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Genome Res. 2011 21: 1462-1477 originally published online June 17, 2011
Access the most recent version at doi:10.1101/gr.121426.111

Supplemental Material http://genome.cshlp.org/content/suppl/2011/06/15/gr.121426.111.DC1.html

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Deep small RNA sequencing from the nematode *Ascaris* reveals conservation, functional diversification, and novel developmental profiles

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Eukaryotic cells express several classes of small RNAs that regulate gene expression and ensure genome maintenance. Endogenous siRNAs (endo-siRNAs) and Piwi-interacting RNAs (piRNAs) mainly control gene and transposon expression in the germline, while microRNAs (miRNAs) generally function in post-transcriptional gene silencing in both somatic and germline cells. To provide an evolutionary and developmental perspective on small RNA pathways in nematodes, we identified and characterized known and novel small RNA classes through gametogenesis and embryo development in the parasitic nematode *Ascaris suum* and compared them with known small RNAs of *Caenorhabditis elegans*. piRNAs, Piwi-clade Argonautes, and other proteins associated with the piRNA pathway have been lost in *Ascaris*. miRNAs are synthesized immediately after fertilization in utero, before pronuclear fusion, and before the first cleavage of the zygote. This is the earliest expression of small RNAs ever described at a developmental stage long thought to be transcriptionally quiescent. A comparison of the two classes of *Ascaris* endo-siRNAs, 22G-RNAs and 26G-RNAs, to those in *C. elegans*, suggests great diversification and plasticity in the use of small RNA pathways during spermatogenesis in different nematodes. Our data reveal conserved characteristics of nematode small RNAs as well as features unique to *Ascaris* that illustrate significant flexibility in the use of small RNAs pathways, some of which are likely an adaptation to *Ascaris*' life cycle and parasitism.

[Supplemental material is available for this article.]

Gametogenesis and embryogenesis are developmental periods that see rapid changes in genome organization, gene expression, and cellular identity. Studies of the nematode *Caenorhabditis elegans* have contributed substantially to our understanding of these processes. Nematodes are present in all environments and are one of the most divergent phyla, with >23,000 described species and an estimated 100,000 to 10 million species (Blaxter 2009). Thus, they offer the opportunity for comparative studies of key developmental processes including small RNA pathways.

Many nematodes are parasitic, and adaptation to the parasitic lifestyle often involves an increase in reproductive capacity and overall body size. The nematode *Ascaris* is a large (~25 × 0.5 × 0.5 cm), sexually dimorphic parasite of the vertebrate small intestine. One species infects ~1 billion people worldwide and is considered an important "neglected disease" (Bethony et al. 2006; Hotez 2008). It is estimated that an *Ascaris* female has as many as 25,000,000 eggs at one time and lays 200,000 to 2 million fertilized eggs per day (Cram 1925; Brown and Cort 1927; Olsen et al. 1958; Sinniah 1982). Theodor Boveri studied *Ascaris* at the turn of the 19th Century and first described chromosomes and cytoplasm in heredity, determinate cleavage, and a nematode cell lineage (Satzinger 2008). More recently, *Ascaris* has been used for a variety of physiological, biochemical, and molecular studies.

Ascaris has several attributes that are advantageous for the analysis of gametogenesis, fertilization, zygote maturation, and early development. First, the long and linear reproductive systems (~140 cm for males and 240 cm for females) enable the dissection and isolation of discrete stages of gametogenesis as well as fertilized zygotes undergoing a 12- to 24-h maturation in the uterus that precedes pronuclear fusion and development (Fig. 1A). Second, large numbers of synchronized, developmentally staged embryos and larvae (fertilized zygote through the L2 larvae) can be easily obtained (Fig. 1B). Furthermore, a variety of biochemical and molecular tools for studying RNA transcription, processing, translation, and decay have been developed (Hannon et al. 1990a,b; Maroney et al. 1995; Davis et al. 1999; Cohen et al. 2004; Wallace et al. 2010).

Small noncoding RNAs (~20–30 nucleotides [nt]) have emerged as key players in both transcriptional and post-transcriptional gene regulation; they also play important roles in genome stability and chromatin organization (for reviews, see Ghildiyal and Zamore 2009; Malone and Hannon 2009; Moazed 2009; Bourc'his and Voinnet 2010). While new types of small RNAs are being identified and their classification continues to be revised, a simple system to group small RNAs divides them according to their biogenesis and Argonaute protein binding partners into three major classes: microRNAs (miRNAs), small interfering RNAs (siRNAs), and Piwi-interacting RNAs (piRNAs) (Czech and Hannon 2011). Small RNAs partnered to Argonaute proteins are the core components of the RNA Induced Silencing Complex (RISC). miRNAs are 20–24 nt in size, are derived from genome-encoded hairpins, and function in gene silencing through translational repression or RNA degradation (for reviews, see Bartel 2004, 2009). siRNAs, typically 20–22 nt in size, are often derived from long dsRNA and play a role in heterochromatin formation, silencing of mobile genetic elements, and gene regulation (for reviews, see Okamura and Lai 2008; Carthew and Sontheimer 2009; Ghildiyal and Zamore 2009; Kim et al.

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Article published online before print. Article, supplemental material, and publication date are at http://www.genome.org/cgi/doi/10.1101/gr.121426.111.

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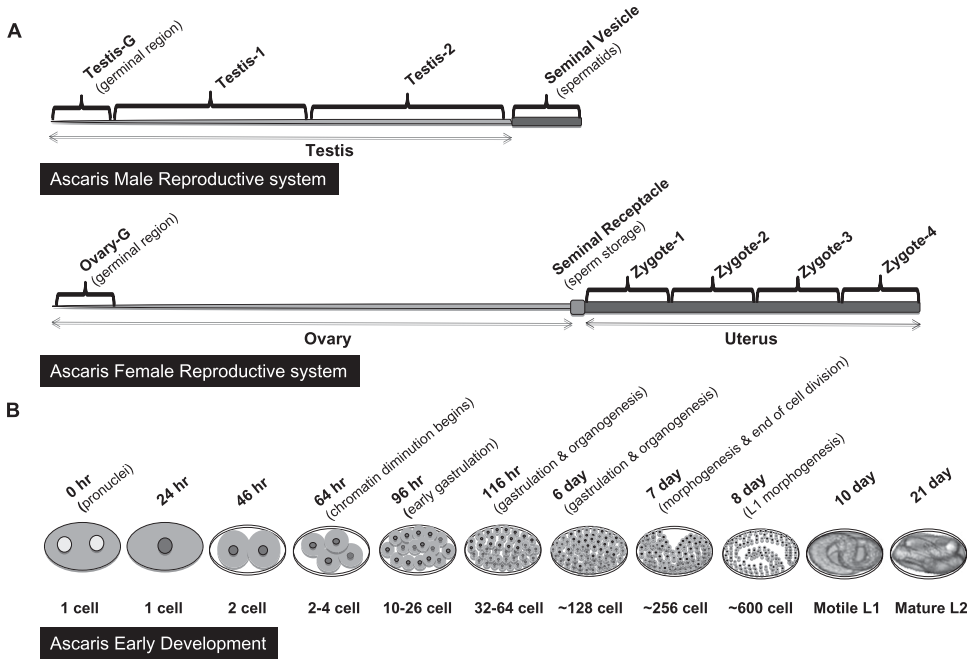


Figure 1. *Ascaris* reproductive systems and early development. (*A*) *Ascaris* male and female reproductive systems. The male seminal vesicle contains spermatids that are activated on fertilization of a female. Sperm are stored in the female seminal receptacle. As mature oocytes move through the seminal receptacle, they are fertilized, and for each fertilized egg, an impermeable layer and chitinous shell is immediately formed around the egg in region one of the uterus (zygote-1). The zygote undergoes maturation as it passes through the uterus (within 12–24 h). Note that the figure is not drawn to scale. Extended male and female reproductive systems are ~140 cm and ~240 cm in length, respectively. (*B*) Early *Ascaris* embryo development. Eggs derived from the region designated as zygote-4 are equivalent to 0-h embryos. Incubation of 0-h embryos at 30°C in high humidity leads to relatively synchronous development (~85%) as illustrated. The maternal to zygotic transition is thought to occur between 46 and 96 h of development (four to 16 cells). *Ascaris* larvae L1 and L2 remain within the chitinous shell. The 0-h embryo is ~100 × 45 μm and does not change in size during development as illustrated. All regions/stages in *A* and *B* were analyzed in the study.

2009). Primary siRNAs in nematodes, fungi, and plants can trigger the generation of secondary siRNAs, a process that involves the action of RNA-dependent RNA polymerases (RdRPs) and serves to amplify the silencing trigger (Ambros et al. 2003b; Chicas et al. 2004; Ruby et al. 2006; Pak and Fire 2007; Sijen et al. 2007). piRNAs are 21- to 30-nt RNAs that specifically associate with Piwi-clade Argonaute proteins and are derived from discrete genomic loci (called piRNA clusters) by a dicer-independent mechanism (for reviews, see Ghildiyal and Zamore 2009; Siomi et al. 2011). piRNAs are present in the germline and are thought to suppress mobile elements and play important roles in spermatogenesis, maintenance of germ cells, and stem cell totipotency (for reviews, see Saito and Siomi 2010; Siomi et al. 2011). Studies in the nematode *C. elegans* have identified a diversity of small RNA classes, including miRNAs, siRNAs (26G- and 22G-RNAs), and piRNA (21U-RNAs) (Lau et al. 2001; Lee and Ambros 2001; Sijen et al. 2001, 2007; Ambros et al. 2003a; Lim et al. 2003; Sijen and Plasterk 2003; Ruby et al. 2006; Pak and Fire 2007; Batista et al. 2008; Das et al. 2008; Wang and Reinke 2008; Claycomb et al. 2009; Gu et al. 2009; Han et al. 2009; Kato et al. 2009; Stoeckius et al. 2009).

We have profiled *Ascaris* small RNAs progressively through discrete regions of the reproductive system and stages of early development by deep sequencing. Our data provide an unprecedented window into the evolution and adaptation of small RNAs and their pathways between the free-living *C. elegans* and a fecund, parasitic nematode that diverged an estimated 400 million years ago (Blaxter 2009). Key findings include remarkable conservation and divergence of nematode miRNAs over 400 million years of evolution. *Ascaris* endo-siRNAs (26G- and 22G-RNAs), particularly in the testis, demonstrate striking adaptability and plasticity in their expression and biogenesis, including the loss of 3′ 2′-*O*-methylation of small RNAs, when compared with that of *C. elegans*. This adaptability may be reflected in part by the loss of piRNAs in *Ascaris*. *Ascaris* small RNAs are transcribed and processed during zygote maturation prior to pronuclear fusion in utero, a developmental stage thought to be transcriptionally quiescent (Leatherman and Jongens 2003; Schier 2007; Tadros and Lipshitz 2009). Finally, small RNAs do not target the major eliminated repeat for *Ascaris* chromatin diminution. Differences in small RNA pathways between *Ascaris* and *C. elegans* likely reflect adaptation to the biology and parasitic lifestyle of *Ascaris*.

Results

Deep sequencing of small RNAs during *Ascaris* gametogenesis, zygote maturation, and early development

We initially demonstrated the presence of *Ascaris* small RNAs on polyacrylamide gels by labeling them at either their 5′ or 3′ termini (Fig. 2A,B). We observed two major groups of small RNAs of 21–24 nt and 32 nt in size. *Ascaris* ~22-nt RNAs in all stages were readily labeled by capping the RNA with capping enzymes (Fig. 2C), suggesting that some *Ascaris* small RNAs have 5′ di- or triphosphate termini. To provide a qualitative assessment of the percentage of 5′ di- or triphosphate RNAs, we first 3′ labeled RNAs with ^{32}P-pCp and then capped the RNAs with GTP. A large percentage of the ~22-nt RNAs increased in size, indicating that the majority of these RNAs could be capped and are 5′ polyphosphate RNAs (Fig. 2D).

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Based on these observations, we prepared and analyzed three types of small RNA libraries: (1) libraries of 18- to 34-nt or 18- to 40-nt RNAs with a 5′ monophosphate (5′ monophosphate libraries), (2) libraries of 18- to 34-nt RNAs with a 5′ monophosphate but enriched for 3′ end modifications (5′ monophosphate, 3′ end modified), and (3) libraries of 18- to 28-nt or 18- to 40-nt RNAs with

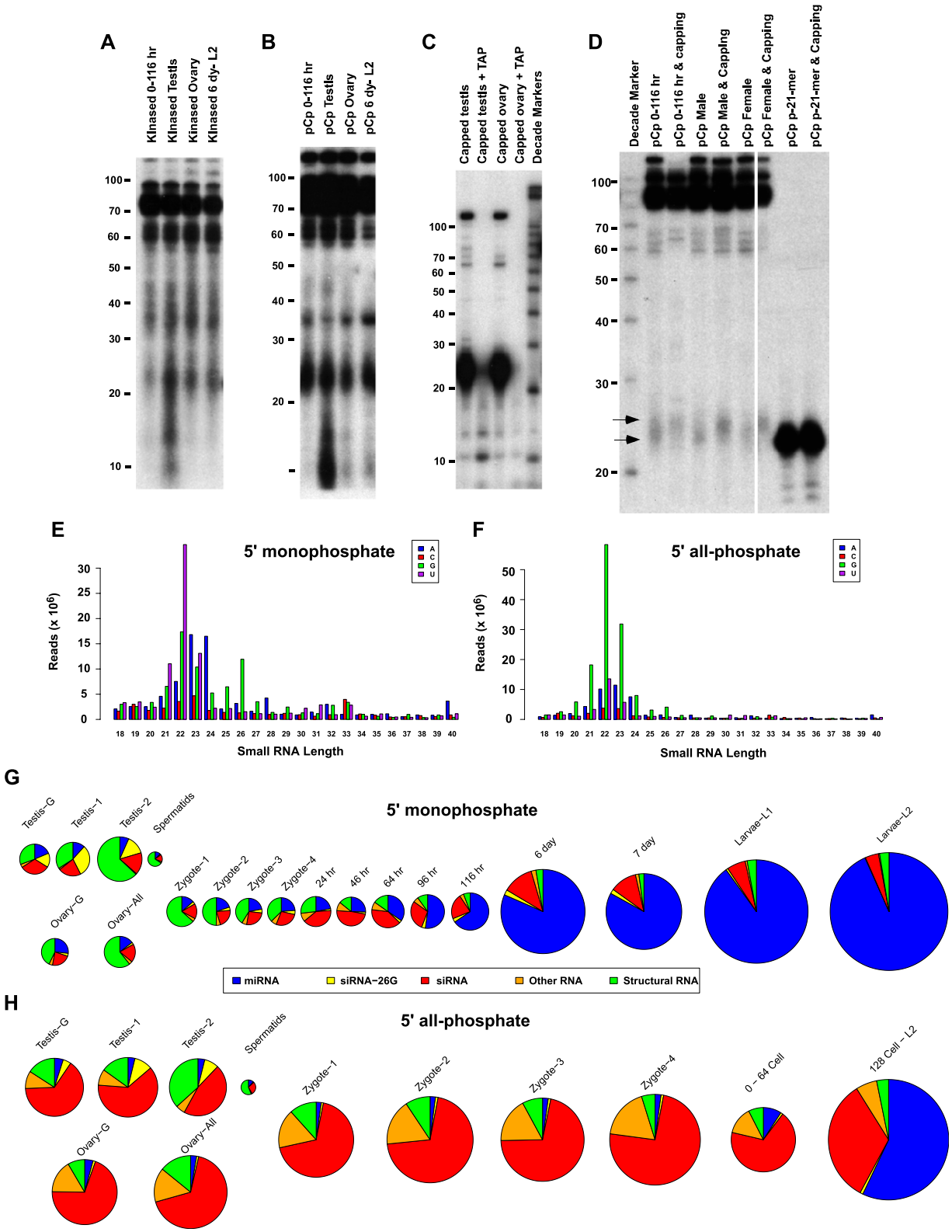


Figure 2. (Legend on next page)

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a 5′ tri-, di-, or monophosphate (5′ all-phosphate; summary of these libraries is provided in Supplemental Table S2). These libraries enabled us to identify all expressed small RNAs and characterize the nature of their 5′ and 3′ ends. We failed to detect any significant enrichment of small RNAs in the 5′ monophosphate, 3′ end modified libraries, suggesting that *Ascaris* small RNAs do not have 3′ modifications (see below). Small RNA libraries were analyzed from different regions of the male and female reproductive systems, spermatids, four stages of zygotes undergoing maturation in the uterus, and staged early embryos from one cell to the larvae to provide an extensive germline and developmental profile (see Fig. 1; Supplemental Table S2). To enable our analysis of the small RNA libraries, we also conducted genome and transcriptome sequencing (for an overview of these data, see Table S1). These data helped us to define different types of small RNAs, their biogenesis, targets, and potential function.

We initiated our analysis by plotting all reads that perfectly matched the genome or transcriptome (J Wang, M Mitreva, M Blaxter, M Berriman, RE Davis, in prep.) as a function of length (Fig. 2E,F; Supplemental Figs. S1–S4). The vast majority of *Ascaris* small RNAs are 21–24 nt in length with a less abundant fraction that is 26 nt in length (Fig. 2E,F; Supplemental Figs. S1–S4). Annotation of our small RNA sequences indicated that the small RNAs 21–24 nt in length are primarily miRNAs and endo-siRNAs, whereas the 26-nt reads show a strong bias to start with guanosine. Thus, in analogy to 26G-RNAs in *C. elegans*, we refer to these small RNAs as 26G-RNAs. We also identified larger RNAs that originate from atypical hairpins (see below). Remaining reads matching abundant cellular RNAs were summarized as "structural RNAs" (snRNAs, snoRNAs, rRNAs, tRNAs, etc.), which made up ~10% of all reads (Fig. 2G,H; Supplemental Table S2). When the small RNA reads between libraries from different stages were compared, we observed that the total number of small RNAs increases progressively (per amount of total RNA/sample), particularly from 128-cell embryos through the larval stages. We found that endo-siRNAs are the predominant small RNA class in the germline. In addition, our data demonstrate a transition in the major type of small RNAs from endo-siRNAs to miRNAs during larval organogenesis and morphogenesis (Fig. 2G,H), as suggested by earlier reports in *C. elegans* (Martinez et al. 2008; Stoeckius et al. 2009). Our data, however, for the first time clearly define the temporal dynamics and identities of these RNA changes.

Lack of piRNA pathway components and small RNAs in *Ascaris*

Piwi-clade proteins and piRNAs have been found in metazoa ranging from animal phyla that diverged before the emergence of the Bilateria (sponges and cnidarians) through worms, flies, and humans (Grimson et al. 2008). piRNAs are derived from distinct genomic loci and are methylated on their 3′ terminal 2′ oxygen by HEN1 (Ghildiyal and Zamore 2009; Siomi et al. 2011). piRNA orthologs in *C. elegans* are only 21 nt in length, have a 5′ terminal U, bind Piwi-clade Argonautes, and are known as 21U-RNAs. These piRNAs are not conserved at the sequence level among *Caenorhabditis* species and do not exhibit complementarity to targets. However, they share a common upstream motif in their genomic loci (Ruby et al. 2006; Batista et al. 2008; Das et al. 2008; Wang and Reinke 2008; de Wit et al. 2009; Kato et al. 2009).

Our data provide several lines of evidence that the piRNA pathway has been lost in *Ascaris*. First, our direct sequencing of discrete regions of both the male and female germlines did not reveal any small RNAs with characteristics of piRNAs (Fig. 3A,B; Supplemental Figs. S1–S4; Supplemental Material on 21U/piRNA). Second, we were not able to identify Piwi-clade Argonaute orthologs using bioinformatics on our extensive genomic (18× coverage of the genome) and cDNA sequence data from testis and ovary tissue (Supplemental Table S1). However, we were able to identify cDNA sequences encoding 10 other Argonautes proteins of the AGO and WAGO clades (Fig. 3C) as well as a variety of proteins associated with small RNA biogenesis and function (Supplemental Table S9). Third, we also failed to detect an ortholog of the HEN1 methyltransferase in the *Ascaris* genome or germline transcriptome. In addition, no small RNAs were identified with 3′ methyl modifications (Fig. 3D–H). Notably, Piwi Argonaute and Hen1 orthologs are also not identifiable in a related parasite, *Brugia malayi* (Ghedin et al. 2007). Given that piRNAs have been shown to be present in metazoa that emerged even before the first bilateral animals (Grimson et al. 2008), the most parsimonious explanation for the absence of piRNAs in *Ascaris* is that these small RNAs and their associated proteins, Piwi and Hen1, have been lost.

Ascaris miRNAs conservation and expression

We next used de novo analyses to identify miRNAs as described in the Supplemental Material. We identified 97 miRNAs that were grouped into 59 *Ascaris* seed families (Fig. 4; Supplemental Fig. S5; Supplemental Tables S3–S5). The seed sequences for 78 (80%) *Ascaris* miRNAs are conserved in other eukaryotic miRNAs (Supplemental Table S4). When considering the miRNAs and their hairpin conservation on the sequence level (see Supplemental Methods), 64 (66%) of the *Ascaris* miRNAs are conserved in other metazoa (Supplemental Table S5). With respect to nematodes, the majority of known miRNAs in the closely related parasitic nematode *B. malayi* were found in Ascaris (Supplemental Table S5). However, to date only ~30 *B. malayi* miRNAs are known; many of these were defined only by computational methods and sequence conservation, and thus they likely represent the most conserved miRNAs (Poole et al. 2010). For more distantly related nematodes, about 30% and ~24% of known miRNAs *Caenorhabditis* and *Pristionchus* are conserved in *Ascaris*, respectively (Supplemental Table S5). A high percentage of conserved miRNAs among closely related nematodes

Figure 2. Characteristics of *Ascaris* small RNAs. (*A*) 5′ end-labeled *Ascaris* small RNAs. Low-molecular-weight (LMW) enriched RNAs were treated with calf alkaline phosphatase and then 5′ end labeled with ^{32}P using T4 polynucleotide kinase. RNAs in *A–D* were resolved on 12.5% denaturing PAGE and autoradiographed. (*B*) 3′ end-labeled *Ascaris* small RNAs. LMW enriched RNAs were 3′ end-labeled using ^{32}pCp and T4 RNA ligase. (*C*) *Ascaris* small RNAs ~22 nt in length can be cap-labeled. LMW enriched RNAs were capped using ^{32}P-α-GTP and vaccinia guanylyltransferase. Samples were treated with tobacco acid pyrophosphatase (TAP) to remove the cap to confirm cap-labeling. Note the significant labeling of RNAs ~22 nt in length. (*D*) The majority of germline and early embryo 22-nt RNAs have 5′ polyphosphates. pCp-labeled small RNAs shown in *B* were treated with GTP and vaccinia guanylyltransferase. The *lower* and *upper* arrows mark the average position of the labeled small RNAs prior to and after capping. Note that the majority of the ^{32}pCp-labeled RNAs are shifted to a longer length. (*E,F*) Size distribution of analyzed *Ascaris* small RNAs. (*E*) All 28 5′ monophosphate libraries characterized combined. (*F*) All 19 5′ all-phosphate (5′ tri-, di-, and monophosphate) libraries characterized combined. In these and all subsequent size distribution figures, small RNAs starting with A, C, G, and U in different sizes are plotted against their read frequencies (raw reads, before normalization). (*G,H*) Comparison, classification, and levels of *Ascaris* small RNAs characterized. (*G*) 5′ monophosphate RNAs. (*H*) 5′ all-phosphate libraries derived from different developmental stages. Area of the circles is proportional to the amount of small RNAs present in each stage or tissue after normalization (see text).

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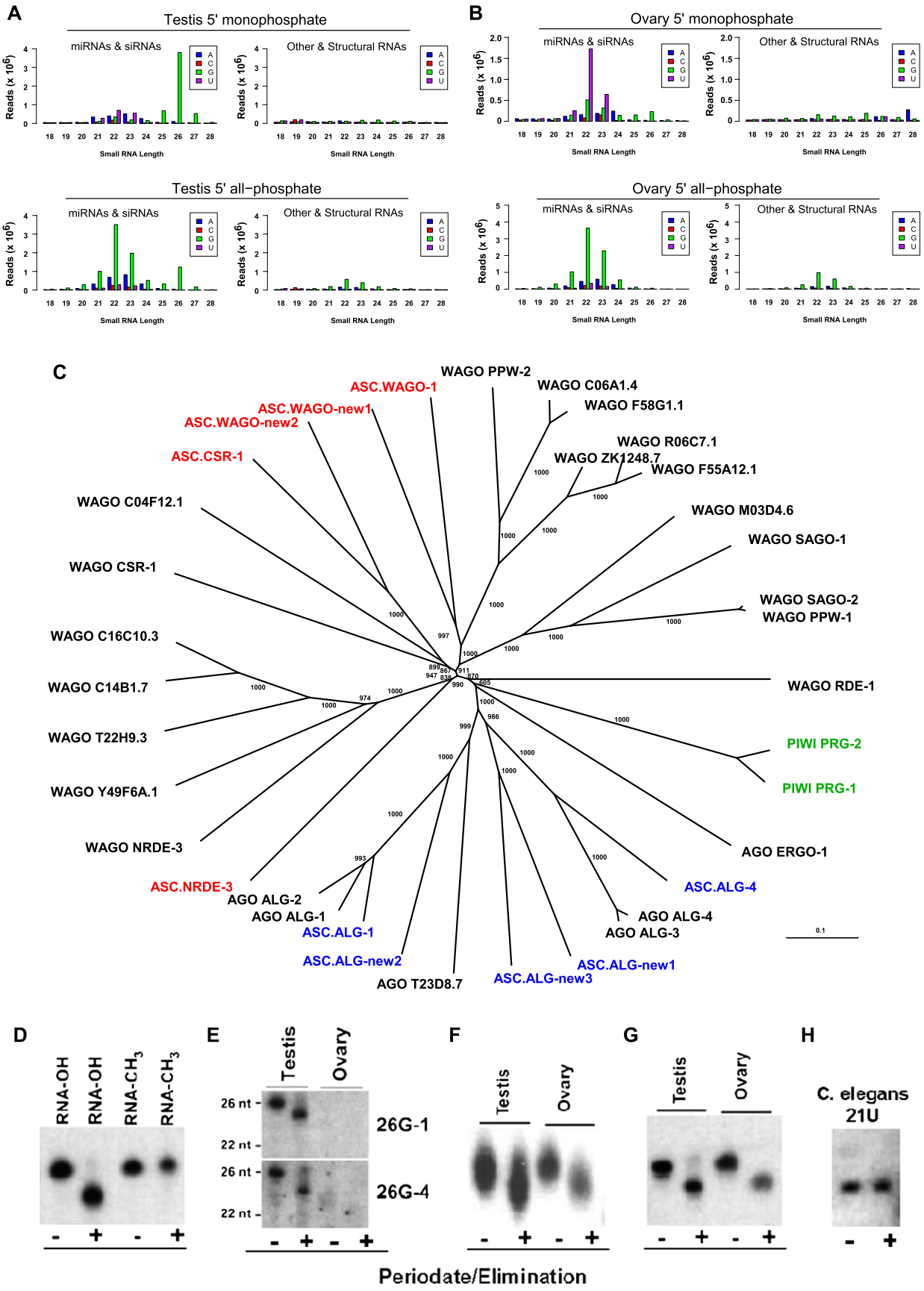


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has also been observed within the *Caenorhabditis* group (>90%), and between *Caenorhabditis* and *Pristionchus* (~70%) (de Wit et al. 2009). When *Ascaris* miRNAs are compared with those of fruit flies and humans, conservation drops to ~18% and ~5%, respectively. Interestingly, of the 33 *Ascaris*-specific miRNAs, 16 are derived from polycistronic loci, and these miRNAs are primarily expressed in the germline, zygote maturation, and early embryos (Fig. 4; Supplemental Fig. S7; Supplemental Tables S3–S5).

Ascaris miRNAs are dynamically expressed during development. The range of *Ascaris* miRNA abundances in individual developmental stages is very dynamic, spanning six orders of magnitude. To validate the small RNA abundance as determined by the small RNA reads in the libraries, we performed Northern blotting for 42 individual miRNAs (43%) covering different expression patterns (Fig. 4). We found a very strong correlation between Northern blot data and read frequencies, with a mean and median Pearson correlation coefficient *r*-value of 0.85 and 0.91, respectively (Supplemental Table S3), demonstrating that our sequencing profiles are quantitative. Based on their expression patterns, *Ascaris* miRNAs were divided into four groups: (1) germline expressed miRNAs; (2) miRNAs predominating in the zygote, early, and middle embryo stages; (3) late embryo and larval expressed miRNAs; and (4) other miRNAs (Fig. 4). Of these 97 miRNAs, none were highly expressed throughout development. This argues against the idea of "housekeeping" miRNAs necessary for basic cellular functions. Several miRNAs are highly expressed during early development and then lost over a narrow developmental window (two- to 128-cell embryos). These miRNAs are often derived from polycistronic loci with similar seeds, suggesting coordinated target regulation (Supplemental Fig. S7). Information on the features of *Ascaris* miRNAs such as miRNA/miRNA* sequences and frequencies, hairpin sequences, polycistronic clusters, expression profiles, RNA editing, nontemplated 3′ end modifications, as well as comparison of seed families and miRNAs with other organisms is provided in Supplemental Material. Overall, our data suggest that while there is high conservation of some miRNAs within nematode lineages, there is also significant miRNA evolution and diversity.

Early expression of *Ascaris* miRNAs during zygote maturation

Surprisingly, at least 15 miRNAs appear immediately after fertilization, before pronuclear fusion, and during maturation of the zygote (Figs. 4, 5A; Supplemental Fig. S6). Note that immediately following fertilization, the zygote synthesizes a chitinous shell followed by an impermeable layer that surrounds the zygote. Northern blot analysis for these new zygotic miRNAs did not identify any mature miRNA or miRNA precursors in *Ascaris* spermatids or oocytes, nor did we see accumulations of primary or pre-miRNAs in the early zygotes, suggesting that these miRNAs are likely derived from new transcription (see Supplemental Fig. S6A). These miRNAs increase in abundance as the zygote matures in the uterus. Other miRNAs also appear or increase in frequency as early as the one- to two-cell stage, and they increase as the embryo develops (Fig. 4; Supplemental Table S3). A recent study on early *C. elegans* embryos (Wu et al. 2010) described a miRNA seed family whose miRNAs (miR-35-42) were of maternal origin. Our data show the corresponding seed family in *Ascaris* (36a/36b/36c/36d/36e/36f/5348) is of embryonic origin.

Ascaris endo-siRNAs in gametogenesis and embryogenesis

We identified a large number of dynamically expressed small RNAs that are not miRNAs, do not appear to be derived from hairpin structures, and are not related to structural RNAs (rRNA, tRNA, snRNAs, etc.). We have defined these *Ascaris* small RNAs as endo-siRNAs. These RNAs are enriched in the germline and early embryos of *Ascaris* (Fig. 2G,H; Supplemental Figs. S1–S4). Most of these small RNAs start with G and are either 22 nt or 26 nt in length, reminiscent of *C. elegans* 22G- and 26G-RNAs. *C. elegans* 22G-RNAs function in chromosome segregation, transposon silencing, and gene regulation (Ambros et al. 2003b; Lim et al. 2003; Ruby et al. 2006; Pak and Fire 2007; Sijen et al. 2007; Claycomb et al. 2009; Gent et al. 2009; Gu et al. 2009; van Wolfswinkel et al. 2009; Vasale et al. 2010; Zhang et al. 2011) *C. elegans* has two classes of 26G-RNAs that regulate gene expression associated with spermatogenesis (Class I) and early zygotic development (Class II) (Han et al. 2009; Conine et al. 2010; Gent et al. 2010; Vasale et al. 2010; Zhang et al. 2011).

A subset of *Ascaris* endo-siRNAs correspond to repetitive elements, such as DNA transposons and retrotransposons, and are expressed at relatively high levels as has been observed in *C. elegans* (Supplemental Table S8; Gu et al. 2009). However, most of the *Ascaris* endo-siRNAs are not highly expressed and correspond either to unique genome sequences or to a broad spectrum of different mRNA transcripts (Fig. 6). For the mRNA-matching endo-siRNAs, the majority are in the antisense orientation (Fig. 6A,B). Most of these RNAs start with G and are of two distinct lengths, 22 nt and 26 nt (Fig. 6A). Based on the orientation of the endo-siRNAs to mRNAs, their length, and starting bases, we grouped them into the four classes: (1) *As.22G*, 21- to 24-nt small RNAs beginning with a G and antisense to mRNAs; (2) *As.26G*, 25- to 27-nt small RNAs beginning with G and antisense to mRNAs; (3) *As.22H*, other small RNAs antisense to mRNAs that do not begin with G; and (4) *Sense*, small RNAs sense to mRNAs. A comparison between 17 pairs of 5′ monophosphate and 5′ all-phosphate libraries definitively demonstrates that *As.22G* and *As.22H* are highly enriched in the 5′ all-phosphate libraries, in contrast to *As.26G* and *Sense* RNA that

Figure 3. *Ascaris* lacks the piRNA pathway. (*A*,*B*) No piRNAs are present in *Ascaris*, as illustrated by the size distribution of *Ascaris* germline small RNAs. (*A*) Testis small RNAs. (*B*) Ovary small RNAs. Raw reads (before normalization) from the libraries are plotted. Note that no 21U or other U-initiated small RNAs are enriched in either the testis or ovary after miRNAs and siRNAs are removed. This is also observed for other germline and embryo libraries (see Supplemental Data). (*C*) *Ascaris* lacks Piwi-clade Argonaute protein. ClustalX was used to generate an alignment of *Ascaris* and *C. elegans* Argonaute proteins. The alignment was used to generate a distance matrix and then analyzed by neighbor-joining and bootstrapping methods using PHYLIP software. TreeView (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html) was used to display the resulted tree. Numbers on the branches show the support value for 1000 bootstraps. Argonaute proteins from *Ascaris* are colored in blue and red for AGO-clade and WAGO-clade proteins, respectively. *C. elegans* Piwi-clade Argonautes are colored in green. Accession numbers for the *Ascaris* proteins can be found in Supplemental Table S9. Note that *Ascaris* also lacks an ortholog of *C. elegans* RDE-1. (*D*) RNAs with a 2′-O-methyl are resistant to periodate treatment and β-elimination. Control RNAs (22 nt) were 5′ labeled by kinasing and then either mock treated (−) or treated with periodate followed by β-elimination (+).(*E*) *Ascaris* 26G-RNAs are not resistant to periodate/β-elimination and thus are not 3′ modified. Northern blots of *Ascaris* RNAs treated with periodate/β-elimination and probed with *Ascaris* 26G-1 and 26G-4 probes. (*F*) *Ascaris* 22G-RNAs are not 3′ modified. Northern blot as in *E* using an *Ascaris* 22G-RNA probe. (*G*) *Ascaris* miRNAs are not 3′ modified. Northern blot as in *E* using an *Ascaris* miRNA probe (asu-miR-5342). (*H*) *C. elegans* 21U RNAs are 3′ modified and resistant to periodate/β-elimination. Northern blot of *C. elegans* RNAs treated with periodate/β-elimination and probed with a *C. elegans* 21U-RNA probe.

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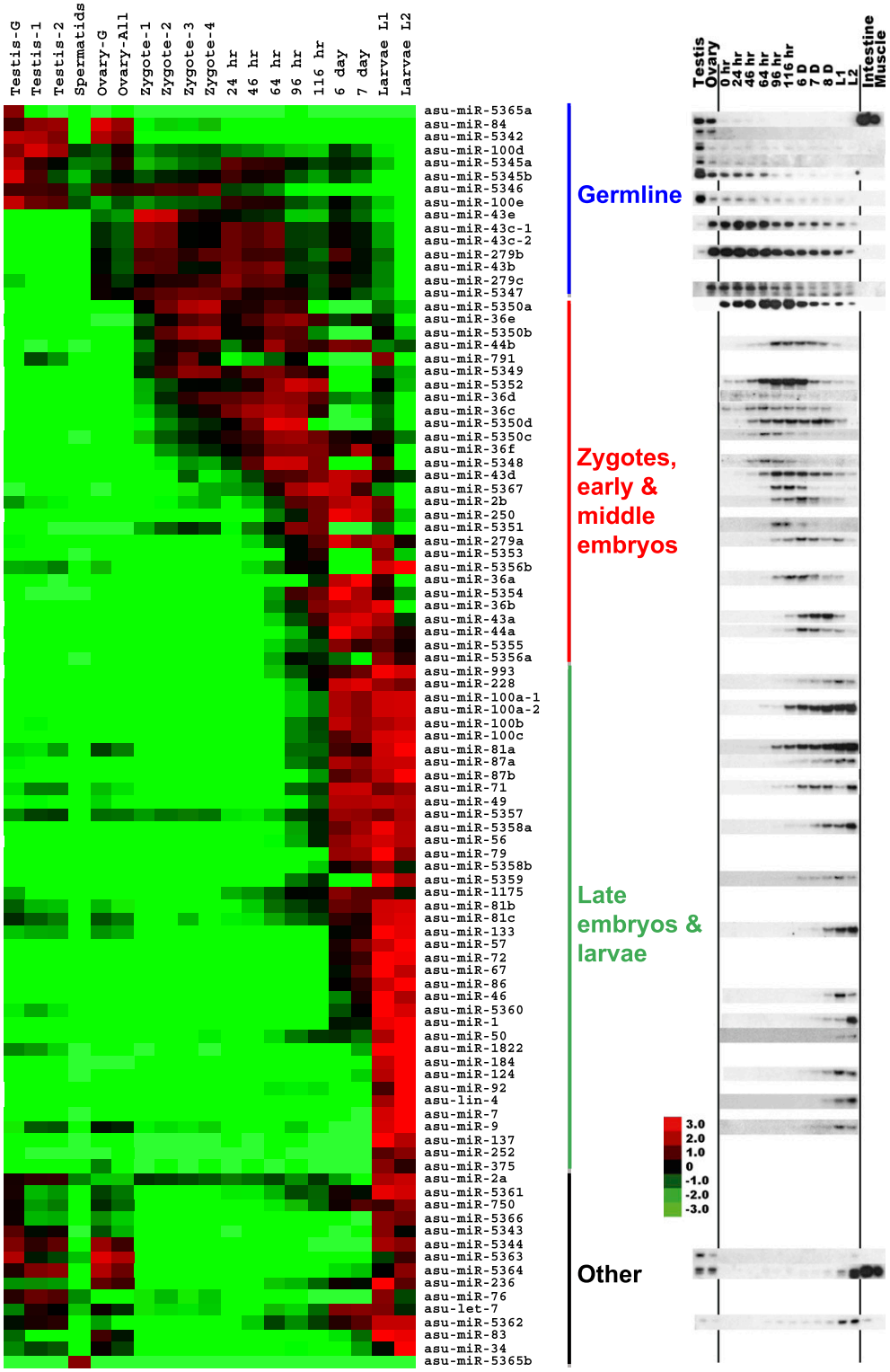


Figure 4. Dynamic miRNA expression profiles in *Ascaris* development. Heatmap and Northern Blot expression profiles of *Ascaris* miRNAs. For each miRNA, colors represent $\log_2$ values of fold changes to the average read frequencies of the miRNA during development. Heatmap expression profiles represent normalized mature miRNA read numbers.

are not enriched (Fig. 6B,C,E). The percentage and enrichment of 22-nt RNAs (*As.22G* and *As.22H*) in the 5′ all-phosphate libraries is consistent with most ~22-nt RNAs in *Ascaris* having 5′ termini with di- or triphosphates (Fig. 2D). Enzymatic treatment of RNA followed by Northern blot analyses further demonstrated that *Ascaris* 22-nt RNAs have 5′ polyphosphates (Fig. 5D–F).

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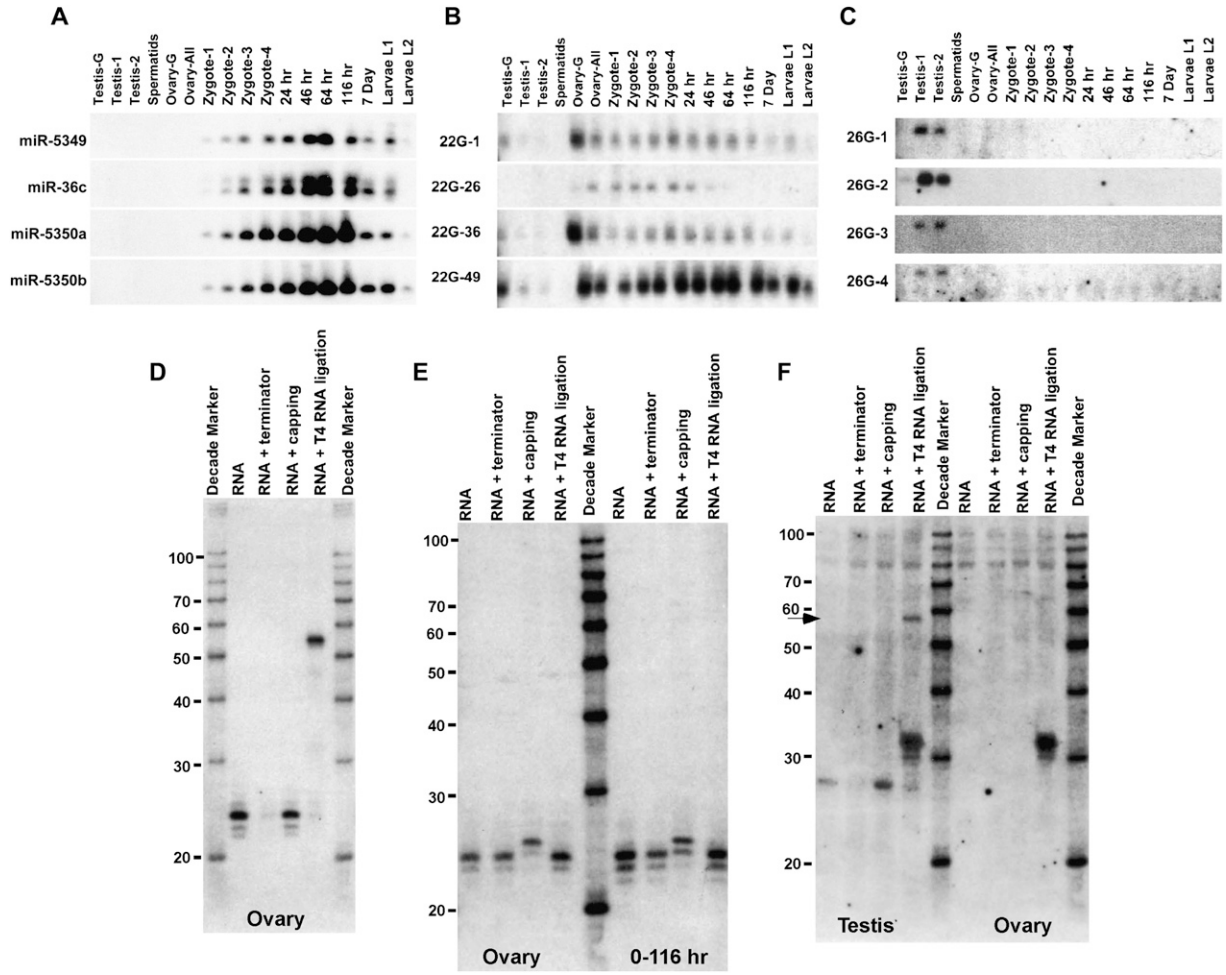


Figure 5. *Ascaris* small RNAs expression and their 5′ phosphate termini. (*A*) Northern blots illustrating intrauterine zygotic expression of miRNAs (for whole blots, see Supplemental Fig. S6A). (*B*) Northern blots illustrating dynamic expression of 22G-RNAs. (C) Northern blots illustrating expression of testis-specific 26G-RNAs. (*D*) *Ascaris* miRNAs have a 5′ monophosphate. Northern blot of *Ascaris* LMW RNA untreated or treated with terminator, GTP and guanylyltransferase (capping), or ligation of an RNA oligonucleotide (T4 RNA ligation) and probed with asu-miR-5347 probe. Note that the miRNA is degraded by terminator, is uncapped, and can be ligated to an RNA oligonucleotide, indicating the 5′ end is a monophosphate. (*E*) *Ascaris* 22G-RNAs have 5′ polyphosphates. Northern blot as in *D* probed with a 22G-RNA probe. Note that the 22G-RNA can be capped but is not susceptible to terminator or T4 RNA ligation, suggesting the 5′ end of the RNA is a di- or triphosphate. (*F*) *Ascaris* 26G-RNAs have a 5′ monophosphate. Northern blot as in *D* probed with a 26G-RNA probe. Note that the 26G-RNA is testis specific and is degraded by terminator, is uncapped, and can be ligated to an RNA oligonucleotide, indicating the 5′ end is a monophosphate. The band at ~32 nt in the RNA+T4 RNA ligation is an artifact in the ovary.

Ascaris As.26G RNAs are specifically expressed in testis (Figs. 2G,H and 5C,F). These RNAs have features similar to *C. elegans* Class I 26G-RNAs that are involved in spermatogenesis (Ruby et al. 2006; Han et al. 2009; Conine et al. 2010) and are believed to be their orthologs: Both of them are 26 nt in length, start with G, and have 5′ monophosphates (Fig. 5F); both are antisense to testis-enriched mRNAs associated with spermatogenesis (see below). *Ascaris* also has an orthologous testis-specific Argonaute protein to *C. elegans* testis-specific Argonautes ALG-3/4 that are associated with Class I 26G-RNAs (Fig. 2C; Supplemental Table S9). *Ascaris* appears to lack the *C. elegans* early zygotic development (Class II) 26G-RNAs (Fig. 2G,H; Vasale et al. 2010). Interestingly, unlike *C. elegans* 26G-RNAs, *Ascaris* 26G-RNAs are not 3′ modified as shown in β-elimination analyses (Fig. 3D–F).

The distribution of endo-siRNAs on their corresponding mRNA targets differs between *Ascaris* and *C. elegans*. 22G-RNAs in *C. elegans* show enrichment at both mRNA termini, and it has been suggested that the initiating events for 22G synthesis originate at the 3′ end of the mRNA template followed by progressive 5′ cycles of transcription by RdRP (Gu et al. 2009). In contrast, *Ascaris* 22G-RNAs and 22H-RNAs are distributed across their mRNA targets increasing in frequency toward the 5′ end with an abrupt drop-off at the boundary between the 5′ untranslated region (UTR) and open reading frame (ORF) (Figs. 6D, 7A,C). This may indicate a 5′ bias in the recruitment of RdRP complexes in *Ascaris*. Alternatively, initial formation of small RNAs at the 3′ end of the mRNA could lead to progressively increased 5′ recruitment of RdRP complexes. The observed differences in the distribution of 22G-RNAs on their target mRNAs suggest significant differences in the biogenesis of 22G-RNAs between *Ascaris* and *C. elegans*. Interestingly, *Ascaris* 26G-RNAs show a distinct pattern with the small RNAs mainly associated with ORFs (Figs. 6D, 7A,C). The primary distribution of *Ascaris* 26G-RNAs on mRNA ORFs leads us to speculate that the regions of the mRNA targeted (and perhaps what mRNAs get targeted)

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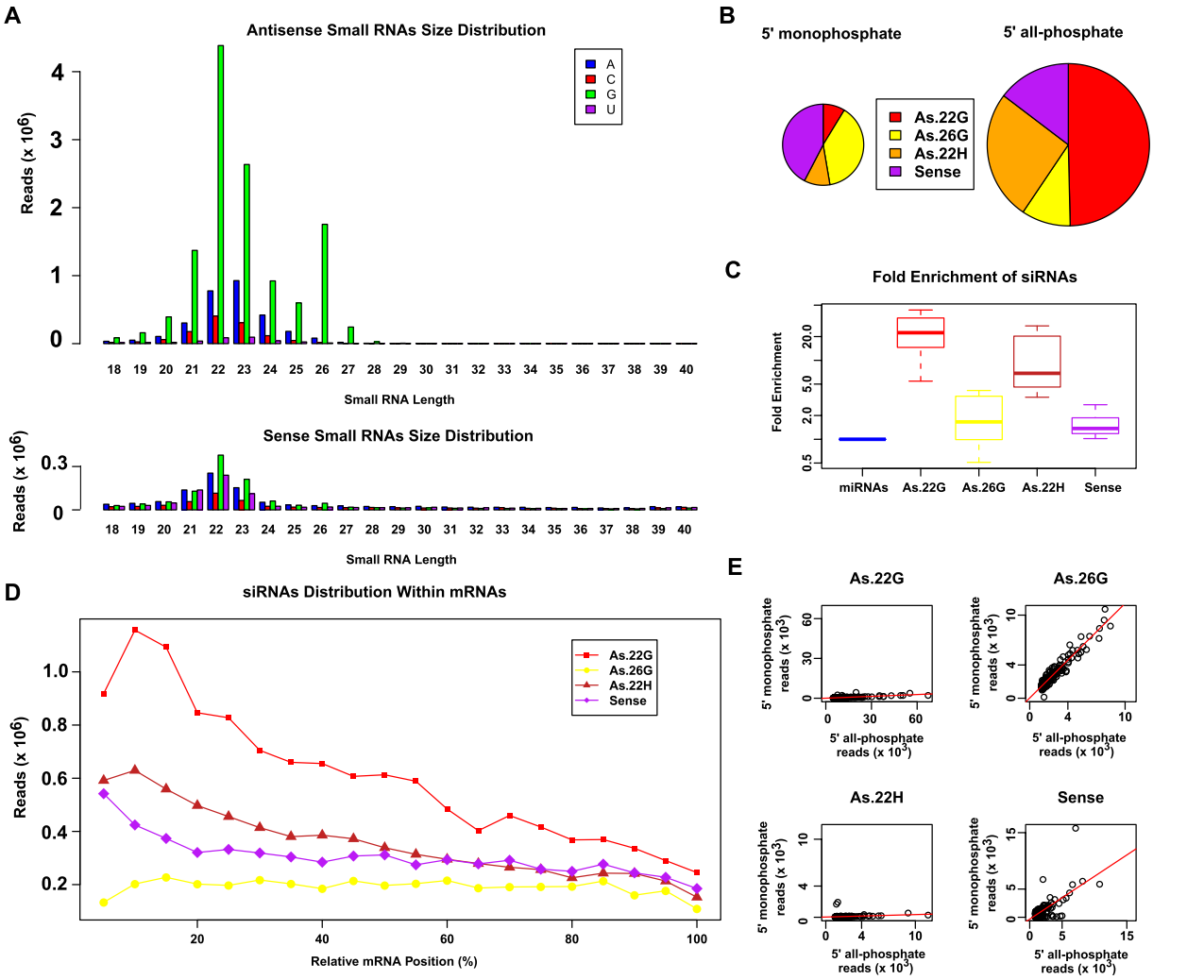


Figure 6. *Ascaris* endo-siRNAs to mRNAs. (*A*) Size distribution of small RNA raw reads corresponding to mRNAs from 17 5′ all-phosphate libraries. (*Upper* panel) Antisense small RNAs; (*lower* panel) sense small RNAs. (*B*) Comparison, classification, and levels of normalized small RNAs corresponding to mRNAs. Area of the circles is proportional to the amount of different types of small RNAs (see text) present in the 5′-mono- and 5′-all-phosphate libraries. (*C*) Twenty-two-nucleotide small RNAs are polyphosphate RNAs, whereas 26G-RNAs are monophosphate RNAs. miRNAs were used to normalize the reads between 5′ monophosphate and 5′ all-phosphate libraries. In these and all subsequent box-and-whisker plots, the *top* and *bottom* ends of each box represent the 75th and 25th percentile, respectively; the *middle* line represents the median value; the extended lines illustrate the range (highest and lowest value); and dots represent values beyond the extremes of the whisker. (*D*) siRNA distribution on mRNA transcripts. Different types of small RNA reads from 5′ all-phosphate libraries are plotted for 8279 full-length cDNAs. Each mRNA is equally divided into 20 bins, and small RNAs mapped to each bin were counted. Plotted is the sum of the counts (*y*-axis) against the relative position (*x*-axis) on the cDNA from 5′ to 3′, with the 5′ end of the mRNA designated as 1 and the site of polyadenylation at the 3′ end designated as 100. (*E*) Twenty-two-nucleotide monophosphate RNAs are likely derived from 22-nt polyphosphate RNAs. Plots illustrate a comparison of small RNA reads between 5′ all-phosphate libraries (*x*-axis) and 5′ monophosphate libraries (*y*-axis). The data sets are the top 200 siRNAs in read frequency.

may be associated with some aspect of translation or the location of 80S ribosomes on mRNAs.

Another type of 22-nt RNAs in *Ascaris* match the genome but not our comprehensive transcriptome data. These small RNAs most likely correspond to nonpolyadenylated transcripts, RNA intermediates, or nonexpressed loci as observed in *C. elegans* (see other RNA in Fig.2G,H).

We observed small RNAs to the sense strand of mRNAs that do not show a preference for the first base and have a broader size distribution up to 40 nt (Fig. 6A). This resembles the distribution of degraded structural RNAs (Supplemental Figs. S1–S4), suggesting they might be mRNA degradation products. However, we also observed a small peak of RNAs 21–23 nt in length for the sense small RNAs, suggesting these small RNAs could potentially be another functional small RNA class (Fig. 6A).

Ascaris 26G-/22G-RNA targets and small RNA diversification in spermatogenesis

To gain insights into the biological roles of *Ascaris* 26G- and 22G-RNAs, we defined a set of exemplary small RNA targeted mRNAs using a cutoff of a minimum of 100 reads/mRNA/million reads for 26G-RNAs or 22G-RNAs in any of the 5′ all-phosphate library (Fig. 7; Supplemental Figs. S9, S10; Supplemental Table S7). This generated 184 and 173 mRNAs for the 26G- and 22G-RNA targets, respectively, with an overlap of 16 targets (Fig. 7D). We refined these

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targets based on the 26G/22G ratio (see Supplemental Methods), and 182 and 159 exemplary targets for 26G- and 22G-RNAs were presented (Fig. 7; Supplemental Figs. S9, S10; Supplemental Table S7). The 182 exemplary mRNAs targeted by 26G-RNAs mainly encode three types of proteins: (1) protein kinases (51), (2) protein phosphatases (24), and (3) major sperm proteins (18). These proteins

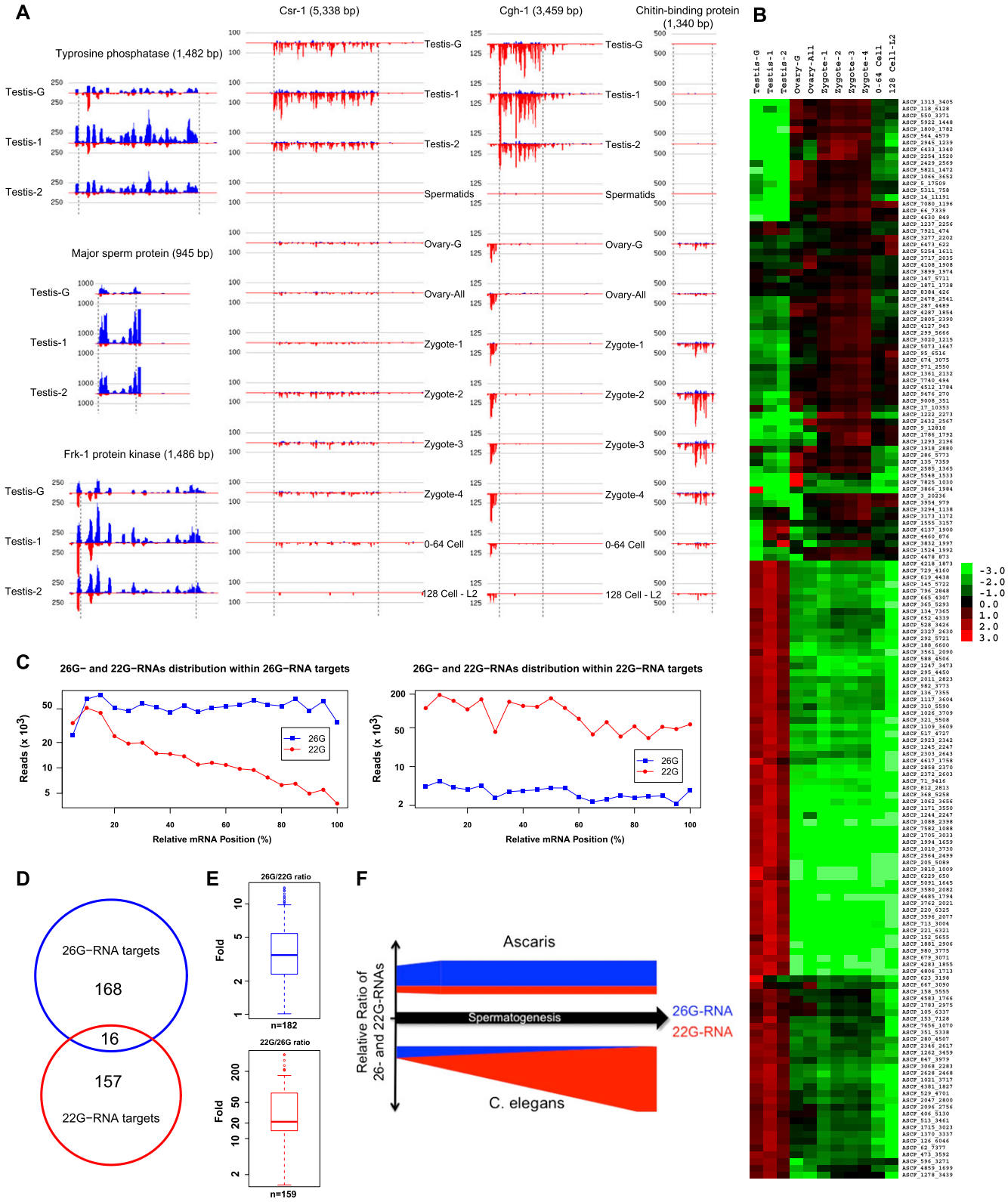


Figure 7. (Legend on next page)

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are known to be associated with *C. elegans* spermatogenesis (Reinke et al. 2000). A comparison of RNA-seq reads from *Ascaris* testis, ovary, embryo, and larvae showed that the 182 mRNAs targeted by 26G-RNAs are highly enriched in the testis (Supplemental Table S7). In contrast, the 159 exemplary mRNA targeted by 22G-RNAs encode a functionally diverse population of proteins important in development and are more abundant in the *Ascaris* ovary (Supplemental Table S7). More than a dozen of these mRNAs encode DNA/chromatin binding proteins, such as transcription factors MEF-2, NHR-25, and FZR-1, as well as histone H3 and H4. The expression of the 22G-RNAs is highly dynamic (Fig. 7B). Their expression profiles appear to match their potential biological roles: 22G-RNAs increase dramatically during and after eggshell formation occurs against the mRNA encoding a chitin-binding protein (ASCF_6433_1340) (Fig. 7A); 22G-RNAs are specifically expressed in the germinal regions of the ovary against histone mRNAs (ASCF_5548_1533 and ASCF_7825_1030) (Supplemental Fig. S9); and 22G-RNAs are highly expressed in the testis against the CGH-1 mRNA, which encodes a protein involved in mRNA regulation (ASCF_1262_3459) (Fig. 7A). Interestingly for CGH-1, not only the level but also the distributions of 22G-RNAs on the mRNA are developmentally regulated.

Ascaris ~28-nt RNAs derived from atypical hairpins

5′ and 3′ labeling of *Ascaris* small RNAs revealed RNAs of ~32 nt with 5′ monophosphates (Fig. 2A,B). Many of these small RNAs are derived from snoRNAs and tRNAs, but a small subset of ~28-nt RNAs in 5′ monophosphate libraries exhibited differential expression patterns and are derived from atypical genomic hairpins (Supplemental Figs. S11, 12). These small RNAs show 5′ end homogeneity with a corresponding lower abundance RNA from the other side of the hairpin. Several are derived from families (Up5 has five members, and Up2 has two members). These small RNAs are more abundant in the zygote and one-cell embryos (0 and 24 h) (Supplemental Fig. S11B). Northern blot analysis for these small RNAs indicated size heterogeneity (28–32 nt in length) and putative, more abundant precursor transcripts of 70–80 nt (Supplemental Fig. S11C). These precursor transcripts do not correspond to snoRNA sequences or their derivatives, and they are not conserved in other studied nematodes. The enrichment of several of these RNAs in the zygote and early embryos suggests developmentally regulated expression. A low ratio of small RNA to a larger precursor RNA was previously observed for snoRNA or tRNA-derived small RNA, several of which were shown to be involved in RNA silencing (Ender et al. 2008; Taft et al. 2009; Haussecker et al. 2010). Thus, these small RNAs potentially represent a novel small silencing RNA class in *Ascaris*.

Discussion

This is the first study in nematodes to systematically catalog the expression of small RNAs through regions of the male and female reproductive systems, during zygote maturation, and all stages of early development. We characterized the differential expression profiles of miRNAs, 22G endo-siRNAs, 26G endo-siRNAs, other endo-siRNAs, and larger RNAs derived from atypical hairpins. Few comparative small RNA analyses have been carried out on nematodes, particularly from distant phylogenetic species (de Wit et al. 2009; Poole et al. 2010). Our comparative analyses demonstrate significant conservation of some miRNAs and endogenous siRNA classes between *Ascaris suum* and *C. elegans*. However, there is also considerable diversity in miRNAs as well as adaptation of endo-siRNA biogenesis and their targets. In particular, piRNAs and protein components of the piRNA pathway have been lost in *Ascaris*. Furthermore, endo-siRNAs involved in *Ascaris* spermatogenesis have increased and diverged as compared with *C. elegans*, perhaps to complement the functional consequences of piRNA loss.

Ascaris miRNAs and endo-siRNAs are differentially expressed during gametogenesis and throughout development to the L2 larvae. Endo-siRNAs are the dominant class of small RNAs in the male and female germline and through the 10- to 26-cell stage of development. Thereafter, the number and abundance of specific miRNAs increase and predominate in the larvae, while the levels of endo-siRNAs significantly decrease (Fig. 2G,H). This transition indicates that siRNA pathways are dominant in the germline, whereas miRNA pathways prevail in embryo and larval development. This transition is likely to be the case in *C. elegans* (Martinez et al. 2008; Stoeckius et al. 2009), but no high-resolution staged samples or quantitative measurements have been used to indicate the exact developmental time and scale of this transition.

Expression of small RNAs prior to pronuclear fusion during zygotic maturation

A key and unexpected finding is that small RNAs are synthesized in the zygote within the uterus before pronuclear fusion. Following fertilization in most metazoa, new zygotic transcription does not occur until the maternal to zygotic transition, which in nematodes begins at the four- to eight-cell stage (Cleavinger et al. 1989; Edgar et al. 1994; Baugh et al. 2003). Previous studies in *Ascaris* indicated that maternal rRNAs are not contributed to the oocyte as observed in most metazoa, but that rRNAs for early development are newly transcribed in the male pronucleus immediately following fertilization (Kaulenas and Fairbairn 1968). The *Ascaris* zygote undergoes maturation during the 12- to 24-h it passes through the uterus; this maturation is necessary for subsequent early development (Fairbairn

Figure 7. *Ascaris* 26G-RNAs and 22G-RNAs targets. (*A*) Examples of distribution of 26G- and 22G-RNAs to mRNAs throughout development. Note that all small RNAs are antisense. (Red) 22G-RNAs; (blue) 26G-RNAs. Vertical dashed lines indicate the start and stop of the ORF. Numbers on *left* indicate the normalized read frequency of the gray line. Note that for 26G-RNA targets, only the profiles from testis 26G-RNAs are shown; for their complete profiles, see Supplemental Table S7 and Supplemental Figures S9 and S10. (*B*) Dynamic expression profiles of 22G-RNAs to 159 exemplary targets (see text). Normalized *As.22G* RNA reads mapping to each target mRNA were used for the heatmap. For each target, colors represent $\log_2$ values of fold changes to the average read frequencies of the *As.22G* RNAs during development. (*C*) Distribution of 26G- and 22G-RNAs on mRNAs predominantly targeted by one of the two types of small RNAs. Only mRNAs identified as near full length are used and include 138 26G-targeted mRNAs and 97 22G-targeted mRNAs (see Supplemental Table S7; Supplemental Figs. S9, S10). Plotted is the sum of the counts (*y*-axis) against the relative position (*x*-axis) on the cDNA from 5′ to 3′, with the 5′ end of the mRNA designated as 1 and the site of polyadenylation at the 3′ end designated as 100. (*D*) Venn diagram illustrating the relationship between the mRNAs targeted by 26G- or 22G-RNAs. (*E*) Ratio of defined testis 26G-RNA/22G-RNAs mRNA targets. (*Upper* panel) 26G-RNA targets, the 26G/22G ratio; (*lower* panel) 22G-RNA targets. (*F*) Expression profile of 26G-RNAs and 22G-RNAs in spermatogenesis is different for *Ascaris* and *C. elegans* (see Discussion). Note that for *C. elegans*, the total level of 26G-RNAs decreases during spermatogenesis with a concomitant and dramatic increase in 22G-RNAs targeting the same mRNAs. In contrast, the ratio of *Ascaris* 26G/22G RNAs to mRNAs remains the same during spermatogenesis and the 26G-RNAs are always the dominant small RNA species. Note that the figure does not represent absolute levels of the RNAs.

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1957). A study from Muller's group demonstrated that mRNA derived from the FERT-1 gene are transcribed during intrauterine zygote maturation (Spicher et al. 1994). It remains to be determined whether the miRNAs synthesized prior to pronuclear fusion are derived from the male or female pronucleus or both. Thus, gene expression in post-fertilization development in *Ascaris* exhibits a number of novel features including miRNA transcription occurring during zygote maturation, earlier than in any system yet described and at a developmental stage long thought to be quiescent. When the mature eggs (zygote-4 or 0 h) are released from the *Ascaris* uterus and then passed from the mammalian host to the external environment, development begins with pronuclear fusion (Fig. 1), and additional new miRNAs appear at the one- to two-cell stage of development (Figs. 4, 5A). Our data suggest that RNA pol II transcription starts earlier in embryogenesis than previously thought for either *Ascaris* or *C. elegans* (Cleavinger et al. 1989; Edgar et al. 1994; Baugh et al. 2003).

Role of small RNAs in early embryo development

Notably, *Ascaris* 22G endo-siRNAs are also synthesized in the zygote prior to pronuclear fusion and get contributed to early embryos. Studies in *C. elegans* demonstrated that dicer and miRNA-associated ALG-1/2 Argonaute mutants led to discrete developmental phenotypes. However, recent studies in mice suggest that early developmental phenotypes of dicer mutants may not be directly related to the loss or reduction of miRNAs but to the alteration of endogenous siRNA pathways (Ma et al. 2010; Suh et al. 2010). Endo-siRNAs that are maternally contributed or differentially expressed during early development may play a role in the maternal to zygotic transition and other important roles in early development, including the onset of primordial germ cells. Additional studies are needed to clarify the roles of these endogenous siRNAs during early development.

Elimination of individual miRNAs or miRNA seed families in *C. elegans* leads to developmental phenotypes including death of embryos or early larvae and defects in locomotion, body size, egg laying, and dauer larvae formation (Miska et al. 2007; Alvarez-Saavedra and Horvitz 2010; Brenner et al. 2010; Shaw et al. 2010). Multiple *Ascaris* miRNAs expressed in early development also belong to the same seed families and share similar expression patterns (Supplemental Table S4), such as *Ascaris* seed family miR-36a/36b/36c/36d/36e/36f/5348 (*C. elegans* miR-35/36/37/38/39/40/41/42), miR-791/5350a/5350b/5350c/5350d/5351/5367 (*C. elegans* miR-790/791), miR-44a/279a/279b/279c (*C. elegans* miR-44/45/61/247), and miR-2a/2b/43a/43b/43c/43d/43e/250 (*C. elegans* miR-2/43/250/797). Our studies clearly demonstrate the timing for the specific developmental expression of these miRNAs and their conserved seed families (Fig. 4; Supplemental Tables S3, S4). In several cases, miRNAs in the same seed families are expressed in a narrow window during embryogenesis. Redundant seed families could ensure silencing at key points in development and/or expression of appropriate seed miRNAs in different cells during early development. It will be interesting to determine the targets for these miRNA in *Ascaris* and compare them with those in *C. elegans*.

We observed a dozen miRNAs maternally contributed to the zygote, but no clear example of paternal miRNA contributions. In *C. elegans*, maternally contributed and some zygotic miRNAs (Kato et al. 2009; Stoeckius et al. 2009; Wu et al. 2010) appear to play important roles in early development (Miska et al. 2007; Alvarez-Saavedra and Horvitz 2010; Brenner et al. 2010; Shaw et al. 2010) as they do in mice, *Xenopus*, and flies (Bernstein et al. 2003; Leaman et al. 2005; Martello et al. 2007; Tang et al. 2007). miRNAs are also known to contribute to the maternal to zygotic transition in zebrafish and flies, although the miRNAs involved are not conserved (Giraldez et al. 2006). *Ascaris* 22G-RNAs are also maternally contributed, synthesized in the zygote prior to nuclear fusion, and differentially expressed through the 24-cell stage of embryos. The role of germline contributed small RNAs, early zygotic transcription of miRNAs in *Ascaris* and *C. elegans*, and new endo-siRNAs during early development remain to be determined. Interestingly, the majority of the miRNAs unique to *Ascaris* are derived from the germline, zygote, and early stages of development, whereas those *Ascaris* miRNAs conserved in *C. elegans* are expressed in later stages of development (26 cell–L2). We hypothesize that the *Ascaris*-specific miRNAs are related to *Ascaris* sexual dimorphism and differences associated with *Ascaris* development and metabolism.

Small RNAs in *Ascaris* spermatogenesis

Ascaris has lost the piRNA pathway. Considering the important role of piRNAs in spermatogenesis and silencing mobile elements in the germline with the exceptional reproductive capacity in *Ascaris* (see above), other small RNAs or other mechanisms must serve this key function in *Ascaris*. Consistent with this hypothesis, *Ascaris* 26G- and 22G-RNAs are the dominant *Ascaris* testis small RNAs. Based on analysis of the biogenesis of *C. elegans* 22G-RNAs in dicer mutants, Gu et al. (2009) proposed that 22G-RNAs are generated through a dicer (DCR-1) independent pathway. They further noted that the WAGO 22G-RNA system in *C. elegans* is similar in many respects to *Drosophila* and vertebrate piRNA pathways. In addition, piRNAs in *C. elegans* have been demonstrated to act upstream of 22G-RNA biogenesis (Batista et al. 2008; Das et al. 2008). Thus, *Ascaris* 26G- and 22G-RNAs may have adapted to serve additional roles typically played by *C. elegans* piRNAs. Functional overlap of piRNA, 26G-, and 22G-RNAs, including targeting mobile elements, likely occurs in *C. elegans* as temperature-sensitive spermatogenesis defects resulting from Piwi-related PRG-1 mutants are similar to those observed for 26G- and 22G-RNA defects (Batista et al. 2008; Wang and Reinke 2008; Conine et al. 2010).

Spermatogenesis is a very temperature-sensitive process in *C. elegans* (L'Hernault 2009). Many of the mutations in the male germline and spermatogenesis cause temperature-sensitive phenotypes (Batista et al. 2008; Das et al. 2008; Wang and Reinke 2008; Gu et al. 2009; Conine et al. 2010). *Ascaris* germline maturation, gametogenesis, sexual reproduction, and zygote maturation occur at 37°C in the vertebrate host. We speculate that the adaptation to these processes at 37°C may have altered the role of these temperature-sensitive pathways including the loss of the 21U-RNAs (piRNAs) and 22G-RNAs amplification in the testis. Furthermore, the increased expression and additional targets of *Ascaris* 26G-RNAs may be an adaptation to the loss or changes in function of 21U- and 22G-RNA pathways. We also failed to detect piRNA pathway components in other nematode parasites of vertebrates, *B. malayi* and *Trichinella*, in which spermatogenesis also takes place at 37°C (Ghedin et al. 2007; Mitreva et al. 2011), further suggesting that this may be an adaption to a parasitic life cycle at higher temperatures.

The small RNAs involved in *Ascaris* spermatogenesis appear to illustrate functional diversification compared with those in *C. elegans*. Several lines of evidence suggest that *C. elegans* testis (and embryo soma) 26G-RNAs function as primary siRNAs targeting mRNAs for the synthesis of much more abundant 22G secondary siRNAs (Gent et al. 2009, 2010; Han et al. 2009; Conine et al. 2010;

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Vasale et al. 2010). During *C. elegans* spermatogenesis, 26G-RNAs are first produced in distal regions of the testis and subsequently target mRNAs for production of amplified levels of secondary siRNAs in the proximal testis (Fig. 7F). Our analysis of small RNAs throughout the *Ascaris* male germline (see Fig. 1; Supplemental Table S2) identified distinct expression patterns for 26G- and 22G-RNAs involved in spermatogenesis (Fig. 7F). Although these two small RNA types are both present in the testis, most of *Ascaris* 26G- and 22G-RNAs have distinct sets of targets: The majority of *Ascaris* testis 22G-RNAs target nonspermatogenesis-related mRNAs, while *Ascaris* 26G-RNAs almost exclusively target mRNAs involved in spermatogenesis. For these spermatogenesis-related transcripts, the level of the 26G-RNAs stays high and their ratio to 22G-RNAs associated with these mRNAs is constant throughout spermatogenesis. This reveals a different relationship between 26G- and 22G-RNAs in *Ascaris* compared with *C. elegans* for spermatogenesis related genes. *Ascaris* 26G-RNAs are the major type of testis endo-siRNA targeting mRNAs involved in spermatogenesis. In addition, 26G-RNAs show a bias for the ORF of the mRNA, whereas the less abundant 22G-RNAs show a bias for targeting the 5′ ends of mRNAs (Fig. 7C,F).

Biogenesis of *Ascaris* endo-siRNAs

Small RNAs produced by RdRPs typically have a 5′ terminal G with polyphosphates (Ambros et al. 2003b; Chicas et al. 2004; Ruby et al. 2006; Pak and Fire 2007; Sijen et al. 2007). 26G-RNAs in *C. elegans* and *Ascaris* have a 5′ monophosphate. It has been suggested that *C. elegans* 26G-RNAs may be derived from dsRNAs formed by RdRPs followed by Dicer cleavage (Han et al. 2009; Conine et al. 2010; Gent et al. 2010; Vasale et al. 2010; Ketting 2011). An alternative hypothesis is that these 26G-RNAs are synthesized by RdRPs with 5′ polyphosphates, followed by trimming of their 5′ terminal phosphates (Ruby et al. 2006). Many questions remain regarding the biogenesis of nematode 26G-RNAs. The absence of the 3′ modification in the *Ascaris* 26G-RNAs raises a number of questions regarding their biogenesis in *Ascaris*, and the potential roles of these 3′ modifications in the *C. elegans* orthologs.

We also observed *Ascaris* 22G-RNAs in our 5′ monophosphate libraries (Fig. 2G), suggesting *Ascaris* may also have 5′ monophosphate 22G-RNAs. For each unique *Ascaris* 22G-RNAs, we found the ratios between 5′ monophosphate and 5′ all-phosphate libraries are constant, suggesting that these monophosphate 22G-RNAs are likely derived from polyphosphate 22G-RNAs (Fig. 6E). Whether these represent intermediates in the turnover or biogenesis of the 22G-RNAs or whether discrete phosphate removal is associated with alternate functions of these small RNAs remains to be determined. We noticed that *As.22H* RNAs have very similar features to *As.22G* (Fig. 6) except that they start with different bases, suggesting that *As.22H* are likely to be generated by RdRPs. Based on their frequency, we speculate that *Ascaris* RdRPs have a strong preference for G (74%) as the initial base, followed by A (17%), C (7%), and U (2%).

Small RNAs and chromatin diminution

Chromatin diminution eliminates specific DNA sequences from the genome of somatic cells in various organisms, typically during early development (Muller and Tobler 2000; Goday and Esteban 2001). In *Ascaris*, chromatin diminution occurs during the third through fifth cleavage (four- to 16-cell stage) with the loss of ~25% of the genome (Muller and Tobler 2000). Fifty percent of the eliminated DNA (~40 Mb, >300,000 copies) is the highly repetitive satellite DNA that consists primarily of several variants of a 121-bp element (Muller et al. 1982; Streeck et al. 1982).

Elimination of DNA during macronuclear rearrangement in *Tetrahymena* and other ciliates is associated with small RNAs (Mochizuki and Gorovsky 2004; Yao and Chao 2005). Our initial interest in *Ascaris* small RNAs was to determine whether small RNAs were mechanistically involved in chromatin diminution. We therefore searched for small RNAs corresponding to the eliminated repetitive DNA in the germline and during early development. We detected small RNAs corresponding to the eliminated satellite DNA in our sequence reads at frequencies of only ~200/million reads. One would predict that targeting >300,000 copies of a dispersed, repetitive sequence for elimination would require much higher levels of small RNAs, particularly when we observed small RNA reads as high as 1000–250,000 reads/million for endo-siRNAs and miRNAs, respectively. We also did not observe an increase in the expression profiles of small RNAs that target the 121-bp repeats or any small RNAs that were stage or tissue specific that correlated with chromatin diminution (data not shown). We conclude that there is no apparent correlation between small RNAs, the 121-bp repeat, and DNA elimination in *Ascaris*.

C. elegans CSR-1 Argonaute and 22G-RNAs are required for holocentric chromosome segregation (Claycomb et al. 2009). Claycomb et al. (2009) suggested during chromatin diminution in *Ascaris* the eliminated regions (e.g., heterochromatic domains and eliminated repeat elements) might not be targeted by small RNAs for retention and chromosome segregation. Chromosome breaks during diminution in the somatic lineages would lead to chromosome fragmentation. Chromosome fragments to be retained would be targeted by CSR-1 Argonaute and 22G-RNAs forming a functional holocentric chromosome, whereas regions for elimination would not be efficiently targeted and not segregated. Experiments are in progress to define the somatic and germline genome in *Ascaris* to identify the retained and eliminated chromosomal regions and to examine the association of *Ascaris* CSR-1 Argonaute with these regions.

Methods

Library preparation, sequencing, and reads processing

Small RNA libraries were prepared and sequenced as previously described (Brennecke et al. 2007; Grimson et al. 2008). Computational analysis and annotation of miRNAs, endo-siRNAs, and other cellular RNAs were carried out as described (see Supplemental Material). For genomic libraries, genomic DNA (>50 kb in length) was isolated on CsCl gradients from 32- to 64-cell embryos or from adult tissues using standard methods. Somatic cells predominate in the 32- to 64-cell embryos with only ~5% germline cells. The *A. suum* genome was sequenced using a whole-genome shotgun strategy using three sequencing platforms, capillary paired-end Sanger sequence of size fractionated 6-kb cloned sequences and direct 454 titanium and Illumina sequencing (see Supplemental Material).

cDNA libraries were prepared from polyadenylated RNA (2× oligo-dT purified using μMACS mRNA Isolation Kit, Miltenyi Biotec). RNA was treated for 75–150 sec with RNA fragmentation buffer (Ambion) at 70°C to generate RNA fragments 150–400 nt in length. cDNA was prepared by random priming (3–6 μg of random hexamers/1 μg of A+ RNA), and second-stranded cDNA synthesis was carried out using a SuperScript Double-Stranded cDNA Synthesis Kit (Invitrogen). Illumina (Solexa) paired-end adaptors were added to the blunt cDNA as described by Illumina, cDNA fragments 300–400 bp in length were gel purified, the fragments were amplified using 17 PCR cycles and paired-end 76- to 100-base

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sequences were generated as described on the Illumina GAII platform (details of *Ascaris* samples, library preparation, sequencing, assembly, analysis, and annotation can be found in the Supplemental Materials).

Small RNA labeling and Northern blot analyses

Total RNA was isolated using TRIzol (Invitrogen), and small RNA samples were 5′ labeled by first treating with calf alkaline phosphatase (Roche) followed by phosphorylation with T4 polynucleotide kinase (NEB) and ^{32}P-γ-ATP. Small RNA samples were 3′ labeled using T4 RNA ligase (NEB) and ^{32}P-pCp as described by the manufacturer. RNAs were capped using cold GTP or ^{32}P-α-GTP and guanylyltransferase as described (Cohen et al. 2004).

Northern blots were prepared using 7.5 or 20 μg of total RNA and 5 μg of low-molecular-weight enriched RNA (mirVana miRNA isolation kit with modification). To characterize the 5′ ends of small RNAs, 10 μg of low-molecular-weight enriched small RNAs was treated with Terminator (Epicentre), guanylyltransferase and GTP, or T4 RNA ligase (NEB) and an RNA oligonucleotide. Periodate treatment and β-elimination of RNA were carried out as described (Vagin et al. 2006; Czech et al. 2009). RNAs were separated on denaturing 12.5% or 15% polyacrylamide gels and transferred to Hybond N+ using semi-dry electroblotting (Trans-Blot Semi-Dry transfer cell, BioRad); the membranes were ultraviolet cross-linked and baked at 80°C. Membranes were probed with 5′ end-labeled DNA oligonucleotides.

Bioinformatics

Bioinformatic analyses are described in the Supplemental Material.

Data access

The transcriptome and small RNA data from this study have been submitted to the NCBI Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo) under accession numbers GSE26956 and GSE26957. The transcriptome assembly has been submitted to NCBI Transcriptome Shotgun Assembly Sequence Database (http://www.ncbi.nlm.nih.gov/genbank/TSA.html) under accession numbers JI163767–JI182837 and JI210738–JI257410. The genomic sequence reads and assembly data from this study have been submitted to the NCBI Sequence Read Archive (http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi) under accession number SRP005397 and GenBank accession number AEUI00000000.]

Acknowledgments

We thank Richard Komuniecki, Bruce Bamber, Amanda Korchnak, Vera Hapiak, Jeff Myers, and Routh Packing Co. for their support and hospitality in collecting *Ascaris* material. We thank David Bartel for helpful discussions and suggestions, Chris Hittinger and Jim Dover for advice on library preparation and sequencing, Tom Evans for samples of *C. elegans*, and Yingfeng Luo and Songnian Hu at the Beijing Institute of Genomics for computer resources. We also thank Mark Johnston for his comments on the manuscript and the reviewers for their constructive comments and suggestions. B.C. is supported by a PhD fellowship from the Boehringer Ingelheim Fonds. This work was supported in part by grants to R.E.D. (NIH AI0149558 and AI078087), to M.M. (NIH AI081803), and to G.J.H. (grants from the NIH and a kind gift from K.W. Davis). G.J.H. is an investigator of the HHMI.

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Received January 25, 2011; accepted in revised form June 8, 2011.

SUPPLEMENTAL MATERIAL

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Deep Small RNA Sequencing from Nematode *Ascaris* Reveals Conservation, Functional Diversification, and Novel Developmental Profiles

Supplemental Materials and Methods

Supplemental Results and Discussion

Supplemental References

Supplemental Materials and Methods

Ascaris material and RNA preparation. Eggs in the uterus near the vulva (proximal uterus, Zygote-4, Figure 1) of *Ascaris suum* (parasite of pigs) are fertilized (without pro-nuclear fusion) and have developed a mechanically and chemically resistant shell/membrane. These eggs can be isolated in large quantities from the proximal region of uteri (~45 ml of packed eggs/1000 worms) by treatment of dissected uteri with 0.5 N NaOH, and the eggs can be stored at 4°C for many years. Upon incubation at 30°C with high humidity and aeration, the eggs undergo slow and relatively synchronous development ($\geq$ 85%), enabling collection of embryos at various stages (see Figure 1). Early *Ascaris* development (Muller 1903) through the L2 is similar to that of *C. elegans* (Sulston et al. 1983), except that it occurs much slower (10 days to reach L1 in *Ascaris* vs. ~13 hr to L1 in C*. elegans*). Unlike *C. elegans* whose larvae are free-living and feeding, the *Ascaris* L1 and L2 larvae remain within the egg.

Ascaris has separate sexes and their adult male and female reproductive systems are on average ~140 and 240 cm, respectively. Discrete regions of the reproductive systems can be obtained (Figure 1). In males, we collected the germinal zone (Testis-G), two regions of the testis (Testis-1 and Testis-2), and spermatids from the seminal vesicle. In females, we collected the germinal region of the ovary (Ovary-G), the ovary (Ovary-All), and four regions of the uterus that contain the newly fertilized and shelled zygotes (Zygote 1-4) undergoing maturation necessary for pronuclear fusion and subsequent development (Figure 1) (Fairbairn 1957; Kaulenas and Fairbairn 1968).

For the germinal zone of the testis and ovary (Figure 1), the distal 5 cm of the gonad was isolated from live worms and stored at -80°C. Other regions of the gonads were dissected from live worms and either frozen immediately at -80°C or lysed by homogenization in Trizol and then frozen. *Ascaris* fertilized eggs were harvested from 4 regions of female uteri (Zygote 1-4) by treatment with 0.5 N NaOH, followed by extensive washing in water, and then stored at 4 °C with 5 volumes of PBS (pH 2.0). For embryonation, the fertilized eggs from final proximal region of the uterus (Zygote-4 = 0 hr embryos) were incubated at 30 °C in PBS (pH 2.0) with constant (100 rpm) shaking for the desired time. The outer shell/membranes were de-coated with 0.4 N KOH/1.4% sodium hypochlorite at 4 °C (zygotes from regions 1-4) or 30°C (developing embryos and larvae) for 180 or 90 minutes, respectively, prior to RNA

preparation. RNA from fertilized eggs in the uterus and early embryos (0 hr to 8 days) were extracted directly with Trizol (Invitrogen). Frozen L1, L2, testis and ovary samples were first ground with a mortar and pestle in liquid nitrogen and then extracted with Trizol.

Small RNA library preparation, sequencing and reads processing. Libraries were prepared and sequenced as previously described (Brennecke et al. 2007; Grimson et al. 2008) with some modifications. In brief, small RNAs (18–34 or 18-40 nt) were gel purified from 25 µg of total RNA using denaturing polyacrylamide–urea gels. Prior to gel purification of the RNAs, two small RNA spikes (p-AACUGUGUCUUUUCUGAAUAGA and p-UAUUUAGAAUGGCGCUGAUCUG) corresponding to mammal specific small RNAs were added to the samples for subsequent library read normalization. Periodate-treated libraries were generated as described (Vagin et al. 2006; Czech et al. 2009). For 5' all-phosphate libraries, 18-28 or 18-40 nt RNAs were treated with RNA 5' polyphosphatase (Epicentre, Madison, WI) to convert all tri- and dephosphorylated RNAs into 5' monophosphates prior to library construction. Libraries were sequenced on an Illumina GAII obtaining 5-25 million reads of 36-40 nt in length. Following removal of the adaptor sequences from the sequence reads, reads were collapsed to non-redundant datasets and then short reads (<= 17 bp) and low complexity reads (including poly A/C/G/ or T, di-nucleotide repeats, etc) were removed. We mapped all processed reads to *Ascaris* genomic and mRNA sequences (Table S1) using BLAST (E-value cutoff: 1e-2) and perfectly-matched reads (no gaps or mismatches across their entire length) were further analyzed (Table S2). Because the data are derived from wild *Ascaris* populations corresponding to hundreds of individuals, the sequences are highly polymorphic. Therefore, selection of only perfectly matching small RNAs is an extremely stringent criterion. Allowing one or two mismatches did not change the general picture of small RNAs identified.

Small RNA read normalization. In order to compare small RNA reads between different stages in 5' monophosphate libraries, we added two small RNA spikes at difference concentrations. Following sequencing, we observed an average of 255,531 high spike reads and an average of 7,429 low spike reads in the libraries. Using one of the 5' monophosphate libraries (Ovary-G) as a standard by setting its read number to 10 million, we compared all the spike reads in other libraries to the spike reads in the standardized Ovary-G. For each library, we normalized its read numbers by multiply the raw value by the

fold change to standard (Table S2), which was derived from the average $\log_2$ ratio fold changes of the two spikes in this library to spikes in the standardized library, and all normalized reads are rounded to integer (Table S2). While the fold change between spikes (spike1/spike2) in most stages (26 out of 28) is close to the average (34.4 fold), we observed an ~6.3X fluctuation in L2 and ~20 X in 8 day. As spike reads become lower, we expect larger fluctuation between spikes (the cases in 6 day, 7 day, 8 day, L1 and L2). Day 8 was significantly out of range from average and thus is not included in our comparative analysis of read frequencies between stages.

We normalized the read frequencies in the 5' all-phosphate libraries using miRNA reads. Since for 5' all-phosphate libraries on the same samples, we also prepared 5' monophosphate libraries, the miRNAs reads should be represented equally in each of the two pairs of libraries. For analysis of 0 - 64 cell and 128 cell – L2 5' all-phosphate libraries, their 5' monophosphate miRNAs data were derived from 0 hr - 116 hr 5' monophosphate libraries and 6 day - L2, respectively (Table S2). All reads in these 28 5' monphosphate and 19 5' all-phosphate libraries are comparable as they are normalized to our standard library (10 million 5' monophosphate reads in Ovary-G).

Expression profiles of miRNAs and siRNAs were clustered by using the Cluster 3.0 program (Eisen et al. 1998) (http://bonsai.ims.u-tokyo.ac.jp/~mdehoon/software/cluster/software.htm) followed by manual adjustment. The TreeView program (http://jtreeview.sourceforge.net/) was used to display the heatmaps.

MicroRNA identification and analysis. Following removal of small RNA sequence corresponding to *Ascaris* rRNA, tRNA, snRNA, snoRNA, and mitochondrial DNA, the remaining reads were clustered to identify potential miRNA hairpins (presence of neighboring matches within 50 nucleotides of each other with at least one of the matches $\geq$ 2,000 reads). Sequences of the clusters were then examined by mfold (Mathews et al. 1999). If the free energy of a potential hairpin was less than -20 kcal/mol, the most frequent reads located on one arm of a predicted hairpin, and the reads were involved in $\geq$ 15 base-pairings, the potential miRNA hairpin was further examined manually. miRNAs were defined using a combination of the following criteria: 1) RNAs derived from a unique and relatively stable genomic hairpin predicted by RNA folding, 2) the RNA sequence is within one arm of the genomic hairpin, 3) at least 15 nt of the RNA is involved in hairpin base-pairing, 4) presence of a RNA* reads in the other arm of the

hairpin, 5) RNA and RNA* have 2 nt overhangs, and 6) 5' terminal homogeneity of the small RNA. Additional low-frequency miRNAs were identified by sequence homology to miRBase and by searching 500 bp flank regions of established miRNAs to look for miRNAs in polycistronic loci.

We used miRBase (version 16.0) to identify *Ascaris* miRNAs orthologs. We first searched pairs of miRNAs that shared the seed region (2-8). For all such pairs, we aligned the mature miRNAs with EMBOSS:needle software (http://emboss.sourceforge.net/apps/cvs/emboss/apps/needle.html) that uses Needleman-Wunsch (NW) algorithm, with the default scoring matrix (match score 5, mismatch -4, gap penalty 10, and gap extension penalty 0.5). miRNA hairpin sequences were also aligned after the hairpin sequences were trimmed according to miRNA and miRNA* positions flanking 2 nucleotides. miRNA pairs with both high sequence similarities for their mature miRNAs and hairpins were considered as homologous. The cutoff scores for high similarities were defined as following: for each NW alignment, the ratio of the alignment score over the alignment length reflects how similar the sequences are. We used all miRNA pairs that do not share the seed sequences as the background, and their ratios were calculated and the median value (0.60 for mature miRNA alignment and 0.57 for hairpin alignment) was defined as the background. Seed-matched pair alignments 2-fold or more above background (1.20 for mature miRNA and 1.14 for hairpin) were considered having high sequence similarities and considered orthologous miRNAs.

Endo-siRNA identification and analysis. After removal of small RNAs corresponding to structural RNAs (rRNAs, tRNAs, snRNAs/snoRNAs, etc.) and miRNAs, the remaining genome- and mRNA-matched small RNAs were categorized into two types, siRNAs and Other small RNAs. The *siRNAs* are defined as small RNAs mapped to our *Ascaris* polyA-selected mRNA database and the *Other RNAs* are genome-matched RNAs that don't have mRNA matches. In order to distinguish sense and antisense small RNAs, we annotated our mRNA data (Table S1) and used them for the analysis. siRNA positions on the mRNAs were analyzed by using the 8,279 near-full length mRNAs (Table S1). We used a cutoff of 100 reads of small RNA/mRNA/million reads for each individual 5' all-phosphate library to define a curated set of 26G and 22G-targets (see text). A closer examination of 16 overlapping mRNAs targets of 26G and 22G-RNAs revealed that they have distinct 22G/22G ratios: 14 of them have a high 26G/22G

ratio, similar to the other 168 26G-RNA targets, while the other 2 overlap mRNAs have a high 22G/26G ratio, similar to the other 157 22G-RNA targets (Figure 6E and Table S7). We found the overlap is largely due to the "low" cutoff we have selected, and when lower ones were used, we see more overlap targets, but the ratio of 26G- and 22G RNAs remains constant (data not shown). We applied this constant 26G/22G ratio feature to refine the targets (see text).

21U/piRNA analysis. Several approaches were used to identify potential *Ascaris* orthologs of *C. elegans* 21U RNAs (piRNAs). First, we looked for *Ascaris* genomic regions enriched with 21nt RNAs starting with U (*Ascaris* 21U-RNAs) from the germline libraries. We used a cutoff of 21U-RNA % > 95% and reads per kb > 25 and identified only 92 *Ascaris* genomic loci that met these criteria. Using the same approach *on C. elegans*, we were able to identify 1,198 potential piRNA loci in the smaller *C. elegans* genome producing 4,749 unique small RNA reads with a total of 30,710 reads, and 94% of these small RNAs were defined as 21U-RNAs (Ruby et al. 2006; Batista et al. 2008). Thus, although our approach can identify 21U-RNAs clusters with high probability in *C. elegans*, few can be identified in *Ascaris*. *C. elegans* 21U-RNAs are derived from across an entire 21U genomic locus with each small RNA present at low frequency. In contrast, most of the potential 92 *Ascaris* 21U-RNA's loci are represented by only a few individual species at high-frequency, further suggesting they are unlikely to be orthologous to *C. elegans* 21U-RNA. Second, after we removed all RNAs types we could define, we looked for U-initiated RNA enrichment in all libraries. No U-intiated RNAs were identified (Figure 3 A-B, Fig. S1-4). Third, we used a position-specific scoring matrix based on a 21U-RNA motif defined in *C. elegans* (http://web.wi.mit.edu/bartel/pub/softwareDocs/TouRnaMotif/Introduction.html) to predict 21U-RNAs loci. Using moderate stringency (score cutoff, 15.5), we predicted 33,411 *C. elegans* potential 21U-RNAs of which 10,468 (31.3%) are true 21U-RNAs, representing 67% (total read number) of all known 21U-RNAs. In contrast, only 8,746 potential 21U-RNAs were predicted for the *Ascaris* genome and only 32 of these were present in our small RNA libraries. The 21U-RNA motif among different nematodes is diverse in regions outside the core GTTTC motif (de Wit et al. 2009). To check whether motifs from other nematodes can be used to predicted 21U-RNA in *Ascaris*, we used the matrix based on the diverged 21U-RNA motif derived from *Pristionchus pacificus* (de Wit et al. 2009). We were able to predict 88%

(988 of the 1,123) of the known 21U-RNAs in *P. pacificus* (score cutoff, 20). While for *Ascaris*, only 96 out of 17,944 potential 21U-RNAs were found in our libraries. Last, in an effort to enrich for piRNAs, we prepared periodate treated small RNA libraries to enrich for small RNAs with 3'-modifications, but did not identify any 21U RNAs enriched in any of the libraries.

Genomic DNA library preparation, sequencing and assembly. The *Ascaris* genome is 290 ± 30 and 394 ± 40 Mb (somatic and germline, respectively) based on our sequencing and measurement of DNA content of nuclei (fuelgen staining). The *A. suum* genome was sequenced by a whole-genome shotgun strategy using three sequencing platforms: paired-end Sanger sequencing, direct 454 titanium sequencing and Illumina paired-end sequencing (Table S1). For Sanger sequencing, DNA was size fractioned to enrich for ~5.5 kb fragments as previously described (Abubucker et al. 2008). The Sanger sequencing generated 451,630 reads with an average length of 826 bases. For 454 Titanium sequencing, 6.6 µg of genomic DNA was fragmented via nebulization, DNA fragments of 500-800 bp in size were isolated, and their ends were polished and ligated to 454 Titanium library adaptors using reagents from the Titanium General Library Kit (454 Roche). The DNA library was sequenced on the Genome Sequencer instrument using the GS FLX Titanium Sequencing Kit XLR70 (Roche 454). A total of 2.66 million reads were generated with an average length of 350 bases (see Table S1). For Illumina sequencing, genomic DNA was fragmented using a Bioruptor sonicator (Diagenode), Solexa paired-end adaptors were added to the DNA as described by Illumina, DNA fragments with an insertion of 300-400 bp in length were gel purified, and then PCR amplified. Forty-one million paired-end reads with an average length of 100 nt were generated on the Illumina GAII.

Genomic reads from Sanger and 454 platforms were combined and assembled by using Newbler (Roche), and genomic reads from Illumina were assembled with Velvet (Zerbino and Birney 2008). We combined the two assemblies by using Phrap (http://www.phrap.org/), and all the assemblies were evaluated by using Tablet assembly viewer (http://bioinf.scri.ac.uk/tablet/). Scaffolds were built by using the paired-end Sanger reads and Illumina reads. The final assembly consists of 86,678 scaffolds with an N50 of 11,773 bp (the largest scaffold is of 185,246 bp) and ~273 Mb of assembled sequence (Table S1). This assembly was used to define the genome origin of small RNAs and their potential biogenesis.

Ascaris rRNA sequences were identified using database sequences and tRNA sequences were identified by using tRNAscan-SE program (Lowe and Eddy 1997).

cDNA library preparation, sequencing, assembly and annotation. cDNA libraries were prepared from polyadenylated RNA (2x oligo-dT purified using μMACS™ mRNA Isolation Kit, Miltenyi Biotec). Two types of libraries were prepared: 1) sheared, full-length cDNA synthesized using a combination of oligo-dT and random hexamer priming and 2) cDNA prepared from RNA first chemically sheared and then double-stranded cDNA prepared using ramom hexamer priming. For the chemically sheared library, RNA was treated for 75-150 sec with RNA fragmentation buffer (Ambion) at 70°C to generate RNA fragments 150-400 nt in length. First stand cDNA was prepared by random priming (3-6 μg random hexamers/1 μg of A+ RNA) and second stranded cDNA synthesis was carried out using a SuperScript® Double-Stranded cDNA Synthesis Kit (Invitrogen). Solexa paired-end adaptors were added to the blunt cDNA as described by Illumina, cDNA fragments of 300-400 bp in length were gel purified, the fragments amplified using 17 PCR cycles, and paired-end, 76-120 nt reads were generated as described on the Illumina GAII. All the libraries we have sequenced are listed in Table S1. Six libraries are chemically sheared first; these are Embryo (pooled RNA from early embryos development (0, 24, 46, 64, 96, and 116 hr embryos)), Larvae (larval development and larvae (6, 7, and 8 day embryos and L1 and L2 larvae)), Testis (testis germimal zone), Ovary (ovary germinal zone), complete female reproductive system, and whole males. One library is full-length sheared cDNAs from mixed samples of all of the RNAs in other six libraries.

Reads from each cDNA library were initially assembled with Velvet (Zerbino and Birney 2008). We built a set of reference sequences by combining all these assemblies together. Using these reference sequences, we assembled each library again and an improved assembly for each library was obtained. We then built an improved reference sequences and iterated this cycle until no further improvement was achieved. All the assemblies were checked with Tablet (http://bioinf.scri.ac.uk/tablet/) by using a cutoff of 5% mismatch for mis-assembled contigs. Other obvious chimera contigs (after annotation, see below) were split. The final assembly (Table S1) was improved by scaffolding, genomic sequences, and available ESTs.

We used the UniProt (http://www.uniprot.org/) and WormBase (http://www.wormbase.org/) to annotate the cDNAs by using BlastX. cDNAs with database matches with an E-value <= 1e-10 were annotated. cDNAs were further categorized using Pfam 24.0 (http://pfam.janelia.org/). The strand of cDNAs were identified using BlastX annotation, the presence of a polyA tail and/or splice leader sequence (Nilsen et al. 1989).

Supplemental Results and Discussion

***Ascaris* miRNA gene organization and expression, processing, editing, and nucleotide addition.** We identified 13 putative polycistronic miRNA loci encoding 33 miRNAs (see Figure S7). miRNAs derived from polycistronic loci are predominantly expressed before day 8 of development and often simultaneously express miRNAs with the same seed sequence. RT-PCR analysis demonstrated that most of the predicted polycistronic loci generate polycistronic primary transcripts, and a number of the primary transcripts are spliced leader trans-spliced and polyadenylated (data not shown). For most of these loci, the individual miRNAs from a single locus are not equally expressed (see Table S3 and Figure S7). While it remains possible that some of these miRNAs have their own promoters, **the data suggest they are either differentially processed or have different half-lives or both.**

No *Ascaris* miRNAs were identified as mirtrons (Ruby et al. 2007) whereas C. elegans has four. *Ascaris* miR-100a-2 is an offset RNA, as recently described in tunicates (see Figure S5) (Shi et al. 2009). Variation in the processing of miRNAs was also observed. As illustrated in Figure 4, the asu-miR-5347 hairpin produces two different sizes of mature miRNAs, 21 and 23 nt. The 23 nt miRNA is maternally contributed and the 21 nt miRNA is produced from the 96 hr – L2 stages of development. Independent miRNAs are derived from the same miRNA hairpin precursor as illustrated by the significant expression of several *Ascaris* miRNA*s (Table S3). miRNA* levels are typically observed at very low frequencies compared to the miRNA. This is observed for most of miRNA* detected in the libraries (on average ~1% of the miRNA reads). However, we observed that 16 *Ascaris* mRNA* reads (16.5% of the miRNA*) accumulate to 15% or more of the mature miRNA reads (Table S3). Several recent and comprehensive studies have made similar observations in flies, including evidence that the miRNA* is functional (Okamura et al. 2008; Czech et al. 2009; Okamura et al. 2009). Interestingly, miRNA strand selection (Liu et al. 2008; Okamura et al. 2008; de Wit et al. 2009) also appears to change in the evolution of the *Ascaris* miRNA locus. *Ascaris* miR-79 and miR-9 hairpins are paralogs having apparently been derived from duplication, yet the mature miRNAs produced from the two hairpins are derived from opposite sides of the hairpin. Thus, the mature miR-79 miRNA is 3p whereas the mature miR-9 is 5p (Figure S8).

Five *Ascaris* miRNAs undergo miRNA editing, four of which have A->I (G) editing, one exhibits C->U editing, and two are edited within their seed sequences (asu-miR-100d and asu-miR-5354) (Table S6). miRNA 3'-uridylation and 3'-adenylation (~3% of the reads) were observed for most of the *Ascaris* miRNAs. Eleven miRNAs exhibited significant levels of 3'-addition (Table S6) and a combination of polyuridylation and polyadenylation was often observed on the same miRNA. When truncated miRNAs are observed (asu-miR-1/2a/43e/56/750/5347), they exhibit much higher levels of 3' addition than the full-length miRNAs. This may correlate with marking the truncated miRNA for degradation (Chatterjee and Grosshans 2009).

***Ascaris* small RNA protein machinery.** *C. elegans* has a diverse set of Argonaute proteins including 5 Ago proteins, 3 PIWI Argonautes, and 18 worm specific Argonautes (WAGOs) (Yigit et al. 2006). A search for Argonaute-related proteins in the *Ascaris* genomic and transcriptome sequence led to the identification of 5 general Ago-clade proteins (2 corresponding to *C. elegans* Alg-1/Alg-2 and Alg-3/Alg-4), 5 WAGOs (corresponding to *C. elegans* csr-1, Wago-1, and nrde-3; the other two *Ascaris* WAGOs cannot be assigned to a *C. elegans* ortholog), but no PIWI orthologs (see Figure 3B and Table S9). Ago-, PIWI-, and WAGO-clade Argonautes associate with miRNAs and 26G-RNAs, piRNAs, and 22G-RNAs, respectively. *Ascaris* orthologs of pasha, drosha, dicer, three RNA-dependent RNA polymerases, and orthologs of many key proteins in *C. elegans* RNA interference pathways were also identified (eri-1, dcr-1, cde-1, mut-7, drh-3, ekl-1, ain-1, nlh-2, and nrde-2).

Ascaris small RNAs and transposons. Only 1-2% of all *Ascaris* small RNAs correspond to mobile elements. Over 90% of these correspond to LT and non-LTR retrotransposons. Small RNAs corresponding to these elements are expressed at relatively high frequency compared to other non-miRNA small RNAs (see Table S8).

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Supplemental Tables and Figure Legends

Deep Small RNA Sequencing from the Nematode Ascaris Reveals Conservation, Functional Diversification, and Novel Developmental Profiles

SUPPLEMENTAL TABLES

Table S1. *Ascaris* genome and cDNA: genome sequencing and assembly statistics, reads and functional coverage, and cDNA sequencing and assembly statistics.

Table S2. *Ascaris* small RNA libraries: sequencing statistics, reads normalization, and types of analyzed small RNAs.

Table S3. *Ascaris* miRNAs: mature miRNA, miRNA*, and miRNA hairpin sequences; seed families, polycistronic clusters, other features of miRNAs, miRNA/miRNA* read frequencies, and expression profiles and quantification of miRNA Northern blots.

Table S4. *Ascaris* miRNA seed families: miRNA seed family comparison between *Ascaris* and *C. elegans*.

Table S5. *Ascaris* miRNA compared to other organisms: comparison of *Ascaris* miRNAs to miRNAs from other nematodes, flies and humans.

Table S6. *Ascaris* miRNA editing and 3' addition: *Ascaris* miRNAs with editing or 3' addition (modifications that exceed 5% of the mature miRNA).

Table S7. *Ascaris* siRNA targets: curated mRNA targets of *Ascaris* 26G-RNAs and 22G-RNAs. Targets were identified as a minimum of 100 reads of small RNA/mRNA/million reads in at least one of the 5'-all-phosphate libraries.

Table S8. *Ascaris* siRNA read frequency: comparison of the read frequency of different types of siRNAs in *Ascaris*.

Table S9. *Ascaris* small RNA machinery: *Ascaris* proteins involved in different small RNA pathways and a comparison to those in *C. elegans* and other organisms.

SUPPLEMENTAL FIGURES

Figure S1. Size distribution of analyzed *Ascaris* 5' monophosphate small RNAs. Each figure provides the size distribution of the **raw small RNA reads** derived from different samples.

Figure S2. Size distribution of *Ascaris* 5' monophosphate miRNAs, siRNAs, and 28-32 nt RNAs. Each figure provides the size distribution of the **raw small RNA reads** derived from different samples.

Figure S3. Size distribution of analyzed *Ascaris* 5' All-phosphate small RNAs. Each figure provides the size distribution of the raw small RNA reads derived from different samples.

Figure S4. Size distribution of *Ascaris* 5' All-phosphate miRNAs, siRNAs, and 28-32 nt RNAs. Each figure provides the size distribution of the raw small RNA reads derived from different samples.

Figure S5. *Ascaris* miRNA hairpins with small RNA reads. Each miRNA hairpin sequence is illustrated with the Mfold predicted structure with the lowest free energy. These are followed by information on mapped small RNA's position, length, and frequency (raw small RNA reads from all stages). miRNAs are shown in red and miRNA* in blue. For simplicity, only small RNAs with read frequency either over 0.05% of the mature miRNA or over 100 are shown, with the exception for those low-frequency miRNA*s that have read numbers lower than 0.05% of the mature miRNAs.

Figure S6. *Ascaris* miRNAs expressed during zygote maturation and 1-4 cell embryos. A. Northern blots of 4 miRNAs expressed during intrauterine zygote maturation. Note the absence of pre-miRNAs in stages preceding the appearance of the

mature miRNAs suggesting the new miRNAs are derived from new transcription. **B.** Transcription of many miRNAs begins as early as the 1-4 cell embryos. Note the scale is logarithmic and the reads are normalized.

Figure S7. *Ascaris* polycistronic loci and miRNA expression. Each miRNA is illustrated as a box containing a red area indicating whether the miRNA is derived from the 5' or 3' arm of the hairpin, 5p or 3p, respectively. The sequence above the miRNA box is the seed sequence for the miRNA; red seed sequences represent those expressed at the same time during a developmental stage. The number below the box is the total of the raw miRNA reads in all stages examined.

Figure S8. *Ascaris* miRNA 5p and 3p shift with miRNA duplication. Illustration of parologous asu-miR-9 and asu-miR-79 apparently derived from gene duplication. **A.** alignment of hairpin sequences of asu-miR-9 and asu-miR-79. **B** and **D.** Small RNAs mapped to asu-miR-9 (**B**) and asu-miR-79 (**D**) as described in Figure S5 (reads are from Fig. S5). **C** and **E.** Predicted secondary structure of asu-miR-9 (**C**) and asu-miR79 (**E**) hairpins.

Figure S9. Frequency and distribution of 22G/26G-RNAs on 26G-RNA targets. Note that all small RNAs are antisense. Red, 22G-RNAs; blue, 26G-RNAs. Vertical dashed lines indicate the start and stop of the ORF. Numbers on left indicate the normalized read frequency of the gray line. (see separate FigS9.26G-RNA_targets.pdf)

Figure S10. Frequency and distribution of 22G/26G-RNAs on 22G-RNA targets. Note that all small RNAs are antisense. Red, 22G-RNAs; blue, 26G-RNAs. Vertical dashed lines indicate the start and stop of the ORF. Numbers on left indicates the normalized read frequency of the gray line. (see separate FigS10.22G-RNA_targets.pdf).

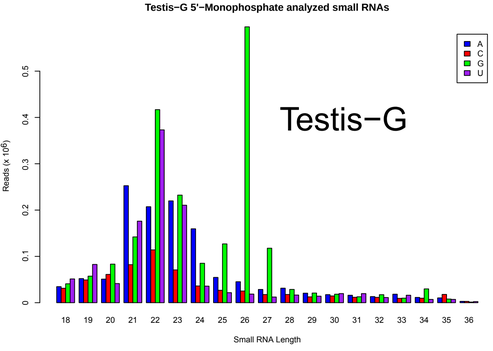
Figure S11. Larger *Ascaris* small RNAs derived from atypical genomic hairpins.

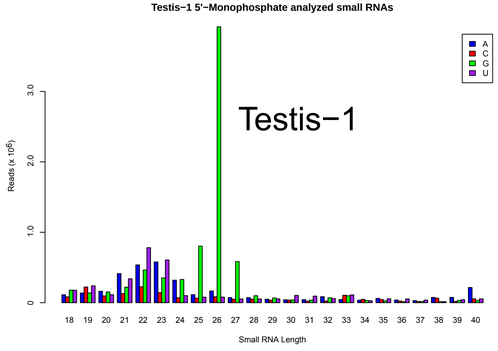
A. Illustration of the lowest free energy structures predicted by Mfold for atypical hairpins. Blue shading represents the major and yellow the minor small RNA derived from the hairpin. See Figure S12 for small RNAs and their total raw read frequencies from the atypical hairpins.

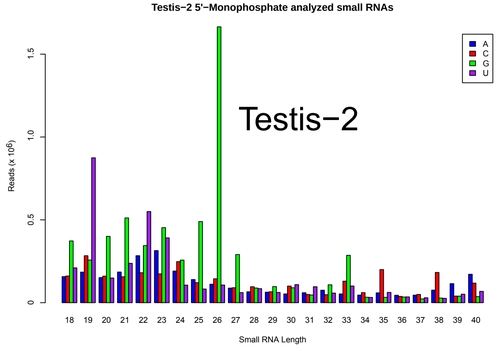
B. Small RNA read expression profiles (normalized) for small RNAs derived from atypical hairpins.

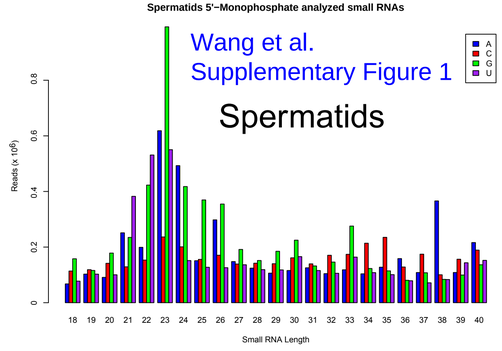
C. Northern blots demonstrating small RNAs derived from atypical hairpins.

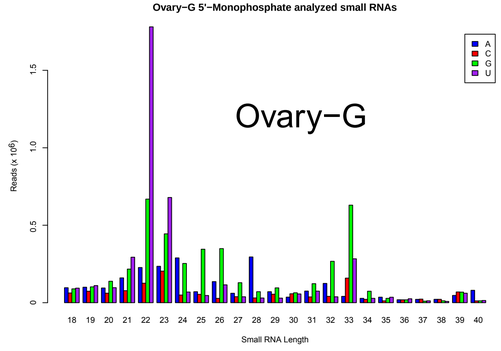
Figure S12. *Ascaris* small RNAs derived from atypical hairpins. *Ascaris* atypical hairpins and alignment of derived small RNAs and their total raw read frequencies described in Figure S11. Blue represents the major and yellow the minor small RNA derived from the atypical hairpin.

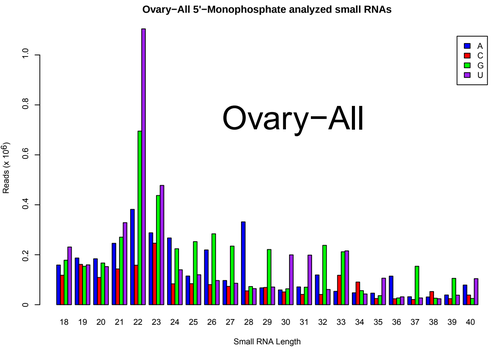

Testis−G 5'−Monophosphate analyzed small RNAs
Testis−G
A
C
G
U
Reads (x 10^6)
Small RNA Length

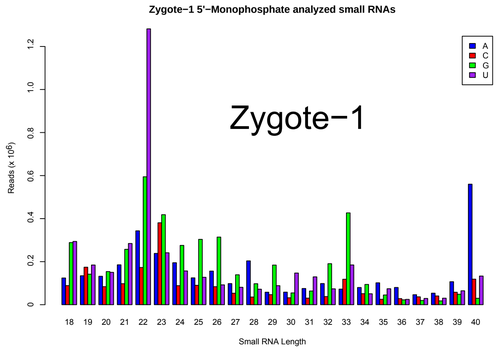

Testis−1 5'−Monophosphate analyzed small RNAs
Testis−1
A
C
G
U
Reads (x 10^6)
Small RNA Length

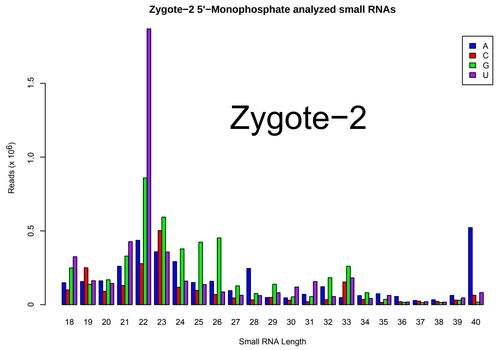

Testis−2 5'−Monophosphate analyzed small RNAs
Testis−2
A
C
G
U
Reads (x 10^6)
Small RNA Length

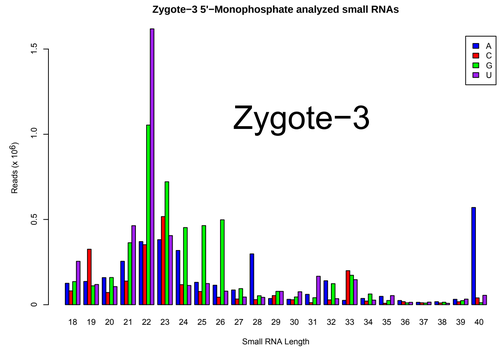

Spermatids 5'−Monophosphate analyzed small RNAs
Wang et al.
Supplementary Figure 1
Spermatids
A
C
G
U
Reads (x 10^6)
Small RNA Length

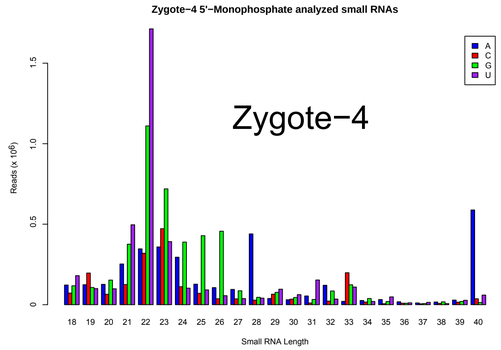

Ovary−G 5'−Monophosphate analyzed small RNAs
Ovary−G
A
C
G
U
Reads (x 10^6)
Small RNA Length

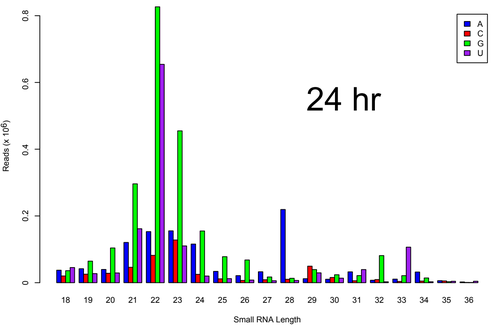

Ovary−All 5'−Monophosphate analyzed small RNAs
Ovary−All
A
C
G
U
Reads (x 10^6)
Small RNA Length

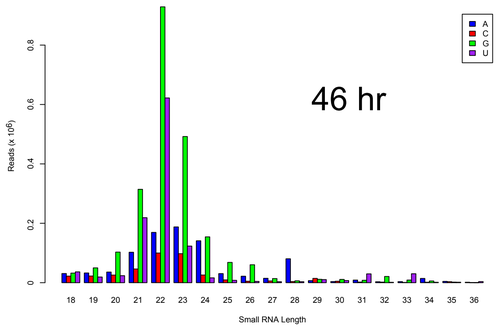

Zygote−1 5'−Monophosphate analyzed small RNAs
Zygote−1
A
C
G
U
Reads (x 10^6)
Small RNA Length

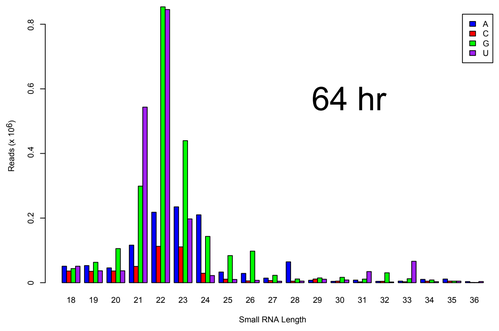

Zygote−2 5'−Monophosphate analyzed small RNAs
Zygote−2
A
C
G
U
Reads (x 10^6)
Small RNA Length

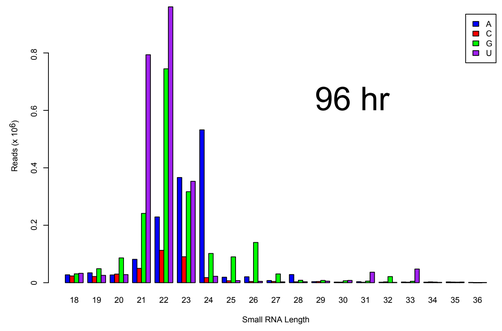

Zygote−3 5'−Monophosphate analyzed small RNAs
Zygote−3
A
C
G
U
Reads (x 10^6)
Small RNA Length

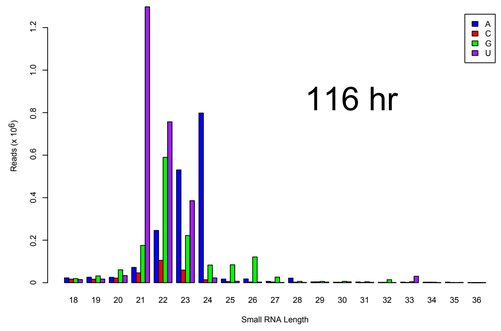

Zygote−4 5'−Monophosphate analyzed small RNAs
Zygote−4
A
C
G
U
Reads (x 10^6)
Small RNA Length

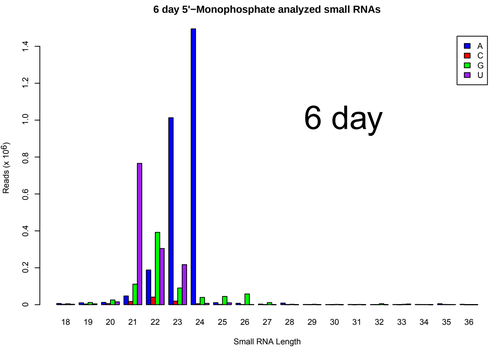

24 hr 5'−Monophosphate analyzed small RNAs
24 hr
A
C
G
U
Reads (x 10^6)
Small RNA Length

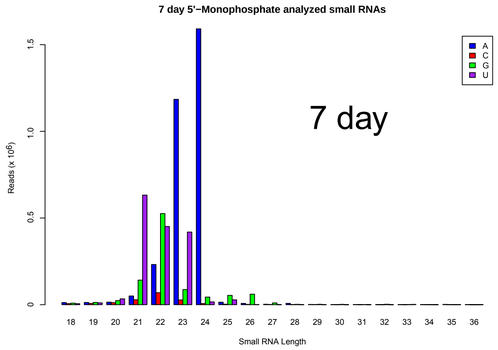

46 hr 5'−Monophosphate analyzed small RNAs
46 hr
A
C
G
U
Reads (x 10^6)
Small RNA Length

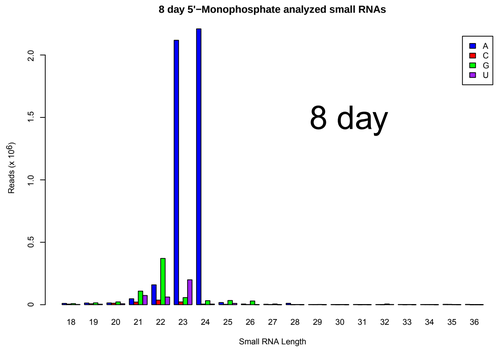

64 hr 5'−Monophosphate analyzed small RNAs
64 hr
A
C
G
U
Reads (x 10^6)
Small RNA Length

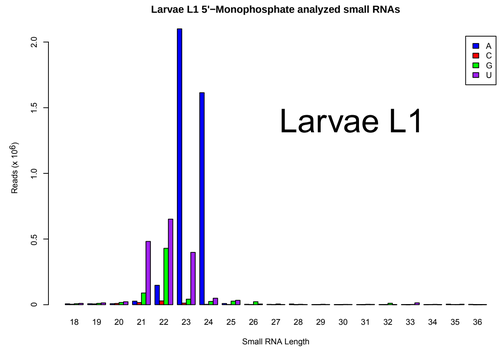

96 hr 5'−Monophosphate analyzed small RNAs
96 hr
A
C
G
U
Reads (x 10^6)
Small RNA Length

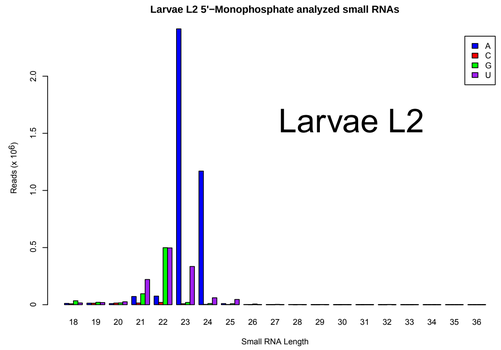

116 hr 5'−Monophosphate analyzed small RNAs
116 hr
A
C
G
U
Reads (x 10^6)
Small RNA Length

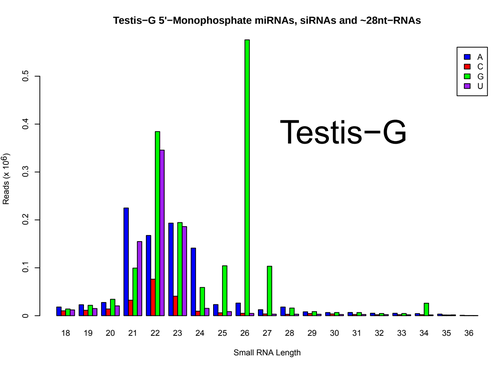

6 day 5'−Monophosphate analyzed small RNAs
6 day
A
C
G
U
Reads (x 10^6)
Small RNA Length

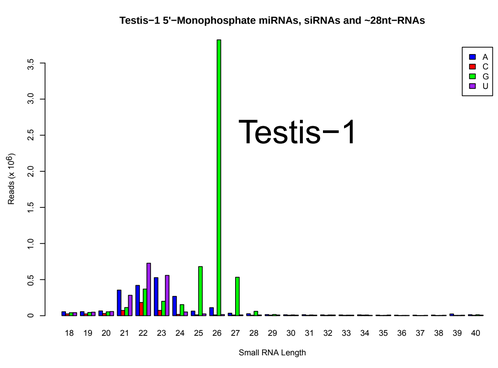

7 day 5'−Monophosphate analyzed small RNAs
7 day
A
C
G
U
Reads (x 10^6)
Small RNA Length

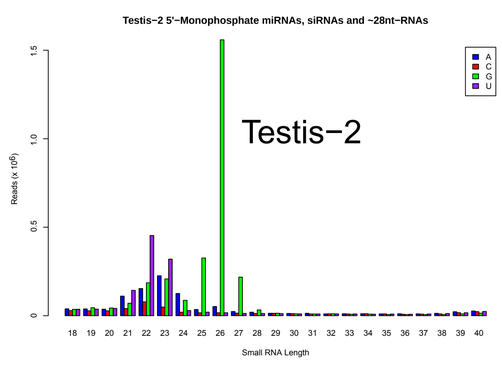

8 day 5'−Monophosphate analyzed small RNAs
8 day
A
C
G
U
Reads (x 10^6)
Small RNA Length

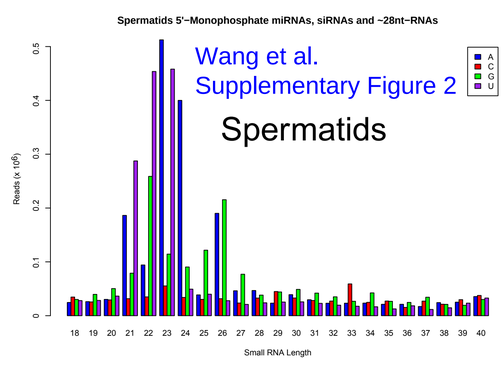

Larvae L1 5'−Monophosphate analyzed small RNAs
Larvae L1
A
C
G
U
Reads (x 10^6)
Small RNA Length

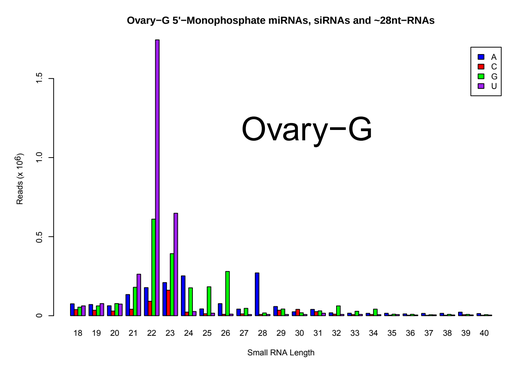

Larvae L2 5'−Monophosphate analyzed small RNAs
Larvae L2
A
C
G
U
Reads (x 10^6)
Small RNA Length

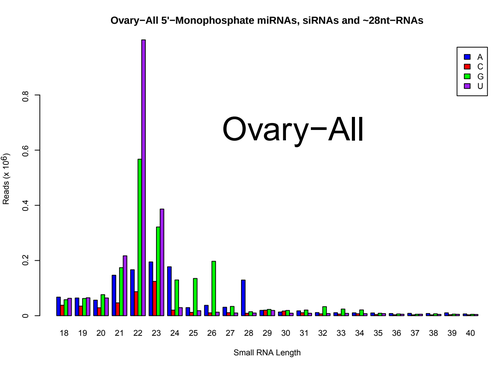

Testis−G 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Testis−G
Reads (x 10^6)
Small RNA Length
A
C
G
U

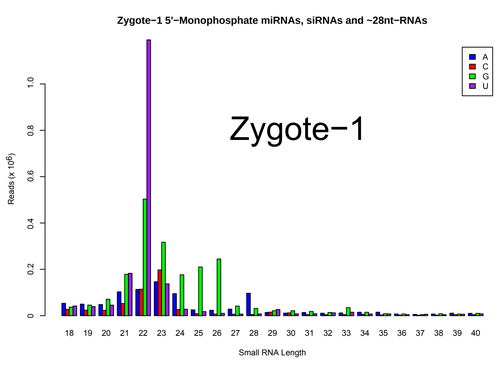

Testis−1 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Testis−1
Reads (x 10^6)
Small RNA Length
A
C
G
U

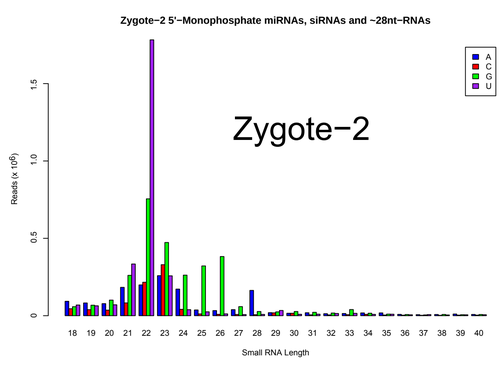

Testis−2 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Testis−2
Reads (x 10^6)
Small RNA Length
A
C
G
U

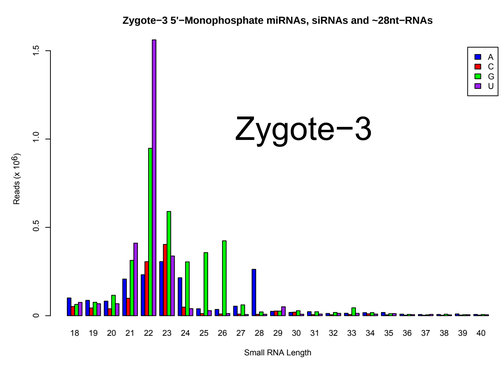

Spermatids 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Wang et al.
Supplementary Figure 2
Spermatids
Reads (x 10^6)
Small RNA Length
A
C
G
U

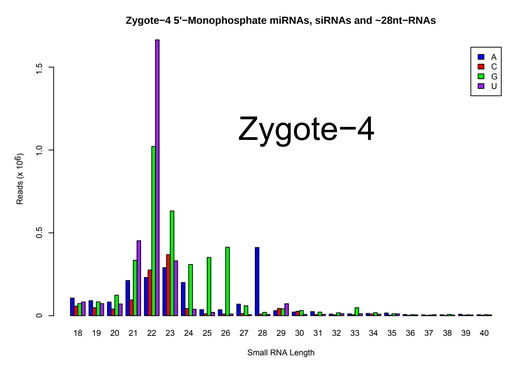

Ovary−G 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Ovary−G
Reads (x 10^6)
Small RNA Length
A
C
G
U

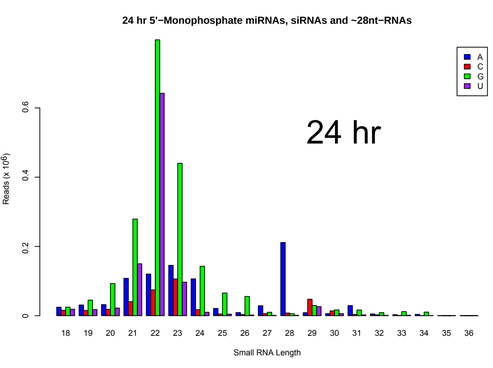

Ovary−All 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Ovary−All
Reads (x 10^6)
Small RNA Length
A
C
G
U

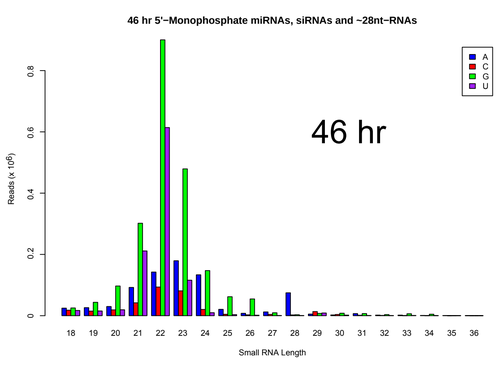

Zygote−1 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−1
Reads (x 10^6)
Small RNA Length
A
C
G
U

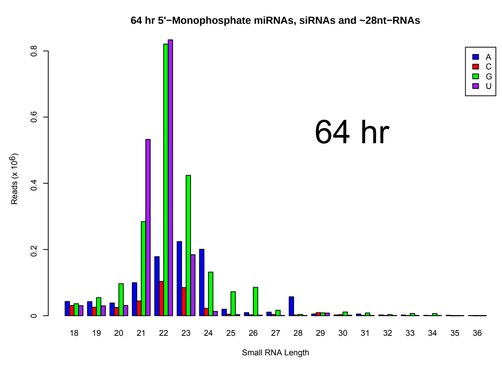

Zygote−2 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−2
Reads (x 10^6)
Small RNA Length
A
C
G
U

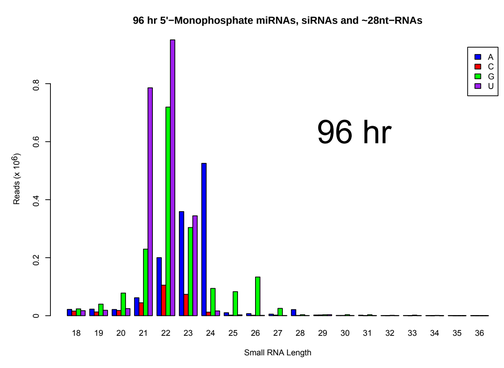

Zygote−3 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−3
Reads (x 10^6)
Small RNA Length
A
C
G
U

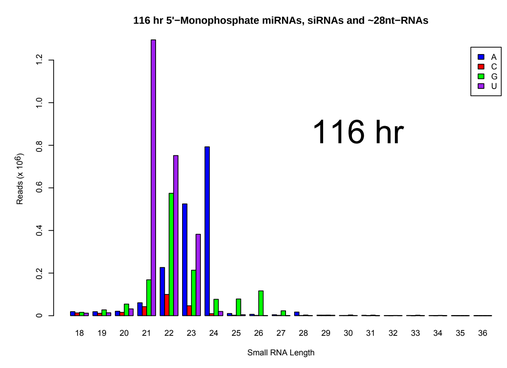

Zygote−4 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−4
Reads (x 10^6)
Small RNA Length
A
C
G
U

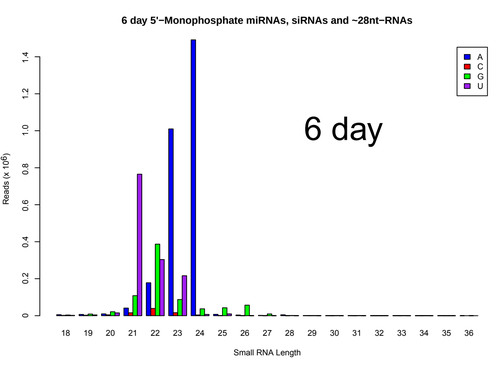

24 hr 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
24 hr
Reads (x 10^6)
Small RNA Length
A
C
G
U

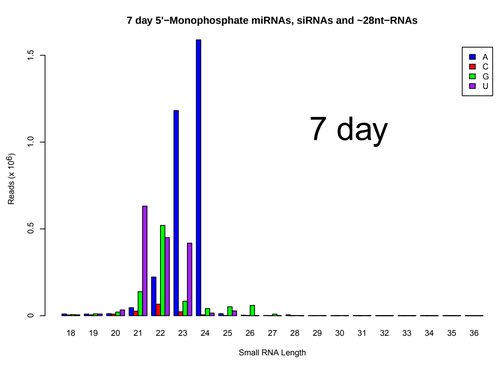

46 hr 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
46 hr
Reads (x 10^6)
Small RNA Length
A
C
G
U

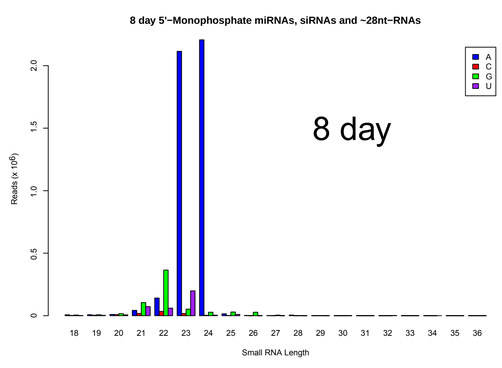

64 hr 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
64 hr
Reads (x 10^6)
Small RNA Length
A
C
G
U

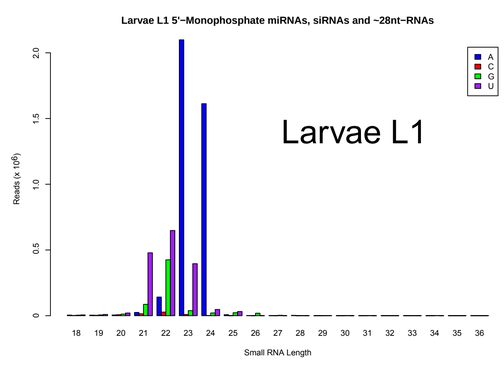

96 hr 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
96 hr
Reads (x 10^6)
Small RNA Length
A
C
G
U

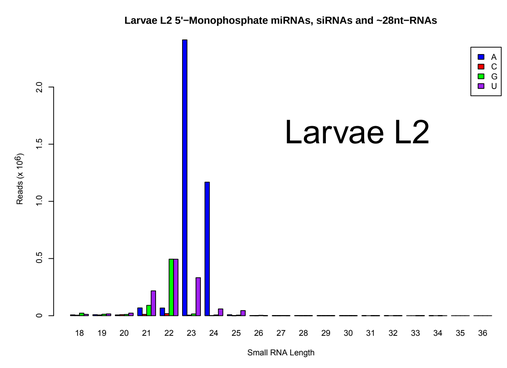

116 hr 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
116 hr
Reads (x 10^6)
Small RNA Length
A
C
G
U


6 day 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
6 day
Reads (x 10^6)
Small RNA Length
A
C
G
U

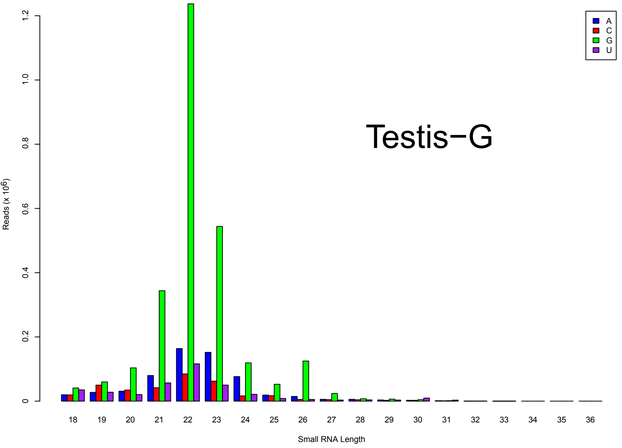

7 day 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
7 day
Reads (x 10^6)
Small RNA Length
A
C
G
U

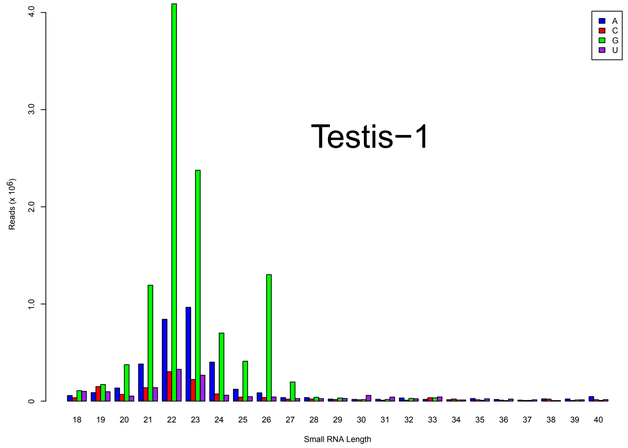

8 day 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
8 day
Reads (x 10^6)
Small RNA Length
A
C
G
U

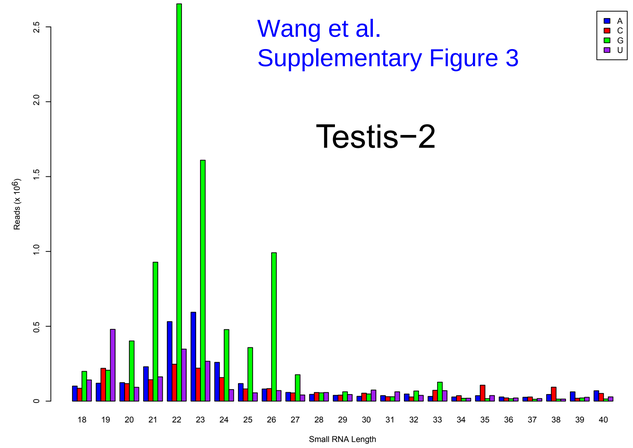

Larvae L1 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Larvae L1
Reads (x 10^6)
Small RNA Length
A
C
G
U

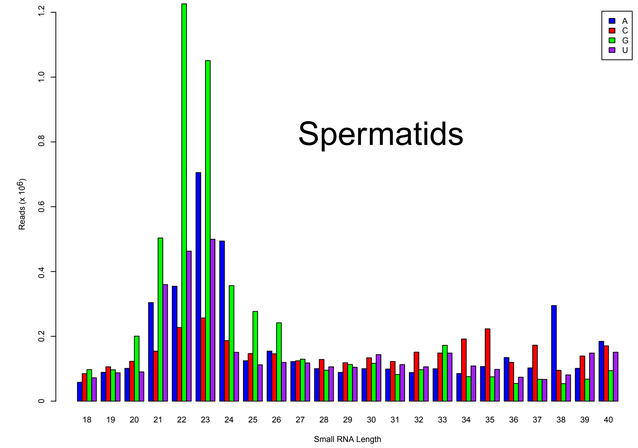

Larvae L2 5′−Monophosphate miRNAs, siRNAs and ~28nt−RNAs
Larvae L2
Reads (x 10^6)
Small RNA Length
A
C
G
U

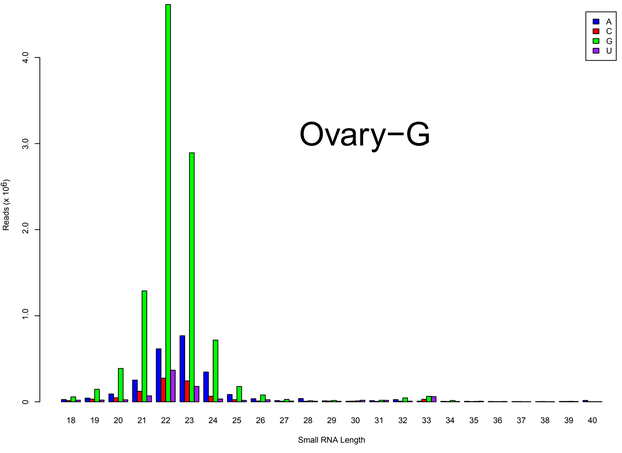
Wang et al.
Supplementary Figure 3

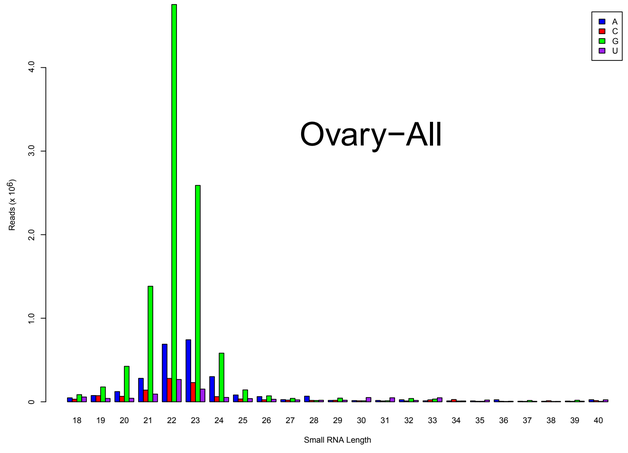


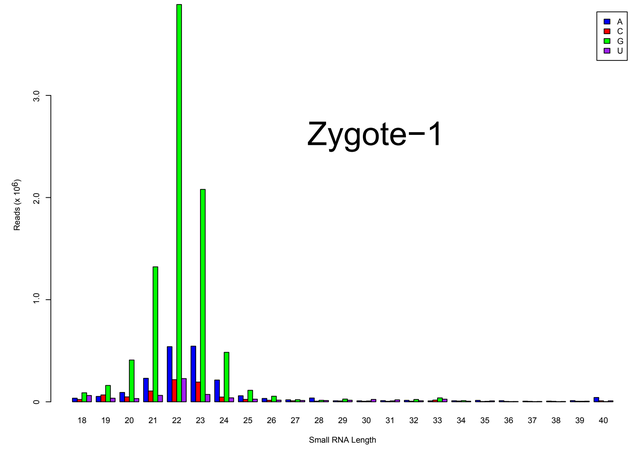


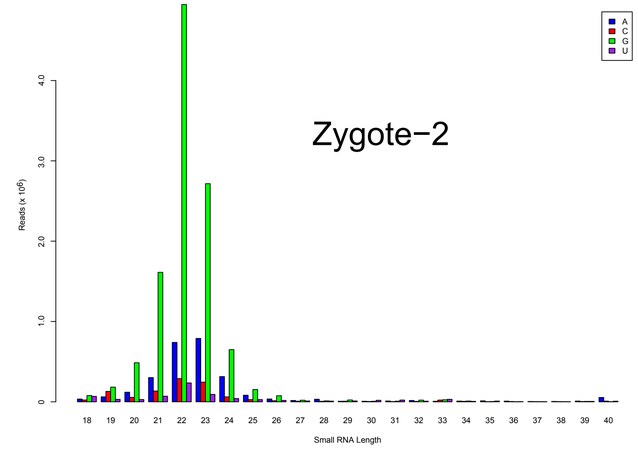


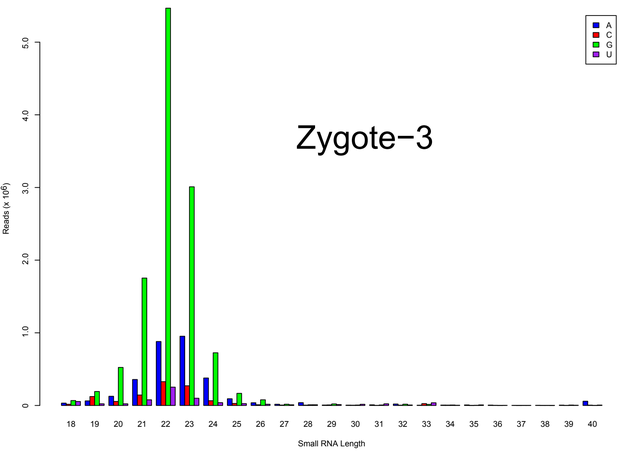


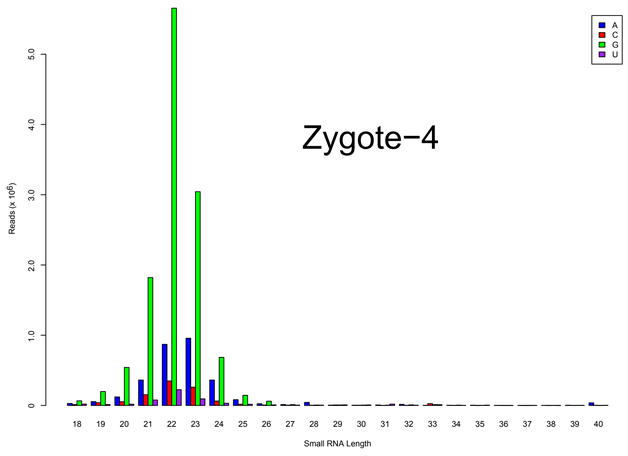


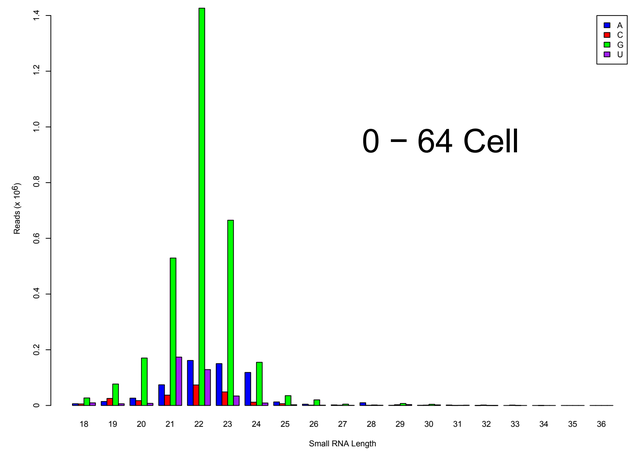


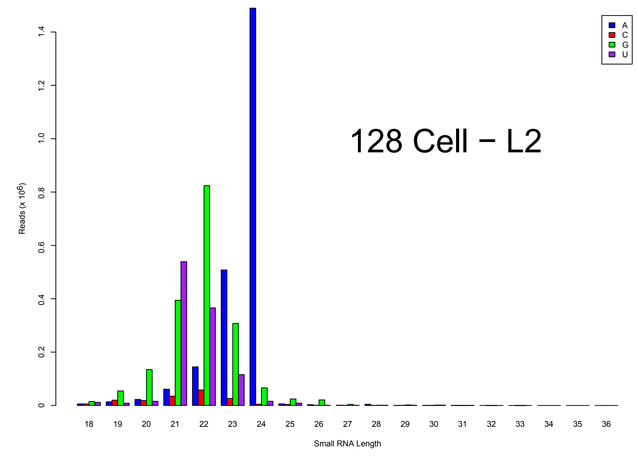


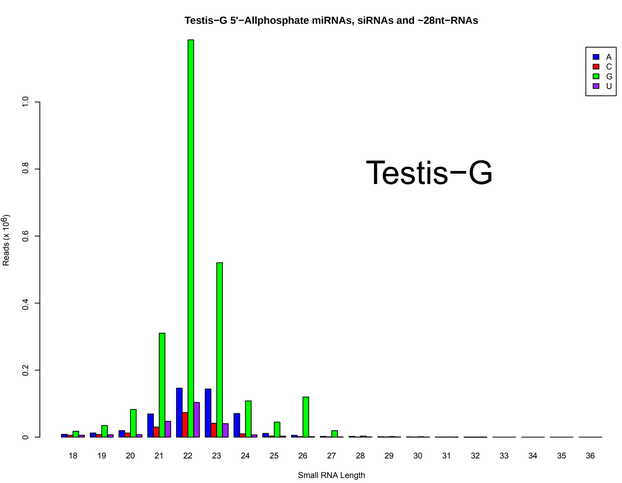


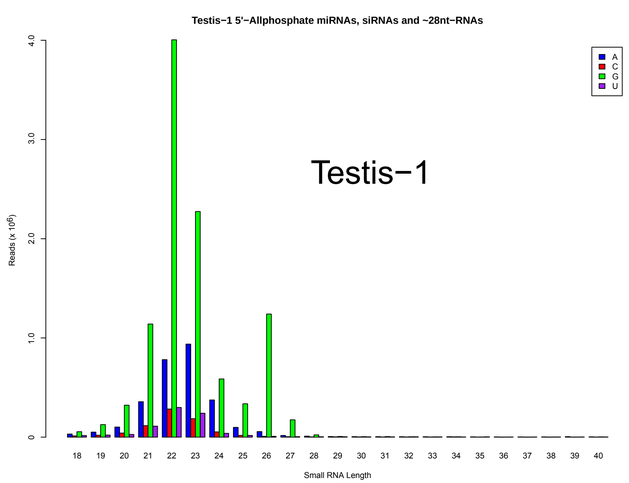


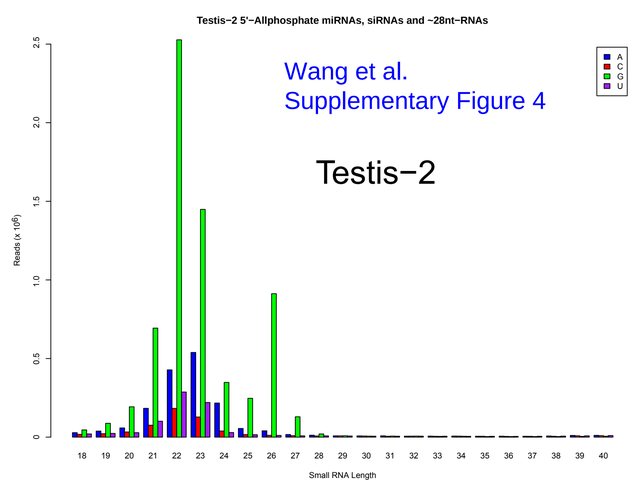


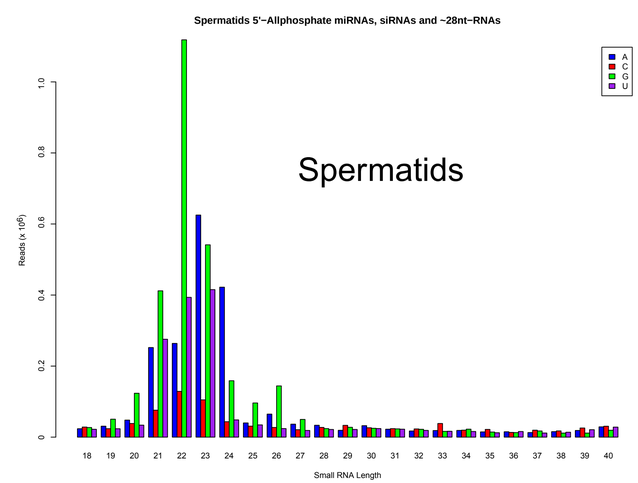


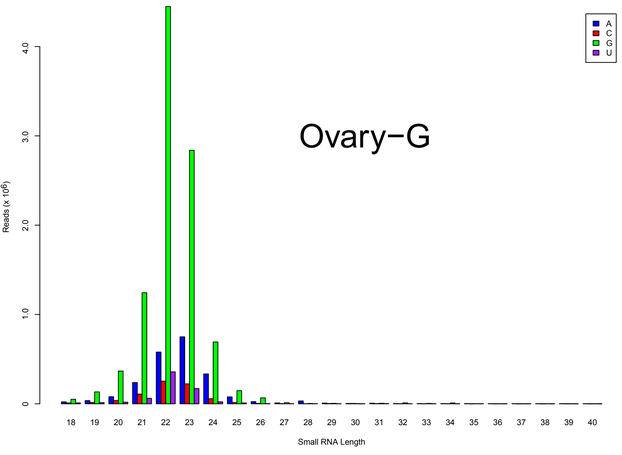


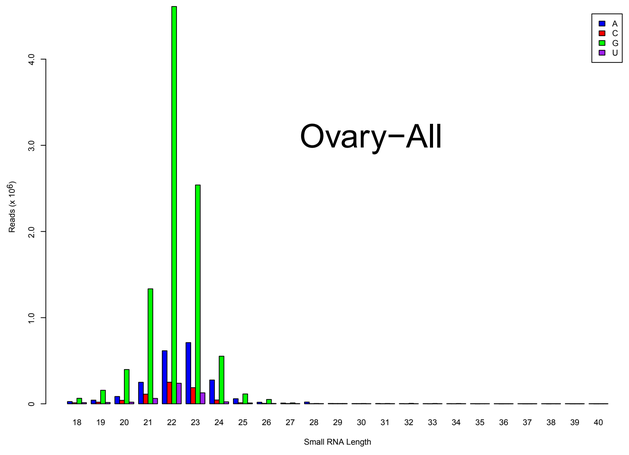

Testis−G 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Testis−G
A
C
G
U
Reads (x 10^6)
Small RNA Length

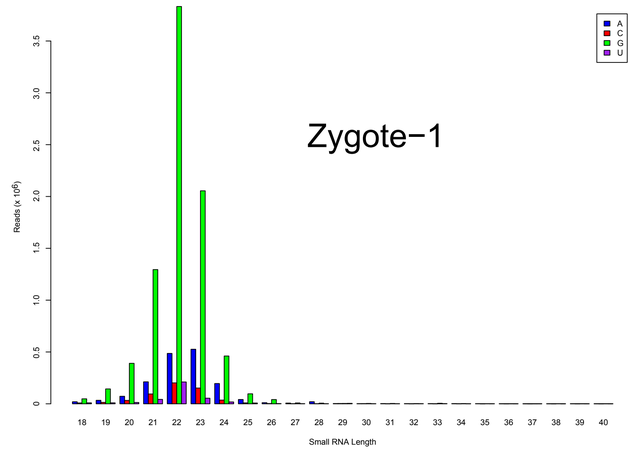

Testis−1 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Testis−1
A
C
G
U
Reads (x 10^6)
Small RNA Length

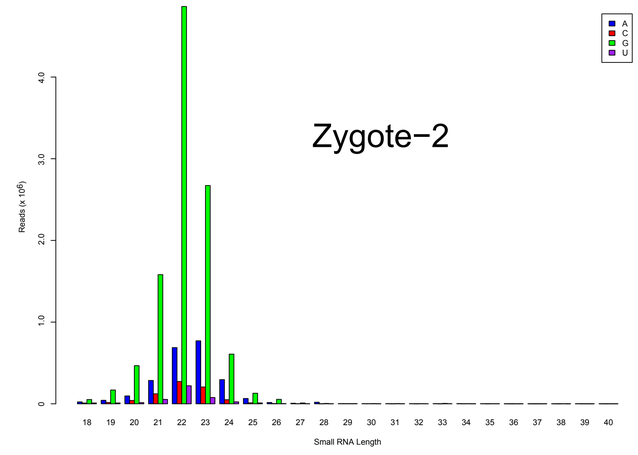

Testis−2 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Wang et al.
Supplementary Figure 4
Testis−2
A
C
G
U
Reads (x 10^6)
Small RNA Length

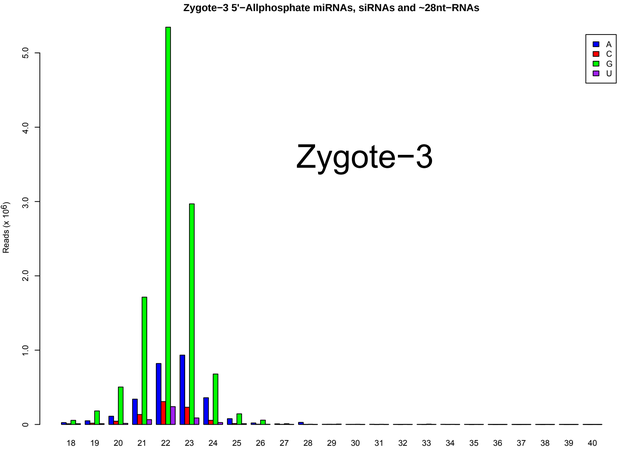

Spermatids 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Spermatids
A
C
G
U
Reads (x 10^6)
Small RNA Length

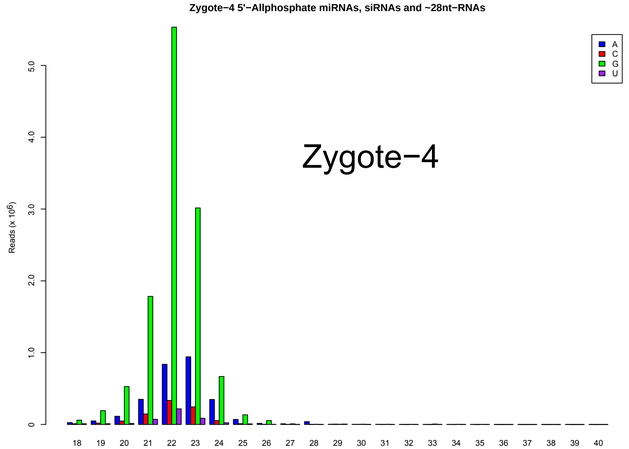

Ovary−G 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Ovary−G
A
C
G
U
Reads (x 10^6)
Small RNA Length

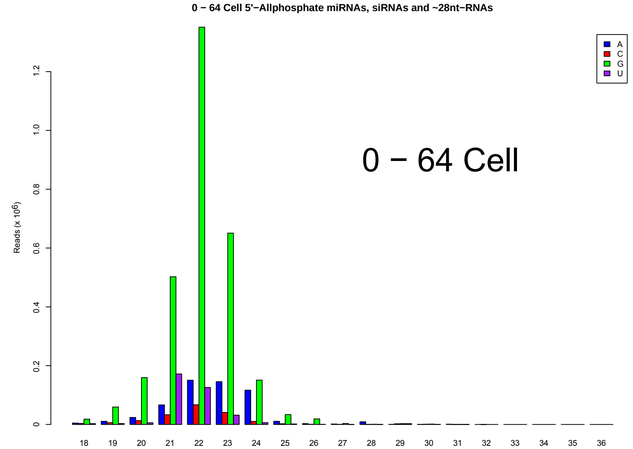

Ovary−All 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Ovary−All
A
C
G
U
Reads (x 10^6)
Small RNA Length

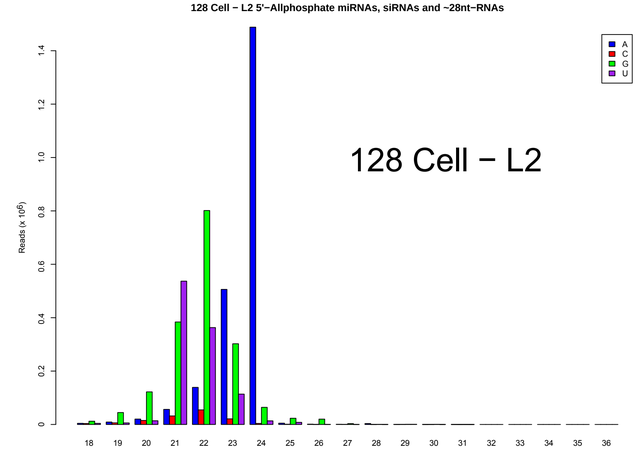

Zygote−1 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−1
A
C
G
U
Reads (x 10^6)
Small RNA Length


Zygote−2 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−2
A
C
G
U
Reads (x 10^6)
Small RNA Length


Zygote−3 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−3
A
C
G
U
Reads (x 10^6)
Small RNA Length


Zygote−4 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
Zygote−4
A
C
G
U
Reads (x 10^6)
Small RNA Length


0 − 64 Cell 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
0 − 64 Cell
A
C
G
U
Reads (x 10^6)
Small RNA Length


128 Cell − L2 5'−Allphosphate miRNAs, siRNAs and ~28nt−RNAs
128 Cell − L2
A
C
G
U
Reads (x 10^6)
Small RNA Length

```
#asu-lin-4
UUGCGACCUUCUCCCUGAGACCUCUGCUGUGACAGUACGCAGGGUCACAGUAAGAGCACCUCAGGGGCCAGGUCUCA
.((.(((((..(((((((((..((((((((((((.(....)...)))))))).))))...)))))))))..)))))).))
Total sRNA: 106647 shared 5' end with miRNA: 1857 shared 3' end with miRNA: 1322
miRNA
..........UCCCUGAGACCUCUGCUGUGA.......................................... 21 85225
Shared 5' Terminus
..........UCCCUGAGACCUCUGCUG.............................................. 18 153
..........UCCCUGAGACCUCUGCUGU............................................. 19 359
..........UCCCUGAGACCUCUGCUGUG............................................ 20 1037
..........UCCCUGAGACCUCUGCUGUGAC.......................................... 22 308
Shared 3' Terminus
............CUGAGACCUCUGCUGUGA.......................................... 18 219
............CCUGAGACCUCUGCUGUGA.......................................... 19 1064
Subsequence
Others
.........................................CACAGUAAGAGCACCUCAGGGGCC........ 24 42
.........................................CACAGUAAGAGCACCUCAGGGGCCA....... 25 31
.........................................ACAGUAAGAGCACCUCAGG............ 19 113
.........................................ACAGUAAGAGCACCUCAGGG........... 20 169
.........................................ACAGUAAGAGCACCUCAGGGG.......... 21 430
.........................................ACAGUAAGAGCACCUCAGGGGC......... 22 1316
.........................................ACAGUAAGAGCACCUCAGGGGCC........ 23 13012
.........................................ACAGUAAGAGCACCUCAGGGGCCA....... 24 2596
.........................................CAGUAAGAGCACCUCAGGGGCC........ 22 109
.........................................AGUAAGAGCACCUCAGGGGCC........ 21 83
.........................................GUAAGAGCACCUCAGGGGCC........ 20 53
.........................................GUAAGAGCACCUCAGGGGCCA....... 21 74


#asu-let-7
UCUGCUCGUUGAGGUAGUAGGUUGUAUAGUUGCGAGCUGCAUCCUUUCGAGAAACUGUCCAGCCUGCUAGCUUGCCGCGCGGAC
(((((.((..(((.((((((((((.((((((.((((.........))))...))))))).)))))))))).)))..)).)))))
Total sRNA: 103298 shared 5' end with miRNA: 15114 shared 3' end with miRNA: 422
miRNA
.........UGAGGUAGUAGGUUGUAUAGUU.......................................................... 22 87428
Shared 5' Terminus
.........UGAGGUAGUAGGUUGUAU.............................................................. 18 298
.........UGAGGUAGUAGGUUGUAUA............................................................. 19 889
.........UGAGGUAGUAGGUUGUAUAG............................................................ 20 1175
.........UGAGGUAGUAGGUUGUAUAGU........................................................... 21 9793
.........UGAGGUAGUAGGUUGUAUAGUUG.......................................................... 23 2166
.........UGAGGUAGUAGGUUGUAUAGUUGC......................................................... 24 793
Shared 3' Terminus
............GUAGUAGGUUGUAUAGUU.......................................................... 18 96
............GGUAGUAGGUUGUAUAGUU.......................................................... 19 273
..........GAGGUAGUAGGUUGUAUAGUU.......................................................... 21 38
Subsequence
Others
.....................................................CUGUCCAGCCUGCUAGCUUGCC........ 22 125


#asu-miR-1
UUCUGUUGCAUCGUACUUCUUUACAUCGCCAUACUGGUAUUUCAAAGAGCUAUGGAAUGUAAAGAAGUAUGUAGUUACUGAA
.((.((.((..((((((((((((((((..(((((((..(......)..)).)))))).))))))))))))))))..)).)).)).
Total sRNA: 487949 shared 5' end with miRNA: 157276 shared 3' end with miRNA: 1232
miRNA
.................................................UGGAAUGUAAAGAAGUAUGUA......... 21 327886
Shared 5' Terminus
.................................................UGGAAUGUAAAGAAGUAU............ 18 1823
.................................................UGGAAUGUAAAGAAGUAUG........... 19 4813
.................................................UGGAAUGUAAAGAAGUAUGU.......... 20 143184
.................................................UGGAAUGUAAAGAAGUAUGUAG........ 22 7348
.................................................UGGAAUGUAAAGAAGUAUGUAGU....... 23 102
Shared 3' Terminus
.....................................................AAUGUAAAGAAGUAUGUA......... 18 360
.....................................................GAAUGUAAAGAAGUAUGUA......... 19 191
.....................................................GGAAUGUAAAGAAGUAUGUA......... 20 148
.....................................................AUGGAAUGUAAAGAAGUAUGUA......... 22 452
Subsequence
Others
```

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..........CGUACUUCUUUACAUCGCCAUA.................................................... 22 213
.............................CUGGUAUUUCAAAGAGCUA.............................. 19 515
.................................................AUGGAAUGUAAAGAAGUAUGU.......... 21 177


#asu-miR-2a
GUUCCAGCACGUCAAAGUGGUGGUGAUUUGUUGUGGAUAAGCUCAUAUCACAGCCAGCUUUGAUGUGCUGUGGCAGUC
((..((((((((((((((((.(((((.((..((......)).)).)))))).)))).)))))))))))))..))....
Total sRNA: 155050 shared 5' end with miRNA: 60059 shared 3' end with miRNA: 429
miRNA
.........................................UAUCACAGCCAGCUUUGAUGUGC.......... 23 93033
Shared 5' Terminus
.........................................UAUCACAGCCAGCUUUGA.............. 18 2976
.........................................UAUCACAGCCAGCUUUGAU............. 19 1695
.........................................UAUCACAGCCAGCUUUGAUG............ 20 172
.........................................UAUCACAGCCAGCUUUGAUGU........... 21 9753
.........................................UAUCACAGCCAGCUUUGAUGUG.......... 22 45086
.........................................UAUCACAGCCAGCUUUGAUGUGCU........ 24 376
Shared 3' Terminus
.................................................CAGCCAGCUUUGAUGUGC.......... 18 40
................................................ACAGCCAGCUUUGAUGUGC.......... 19 307
.............................................AUCACAGCCAGCUUUGAUGUGC.......... 22 41
Subsequence
................................................ACAGCCAGCUUUGAUGUG.......... 18 181
Others
........ACGUCAAAGUGGUGGUGAUUUG.................................................... 22 131
........CGUCAAAGUGGUGGUGAUUUG.................................................... 21 940
........CGUCAAAGUGGUGGUGAUUUGUUGUGGAUAAGCUCA.................................... 36 65


#asu-miR-2b
GAACUCUGGCGUGCUUAAUCGUUCAGUGAUUCAUAGUGAAUAGCUUGUAUCACAGUUCGAUUUGGCCCGCUAGUGUCACUG
((...((((((.(((.(((((..(.(((((.((.(((.....)))))).)))))..)..)))))).)))..)))))..))....
Total sRNA: 1981399 shared 5' end with miRNA: 367975 shared 3' end with miRNA: 2586
miRNA
.............................................UAUCACAGUUCGAUUUGGCCCG........... 22 1600387
Shared 5' Terminus
.............................................UAUCACAGUUCGAUUUGG.............. 18 2312
.............................................UAUCACAGUUCGAUUUGGC............. 19 16207
.............................................UAUCACAGUUCGAUUUGGCC............ 20 106888
.............................................UAUCACAGUUCGAUUUGGCCC........... 21 234824
.............................................UAUCACAGUUCGAUUUGGCCCGC......... 23 7623
.............................................UAUCACAGUUCGAUUUGGCCCGCU........ 24 119
Shared 3' Terminus
.................................................ACAGUUCGAUUUGGCCCG........... 18 1800
................................................CACAGUUCGAUUUGGCCCG........... 19 205
...............................................UCACAGUUCGAUUUGGCCCG........... 20 203
.............................................AUCACAGUUCGAUUUGGCCCG........... 21 276
Subsequence
Others
..........UGCUUAAUCGUUCAGUGAUUC.................................................. 21 191
..........UGCUUAAUCGUUCAGUGAUUCA................................................. 22 9773


#asu-miR-7
ACUCCCGGGUGGAAGACUGGUGAUUUUGUUGUUUGAGCUCAUCCAUAACAGCAAAUCCGUAGUCUCCACCUGGCAACUCCUAA
....((((((((((.(((((..(((((.((((((.((.....)).)))))))))))..))))))))))))))).........
Total sRNA: 7946 shared 5' end with miRNA: 1667 shared 3' end with miRNA: 50
miRNA
.........UGGAAGACUGGUGAUUUUGUUGUU................................................ 24 6168
Shared 5' Terminus
.........UGGAAGACUGGUGAUUUU...................................................... 18 32
.........UGGAAGACUGGUGAUUUUG..................................................... 19 17
.........UGGAAGACUGGUGAUUUUGU.................................................... 20 25
.........UGGAAGACUGGUGAUUUUGUU................................................... 21 43
.........UGGAAGACUGGUGAUUUUGUUG.................................................. 22 34
.........UGGAAGACUGGUGAUUUUGUUGU................................................. 23 907
.........UGGAAGACUGGUGAUUUUGUUGUUU............................................... 25 609
Shared 3' Terminus
..............ACUGGUGAUUUUGUUGUU.................................................. 18 6
.............GACUGGUGAUUUUGUUGUU.................................................. 19 24
```

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.............AGACUGGUGAUUUUGUUGUU..................................................... 20 13
.............AAGACUGGUGAUUUUGUUGUU..................................................... 21 3
............GAAGACUGGUGAUUUUGUUGUU..................................................... 22 3
Subsequence
............GAAGACUGGUGAUUUUGUUGU..................................................... 21 4
.............AGACUGGUGAUUUUGUUGU..................................................... 19 3
..............GACUGGUGAUUUUGUUGU..................................................... 18 6
Others
..............GACUGGUGAUUUUGUUGUUU.................................................... 20 3
................................................CAGCAAAUCCGUAGUCUCCACC.............. 22 32


#asu-miR-9
GCAAUUUCUUUGGUUAUCUAGCUGUAUGAGUACCGCGUUUAGUCGUCAUAAAGCUGGACGACCGAAGUAAUGGCCGCU
((.(((.(((((((..(((((((.(((((..((........))..)))))).)))))))..)))))))..))).))....
Total sRNA: 605982 shared 5' end with miRNA: 234930 shared 3' end with miRNA: 1974
miRNA
......UCUUUGGUUAUCUAGCUGUAUGA..................................................... 23 343507
Shared 5' Terminus
......UCUUUGGUUAUCUAGCUG.......................................................... 18 430
......UCUUUGGUUAUCUAGCUGU......................................................... 19 3810
......UCUUUGGUUAUCUAGCUGUA........................................................ 20 2709
......UCUUUGGUUAUCUAGCUGUAU....................................................... 21 22291
......UCUUUGGUUAUCUAGCUGUAUG...................................................... 22 204274
......UCUUUGGUUAUCUAGCUGUAUGAG..................................................... 24 1354
Shared 3' Terminus
..........UGGUUAUCUAGCUGUAUGA...................................................... 19 190
.........UUGGUUAUCUAGCUGUAUGA...................................................... 20 555
........UUUGGUUAUCUAGCUGUAUGA...................................................... 21 331
.......CUUUGGUUAUCUAGCUGUAUGA...................................................... 22 230
.....UUCUUUGGUUAUCUAGCUGUAUGA...................................................... 24 616
Subsequence
.......CUUUGGUUAUCUAGCUGUAUG....................................................... 21 131
........UUUGGUUAUCUAGCUGUAUG....................................................... 20 195
.........UUGGUUAUCUAGCUGUAUG....................................................... 19 318
..........UGGUUAUCUAGCUGUAUG....................................................... 18 135
Others
.....UUCUUUGGUUAUCUAGCUGUAUG...................................................... 23 1324
................................................AUAAAGCUGGACGACCGAAG.............. 20 101
................................................AUAAAGCUGGACGACCGAAGU............. 21 1184
................................................AUAAAGCUGGACGACCGAAGUA............ 22 3550
................................................AUAAAGCUGGACGACCGAAGUAA........... 23 16125
................................................AUAAAGCUGGACGACCGAAGUAAU.......... 24 139
.................................................UAAAGCUGGACGACCGAAGUA............ 21 196
.................................................UAAAGCUGGACGACCGAAGUAA........... 22 1557


#asu-miR-34
UAAGUCACCGGCUGGCAGUGUGGUUAGCUGGUUGUCAGAUGUGAGACAACGGCUAUCACCACUGCCGUCCUGGUGGUUCGUCC
..(..((((((.(((((((((((.(((((.(((((........)))))))))))))).)))))))..))))))..)..)))
Total sRNA: 1812490 shared 5' end with miRNA: 171673 shared 3' end with miRNA: 9167
miRNA
............UGGCAGUGUGGUUAGCUGGUUGU................................................ 23 1630779
Shared 5' Terminus
............UGGCAGUGUGGUUAGCUG...................................................... 18 997
............UGGCAGUGUGGUUAGCUGG..................................................... 19 13677
............UGGCAGUGUGGUUAGCUGGU.................................................... 20 6700
............UGGCAGUGUGGUUAGCUGGUU................................................... 21 22983
............UGGCAGUGUGGUUAGCUGGUUG.................................................. 22 113359
............UGGCAGUGUGGUUAGCUGGUUGUC................................................ 24 13437
............UGGCAGUGUGGUUAGCUGGUUGUCA............................................... 25 168
............UGGCAGUGUGGUUAGCUGGUUGUCAGAUGUGA....................................... 32 104
Shared 3' Terminus
..................GUGUGGUUAGCUGGUUGU.............................................. 18 3461
.................AGUGUGGUUAGCUGGUUGU.............................................. 19 2177
...............CAGUGUGGUUAGCUGGUUGU.............................................. 20 1249
..............GCAGUGUGGUUAGCUGGUUGU.............................................. 21 290
.............GGCAGUGUGGUUAGCUGGUUGU.............................................. 22 647
...........CUGGCAGUGUGGUUAGCUGGUUGU.............................................. 24 1342
Subsequence
...............CAGUGUGGUUAGCUGGUUG.............................................. 19 101
```

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.................AGUGUGGUUAGCUGGUUG..................................................... 18 157
Others
.............................................AACGGCUAUCACCACUGCCGUCC.............. 23 104


#asu-miR-36a
CGGUGUGUAGUGGAUGUACCCUCGGUUCGAUGUUUCUUUACUAUCAUCACCGGGUAUACAUUCAUCAAAUACCGUAGCUCA
((((((...((((((((((..((((((..((((............))))))))))..))))))))).))))))).......
Total sRNA: 173670 shared 5' end with miRNA: 19549 shared 3' end with miRNA: 549
miRNA
.............................................UCACCGGGUAUACAUUCAUCAA.............. 22 141418
Shared 5' Terminus
.............................................UCACCGGGUAUACAUUCA.................. 18 58
.............................................UCACCGGGUAUACAUUCAU.................. 19 81
.............................................UCACCGGGUAUACAUUCAUC................. 20 550
.............................................UCACCGGGUAUACAUUCAUCA................ 21 15617
.............................................UCACCGGGUAUACAUUCAUCAAA.............. 23 3238
Shared 3' Terminus
................................................CGGGUAUACAUUCAUCAA.............. 18 96
................................................ACCGGGUAUACAUUCAUCAA.............. 20 265
................................................CACCGGGUAUACAUUCAUCAA.............. 21 52
.............................................AUCACCGGGUAUACAUUCAUCAA.............. 23 89
Subsequence
Others
........AGUGGAUGUACCCUCGGUUCGA..................................................... 22 103
........AGUGGAUGUACCCUCGGUUCGAU.................................................... 23 323
........AGUGGAUGUACCCUCGGUUCGAUG................................................... 24 11061
........AGUGGAUGUACCCUCGGUUCGAUGU.................................................. 25 408


#asu-miR-36b
GUGGCCGAUCGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGGUGCUCACCGGGUGAACAUUCAUUAUCGGCCCAUUG
(.(((((((.((((((((((..(..((((.((((.(((....)))))))..))))).)..)))))))))..)))))))....
Total sRNA: 24273 shared 5' end with miRNA: 1684 shared 3' end with miRNA: 76
miRNA
.............................................UCACCGGGUGAACAUUCAUUAU.......... 22 14919
Shared 5' Terminus
.............................................UCACCGGGUGAACAUUCA.............. 18 42
.............................................UCACCGGGUGAACAUUCAU.............. 19 6
.............................................UCACCGGGUGAACAUUCAUU............. 20 170
.............................................UCACCGGGUGAACAUUCAUUA............ 21 1448
.............................................UCACCGGGUGAACAUUCAUUAUC.......... 23 17
Shared 3' Terminus
..................................................CGGGUGAACAUUCAUUAU.......... 18 5
.................................................CCGGGUGAACAUUCAUUAU.......... 19 9
................................................ACCGGGUGAACAUUCAUUAU.......... 20 29
.............................................CACCGGGUGAACAUUCAUUAU.......... 21 6
.........................................CUCACCGGGUGAACAUUCAUUAU.......... 23 27
Subsequence
.............................................ACCGGGUGAACAUUCAUUA.......... 19 5
Others
.........CGUGAGUGUUUGCGACGGUUA..................................................... 21 19
.........CGUGAGUGUUUGCGACGGUUAG.................................................... 22 51
.........CGUGAGUGUUUGCGACGGUUAGC................................................... 23 6891
.........CGUGAGUGUUUGCGACGGUUAGCG.................................................. 24 5
.........CGUGAGUGUUUGCGACGGUUAGCGUC................................................ 26 5
.........CGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGG....................................... 35 9
.........CGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGGU...................................... 36 20
.........CGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGGUG..................................... 37 46
.........CGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGGUGC.................................... 38 321
.........CGUGAGUGUUUGCGACGGUUAGCGUCUGGUAUCGGUGCU................................... 39 14
..........GUGAGUGUUUGCGACGGUUAGC.................................................. 22 21
......................CGGUUAGCGUCUGGUAUCGGU.......................................... 21 12
......................CGGUUAGCGUCUGGUAUCGGUG......................................... 22 12
.....................GGUUAGCGUCUGGUAUCGGUGC.......................................... 22 5
.............................................CUCACCGGGUGAACAUUCAUUA.......... 22 14
```

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#asu-miR-36c
ACGUGACGGGGAUUCUACUUUUGGUGAAGCGAGCUCAGAUGACUUCACCGGGCUCGAAUCCCUGUCCUGUCAUGAUUC
(((.((((((((((....((((((((((........)).)))))))))...)))))))))).)))........
Total sRNA: 948146 shared 5' end with miRNA: 72559 shared 3' end with miRNA: 132796
miRNA
.........................................UCACCGGGCUCGAAUCCCUGUC............ 22 641611
Shared 5' Terminus
.........................................UCACCGGGCUCGAAUCCC................ 18 130
.........................................UCACCGGGCUCGAAUCCCU............... 19 402
.........................................UCACCGGGCUCGAAUCCCUG.............. 20 172
.........................................UCACCGGGCUCGAAUCCCUGU............. 21 70135
.........................................UCACCGGGCUCGAAUCCCUGUCC........... 23 1712
Shared 3' Terminus
.............................................CGGGCUCGAAUCCCUGUC............ 18 133
............................................ACCGGGCUCGAAUCCCUGUC............ 20 2500
.............................................CACCGGGCUCGAAUCCCUGUC............ 21 5879
..........................................UUCACCGGGCUCGAAUCCCUGUC............ 23 124075
.......................................CUUCACCGGGCUCGAAUCCCUGUC............ 24 121
Subsequence
.........................................CACCGGGCUCGAAUCCCUGU............. 20 488
Others
.....ACGGGGAUUCUACUUUUGGUGA..................................................... 22 118
.....ACGGGGAUUCUACUUUUGGUGAA.................................................... 23 181
.....ACGGGGAUUCUACUUUUGGUGAAG................................................... 24 139
......CGGGGAUUCUACUUUUGGU....................................................... 19 126
......CGGGGAUUCUACUUUUGGUG...................................................... 20 162
......CGGGGAUUCUACUUUUGGUGA..................................................... 21 286
......CGGGGAUUCUACUUUUGGUGAA.................................................... 22 1788
......CGGGGAUUCUACUUUUGGUGAAG................................................... 23 51389
......CGGGGAUUCUACUUUUGGUGAAGC.................................................. 24 31070
.......GGGGAUUCUACUUUUGGUGAAG.................................................... 22 331
.......GGGGAUUCUACUUUUGGUGAAGC................................................... 23 555
.........................AGCGAGCUCAGAUGACUUC.................................... 19 258
.........................................UUCACCGGGCUCGAAUCC.................. 18 147
.........................................UUCACCGGGCUCGAAUCCCUGU.............. 22 13240
.........................................CACCGGGCUCGAAUCCCUGUCC........... 22 188


#asu-miR-36d
AUCUCGCGUGGCAGGGAUUCCGCUUUUGGUGACGUGGAGAAGAAUCUUCACCGGGCAAGAAUCCCUGUCAUGUUGCCU
.....(((((((((((((((.(((..((((((...(((......)))))))))))))..)))))))))))))).....
Total sRNA: 1388325 shared 5' end with miRNA: 227465 shared 3' end with miRNA: 9200
miRNA
.............................................UCACCGGGCAAGAAUCCCUGUC......... 22 1110857
Shared 5' Terminus
.............................................UCACCGGGCAAGAAUCCC.............. 18 126
.............................................UCACCGGGCAAGAAUCCCU............. 19 534
.............................................UCACCGGGCAAGAAUCCCUG............ 20 403
.............................................UCACCGGGCAAGAAUCCCUGU.......... 21 113939
.............................................UCACCGGGCAAGAAUCCCUGUCA........ 23 112415
Shared 3' Terminus
.....................................................CGGGCAAGAAUCCCUGUC......... 18 2160
....................................................CCGGGCAAGAAUCCCUGUC......... 19 308
...................................................ACCGGGCAAGAAUCCCUGUC......... 20 4149
.................................................CACCGGGCAAGAAUCCCUGUC......... 21 288
...............................................UUCACCGGGCAAGAAUCCCUGUC......... 23 2207
Subsequence
...................................................ACCGGGCAAGAAUCCCUGU.......... 19 202
Others
..........GCAGGGAUUCCGCUUUUGGUGACG.............................................. 24 307
...........CAGGGAUUCCGCUUUUGG.................................................... 18 114
...........CAGGGAUUCCGCUUUUGGUGA................................................. 21 434
...........CAGGGAUUCCGCUUUUGGUGAC................................................ 22 319
...........CAGGGAUUCCGCUUUUGGUGACG............................................... 23 36824
...........CAGGGAUUCCGCUUUUGGUGACGU.............................................. 24 576
............AGGGAUUCCGCUUUUGGUGACG................................................ 22 215
.............................................UUCACCGGGCAAGAAUCCCUGU.......... 22 465
.............................................UUCACCGGGCAAGAAUCCCUGUCA........ 24 245
...............................................CACCGGGCAAGAAUCCCUGUCA........ 22 154
...............................................ACCGGGCAAGAAUCCCUGUCA........ 21 364
```

```
#asu-miR-36e
AUGUGACGUGACGGGGAUUCUACUCUUGGUGAAGCGAGCUCAGAUGACUUCACCGGGCUCGAAUCCUUGUCCUGUCAUGAU
..((((((.((((((((((....((((((((((........)).)))))))))...)))))))))).))))))...
Total sRNA: 157812 shared 5' end with miRNA: 6323 shared 3' end with miRNA: 26245
miRNA
.............................................UCACCGGGCUCGAAUCCUUGUC..... 22 108762
Shared 5' Terminus
.............................................UCACCGGGCUCGAAUCCU..... 18 138
.............................................UCACCGGGCUCGAAUCCUU..... 19 141
.............................................UCACCGGGCUCGAAUCCUUG..... 20 107
.............................................UCACCGGGCUCGAAUCCUUGU..... 21 5793
.............................................UCACCGGGCUCGAAUCCUUGUCC..... 23 141
Shared 3' Terminus
..................................................CGGGCUCGAAUCCUUGUC..... 18 159
.................................................CCGGGCUCGAAUCCUUGUC..... 19 50
................................................ACCGGGCUCGAAUCCUUGUC..... 20 620
...............................................CACCGGGCUCGAAUCCUUGUC..... 21 1176
............................................UUCACCGGGCUCGAAUCCUUGUC..... 23 24228
Subsequence
.............................................CACCGGGCUCGAAUCCUUGU..... 20 118
Others
.........ACGGGGAUUCUACUCUUGGUGA..... 22 38
...........CGGGGAUUCUACUCUUGGUGA..... 21 149
...........CGGGGAUUCUACUCUUGGUGAA..... 22 653
...........CGGGGAUUCUACUCUUGGUGAAG..... 23 10652
...........CGGGGAUUCUACUCUUGGUGAAGC..... 24 1939
............GGGGAUUCUACUCUUGGUGAAG..... 22 72
............GGGGAUUCUACUCUUGGUGAAGC..... 23 45
.............................AGCGAGCUCAGAUGACUUC..... 19 258
.................................................UUCACCGGGCUCGAAUCC..... 18 147
.................................................UUCACCGGGCUCGAAUCCU..... 19 40
.................................................UUCACCGGGCUCGAAUCCUU..... 20 42
.................................................UUCACCGGGCUCGAAUCCUUG..... 21 37
.................................................UUCACCGGGCUCGAAUCCUUGU..... 22 2040


#asu-miR-36f
CUGGAGCGUGACAUGGAUUCAGCUAUCUGUGGAGUAGUGCCUUCAAAACAAAUUCUUCACCGGGCUGCAAUCCUUGUCACGCCGGUCU
(((..(((((((((.((((((((((....((((((.(((.............)))))))))..)))))).)))))).)))))))))...
Total sRNA: 91903 shared 5' end with miRNA: 7951 shared 3' end with miRNA: 2300
miRNA
.....................................................UCACCGGGCUGCAAUCCUUGUCA..... 23 73099
Shared 5' Terminus
.....................................................UCACCGGGCUGCAAUCCU..... 18 63
.....................................................UCACCGGGCUGCAAUCCUU..... 19 36
.....................................................UCACCGGGCUGCAAUCCUUG..... 20 44
.....................................................UCACCGGGCUGCAAUCCUUGU..... 21 939
.....................................................UCACCGGGCUGCAAUCCUUGUC..... 22 6855
Shared 3' Terminus
.........................................................CCGGGCUGCAAUCCUUGUCA..... 20 28
........................................................ACCGGGCUGCAAUCCUUGUCA..... 21 362
.......................................................CACCGGGCUGCAAUCCUUGUCA..... 22 1608
.....................................................UUCACCGGGCUGCAAUCCUUGUCA..... 24 279
Subsequence
.....................................................CACCGGGCUGCAAUCCUUGUC..... 21 59
......................................................ACCGGGCUGCAAUCCUUGUC..... 20 29
Others
.........ACAUGGAUUCAGCUAUCUGUGG..... 22 48
.........ACAUGGAUUCAGCUAUCUGUGGA..... 23 6010
.........ACAUGGAUUCAGCUAUCUGUGGAG..... 24 1627
.........ACAUGGAUUCAGCUAUCUGUGGAGU..... 25 490
...........CAUGGAUUCAGCUAUCUGUGGAG..... 23 44
.....................................................UUCACCGGGCUGCAAUCCUUGUC..... 23 36


#asu-miR-43a
CCCGGCGAUAGUAAGUACUGCGAUAUGCUGCAAGAACACAAACACAUAUCACAGUCUACUUGCUGUCUCCGGUUCGCUG
.((((.(((((((((((((((.((((((.((...........)))))))).))))..)))))))))).))))).......
Total sRNA: 175734 shared 5' end with miRNA: 61851 shared 3' end with miRNA: 722
miRNA
.........................................UAUCACAGUCUACUUGCUGUCUC..... 23 92981
```

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Shared 5' Terminus
.............................................UAUCACAGUCUACUUGCU.............. 18 474
.............................................UAUCACAGUCUACUUGCUGU............. 20 973
.............................................UAUCACAGUCUACUUGCUGUC............ 21 999
.............................................UAUCACAGUCUACUUGCUGUCU........... 22 58649
.............................................UAUCACAGUCUACUUGCUGUCUCC......... 24 743
Shared 3' Terminus
.....................................................CAGUCUACUUGCUGUCUC.......... 18 164
.....................................................ACAGUCUACUUGCUGUCUC.......... 19 86
....................................................AUCACAGUCUACUUGCUGUCUC.......... 22 31
...................................................AUAUCACAGUCUACUUGCUGUCUC.......... 24 416
Subsequence
.....................................................ACAGUCUACUUGCUGUCU........... 18 99
Others
......GAUAGUAAGUACUGCGAUA.................................................... 19 64
......GAUAGUAAGUACUGCGAUAU................................................... 20 326
......GAUAGUAAGUACUGCGAUAUG.................................................. 21 16932
.......AUAGUAAGUACUGCGAUAUG.................................................. 20 732
.........................CUGCAAGAACACAAACACA.................................. 19 890
.............................................ACAUAUCACAGUCUACUUGCUGUCU........... 25 93
............................................CAUAUCACAGUCUACUUGCUGUCU........... 24 51
...........................................AUAUCACAGUCUACUUGCUGUCU........... 23 721


#asu-miR-43b
UAUAGCGGCACGUGGCAAAGGUGCUGCGAUGCGCCGCGUUAAAUCGUAUCACAGUUCUUUGUCACCUUUUGCUUCACACGC
...(((((...((((((((((.((((.((((((...........))))))..)))))))))))))...)))))).......
Total sRNA: 1240795 shared 5' end with miRNA: 122247 shared 3' end with miRNA: 5305
miRNA
.............................................UAUCACAGUUCUUUGUCACCUU............. 22 1111980
Shared 5' Terminus
.............................................UAUCACAGUUCUUUGUCA................ 18 5568
.............................................UAUCACAGUUCUUUGUCAC............... 19 5641
.............................................UAUCACAGUUCUUUGUCACC.............. 20 30462
.............................................UAUCACAGUUCUUUGUCACCU............. 21 74263
.............................................UAUCACAGUUCUUUGUCACCUUU........... 23 6223
Shared 3' Terminus
.....................................................ACAGUUCUUUGUCACCUU............. 18 3157
....................................................CACAGUUCUUUGUCACCUU............. 19 427
...................................................UCACAGUUCUUUGUCACCUU............. 20 250
..................................................AUCACAGUUCUUUGUCACCUU............. 21 1426
Subsequence
Others
..........CGUGGCAAAGGUGCUGCGAUGCG.............................................. 23 648


#asu-miR-43c-1
UGCGUACAGCAGCGCGUGGCAAGGAUACUGCGAUGCGUCAUGUUGCAUCGUAUCACAGUUCUUUGUCACCCUUUGCAUCACGCA
.((((...((((.(.((((((((((.((((.((((((...........)))))).)))))))))))))).).)))).)))).
Total sRNA: 2911161 shared 5' end with miRNA: 140358 shared 3' end with miRNA: 11885
miRNA
.................................................UAUCACAGUUCUUUGUCACCCU............ 22 2744612
Shared 5' Terminus
.................................................UAUCACAGUUCUUUGUCA................ 18 5568
.................................................UAUCACAGUUCUUUGUCAC............... 19 5641
.................................................UAUCACAGUUCUUUGUCACC.............. 20 30462
.................................................UAUCACAGUUCUUUGUCACCC............. 21 92878
.................................................UAUCACAGUUCUUUGUCACCCUU........... 23 5580
.................................................UAUCACAGUUCUUUGUCACCCUUU.......... 24 229
Shared 3' Terminus
.....................................................ACAGUUCUUUGUCACCCU............ 18 6826
....................................................CACAGUUCUUUGUCACCCU............ 19 870
...................................................UCACAGUUCUUUGUCACCCU............ 20 616
..................................................AUCACAGUUCUUUGUCACCCU............ 21 3461
Subsequence
.....................................................AUCACAGUUCUUUGUCACCC............. 20 104
Others
.............CGUGGCAAGGAUACUGCGAUG.......................................... 21 202
.............CGUGGCAAGGAUACUGCGAUGC......................................... 22 443
.............CGUGGCAAGGAUACUGCGAUGCG........................................ 23 11997
................GGCAAGGAUACUGCGAUGCGUC...................................... 22 104
```

#asu-miR-43c-2
ACAGCGGCGCGUGGCAAAGAUACUGCGAUGCGCCGCGUUACAUCGUAUCACAGUUCUUUGUCACCCUUUGCUUUACG
..(((((.(.((((((((((.((((.((((((..(.....)..)))))).)))))))))))))).).)))))).....
Total sRNA: 2904371 shared 5' end with miRNA: 140358 shared 3' end with miRNA: 11870
miRNA
.....UAUCACAGUUCUUUGUCACCCU..... 22 2744612
Shared 5' Terminus
.....UAUCACAGUUCUUUGUCA..... 18 5568
.....UAUCACAGUUCUUUGUCAC..... 19 5641
.....UAUCACAGUUCUUUGUCACC..... 20 30462
.....UAUCACAGUUCUUUGUCACCC..... 21 92878
.....UAUCACAGUUCUUUGUCACCCUU..... 23 5580
.....UAUCACAGUUCUUUGUCACCCUUU..... 24 229
Shared 3' Terminus
.....ACAGUUCUUUGUCACCCU..... 18 6826
.....CACAGUUCUUUGUCACCCU..... 19 870
.....UCACAGUUCUUUGUCACCCU..... 20 616
.....AUCACAGUUCUUUGUCACCCU..... 21 3461
Subsequence
.....AUCACAGUUCUUUGUCACCC..... 20 104
Others
.....CGUGGCAAAGAUACUGCGAUGC..... 22 135
.....CGUGGCAAAGAUACUGCGAUGCG..... 23 6699

#asu-miR-43d
GGCAGUAACCCGAUGUGGCUGCGAUACUGUUUGCACAUGGCCGAGUAUCACAGUCUUAUCCGGUCACCGCCUCUU
(((.((.(((.((((.(((((.((((((....((.....))..))))))).)))))..))))..))).)).))))....
Total sRNA: 743362 shared 5' end with miRNA: 75266 shared 3' end with miRNA: 1075
miRNA
.....UAUCACAGUCUUAUCCGGUCA..... 21 549241
Shared 5' Terminus
.....UAUCACAGUCUUAUCCGGU..... 19 1328
.....UAUCACAGUCUUAUCCGGUC..... 20 2545
.....UAUCACAGUCUUAUCCGGUCAC..... 22 71332
Shared 3' Terminus
.....CACAGUCUUAUCCGGUCA..... 18 114
.....AUCACAGUCUUAUCCGGUCA..... 20 159
.....GUAUCACAGUCUUAUCCGGUCA..... 22 758
Subsequence
Others
.....UAACCCGAUGUGGCUGCGAUACU..... 23 151
.....AACCCGAUGUGGCUGCGA..... 18 433
.....AACCCGAUGUGGCUGCGAU..... 19 915
.....AACCCGAUGUGGCUGCGAUA..... 20 816
.....AACCCGAUGUGGCUGCGAUAC..... 21 4544
.....AACCCGAUGUGGCUGCGAUACU..... 22 106650
.....AACCCGAUGUGGCUGCGAUACUG..... 23 109
.....ACCCGAUGUGGCUGCGAUACU..... 21 1812
.....ACCCGAUGUGGCUGCGAUACUG..... 22 1073
.....AUCACAGUCUUAUCCGGUCAC..... 21 517
.....ACAGUCUUAUCCGGUCAC..... 18 378

#asu-miR-43e
UGCACAGCACGCGGUAGCAGAGGUGCUGCGAUACGCUGUGUAGUAUCAUAUCACAGUUCUUUGCUACCUCGUGCUUCGCA
.((..((((((.((((((((((.((((.((((.(((....))).)))).)))))))))))))))).))))))..)).
Total sRNA: 342730 shared 5' end with miRNA: 48775 shared 3' end with miRNA: 2631
miRNA
.....UAUCACAGUUCUUUGCUACCUC..... 22 278943
Shared 5' Terminus
.....UAUCACAGUUCUUUGCUA..... 18 288
.....UAUCACAGUUCUUUGCUAC..... 19 700
.....UAUCACAGUUCUUUGCUACC..... 20 2656
.....UAUCACAGUUCUUUGCUACCU..... 21 32492
.....UAUCACAGUUCUUUGCUACCUCG..... 23 12484
.....UAUCACAGUUCUUUGCUACCUCGU..... 24 128
Shared 3' Terminus
.....ACAGUUCUUUGCUACCUC..... 18 954
.....UCACAGUUCUUUGCUACCUC..... 20 151
.....AUCACAGUUCUUUGCUACCUC..... 21 1276

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.............................................AUAUCACAGUUCUUUGCUACCUC.......... 23 173
Subsequence
..............................................AUCACAGUUCUUUGCUACCU........... 20 100
Others
.........CGCGGUAGCAGAGGUGCUGCGAU.............................................. 23 409
...........CGGUAGCAGAGGUGCUGCGAU.............................................. 21 258
...........CGGUAGCAGAGGUGCUGCGAUA............................................. 22 785
...........CGGUAGCAGAGGUGCUGCGAUAC............................................ 23 1355
...........CGGUAGCAGAGGUGCUGCGAUACG........................................... 24 5956
............GGUAGCAGAGGUGCUGCGAUACG.......................................... 23 781
.......................CUGCGAUACGCUGUGUAGUAUCA................................ 23 94
...................................................AUCACAGUUCUUUGCUACCUCG......... 22 386
....................................................UCACAGUUCUUUGCUACCUCG......... 21 194
....................................................UCACAGUUCUUUGCUACCUCGU........ 22 290
....................................................UCACAGUUCUUUGCUACCUCGUG....... 23 185


#asu-miR-44a
CAGACGUGAAACUGGAUGUCUCUCGCAGUCAUACGGUAUAUAGAGUUCUAUGACUAGAGACACAUUCAGCUUGGCGGCUG
(((.(((.((.(((((((((.((((..(((((((.((.........)))))))))..))))..)))))))))..)).)))))
Total sRNA: 774872 shared 5' end with miRNA: 48446 shared 3' end with miRNA: 1277
miRNA
...................................................UGACUAGAGACACAUUCAGCU......... 21 691583
Shared 5' Terminus
...................................................UGACUAGAGACACAUUCA............ 18 2993
...................................................UGACUAGAGACACAUUCAG........... 19 4932
...................................................UGACUAGAGACACAUUCAGC.......... 20 26138
...................................................UGACUAGAGACACAUUCAGCUU........ 22 14373
Shared 3' Terminus
.....................................................CUAGAGACACAUUCAGCU......... 18 532
......................................................ACUAGAGACACAUUCAGCU......... 19 355
.......................................................GACUAGAGACACAUUCAGCU......... 20 155
.....................................................AUGACUAGAGACACAUUCAGCU......... 22 223
Subsequence
Others
...........CUGGAUGUCUCUCGCAGU.................................................. 18 117
...........CUGGAUGUCUCUCGCAGUCAU.............................................. 21 391
...........CUGGAUGUCUCUCGCAGUCAUA............................................. 22 32577


#asu-miR-44b
AGUAAGCUACUGGAUGUGUGUCAUAGUCAUGACGUGUGAUCAACAUGACUAGAUAUCACAUUCAGUGGUAUAUUU
((((.(((((((((((((((((.(((((((...((....)).)))))))))))))).))))))))))))).))))).
Total sRNA: 143950 shared 5' end with miRNA: 8104 shared 3' end with miRNA: 311
miRNA
........ACUGGAUGUGUGUCAUAGUCAUG.............................................. 23 70723
Shared 5' Terminus
........ACUGGAUGUGUGUCAUAG.................................................... 18 59
........ACUGGAUGUGUGUCAUAGU................................................... 19 291
........ACUGGAUGUGUGUCAUAGUC.................................................. 20 203
........ACUGGAUGUGUGUCAUAGUCA................................................. 21 587
........ACUGGAUGUGUGUCAUAGUCAU................................................ 22 6185
........ACUGGAUGUGUGUCAUAGUCAUGA.............................................. 24 715
........ACUGGAUGUGUGUCAUAGUCAUGACGUGUGAUCAACA.................................. 37 47
Shared 3' Terminus
..........UGGAUGUGUGUCAUAGUCAUG.............................................. 21 146
.........CUGGAUGUGUGUCAUAGUCAUG.............................................. 22 86
.......UACUGGAUGUGUGUCAUAGUCAUG.............................................. 24 63
Subsequence
Others
.......UACUGGAUGUGUGUCAUAGUCA................................................ 22 76
.......UACUGGAUGUGUGUCAUAGUCAU............................................... 23 35
.............................................UGACUAGAUAUCACAUUCA........... 19 69
.............................................UGACUAGAUAUCACAUUCAGU......... 21 878
.............................................UGACUAGAUAUCACAUUCAGUG........ 22 755
.............................................UGACUAGAUAUCACAUUCAGUGG....... 23 60481
.............................................UGACUAGAUAUCACAUUCAGUGGU...... 24 1980
..............................................GACUAGAUAUCACAUUCAGUGGU...... 23 44
...............................................CUAGAUAUCACAUUCAGU......... 18 48
.............................................CUAGAUAUCACAUUCAGUGG....... 20 74
............................................UAGAUAUCACAUUCAGUGG....... 19 40
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.................................................AGAUAUCACAUUCAGUGG....... 18 33


#asu-miR-46
GCAGACGGCUAAGAGAGCCAUCUGUUGACAGUCGUCAAUUGCCCACUGUCAUGGAGUUGCUCUCUUCAGAUGCCUGC
((((.((.((((((((((..(((((.((((((.(.(....).).)))))))))))...)))))))).)).)).))))
Total sRNA: 47137 shared 5' end with miRNA: 2360 shared 3' end with miRNA: 1085
miRNA
.............................................UGUCAUGGAGUUGCUCUCUUCA......... 22 35988
Shared 5' Terminus
.............................................UGUCAUGGAGUUGCUCUC............. 18 17
.............................................UGUCAUGGAGUUGCUCUCU............ 19 77
.............................................UGUCAUGGAGUUGCUCUCUU........... 20 91
.............................................UGUCAUGGAGUUGCUCUCUUC.......... 21 588
.............................................UGUCAUGGAGUUGCUCUCUUCAG........ 23 1573
.............................................UGUCAUGGAGUUGCUCUCUUCAGA....... 24 14
Shared 3' Terminus
..............................................AUGGAGUUGCUCUCUUCA......... 18 47
.............................................CAUGGAGUUGCUCUCUUCA......... 19 32
............................................UCAUGGAGUUGCUCUCUUCA......... 20 15
...........................................GUCAUGGAGUUGCUCUCUUCA......... 21 15
..........................................CUGUCAUGGAGUUGCUCUCUUCA......... 23 974
Subsequence
Others
.........UAAGAGAGCCAUCUGUUGACAGU.......................................... 23 22
.........AAGAGAGCCAUCUGUUGACA............................................ 20 38
.........AAGAGAGCCAUCUGUUGACAG........................................... 21 180
.........AAGAGAGCCAUCUGUUGACAGU.......................................... 22 6827
.........AAGAGAGCCAUCUGUUGACAGUC......................................... 23 347
..........AGAGAGCCAUCUGUUGACAGU.......................................... 21 25
..........AGAGAGCCAUCUGUUGACAGUC......................................... 22 24
............GAGCCAUCUGUUGACAGU............................................ 18 38
.............................................CUGUCAUGGAGUUGCUCUCUUC......... 22 59


#asu-miR-49
UGCGCGGUGCGUAGUUUCAUAUGGGUAUGCUCCGUUGUGUAUUUUCGAAGCACCAUGUGAAGCUGCUAUCCGAACGGCGA
.((.(((...(((((((((((((...((((.((..(.....)..)).)))))))))))))))))...)))....)).
Total sRNA: 251800 shared 5' end with miRNA: 17780 shared 3' end with miRNA: 4903
miRNA
.............................................AAGCACCAUGUGAAGCUGCUAU.......... 22 227971
Shared 5' Terminus
.............................................AAGCACCAUGUGAAGCUG.............. 18 1071
.............................................AAGCACCAUGUGAAGCUGC............. 19 203
.............................................AAGCACCAUGUGAAGCUGCU............ 20 3940
.............................................AAGCACCAUGUGAAGCUGCUA........... 21 12501
Shared 3' Terminus
...................................................ACCAUGUGAAGCUGCUAU.......... 18 4444
................................................CACCAUGUGAAGCUGCUAU.......... 19 304
.............................................GCACCAUGUGAAGCUGCUAU.......... 20 84
Subsequence
Others
.........CGUAGUUUCAUAUGGGUAUGCUCCG.......................................... 25 925


#asu-miR-50
GGCGUUGAUAUGUCUGGUAUUCUUGGGUUGGGUCUUCGUCAACCAGUAUCUCAGACGUAUCAUCGUUGUGCAUUG
((((.((((((((((..((.....((((((.......))))))...)).)).))))))))))).))))........
Total sRNA: 244008 shared 5' end with miRNA: 36216 shared 3' end with miRNA: 1399
miRNA
.....UGAUAUGUCUGGUAUUCUUGGGUU.......................................... 24 198340
Shared 5' Terminus
.....UGAUAUGUCUGGUAUUCUU................................................ 19 68
.....UGAUAUGUCUGGUAUUCUUGG.............................................. 21 185
.....UGAUAUGUCUGGUAUUCUUGGG............................................. 22 1092
.....UGAUAUGUCUGGUAUUCUUGGGU............................................ 23 33878
.....UGAUAUGUCUGGUAUUCUUGGGUUG.......................................... 25 860
Shared 3' Terminus
.........UGUCUGGUAUUCUUGGGUU............................................. 19 193
.........AUGUCUGGUAUUCUUGGGUU........................................... 20 442
.......UAUGUCUGGUAUUCUUGGGUU............................................ 21 143
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.......AUAUGUCUGGUAUUCUUGGGUU..................................................... 22 103
......GAUAUGUCUGGUAUUCUUGGGUU..................................................... 23 128
....UUGAUAUGUCUGGUAUUCUUGGGUU..................................................... 25 324
Subsequence
.........AUGUCUGGUAUUCUUGGGU..................................................... 19 118
Others
....UUGAUAUGUCUGGUAUUCUUGGGU..................................................... 24 74
.....................................ACCAGUAUCUCAGACGUAUCAU.................... 22 656
.....................................ACCAGUAUCUCAGACGUAUCAUC................... 23 898
......................................CCAGUAUCUCAGACGUAUCAU.................... 21 1194
......................................CCAGUAUCUCAGACGUAUCAUC................... 22 4246


#asu-miR-56
UGGACGGCCGGGUGGCAGACUAUCGUGGGUAUGUGCAUAUAUAUUCAUACCCGUAAGUCUCCAUCGAGCUCCGGCUGUC
..((((((((((((.(((((....(((((((.............))))))))..))))))))).....)))))))))
Total sRNA: 263876 shared 5' end with miRNA: 30111 shared 3' end with miRNA: 850
miRNA
.............................................UACCCGUAAGUCUCCAUCGAG.......... 21 232332
Shared 5' Terminus
.............................................UACCCGUAAGUCUCCAUC............. 18 2237
.............................................UACCCGUAAGUCUCCAUCG............. 19 1983
.............................................UACCCGUAAGUCUCCAUCGA............ 20 15647
.............................................UACCCGUAAGUCUCCAUCGAGC.......... 22 9993
.............................................UACCCGUAAGUCUCCAUCGAGCU......... 23 251
Shared 3' Terminus
..................................................CCGUAAGUCUCCAUCGAG.......... 18 89
.............................................AUACCCGUAAGUCUCCAUCGAG.......... 22 662
Subsequence
Others
.............................................AUACCCGUAAGUCUCCAUCGA............ 21 301


#asu-miR-57
GUGGUUUCGUCUACCCUGUAGUACCGAGCUGUGUUUGAGUGAUUAUGCAUACACGAUCGGUUGCCGGGUGAAUGACGCUGCCC
(..((.((((.(((((.(((..(((((..(((((.((.((....)).)).)))))).)))))))).)))))).))))..)..
Total sRNA: 837154 shared 5' end with miRNA: 152202 shared 3' end with miRNA: 3927
miRNA
..........UACCCUGUAGUACCGAGCUGUGUUU.............................................. 25 677202
Shared 5' Terminus
..........UACCCUGUAGUACCGAGC..................................................... 18 1679
..........UACCCUGUAGUACCGAGCU.................................................... 19 4626
..........UACCCUGUAGUACCGAGCUG................................................... 20 1964
..........UACCCUGUAGUACCGAGCUGU.................................................. 21 4194
..........UACCCUGUAGUACCGAGCUGUG................................................. 22 3104
..........UACCCUGUAGUACCGAGCUGUGU................................................ 23 21968
..........UACCCUGUAGUACCGAGCUGUGUU.............................................. 24 113870
..........UACCCUGUAGUACCGAGCUGUGUUUG............................................ 26 716
Shared 3' Terminus
................UAGUACCGAGCUGUGUUU.............................................. 18 170
................GUAGUACCGAGCUGUGUUU.............................................. 19 1035
................UGUAGUACCGAGCUGUGUUU............................................. 20 802
...............CUGUAGUACCGAGCUGUGUUU............................................. 21 985
..............CCUGUAGUACCGAGCUGUGUUU............................................ 22 166
............ACCCUGUAGUACCGAGCUGUGUUU............................................ 24 233
.........CUACCCUGUAGUACCGAGCUGUGUUU.............................................. 26 417
Subsequence
...............CUGUAGUACCGAGCUGUGUU.............................................. 20 146
................UGUAGUACCGAGCUGUGUU.............................................. 19 229
................GUAGUACCGAGCUGUGUU.............................................. 18 423
Others
.................................................UACACGAUCGGUUGCCGGGUGAA.......... 23 117
.................................................ACACGAUCGGUUGCCGGGUGA........... 21 188
.................................................ACACGAUCGGUUGCCGGGUGAA.......... 22 2323


#asu-miR-67
GGGCACUUAGCUCGCUCGGCUGGUUGUUAGAUGUUUCUGAUGUUCAUCACAACCUCCUUGAGUGAGUUGAAAGCCCUC
((((..(((((((((((((..((((((..((((...(....)..))))))))))...))))))))))))))..)))))..
Total sRNA: 55470 shared 5' end with miRNA: 9136 shared 3' end with miRNA: 1776
miRNA
```

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.........................................UCACAACCUCCUUGAGUGAGUUGA........ 24 43482
Shared 5' Terminus
.........................................UCACAACCUCCUUGAGUGA............. 19 169
.........................................UCACAACCUCCUUGAGUGAG............ 20 82
.........................................UCACAACCUCCUUGAGUGAGU........... 21 2641
.........................................UCACAACCUCCUUGAGUGAGUU.......... 22 602
.........................................UCACAACCUCCUUGAGUGAGUUG......... 23 5360
.........................................UCACAACCUCCUUGAGUGAGUUGAA....... 25 268
Shared 3' Terminus
.....................................................CCUCCUUGAGUGAGUUGA........ 18 191
....................................................ACCUCCUUGAGUGAGUUGA........ 19 964
...................................................AACCUCCUUGAGUGAGUUGA........ 20 319
..................................................CAACCUCCUUGAGUGAGUUGA........ 21 45
................................................ACAACCUCCUUGAGUGAGUUGA........ 22 221
.............................................AUCACAACCUCCUUGAGUGAGUUGA........ 25 26
Subsequence
................................................ACAACCUCCUUGAGUGAGU........... 19 27
................................................ACAACCUCCUUGAGUGAGUUG......... 21 34
..............................................CAACCUCCUUGAGUGAGU........... 18 30
..............................................CAACCUCCUUGAGUGAGUUG......... 20 27
............................................AACCUCCUUGAGUGAGUUG......... 19 26
............................................ACCUCCUUGAGUGAGUUG......... 18 46
Others
........AGCUCGCUCGGCUGGUUGUUAGA.............................................. 23 20
........AGCUCGCUCGGCUGGUUGUUAGAU............................................. 24 61
........AGCUCGCUCGGCUGGUUGUUAGAUG............................................ 25 392
........AGCUCGCUCGGCUGGUUGUUAGAUGU........................................... 26 318
.............................................ACCUCCUUGAGUGAGUUGAA....... 20 23


#asu-miR-71
GGGAAUGUGGUGAAAGACAUGGGUAGUGAGACGUUACAUUGAGUCGUAUCACUAUUCUGUUUUUCGCCUCGUAUCCUCG
(((((((.(((((((((((.((((((((((.(((...........))).)))))))))))))))))))).))).))))..
Total sRNA: 3056485 shared 5' end with miRNA: 807129 shared 3' end with miRNA: 4462
miRNA
..........UGAAAGACAUGGGUAGUGAGACG.............................................. 23 2241933
Shared 5' Terminus
..........UGAAAGACAUGGGUAGUG.................................................... 18 4080
..........UGAAAGACAUGGGUAGUGA................................................... 19 66987
..........UGAAAGACAUGGGUAGUGAG.................................................. 20 41780
..........UGAAAGACAUGGGUAGUGAGA................................................. 21 269458
..........UGAAAGACAUGGGUAGUGAGAC................................................ 22 412823
..........UGAAAGACAUGGGUAGUGAGACGU.............................................. 24 11188
..........UGAAAGACAUGGGUAGUGAGACGUU............................................ 25 583
Shared 3' Terminus
..............GACAUGGGUAGUGAGACG.................................................. 18 1555
.............AGACAUGGGUAGUGAGACG.................................................. 19 659
............AAGACAUGGGUAGUGAGACG.................................................. 20 814
...........AAAGACAUGGGUAGUGAGACG.................................................. 21 494
..........GAAAGACAUGGGUAGUGAGACG.................................................. 22 796
.........GUGAAAGACAUGGGUAGUGAGACG.............................................. 24 103
Subsequence
...........GAAAGACAUGGGUAGUGAGAC.................................................. 21 131
............AAGACAUGGGUAGUGAGA.................................................... 18 110
............AAGACAUGGGUAGUGAGAC.................................................. 19 120
Others
.........GUGAAAGACAUGGGUAGUGAGAC.............................................. 23 180
..........GAAAGACAUGGGUAGUGAGACGU.............................................. 23 148
.....................................................UAUCACUAUUCUGUUUUUCGC..... 21 169
.....................................................UAUCACUAUUCUGUUUUUCGCC.... 22 1554

#asu-miR-72
CGUGGGACCAGGCAAGAUGUUGGCAUAGCUGAACGAAGCUUCGGAUUCAGCCGUGCUACAUAAGGCCAUGCUCCCGCG
(((((((.(((((...((((.((((..(((((.(((....)))...)))))..)))))))))...))).)).)))))))
Total sRNA: 141284 shared 5' end with miRNA: 5450 shared 3' end with miRNA: 915
miRNA
.........AGGCAAGAUGUUGGCAUAGCUGA.............................................. 23 134811
Shared 5' Terminus
.........AGGCAAGAUGUUGGCAUA.................................................... 18 89
.........AGGCAAGAUGUUGGCAUAG................................................... 19 64
.........AGGCAAGAUGUUGGCAUAGCU................................................. 21 728
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.........AGGCAAGAUGUUGGCAUAGCUG.......................................... 22 1275
.........AGGCAAGAUGUUGGCAUAGCUGAA....................................... 24 3267
Shared 3' Terminus
.............AGAUGUUGGCAUAGCUGA.......................................... 18 105
.............AAGAUGUUGGCAUAGCUGA......................................... 19 528
............CAAGAUGUUGGCAUAGCUGA.......................................... 20 125
...........GCAAGAUGUUGGCAUAGCUGA.......................................... 21 51
..........GGCAAGAUGUUGGCAUAGCUGA.......................................... 22 55
........CAGGCAAGAUGUUGGCAUAGCUGA.......................................... 24 51
Subsequence
Others
.............................................AGCCGUGCUACAUAAGGCCAUGC....... 23 23


#asu-miR-76
AUGGCCGCUGGCUGGUCGGgUUUUCUAUCAGCGAAUAUUUCGCUGAAAUUAUUCGUUGUUUAUGAAACCUGCUUAGCCGGUUG
......(((((((((.(((((((((.((.(((((((((((((...)))).))))))))).))).)))))))).))))))))..
Total sRNA: 43969 shared 5' end with miRNA: 12056 shared 3' end with miRNA: 66
miRNA
..................................................UUCGUUGUUUAUGAAACCUGCUU......... 23 31328
Shared 5' Terminus
..................................................UUCGUUGUUUAUGAAACC.............. 18 43
..................................................UUCGUUGUUUAUGAAACCU............. 19 166
..................................................UUCGUUGUUUAUGAAACCUG............ 20 483
..................................................UUCGUUGUUUAUGAAACCUGC........... 21 424
..................................................UUCGUUGUUUAUGAAACCUGCU.......... 22 10867
..................................................UUCGUUGUUUAUGAAACCUGCUUA........ 24 72
Shared 3' Terminus
.....................................................GUUGUUUAUGAAACCUGCUU......... 20 27
..................................................UCGUUGUUUAUGAAACCUGCUU......... 22 24
Subsequence
Others
..............UCGGGUUUUCUAUCAGCGAAU..................................... 21 21
..............UCGGGUUUUCUAUCAGCGAAUA.................................... 22 189
..............CGGGUUUUCUAUCAGCGAAUA..................................... 21 12
.........................................AAAUUAUUCGUUGUUUAUGAA.............. 21 32
.........................................AAAUUAUUCGUUGUUUAUGAAA............. 22 100
.........................................AAUUAUUCGUUGUUUAUGAAA.............. 21 27
..................................................UAUUCGUUGUUUAUGAAACCUGCU.......... 24 51


#asu-miR-79
UUGUCUUUCCCUUUGGUUAUCUGGCUGUAUGAGUGAGCCAUAACAUCAUAAAGCUAGGUUACCAAAGCUAAGCACAAU
(((((((...(((((((.(((((((.(((((((........)).)))))).)))))))).)))))))..))).)))).
Total sRNA: 316210 shared 5' end with miRNA: 6335 shared 3' end with miRNA: 1262
miRNA
.............................................AUAAAGCUAGGUUACCAAAGCU......... 22 304277
Shared 5' Terminus
.............................................AUAAAGCUAGGUUACCAA.............. 18 456
.............................................AUAAAGCUAGGUUACCAAA............. 19 635
.............................................AUAAAGCUAGGUUACCAAAG............ 20 1328
.............................................AUAAAGCUAGGUUACCAAAGC........... 21 3254
.............................................AUAAAGCUAGGUUACCAAAGCUA......... 23 575
Shared 3' Terminus
.............................................UAAAGCUAGGUUACCAAAGCU......... 21 927
.........................................CAUAAAGCUAGGUUACCAAAGCU......... 23 162
Subsequence
Others
.........CCUUUGGUUAUCUGGCUGUAUG.......................................... 22 288
.........CCUUUGGUUAUCUGGCUGUAUGA......................................... 23 1072
..........CUUUGGUUAUCUGGCUGUAUGA......................................... 22 1205
...........UUUGGUUAUCUGGCUGUAUGA......................................... 21 1424


#asu-miR-81a
ACGGGCACUAGGCCUUCACUGUGAAUCUGCAGAAUGCCUGUUAUACUGUCUGAGAUCAUUGUGAAAGCUAUUUGCCUUGCUUG
..(((((...(((.(((((.((((.(((.((((.............)))))))))).)))))..)))...)))))).....
Total sRNA: 25753127 shared 5' end with miRNA: 2374363 shared 3' end with miRNA: 37135
miRNA
.............................................UGAGAUCAUUGUGAAAGCUAUU........... 22 23338358
Shared 5' Terminus
```

```
.................................................UGAGAUCAUUGUGAAAGC.............. 18 99482
.................................................UGAGAUCAUUGUGAAAGCU............. 19 331760
.................................................UGAGAUCAUUGUGAAAGCUA............ 20 397282
.................................................UGAGAUCAUUGUGAAAGCUAU........... 21 1321254
.................................................UGAGAUCAUUGUGAAAGCUAUUU......... 23 224124
.................................................UGAGAUCAUUGUGAAAGCUAUUUG........ 24 174
.................................................UGAGAUCAUUGUGAAAGCUAUUUGC....... 25 181
Shared 3' Terminus
.....................................................AUCAUUGUGAAAGCUAUU.......... 18 15784
....................................................GAUCAUUGUGAAAGCUAUU.......... 19 6756
...................................................AGAUCAUUGUGAAAGCUAUU.......... 20 1848
....................................................GAGAUCAUUGUGAAAGCUAUU.......... 21 4801
.................................................CUGAGAUCAUUGUGAAAGCUAUU.......... 23 6993
...............................................UCUGAGAUCAUUGUGAAAGCUAUU.......... 24 933
Subsequence
....................................................GAGAUCAUUGUGAAAGCU............. 18 141
....................................................GAGAUCAUUGUGAAAGCUAU........... 20 295
.....................................................GAUCAUUGUGAAAGCUAU........... 18 484
Others
.................................................CUGAGAUCAUUGUGAAAGCUA............ 21 109
.................................................CUGAGAUCAUUGUGAAAGCUAU........... 22 587
....................................................GAGAUCAUUGUGAAAGCUAUUU......... 22 366
...................................................AGAUCAUUGUGAAAGCUAUUUG........ 22 159
....................................................GAUCAUUGUGAAAGCUAUUU......... 20 108
.....................................................AUCAUUGUGAAAGCUAUUU......... 19 176
.....................................................UCAUUGUGAAAGCUAUUU......... 18 116


#asu-miR-81b
UUGUUCUCAAAACGGGUGUGCAUGCAGAUCAUGGUGUAAUAUAGCUCAUGAGAUCAUGCCACAUCUGUCUUGAAAGCCA
..(((.((((.(((((((((((((.(..((((((.((......))))))))..)))))).)))))))).)))).)))..
Total sRNA: 190302 shared 5' end with miRNA: 26768 shared 3' end with miRNA: 299
miRNA
................................................UGAGAUCAUGCCACAUCUGUCU......... 22 163077
Shared 5' Terminus
................................................UGAGAUCAUGCCACAUCU............. 18 163
................................................UGAGAUCAUGCCACAUCUG............ 19 97
................................................UGAGAUCAUGCCACAUCUGU........... 20 3577
................................................UGAGAUCAUGCCACAUCUGUC.......... 21 5221
................................................UGAGAUCAUGCCACAUCUGUCUU........ 23 17699
Shared 3' Terminus
.....................................................AUCAUGCCACAUCUGUCU......... 18 79
....................................................GAUCAUGCCACAUCUGUCU......... 19 79
................................................AUGAGAUCAUGCCACAUCUGUCU......... 23 76
Subsequence
Others
..........ACGGGUGUGCAUGCAGAUCAUG.......................................... 22 65


#asu-miR-81c
GAUUCCGAGGCGGAUGUGCAUGAGAUCAUGUAUCUAUAAAAUUUCAUGAGAUCAUGUUACAUCCGACUUGGCGUCUC
(((.(((((.(((((((((((((..(((((.............)))))..)))))).)))))))).)))))).)))..
Total sRNA: 358936 shared 5' end with miRNA: 33814 shared 3' end with miRNA: 428
miRNA
................................................UGAGAUCAUGUUACAUCCGACU......... 22 324317
Shared 5' Terminus
................................................UGAGAUCAUGUUACAUCC............. 18 6066
................................................UGAGAUCAUGUUACAUCCG............ 19 1376
................................................UGAGAUCAUGUUACAUCCGA........... 20 10285
................................................UGAGAUCAUGUUACAUCCGAC.......... 21 10737
................................................UGAGAUCAUGUUACAUCCGACUU........ 23 5342
Shared 3' Terminus
.....................................................AUCAUGUUACAUCCGACU......... 18 159
Subsequence
Others
.........GCGGAUGUGCAUGAGAUCAUG.......................................... 21 285
```

#asu-miR-83
GAUCUCUGAAUCCUGAAUUUGUUUGUGUGCUGGACAGAACCCAUCUCUAGCACCAUUUAAAUUCAGCAUUUCUGAGGU
.(((((.(((..((((((((((..((.(((((((((..((.....)))))))))))))..))))))))).)))).)))))
Total sRNA: 462460 shared 5' end with miRNA: 13599 shared 3' end with miRNA: 2051
miRNA
.....UAGCACCAUUUAAAUUCAGCAU..... 22 445335
Shared 5' Terminus
.....UAGCACCAUUUAAAUUCA..... 18 156
.....UAGCACCAUUUAAAUUCAG..... 19 3559
.....UAGCACCAUUUAAAUUCAGC..... 20 1275
.....UAGCACCAUUUAAAUUCAGCA..... 21 7774
.....UAGCACCAUUUAAAUUCAGCAUU..... 23 822
Shared 3' Terminus
.....ACCAUUUAAAUUCAGCAU..... 18 1489
.....CACCAUUUAAAUUCAGCAU..... 19 107
.....AGCACCAUUUAAAUUCAGCAU..... 21 174
.....CUAGCACCAUUUAAAUUCAGCAU..... 23 172
Subsequence
Others
.....CCUGAAUUUGUUUGUGUGCUGGA..... 23 1384

#asu-miR-84
AAGGCCGAUGAGGUAGUUUAUAAAGCUGCGAGUGUGUUUUCCUUCGCAGAUUUUAGGCUAUCUCGACAGCCUUGAU
(((((.(.(((((((((((.....(((((((.(......).)))))))....)))))))))))).).)))))...
Total sRNA: 3860437 shared 5' end with miRNA: 298112 shared 3' end with miRNA: 6306
miRNA
.....UGAGGUAGUUUAUAAAGCUGCGA..... 23 3555497
Shared 5' Terminus
.....UGAGGUAGUUUAUAAAGC..... 18 1185
.....UGAGGUAGUUUAUAAAGCU..... 19 49438
.....UGAGGUAGUUUAUAAAGCUG..... 20 11857
.....UGAGGUAGUUUAUAAAGCUGC..... 21 948
.....UGAGGUAGUUUAUAAAGCUGCG..... 22 232199
.....UGAGGUAGUUUAUAAAGCUGCGAG..... 24 1677
.....UGAGGUAGUUUAUAAAGCUGCGAGU..... 25 620
.....UGAGGUAGUUUAUAAAGCUGCGAGUGU..... 27 140
Shared 3' Terminus
.....UAGUUUAUAAAGCUGCGA..... 18 4909
.....GUAGUUUAUAAAGCUGCGA..... 19 609
.....GGUAGUUUAUAAAGCUGCGA..... 20 219
.....GAGGUAGUUUAUAAAGCUGCGA..... 22 461
Subsequence
Others
.....GCAGAUUUUAGGCUAUCUCGAC..... 22 260

#asu-miR-86
GGCCAGUUAAGUGAAUGCUUUGCCACAGUCUUAGCAAUGAAAUAAGCUGGGCUGAGGUUCACUUACGCUGGAGGCU
..((((((((((((.(((.(((.(((.((((.........)))))))))).)))))))))))).)))).....
Total sRNA: 15878 shared 5' end with miRNA: 1137 shared 3' end with miRNA: 89
miRNA
.....UAAGUGAAUGCUUUGCCACAGUCU..... 24 14638
Shared 5' Terminus
.....UAAGUGAAUGCUUUGCCA..... 18 29
.....UAAGUGAAUGCUUUGCCAC..... 19 26
.....UAAGUGAAUGCUUUGCCACA..... 20 64
.....UAAGUGAAUGCUUUGCCACAG..... 21 5
.....UAAGUGAAUGCUUUGCCACAGU..... 22 289
.....UAAGUGAAUGCUUUGCCACAGUC..... 23 706
.....UAAGUGAAUGCUUUGCCACAGUCUU..... 25 17
Shared 3' Terminus
.....AAUGCUUUGCCACAGUCU..... 18 6
.....GAAUGCUUUGCCACAGUCU..... 19 11
.....UGAAUGCUUUGCCACAGUCU..... 20 20
.....GUGAAUGCUUUGCCACAGUCU..... 21 9
.....AGUGAAUGCUUUGCCACAGUCU..... 22 5
.....AAGUGAAUGCUUUGCCACAGUCU..... 23 7
.....UUAAGUGAAUGCUUUGCCACAGUCU..... 25 31
Subsequence
Others

```
.........................................CUGGGCUGAGGUUCACUUACG......... 21 4


#asu-miR-87a
UCCGCCACUCCGCCUGACACUAGGUCUCAACCUCUGUUGAUUUGAGCAGGUGAGCAAAGUCUCAGGUGUUGUGGCGG
.(((((((..(((((((.(((..(.((((...((((((......)))))))))))..))).)))))))..)))))))
Total sRNA: 809177 shared 5' end with miRNA: 63679 shared 3' end with miRNA: 2544
miRNA
.................................................GUGAGCAAAGUCUCAGGUGUUG...... 22 742462
Shared 5' Terminus
.................................................GUGAGCAAAGUCUCAGGU.......... 18 317
.................................................GUGAGCAAAGUCUCAGGUG......... 19 382
.................................................GUGAGCAAAGUCUCAGGUGU........ 20 886
.................................................GUGAGCAAAGUCUCAGGUGUU....... 21 23637
.................................................GUGAGCAAAGUCUCAGGUGUUGU..... 23 38448
Shared 3' Terminus
.....................................................GCAAAGUCUCAGGUGUUG...... 18 894
....................................................AGCAAAGUCUCAGGUGUUG...... 19 277
.................................................UGAGCAAAGUCUCAGGUGUUG...... 21 243
................................................GGUGAGCAAAGUCUCAGGUGUUG...... 23 1033
Subsequence
Others
.........CCGCCUGACACUAGGUCUCAACCU.......................................... 24 100


#asu-miR-87b
AGAGUGCUCGACGCCUGGAACUUAGACUCAACCUCAGUGUAAUUGCGUAGGUGAGCAAAGUUUCAGGUGUUCGAGCGCCUUCU
((.((((((((((((((((((.(.((((.(((..((......))..))))))))).))))))))))))).))))))...
Total sRNA: 5157488 shared 5' end with miRNA: 781657 shared 3' end with miRNA: 10154
miRNA
.................................................GUGAGCAAAGUUUCAGGUGUUC.......... 22 4361118
Shared 5' Terminus
.................................................GUGAGCAAAGUUUCAGGU.............. 18 18216
.................................................GUGAGCAAAGUUUCAGGUG............. 19 4841
.................................................GUGAGCAAAGUUUCAGGUGU............ 20 30822
.................................................GUGAGCAAAGUUUCAGGUGUU........... 21 680984
.................................................GUGAGCAAAGUUUCAGGUGUUCG......... 23 45108
.................................................GUGAGCAAAGUUUCAGGUGUUCGA........ 24 1664
Shared 3' Terminus
.....................................................GCAAAGUUUCAGGUGUUC.......... 18 2996
....................................................AGCAAAGUUUCAGGUGUUC.......... 19 965
...................................................GAGCAAAGUUUCAGGUGUUC.......... 20 554
..................................................UGAGCAAAGUUUCAGGUGUUC.......... 21 2032
................................................GGUGAGCAAAGUUUCAGGUGUUC.......... 23 3572
Subsequence
.....................................................UGAGCAAAGUUUCAGGUGUU........... 20 489
....................................................AGCAAAGUUUCAGGUGUU........... 18 111
Others
.........ACGCCUGGAACUUAGACUCAACCU.......................................... 24 104
..........CGCCUGGAACUUAGACUCAACC.......................................... 22 540
..........CGCCUGGAACUUAGACUCAACCU......................................... 23 1779
.................................................GGUGAGCAAAGUUUCAGGUGUU........... 22 718
.....................................................GCAAAGUUUCAGGUGUUCG.......... 19 166


#asu-miR-92
GACACAGUCAGGCCGAGUCGUCUGCAUUAUUCGGAAGCAGCAAACGGCAAUAUUGCACUCGUCCCGGCCUGAGUGCGCGUUCA
(.(.((.(((((((((.(.((..((((.(((.(....)..((.....)).)))).))))..)).).)))))))).)).)).....
Total sRNA: 17912 shared 5' end with miRNA: 1676 shared 3' end with miRNA: 106
miRNA
.................................................UAUUGCACUCGUCCCGGCCUGA.......... 22 13005
Shared 5' Terminus
.................................................UAUUGCACUCGUCCCGGC.............. 18 434
.................................................UAUUGCACUCGUCCCGGCC.............. 19 98
.................................................UAUUGCACUCGUCCCGGCCU............. 20 341
.................................................UAUUGCACUCGUCCCGGCCUG............ 21 574
.................................................UAUUGCACUCGUCCCGGCCUGAG.......... 23 218
.................................................UAUUGCACUCGUCCCGGCCUGAGU......... 24 11
Shared 3' Terminus
.....................................................GCACUCGUCCCGGCCUGA.......... 18 10
...................................................UUGCACUCGUCCCGGCCUGA.......... 20 15
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.................................................AUUGCACUCGUCCCGGCCUGA.......... 21 68
.................................................AUAUUGCACUCGUCCCGGCCUGA.......... 23 9
Subsequence
Others
.........AGGCCGAGUCGUCUGCAU..................................................... 18 6
.........AGGCCGAGUCGUCUGCAUU.................................................... 19 40
.........AGGCCGAGUCGUCUGCAUUA................................................... 20 34
.........AGGCCGAGUCGUCUGCAUUAU.................................................. 21 664
.........AGGCCGAGUCGUCUGCAUUAUU................................................. 22 2294


#asu-miR-100a-1
GGCGGUAAACCCGUAGAUCCGAACUUGUGUUGUGUAUUUGGUAACGCAAUUCGCCUCUCGGGUGCAUCGCUGAUUAG
((((((..(((((.(((..((((.(((((((((.........)))))))))))..)))))))..))))))).....
Total sRNA: 26254824 shared 5' end with miRNA: 12490303 shared 3' end with miRNA: 60351
miRNA
.......AACCCGUAGAUCCGAACUUGUGUU.............................................. 24 13669488
Shared 5' Terminus
.......AACCCGUAGAUCCGAACU..................................................... 18 15136
.......AACCCGUAGAUCCGAACUU.................................................... 19 14911
.......AACCCGUAGAUCCGAACUUG................................................... 20 6824
.......AACCCGUAGAUCCGAACUUGU.................................................. 21 164292
.......AACCCGUAGAUCCGAACUUGUG.................................................. 22 238228
.......AACCCGUAGAUCCGAACUUGUGU................................................. 23 12030377
.......AACCCGUAGAUCCGAACUUGUGUUG............................................... 25 19113
.......AACCCGUAGAUCCGAACUUGUGUUGU.............................................. 26 1374
Shared 3' Terminus
............UAGAUCCGAACUUGUGUU.................................................. 18 1119
............GUAGAUCCGAACUUGUGUU.................................................. 19 13262
..........CGUAGAUCCGAACUUGUGUU.................................................. 20 23157
.........CCGUAGAUCCGAACUUGUGUU.................................................. 21 7899
.........CCCGUAGAUCCGAACUUGUGUU................................................. 22 1213
........ACCCGUAGAUCCGAACUUGUGUU................................................. 23 3766
......AAACCCGUAGAUCCGAACUUGUGUU................................................ 25 9930
Subsequence
........ACCCGUAGAUCCGAACUUGUGU.................................................. 22 2503
.........CCCGUAGAUCCGAACUUGUGU.................................................. 21 1124
..........CCGUAGAUCCGAACUUGUG.................................................. 19 103
.........CCGUAGAUCCGAACUUGUGU.................................................. 20 4013
..........CGUAGAUCCGAACUUGUG................................................... 18 333
..........CGUAGAUCCGAACUUGUGU.................................................. 19 8612
............GUAGAUCCGAACUUGUGU.................................................. 18 8987
Others
......AAACCCGUAGAUCCGAACUUGUG.................................................. 23 475
......AAACCCGUAGAUCCGAACUUGUGU................................................. 24 6456
.............................................CGCAAUUCGCCUCUCGGGUGCA.......... 22 1610


#asu-miR-100a-2
CGAUUCAUUGUGUACUGAAGCAGGGGUGUGUGCGGUCAACCCGUAGAUCCGAACUUGUGUUGGGUUUGGUAACAUGAGCUCGGCACUCGGGUAGACUGCGUCAUCCCAGCCCGCCACCCAAUGCCCG
.....(((((.((..((..((.((((((...((((((.(((((.((..((((.((..(((((.......)))))..))).))))..)))))))..))))))..))))))).))..)).))))....
Total sRNA: 26273001 shared 5' end with miRNA: 12489821 shared 3' end with miRNA: 51766
miRNA
.....................................AACCCGUAGAUCCGAACUUGUGUU.......................................................................... 24 13669488
Shared 5' Terminus
.....................................AACCCGUAGAUCCGAACU.............................................................................. 18 15136
.....................................AACCCGUAGAUCCGAACUU............................................................................. 19 14911
.....................................AACCCGUAGAUCCGAACUUG............................................................................ 20 6824
.....................................AACCCGUAGAUCCGAACUUGU........................................................................... 21 164292
.....................................AACCCGUAGAUCCGAACUUGUG.......................................................................... 22 238228
.....................................AACCCGUAGAUCCGAACUUGUGU........................................................................ 23 12030377
.....................................AACCCGUAGAUCCGAACUUGUGUUG...................................................................... 25 19113
.....................................AACCCGUAGAUCCGAACUUGUGUUGG..................................................................... 26 297
.....................................AACCCGUAGAUCCGAACUUGUGUUGGGU.................................................................... 28 114
.....................................AACCCGUAGAUCCGAACUUGUGUUGGGUU................................................................... 29 137
.....................................AACCCGUAGAUCCGAACUUGUGUUGGGUUU.................................................................. 30 118
.....................................AACCCGUAGAUCCGAACUUGUGUUGGGUUUG................................................................. 31 127
Shared 3' Terminus
.......................................UAGAUCCGAACUUGUGUU.............................................................................. 18 1119
.....................................GUAGAUCCGAACUUGUGUU.............................................................................. 19 13262
....................................CGUAGAUCCGAACUUGUGUU.............................................................................. 20 23157
...................................CCGUAGAUCCGAACUUGUGUU.............................................................................. 21 7899
....................................CCCGUAGAUCCGAACUUGUGUU............................................................................. 22 1213
...................................ACCCGUAGAUCCGAACUUGUGUU............................................................................. 23 3766
.................................CAACCCGUAGAUCCGAACUUGUGUU............................................................................ 25 1275
Subsequence
....................................ACCCGUAGAUCCGAACUUGUGU.............................................................................. 22 2503
....................................CCCGUAGAUCCGAACUUGUGU.............................................................................. 21 1124
...................................CCGUAGAUCCGAACUUGUG.............................................................................. 19 103
....................................CCGUAGAUCCGAACUUGUGU.............................................................................. 20 4013
....................................CGUAGAUCCGAACUUGUG................................................................................ 18 333
....................................CGUAGAUCCGAACUUGUGU.............................................................................. 19 8612
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.....................................GUAGAUCCGAACUUGUGU..................................................................... 18 8987
Others
...............GAAGCAGGGGUGUGUGCGGUC.................................................................................... 21 32
.................................CAACCCGUAGAUCCGAACUUGUGU.................................................................... 24 1110
.....................................................................CAUGAGCUCGGCACUCGGGUAG.............................. 22 794
.....................................................................CAUGAGCUCGGCACUCGGGUAGA............................. 23 19858
.....................................................................AUGAGCUCGGCACUCGGGUAG.............................. 21 192
.....................................................................AUGAGCUCGGCACUCGGGUAGA............................. 22 7374
.....................................................................UGAGCUCGGCACUCGGGUAGA.............................. 21 3902
.....................................................................................CUGCGUCAUCCCAGCCCGC.............. 19 209
.....................................................................................CUGCGUCAUCCCAGCCCGCC............. 20 652
.....................................................................................CUGCGUCAUCCCAGCCCGCCA............ 21 296
.....................................................................................CUGCGUCAUCCCAGCCCGCCACC......... 23 378
.....................................................................................CUGCGUCAUCCCAGCCCGCCACCC........ 24 183
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#asu-miR-100b

```
GCUCUCGGUCAACCCGUAGAUUCGAAUUUGUGUUUACAUAAUGGAAUAACACUGUUCGAUUCUCGGGUAGAUCGAAUGCU
((..((((((.((((((.(((.(((((((..((((((..(.....)....)))))).))))))).)))))))).))))))..)).
Total sRNA: 2129287 shared 5' end with miRNA: 549294 shared 3' end with miRNA: 6617
miRNA
..........AACCCGUAGAUUCGAAUUUGUGUU.......................................... 24 1569878
Shared 5' Terminus
..........AACCCGUAGAUUCGAAUU.................................................. 18 510
..........AACCCGUAGAUUCGAAUUU................................................. 19 922
..........AACCCGUAGAUUCGAAUUUG................................................ 20 524
..........AACCCGUAGAUUCGAAUUUGU.............................................. 21 7750
..........AACCCGUAGAUUCGAAUUUGUG............................................. 22 4713
..........AACCCGUAGAUUCGAAUUUGUGU............................................ 23 443666
..........AACCCGUAGAUUCGAAUUUGUGUUU.......................................... 25 90653
..........AACCCGUAGAUUCGAAUUUGUGUUUA......................................... 26 310
Shared 3' Terminus
..............UAGAUUCGAAUUUGUGUU.............................................. 18 760
.............GUAGAUUCGAAUUUGUGUU............................................. 19 1532
............CGUAGAUUCGAAUUUGUGUU............................................ 20 1758
...........CCGUAGAUUCGAAUUUGUGUU............................................ 21 639
..........CCCGUAGAUUCGAAUUUGUGUU............................................ 22 180
..........ACCCGUAGAUUCGAAUUUGUGUU........................................... 23 737
.........CAACCCGUAGAUUCGAAUUUGUGUU.......................................... 25 996
Subsequence
..........ACCCGUAGAUUCGAAUUUGUGU............................................ 22 196
...........CCGUAGAUUCGAAUUUGUGU............................................. 20 157
............CGUAGAUUCGAAUUUGUGU............................................ 19 412
.............GUAGAUUCGAAUUUGUGU............................................ 18 310
Others
.........CAACCCGUAGAUUCGAAUUUGUGU.......................................... 24 618
.........CAACCCGUAGAUUCGAAUUUGUGUUU........................................ 26 129
............CGUAGAUUCGAAUUUGUGUUU.......................................... 21 141
.................................................CACUGUUCGAUUCUCGGGUAGA..... 22 894
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#asu-miR-100c

```
AGCCGGUGUGCGGUGUACCCGUAGCUCCGAAAUCGUGUCAGCAUUUGAAUACACGUUUCGUUGCUCGGGUGCCCUGCGCAUAUUUCCG
..((((((((((.(((((((.(((..(((((.(((((...(....)...)))))))))..))))))))))..)))))))).....)))
Total sRNA: 3790545 shared 5' end with miRNA: 91977 shared 3' end with miRNA: 11201
miRNA
..............UACCCGUAGCUCCGAAAUCGUGU....................................................... 23 3682744
Shared 5' Terminus
..............UACCCGUAGCUCCGAAAU.............................................................. 18 1606
..............UACCCGUAGCUCCGAAAUC............................................................. 19 7389
..............UACCCGUAGCUCCGAAAUCG............................................................ 20 3914
..............UACCCGUAGCUCCGAAAUCGU........................................................... 21 27696
..............UACCCGUAGCUCCGAAAUCGUG.......................................................... 22 48906
..............UACCCGUAGCUCCGAAAUCGUGUC....................................................... 24 2225
..............UACCCGUAGCUCCGAAAUCGUGUCA...................................................... 25 114
Shared 3' Terminus
.................GUAGCUCCGAAAUCGUGU.......................................................... 18 3980
................CGUAGCUCCGAAAUCGUGU.......................................................... 19 4454
...............CCGUAGCUCCGAAAUCGUGU.......................................................... 20 1074
..............CCCGUAGCUCCGAAAUCGUGU.......................................................... 21 467
.............ACCCGUAGCUCCGAAAUCGUGU.......................................................... 22 854
............GUACCCGUAGCUCCGAAAUCGUGU.......................................................... 24 369
Subsequence
Others
..................................................ACGUUUCGUUGCUCGGGUGC.................. 20 213
```

```
.................................................ACGUUUCGUUGCUCGGGUGCC..... 21 3900


#asu-miR-100d
GAUGGGCGGUGAACCCGUAUGCUGUUGGGUGUGUUGGGUUCGGUGACACGCUACGGUGUUCGGGUCCACCGAGGCGUC
((((..(((((.(((((.(((((((..(((((((.........)))))))))))))))).)))))..)))))...))))
Total sRNA: 2518817 shared 5' end with miRNA: 664035 shared 3' end with miRNA: 13557
miRNA
..........AACCCGUAUGCUGUUGGGUGUGU..................................... 23 1837370
Shared 5' Terminus
..........AACCCGUAUGCUGUUGGG..................................... 18 1980
..........AACCCGUAUGCUGUUGGGU..................................... 19 28601
..........AACCCGUAUGCUGUUGGGUG..................................... 20 1388
..........AACCCGUAUGCUGUUGGGUGU..................................... 21 346435
..........AACCCGUAUGCUGUUGGGUGUG..................................... 22 29059
..........AACCCGUAUGCUGUUGGGUGUGU..................................... 24 255728
..........AACCCGUAUGCUGUUGGGUGUGUUG..................................... 25 643
..........AACCCGUAUGCUGUUGGGUGUGUUGG..................................... 26 107
Shared 3' Terminus
..............GUAUGCUGUUGGGUGUGU..................................... 18 3912
.............CGUAUGCUGUUGGGUGUGU..................................... 19 5789
............CCGUAUGCUGUUGGGUGUGU..................................... 20 2460
...........CCCGUAUGCUGUUGGGUGUGU..................................... 21 384
..........ACCCGUAUGCUGUUGGGUGUGU..................................... 22 1003
Subsequence
............CCGUAUGCUGUUGGGUGU..................................... 18 650
............CCGUAUGCUGUUGGGUGUG..................................... 19 143
.............CGUAUGCUGUUGGGUGUG..................................... 18 365
Others
..........ACCCGUAUGCUGUUGGGUGUGUU..................................... 23 143
............CCGUAUGCUGUUGGGUGUGUU..................................... 21 527
.............CGUAUGCUGUUGGGUGUGUU..................................... 20 788
..............GUAUGCUGUUGGGUGUGUU..................................... 19 450
...............UAUGCUGUUGGGUGUGUU..................................... 18 108
.............................................CACGCUACGGUGUUCGGGUCC.......... 21 11


#asu-miR-100e
UGUGUGCGGUGAACCUGAGGACCGUAUGCUGUGUUUGGAUAGGUAACACGCAACGGUGUUCGGGUCCACUAAAGCAUCC
.((((..((((.(((((((.(((((.(((.(((((.........)))))))))))))).)))))))..))))...))))..
Total sRNA: 724731 shared 5' end with miRNA: 319436 shared 3' end with miRNA: 5719
miRNA
..........AACCUGAGGACCGUAUGCUGUGUU..................................... 24 396545
Shared 5' Terminus
..........AACCUGAGGACCGUAUGC..................................... 18 2302
..........AACCUGAGGACCGUAUGCU..................................... 19 5305
..........AACCUGAGGACCGUAUGCUG..................................... 20 2814
..........AACCUGAGGACCGUAUGCUGU..................................... 21 7026
..........AACCUGAGGACCGUAUGCUGUG..................................... 22 7368
..........AACCUGAGGACCGUAUGCUGUGU..................................... 23 261921
..........AACCUGAGGACCGUAUGCUGUGUUU..................................... 25 32631
Shared 3' Terminus
...............AGGACCGUAUGCUGUGUU..................................... 18 119
..............GAGGACCGUAUGCUGUGUU..................................... 19 1045
.............UGAGGACCGUAUGCUGUGUU..................................... 20 3479
............CUGAGGACCGUAUGCUGUGUU..................................... 21 779
...........CCUGAGGACCGUAUGCUGUGUU..................................... 22 115
...........ACCUGAGGACCGUAUGCUGUGUU..................................... 23 177
Subsequence
...........ACCUGAGGACCGUAUGCUGUGU..................................... 22 124
............CUGAGGACCGUAUGCUGUGU..................................... 20 342
.............UGAGGACCGUAUGCUGUGU..................................... 19 1038
..............GAGGACCGUAUGCUGUGU..................................... 18 368
Others
.........UGAACCUGAGGACCGUAUGCUGUGU..................................... 25 117
.............UGAGGACCGUAUGCUGUGUUU..................................... 21 167
.............................................CACGCAACGGUGUUCGGGUCCA.......... 22 348
```

```
#asu-miR-124
UUUGCGACACGCCUUCACCGGUGACUUUGGUGUGAAGCAGCCUACUAAGGCACGCGGUGAAUGCCAAUCGCUCUUG
...((((...((.((((((((((.(((((((.(......).)))))))))).)))))))).))...)))).....
Total sRNA: 40873 shared 5' end with miRNA: 14305 shared 3' end with miRNA: 123
miRNA
.........................................UAAGGCACGCGGUGAAUGCCA......... 21 26085
Shared 5' Terminus
.........................................UAAGGCACGCGGUGAAUG............. 18 1444
.........................................UAAGGCACGCGGUGAAUGC............ 19 363
.........................................UAAGGCACGCGGUGAAUGCC........... 20 1327
.........................................UAAGGCACGCGGUGAAUGCCAA......... 22 10919
.........................................UAAGGCACGCGGUGAAUGCCAAU........ 23 252
Shared 3' Terminus
.............................................GGCACGCGGUGAAUGCCA......... 18 13
.........................................CUAAGGCACGCGGUGAAUGCCA......... 22 95
Subsequence
Others
.........CGCCUUCACCGGUGACUUUGGU.......................................... 22 33
.........................................CUAAGGCACGCGGUGAAU.............. 18 16
.........................................CUAAGGCACGCGGUGAAUG............. 19 11
.........................................CUAAGGCACGCGGUGAAUGC............ 20 9
.........................................CUAAGGCACGCGGUGAAUGCC........... 21 21
.........................................CUAAGGCACGCGGUGAAUGCCA.......... 23 88
.............................................GCACGCGGUGAAUGCCAA......... 18 128


#asu-miR-133
CCGUUCACGUACCUGGUUGUAGCCGAGCCAAAUUGUGUUUAGUGUAUCAAUUGGUCCCCUUCAACCAGCUACGAAAAGCG
.((((..((((.(((((((.((..(..((((.(((.............)))))))..).)).)))))))..))))...))))
Total sRNA: 39520 shared 5' end with miRNA: 6780 shared 3' end with miRNA: 283
miRNA
.............................................AUUGGUCCCCUUCAACCAGCUA......... 22 13117
Shared 5' Terminus
.............................................AUUGGUCCCCUUCAACCA............. 18 19
.............................................AUUGGUCCCCUUCAACCAG............ 19 79
.............................................AUUGGUCCCCUUCAACCAGC........... 20 69
.............................................AUUGGUCCCCUUCAACCAGCU.......... 21 6602
.............................................AUUGGUCCCCUUCAACCAGCUAC........ 23 11
Shared 3' Terminus
...................................................GUCCCCUUCAACCAGCUA......... 18 21
.................................................GGUCCCCUUCAACCAGCUA......... 19 6
.............................................UUGGUCCCCUUCAACCAGCUA......... 21 251
Subsequence
.............................................UUGGUCCCCUUCAACCAGCU.......... 20 102
Others
..........CCUGGUUGUAGCCGAGCC.................................................. 18 109
..........CCUGGUUGUAGCCGAGCCA................................................. 19 48
..........CCUGGUUGUAGCCGAGCCAA................................................ 20 56
..........CCUGGUUGUAGCCGAGCCAAA............................................... 21 217
..........CCUGGUUGUAGCCGAGCCAAAU.............................................. 22 727
..........CCUGGUUGUAGCCGAGCCAAAUU............................................. 23 6136
..........CCUGGUUGUAGCCGAGCCAAAUUG............................................ 24 10637
..........CCUGGUUGUAGCCGAGCCAAAUUGU........................................... 25 999
..........CCUGGUUGUAGCCGAGCCAAAUUGUG.......................................... 26 16
..........CCUGGUUGUAGCCGAGCCAAAUUGUGU......................................... 27 6
...........CUGGUUGUAGCCGAGCCAAAU.............................................. 21 5
...........CUGGUUGUAGCCGAGCCAAAUU............................................. 22 17
...........CUGGUUGUAGCCGAGCCAAAUUG............................................ 23 35
...........CUGGUUGUAGCCGAGCCAAAUUGU........................................... 24 6
.............GGUUGUAGCCGAGCCAAAUUG............................................ 21 6
............GUUGUAGCCGAGCCAAAUU.............................................. 19 19
............GUUGUAGCCGAGCCAAAUUG............................................ 20 18
............GUUGUAGCCGAGCCAAAUUGU........................................... 21 5
.............UUGUAGCCGAGCCAAAUU.............................................. 18 6
.............UUGUAGCCGAGCCAAAUUG............................................ 19 15
..............UGUAGCCGAGCCAAAUUG............................................ 18 6
..............GUAGCCGAGCCAAAUUGU............................................ 18 5
.......................AGCCAAAUUGUGUUUAGUGUA................................. 21 8
```

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#asu-miR-137
AGCAAAAGGUAUUCUCCGGUAAUGACAUAGUGCAUUGAAAGCUGUUAUUGCUUGAGAAUACAAAUUGUUGUCCGGC
(((((...(((((((((.((((((((((....((.......)))))))))))).)))))))))...)))))......
Total sRNA: 5713 shared 5' end with miRNA: 202 shared 3' end with miRNA: 12
miRNA
.........................................UUAUUGCUUGAGAAUACAAAU.......... 21 5447
Shared 5' Terminus
.........................................UUAUUGCUUGAGAAUACA.............. 18 6
.........................................UUAUUGCUUGAGAAUACAA............. 19 13
.........................................UUAUUGCUUGAGAAUACAAA............ 20 96
.........................................UUAUUGCUUGAGAAUACAAAUU......... 22 87
Shared 3' Terminus
.........................................AUUGCUUGAGAAUACAAAU.......... 19 3
.........................................UAUUGCUUGAGAAUACAAAU.......... 20 4
.........................................GUUAUUGCUUGAGAAUACAAAU.......... 22 2
.........................................UGUUAUUGCUUGAGAAUACAAAU.......... 23 3
Subsequence
Others
......AGGUAUUCUCCGGUAAUGACA.................................................. 21 30
......AGGUAUUCUCCGGUAAUGACAU................................................. 22 9
.....................................CUGUUAUUGCUUGAGAAUACAAA............ 23 7


#asu-miR-184
UGAUUUUGAGUGCUUAUCAGCUGCCAGCCCUGUUGCAACUUGAAACUGGACGGAAGACUGAUAAGAGCCUCAAUUUUGCCC
.((..((((((..((((((((((.((..((..(((.(.....).))).))..)).)).)))))))))...))))))..))....
Total sRNA: 9876 shared 5' end with miRNA: 4619 shared 3' end with miRNA: 21
miRNA
.........................................UGGACGGAAGACUGAUAAGAGC.......... 22 5145
Shared 5' Terminus
.........................................UGGACGGAAGACUGAUAA.............. 18 5
.........................................UGGACGGAAGACUGAUAAG............. 19 17
.........................................UGGACGGAAGACUGAUAAGA............ 20 157
.........................................UGGACGGAAGACUGAUAAGAG........... 21 469
.........................................UGGACGGAAGACUGAUAAGAGCC......... 23 2663
.........................................UGGACGGAAGACUGAUAAGAGCCU........ 24 1295
.........................................UGGACGGAAGACUGAUAAGAGCCUC....... 25 13
Shared 3' Terminus
.................................................CGGAAGACUGAUAAGAGC.......... 18 2
...............................................GACGGAAGACUGAUAAGAGC.......... 20 4
.........................................CUGGACGGAAGACUGAUAAGAGC.......... 23 13
Subsequence
Others
.........UGCUUAUCAGCUGCCAGCCCUGU.............................................. 23 12
.........UGCUUAUCAGCUGCCAGCCCUGUU............................................. 24 5
.........GCUUAUCAGCUGCCAGCCCUGUU.............................................. 23 3
.........................................CUGGACGGAAGACUGAUAAG............ 20 2
.........................................CUGGACGGAAGACUGAUAAGAGCC......... 24 38
...............................................GGACGGAAGACUGAUAAGAGCC......... 22 4
...............................................GGACGGAAGACUGAUAAGAGCCU........ 23 6
.................................................GGAAGACUGAUAAGAGCC.......... 18 2
.................................................GGAAGACUGAUAAGAGCCU........ 19 8


#asu-miR-228
CGUACACUCAAUGGCACUAGAUGAAUUCACGGUCCUUUUUGCUGUUCCGUGUAUUCACCAGUUCCAUAGAGUUGCGUUGGC
((((.((((.((((.(((.(.(((((.(((((..(........)..)))))).)))))).))).)))).)))))).....
Total sRNA: 107629 shared 5' end with miRNA: 22084 shared 3' end with miRNA: 449
miRNA
.........AAUGGCACUAGAUGAAUUCACGG.............................................. 23 84630
Shared 5' Terminus
.........AAUGGCACUAGAUGAAUU.................................................... 18 99
.........AAUGGCACUAGAUGAAUUC................................................... 19 64
.........AAUGGCACUAGAUGAAUUCA.................................................. 20 284
.........AAUGGCACUAGAUGAAUUCAC................................................. 21 330
.........AAUGGCACUAGAUGAAUUCACG................................................ 22 15979
.........AAUGGCACUAGAUGAAUUCACGGU.............................................. 24 5323
Shared 3' Terminus
.............CACUAGAUGAAUUCACGG.................................................. 18 155
............GCACUAGAUGAAUUCACGG.................................................. 19 61
............GGCACUAGAUGAAUUCACGG.................................................. 20 77
```

```
.........AUGGCACUAGAUGAAUUCACGG..................................................... 22 104
........CAAUGGCACUAGAUGAAUUCACGG..................................................... 24 34
Subsequence
............GGCACUAGAUGAAUUCACG..................................................... 19 34
Others
.........AUGGCACUAGAUGAAUUCACGGU.................................................... 23 224
................................................UGUAUUCACCAGUUCCAUAGAG.......... 22 12


#asu-miR-236
UGUUGAUUGGCUGUCGUCCUACCUGCAAGUUAUUAGAGUGAAUAAUGACGUCUAAUACUGUCAGGUAAUGACGACAGCUUGUCC
....(((.((((((((((.((((((..(((.(((((((.........)).)))))))))..))))))..)))))))))).))).
Total sRNA: 89106 shared 5' end with miRNA: 4147 shared 3' end with miRNA: 180
miRNA
................................................UAAUACUGUCAGGUAAUGACGA.......... 22 84733
Shared 5' Terminus
................................................UAAUACUGUCAGGUAAUG.............. 18 71
................................................UAAUACUGUCAGGUAAUGA............. 19 40
................................................UAAUACUGUCAGGUAAUGAC............ 20 73
................................................UAAUACUGUCAGGUAAUGACG........... 21 3621
................................................UAAUACUGUCAGGUAAUGACGAC......... 23 338
Shared 3' Terminus
..........................................................ACUGUCAGGUAAUGACGA.......... 18 71
.........................................................AAUACUGUCAGGUAAUGACGA.......... 21 36
................................................CUAAUACUGUCAGGUAAUGACGA.......... 23 37
Subsequence
Others
..............GUCCUACCUGCAAGUUAUUAGA..................................................... 22 1


#asu-miR-250
GACGGCAUCUAACUGGCAGUUGACUGUUGAUCCGUCGUAUCGAAUCGAAUCACAGCCAAACUGUUGGUUAGGUUCAGUU
(((.(.(((((((..((((((..((((.(((.(((((...))))..)).)))))))...)))))))..)))))))).).)))
Total sRNA: 14264 shared 5' end with miRNA: 552 shared 3' end with miRNA: 57
miRNA
.............................................AAUCACAGCCAAACUGUUGGUUA......... 23 10049
Shared 5' Terminus
.............................................AAUCACAGCCAAACUGUU.............. 18 4
.............................................AAUCACAGCCAAACUGUUG............. 19 23
.............................................AAUCACAGCCAAACUGUUGGU........... 21 58
.............................................AAUCACAGCCAAACUGUUGGUU.......... 22 374
.............................................AAUCACAGCCAAACUGUUGGUUAG........ 24 92
Shared 3' Terminus
.....................................................CAGCCAAACUGUUGGUUA......... 18 6
..................................................ACAGCCAAACUGUUGGUUA......... 19 34
.............................................AUCACAGCCAAACUGUUGGUUA......... 22 14
Subsequence
.....................................................ACAGCCAAACUGUUGGUU.......... 18 5
Others
.........AACUGGCAGUUGACUGUUGAUCCG.................................................. 24 4
...........ACUGGCAGUUGACUGUUG....................................................... 18 8
..........ACUGGCAGUUGACUGUUGA...................................................... 19 28
...........ACUGGCAGUUGACUGUUGAU..................................................... 20 40
...........ACUGGCAGUUGACUGUUGAUC.................................................... 21 26
...........ACUGGCAGUUGACUGUUGAUCC................................................... 22 184
...........ACUGGCAGUUGACUGUUGAUCCG.................................................. 23 2967
...........ACUGGCAGUUGACUGUUGAUCCGU................................................. 24 98
...........ACUGGCAGUUGACUGUUGAUCCGUCGUAUCGAAUC...................................... 35 10
...........ACUGGCAGUUGACUGUUGAUCCGUCGUAUCGAAUCG..................................... 36 7
............CUGGCAGUUGACUGUUGAUCCG.................................................. 22 42
.............UGGCAGUUGACUGUUGAUCCG.................................................. 21 16
.....................ACUGUUGAUCCGUCGUAUCGAA.......................................... 22 8
.....................ACUGUUGAUCCGUCGUAUCGAAU......................................... 23 10
......................CUGUUGAUCCGUCGUAUCGA.......................................... 20 8
......................CUGUUGAUCCGUCGUAUCGAA......................................... 21 31
......................CUGUUGAUCCGUCGUAUCGAAU........................................ 22 44
.......................UGUUGAUCCGUCGUAUCGAAUCG...................................... 23 4
```

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#asu-miR-252
GGGACCAGCCUAAGUAGUAGUGCCGCAGGUAACAUGACUUGGGAUUACCUGCUCCCUGCUGCUUAACUUGGUACCGCUUUACG
((.(((((..((((((((((.(..((((((((((.....))...))))))))..))))))))))..))))))..)).........
Total sRNA: 358 shared 5' end with miRNA: 13 shared 3' end with miRNA: 4
miRNA
.........CUAAGUAGUAGUGCCGCAGGUAA.................................................... 23 339
Shared 5' Terminus
.........CUAAGUAGUAGUGCCGCA.......................................................... 18 3
.........CUAAGUAGUAGUGCCGCAG......................................................... 19 2
.........CUAAGUAGUAGUGCCGCAGGU....................................................... 21 3
.........CUAAGUAGUAGUGCCGCAGGUA...................................................... 22 5
Shared 3' Terminus
.........UAAGUAGUAGUGCCGCAGGUAA...................................................... 22 4
Subsequence
Others
.............................................ACCUGCUCCCUGCUGCUUAACU.............. 22 1


#asu-miR-279a
CAUUGCCACAUUCUUUGCUGGGCAUGGCUCUAUGUCAUGCUAUCUAGUUUCAUGACUAGAUCCAUACUCAGCUAGGGGUGUG
......(((((((((.((((((.((((.((((.((((((..((...))..))..)))))))))).))))).))))))).)))))
Total sRNA: 5484173 shared 5' end with miRNA: 30653 shared 3' end with miRNA: 15800
miRNA
.....................................................UGACUAGAUCCAUACUCAGCU......... 21 5436217
Shared 5' Terminus
.....................................................UGACUAGAUCCAUACUCA............ 18 208
.....................................................UGACUAGAUCCAUACUCAG........... 19 2987
.....................................................UGACUAGAUCCAUACUCAGC.......... 20 10441
.....................................................UGACUAGAUCCAUACUCAGCUA........ 22 16711
.....................................................UGACUAGAUCCAUACUCAGCUAG....... 23 304
Shared 3' Terminus
.......................................................CUAGAUCCAUACUCAGCU......... 18 1809
......................................................ACUAGAUCCAUACUCAGCU......... 19 1319
.....................................................GACUAGAUCCAUACUCAGCU......... 20 1168
....................................................AUGACUAGAUCCAUACUCAGCU......... 22 11431
Subsequence
Others
................CUGGGCAUGGCUCUAUGU.................................................. 18 338
................CUGGGCAUGGCUCUAUGUCAUG.............................................. 22 432
.....................................................AUGACUAGAUCCAUACUCAGC.......... 21 152


#asu-miR-279b
AUUCGGCGUCACUGGAACUGGUUUGCAGUCUAGUGCAUGCAAUAUGAAGUCAUGACUAGACUGAUAACCAGCUCUAGUUUCGUUC
....((((..((((((.((((((..(((((((((.(((((........).)))))))))))))..))))))).))))))..)))).
Total sRNA: 1709827 shared 5' end with miRNA: 30869 shared 3' end with miRNA: 4070
miRNA
.....................................................UGACUAGACUGAUAACCAGCUC........... 22 1650149
Shared 5' Terminus
.....................................................UGACUAGACUGAUAACCA............... 18 2524
.....................................................UGACUAGACUGAUAACCAG.............. 19 865
.....................................................UGACUAGACUGAUAACCAGC............. 20 1568
.....................................................UGACUAGACUGAUAACCAGCU............ 21 23687
.....................................................UGACUAGACUGAUAACCAGCUCU.......... 23 2222
Shared 3' Terminus
.......................................................UAGACUGAUAACCAGCUC........... 18 995
......................................................CUAGACUGAUAACCAGCUC........... 19 719
.....................................................ACUAGACUGAUAACCAGCUC........... 20 827
....................................................GACUAGACUGAUAACCAGCUC........... 21 1322
...................................................AUGACUAGACUGAUAACCAGCUC........... 23 192
Subsequence
Others
..............AACUGGUUUGCAGUCUAGUGCAU.................................................. 23 150
..............AACUGGUUUGCAGUCUAGUGCAUG................................................. 24 120
..............ACUGGUUUGCAGUCUAGU....................................................... 18 766
..............ACUGGUUUGCAGUCUAGUGC.................................................... 20 356
..............ACUGGUUUGCAGUCUAGUGCA................................................... 21 303
..............ACUGGUUUGCAGUCUAGUGCAU.................................................. 22 14419
..............ACUGGUUUGCAGUCUAGUGCAUG................................................. 23 7993
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#asu-miR-279c
UUACUGGGCGUCACUGGAGCUGGCUUACCGUCUAGUGCAUGUAAUGUGAAAUCAUGACUAGACUGGUAACCUGCUCUAGUUUCGUUCCU
.....(((((..(((((((((.((.((((((((((((.((((...........)))))))))))).)))))))..)))))))..)))))..
Total sRNA: 1161787 shared 5' end with miRNA: 91574 shared 3' end with miRNA: 1607
miRNA
.....................................................UGACUAGACUGGUAACCUGCUC..... 22 1066048
Shared 5' Terminus
.....................................................UGACUAGACUGGUAACCU..... 18 3767
.....................................................UGACUAGACUGGUAACCUG..... 19 3201
.....................................................UGACUAGACUGGUAACCUGC..... 20 3575
.....................................................UGACUAGACUGGUAACCUGCU..... 21 68507
.....................................................UGACUAGACUGGUAACCUGCUCU..... 23 12462
Shared 3' Terminus
.....................................................UAGACUGGUAACCUGCUC..... 18 367
.....................................................CUAGACUGGUAACCUGCUC..... 19 320
.....................................................ACUAGACUGGUAACCUGCUC..... 20 243
.....................................................GACUAGACUGGUAACCUGCUC..... 21 440
.....................................................AUGACUAGACUGGUAACCUGCUC..... 23 223
Subsequence
Others
UUACUGGGCGUCACUGGA.......................................................................... 18 454
.................GCUGGCUUACCGUCUAGUGCAU.......................................................... 22 816
.................GCUGGCUUACCGUCUAGUGCAUG......................................................... 23 247


#asu-miR-375
GUUUUCACUCUUCGCAAGCGAACUGAUCAAAACCCACACUCGGUGACGGACGUUUUGUUCGUUUUGCUUGCGAUCAGUGCGAGCGUAC
((((.((((..((((((((((.(((.((((((.....(((....))).)).)))))).)))).)))))))))..)))).))))....
Total sRNA: 549888 shared 5' end with miRNA: 107381 shared 3' end with miRNA: 3132
miRNA
.....................................................UUUGUUCGUUUUGCUUGCGAUCA..... 23 398062
Shared 5' Terminus
.....................................................UUUGUUCGUUUUGCUUGC..... 18 516
.....................................................UUUGUUCGUUUUGCUUGCG..... 19 1364
.....................................................UUUGUUCGUUUUGCUUGCGA..... 20 2096
.....................................................UUUGUUCGUUUUGCUUGCGAU..... 21 24162
.....................................................UUUGUUCGUUUUGCUUGCGAUC..... 22 78858
.....................................................UUUGUUCGUUUUGCUUGCGAUCAG..... 24 340
Shared 3' Terminus
.....................................................UCGUUUUGCUUGCGAUCA..... 18 608
.....................................................UUCGUUUUGCUUGCGAUCA..... 19 718
.....................................................UUGUUCGUUUUGCUUGCGAUCA..... 22 1584
.....................................................UUUGUUCGUUUUGCUUGCGAUCA..... 24 148
Subsequence
.....................................................UUGUUCGUUUUGCUUGCGAU..... 20 108
.....................................................UUGUUCGUUUUGCUUGCGAUC..... 21 435
Others
..........UUCGCAAGCGAACUGAUC.............................................................. 18 280
..........UUCGCAAGCGAACUGAUCA............................................................. 19 132
..........UUCGCAAGCGAACUGAUCAA............................................................ 20 188
..........UUCGCAAGCGAACUGAUCAAA........................................................... 21 1453
..........UUCGCAAGCGAACUGAUCAAAA.......................................................... 22 10691
..........UUCGCAAGCGAACUGAUCAAAAC......................................................... 23 27361
.....................................................UUUUGUUCGUUUUGCUUGCGAUC..... 23 164


#asu-miR-750
UGGCAGUUGGAGGUUAGAUCUCGGGCAGAGCAUAUUCGGUUAUGCCAGAUCUAUUACUUCCAACUGACAUCGACUCGU
((.((((((((((((((((..((((.(((.......))).))))))))))..))))))))))).))..........
Total sRNA: 80018 shared 5' end with miRNA: 9161 shared 3' end with miRNA: 489
miRNA
.........................................CCAGAUCUAUUACUUCCAACUGA........... 23 56799
Shared 5' Terminus
.........................................CCAGAUCUAUUACUUCCA..... 18 267
.........................................CCAGAUCUAUUACUUCCAA..... 19 1052
.........................................CCAGAUCUAUUACUUCCAAC..... 20 215
.........................................CCAGAUCUAUUACUUCCAACU..... 21 886
.........................................CCAGAUCUAUUACUUCCAACUG..... 22 6716
Shared 3' Terminus
.............................................UCUAUUACUUCCAACUGA........... 18 68
.............................................AUCUAUUACUUCCAACUGA........... 19 22
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.............................................GAUCUAUUACUUCCAACUGA.......... 20 61
.............................................AGAUCUAUUACUUCCAACUGA.......... 21 21
.............................................CAGAUCUAUUACUUCCAACUGA.......... 22 316
Subsequence
.............................................CAGAUCUAUUACUUCCAACUG........... 21 24
Others
....AGUUGGAGGUUAGAUCUC....................................................... 18 19
....AGUUGGAGGUUAGAUCUCG...................................................... 19 148
....AGUUGGAGGUUAGAUCUCGG..................................................... 20 491
....AGUUGGAGGUUAGAUCUCGGG.................................................... 21 984
....AGUUGGAGGUUAGAUCUCGGGC................................................... 22 1450
....AGUUGGAGGUUAGAUCUCGGGCA.................................................. 23 10296
....AGUUGGAGGUUAGAUCUCGGGCAG................................................. 24 41
......UUGGAGGUUAGAUCUCGGGCA.................................................. 21 21


#asu-miR-791
GCUUGUUGGGGUGCUGGUCUGCUCCGUGUCCAAAGUUAUGUAUAGUCACUUUGGCACUCUCCAGGCCUGCACACUACAGCCUU
(((.((.((.((((.((((((....(((.(((((((.((.....)).)))))))))....))))))..))))..)))))))...
Total sRNA: 27404 shared 5' end with miRNA: 1205 shared 3' end with miRNA: 114
miRNA
.............................................UUUGGCACUCUCCAGGCCUGCA........... 22 15738
Shared 5' Terminus
.............................................UUUGGCACUCUCCAGGCC............... 18 40
.............................................UUUGGCACUCUCCAGGCCU.............. 19 43
.............................................UUUGGCACUCUCCAGGCCUG............. 20 90
.............................................UUUGGCACUCUCCAGGCCUGC............ 21 917
.............................................UUUGGCACUCUCCAGGCCUGCAC.......... 23 110
Shared 3' Terminus
.....................................................GCACUCUCCAGGCCUGCA........... 18 21
.....................................................UUGGCACUCUCCAGGCCUGCA........... 21 34
.....................................................CUUUGGCACUCUCCAGGCCUGCA........... 23 51
Subsequence
Others
............CUGGUCUGCUCCGUGUCC.......................................................... 18 21
............CUGGUCUGCUCCGUGUCCA......................................................... 19 9
............CUGGUCUGCUCCGUGUCCAAA...................................................... 21 25
............CUGGUCUGCUCCGUGUCCAAAG..................................................... 22 229
............CUGGUCUGCUCCGUGUCCAAAGU.................................................... 23 6477
............CUGGUCUGCUCCGUGUCCAAAGUU................................................... 24 2498
............CUGGUCUGCUCCGUGUCCAAAGUUA.................................................. 25 31
............UGGUCUGCUCCGUGUCCAAAG....................................................... 21 6
............UGGUCUGCUCCGUGUCCAAAGU...................................................... 22 238
............UGGUCUGCUCCGUGUCCAAAGUU..................................................... 23 391
............UGGUCUGCUCCGUGUCCAAAGUUA.................................................... 24 7
.....................................................CUUUGGCACUCUCCAGGCCU............... 20 6
.....................................................CUUUGGCACUCUCCAGGCCUG.............. 21 11
.....................................................CUUUGGCACUCUCCAGGCCUGC............. 22 49
.....................................................UUGGCACUCUCCAGGCCUGCAC.......... 22 10


#asu-miR-993
CGGAUGGUUUACCCUGUAGAAGCGUGUUUAUCUGCACAUUUCAAAAUAAGCUCGUCUCUACAGGCAGGACCUUCCAG
.(((.(((((..(((((((((..((.((((((.............))))))..))..)))))))))..)))))..)))..
Total sRNA: 150316 shared 5' end with miRNA: 55772 shared 3' end with miRNA: 2773
miRNA
.............................................UAAGCUCGUCUCUACAGGCAGG......... 22 86343
Shared 5' Terminus
.............................................UAAGCUCGUCUCUACAGG.............. 18 1377
.............................................UAAGCUCGUCUCUACAGGC............. 19 2139
.............................................UAAGCUCGUCUCUACAGGCA............ 20 3852
.............................................UAAGCUCGUCUCUACAGGCAG........... 21 3866
.............................................UAAGCUCGUCUCUACAGGCAGGA......... 23 44491
.............................................UAAGCUCGUCUCUACAGGCAGGAC........ 24 46
Shared 3' Terminus
.....................................................CUCGUCUCUACAGGCAGG......... 18 479
.....................................................AAGCUCGUCUCUACAGGCAGG......... 21 29
.....................................................AUAAGCUCGUCUCUACAGGCAGG......... 23 2235
Subsequence
Others
.........UACCCUGUAGAAGCGUGUUUAU.............................................. 22 420
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.........UACCCUGUAGAAGCGUGUUUAUC.......................................... 23 168
.........UACCCUGUAGAAGCGUGUUUAUCU......................................... 24 42
.........ACCCUGUAGAAGCGUGUUUA............................................. 20 48
.........ACCCUGUAGAAGCGUGUUUAU............................................ 21 739
.........ACCCUGUAGAAGCGUGUUUAUC........................................... 22 1455
.........ACCCUGUAGAAGCGUGUUUAUCU.......................................... 23 1249
.........................................AUAAGCUCGUCUCUACAGGCA.......... 21 103
.........................................AUAAGCUCGUCUCUACAGGCAG......... 22 439
.........................................AUAAGCUCGUCUCUACAGGCAGGA........ 24 430
..........................................AAGCUCGUCUCUACAGGCAGGA........ 22 42


#asu-miR-1175
GACGGUCAAAAAAGUGGAGGAUUGGGUCUGCACUGAAUGACAUGGCAUAGUGAGAUUCUCAUUCCUCCAUUUUAGCUGCCU
...(((....((((((((((.(((((((.((((..(((......)))))))))..)))).)))))))))))....))).
Total sRNA: 8793 shared 5' end with miRNA: 454 shared 3' end with miRNA: 58
miRNA
...........AAGUGGAGGAUUGGGUCUGCACU....................................... 23 7009
Shared 5' Terminus
...........AAGUGGAGGAUUGGGUCU............................................ 18 16
...........AAGUGGAGGAUUGGGUCUG........................................... 19 9
...........AAGUGGAGGAUUGGGUCUGC.......................................... 20 23
...........AAGUGGAGGAUUGGGUCUGCA......................................... 21 69
...........AAGUGGAGGAUUGGGUCUGCAC........................................ 22 320
...........AAGUGGAGGAUUGGGUCUGCACUG...................................... 24 3
...........AAGUGGAGGAUUGGGUCUGCACUGAAUGACAUGGCAUAG....................... 39 10
Shared 3' Terminus
..............GGAGGAUUGGGUCUGCACU.......................................... 19 8
............UGGAGGAUUGGGUCUGCACU.......................................... 20 7
............GUGGAGGAUUGGGUCUGCACU......................................... 21 3
...........AGUGGAGGAUUGGGUCUGCACU.......................................... 22 22
..........AAAGUGGAGGAUUGGGUCUGCACU........................................ 24 17
Subsequence
Others
.................................................UGAGAUUCUCAUUCCUCC.......... 18 60
.................................................UGAGAUUCUCAUUCCUCCA......... 19 97
.................................................UGAGAUUCUCAUUCCUCCAU........ 20 95
.................................................UGAGAUUCUCAUUCCUCCAUU....... 21 258
.................................................UGAGAUUCUCAUUCCUCCAUUU...... 22 706
.................................................UGAGAUUCUCAUUCCUCCAUUUU..... 23 6


#asu-miR-1822
UCCUAGCGUACGUCUUUCAUUCGGUUCAGCUAUCGGUGAAUUUCGCUCCGAGCUGCCCUAUGAAGGACUGUCGCUAUUACG
...(((((.((((((((((..((..(((((...((((.....))))...)))))))..)))))))))).)))))).....
Total sRNA: 19239 shared 5' end with miRNA: 137 shared 3' end with miRNA: 297
miRNA
................................................GAGCUGCCCUAUGAAGGACUGU...... 22 18540
Shared 5' Terminus
................................................GAGCUGCCCUAUGAAGGA.......... 18 47
................................................GAGCUGCCCUAUGAAGGACU........ 20 9
................................................GAGCUGCCCUAUGAAGGACUG....... 21 38
................................................GAGCUGCCCUAUGAAGGACUGUC..... 23 37
Shared 3' Terminus
..................................................UGCCCUAUGAAGGACUGU...... 18 242
.................................................CUGCCCUAUGAAGGACUGU...... 19 28
................................................AGCUGCCCUAUGAAGGACUGU...... 21 11
...............................................CGAGCUGCCCUAUGAAGGACUGU...... 23 13
Subsequence
Others
..........CGUCUUUCAUUCGGUUCAG............................................ 19 76
..........CGUCUUUCAUUCGGUUCAGCUAUC...................................... 24 8
..........CGUCUUUCAUUCGGUUCAGCUAUCG..................................... 25 35
..........CGUCUUUCAUUCGGUUCAGCUAUCGG.................................... 26 108
..........CGUCUUUCAUUCGGUUCAGCUAUCGGU................................... 27 20


#asu-miR-5342
UGACUUGAGUGCAUUACUCGUCAACCAGUAAUAUUAUGUUUUAAUGACCAUAAUAUCACUGGCUUACGGGAAAUGGCCUUUGGU
..(((.(((..((((.((((((...((((((.(((((((((.((....)).)))))))))..)))))...)))))).))))..)))).)))
Total sRNA: 174961 shared 5' end with miRNA: 35814 shared 3' end with miRNA: 9237
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miRNA
.....................................................UAAUAUCACUGGCUUACGGGAAA.......... 23 122176
Shared 5' Terminus
.....................................................UAAUAUCACUGGCUUACG............... 18 127
.....................................................UAAUAUCACUGGCUUACGGG.............. 20 47
.....................................................UAAUAUCACUGGCUUACGGGA............. 21 1591
.....................................................UAAUAUCACUGGCUUACGGGAA............ 22 33172
.....................................................UAAUAUCACUGGCUUACGGGAAAU.......... 24 847
Shared 3' Terminus
.......................................................UCACUGGCUUACGGGAAA.......... 18 88
......................................................AUCACUGGCUUACGGGAAA.......... 19 97
.....................................................AUAUCACUGGCUUACGGGAAA.......... 21 8030
.....................................................AAUAUCACUGGCUUACGGGAAA.......... 22 989
Subsequence
.....................................................AAUAUCACUGGCUUACGGGAA............ 21 287
.....................................................AUAUCACUGGCUUACGGGA............. 19 105
.....................................................AUAUCACUGGCUUACGGGAA............ 20 1866
Others
..............ACUCGUCAACCAGUAAUAUU.................................................. 20 97
..............ACUCGUCAACCAGUAAUAUUA................................................. 21 374
..............ACUCGUCAACCAGUAAUAUUAU................................................ 22 2148
..............ACUCGUCAACCAGUAAUAUUAUG............................................... 23 2459
..............ACUCGUCAACCAGUAAUAUUAUGU.............................................. 24 70
.....................................................AUAAUAUCACUGGCUUACGGGAA............ 23 47
.....................................................AUAUCACUGGCUUACGGGAAAU.......... 22 155


#asu-miR-5343
CUCAAGGAGAAUAUCAGCAAGAUUGAUCUGGCUGUAUAUAAGUCCAGACCUAUCUGUCGAUAUUGCCUG
....(((..((((((.(((.(((.(.(((((((.......)).)))))).).)))))).)))))).))).
Total sRNA: 2322 shared 5' end with miRNA: 255 shared 3' end with miRNA: 277
miRNA
........GAAUAUCAGCAAGAUUGAUCUGG..................................... 23 1758
Shared 5' Terminus
........GAAUAUCAGCAAGAUUGA.......................................... 18 3
........GAAUAUCAGCAAGAUUGAU......................................... 19 40
........GAAUAUCAGCAAGAUUGAUC........................................ 20 29
........GAAUAUCAGCAAGAUUGAUCU....................................... 21 44
........GAAUAUCAGCAAGAUUGAUCUG...................................... 22 137
........GAAUAUCAGCAAGAUUGAUCUGGC.................................... 24 2
Shared 3' Terminus
............UCAGCAAGAUUGAUCUGG..................................... 18 10
...........AUCAGCAAGAUUGAUCUGG..................................... 19 3
..........UAUCAGCAAGAUUGAUCUGG..................................... 20 2
........AAUAUCAGCAAGAUUGAUCUGG..................................... 22 228
.......AGAAUAUCAGCAAGAUUGAUCUGG.................................... 24 34
Subsequence
.........AAUAUCAGCAAGAUUGAU......................................... 18 2
.........AAUAUCAGCAAGAUUGAUC........................................ 19 1
.........AAUAUCAGCAAGAUUGAUCU....................................... 20 3
.........AAUAUCAGCAAGAUUGAUCUG...................................... 21 12
Others
.......AGAAUAUCAGCAAGAUUGAU......................................... 20 1
.......AGAAUAUCAGCAAGAUUGAUC........................................ 21 1
.......AGAAUAUCAGCAAGAUUGAUCUG...................................... 23 1
..................AUUGAUCUGGCUGUAUAUAAG.............................. 21 1
.........................................CAGACCUAUCUGUCGAUAUUGCC.. 23 1
.........................................AGACCUAUCUGUCGAUAUUGC... 21 2
.........................................AGACCUAUCUGUCGAUAUUGCC.. 22 4


#asu-miR-5344
UUGUUGAACUUUGUACUUCGGCUAAGGUGCUGCUCUAUGGCGGCCAGUACCUUGGCUAGGUGCAACGCUGAAUAGUUGG
(((((.(.(.(((((((.(((((((((((((..(......)..)))))))))))))))))))).).).)))))....
Total sRNA: 1401837 shared 5' end with miRNA: 489263 shared 3' end with miRNA: 2109
miRNA
.........UUUGUACUUCGGCUAAGGUGCUG.................................................. 23 908760
Shared 5' Terminus
.........UUUGUACUUCGGCUAAGG....................................................... 18 2481
.........UUUGUACUUCGGCUAAGGU...................................................... 19 6593
.........UUUGUACUUCGGCUAAGGUG..................................................... 20 21851
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.........UUUGUACUUCGGCUAAGGUGC.......................................................... 21 17434
.........UUUGUACUUCGGCUAAGGUGCU......................................................... 22 426409
.........UUUGUACUUCGGCUAAGGUGCUGC....................................................... 24 2547
.........UUUGUACUUCGGCUAAGGUGCUGCU...................................................... 25 1662
.........UUUGUACUUCGGCUAAGGUGCUGCUC..................................................... 26 583
.........UUUGUACUUCGGCUAAGGUGCUGCUCU.................................................... 27 2743
.........UUUGUACUUCGGCUAAGGUGCUGCUCUA................................................... 28 437
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAU.................................................. 29 4173
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUG................................................. 30 512
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGG................................................ 31 417
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGGC............................................... 32 129
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGGCG.............................................. 33 252
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGGCGGC............................................ 35 229
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGGCGGCCA.......................................... 37 580
.........UUUGUACUUCGGCUAAGGUGCUGCUCUAUGGCGGCCAGU........................................ 39 162
Shared 3' Terminus
..............ACUUCGGCUAAGGUGCUG....................................................... 18 465
............UACUUCGGCUAAGGUGCUG....................................................... 19 146
............GUACUUCGGCUAAGGUGCUG...................................................... 20 450
...........UGUACUUCGGCUAAGGUGCUG....................................................... 21 148
..........UUGUACUUCGGCUAAGGUGCUG....................................................... 22 667
........CUUUGUACUUCGGCUAAGGUGCUG....................................................... 24 229
Subsequence
..........UUGUACUUCGGCUAAGGUGCU........................................................ 21 334
............GUACUUCGGCUAAGGUGCU....................................................... 19 236
Others
.............................................GUACCUUGGCUAGGUGCAACGC.......... 22 102
.............................................UACCUUGGCUAGGUGCAACGC.......... 21 451


#asu-miR-5345a
GUGCGCUCAAUAAGGCACUGGGUUGGUCAGCUGGGGUUUCUUAGCGCAACUGGCCAUUCCAUUGCCUGGUCGAGCUGUC
....((((.((.((((((.(((..(((((((.((.(.(.....).).)).)))))))..))).)))))).)).))))....
Total sRNA: 195673 shared 5' end with miRNA: 94033 shared 3' end with miRNA: 588
miRNA
...........AAGGCACUGGGUUGGUCAGCUG....................................................... 22 96191
Shared 5' Terminus
...........AAGGCACUGGGUUGGUCA.......................................................... 18 499
...........AAGGCACUGGGUUGGUCAG......................................................... 19 2088
...........AAGGCACUGGGUUGGUCAGC........................................................ 20 1952
...........AAGGCACUGGGUUGGUCAGCU...................................................... 21 88718
...........AAGGCACUGGGUUGGUCAGCUGG.................................................... 23 745
Shared 3' Terminus
..............CACUGGGUUGGUCAGCUG....................................................... 18 393
.............GCACUGGGUUGGUCAGCUG....................................................... 19 79
............AGGCACUGGGUUGGUCAGCUG...................................................... 21 108
Subsequence
............AGGCACUGGGUUGGUCAGCU...................................................... 20 54
.............GCACUGGGUUGGUCAGCU....................................................... 18 42
Others
.............................................ACUGGCCAUUCCAUUGCCUG.......... 20 93
.............................................ACUGGCCAUUCCAUUGCCUGG......... 21 346
.............................................ACUGGCCAUUCCAUUGCCUGGU........ 22 4112


#asu-miR-5345b
GUGUGCUCAAUAAGGCACUGGAUUGGUCAGUUGAGUUUUCUGAGCGAAACUGGGCCAUUUCCAUUGUCUGGCCGAG
.....(((....(((((.((((.((((((((((..((((...))))..))))).)))))..))))).)))))....)))
Total sRNA: 1619521 shared 5' end with miRNA: 97677 shared 3' end with miRNA: 8651
miRNA
...........AAGGCACUGGAUUGGUCAGUU...................................................... 21 1512589
Shared 5' Terminus
...........AAGGCACUGGAUUGGUCA......................................................... 18 4283
...........AAGGCACUGGAUUGGUCAG........................................................ 19 5651
...........AAGGCACUGGAUUGGUCAGU...................................................... 20 63983
...........AAGGCACUGGAUUGGUCAGUUG.................................................... 22 20883
...........AAGGCACUGGAUUGGUCAGUUGA................................................... 23 2746
Shared 3' Terminus
..............GCACUGGAUUGGUCAGUU...................................................... 18 935
............GGCACUGGAUUGGUCAGUU....................................................... 19 123
............AGGCACUGGAUUGGUCAGUU...................................................... 20 1158
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.........UAAGGCACUGGAUUGGUCAGUU..................................................... 22 6433
Subsequence
Others
.........UAAGGCACUGGAUUGGUCAGU...................................................... 21 248


#asu-miR-5346
UGCAGUAGAUAGCUGGAGUUGCCCUACGACUGUGUGGAACGGUCCAGUCGUUGGGAAACUCAAGCCAUCGGGUGUUGUCAGU
.(((.(.(((.(((.(((((.(((.(((((((..(......)..)))))))).))).)))))).))).))).).)))......
Total sRNA: 521153 shared 5' end with miRNA: 31570 shared 3' end with miRNA: 9210
miRNA
..............................................UCGUUGGGAAACUCAAGCCAU.............. 21 402510
Shared 5' Terminus
..............................................UCGUUGGGAAACUCAAGC................. 18 2043
..............................................UCGUUGGGAAACUCAAGCC................ 19 4757
..............................................UCGUUGGGAAACUCAAGCCA............... 20 24074
..............................................UCGUUGGGAAACUCAAGCCAUC.............. 22 667
Shared 3' Terminus
...............................................UUGGGAAACUCAAGCCAU.............. 18 119
...............................................GUUGGGAAACUCAAGCCAU.............. 19 2449
...............................................CGUUGGGAAACUCAAGCCAU.............. 20 268
...............................................GUCGUUGGGAAACUCAAGCCAU.............. 22 6090
...............................................AGUCGUUGGGAAACUCAAGCCAU.............. 23 251
Subsequence
...............................................GUUGGGAAACUCAAGCCA............... 18 186
Others
.........AGCUGGAGUUGCCCUACG....................................................... 18 1949
.........AGCUGGAGUUGCCCUACGA...................................................... 19 843
.........AGCUGGAGUUGCCCUACGAC..................................................... 20 624
.........AGCUGGAGUUGCCCUACGACU.................................................... 21 8785
.........AGCUGGAGUUGCCCUACGACUG................................................... 22 60034
.........AGCUGGAGUUGCCCUACGACUGU.................................................. 23 4179
............UGGAGUUGCCCUACGACUG..................................................... 19 102
..............................................GUCGUUGGGAAACUCAAGCC................ 20 127
..............................................GUCGUUGGGAAACUCAAGCCA............... 21 451

#asu-miR-5347
CUCUGCUUACAUUCGGCUUCCCUCAACGCCGCUGCUACCAGCCACAGCAGCGACGGUGUUGACGGAGGUCGAGUGUAGACAGA
.((((..(((((((((((((.(((((((((((((.........))))))...))))))))).))))))))))))))..))))
Total sRNA: 2600512 shared 5' end with miRNA: 772879 shared 3' end with miRNA: 20029
miRNA
..............................................CGACGGUGUUGACGGAGGUCGAG.......... 23 1797736
Shared 5' Terminus
..............................................CGACGGUGUUGACGGAGG................ 18 10231
..............................................CGACGGUGUUGACGGAGGU............... 19 19912
..............................................CGACGGUGUUGACGGAGGUC.............. 20 25209
..............................................CGACGGUGUUGACGGAGGUCG............. 21 224776
..............................................CGACGGUGUUGACGGAGGUCGA............ 22 366845
..............................................CGACGGUGUUGACGGAGGUCGAGU.......... 24 124794
..............................................CGACGGUGUUGACGGAGGUCGAGUG......... 25 835
..............................................CGACGGUGUUGACGGAGGUCGAGUGU........ 26 260
Shared 3' Terminus
....................................................GUGUUGACGGAGGUCGAG.......... 18 1893
...................................................GGUGUUGACGGAGGUCGAG.......... 19 2521
..................................................CGGUGUUGACGGAGGUCGAG.......... 20 600
.................................................ACGGUGUUGACGGAGGUCGAG.......... 21 301
.................................................GACGGUGUUGACGGAGGUCGAG.......... 22 9915
................................................GCGACGGUGUUGACGGAGGUCGAG.......... 24 296
................................................AGCGACGGUGUUGACGGAGGUCGAG.......... 25 4494
Subsequence
.................................................GACGGUGUUGACGGAGGUC.............. 19 136
.................................................GACGGUGUUGACGGAGGUCG............. 20 886
.................................................GACGGUGUUGACGGAGGUCGA............ 21 1679
..................................................CGGUGUUGACGGAGGUCGA............ 19 198
...................................................GGUGUUGACGGAGGUCGA............ 18 651
Others
............CGGCUUCCCUCAACGCCGCUGC.................................................. 22 285
............CGGCUUCCCUCAACGCCGCUGCU................................................. 23 228
..............................................AGCGACGGUGUUGACGGAGG.............. 20 113
..............................................AGCGACGGUGUUGACGGAGGU............. 21 266
..............................................AGCGACGGUGUUGACGGAGGUC............ 22 304
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.............................................AGCGACGGUGUUGACGGAGGUCG..... 23 902
.............................................AGCGACGGUGUUGACGGAGGUCGA..... 24 1563
.............................................AGCGACGGUGUUGACGGAGGUCGAGU..... 26 386
..............................................GCGACGGUGUUGACGGAGGUCG..... 22 128
..............................................GCGACGGUGUUGACGGAGGUCGA..... 23 154
................................................GACGGUGUUGACGGAGGUCGAGU..... 23 563
.................................................GGUGUUGACGGAGGUCGAGU..... 20 200
..................................................GUGUUGACGGAGGUCGAGU..... 19 123
...................................................UGUUGACGGAGGUCGAGU..... 18 324


#asu-miR-5348
CUAGGUACGUGACAGAAGUUGAGUCUAGUUGAGACUGAUAUGUUUCUCACCGGGCAACAACUUCUGUCUCGUGGUAGUAG
...(.((((.(((((((((((.(((..((.(((((.....)))))..))..)))..)))))))))))).))))..)..... 
Total sRNA: 91080 shared 5' end with miRNA: 5711 shared 3' end with miRNA: 1655
miRNA
.............................................UCACCGGGCAACAACUUCUGUC..... 22 80692
Shared 5' Terminus
.............................................UCACCGGGCAACAACUUC..... 18 28
.............................................UCACCGGGCAACAACUUCU..... 19 99
.............................................UCACCGGGCAACAACUUCUG..... 20 77
.............................................UCACCGGGCAACAACUUCUGU..... 21 4266
.............................................UCACCGGGCAACAACUUCUGUCU..... 23 1238
Shared 3' Terminus
................................................CGGGCAACAACUUCUGUC..... 18 1312
................................................CCGGGCAACAACUUCUGUC..... 19 35
................................................ACCGGGCAACAACUUCUGUC..... 20 229
.............................................CACCGGGCAACAACUUCUGUC..... 21 32
............................................CUCACCGGGCAACAACUUCUGUC..... 23 46
Subsequence
Others
............CAGAAGUUGAGUCUAGUUGAG..... 21 51
............CAGAAGUUGAGUCUAGUUGAGA..... 22 2654
............CAGAAGUUGAGUCUAGUUGAGACUGAUAUGUUUC..... 34 185


#asu-miR-5349
UCGUCUUGGGCUGCUCUCGGAUGAGCCAGCUUGAGAAUUCAGAAAUCUGGCACACCCGGUGGCAUUCUAUCCGGCAAUAU
...(((..(((((((.....))).)))))..))).((((....)))).....(((((((....))).))))..... 
Total sRNA: 628684 shared 5' end with miRNA: 75136 shared 3' end with miRNA: 4160
miRNA
..........CUGCUCUCGGAUGAGCCAGCUU..... 22 530659
Shared 5' Terminus
..........CUGCUCUCGGAUGAGCCA..... 18 295
..........CUGCUCUCGGAUGAGCCAG..... 19 693
..........CUGCUCUCGGAUGAGCCAGC..... 20 12917
..........CUGCUCUCGGAUGAGCCAGCU..... 21 58156
..........CUGCUCUCGGAUGAGCCAGCUUGAGAAUUCAGAAA..... 35 2698
Shared 3' Terminus
.............UCUCGGAUGAGCCAGCUU..... 18 636
.............CUCUCGGAUGAGCCAGCUU..... 19 165
...........UGCUCUCGGAUGAGCCAGCUU..... 21 3257
Subsequence
...........UGCUCUCGGAUGAGCCAGCU..... 20 192
Others
......UGGGCUGCUCUCGGAUGAGCCAG..... 23 450
.............................................UCUGGCACACCCGGUGGCAUU..... 21 525
.............................................UCUGGCACACCCGGUGGCAUUC..... 22 17142


#asu-miR-5350a
CCGCCGGAGGAGUUUCUCAGGACUGCUAAAUUGUGAAUCGGCUAAUUUGGCACGCCUGAAAAACUACUCUUGUAGG
((((.((((.((((((.((((((..((((((((((.....)).)))))))))..)))))).)))))).)))).)).)) 
Total sRNA: 184799 shared 5' end with miRNA: 4964 shared 3' end with miRNA: 279
miRNA
.........................................UUUGGCACGCCUGAAAAACUAC..... 22 174408
Shared 5' Terminus
.........................................UUUGGCACGCCUGAAAAA..... 18 1385
.........................................UUUGGCACGCCUGAAAAAC..... 19 181
.........................................UUUGGCACGCCUGAAAAACU..... 20 1074
.........................................UUUGGCACGCCUGAAAAACUA..... 21 2230
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.........................................UUUGGCACGCCUGAAAAACUACU........ 23 94
Shared 3' Terminus
.........................................UUGGCACGCCUGAAAAACUAC......... 21 168
Subsequence
Others
.........AGUUUCUCAGGACUGCUA.................................................. 18 88
.........AGUUUCUCAGGACUGCUAAAU.............................................. 21 289
.........AGUUUCUCAGGACUGCUAAAUU............................................. 22 4586


#asu-miR-5350b
UGCAGGAGGUGGCGUUUCUAAGGUCUGCCAAAUUGUCUGAUCGCAAAUUUGGCACACCUAAGGAGCACUCGUUCCC
....((((..((.((((((.((((.((((((((((.....)).)))))))).)))).))))))..))..)))).
Total sRNA: 667676 shared 5' end with miRNA: 21504 shared 3' end with miRNA: 2836
miRNA
.............................................UUUGGCACACCUAAGGAGCACU....... 22 638804
Shared 5' Terminus
.............................................UUUGGCACACCUAAGGAG........... 18 230
.............................................UUUGGCACACCUAAGGAGC.......... 19 988
.............................................UUUGGCACACCUAAGGAGCA......... 20 2263
.............................................UUUGGCACACCUAAGGAGCAC........ 21 16729
.............................................UUUGGCACACCUAAGGAGCACUC...... 23 1287
Shared 3' Terminus
.....................................................GCACACCUAAGGAGCACU....... 18 187
....................................................GGCACACCUAAGGAGCACU....... 19 187
...................................................UGGCACACCUAAGGAGCACU....... 20 124
.................................................UUGGCACACCUAAGGAGCACU....... 21 2090
..............................................AUUUGGCACACCUAAGGAGCACU....... 23 227
Subsequence
Others
............CGUUUCUAAGGUCUGCCAAAU.......................................... 21 367
............CGUUUCUAAGGUCUGCCAAAUU........................................ 22 3610
.................................................UUGGCACACCUAAGGAGCACUC...... 22 249


#asu-miR-5350c
UGAUAACGCUGGAGGUGGCGUUUCUGAGGUCCGCCAAAUUGCUUUACGACAAACUUGGCACACCUGAGAAACGCCUGCUCCAGU
.......(((((((..((((((((((.((((..(((((.(((........))))..)))))..))))).)))))))))..)))))))
Total sRNA: 31918 shared 5' end with miRNA: 4141 shared 3' end with miRNA: 440
miRNA
.....................................................CUUGGCACACCUGAGAAACGCC......... 22 26134
Shared 5' Terminus
.....................................................CUUGGCACACCUGAGAAA............. 18 44
.....................................................CUUGGCACACCUGAGAAAC............ 19 138
.....................................................CUUGGCACACCUGAGAAACG........... 20 1163
.....................................................CUUGGCACACCUGAGAAACGC.......... 21 2662
.....................................................CUUGGCACACCUGAGAAACGCCU........ 23 132
Shared 3' Terminus
.........................................................GCACACCUGAGAAACGCC......... 18 22
.......................................................UUGGCACACCUGAGAAACGCC......... 21 371
.....................................................ACUUGGCACACCUGAGAAACGCC......... 23 33
Subsequence
.....................................................UUGGCACACCUGAGAAACGC.......... 20 29
Others
...............UGGCGUUUCUGAGGUCCG.......................................... 18 20
...............UGGCGUUUCUGAGGUCCGC......................................... 19 20
...............UGGCGUUUCUGAGGUCCGCC........................................ 20 10
...............UGGCGUUUCUGAGGUCCGCCA...................................... 21 18
...............UGGCGUUUCUGAGGUCCGCCAA..................................... 22 53
...............UGGCGUUUCUGAGGUCCGCCAAA.................................... 23 316
.................CGUUUCUGAGGUCCGCCAAA..................................... 20 12
.................CGUUUCUGAGGUCCGCCAAAU.................................... 21 92
.................CGUUUCUGAGGUCCGCCAAAUU................................... 22 389
.....................................................UUGGCACACCUGAGAAACGCCU........ 22 10
.....................................................UGGCACACCUGAGAAACGCCUG....... 22 13
.....................................................UGGCACACCUGAGAAACGCCUGC...... 23 91
```

#asu-miR-5350d
CGGCGGCCUUUCUCGGGUAAGCUAAAUUGUUUUUGUGCGAAAUUUGGCACGCCCGUGGAAUGCCCAUUGCAGUAU
..(((((.((((.(((((..((((((((((.....))))..))))))..))))))..)))))..))))..)))....)).....
Total sRNA: 80747 shared 5' end with miRNA: 6438 shared 3' end with miRNA: 220
miRNA
.....UUUGGCACGCCCGUGGAAUGCC..... 22 65919
Shared 5' Terminus
.....UUUGGCACGCCCGUGGAA..... 18 44
.....UUUGGCACGCCCGUGGAAU..... 19 251
.....UUUGGCACGCCCGUGGAAUG..... 20 413
.....UUUGGCACGCCCGUGGAAUGC..... 21 5465
.....UUUGGCACGCCCGUGGAAUGCCC..... 23 264
Shared 3' Terminus
.....UUGGCACGCCCGUGGAAUGCC..... 21 167
.....AUUUGGCACGCCCGUGGAAUGCC..... 23 28
Subsequence
.....UUGGCACGCCCGUGGAAUGC..... 20 24
Others
......CCUUUCUCGGGUAAGCUAAA..... 20 25
......CCUUUCUCGGGUAAGCUAAAU..... 21 446
......CCUUUCUCGGGUAAGCUAAAUU..... 22 7557
.......CUUUCUCGGGUAAGCUAAAUU..... 21 24
.....AUUUGGCACGCCCGUGGAAUGC..... 22 23

#asu-miR-5351
GUACCAAGUCAGGUUUUACUAAUGACCAAAUUGUUUCAAGCGAAUUUGGCACAUGUAAUACCUGCCUUGGUUGCU
(((((((.(((((.((((...((.(((((((((.....)).)))))))))...))))).)))))..)))))).)))..
Total sRNA: 10126 shared 5' end with miRNA: 1893 shared 3' end with miRNA: 229
miRNA
.....UUUGGCACAUGUAAUACCUGCC..... 22 7914
Shared 5' Terminus
.....UUUGGCACAUGUAAUACC..... 18 68
.....UUUGGCACAUGUAAUACCU..... 19 84
.....UUUGGCACAUGUAAUACCUG..... 20 43
.....UUUGGCACAUGUAAUACCUGC..... 21 1622
.....UUUGGCACAUGUAAUACCUGCCU..... 23 76
Shared 3' Terminus
.....UUGGCACAUGUAAUACCUGCC..... 21 217
.....AUUUGGCACAUGUAAUACCUGCC..... 23 7
Subsequence
.....UUGGCACAUGUAAUACCU..... 18 3
.....UUGGCACAUGUAAUACCUGC..... 20 10
Others
.........CAGGUUUUACUAAUGACCAAAUU..... 23 9
.........CAGGUUUUACUAAUGACCAAAUUGUUUCAAGCGA..... 34 4
.........CAGGUUUUACUAAUGACCAAAUUGUUUCAAGCGAA..... 35 14
.....AUUUGGCACAUGUAAUACCUGC..... 22 35
.....UUGGCACAUGUAAUACCUGCCU..... 22 4

#asu-miR-5352
AAGUCCCUCAGAAGGCGCUCAGAAUGUGCAUCGUAGUUACUGAAUCGUUGCACAUGUUGAACGACCUGCUGGGUGCCUC
..(..((.(((.(((((.((((.(((((((.((...........)).)))))))..))))..)).)))..)))))..)...
Total sRNA: 366423 shared 5' end with miRNA: 21439 shared 3' end with miRNA: 1090
miRNA
.....UUGCACAUGUUGAACGACCUGCU..... 23 300552
Shared 5' Terminus
.....UUGCACAUGUUGAACGAC..... 18 2863
.....UUGCACAUGUUGAACGACC..... 19 2760
.....UUGCACAUGUUGAACGACCU..... 20 1801
.....UUGCACAUGUUGAACGACCUG..... 21 4740
.....UUGCACAUGUUGAACGACCUGC..... 22 8925
.....UUGCACAUGUUGAACGACCUGCUG..... 24 344
Shared 3' Terminus
.....CAUGUUGAACGACCUGCU..... 18 528
.....ACAUGUUGAACGACCUGCU..... 19 282
Subsequence
Others
.....AAGGCGCUCAGAAUGUGCAU..... 20 115
.....AAGGCGCUCAGAAUGUGCAUC..... 21 1008

```
..........AAGGCGCUCAGAAUGUGCAUCG..................................................... 22 41428
..........AAGGCGCUCAGAAUGUGCAUCGU.................................................... 23 256


#asu-miR-5353
CGCGCACCCUUAGGCGAACAGUGUGCAAUUCGAGUUGAUUAUUUGCAACUCAUUGCGAUUUUGUUCGGCUCAUGGUGUUCG
((.(((((...((.(((((((..((((((..((((((........)))))))))))...)))))))..))...)))))..))
Total sRNA: 8980 shared 5' end with miRNA: 193 shared 3' end with miRNA: 465
miRNA
.................................................UCAUUGCGAUUUUGUUCGGCUCA......... 23 7200
Shared 5' Terminus
.................................................UCAUUGCGAUUUUGUUCG.............. 18 4
.................................................UCAUUGCGAUUUUGUUCGG............. 19 16
.................................................UCAUUGCGAUUUUGUUCGGC............ 20 8
.................................................UCAUUGCGAUUUUGUUCGGCU........... 21 39
.................................................UCAUUGCGAUUUUGUUCGGCUC.......... 22 116
.................................................UCAUUGCGAUUUUGUUCGGCUCAU........ 24 10
Shared 3' Terminus
.....................................................GCGAUUUUGUUCGGCUCA......... 18 3
....................................................UUGCGAUUUUGUUCGGCUCA......... 20 4
...................................................AUUGCGAUUUUGUUCGGCUCA......... 21 11
..................................................CAUUGCGAUUUUGUUCGGCUCA......... 22 3
................................................CUCAUUGCGAUUUUGUUCGGCUCA......... 24 442
Subsequence
Others
..........AGGCGAACAGUGUGCAAUUCGA..................................................... 22 16
..........AGGCGAACAGUGUGCAAUUCGAG.................................................... 23 16
..........AGGCGAACAGUGUGCAAUUCGAGU................................................... 24 949
..........AGGCGAACAGUGUGCAAUUCGAGUU.................................................. 25 92
.................................................CUCAUUGCGAUUUUGUUCGGC............ 21 6
.................................................CUCAUUGCGAUUUUGUUCGGCU........... 22 14
.................................................CUCAUUGCGAUUUUGUUCGGCUC.......... 23 14


#asu-miR-5354
CUUCAACCGAGCGGGUAUGGUUGUGUUCCAAAGCCGGUAGUGAUAGCGACACUUUGGCACAAUCACACCUGCUCAGGCGGAAU
.(((..((((((((((.((((((((..((((((.((.((....)).)).)...)))))))))))))))).)))))))).))..))).
Total sRNA: 19450 shared 5' end with miRNA: 689 shared 3' end with miRNA: 1880
miRNA
..........GCGGGUAUGGUUGUGUUCCAAAGC.................................................. 24 7064
Shared 5' Terminus
..........GCGGGUAUGGUUGUGUUC........................................................ 18 15
..........GCGGGUAUGGUUGUGUUCC....................................................... 19 59
..........GCGGGUAUGGUUGUGUUCCA...................................................... 20 10
..........GCGGGUAUGGUUGUGUUCCAA..................................................... 21 13
..........GCGGGUAUGGUUGUGUUCCAAA.................................................... 22 253
..........GCGGGUAUGGUUGUGUUCCAAAG................................................... 23 335
..........GCGGGUAUGGUUGUGUUCCAAAGCC................................................. 25 3
Shared 3' Terminus
...............AUGGUUGUGUUCCAAAGC.................................................. 18 4
............GGGUAUGGUUGUGUUCCAAAGC.................................................. 22 6
..........CGGGUAUGGUUGUGUUCCAAAGC................................................... 23 1861
.........AGCGGGUAUGGUUGUGUUCCAAAGC.................................................. 25 8
Subsequence
...........CGGGUAUGGUUGUGUUCCAAAG.................................................... 22 41
Others
........................CCAAAGCCGGUAGUGAUAGCGA.................................... 22 8
.......................AAAGCCGGUAGUGAUAGCGACA..................................... 22 17
......................AAGCCGGUAGUGAUAGCGACA....................................... 21 3
.................................CGGUAGUGAUAGCGACAC.................................. 18 102
.....................................UAGCGACACUUUGGCACAAUCA.......................... 22 7
.................................................CUUUGGCACAAUCACACCUGCU.......... 22 28
................................................CUUUGGCACAAUCACACCUGCUC......... 23 8
...................................................UUUGGCACAAUCACACCU.............. 18 12
...................................................UUUGGCACAAUCACACCUG............. 19 18
...................................................UUUGGCACAAUCACACCUGC............ 20 11
..................................................UUUGGCACAAUCACACCUGCU........... 21 2272
..................................................UUUGGCACAAUCACACCUGCUC.......... 22 7073
..................................................UUUGGCACAAUCACACCUGCUCA......... 23 27
...................................................UUGGCACAAUCACACCUGCU.......... 20 8
..................................................UUGGCACAAUCACACCUGCUC......... 21 72
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#asu-miR-5355
CACCGAUUCUGAACACCUCAAGAGAUACAACGCUGUUAUUGGUAACGGUGUGCCCCUUGAGGUGUUUAGAAUGAUGGUGUA
((((((((((((((((((((.(.....(((((((((....)))))))))...)))))))))))))))))))..)))))..
Total sRNA: 8080 shared 5' end with miRNA: 403 shared 3' end with miRNA: 162
miRNA
.........UGAACACCUCAAGAGAUACAACG..................................................... 23 7108
Shared 5' Terminus
.........UGAACACCUCAAGAGAUA.......................................................... 18 38
.........UGAACACCUCAAGAGAUAC......................................................... 19 6
.........UGAACACCUCAAGAGAUACA........................................................ 20 18
.........UGAACACCUCAAGAGAUACAA....................................................... 21 61
.........UGAACACCUCAAGAGAUACAAC...................................................... 22 164
.........UGAACACCUCAAGAGAUACAACGC..................................................... 24 116
Shared 3' Terminus
.............ACCUCAAGAGAUACAACG..................................................... 18 13
............CACCUCAAGAGAUACAACG...................................................... 19 5
...........ACACCUCAAGAGAUACAACG...................................................... 20 5
..........AACACCUCAAGAGAUACAACG...................................................... 21 39
........CUGAACACCUCAAGAGAUACAACG..................................................... 24 98
Subsequence
Others
........CUGAACACCUCAAGAGAUACA........................................................ 21 5
........CUGAACACCUCAAGAGAUACAA....................................................... 22 19
........CUGAACACCUCAAGAGAUACAAC...................................................... 23 70
..........GAACACCUCAAGAGAUACAACGC..................................................... 23 8
..........AACACCUCAAGAGAUACAACGC...................................................... 22 215
.............................................GUGUGCCCCUUGAGGUGUUUAG.............. 22 3
.............................................GUGUGCCCCUUGAGGUGUUUAGA............. 23 66
.............................................GUGUGCCCCUUGAGGUGUUUAGAA............ 24 3
.............................................UGUGCCCCUUGAGGUGUUUAGA............. 22 10


#asu-miR-5356a
UUGCACUUCUUCCCGCCCACGUCGUAAUUAACUGAGAGUAAGGUUCGUCUGUUACUUCCGAGGUGGGAGGAAAGACGUAAAA
....((.((((.((.((((((.(((.((.((((.(((((.....))).)).)))))).)).))).)))))).)).)))).))....
Total sRNA: 10740 shared 5' end with miRNA: 2144 shared 3' end with miRNA: 324
miRNA
.............................................UGUUACUUCCGAGGUGGGAGGAA.......... 23 8009
Shared 5' Terminus
.............................................UGUUACUUCCGAGGUGGG............... 18 5
.............................................UGUUACUUCCGAGGUGGGA.............. 19 18
.............................................UGUUACUUCCGAGGUGGGAG............. 20 11
.............................................UGUUACUUCCGAGGUGGGAGG............ 21 65
.............................................UGUUACUUCCGAGGUGGGAGGA........... 22 1762
.............................................UGUUACUUCCGAGGUGGGAGGAAA......... 24 260
.............................................UGUUACUUCCGAGGUGGGAGGAAAG........ 25 20
.............................................UGUUACUUCCGAGGUGGGAGGAAAGA....... 26 3
Shared 3' Terminus
.....................................................CUUCCGAGGUGGGAGGAA.......... 18 198
....................................................ACUUCCGAGGUGGGAGGAA.......... 19 101
...................................................UACUUCCGAGGUGGGAGGAA.......... 20 15
.............................................CUGUUACUUCCGAGGUGGGAGGAA.......... 24 6
Subsequence
.....................................................UACUUCCGAGGUGGGAGGA........... 19 3
Others
............CCGCCCACGUCGUAAUUAA.................................................... 19 4
............CCGCCCACGUCGUAAUUAACU.................................................. 21 4
............CCGCCCACGUCGUAAUUAACUG................................................. 22 58
............CCGCCCACGUCGUAAUUAACUGA................................................ 23 140
............CGCCCACGUCGUAAUUAACUG.................................................. 21 4
............CGCCCACGUCGUAAUUAACUGA................................................. 22 15
..............CACGUCGUAAUUAACUGA.................................................... 18 6
.....................................................CUUCCGAGGUGGGAGGAAA......... 19 10


#asu-miR-5356b
GCAUUUCUUUUCGUUCACCUCGGAAAUAGUGGAGAAAGUAAAAUUUUUAUCUACUAUUUCCGAGGUGGAAGGGAAGACGUGC
((((.((((..(.(((((((((((((((((((.((((......)))).)))))))))))))))))))).)..)))).))))
Total sRNA: 119818 shared 5' end with miRNA: 4914 shared 3' end with miRNA: 10824
miRNA
.........UCGUUCACCUCGGAAAUAGUGGA..................................................... 23 85260
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Shared 5' Terminus
.........UCGUUCACCUCGGAAAUA..................................................... 18 181
.........UCGUUCACCUCGGAAAUAG.................................................... 19 51
.........UCGUUCACCUCGGAAAUAGU................................................... 20 310
.........UCGUUCACCUCGGAAAUAGUG.................................................. 21 377
.........UCGUUCACCUCGGAAAUAGUGG................................................. 22 3417
.........UCGUUCACCUCGGAAAUAGUGGAG................................................ 24 323
.........UCGUUCACCUCGGAAAUAGUGGAGA............................................... 25 192
.........UCGUUCACCUCGGAAAUAGUGGAGAA.............................................. 26 48
Shared 3' Terminus
..............CACCUCGGAAAUAGUGGA.................................................. 18 30
.............UCACCUCGGAAAUAGUGGA.................................................. 19 293
............UUCACCUCGGAAAUAGUGGA.................................................. 20 111
...........GUUCACCUCGGAAAUAGUGGA.................................................. 21 418
..........CGUUCACCUCGGAAAUAGUGGA.................................................. 22 9926
.........UUCGUUCACCUCGGAAAUAGUGGA................................................. 24 46
Subsequence
..........CGUUCACCUCGGAAAUAGU..................................................... 19 40
..........CGUUCACCUCGGAAAUAGUG.................................................... 20 37
..........CGUUCACCUCGGAAAUAGUGG................................................... 21 240
Others
..........CGUUCACCUCGGAAAUAGUGGAG................................................. 23 2149
.........CGUUCACCUCGGAAAUAGUGGAGA.................................................. 24 112
.................................................UCUACUAUUUCCGAGGUGGAAGGG......... 24 32
..................................................UACUAUUUCCGAGGUGGAAG........... 20 34
..................................................UACUAUUUCCGAGGUGGAAGG.......... 21 160
..................................................UACUAUUUCCGAGGUGGAAGGG......... 22 1716
..................................................UACUAUUUCCGAGGUGGAAGGGA........ 23 13169
..................................................UACUAUUUCCGAGGUGGAAGGGAA....... 24 772
.................................................ACUAUUUCCGAGGUGGAAGGGA........ 22 118
.................................................AUUUCCGAGGUGGAAGGGA........ 19 38


#asu-miR-5357
UCGACUCCUCACCCGAAUCGUUGUUCAUUUGUAUUGCUUGCCUCAAAUGGACAACGAUUUGGGUGAGGAGUUGAGCAG
((((((((((((((((((((((((((((.....))))))))))))))))))))))))))))....
Total sRNA: 304076 shared 5' end with miRNA: 6613 shared 3' end with miRNA: 2119
miRNA
.........................................AAUGGACAACGAUUUGGGUGAG........... 22 243448
Shared 5' Terminus
.........................................AAUGGACAACGAUUUGGGU.............. 19 797
.........................................AAUGGACAACGAUUUGGGUG............. 20 179
.........................................AAUGGACAACGAUUUGGGUGA............ 21 3779
.........................................AAUGGACAACGAUUUGGGUGAGG.......... 23 1744
.........................................AAUGGACAACGAUUUGGGUGAGGA......... 24 88
Shared 3' Terminus
.................................................GACAACGAUUUGGGUGAG........... 18 426
.................................................GGACAACGAUUUGGGUGAG........... 19 653
.........................................AUGGACAACGAUUUGGGUGAG........... 21 597
.......................................AAAUGGACAACGAUUUGGGUGAG........... 23 371
Subsequence
Others
........UCACCCGAAUCGUUGUUCAUUU.................................................. 22 135
........UCACCCGAAUCGUUGUUCAUUUG................................................. 23 2879
.........CACCCGAAUCGUUGUUCAU..................................................... 19 157
.........CACCCGAAUCGUUGUUCAUU.................................................... 20 274
.........CACCCGAAUCGUUGUUCAUUU................................................... 21 1041
.........CACCCGAAUCGUUGUUCAUUUG.................................................. 22 44395
.........CACCCGAAUCGUUGUUCAUUUGU................................................. 23 2274
..........ACCCGAAUCGUUGUUCAUUUG.................................................. 21 235
.........................................AUGGACAACGAUUUGGGUGAGG.......... 22 136


#asu-miR-5358a
GGUGUGGGAGGCGGUUAUGGUAUUGCGCUGGUAUGUUGAUUCUGUGUUCAUACCCGUAAUUGCCAUGACUGUUUCCCGCUCC
((.((((((((((((((((((((..((((((.............))))))))))).)))))))))))))))))..))
Total sRNA: 462035 shared 5' end with miRNA: 46123 shared 3' end with miRNA: 2015
miRNA
.................................................UACCCGUAAUUGCCAUGACUGUU......... 23 403107
Shared 5' Terminus
.................................................UACCCGUAAUUGCCAUGA.............. 18 2728
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.................................................UACCCGUAAUUGCCAUGAC..... 19 436
.................................................UACCCGUAAUUGCCAUGACU.... 20 1129
.................................................UACCCGUAAUUGCCAUGACUG... 21 2811
.................................................UACCCGUAAUUGCCAUGACUGU.. 22 26350
.................................................UACCCGUAAUUGCCAUGACUGUUU 24 12655
Shared 3' Terminus
.....................................................GUAAUUGCCAUGACUGUU..... 18 280
....................................................CGUAAUUGCCAUGACUGUU..... 19 976
...................................................CCGUAAUUGCCAUGACUGUU..... 20 171
..................................................CCCGUAAUUGCCAUGACUGUU..... 21 105
.................................................ACCCGUAAUUGCCAUGACUGUU..... 22 364
................................................AUACCCGUAAUUGCCAUGACUGUU..... 24 118
Subsequence
Others
..........CGGUUAUGGUAUUGCGCUGG.................................................. 20 108
..........CGGUUAUGGUAUUGCGCUGGU................................................. 21 118
..........CGGUUAUGGUAUUGCGCUGGUA................................................ 22 184
..........CGGUUAUGGUAUUGCGCUGGUAU............................................... 23 178
..........CGGUUAUGGUAUUGCGCUGGUAUG.............................................. 24 9019
..........CGGUUAUGGUAUUGCGCUGGUAUGU............................................. 25 411


#asu-miR-5358b
UGUCGGCAACCAUGUUGGUGCGUCGUGGUAUGCUGAUGGUGUAUUCAUACCCGUAAUGCCAACAUGCAUGCUUGCAC
(((.((((..((((((((((...((.((((((..((((...))))))))))))...))))))))))..)))).))).
Total sRNA: 9181 shared 5' end with miRNA: 273 shared 3' end with miRNA: 82
miRNA
.............................................UACCCGUAAUGCCAACAUGCAU........ 22 3706
Shared 5' Terminus
.............................................UACCCGUAAUGCCAACAU............ 18 3
.............................................UACCCGUAAUGCCAACAUG........... 19 13
.............................................UACCCGUAAUGCCAACAUGC.......... 20 60
.............................................UACCCGUAAUGCCAACAUGCA......... 21 188
.............................................UACCCGUAAUGCCAACAUGCAUG....... 23 9
Shared 3' Terminus
.................................................CGUAAUGCCAACAUGCAU........ 18 4
................................................CCGUAAUGCCAACAUGCAU........ 19 2
...............................................CCCGUAAUGCCAACAUGCAU........ 20 2
..............................................ACCCGUAAUGCCAACAUGCAU........ 21 18
............................................AUACCCGUAAUGCCAACAUGCAU........ 23 56
Subsequence
Others
........ACCAUGUUGGUGCGUCGUGGUAU.............................................. 23 12
........ACCAUGUUGGUGCGUCGUGGUAUG............................................. 24 3
.........CCAUGUUGGUGCGUCGUG.................................................. 18 13
.........CCAUGUUGGUGCGUCGUGG................................................. 19 6
.........CCAUGUUGGUGCGUCGUGGU................................................ 20 14
.........CCAUGUUGGUGCGUCGUGGUA............................................... 21 31
.........CCAUGUUGGUGCGUCGUGGUAU.............................................. 22 1400
.........CCAUGUUGGUGCGUCGUGGUAUG............................................. 23 2568
.........CCAUGUUGGUGCGUCGUGGUAUGC............................................ 24 743
.........CCAUGUUGGUGCGUCGUGGUAUGCU........................................... 25 5
.........CCAUGUUGGUGCGUCGUGGUAUGCUGAUGGUGUAUUCA.............................. 38 6
..........CAUGUUGGUGCGUCGUGGUAU.............................................. 21 4
..........CAUGUUGGUGCGUCGUGGUAUG............................................. 22 4
..........CAUGUUGGUGCGUCGUGGUAUGC............................................ 23 5
...........AUGUUGGUGCGUCGUGGUAU.............................................. 20 7
...........AUGUUGGUGCGUCGUGGUAUG............................................. 21 18
...........AUGUUGGUGCGUCGUGGUAUGC............................................ 22 196
...........AUGUUGGUGCGUCGUGGUAUGCU........................................... 23 19
............UGUUGGUGCGUCGUGGUAUG............................................. 20 6
.............................................AUACCCGUAAUGCCAACAUG........... 20 2
.............................................AUACCCGUAAUGCCAACAUGC.......... 21 22
.............................................AUACCCGUAAUGCCAACAUGCA......... 22 7


#asu-miR-5359
ACAAUGUGUGGUCUGGGAUUGUCUAUAUUGGUAAAAGUGAAUGCAUACCAAUAUCCACAAUCCUUGAGCAGGCAAAUGUC
....(((.((.((.(((((((((..((((((((((...((....)).)))))))))..)))))))).)).)).)))......
Total sRNA: 229103 shared 5' end with miRNA: 40968 shared 3' end with miRNA: 576
miRNA
```

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..........UCUGGGAUUGUCUAUAUUGGUA..................................................... 22 181013
Shared 5' Terminus
..........UCUGGGAUUGUCUAUAUU.......................................................... 18 478
..........UCUGGGAUUGUCUAUAUUG......................................................... 19 187
..........UCUGGGAUUGUCUAUAUUGG........................................................ 20 224
..........UCUGGGAUUGUCUAUAUUGGU....................................................... 21 36219
..........UCUGGGAUUGUCUAUAUUGGUAA..................................................... 23 3334
..........UCUGGGAUUGUCUAUAUUGGUAAA.................................................... 24 439
..........UCUGGGAUUGUCUAUAUUGGUAAAA................................................... 25 70
Shared 3' Terminus
............UGGGAUUGUCUAUAUUGGUA..................................................... 20 179
............CUGGGAUUGUCUAUAUUGGUA..................................................... 21 317
Subsequence
............CUGGGAUUGUCUAUAUUGGU...................................................... 20 68
Others
.............................................ACCAAUAUCCACAAUCCUUGAGC.......... 23 214
.............................................CCAAUAUCCACAAUCCUUGAG............ 21 182
.............................................CCAAUAUCCACAAUCCUUGAGC.......... 22 5712
.............................................CAAUAUCCACAAUCCUUGAGC.......... 21 179


#asu-miR-5360
GGUGCCAAAGAACGAAUCGUCGAAUCGGAUGUCUGUGCAUUGUGCGAGAAAUUCGAAUCGACAUUCGACCUGUGGCCAUC
.(.((((.((..((((((.((((((.((((((.(((.(((.....)))))).)))))).)))))))))..)).)))))...
Total sRNA: 488338 shared 5' end with miRNA: 12133 shared 3' end with miRNA: 1316
miRNA
..........ACGAAUCGUCGAAUCGGAUGUCU..................................................... 23 474752
Shared 5' Terminus
..........ACGAAUCGUCGAAUCGGA.......................................................... 18 799
..........ACGAAUCGUCGAAUCGGAU......................................................... 19 567
..........ACGAAUCGUCGAAUCGGAUG........................................................ 20 1395
..........ACGAAUCGUCGAAUCGGAUGU....................................................... 21 4629
..........ACGAAUCGUCGAAUCGGAUGUC..................................................... 22 4712
Shared 3' Terminus
..............UCGUCGAAUCGGAUGUCU..................................................... 18 187
.............AUCGUCGAAUCGGAUGUCU..................................................... 19 322
............AAUCGUCGAAUCGGAUGUCU..................................................... 20 493
...........GAAUCGUCGAAUCGGAUGUCU..................................................... 21 120
...........CGAAUCGUCGAAUCGGAUGUCU..................................................... 22 132
Subsequence
Others
.............................................AAAUUCGAAUCGACAUUCGACC.......... 22 40


#asu-miR-5361
GCUCGAAUUUGGGAUAUCUUGGAAGGUUUCUCGGUUUUUAUGGGCGGAAAGCUUCCAUUUUGUCCCUGAUUCUAU
....(((((.(((((((...(((((((.((((.((.((.....)).)))))))...)))))))...)))))).)))))...
Total sRNA: 4284371 shared 5' end with miRNA: 125304 shared 3' end with miRNA: 9254
miRNA
.........UGGGAUAUCUUGGAAGGUUUCU....................................... 22 4147017
Shared 5' Terminus
.........UGGGAUAUCUUGGAAGGU........................................... 18 20088
.........UGGGAUAUCUUGGAAGGUU.......................................... 19 11985
.........UGGGAUAUCUUGGAAGGUUU......................................... 20 39670
.........UGGGAUAUCUUGGAAGGUUUC........................................ 21 52596
.........UGGGAUAUCUUGGAAGGUUUCUC...................................... 23 872
Shared 3' Terminus
............AUAUCUUGGAAGGUUUCU....................................... 18 4731
............GAUAUCUUGGAAGGUUUCU...................................... 19 2330
...........GGAUAUCUUGGAAGGUUUCU....................................... 20 436
..........GGGAUAUCUUGGAAGGUUUCU...................................... 21 1267
........UUGGGAUAUCUUGGAAGGUUUCU....................................... 23 488
Subsequence
Others
.............................................AAAGCUUCCAUUUUGUCCCUGA...... 22 2433


#asu-miR-5362
UGUGCAGUUAAAUCUCGUCCGGUAGUAUAUGCGAGUUGAAAAGCAUUGCAACCGGUGGAGAUUCCACUGACUUCUCU
.((.((((..((((((..((((((.(((.((((.........)))))))).)))))..))))))..))))))......
Total sRNA: 129020 shared 5' end with miRNA: 8839 shared 3' end with miRNA: 894
```

```
miRNA
.........AAAUCUCGUCCGGUAGUAUAUGC..................................................... 23 117257
Shared 5' Terminus
.........AAAUCUCGUCCGGUAGUA.......................................................... 18 90
.........AAAUCUCGUCCGGUAGUAU......................................................... 19 103
.........AAAUCUCGUCCGGUAGUAUA........................................................ 20 252
.........AAAUCUCGUCCGGUAGUAUAU....................................................... 21 628
.........AAAUCUCGUCCGGUAGUAUAUG...................................................... 22 7731
Shared 3' Terminus
..............UCGUCCGGUAGUAUAUGC..................................................... 18 132
.............CUCGUCCGGUAGUAUAUGC.................................................... 19 371
............UCUCGUCCGGUAGUAUAUGC..................................................... 20 71
...........AUCUCGUCCGGUAGUAUAUGC..................................................... 21 65
..........AAUCUCGUCCGGUAGUAUAUGC..................................................... 22 112
........UAAAUCUCGUCCGGUAGUAUAUGC..................................................... 24 143
Subsequence
Others
.............................................AUUGCAACCGGUGGAGAUUCC.............. 21 112
.............................................AUUGCAACCGGUGGAGAUUCCA............. 22 1848


#asu-miR-5363
UCGUACGCUGAUGGGCAAAGUUUCUGAACCGUGUUGUGUUCAAGGCUAAACGGUUUGGCACUUGCCCAGCACUGUAUGAC
(((((((.((.(((((((.((..(..((((((...((.......))...))))))..).)))))))))).)).)))))))).
Total sRNA: 2478826 shared 5' end with miRNA: 241482 shared 3' end with miRNA: 37205
miRNA
..........AUGGGCAAAGUUUCUGAACCGUGU.................................................... 24 2198129
Shared 5' Terminus
..........AUGGGCAAAGUUUCUGAA.......................................................... 18 3246
..........AUGGGCAAAGUUUCUGAAC......................................................... 19 3066
..........AUGGGCAAAGUUUCUGAACC........................................................ 20 15443
..........AUGGGCAAAGUUUCUGAACCG....................................................... 21 6338
..........AUGGGCAAAGUUUCUGAACCGU...................................................... 22 50075
..........AUGGGCAAAGUUUCUGAACCGUG..................................................... 23 141587
..........AUGGGCAAAGUUUCUGAACCGUGUU................................................... 25 20259
..........AUGGGCAAAGUUUCUGAACCGUGUUG.................................................. 26 436
..........AUGGGCAAAGUUUCUGAACCGUGUUGU................................................. 27 686
..........AUGGGCAAAGUUUCUGAACCGUGUUGUGU.............................................. 29 220
Shared 3' Terminus
................AAAGUUUCUGAACCGUGU.................................................. 18 14091
...............CAAAGUUUCUGAACCGUGU.................................................. 19 1769
..............GCAAAGUUUCUGAACCGUGU.................................................. 20 4517
.............GGCAAAGUUUCUGAACCGUGU.................................................. 21 1697
...........UGGGCAAAGUUUCUGAACCGUGU.................................................. 23 15065
Subsequence
...........UGGGCAAAGUUUCUGAACCGU..................................................... 21 261
...........UGGGCAAAGUUUCUGAACCGUG.................................................... 22 463
.............GGCAAAGUUUCUGAACCGU..................................................... 19 139
..............GCAAAGUUUCUGAACCGU..................................................... 18 138
Others
...........UGGGCAAAGUUUCUGAACCGUGUU................................................... 24 152
................AAAGUUUCUGAACCGUGUU.................................................. 19 363
...................................................ACGGUUUGGCACUUGCCCAGCA......... 22 16


#asu-miR-5364
UGAACUCAGCUAAUGGACUUUACUUCCUCUGCUUAAUUUUUCUGCAGAGGUAUUGUUUAUUGGCUAAGAUCAAAGCUCGAGC
(((.((.(((((((((((..((...(((((((...........)))))))))..))))))))))).)).)))..........
Total sRNA: 553346 shared 5' end with miRNA: 30396 shared 3' end with miRNA: 2129
miRNA
.............................................AGAGGUAUUGUUUAUUGGCUAA.............. 22 520637
Shared 5' Terminus
.............................................AGAGGUAUUGUUUAUUGG.................. 18 3377
.............................................AGAGGUAUUGUUUAUUGGC................. 19 340
.............................................AGAGGUAUUGUUUAUUGGCU................ 20 14155
.............................................AGAGGUAUUGUUUAUUGGCUA............... 21 11761
.............................................AGAGGUAUUGUUUAUUGGCUAAG.............. 23 740
Shared 3' Terminus
..................................................GUAUUGUUUAUUGGCUAA.............. 18 395
.................................................GGUAUUGUUUAUUGGCUAA.............. 19 572
................................................AGGUAUUGUUUAUUGGCUAA.............. 20 740
```

```
.............................................GAGGUAUUGUUUAUUGGCUAA.............. 21 145
.............................................CAGAGGUAUUGUUUAUUGGCUAA.............. 23 277
Subsequence
Others
.......AGCUAAUGGACUUUACUUCCUCUGC..................................................... 25 7

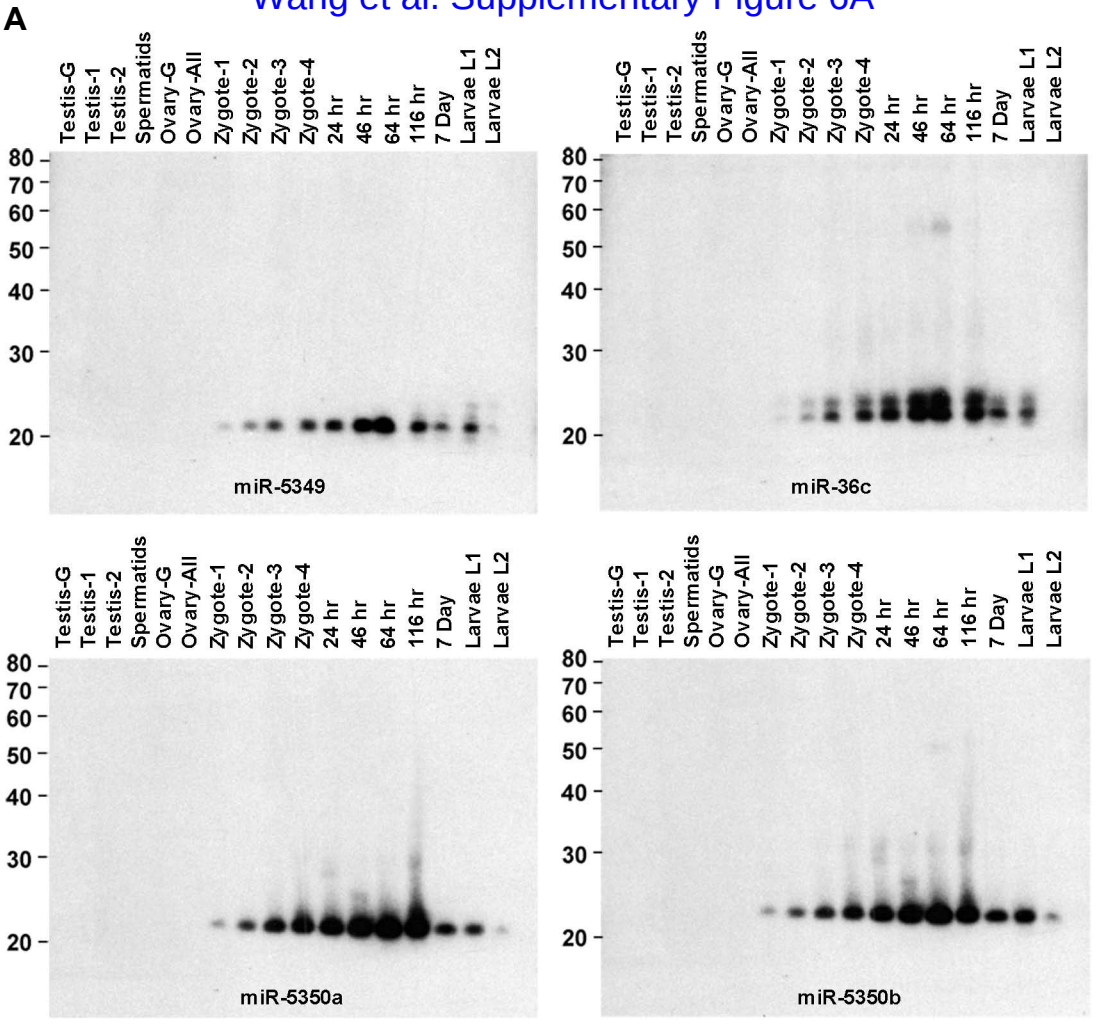

#asu-miR-5365a
UCAGCUAGAUCAGCUGUUCCAUCUUAAUCAUAAAAUCUAAUUCAGGAUGAUUAAGAAGGAACAACUGAUUUUACUGAGUGC
((((..(((((((.((((((.((((((((((....(((.....)))))))))))))).)))))).)))))))..)))).... 
Total sRNA: 101089 shared 5' end with miRNA: 31057 shared 3' end with miRNA: 673
miRNA
.............................................UGAUUAAGAAGGAACAACUGAU............ 22 64267
Shared 5' Terminus
.............................................UGAUUAAGAAGGAACAAC................ 18 126
.............................................UGAUUAAGAAGGAACAACU............... 19 576
.............................................UGAUUAAGAAGGAACAACUG.............. 20 763
.............................................UGAUUAAGAAGGAACAACUGA............. 21 7669
.............................................UGAUUAAGAAGGAACAACUGAUU........... 23 21820
.............................................UGAUUAAGAAGGAACAACUGAUUU.......... 24 102
Shared 3' Terminus
..................................................UAAGAAGGAACAACUGAU............ 18 53
.................................................UUAAGAAGGAACAACUGAU............ 19 62
................................................AUUAAGAAGGAACAACUGAU............ 20 258
...............................................GAUUAAGAAGGAACAACUGAU............ 21 208
............................................AUGAUUAAGAAGGAACAACUGAU............ 23 88
Subsequence
..............................................AUUAAGAAGGAACAACUGA............. 19 35
Others
.........CAGCUGUUCCAUCUUAAUCA..................................................... 20 40
.........CAGCUGUUCCAUCUUAAUCAU.................................................... 21 422
.........CAGCUGUUCCAUCUUAAUCAUA................................................... 22 218
.........................................GAUGAUUAAGAAGGAACAACUGA............. 23 75
.............................................GAUUAAGAAGGAACAACUGAUU........... 22 97
.............................................AUUAAGAAGGAACAACUGAUU............ 21 2172
.............................................AUUAAGAAGGAACAACUGAUUU........... 22 306
..................................................UUAAGAAGGAACAACUGAUU............ 20 41
.................................................UUAAGAAGGAACAACUGAUUU........... 21 32
..................................................UAAGAAGGAACAACUGAUU............ 19 38
...................................................AAGAAGGAACAACUGAUU............ 18 35


#asu-miR-5365b
AAGCAUCAGCUAGAUCAGCUGUUCCAUCUUAAUCAUAAAAUUCAAUUCAGGAUGAUUAAGAAGAAACAACUGAUUUACUGAGUGCAU
..(((((((.(((((((((.((((.(.((((((((((.............)))))))))).).)))).)))))))))))))).))).. 
Total sRNA: 189766 shared 5' end with miRNA: 51790 shared 3' end with miRNA: 562
miRNA
.............................................UGAUUAAGAAGAAACAACUGAU............ 22 130245
Shared 5' Terminus
.............................................UGAUUAAGAAGAAACAAC................ 18 427
.............................................UGAUUAAGAAGAAACAACU............... 19 1815
.............................................UGAUUAAGAAGAAACAACUG.............. 20 1311
.............................................UGAUUAAGAAGAAACAACUGA............. 21 9335
.............................................UGAUUAAGAAGAAACAACUGAUU........... 23 38842
.............................................UGAUUAAGAAGAAACAACUGAUUU.......... 24 59
Shared 3' Terminus
..................................................UAAGAAGAAACAACUGAU............ 18 152
.................................................UUAAGAAGAAACAACUGAU............ 19 138
................................................AUUAAGAAGAAACAACUGAU............ 20 185
...............................................GAUUAAGAAGAAACAACUGAU............ 21 59
Subsequence
Others
..............CAGCUGUUCCAUCUUAAUCAU.................................................... 21 422
..............CAGCUGUUCCAUCUUAAUCAUA................................................... 22 218
...............................................GAUUAAGAAGAAACAACUGAUU........... 22 52
................................................AUUAAGAAGAAACAACUGAUU............ 21 4383
.................................................AUUAAGAAGAAACAACUGAUUU........... 22 329
..................................................UUAAGAAGAAACAACUGAUU............ 20 53
.................................................UUAAGAAGAAACAACUGAUUU........... 21 64
```

```
#asu-miR-5366
CACGAGCACGUAAAUGCACUGUGUUGCUAAUUUGGCUCAUCGAAAAUUAGCAGCAUGGCGCAUUUGCGCGCCAAUGGCCAAAU
...(.((.(((((((((.(((((((((((((((.........)))))))))))))))).))))))))).)))..........
Total sRNA: 31514 shared 5' end with miRNA: 1174 shared 3' end with miRNA: 147
miRNA
.........UAAAUGCACUGUGUUGCUAAUU.................................................... 22 17553
Shared 5' Terminus
.........UAAAUGCACUGUGUUGCU........................................................ 18 91
.........UAAAUGCACUGUGUUGCUA....................................................... 19 40
.........UAAAUGCACUGUGUUGCUAA...................................................... 20 216
.........UAAAUGCACUGUGUUGCUAAU..................................................... 21 474
.........UAAAUGCACUGUGUUGCUAAUUU................................................... 23 334
Shared 3' Terminus
...........AAAUGCACUGUGUUGCUAAUU..................................................... 21 109
Subsequence
Others
........CGUAAAUGCACUGUGUUGCUAAU..................................................... 23 44
.............................GGCUCAUCGAAAAUUAGCAGCA.............................. 22 227
.............................GGCUCAUCGAAAAUUAGCAGCAU............................. 23 165
.......................................GAAAAUUAGCAGCAUGGCGCAU.................... 22 106
.....................................AUUAGCAGCAUGGCGCAUUUGCG.................. 23 195
.....................................UUAGCAGCAUGGCGCAUU...................... 18 58
.....................................UUAGCAGCAUGGCGCAUUU..................... 19 82
.....................................UUAGCAGCAUGGCGCAUUUG.................... 20 519
.....................................UUAGCAGCAUGGCGCAUUUGC................... 21 1395
.....................................UUAGCAGCAUGGCGCAUUUGCG.................. 22 8315

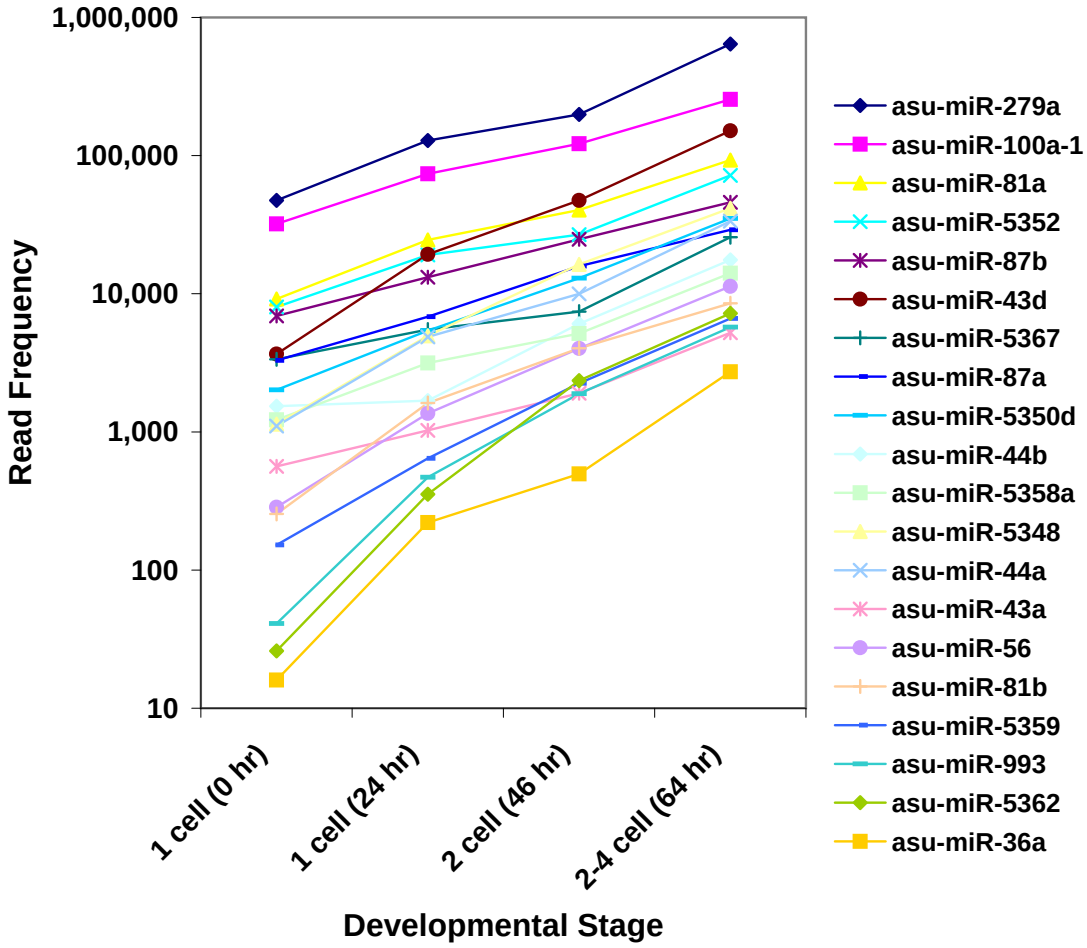

#asu-miR-5367
AAGGCCAAAGCGGCCUCAGAUCUUGCCAAUUUUUCAAUGCGGUUAAAUUGGCACCUCUUAGACCGGCUUGGAGCG
...(((.((((((.((.(((...((((((((((..(......)..)))))))))..))).)).)).)))).).)).
Total sRNA: 150897 shared 5' end with miRNA: 2910 shared 3' end with miRNA: 2025
miRNA
.........................................AUUGGCACCUCUUAGACCGGCU....... 22 145824
Shared 5' Terminus
.........................................AUUGGCACCUCUUAGACCG.......... 19 60
.........................................AUUGGCACCUCUUAGACCGG......... 20 221
.........................................AUUGGCACCUCUUAGACCGGC........ 21 1378
.........................................AUUGGCACCUCUUAGACCGGCUU...... 23 1209
Shared 3' Terminus
.........................................UUGGCACCUCUUAGACCGGCU....... 21 1252
.........................................AAUUGGCACCUCUUAGACCGGCU....... 23 709
Subsequence
Others
.........................................UUGGCACCUCUUAGACCGGCUU...... 22 54
.........GCGGCCUCAGAUCUUGCCAAUUU.................................................. 23 23
```

Wang et al. Supplementary Figure 6A



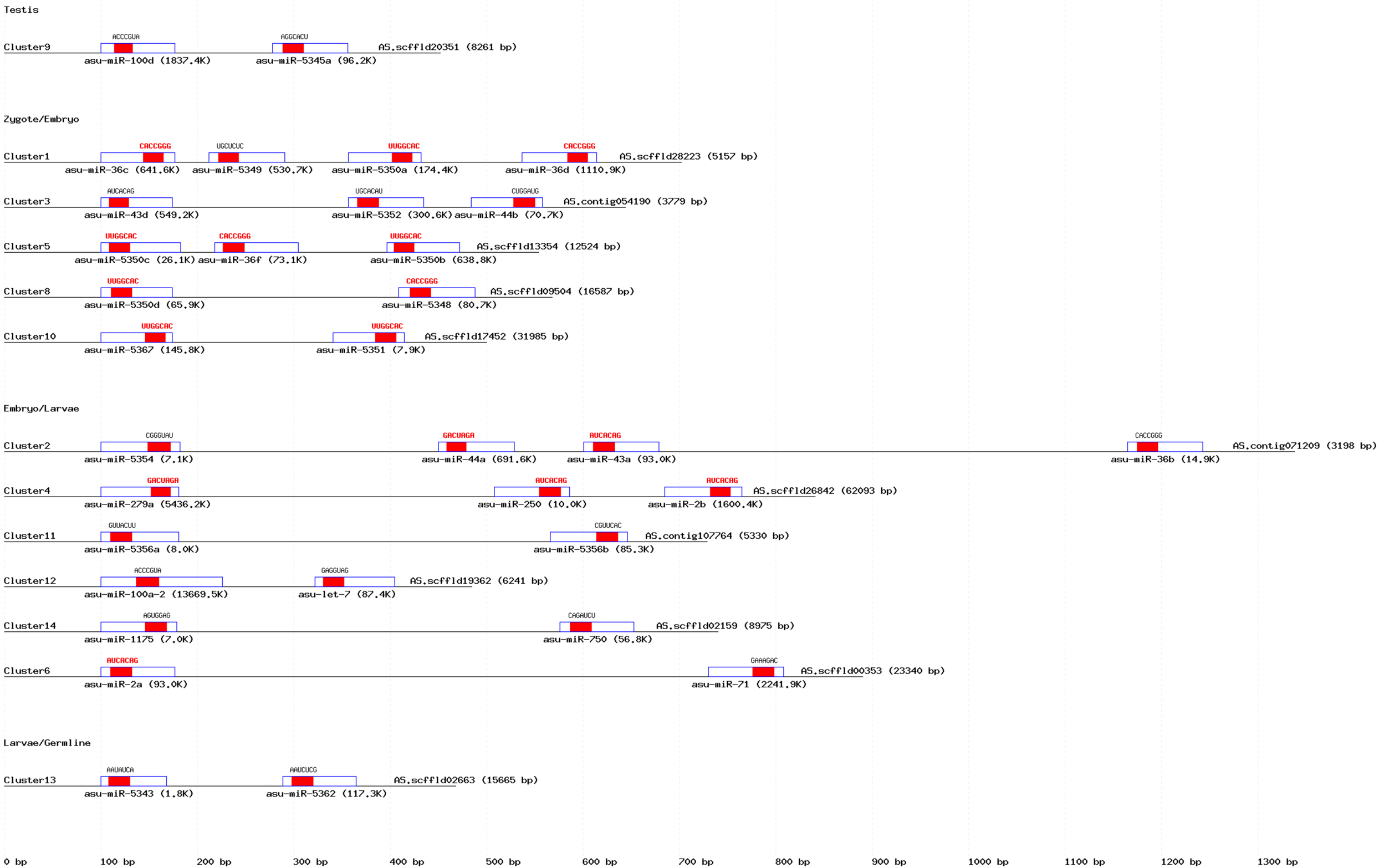
Wang et al.
Supplementary Figure 6B

B



Ascaris polycistronic miRNAs

Wang et al.
Supplementary Figure 7



Wang et al. Supplementary Figure 8

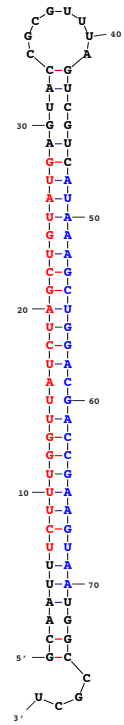
A

```
asu-miR-9  --G-CAAUUUCUUUGGUUAUCUAGCUGUAUGAGUACCGCGUUUAGUCGUCAUAAAGCUGGACGACCGAAG-UAAUGGCCGCU
             | |  |  |||||||||||| ||||||||||    ||   ||  | ||||||||||  |   |||  ||| ||| |  |  |
asu-miR-79 UUGUCUUUCCCUUUGGUUAUCUGGCUGUAUGAGU-GAGC-CAUA-ACAUCAUAAAGCUAGGUUACCAAAGCUAA-GCACAAU
```

B

```
#asu-miR-9
GCAAUUUCUUUGGUUAUCUAGCUGUAUGAGUACCGCGUUUAGUCGUCAUAAAGCUGGACGACCGAAGUAAUGGCCGCU
((.(((.(((((((..(((((((.(((((..((........))..)))))).)))))))..)))))))..))).)).....
Total sRNA: 605982 shared 5' end with miRNA: 234930 shared 3' end with miRNA: 1974
miRNA
......UCUUUGGUUAUCUAGCUGUAUGA.......................................................... 23 343507
Shared 5' Terminus
......UCUUUGGUUAUCUAGCUG.............................................................. 18 430
......UCUUUGGUUAUCUAGCUGU............................................................. 19 3810
......UCUUUGGUUAUCUAGCUGUA............................................................ 20 2709
......UCUUUGGUUAUCUAGCUGUAU........................................................... 21 22291
......UCUUUGGUUAUCUAGCUGUAUG.......................................................... 22 204274
......UCUUUGGUUAUCUAGCUGUAUGAG........................................................ 24 1354
Shared 3' Terminus
..........UGGUUAUCUAGCUGUAUGA.......................................................... 19 190
.........UUGGUUAUCUAGCUGUAUGA......................................................... 20 555
........UUUGGUUAUCUAGCUGUAUGA........................................................ 21 331
.......CUUUGGUUAUCUAGCUGUAUGA......................................................... 22 230
.....UUCUUUGGUUAUCUAGCUGUAUGA........................................................ 24 616
Subsequence
.......CUUUGGUUAUCUAGCUGUAUG.......................................................... 21 131
........UUUGGUUAUCUAGCUGUAUG......................................................... 20 195
.........UUGGUUAUCUAGCUGUAUG......................................................... 19 318
..........UGGUUAUCUAGCUGUAUG.......................................................... 18 135
Others
.....UUCUUUGGUUAUCUAGCUGUAUG......................................................... 23 1324
.....................................................AUAAAGCUGGACGACCGAAG.......... 20 101
.....................................................AUAAAGCUGGACGACCGAAGU......... 21 1184
.....................................................AUAAAGCUGGACGACCGAAGUA........ 22 3550
.....................................................AUAAAGCUGGACGACCGAAGUAA....... 23 16125
.....................................................AUAAAGCUGGACGACCGAAGUAAU...... 24 139
.....................................................UAAAGCUGGACGACCGAAGUA......... 21 196
.....................................................UAAAGCUGGACGACCGAAGUAA........ 22 1557
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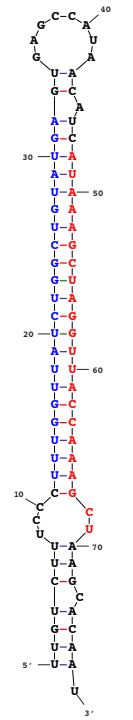
C



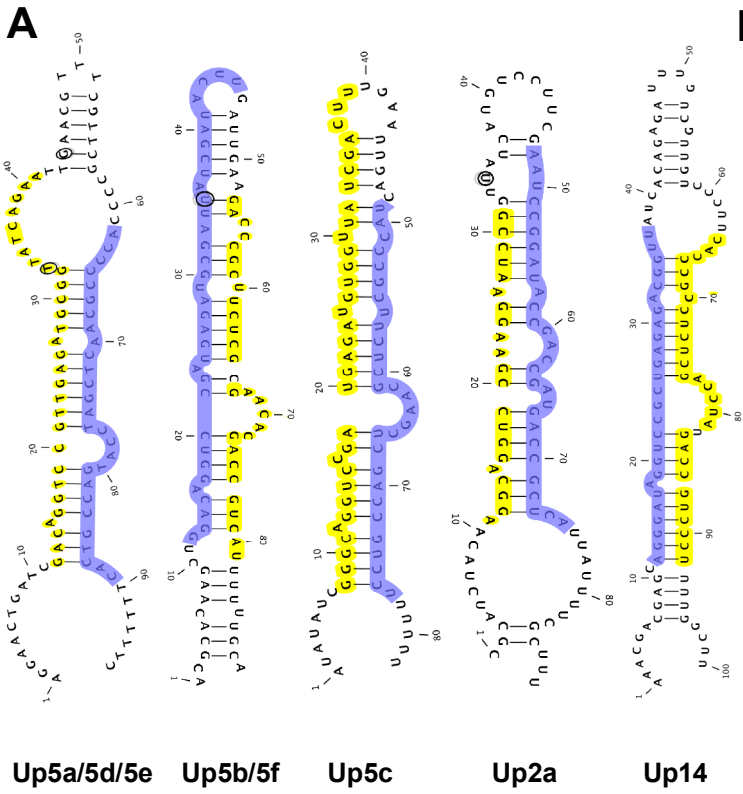
D

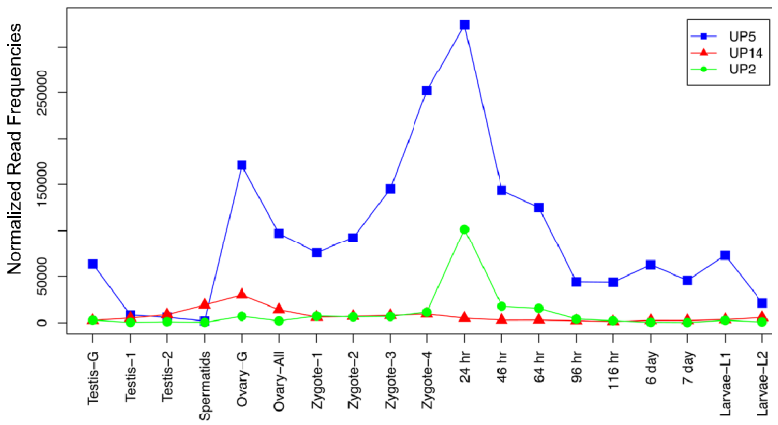
```
#asu-miR-79
UUGUCUUUCCCUUUGGUUAUCUGGCUGUAUGAGUGAGCCAUAACAUCAUAAAGCUAGGUUACCAAAGCUAAGCACAAU
(((((((...((((((.(((((((((.(((((((.........)).)))))).)))))))).)))))))..))).)))).
Total sRNA: 316210 shared 5' end with miRNA: 6335 shared 3' end with miRNA: 1262
miRNA
.....................................................AUAAAGCUAGGUUACCAAAGCU......... 22 304277
Shared 5' Terminus
.....................................................AUAAAGCUAGGUUACCAA............. 18 456
.....................................................AUAAAGCUAGGUUACCAAA............ 19 635
.....................................................AUAAAGCUAGGUUACCAAAG........... 20 1328
.....................................................AUAAAGCUAGGUUACCAAAGC.......... 21 3254
.....................................................AUAAAGCUAGGUUACCAAAGCUA........ 23 575
Shared 3' Terminus
.....................................................UAAAGCUAGGUUACCAAAGCU......... 21 927
....................................................CAUAAAGCUAGGUUACCAAAGCU........ 23 162
Subsequence
Others
.........CCUUUGGUUAUCUGGCUGUAUG....................................................... 22 288
.........CCUUUGGUUAUCUGGCUGUAUGA...................................................... 23 1072
..........CUUUGGUUAUCUGGCUGUAUGA...................................................... 22 1205
...........UUUGGUUAUCUGGCUGUAUGA....................................................... 21 1424
```

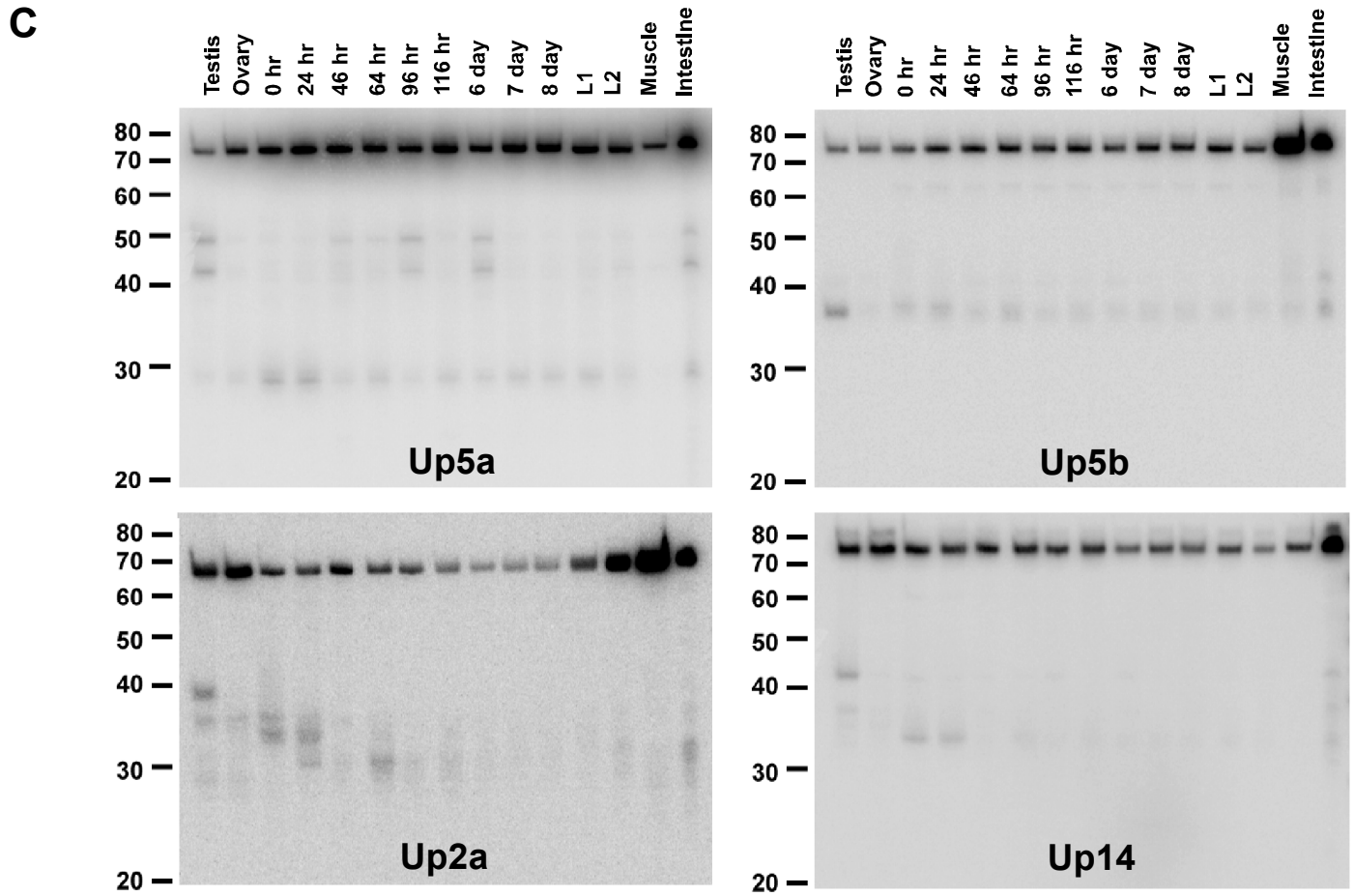
E



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Supplementary Figure 11







Wang et al.
Supplementary Figure 12

#UP14
AAACGACGAGCAGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGAGAUUUGUCGUUGUCCCUUCACCCGCCUCUCGACCUAUGACCGUCCCUUUUGGCUU
Perfectly match

..........AGGGAUAGGUCCGCUGAGA.....	19	11046
..........AGGGAUAGGUCCGCUGAGAGA.....	21	14711
..........AGGGAUAGGUCCGCUGAGAGACG.....	23	121147
..........AGGGAUAGGUCCGCUGAGAGACGG.....	24	11201
..........AGGGAUAGGUCCGCUGAGAGACGGU.....	25	47403
..........AGGGAUAGGUCCGCUGAGAGACGGUU.....	26	1062100
..........AGGGAUAGGUCCGCUGAGAGACGGUUA.....	27	30354
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAG.....	33	12652
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGA.....	34	21545
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGAG.....	35	45875
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGAGA.....	36	22111
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGAGAU.....	37	34000
..........AGGGAUAGGUCCGCUGAGAGACGGUUAUCACAGAGAUUU.....	39	20894
..........GGGAUAGGUCCGCUGAGAGACGGUU.....	25	11337
.....UCACCCGCCUCUCGACCUAUGACCGUCCCU.....	30	19962
.....CACCCGCCUCUCGACCUAUGACCGUCCC.....	28	18477
.....CACCCGCCUCUCGACCUAUGACCGUCCCU.....	29	92321
.....CACCCGCCUCUCGACCUAUGACCGUCCCUU.....	30	16035
.....ACCCGCCUCUCGACCUAUGACCGUCCCU.....	28	15777

Perfectly antisense match

#UP2a
CGCAUCUACAAGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCUUCGAAUCCGGAUACCGACCGAUGACCGCUCAUUAUUUUCGCUUU
Perfectly match

.........AAGGCAGGUCCGAAGGAAUCCG.....	22	15702
.........AAGGCAGGUCCGAAGGAAUCCGGU.....	24	11346
.........AAGGCAGGUCCGAAGGAAUCCGGUU.....	25	16582
.........AAGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCU.....	35	14035
.........AGGCAGGUCCGAAGGAAU.....	18	28173
.........AGGCAGGUCCGAAGGAAUC.....	19	28015
.........AGGCAGGUCCGAAGGAAUCC.....	20	30318
.........AGGCAGGUCCGAAGGAAUCCG.....	21	53303
.........AGGCAGGUCCGAAGGAAUCCGG.....	22	32933
.........AGGCAGGUCCGAAGGAAUCCGGU.....	23	37305
.........AGGCAGGUCCGAAGGAAUCCGGUU.....	24	41828
.........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGU.....	31	18454
.........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUC.....	32	14562
.........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCC.....	33	11952
.........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCU.....	34	18704

```
.........................................CUUCGAAUCCGGAUACCGACCGAUGACCGCUCA.............    33    13569
........................................UUCGAAUCCGGAUACCGACCGAUGACCGCUCA.............    32    32405
.......................................UCGAAUCCGGAUACCGACCGAUGACCGCUCA.............    31    44109
......................................CGAAUCCGGAUACCGACCGAUGACCGCUCA.............    30    49662
.....................................GAAUCCGGAUACCGACCGAUGACCGCUCA.............    29    59460
....................................AAUCCGGAUACCGACCGAUGACCGCUCA.............    28    236230
...................................AUCCGGAUACCGACCGAUGACCGCUCA.............    27    51842
..................................CGGAUACCGACCGAUGACCGCUCA.............    24    12236
.................................GGAUACCGACCGAUGACCGCUCA.............    23    18791
................................GAUACCGACCGAUGACCGCUCA.............    22    20577
...............................AUACCGACCGAUGACCGCUCA.............    21    27896
..............................UACCGACCGAUGACCGCUCA.............    20    15286
.............................CCGACCGAUGACCGCUCA.............    18    56397
Perfectly antisense match


#UP2c
ACGCAUUUGAAAGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCUUCGAAUCCGGAUACCGACCGAUGACCGCUCGUUAUUUUC
Perfectly match
..........AAGGCAGGUCCGAAGGAAUCCG.....................................................    22    15702
..........AAGGCAGGUCCGAAGGAAUCCGGU...................................................    24    11346
..........AAGGCAGGUCCGAAGGAAUCCGGUU..................................................    25    16582
..........AAGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCU........................................    35    14035
...........AGGCAGGUCCGAAGGAAU.........................................................    18    28173
...........AGGCAGGUCCGAAGGAAUC........................................................    19    28015
...........AGGCAGGUCCGAAGGAAUCC.......................................................    20    30318
...........AGGCAGGUCCGAAGGAAUCCG......................................................    21    53303
...........AGGCAGGUCCGAAGGAAUCCGG.....................................................    22    32933
...........AGGCAGGUCCGAAGGAAUCCGGU....................................................    23    37305
...........AGGCAGGUCCGAAGGAAUCCGGUU...................................................    24    41828
...........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGU............................................    31    18454
...........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUC...........................................    32    14562
...........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCC..........................................    33    11952
...........AGGCAGGUCCGAAGGAAUCCGGUUAUCAUGUCCU.........................................    34    18704
.....................................................GAAUCCGGAUACCGACCGAUGACCGCUCG.....    29    13311
....................................................AAUCCGGAUACCGACCGAUGACCGCUCG.....    28    27731
Perfectly antisense match


#UP5a
AGGAACUGAUCGACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGUUUCGUUCGCCCCACCCCGCAACUCGAUCCAUGACCGUCACUUUUUUC
Perfectly match
...........GACAGGUCCGUUGAGAUG.....................................................................    18    16428
...........GACAGGUCCGUUGAGAUGC....................................................................    19    38785
...........GACAGGUCCGUUGAGAUGCG...................................................................    20    65296
...........GACAGGUCCGUUGAGAUGCGG..................................................................    21    76568
```

```
..........GACAGGUCCGUUGAGAUGCGGU.......................................................... 22    179915
..........GACAGGUCCGUUGAGAUGCGGUU......................................................... 23    66307
..........GACAGGUCCGUUGAGAUGCGGUUA........................................................ 24    11140
..........GACAGGUCCGUUGAGAUGCGGUUAUCA..................................................... 27    27767
..........GACAGGUCCGUUGAGAUGCGGUUAUCAG.................................................... 28    55837
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGA................................................... 29    73856
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAA.................................................. 30    258715
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAU................................................. 31    153185
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUU................................................ 32    169246
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUG.............................................. 33    206728
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGA............................................. 34    44979
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGU......................................... 38    28927
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGUU........................................ 39    13896
..........GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGUUU...................................... 40    17056
.....................................................GCCCCACCCCGCAACUCGAUCCAUGACCGUCAC....... 33    16253
....................................................CCCACCCCGCAACUCGAUCCAUGACCGUCAC....... 31    34199
...................................................CCACCCCGCAACUCGAUCCAUGACCGUCAC....... 30    61668
...................................................CACCCCGCAACUCGAUCCAUGACCGUCA........ 28    33875
...................................................CACCCCGCAACUCGAUCCAUGACCGUCAC....... 29    205012
...................................................CACCCCGCAACUCGAUCCAUGACCGUCACU...... 30    14984
..................................................ACCCCGCAACUCGAUCCAUGACCGUC......... 26    13495
..................................................ACCCCGCAACUCGAUCCAUGACCGUCA........ 27    254293
.................................................ACCCCGCAACUCGAUCCAUGACCGUCAC....... 28    1635380
..................................................ACCCCGCAACUCGAUCCAUGACCGUCACU...... 29    137408
.................................................CCCCGCAACUCGAUCCAUGACCGUCAC....... 27    38575
................................................CCCGCAACUCGAUCCAUGACCGUCAC....... 26    15136
...............................................CCGCAACUCGAUCCAUGACCGUCAC....... 25    10652
..............................................GCAACUCGAUCCAUGACCGUCAC....... 23    17511
.............................................CAACUCGAUCCAUGACCGUCAC....... 22    10421
............................................AACUCGAUCCAUGACCGUCAC....... 21    18488
...........................................ACUCGAUCCAUGACCGUCAC....... 20    17885
..........................................CUCGAUCCAUGACCGUCAC....... 19    10182
.........................................UCGAUCCAUGACCGUCAC....... 18    16452
Perfectly antisense match


#UP5b
ACGCACAAGCUGGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUUGAUUGAAGACCCGCUUCUCGCGAACACGACCGUCAUUUUUUGCA
Perfectly match
..........GGACAGGUCCGAUGAGAUG.............................................................  19    56359
..........GGACAGGUCCGAUGAGAUGC............................................................  20    38013
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................................................AAGACCCGCUUCUCGCGAACACGACCGUCAU.....  31    14597
................................................GACCCGCUUCUCGCGAACACGACCGUCA........  28    17298
................................................GACCCGCUUCUCGCGAACACGACCGUCAU.....  29    28185
Perfectly antisense match


#UP5c
AUAUAUCGGGCAGGUCCGAUGAGAUGUGGUUAUCGACUUUGAAUUGACUACCCGCUUCUCGCAAGCUCGACCGUCCUUUUUU
Perfectly match
.......GGGCAGGUCCGAUGAGAUGUGGUUAUCGACUU.....................................  32    14932
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..............................................UACCCGCUUCUCGCAAGCUCGACCGUCCU.....  29    283606
..............................................ACCCGCUUCUCGCAAGCUCGACCGUCCU.....  28    42010
Perfectly antisense match


#UP5d
AGUGUUCGACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGUUUCGUUCGCCCCACCCCGCAACUCGAUCCAUGACCGUCCUUUUAGU
Perfectly match
.......GACAGGUCCGUUGAGAUG.....................................................  18    16428
.......GACAGGUCCGUUGAGAUGC....................................................  19    38785
.......GACAGGUCCGUUGAGAUGCG...................................................  20    65296
.......GACAGGUCCGUUGAGAUGCGG..................................................  21    76568
.......GACAGGUCCGUUGAGAUGCGGU.................................................  22    179915
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Perfectly antisense match

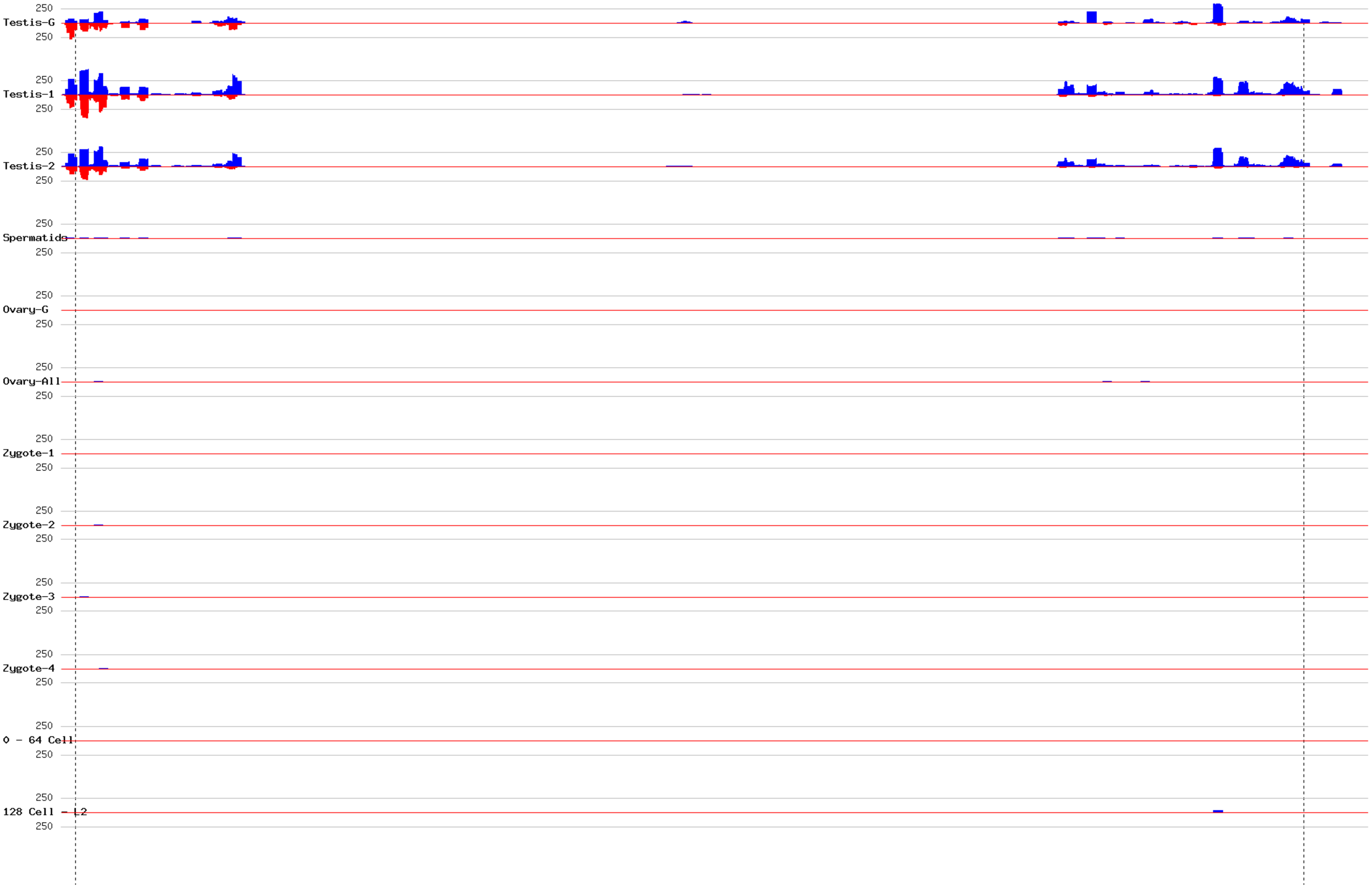

#UP5e
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Perfectly match
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...............GACAGGUCCGUUGAGAUGC....................................................  19    38785
...............GACAGGUCCGUUGAGAUGCG...................................................  20    65296
...............GACAGGUCCGUUGAGAUGCGG..................................................  21    76568
...............GACAGGUCCGUUGAGAUGCGGU.................................................  22    179915
...............GACAGGUCCGUUGAGAUGCGGUU................................................  23    66307
...............GACAGGUCCGUUGAGAUGCGGUUA...............................................  24    11140
...............GACAGGUCCGUUGAGAUGCGGUUAUCA............................................  27    27767
...............GACAGGUCCGUUGAGAUGCGGUUAUCAG...........................................  28    55837
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGA..........................................  29    73856
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAA.........................................  30    258715
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAAU........................................  31    153185
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUU.......................................  32    169246
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUG......................................  33    206728
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...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGU.................................  38    28927
...............GACAGGUCCGUUGAGAUGCGGUUAUCAGAAUUGAACGUU................................  39    13896
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Perfectly antisense match

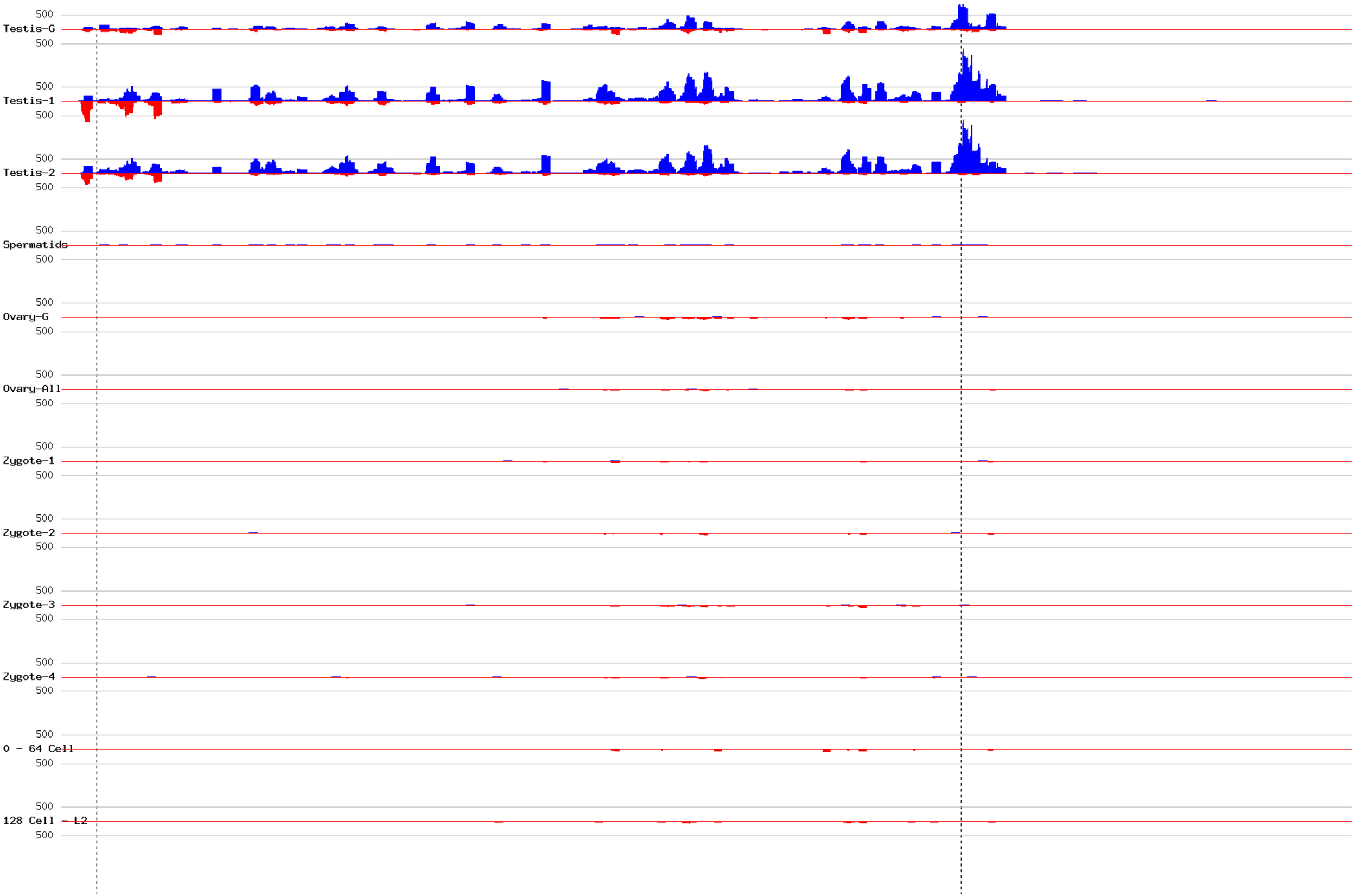

#UP5f
ACAAGCUGGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUUGAUUGAAGACCCGCUUCUCGCAAACACGACCGUCCUUUUU
Perfectly match
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.......GGACAGGUCCGAUGAGAUGC....................................................      20    38013
.......GGACAGGUCCGAUGAGAUGCG...................................................      21    112748
.......GGACAGGUCCGAUGAGAUGCGA..................................................      22    71613
.......GGACAGGUCCGAUGAGAUGCGAU.................................................      23    119205
.......GGACAGGUCCGAUGAGAUGCGAUU................................................      24    217472
.......GGACAGGUCCGAUGAGAUGCGAUUA...............................................      25    36302
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.......GGACAGGUCCGAUGAGAUGCGAUUAUC.............................................      27    153851
.......GGACAGGUCCGAUGAGAUGCGAUUAUCG............................................      28    35130
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGA...........................................      29    30043
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUA.........................................      31    120964
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUACU.......................................      33    85529
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUU......................................      34    227465
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUUG.....................................      35    58316
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUUGA....................................      36    12555
.......GGACAGGUCCGAUGAGAUGCGAUUAUCGAUACUUGAUUG.................................      39    10133
........GACAGGUCCGAUGAGAUGCG....................................................      20    12196
........GACAGGUCCGAUGAGAUGCGA...................................................      21    10715
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........GACAGGUCCGAUGAGAUGCGAUUAUC..............................................      26    13869
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........GACAGGUCCGAUGAGAUGCGAUUAUCGAUACU........................................      32    12435
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..............................GAAGACCCGCUUCUCGCAAACACGACCGUCCU....      32    68415
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...........................GACCCGCUUCUCGCAAACACGACCGUCCU....      29    196006
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Perfectly antisense match
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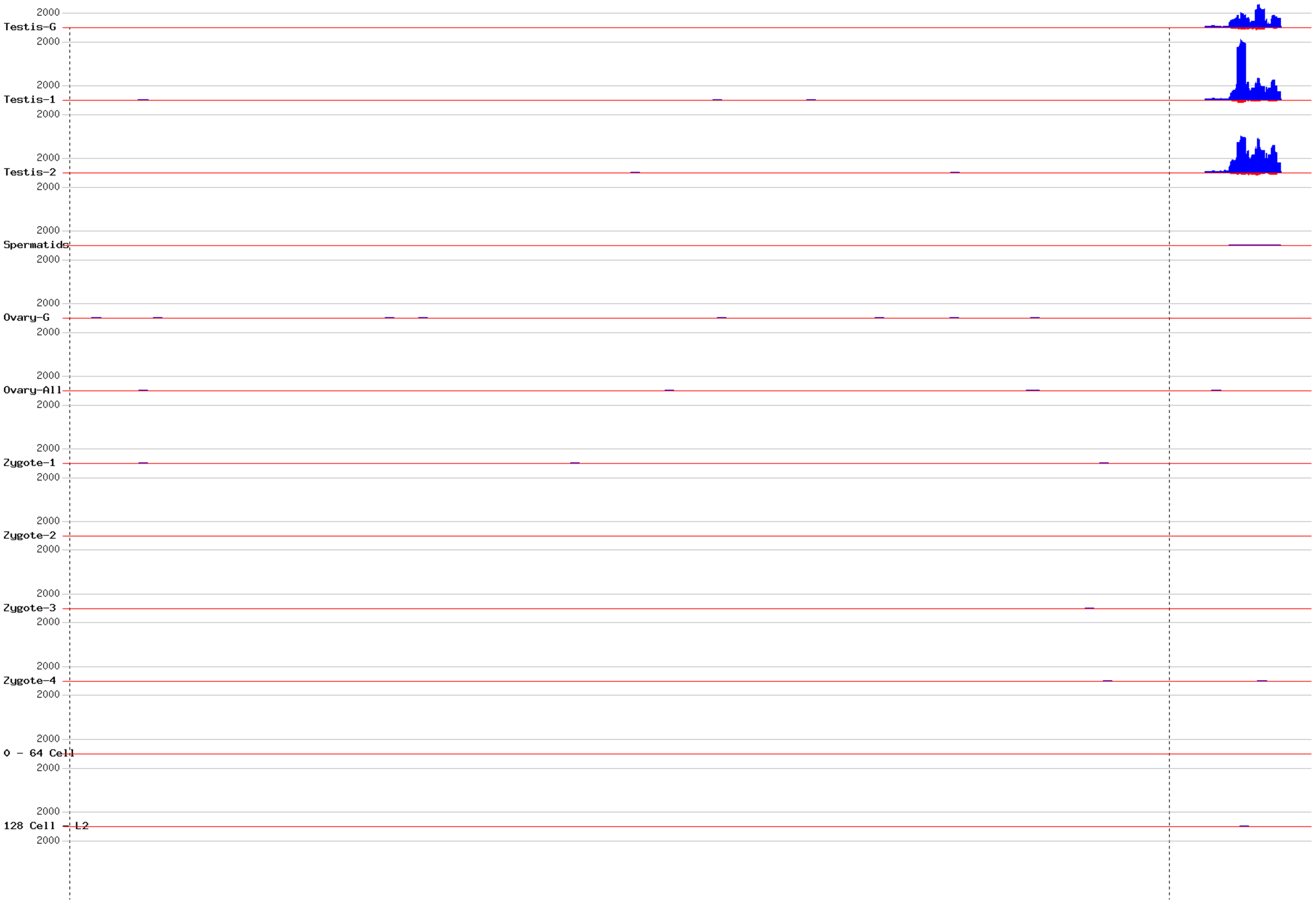
ASCF_1079_3640 Serine/threonine_protein_phosphatase_PP1 3640 bp



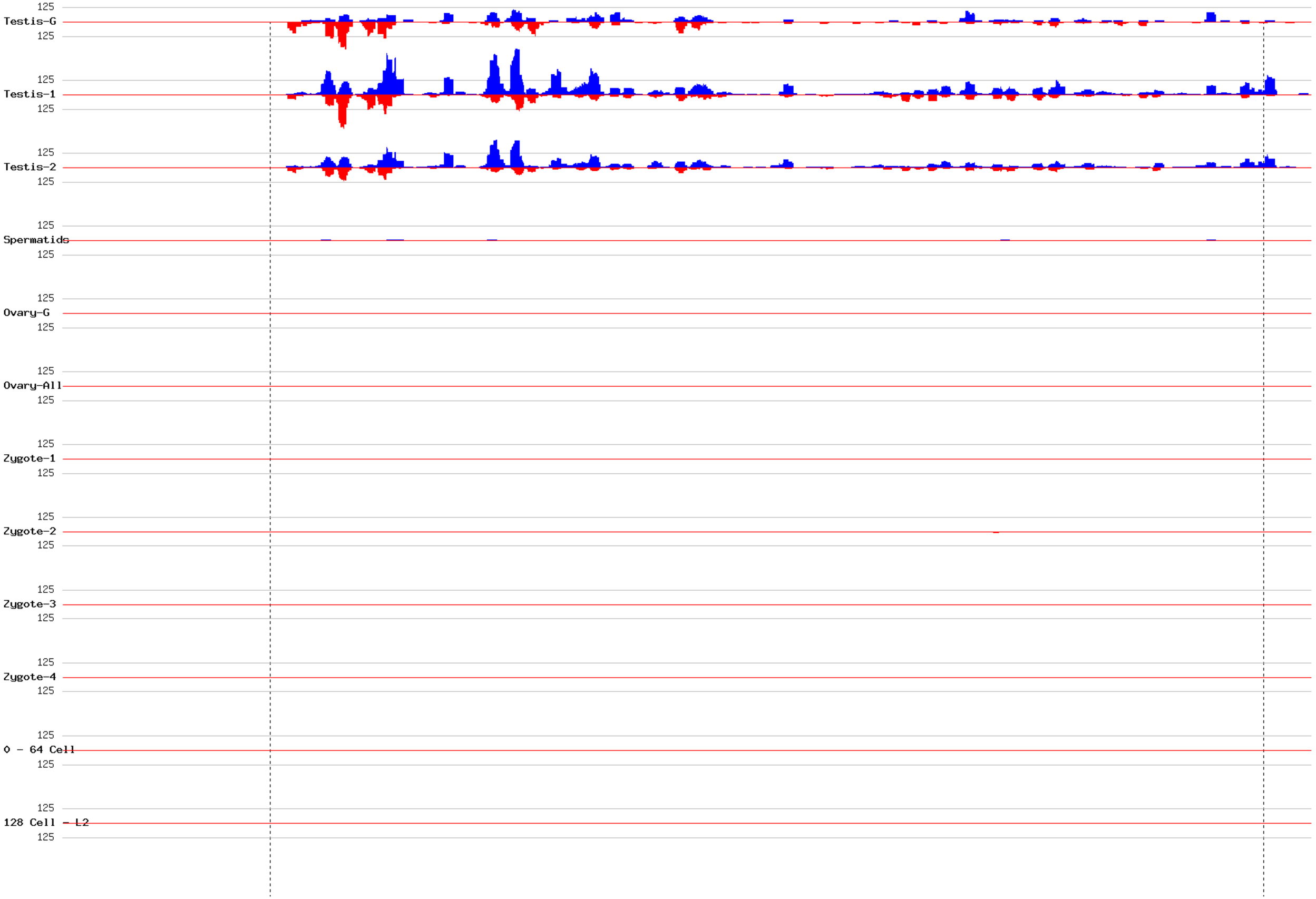
ASCF_1145_3585 6-phosphofructokinase 3585 bp



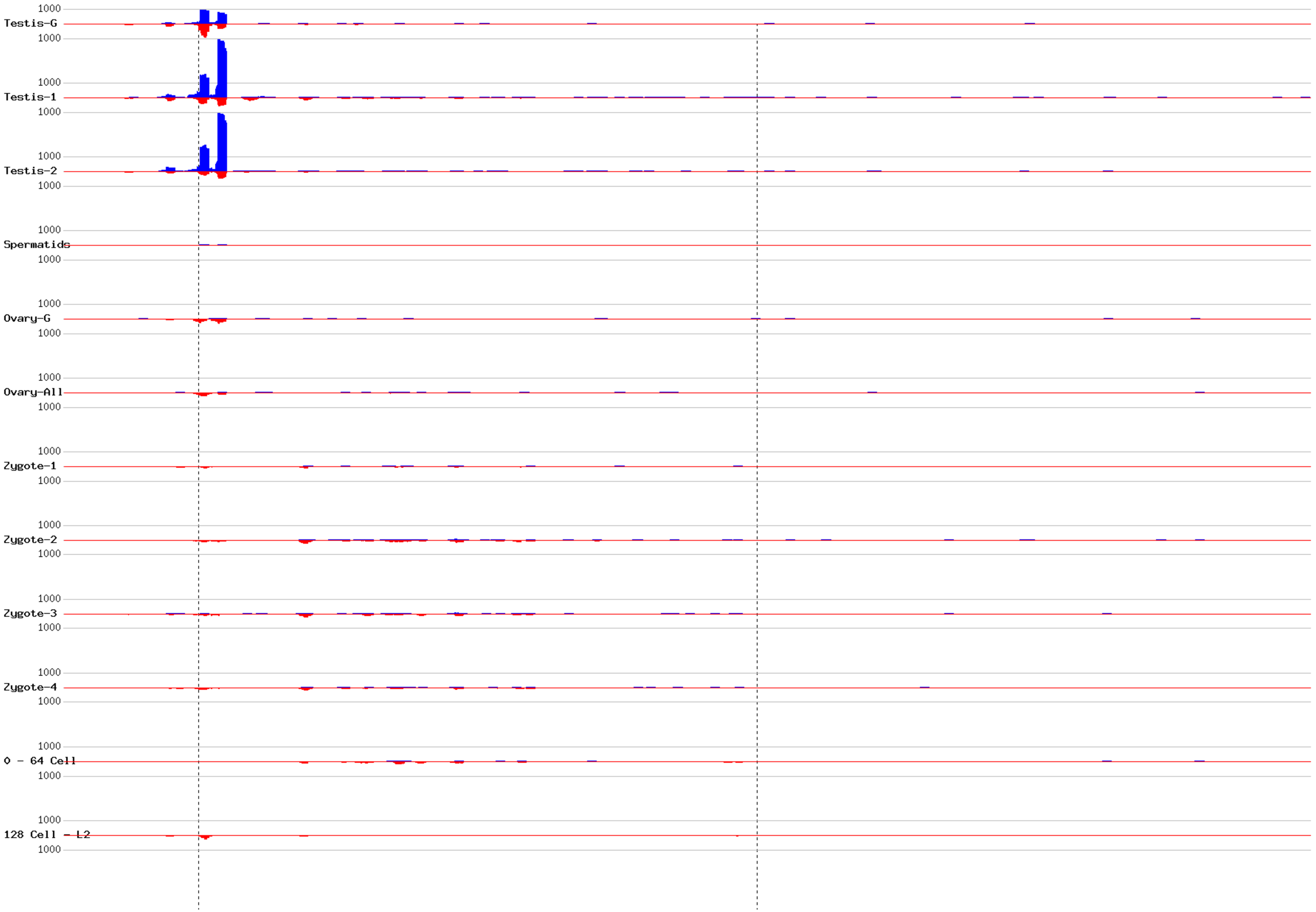
ASCF_1280_3437 Ubiquitin_conjugation_factor 3437 bp



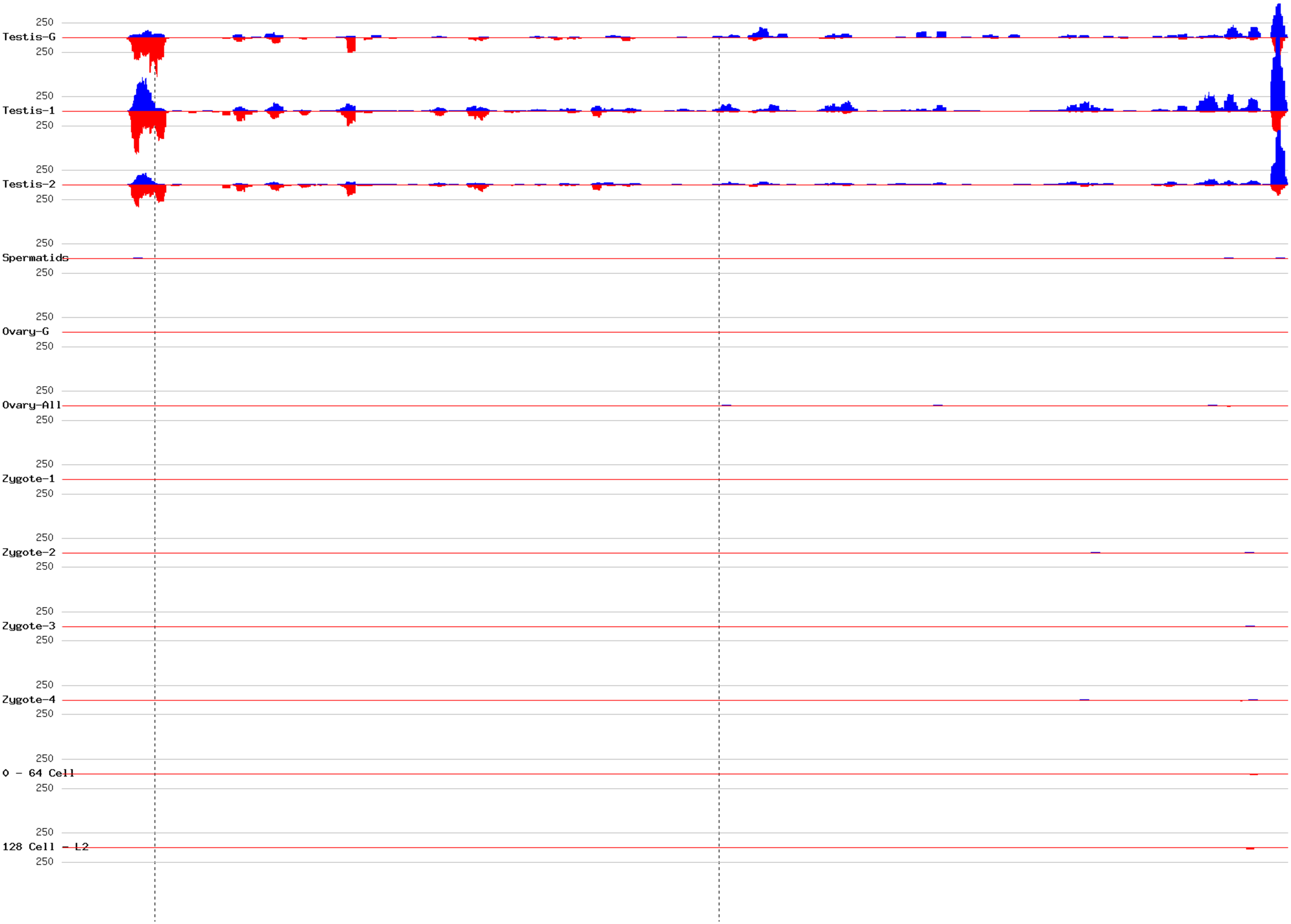
ASCF_1291_3428 Protein-tyrosine_phosphatase_containing_protein 3428 bp



ASCF_1329_3381 Zinc_finger_C2H2_type_family_protein 3381 bp



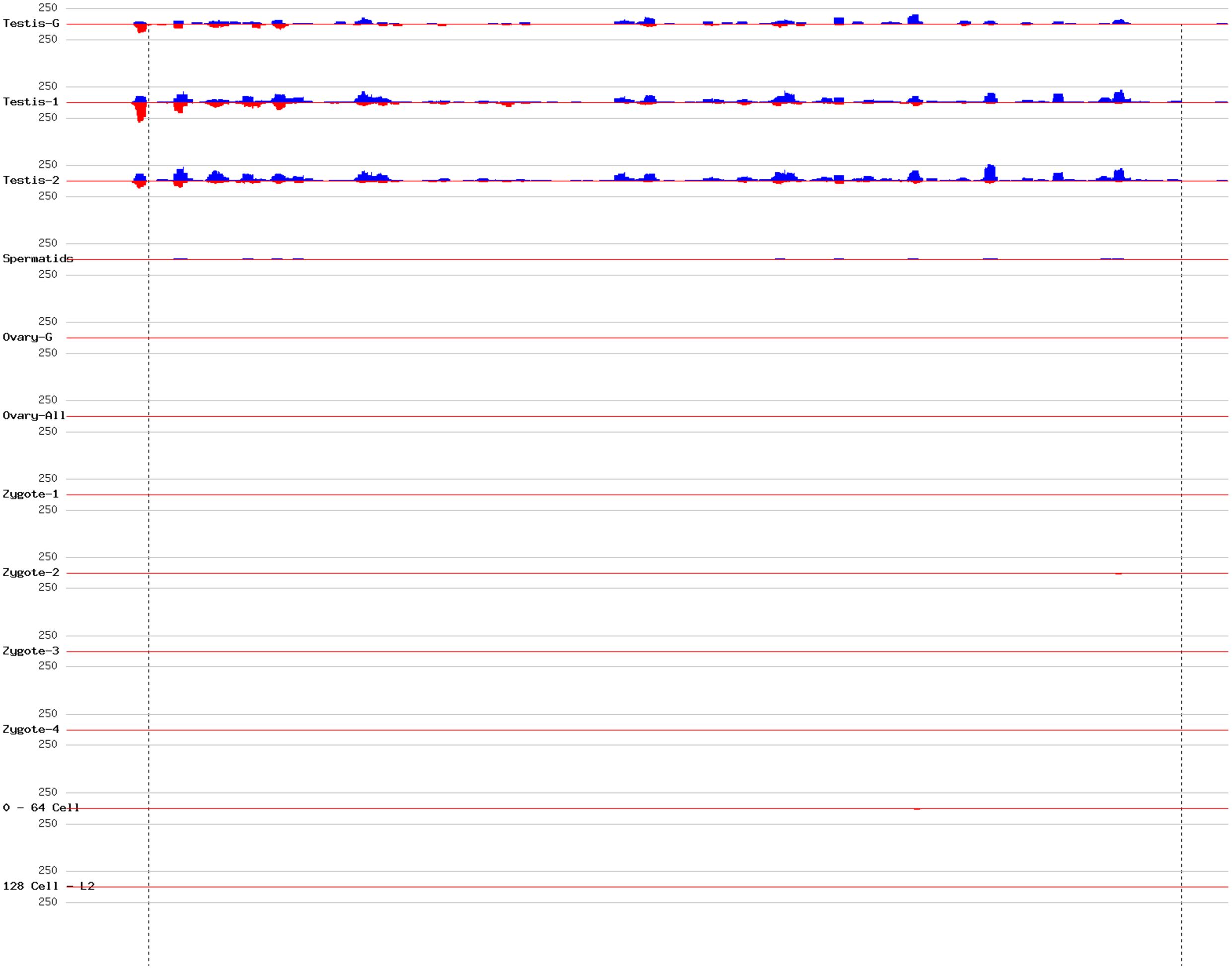
ASCF_1383_3328 Alternative_Splicing_Defective_2 3328 bp



ASCF_1603_3119 Protein_kinase_domain_containing_protein 3119 bp

250
Testis-G
250
250
Testis-1
250
250
Testis-2
250
250
Spermatids
250
250
Ovary-G
250
250
Ovary-All
250
250
Zygote-1
250
250
Zygote-2
250
250
Zygote-3
250
250
Zygote-4
250
250
0 - 64 Cell
250
250
128 Cell - L2
250

ASCF_1802_2962 Hypothetical_protein 2962 bp

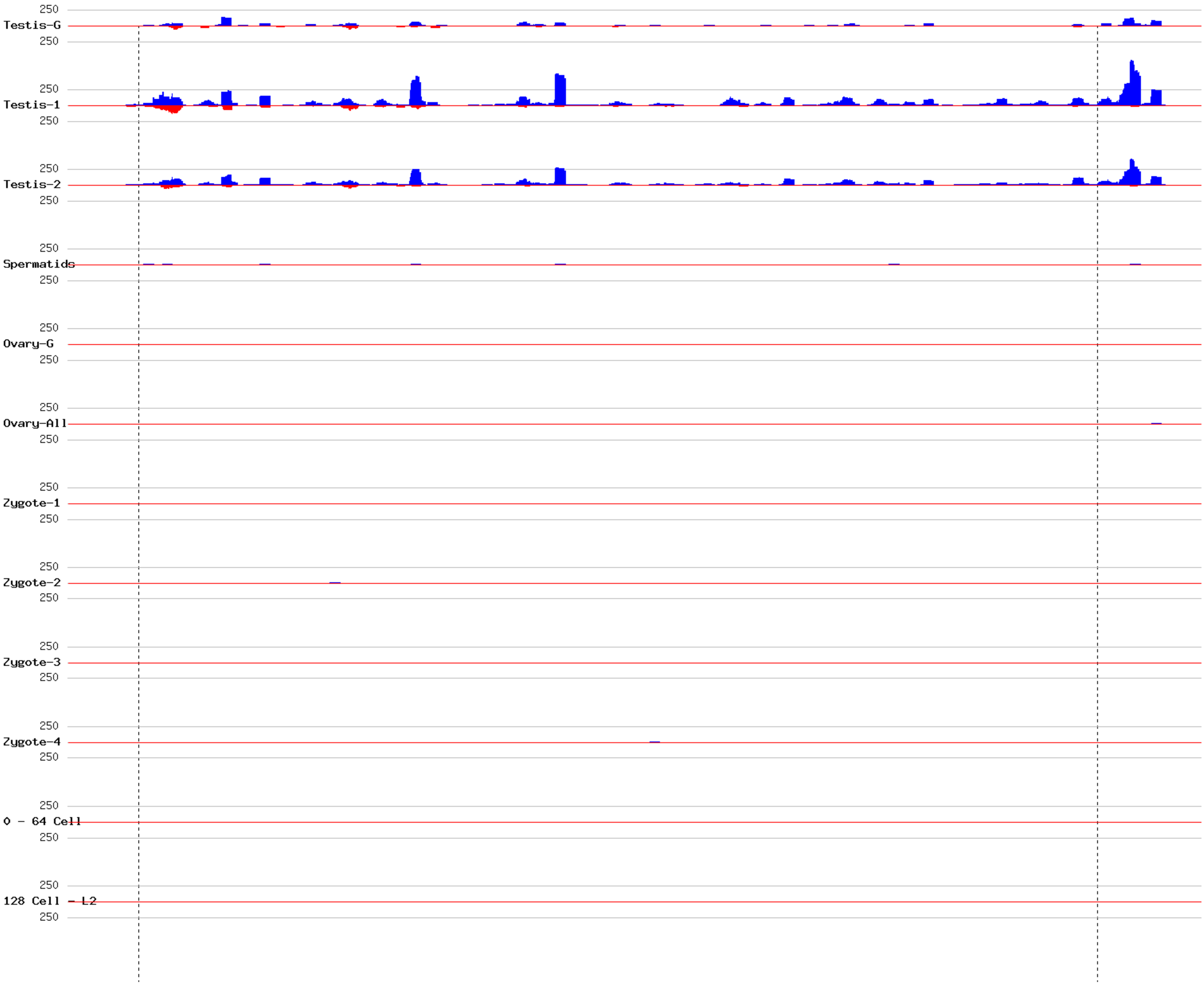


ASCF_1949_2860 Protein-tyrosine_phosphatase_containing_protein 2860 bp

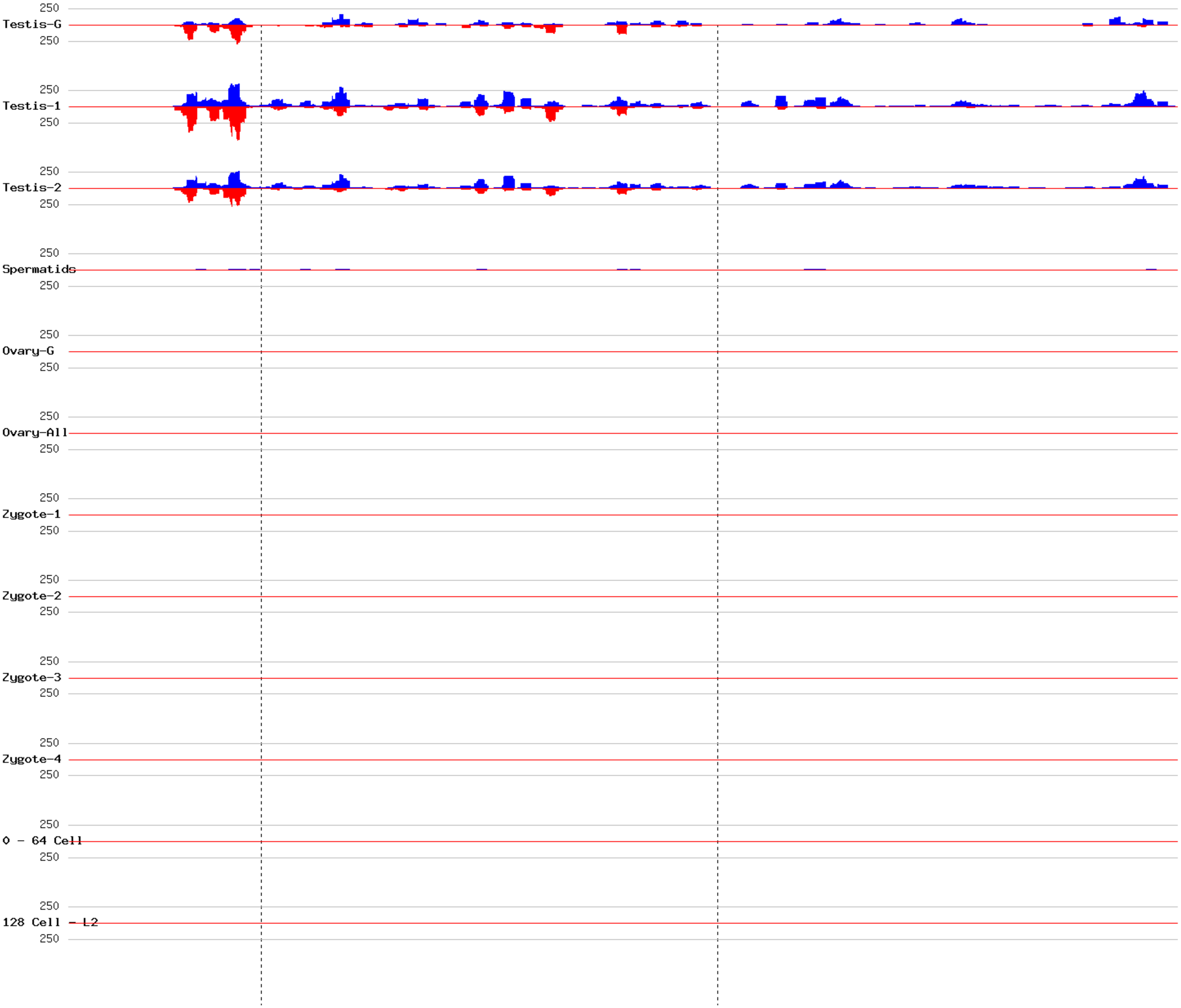
Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

500

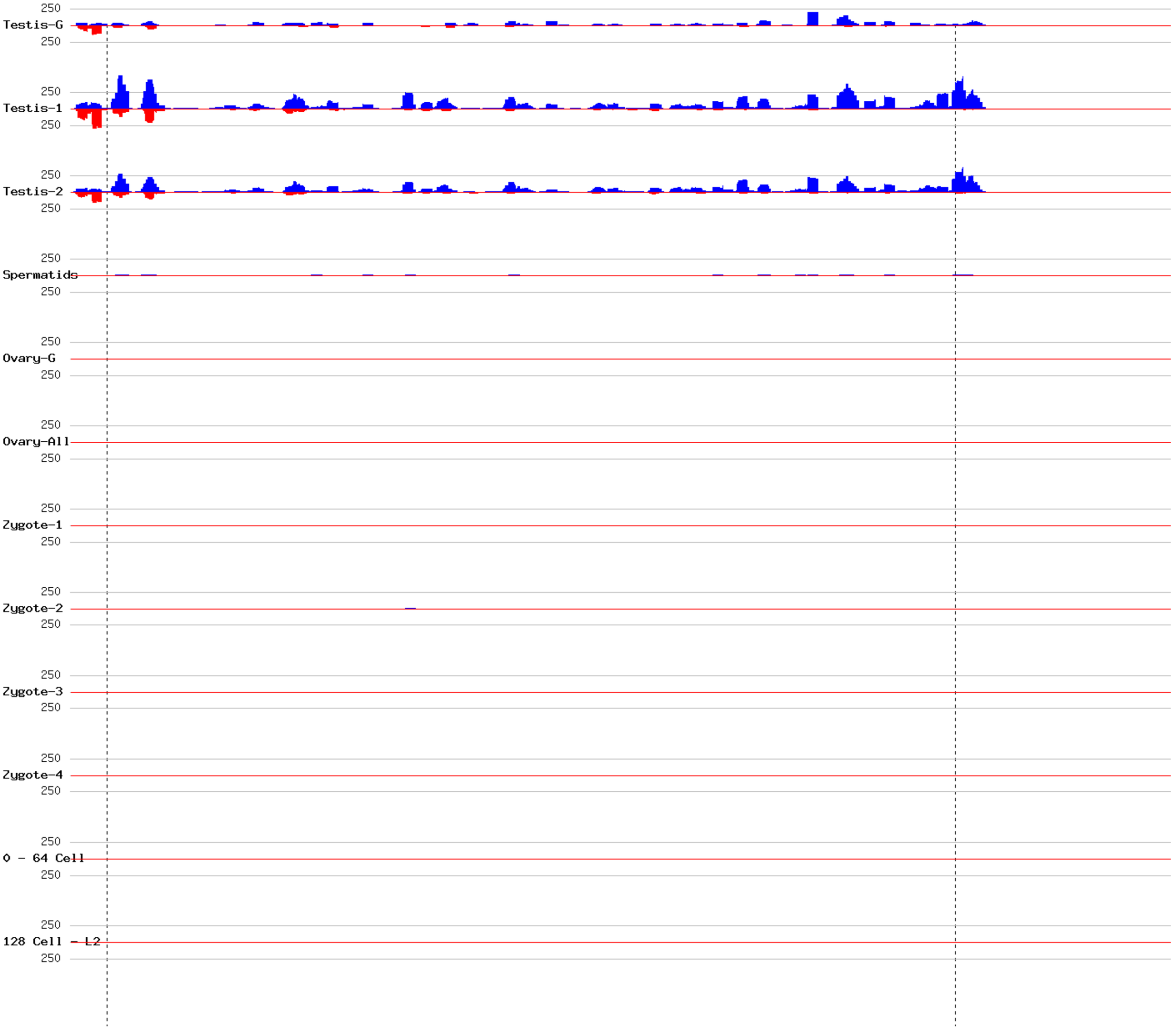
ASCF_1968_2846 Tyrosine-protein_kinase_Fer 2846 bp



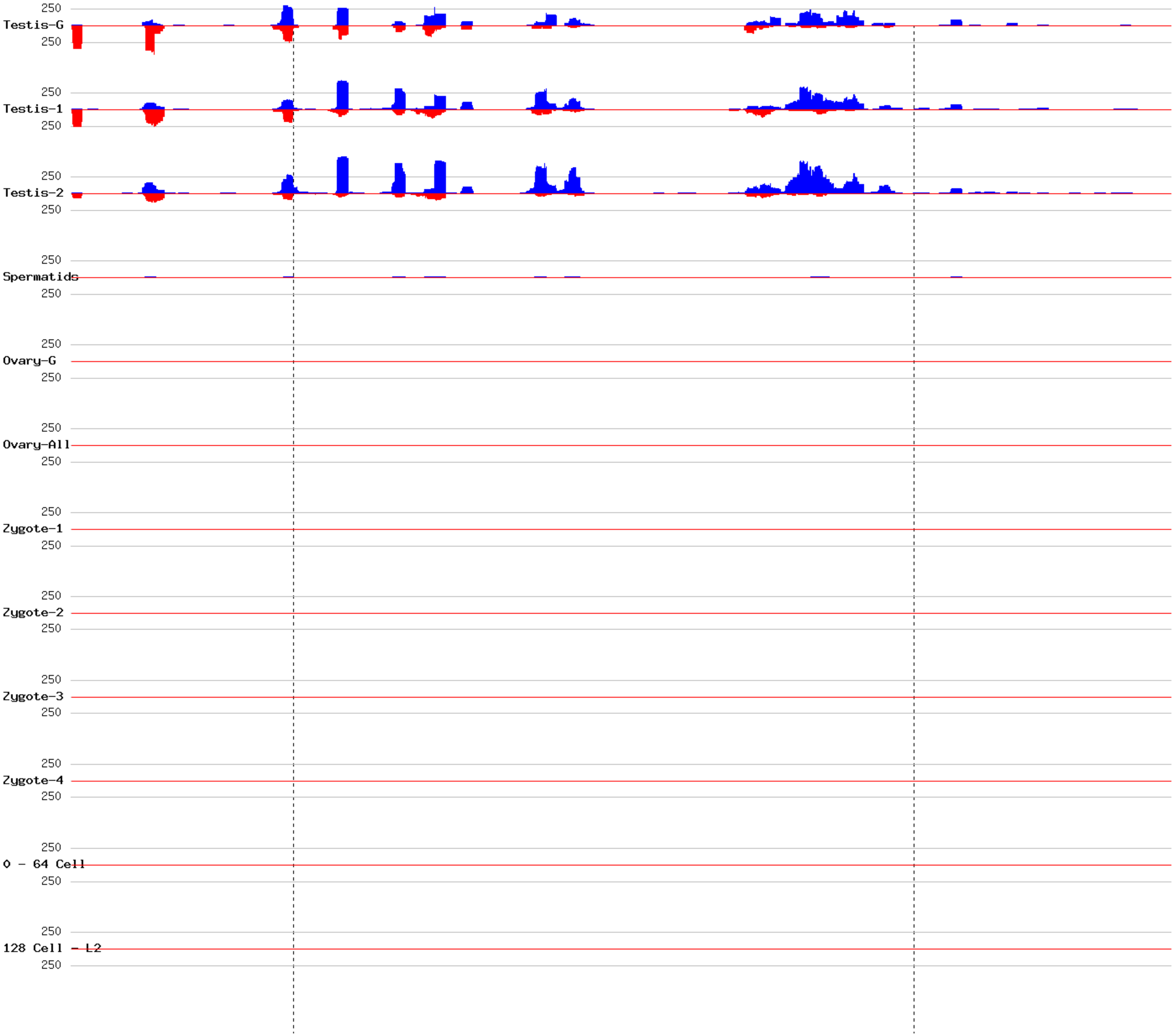
ASCF_2165_2716 Tyrosine-protein_kinase_Fer 2716 bp



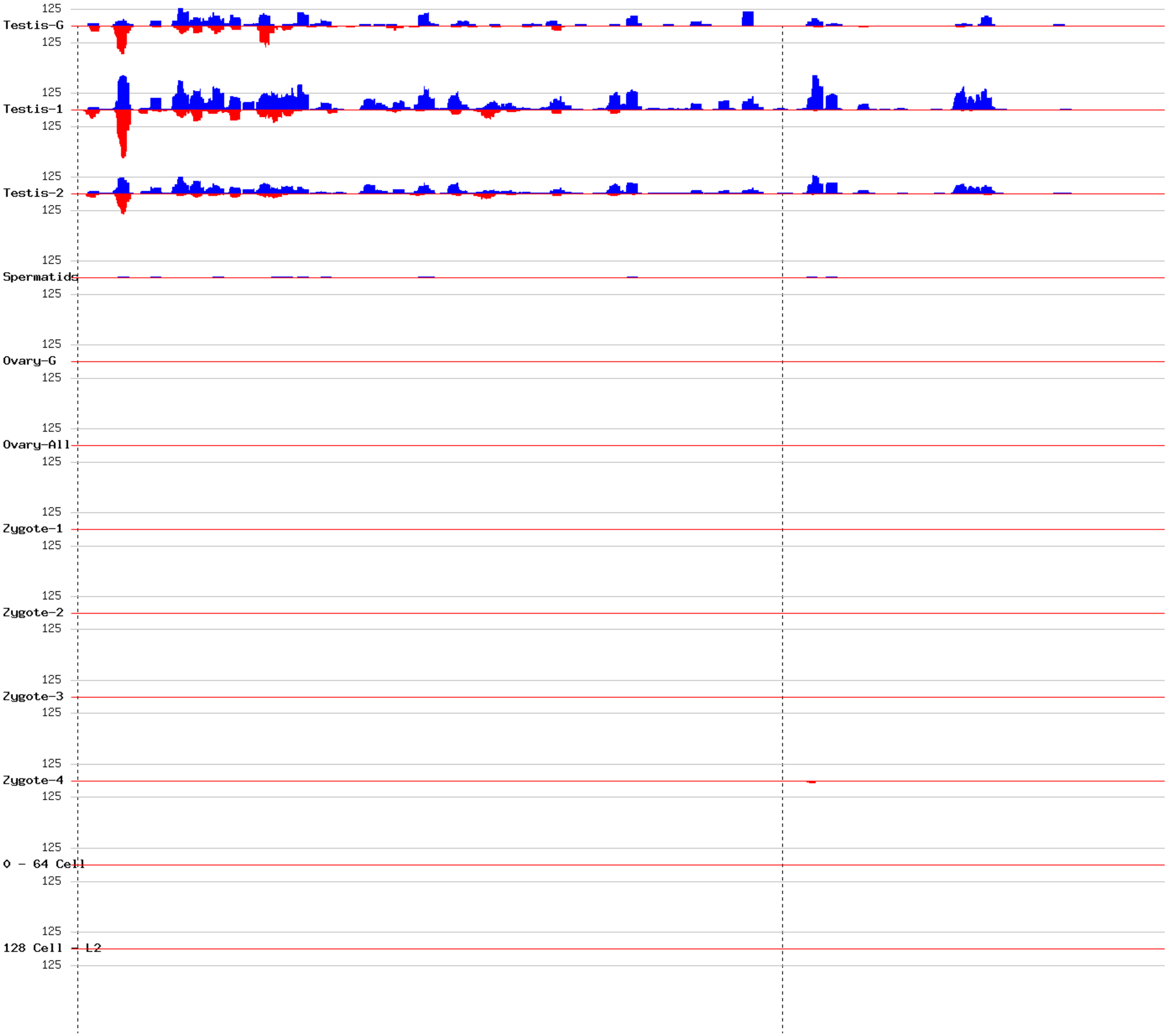
ASCF_2310_2640 Hypothetical_protein 2640 bp



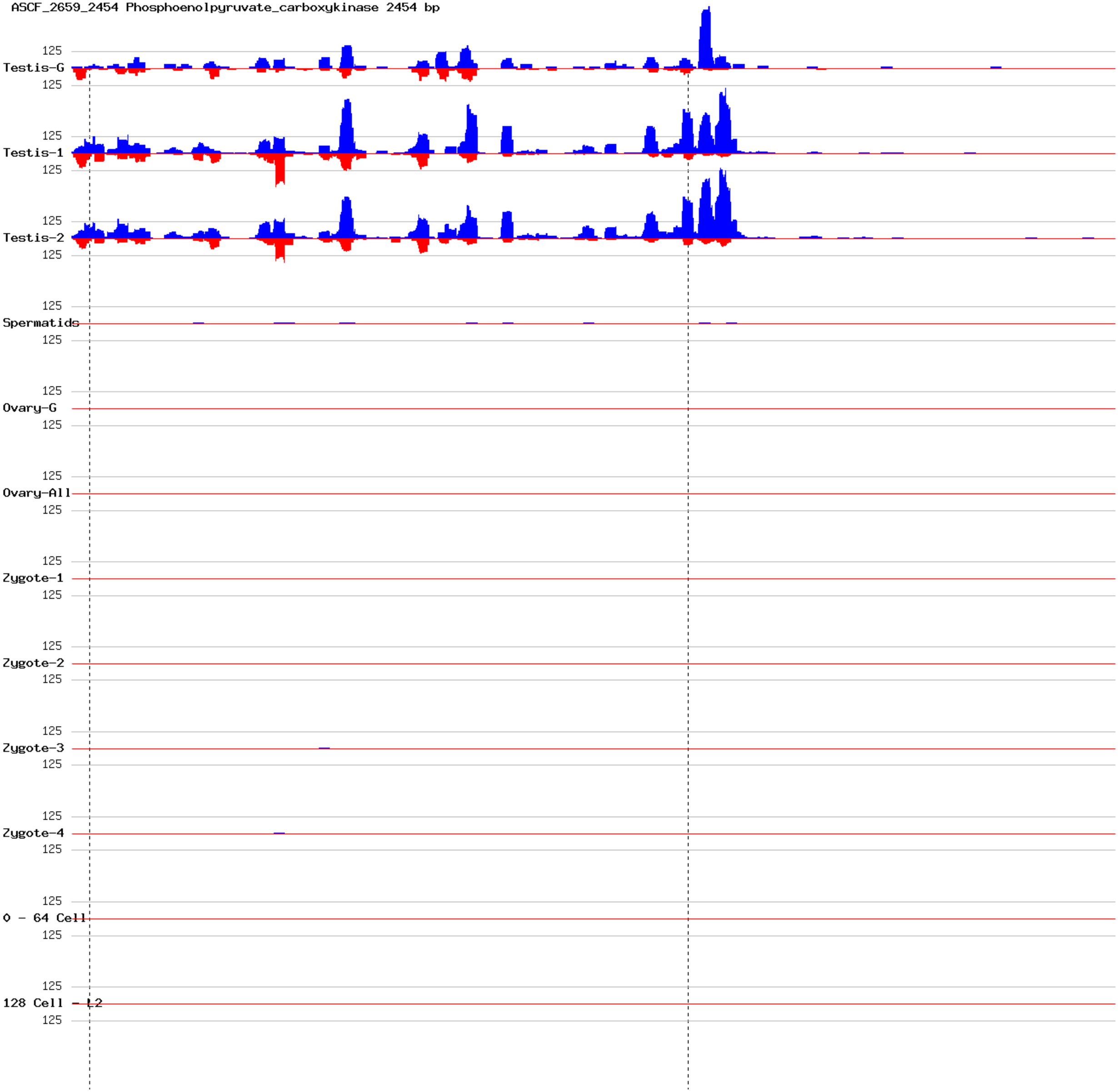
ASCF_2338_2621 Protein_kinase_domain_containing_protein 2621 bp



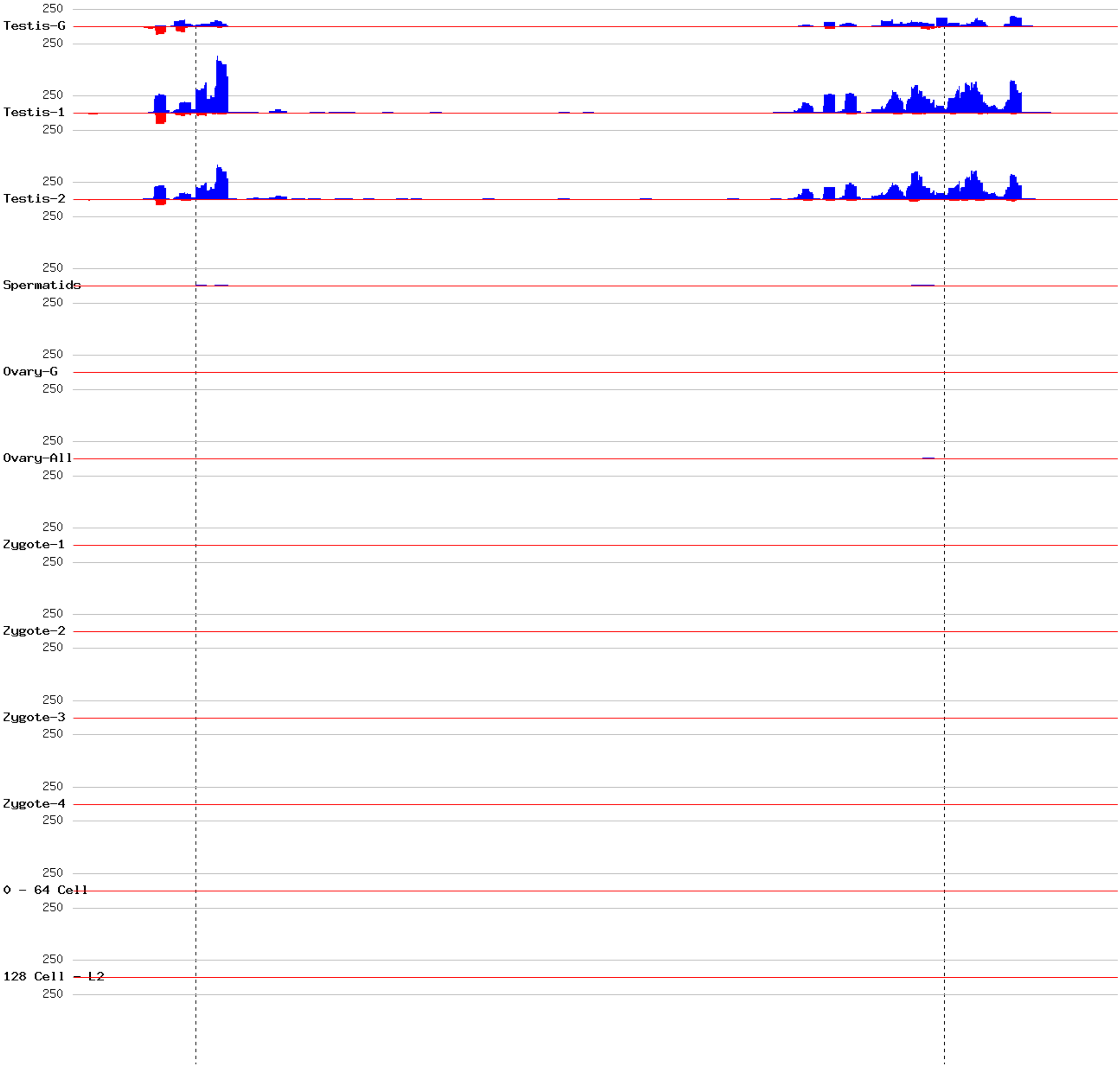
ASCF_2366_2606 Excitatory_amino_acid_transporter 2606 bp



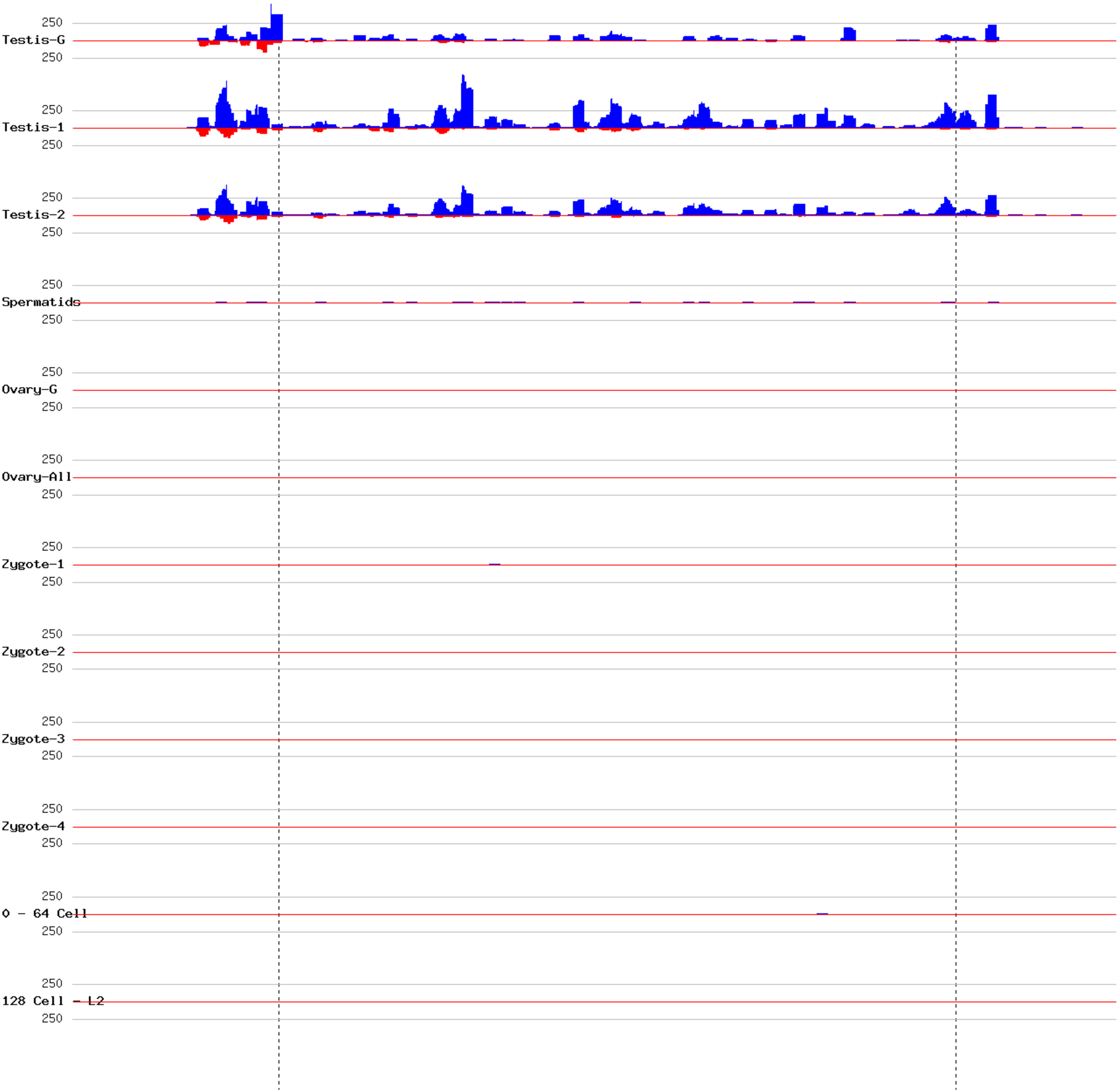
ASCF_2659_2454 Phosphoenolpyruvate_carboxykinase 2454 bp



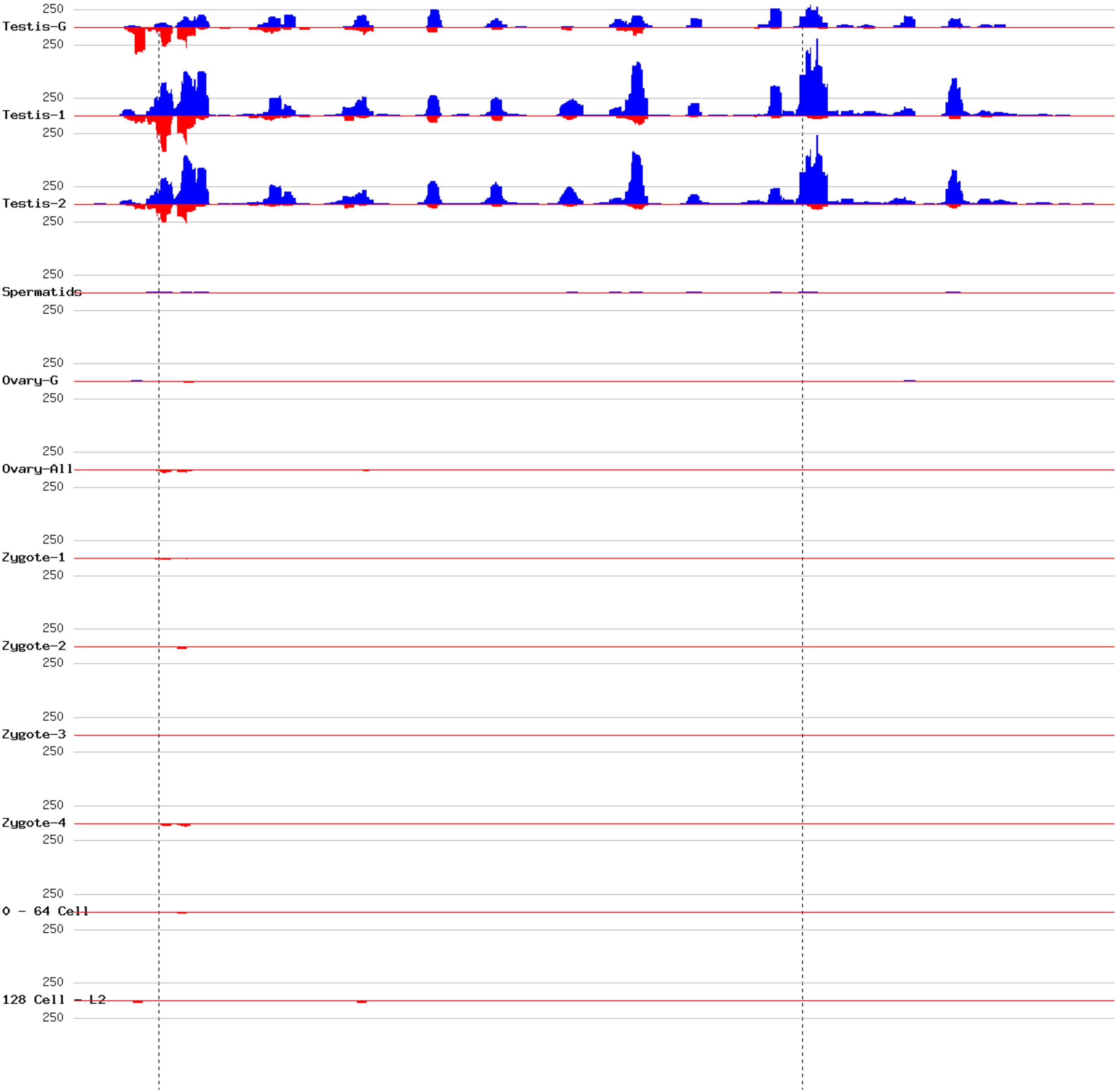
ASCF_2746_2417 Major_sperm_protein 2417 bp



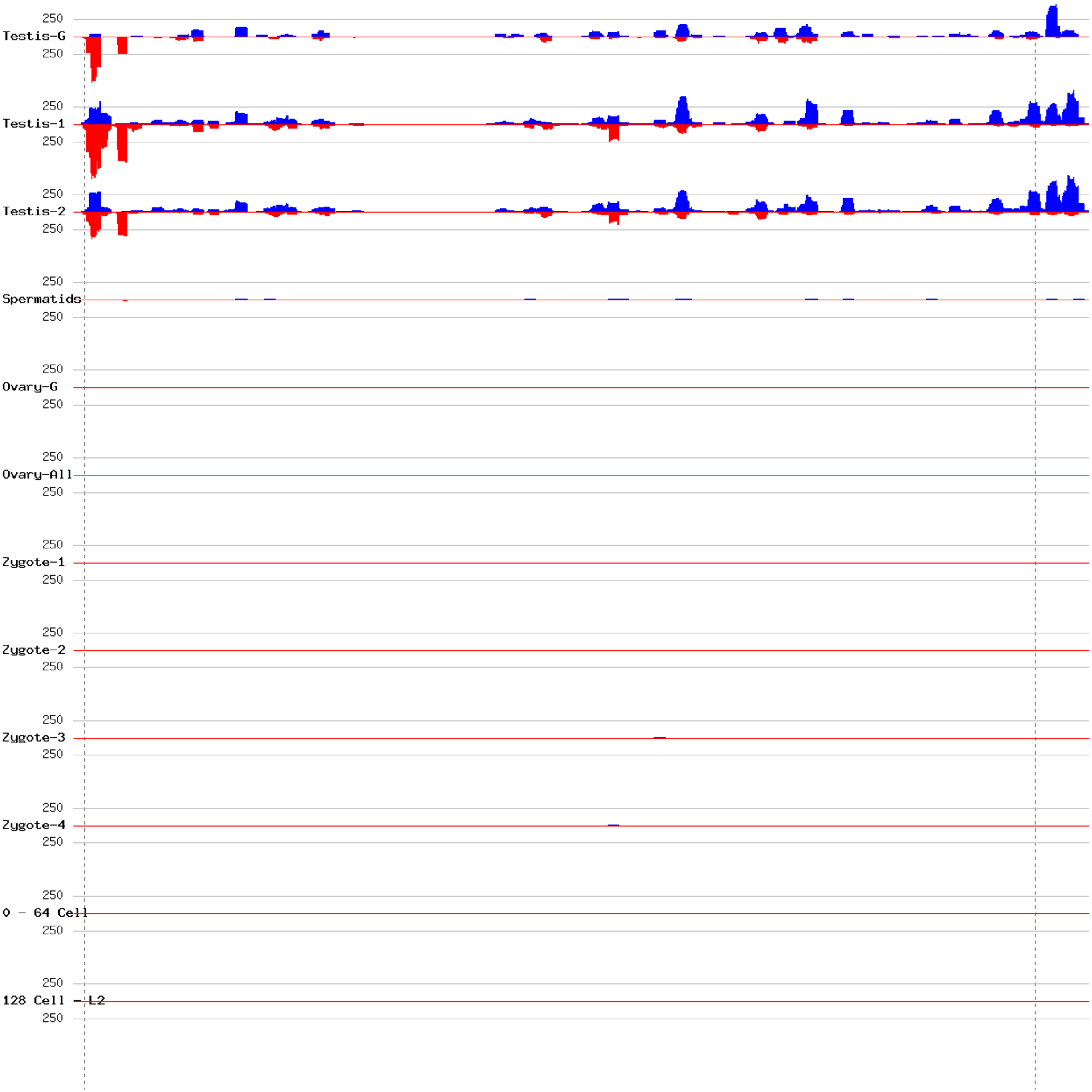
ASCF_2808_2389 Hypothetical_protein 2389 bp



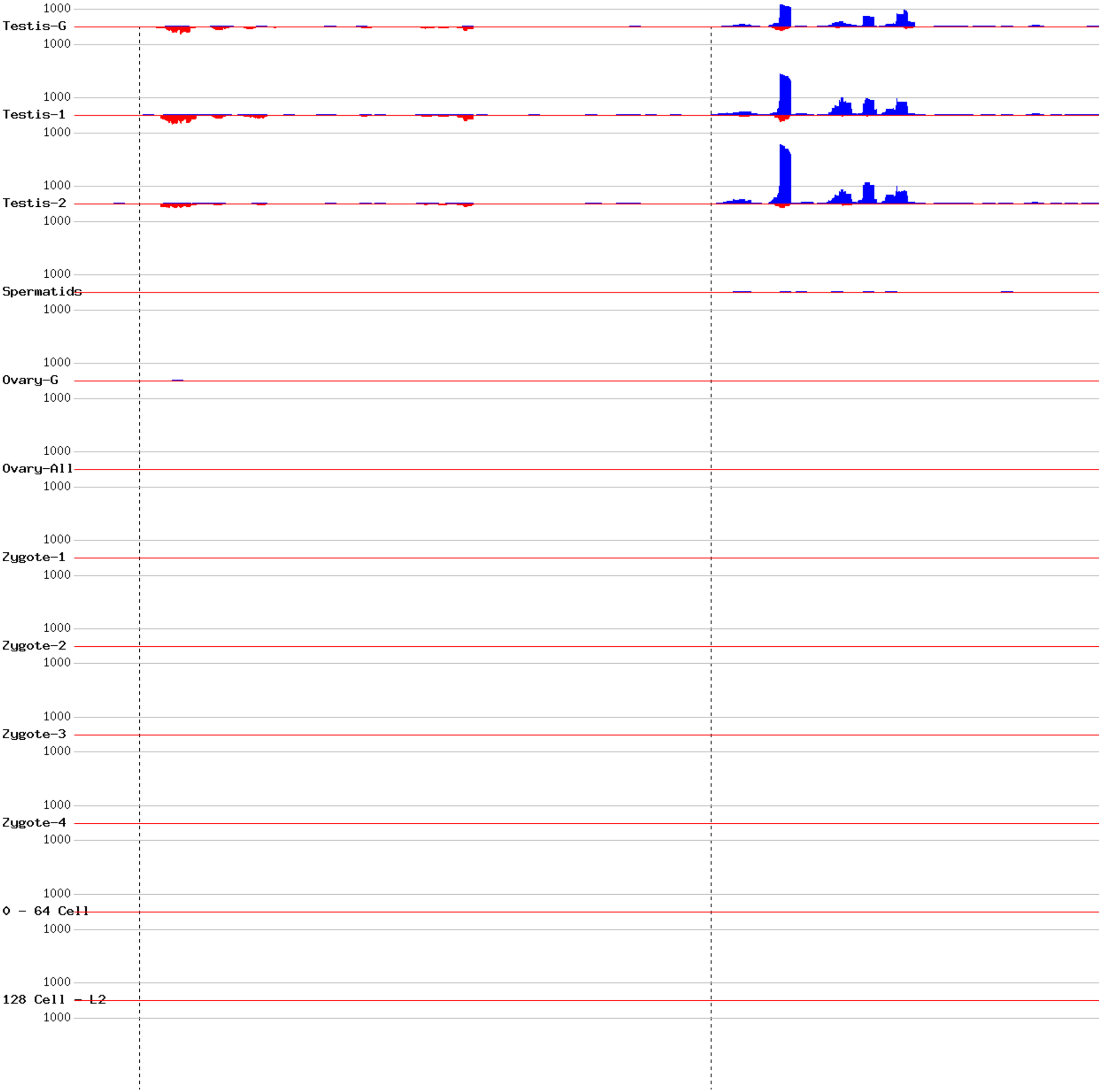
ASCF_2901_2350 S-antigen_protein 2350 bp



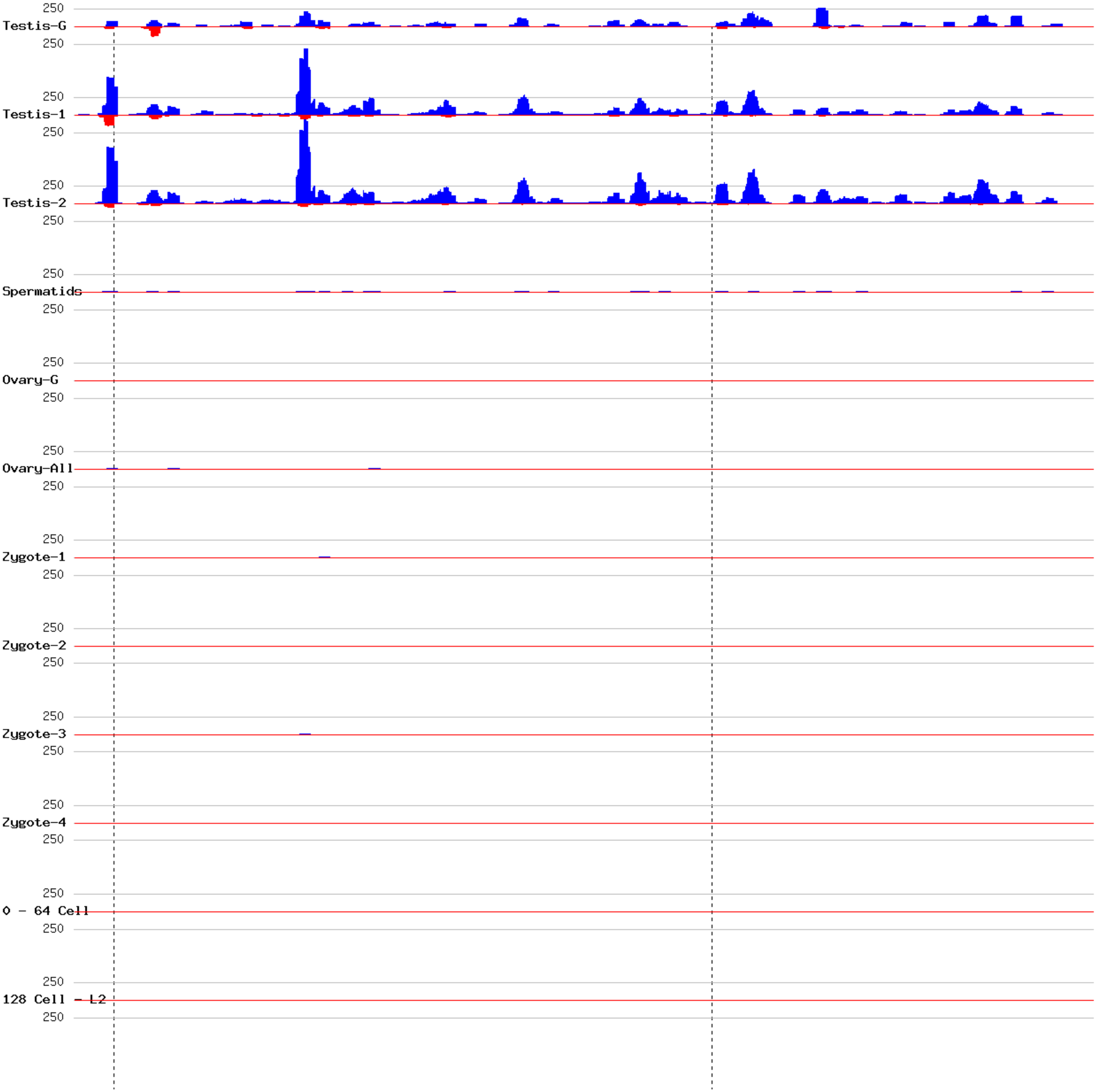
ASCF_2980_2317 Phosphoenolpyruvate_carboxykinase 2317 bp



ASCF_2986_2316 PDZ_domain_containing_protein 2316 bp



ASCF_3013_2305 Armadillo/beta-catenin-like_repeat_family_protein 2305 bp



ASCF_3048_2292 Protein_kinase_domain_containing_protein 2292 bp

125
Testis-G
125

125
Testis-1
125

125
Testis-2
125

125
Spermatids
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125
Ovary-G
125

125
Ovary-All
125

125
Zygote-1
125

125
Zygote-2
125

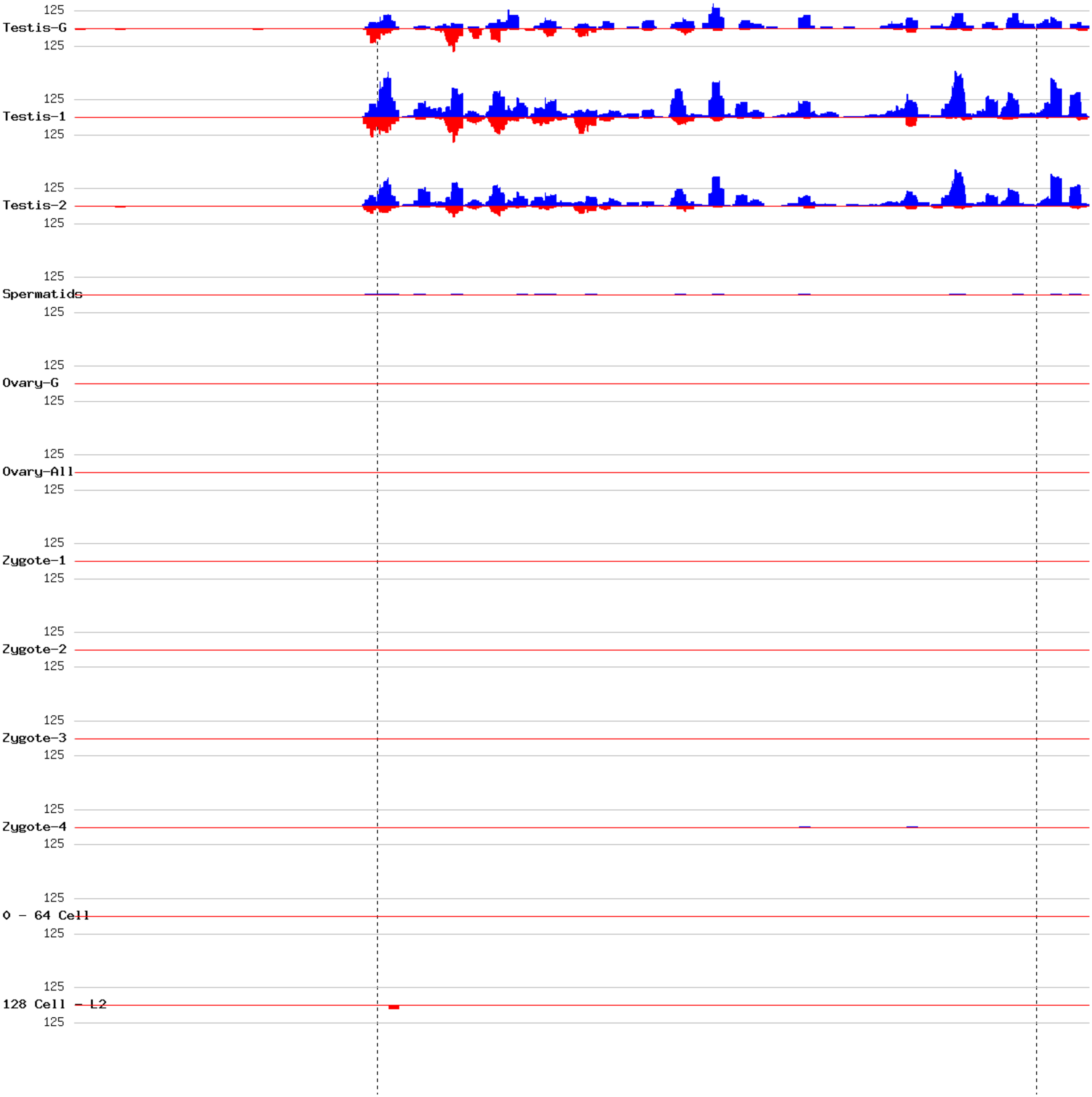
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125
Zygote-4
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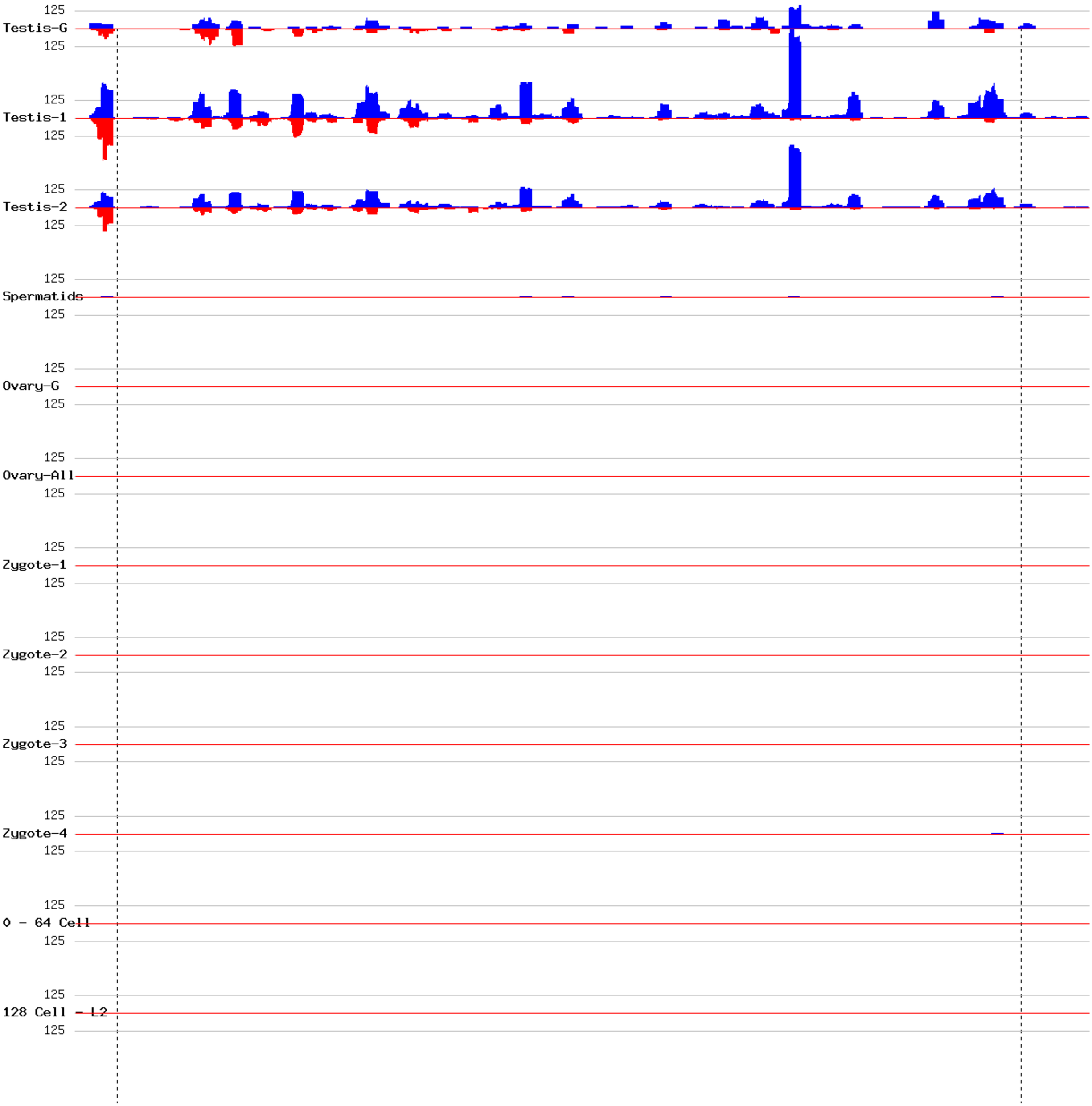
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125

125
128 Cell - L2
125

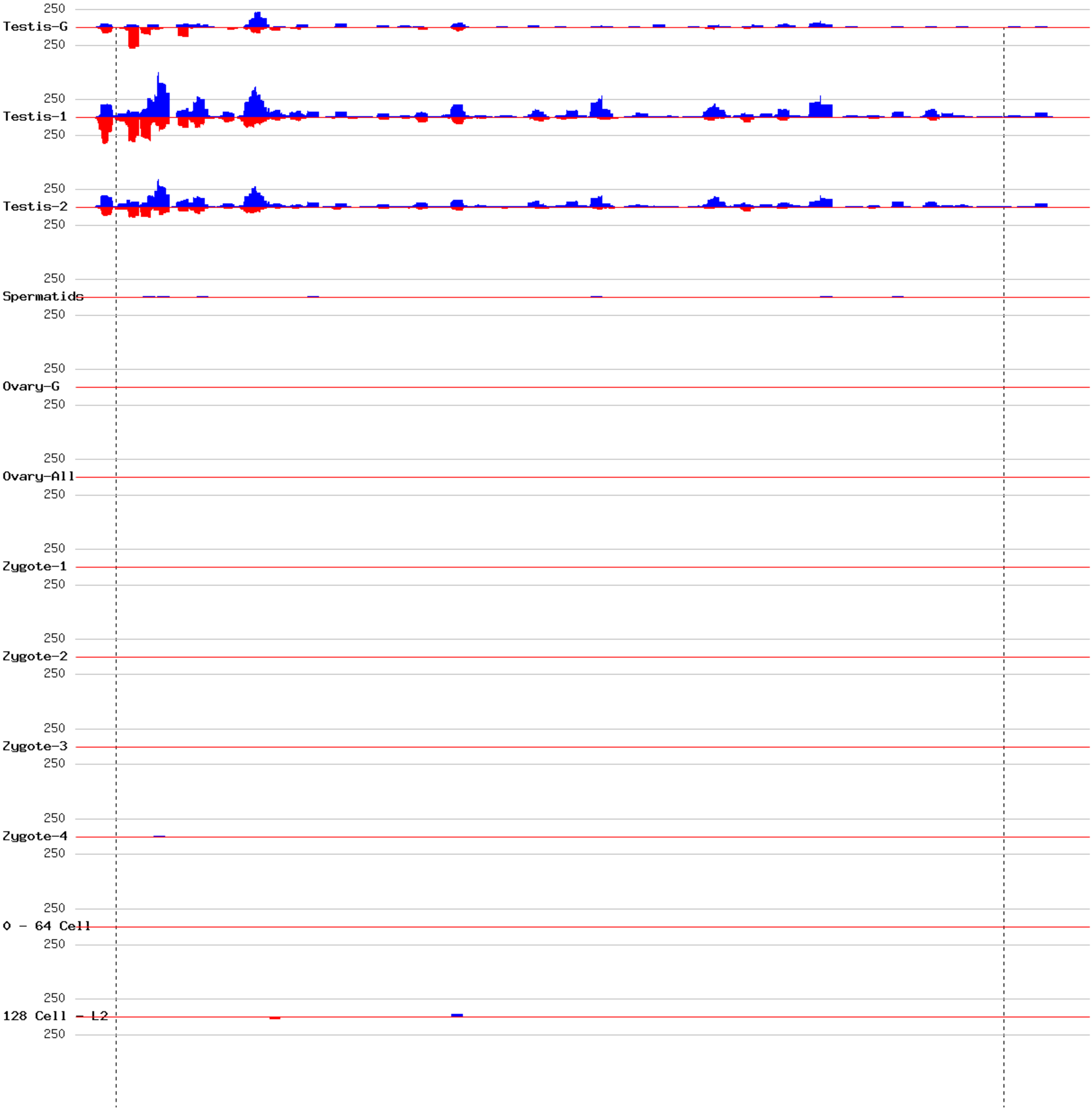
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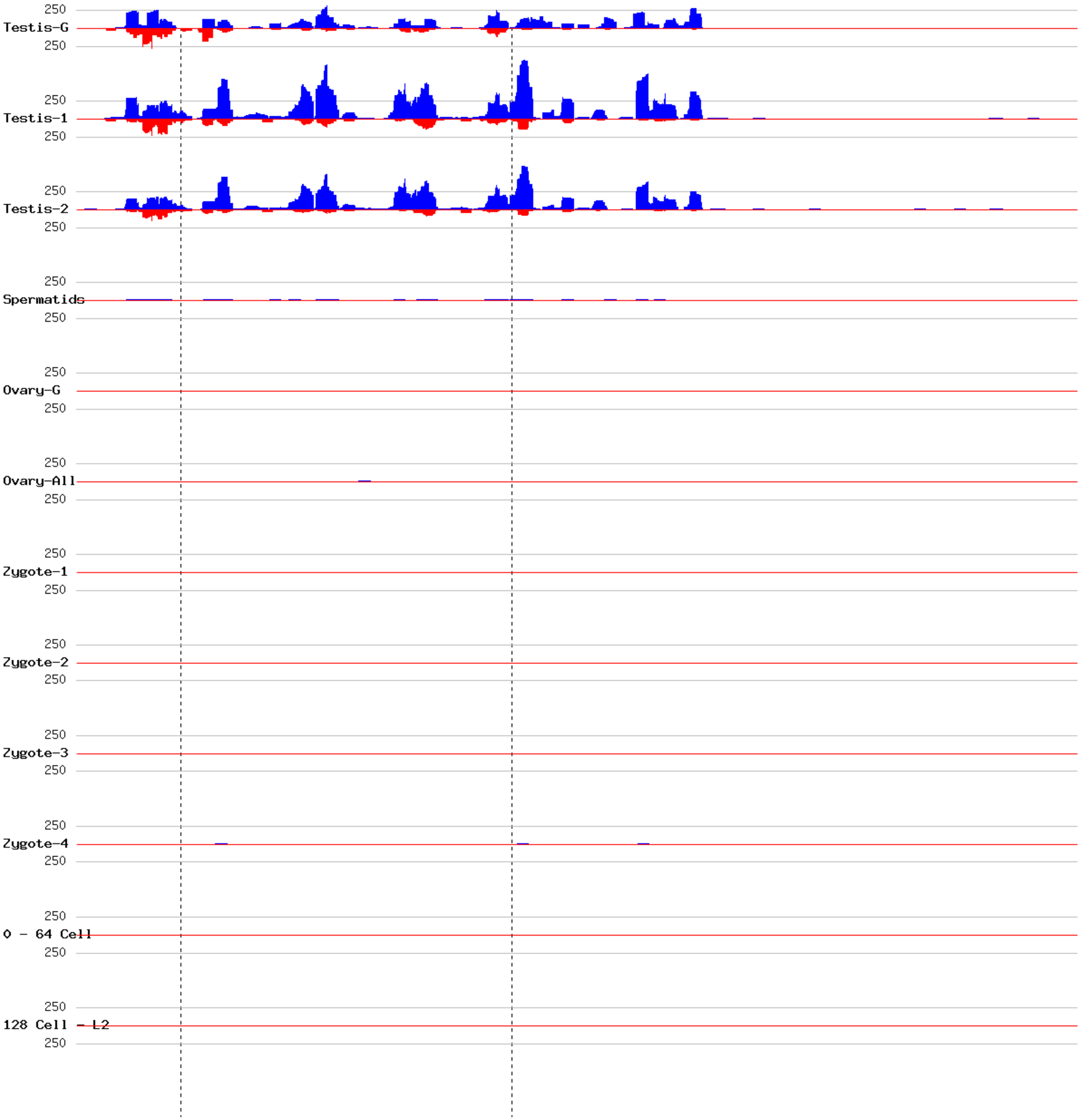
ASCF_3111_2267 TRE-5_protein 2267 bp



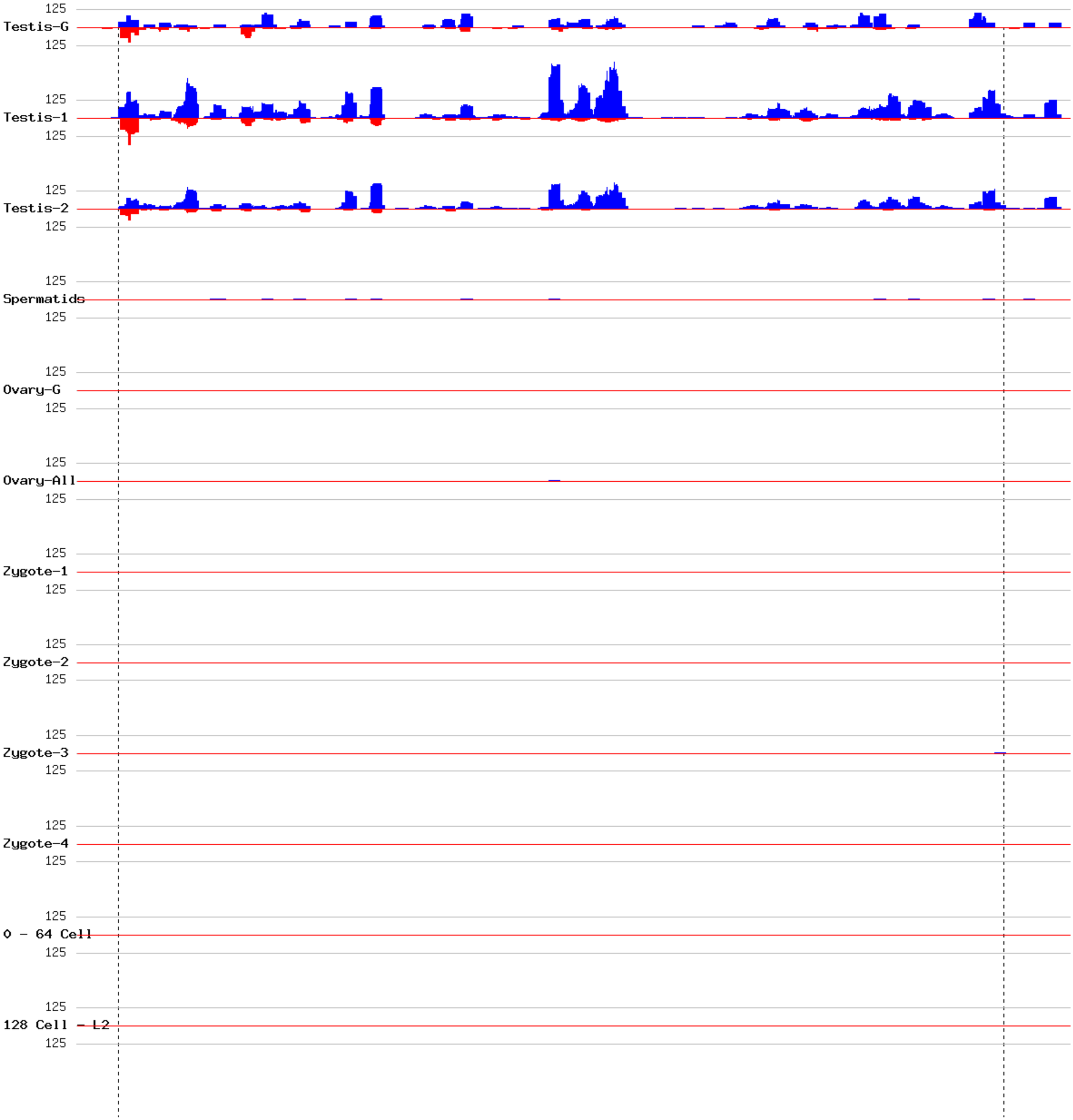
ASCF_3142_2255 Phosphoenolpyruvate_carboxykinase 2255 bp



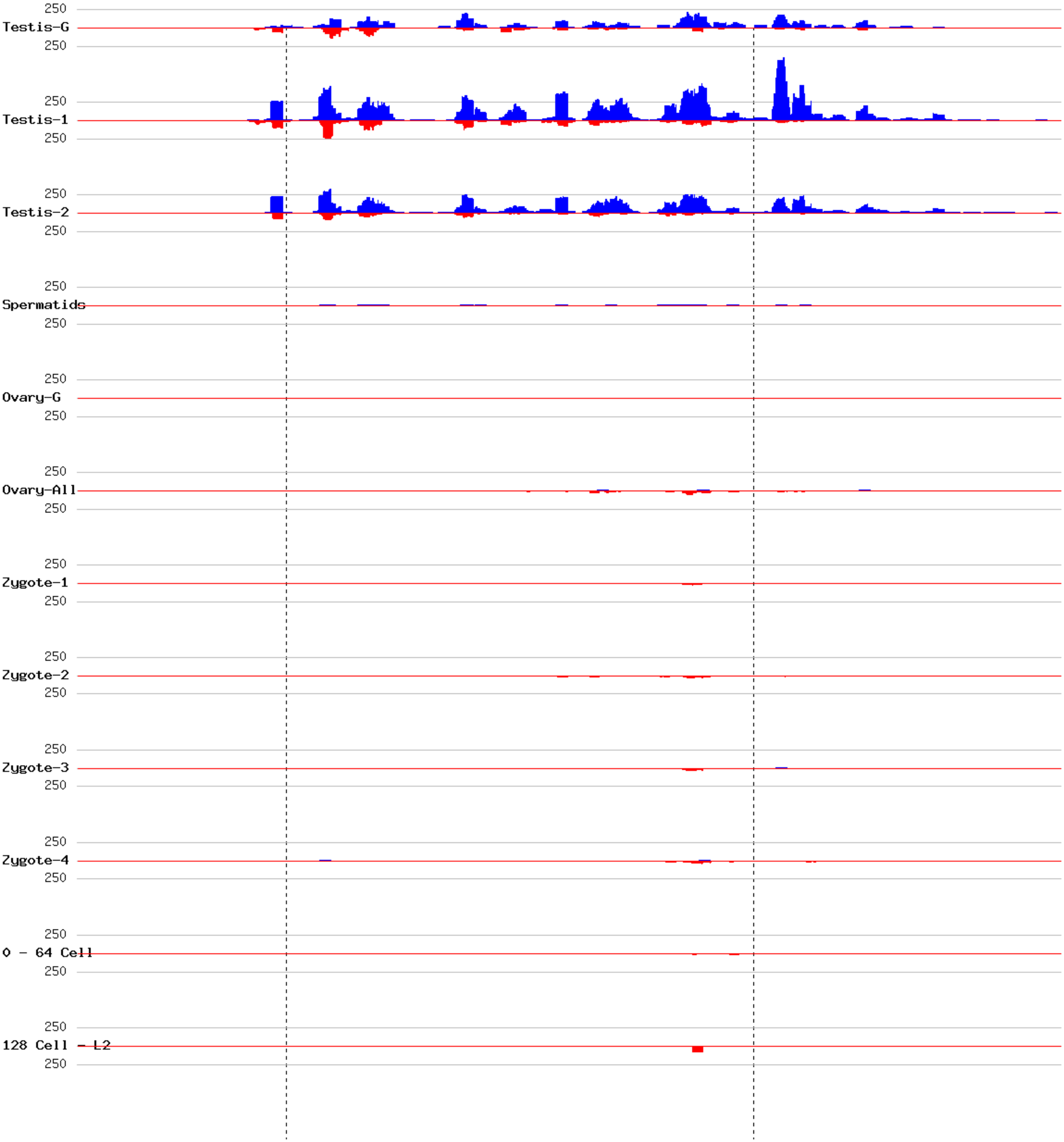
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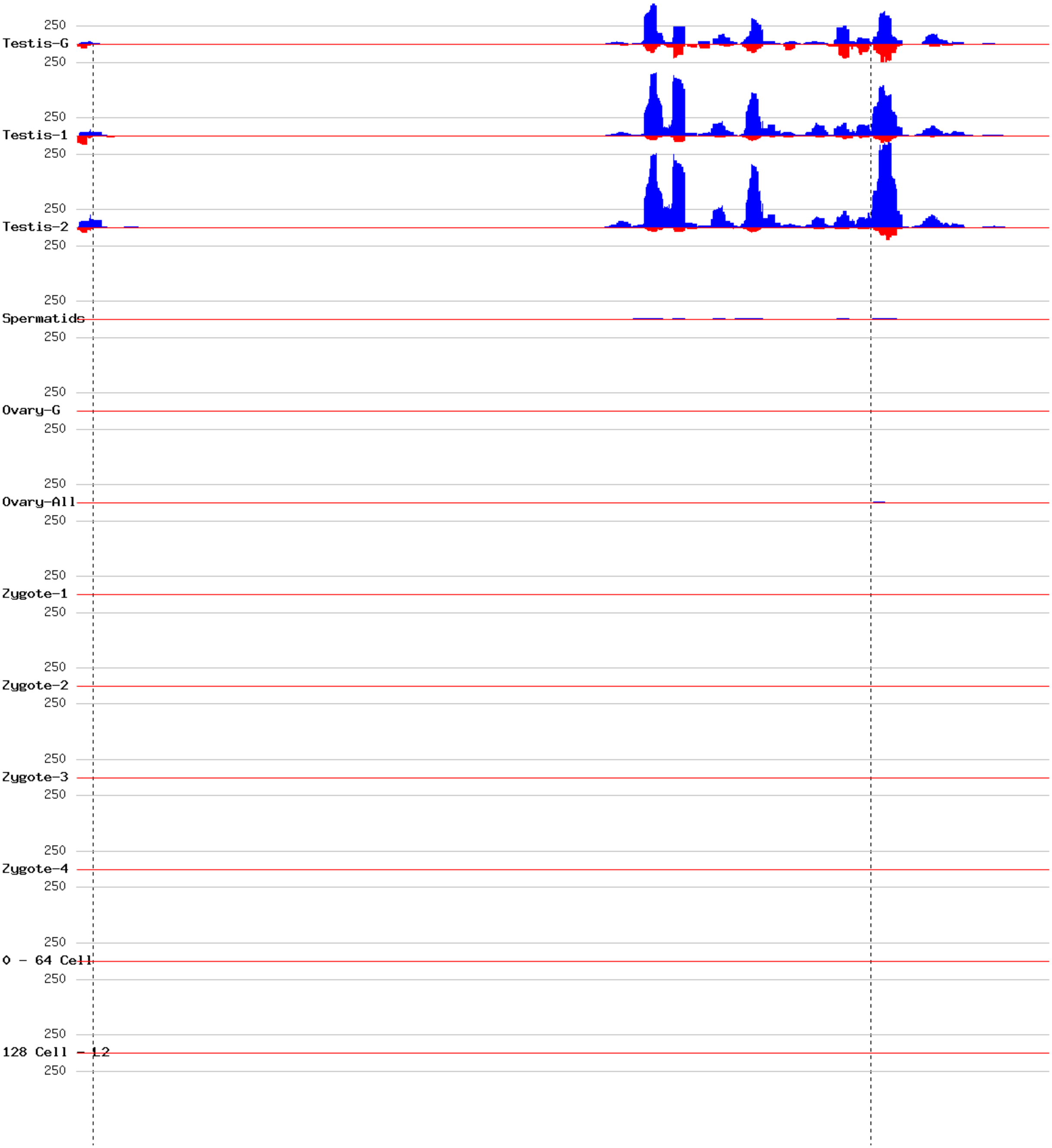
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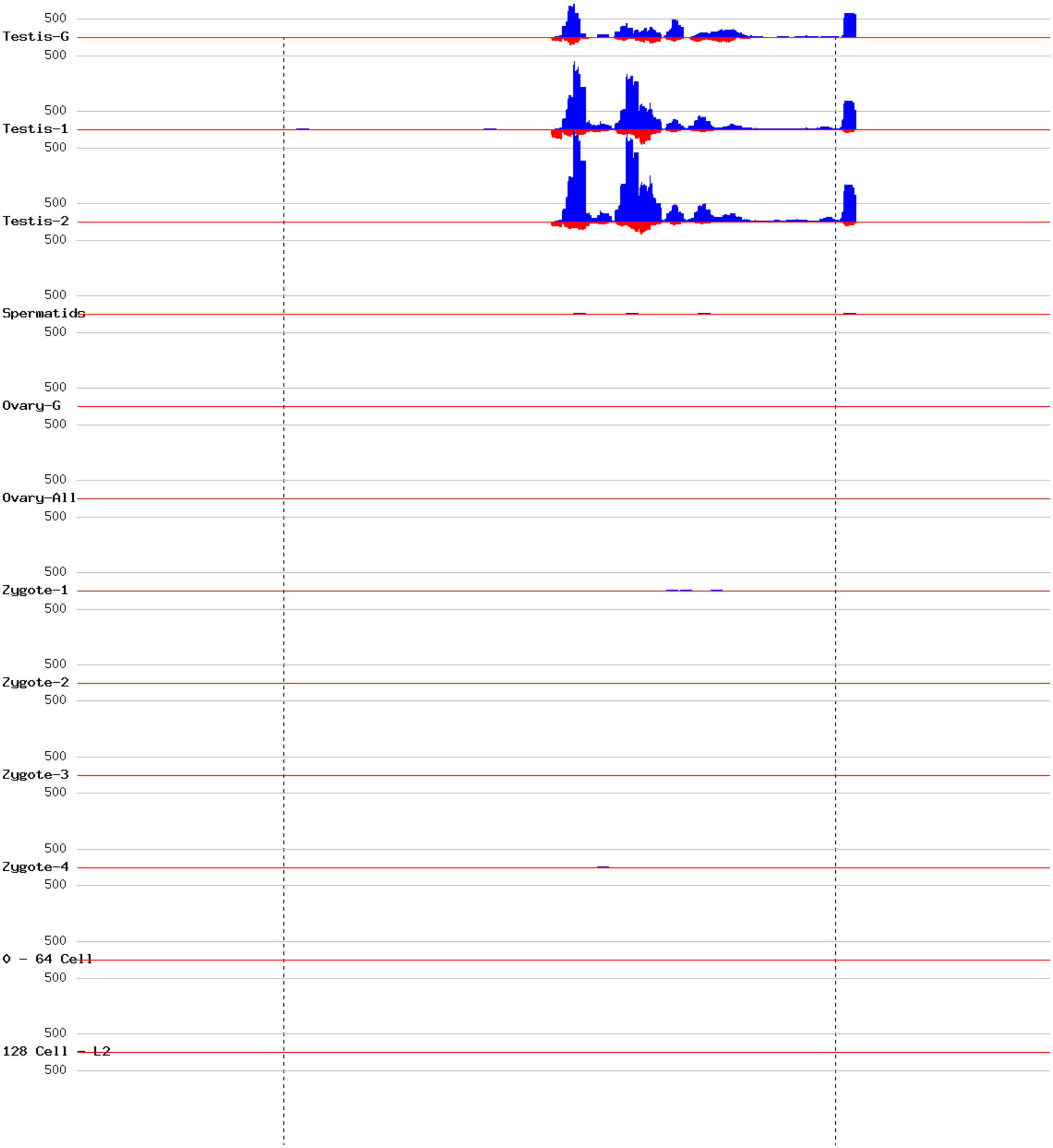
ASCF_3454_2127 Hypothetical_protein 2127 bp



ASCF_3471_2120 Major_sperm_protein 2120 bp



ASCF_3508_2109 Major_sperm_protein 2109 bp



ASCF_3518_2106 Hypothetical_protein 2106 bp

125
Testis-G
125

125
Testis-1
125

125
Testis-2
125

125
Spermatids
125

125
Ovary-G
125

125
Ovary-All
125

125
Zygote-1
125

125
Zygote-2
125

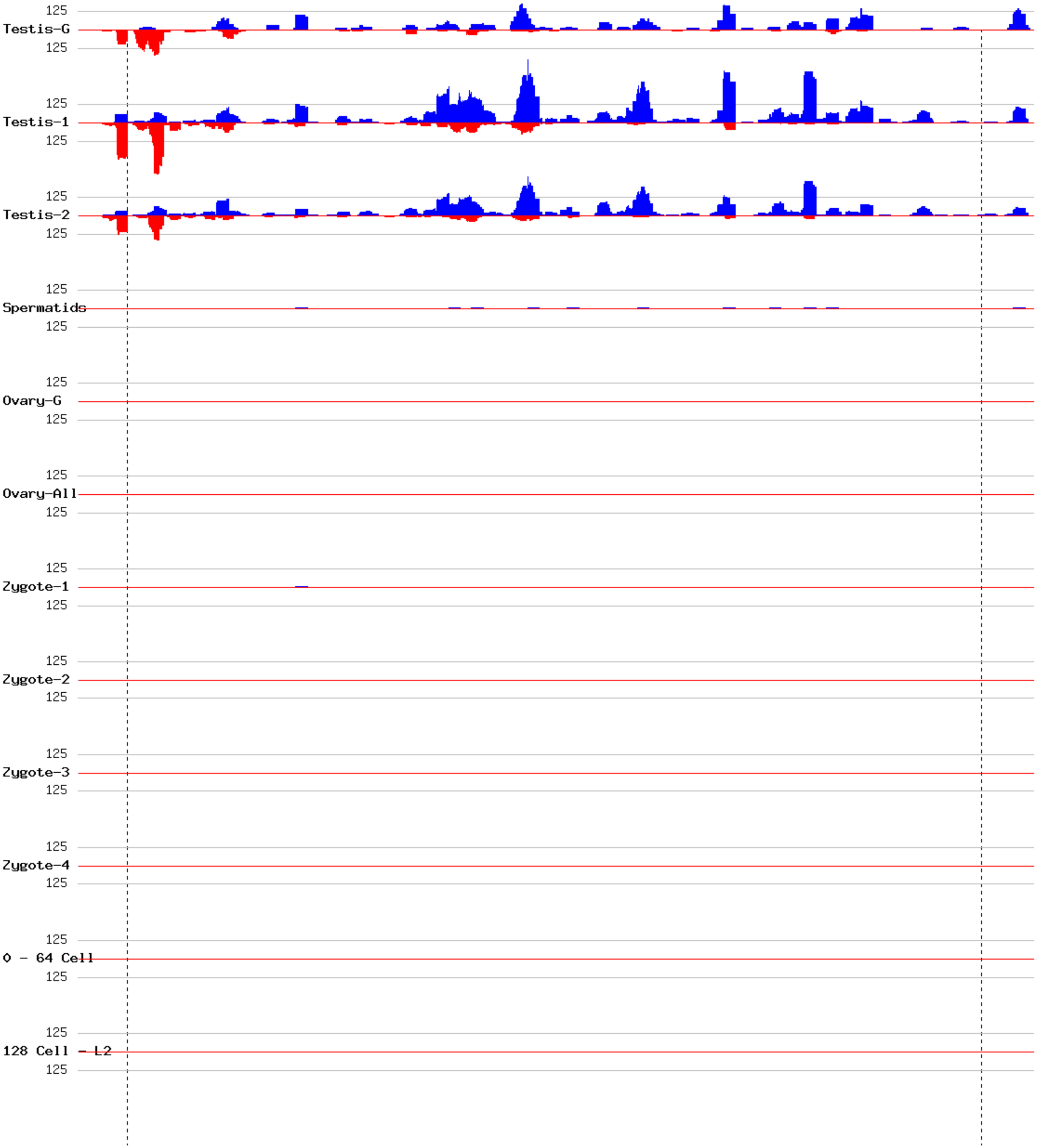
125
Zygote-3
125

125
Zygote-4
125

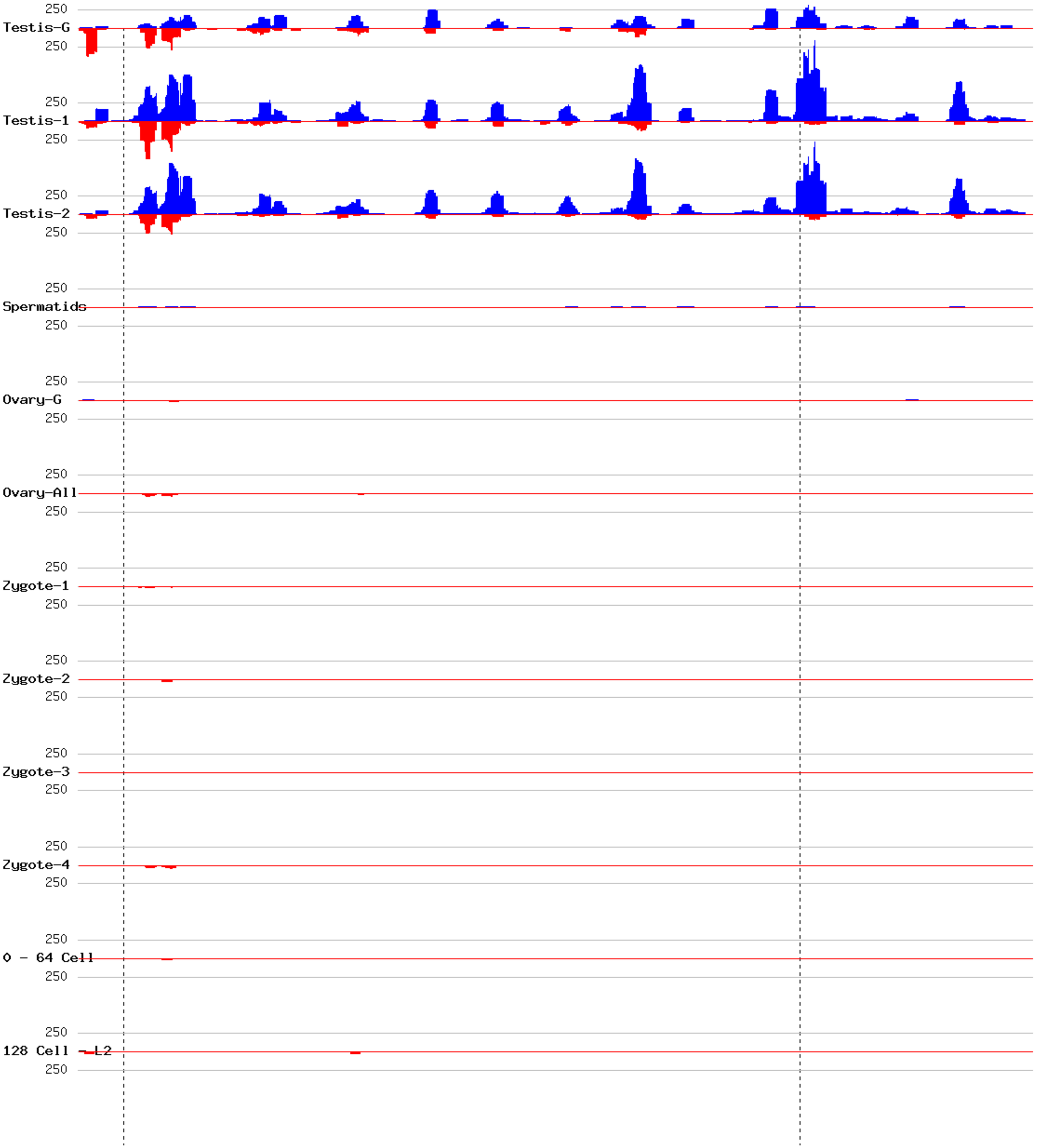
125
0 - 64 Cell
125

125
128 Cell - L2
125

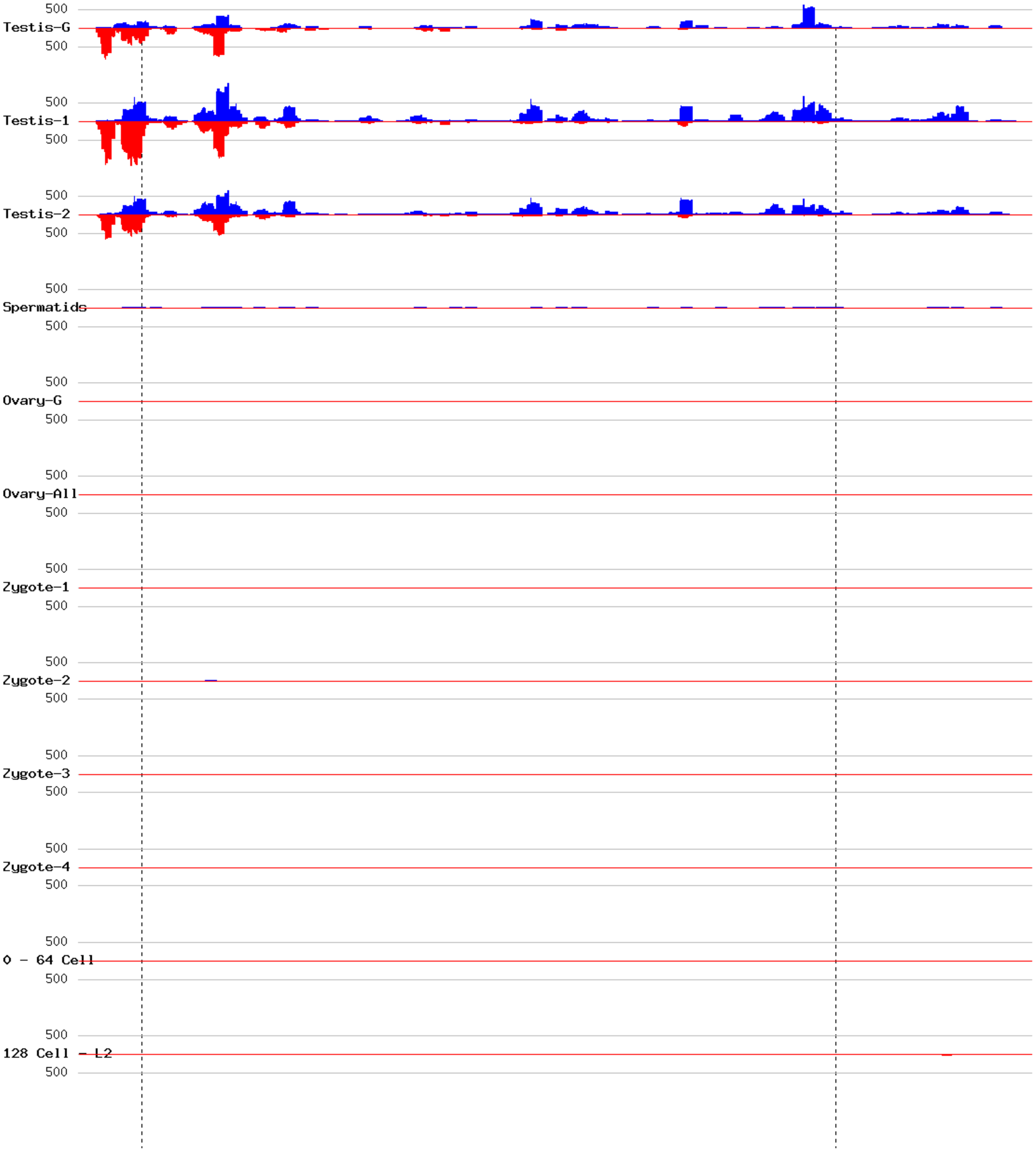
ASCF_3656_2056 Protein-tyrosine_phosphatase_containing_protein 2056 bp



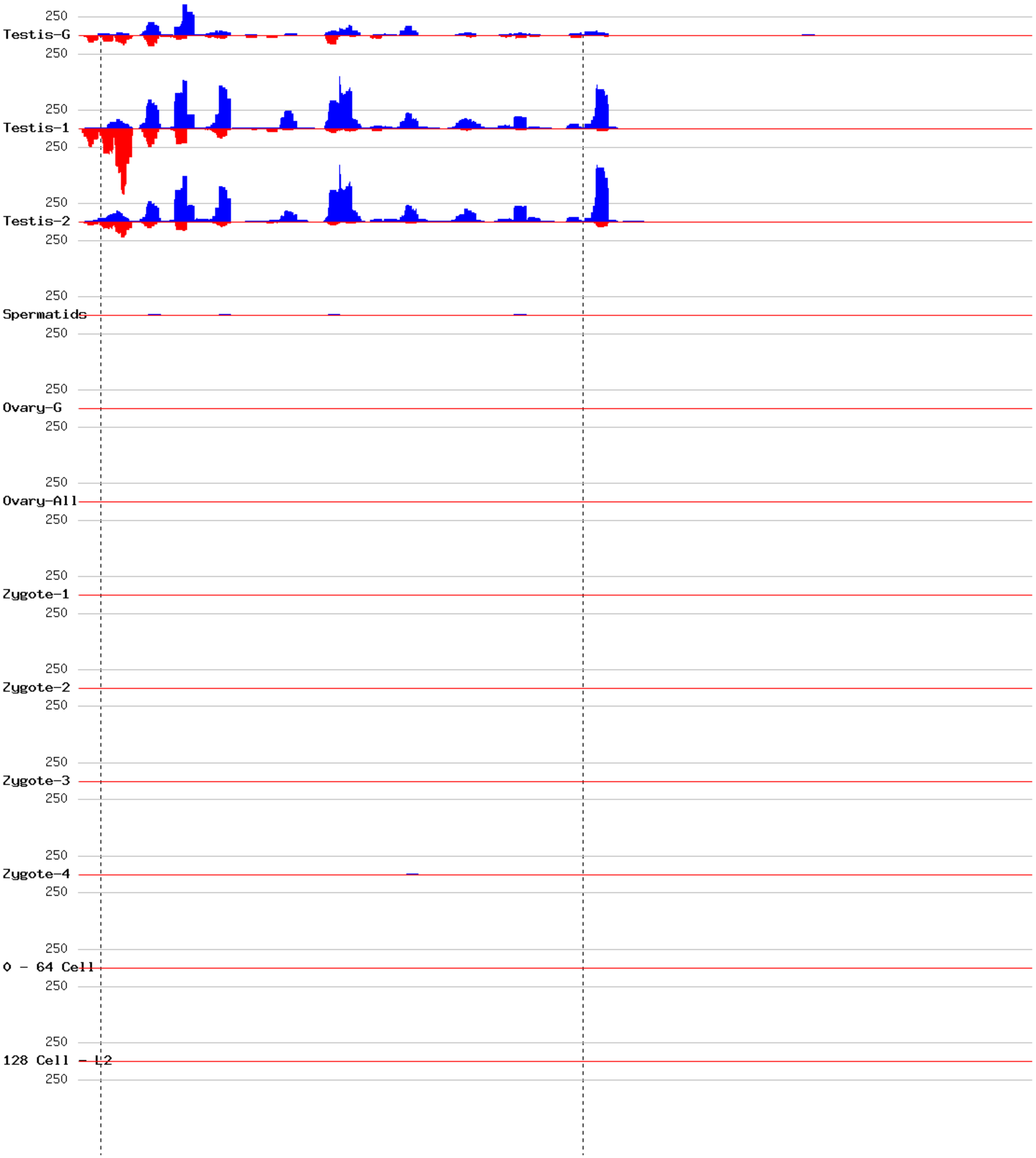
ASCF_3667_2052 S-antigen_protein 2052 bp



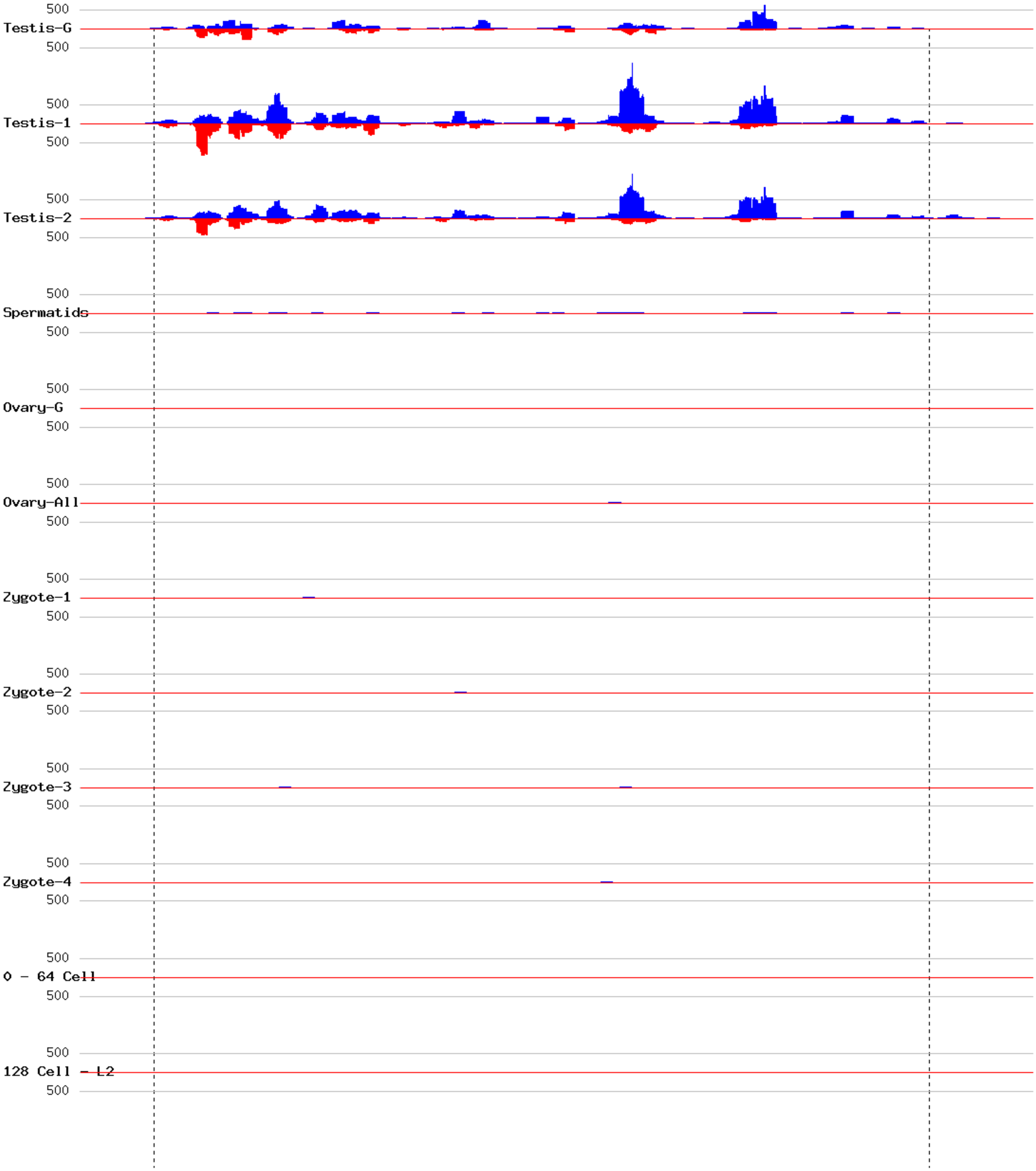
ASCF_3691_2045 Protein_kinase_domain_containing_protein 2045 bp



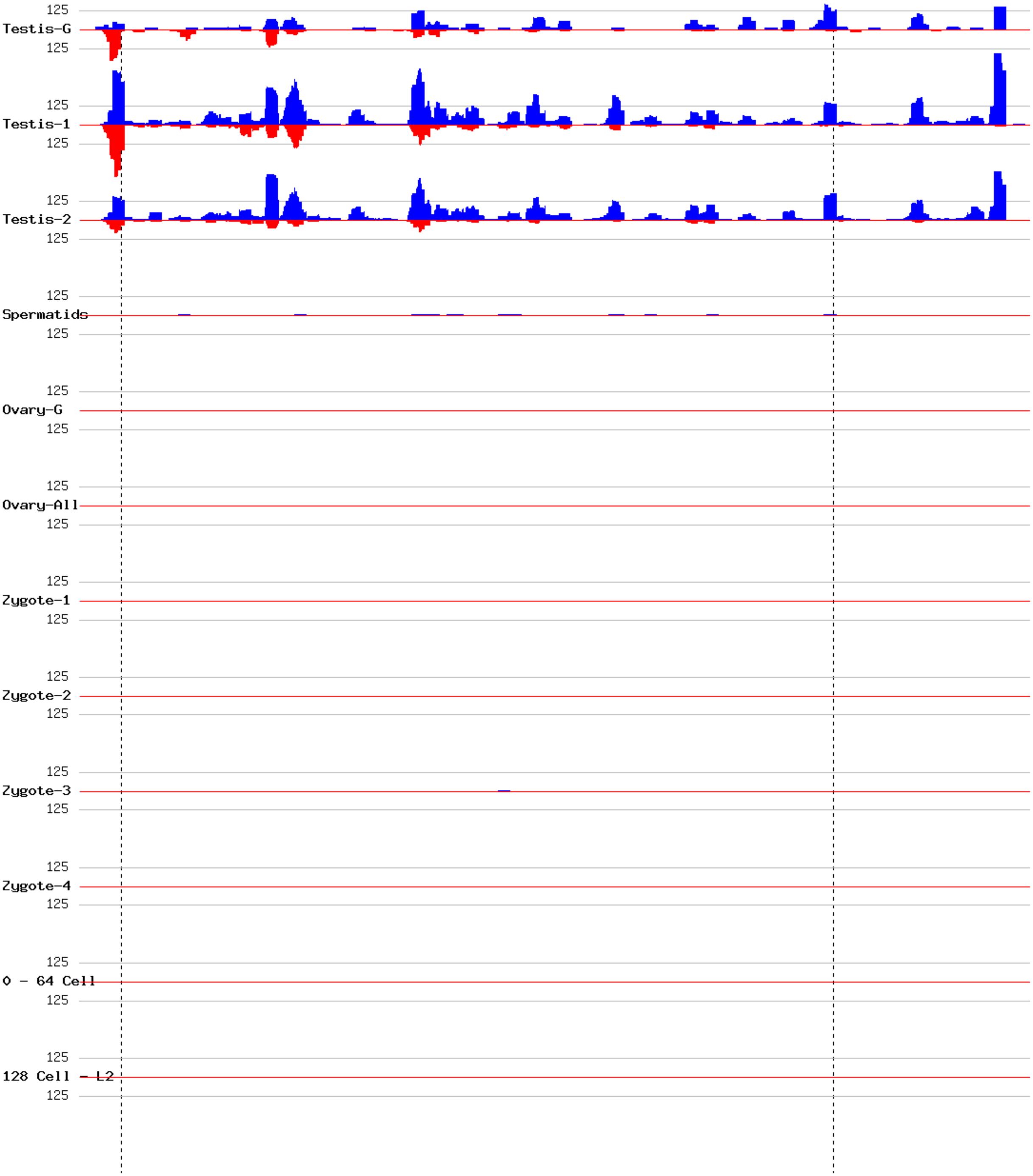
ASCF_3694_2044 MSP_fiber_protein_2 2044 bp



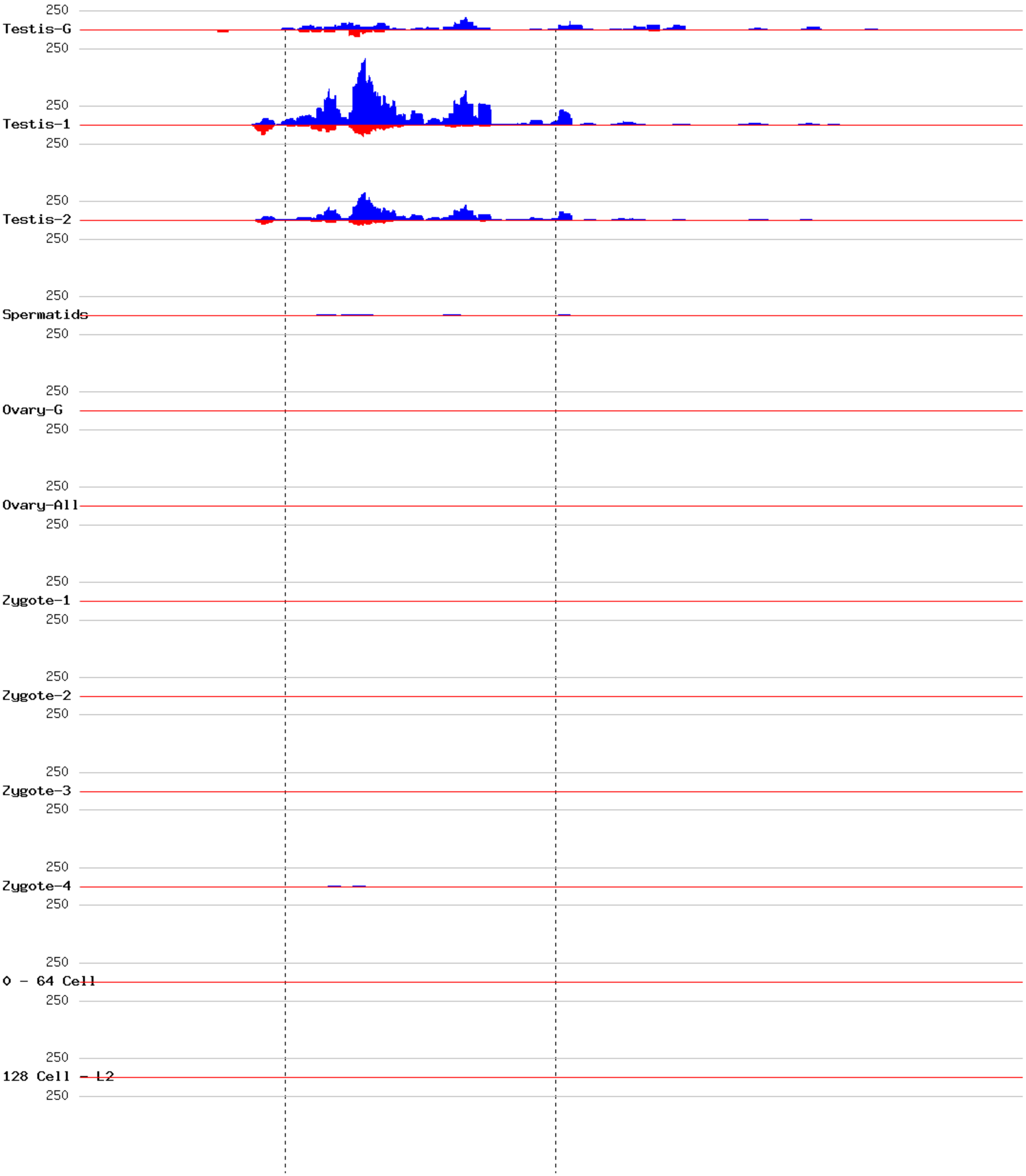
ASCF_3791_2009 Hypothetical_protein 2009 bp



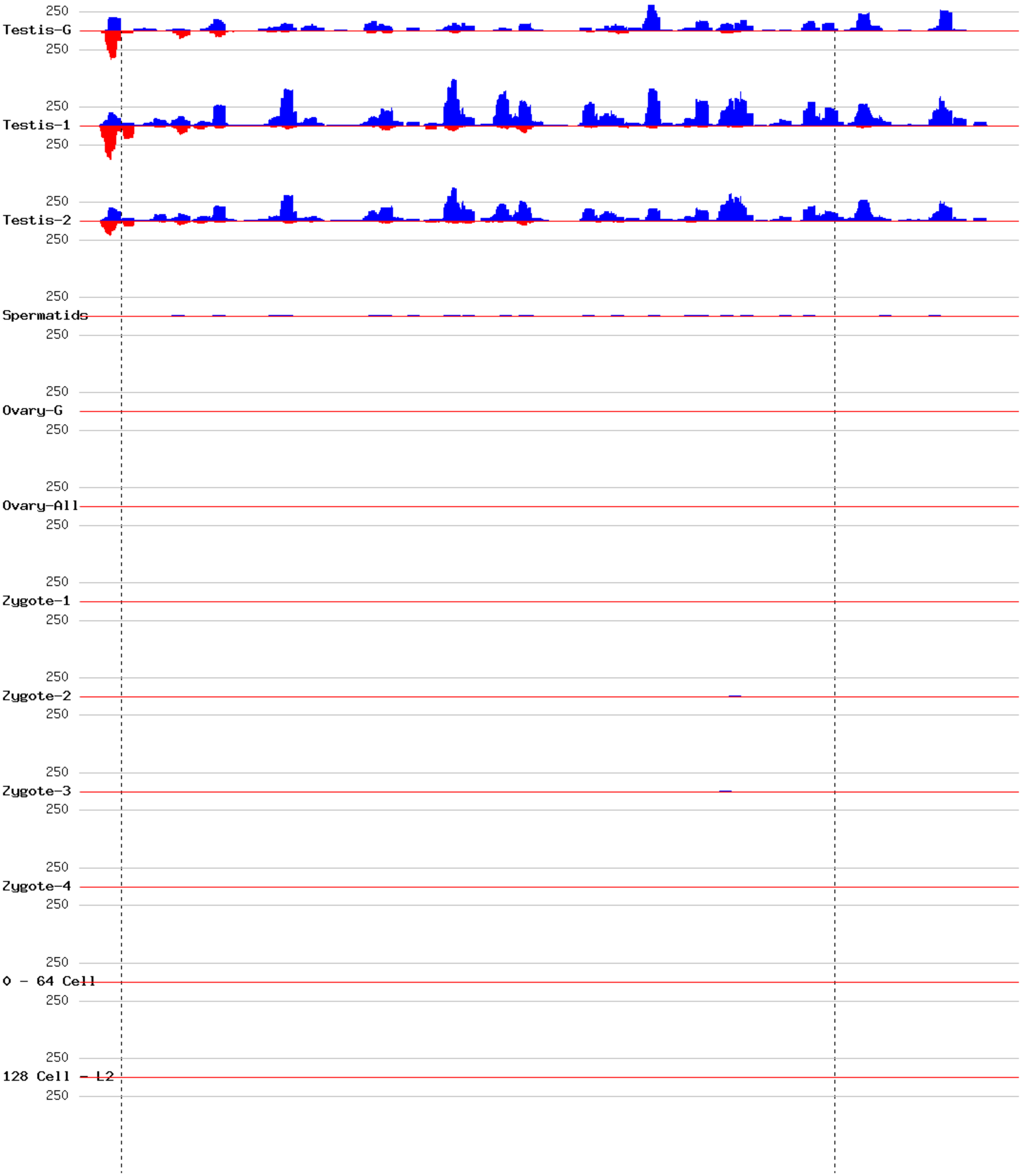
ASCF_3831_1997 Hypothetical_protein 1997 bp



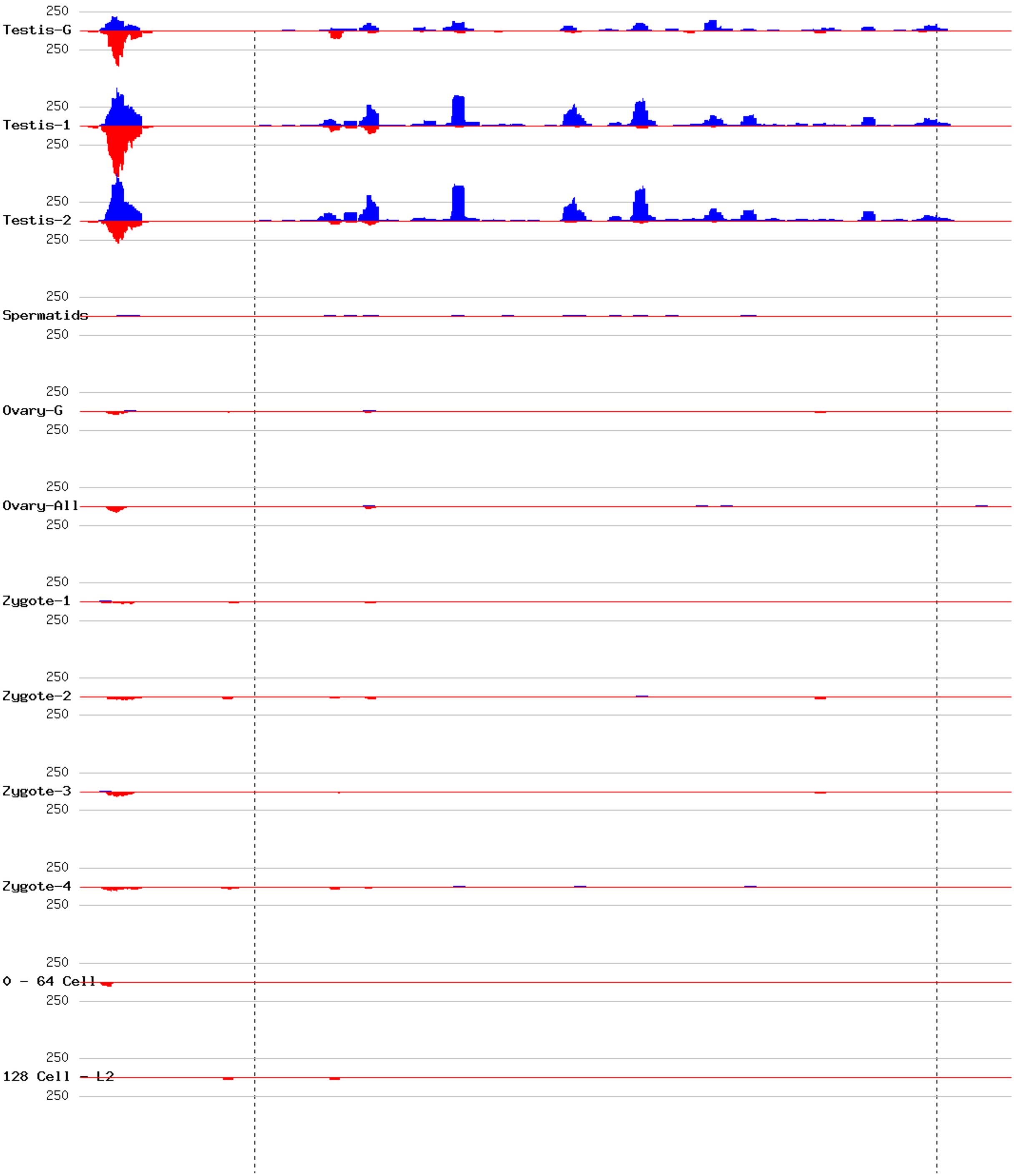
ASCF_3880_1981 Hypothetical_protein 1981 bp



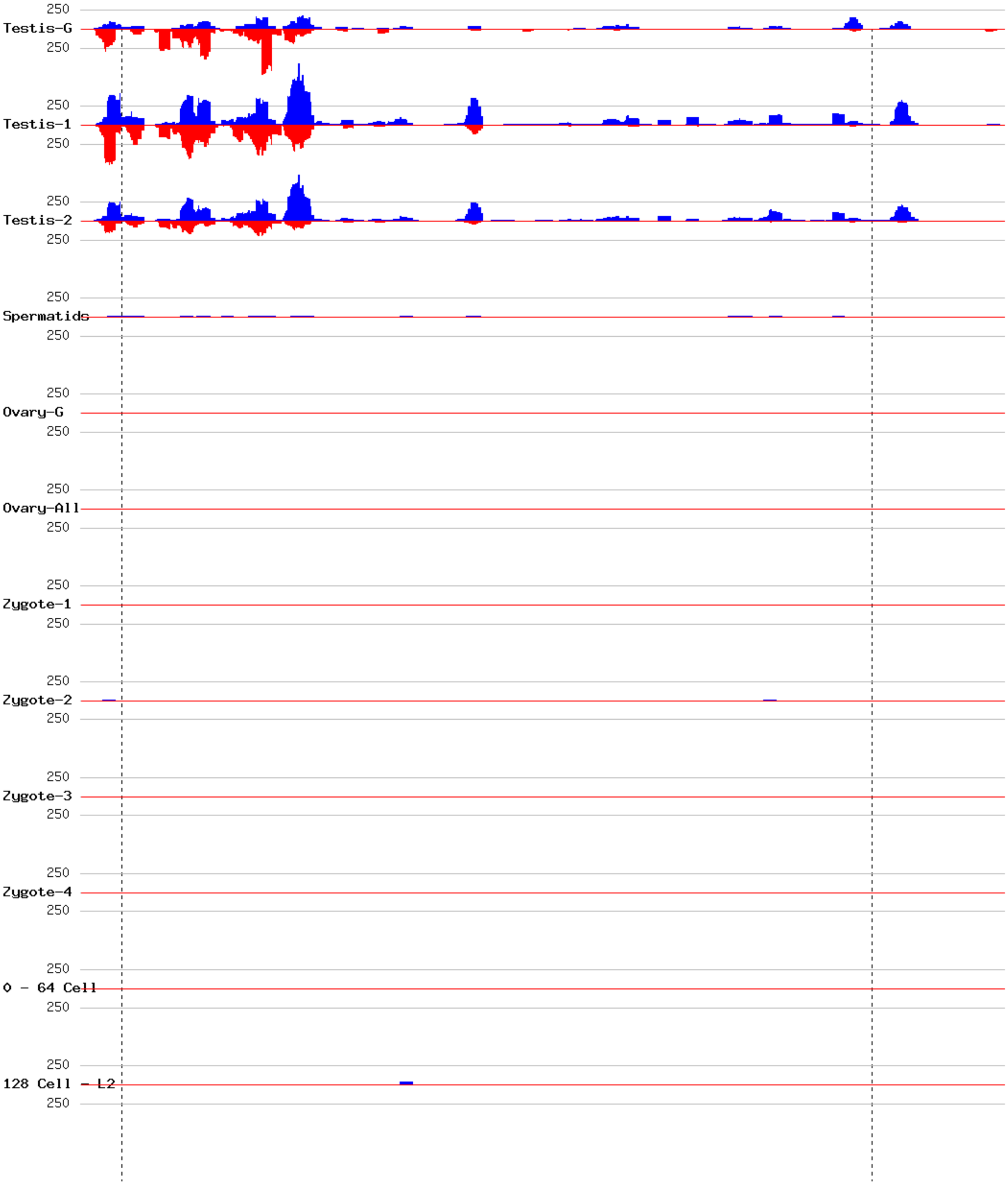
ASCF_3897_1975 Protein_tyrosine_phosphatase 1975 bp



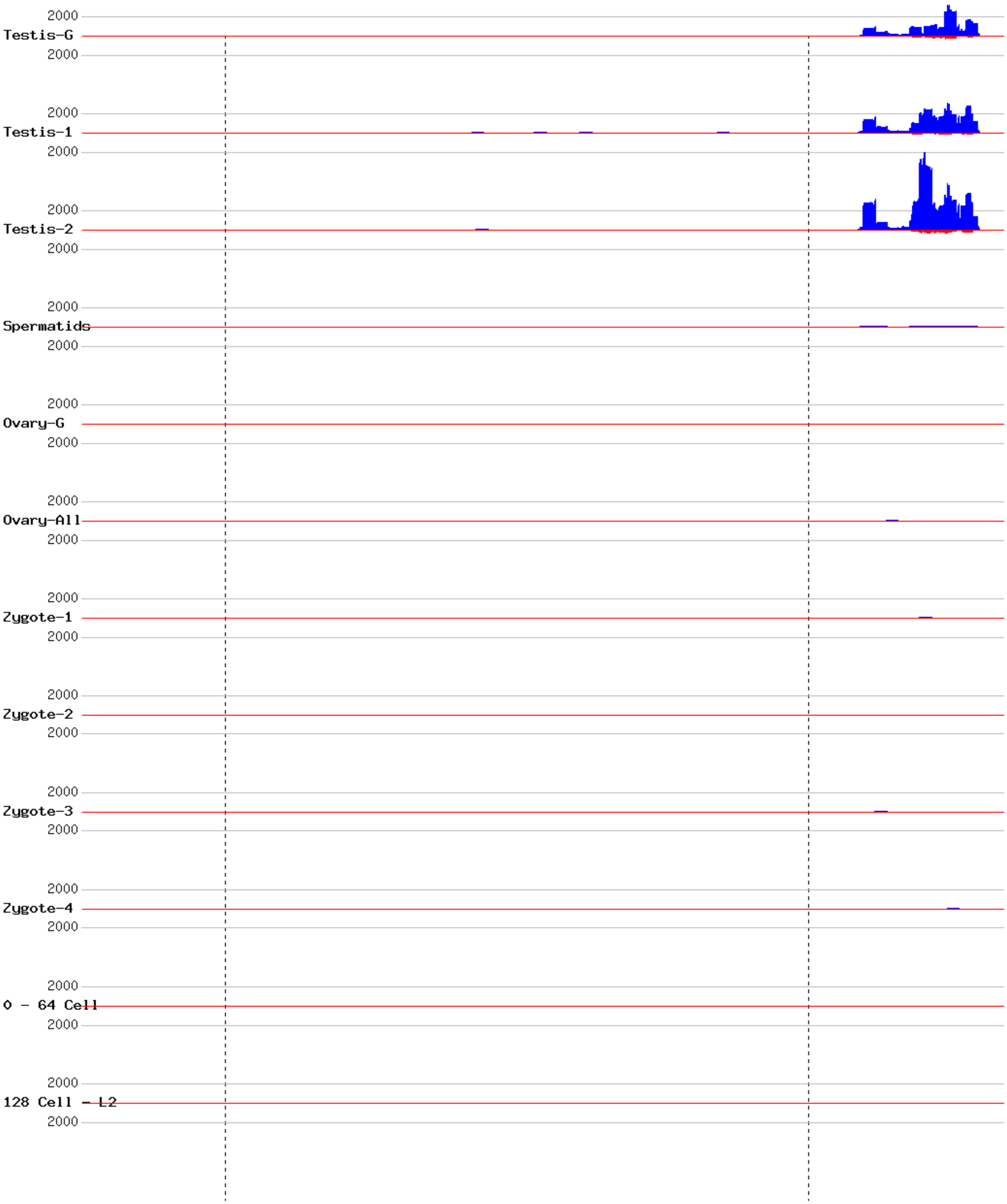
ASCF_3938_1959 Hypothetical_protein 1959 bp



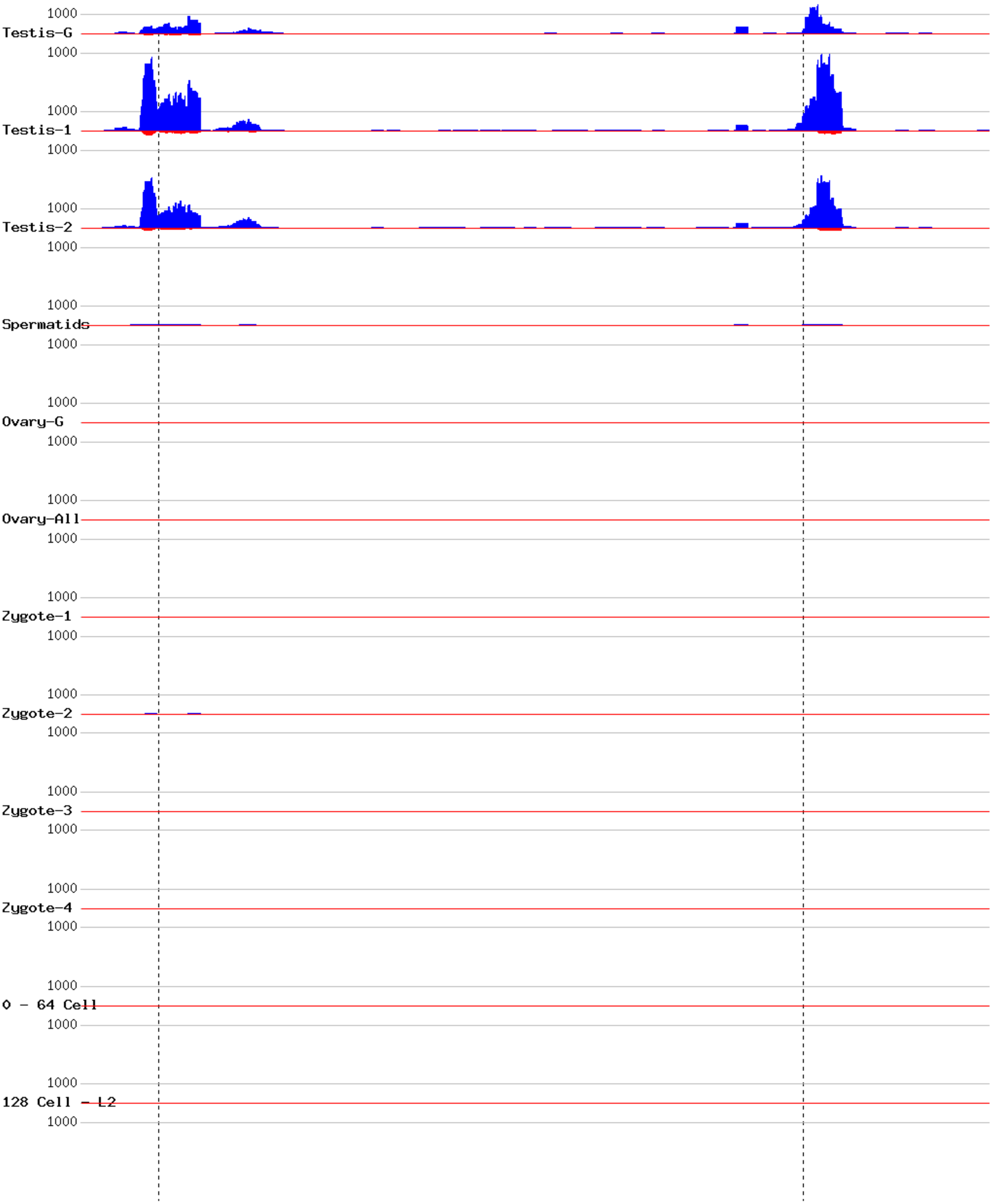
ASCF_4039_1927 Tyrosine-protein_kinase_Fer 1927 bp



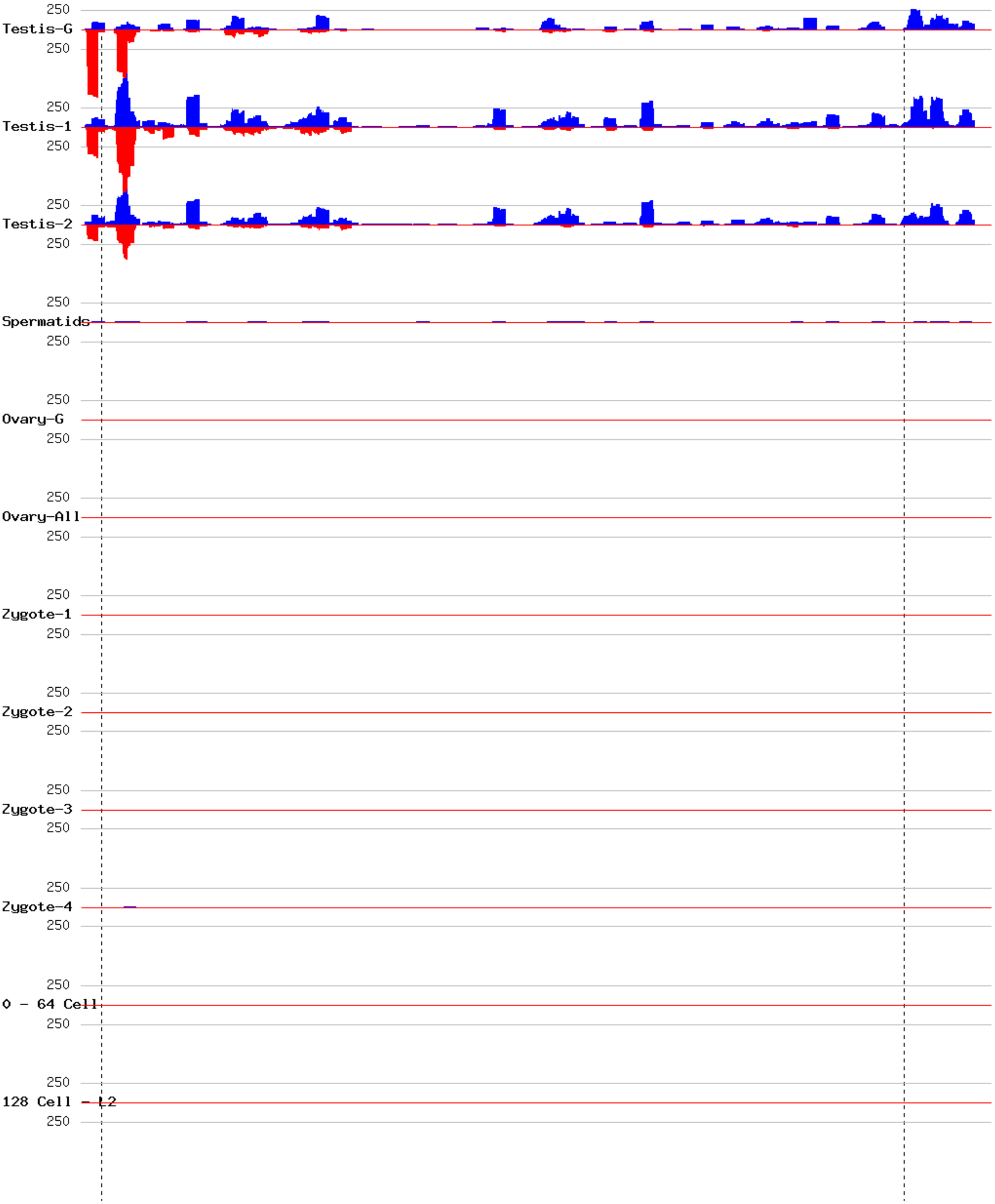
ASCF_4136_1901 Proton-coupled_amino_acid_transporter 1901 bp



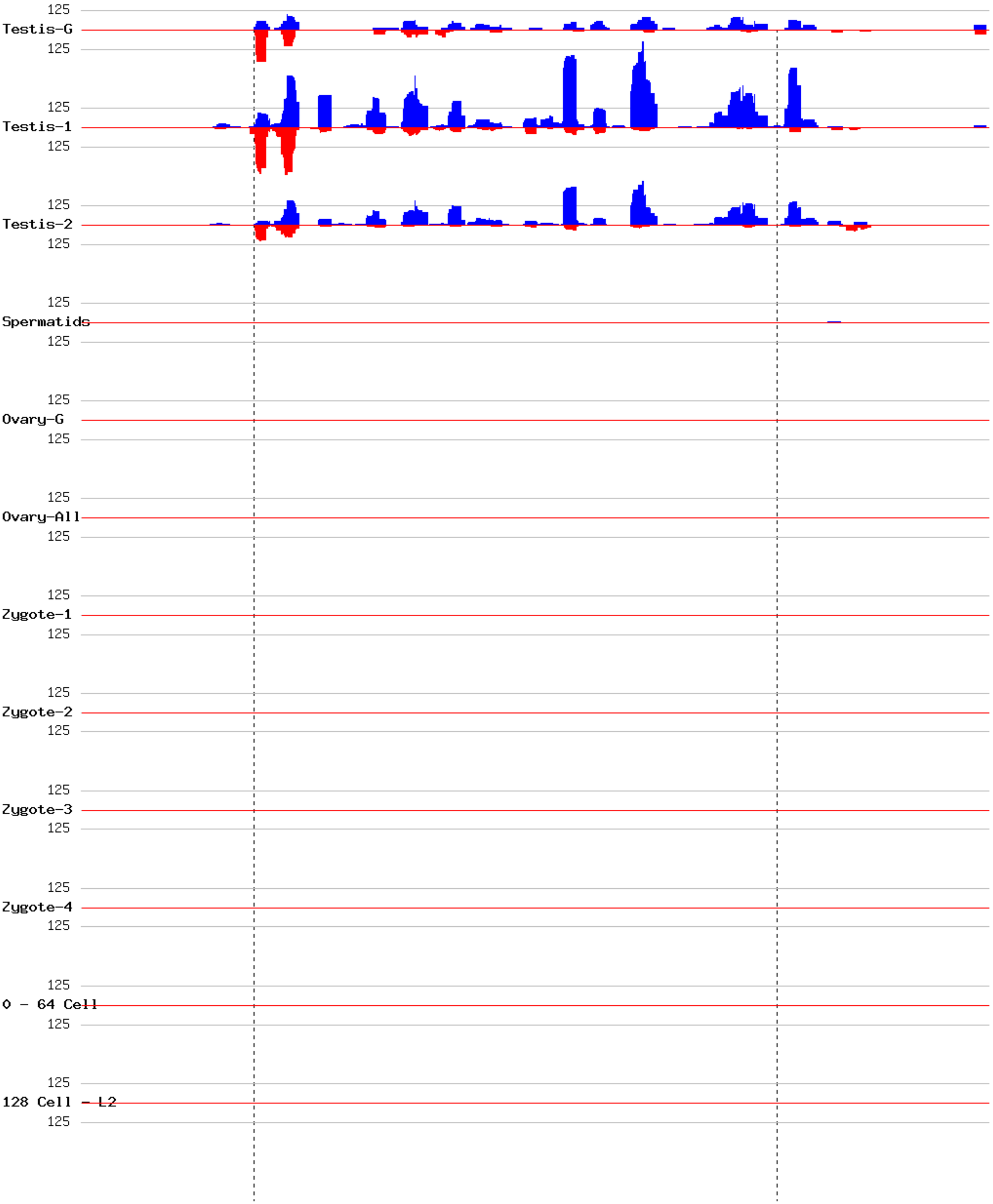
ASCF_4234_1869 Hypothetical_protein 1869 bp



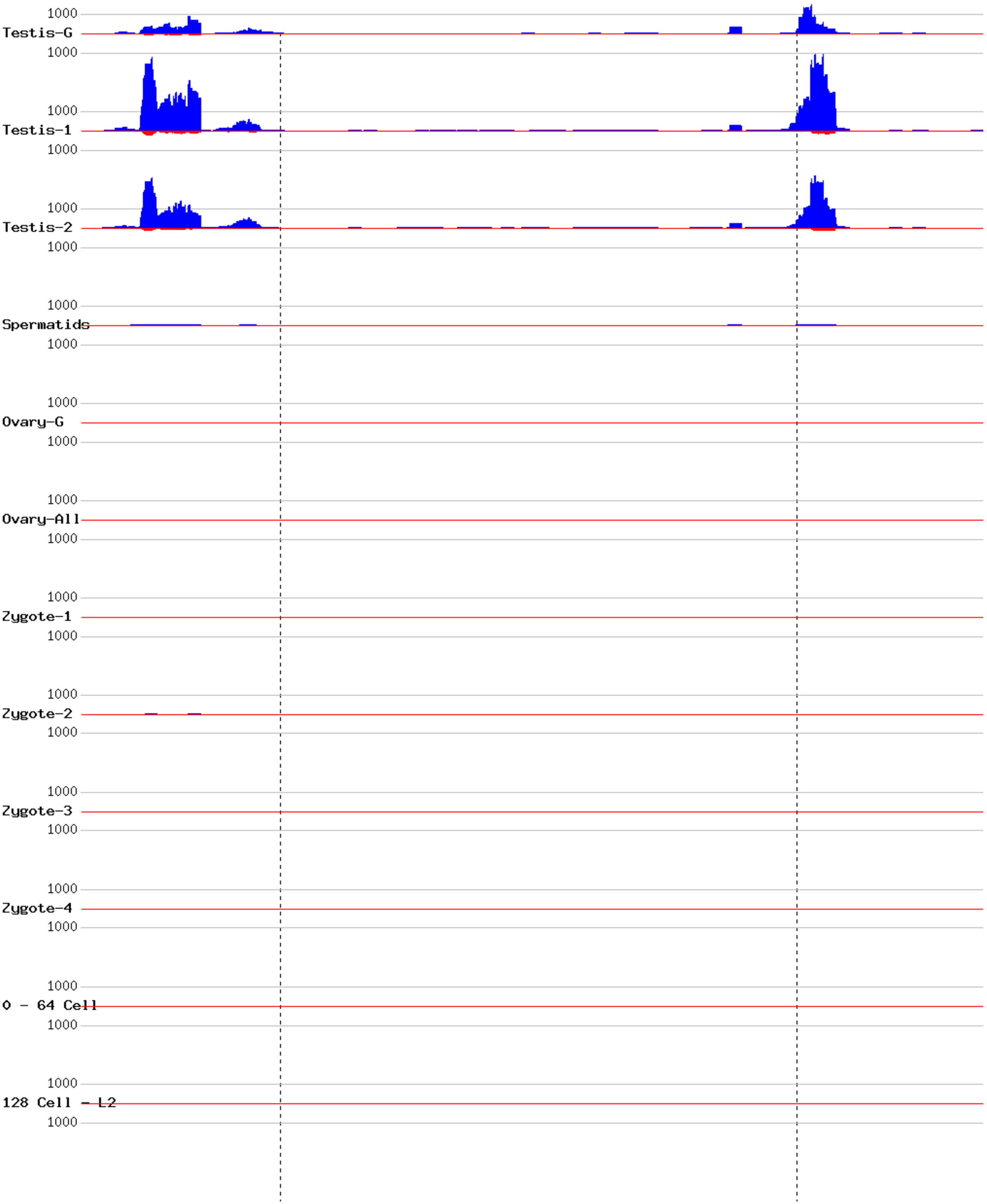
ASCF_4243_1866 Protein_kinase_domain_containing_protein 1866 bp



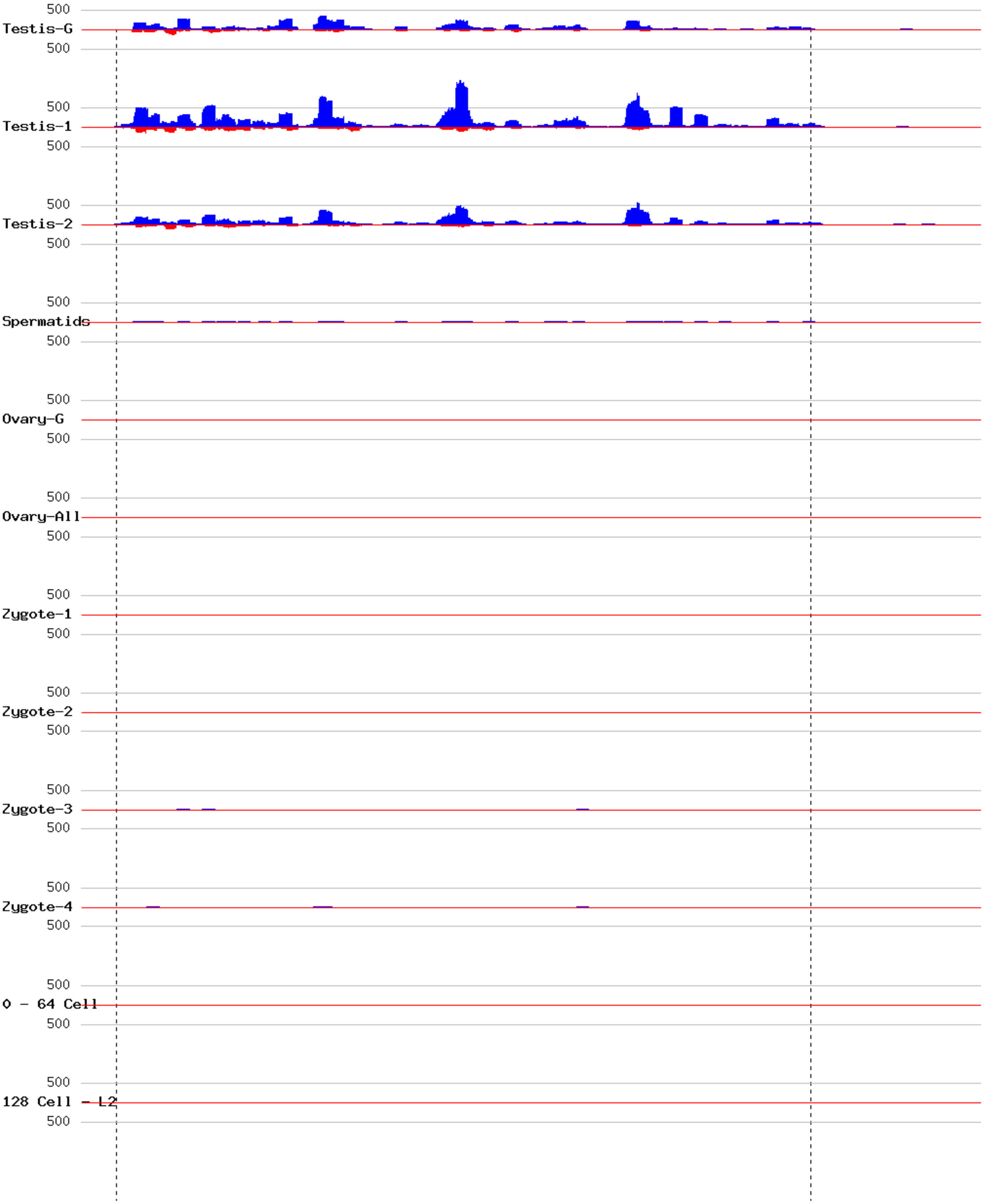
ASCF_4258_1861 Pyruvate_dehydrogenase_E1_component 1861 bp



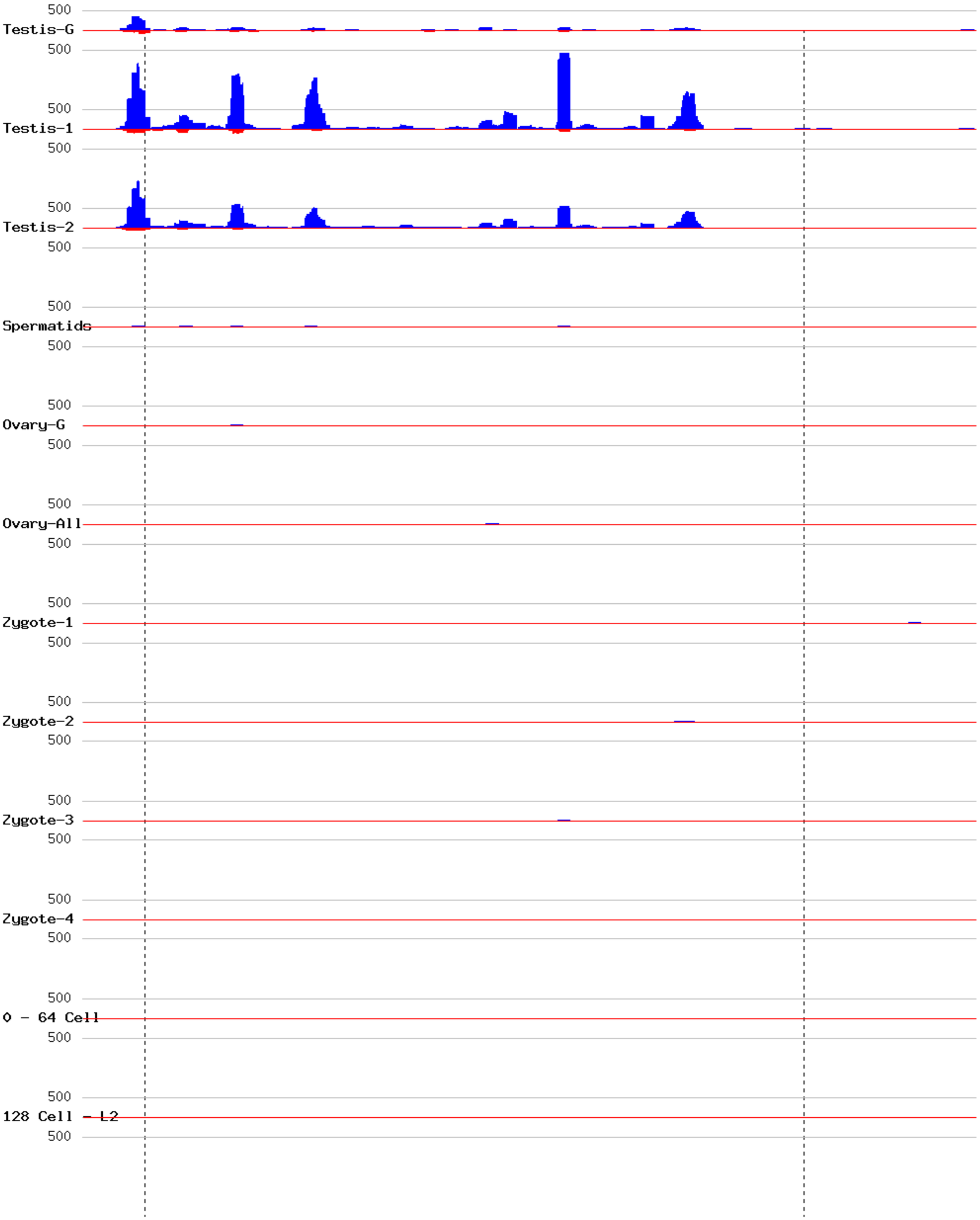
ASCF_4282_1855 Hypothetical_protein 1855 bp



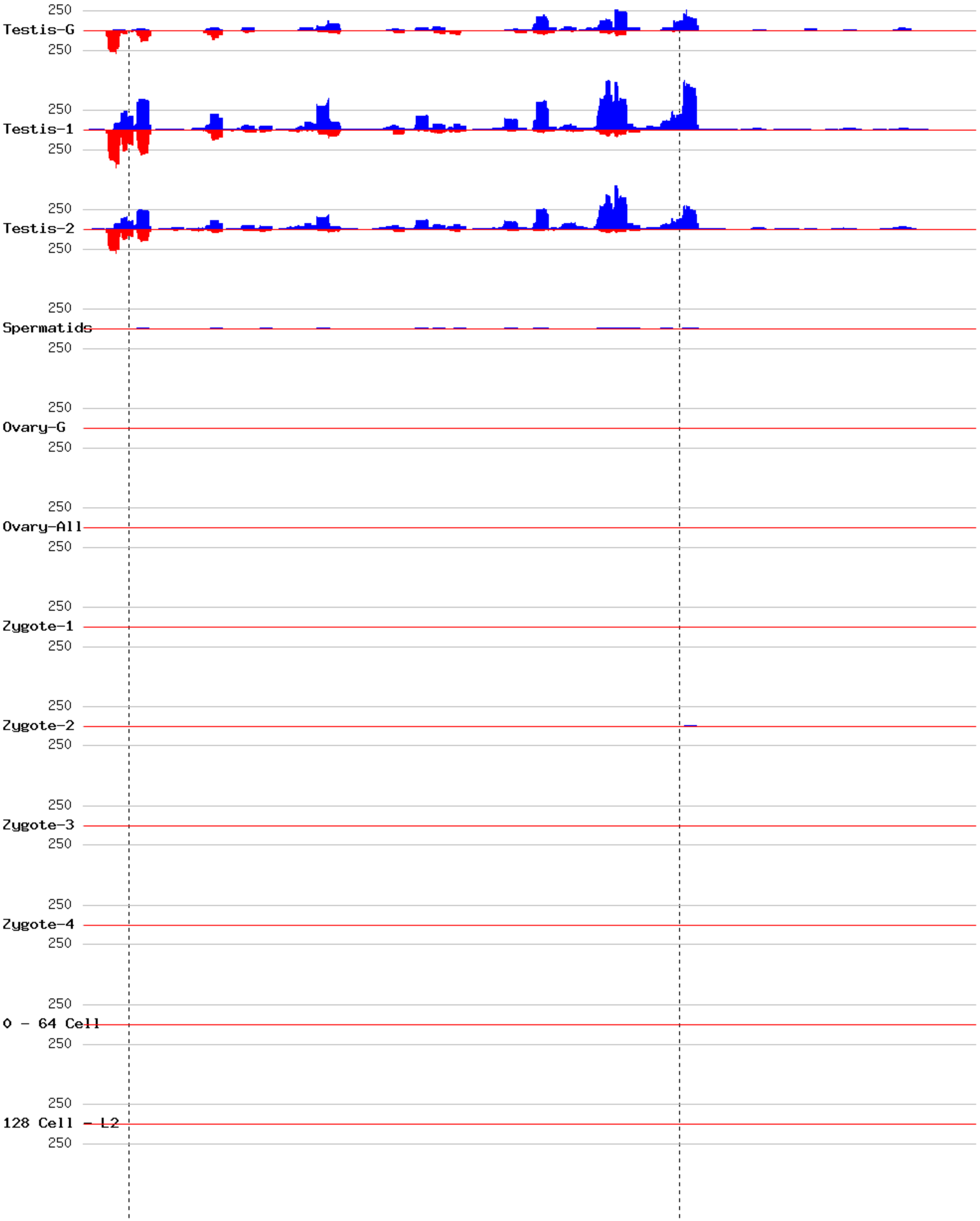
ASCF_4315_1845 Hypothetical_protein 1845 bp



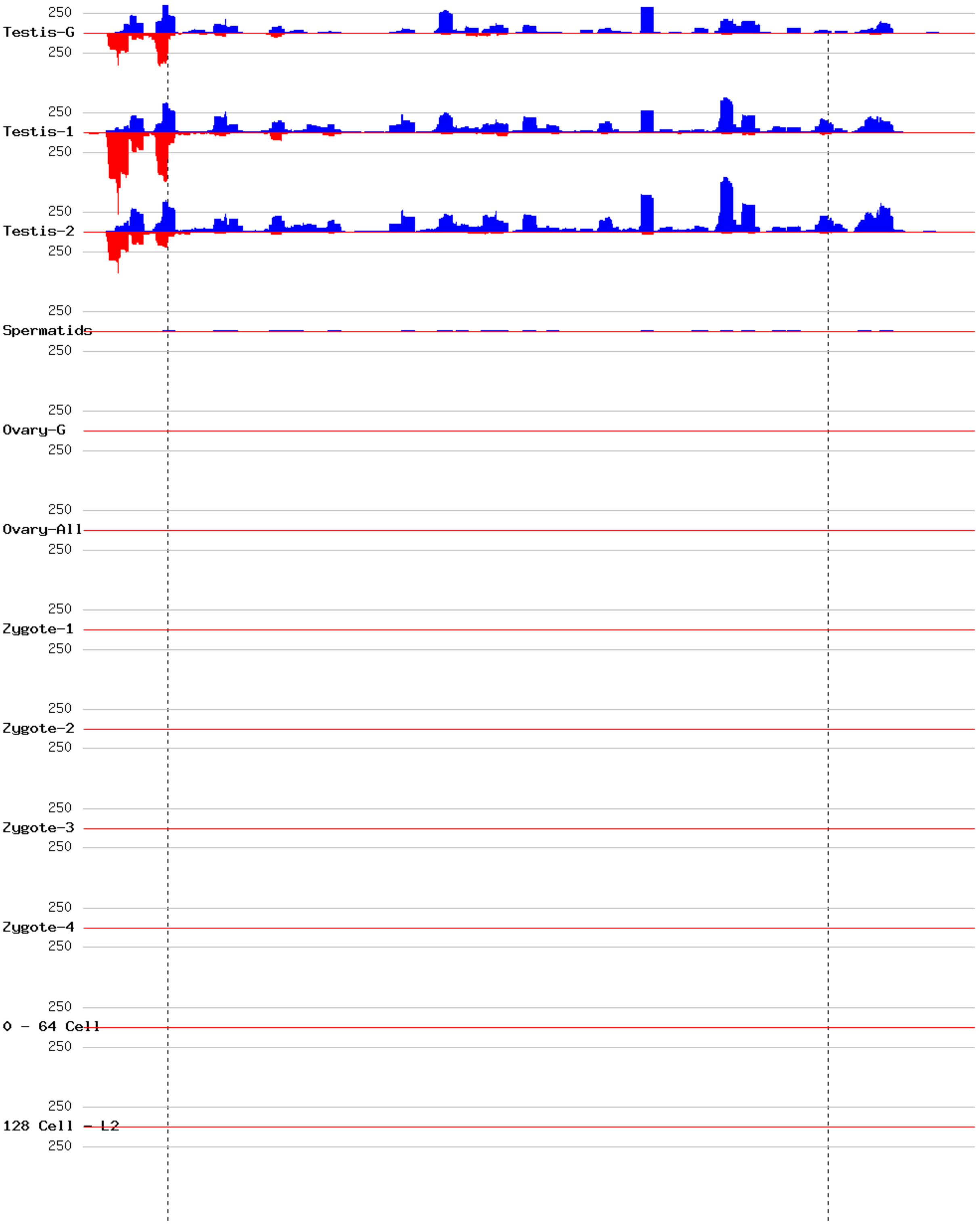
ASCF_4433_1809 Pyruvate dehydrogenase E1 component 1809 bp



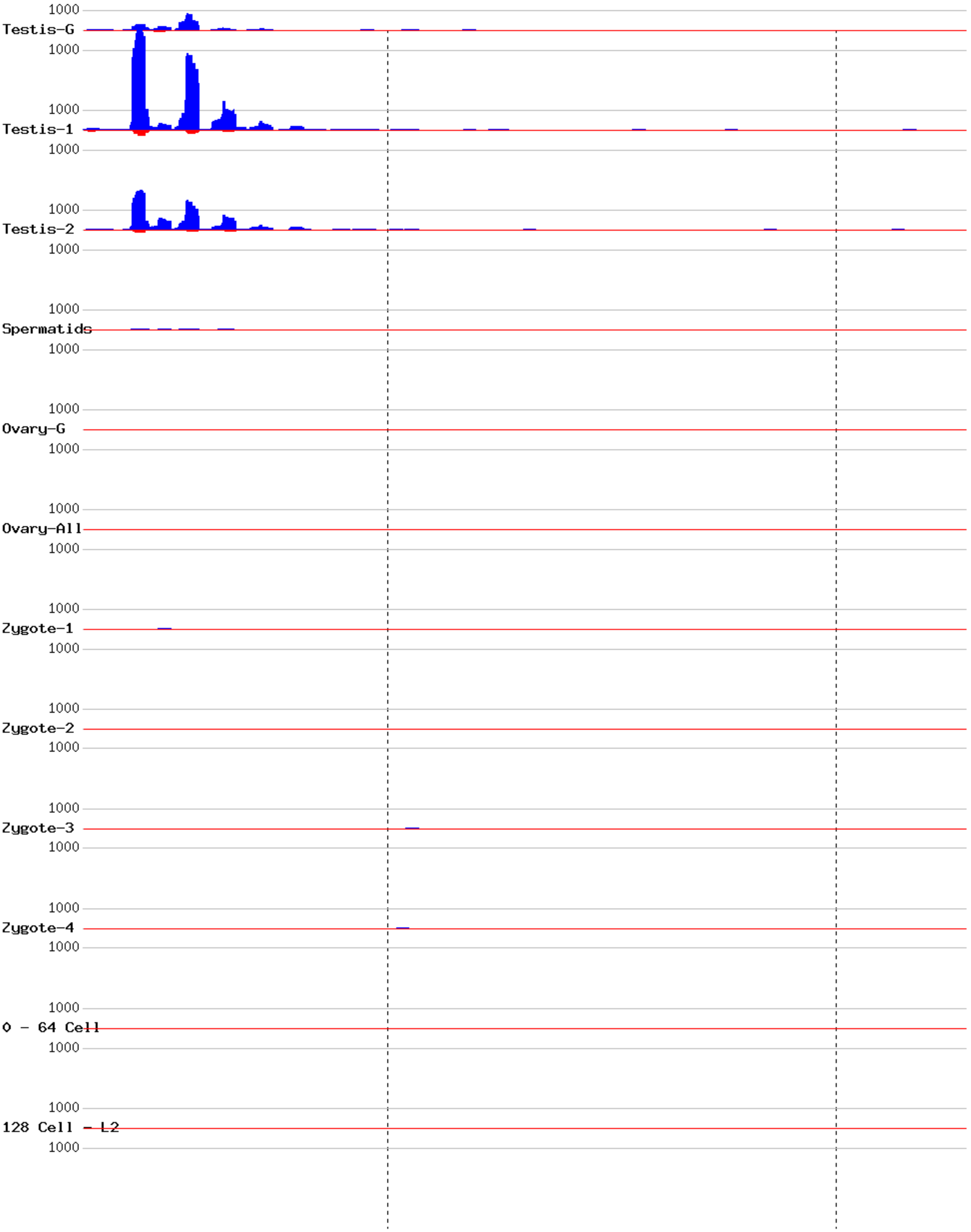
ASCF_4476_1797 Protein-tyrosine_phosphatase_containing_protein 1797 bp



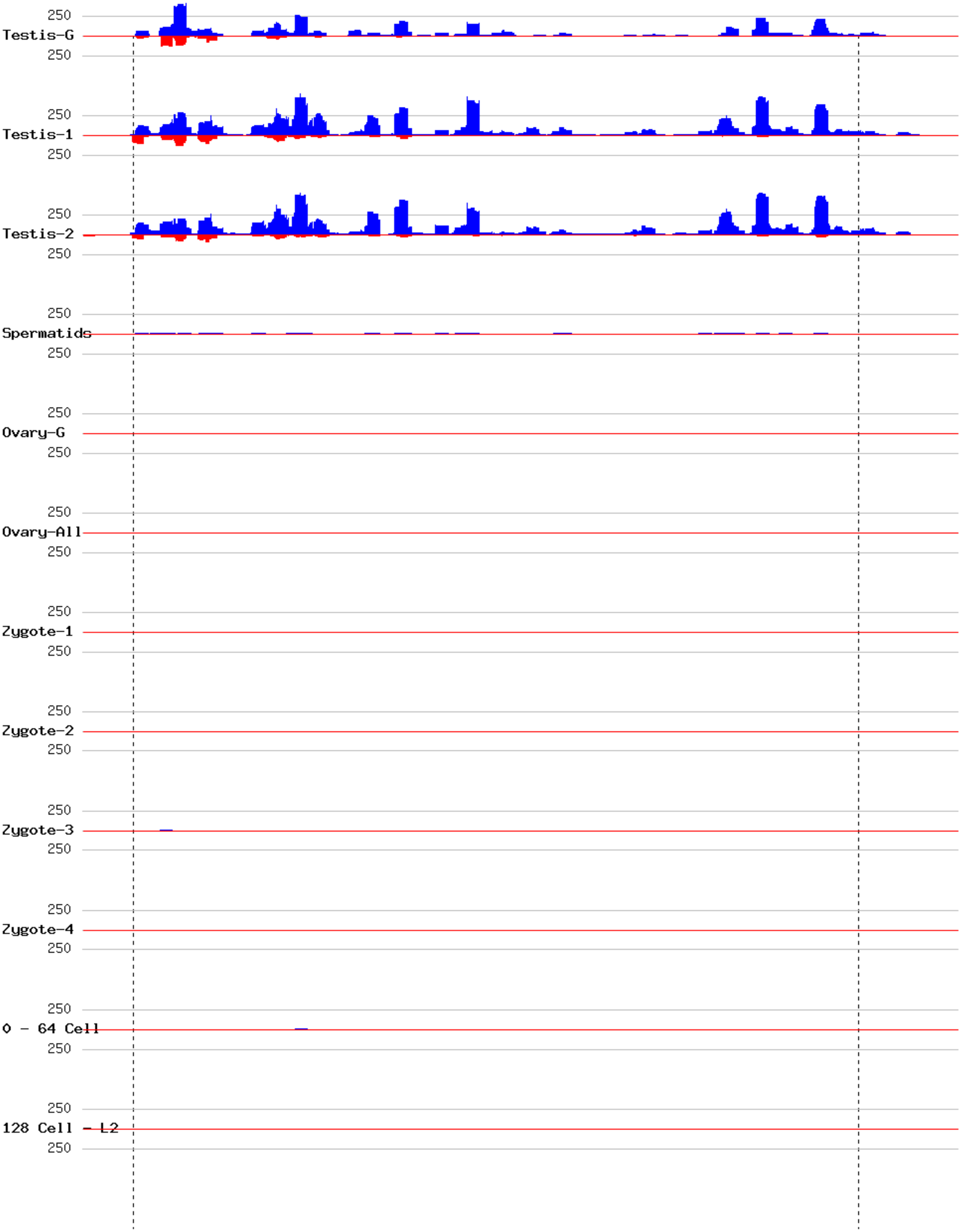
ASCF_4492_1792 Tau-tubulin_kinase 1792 bp



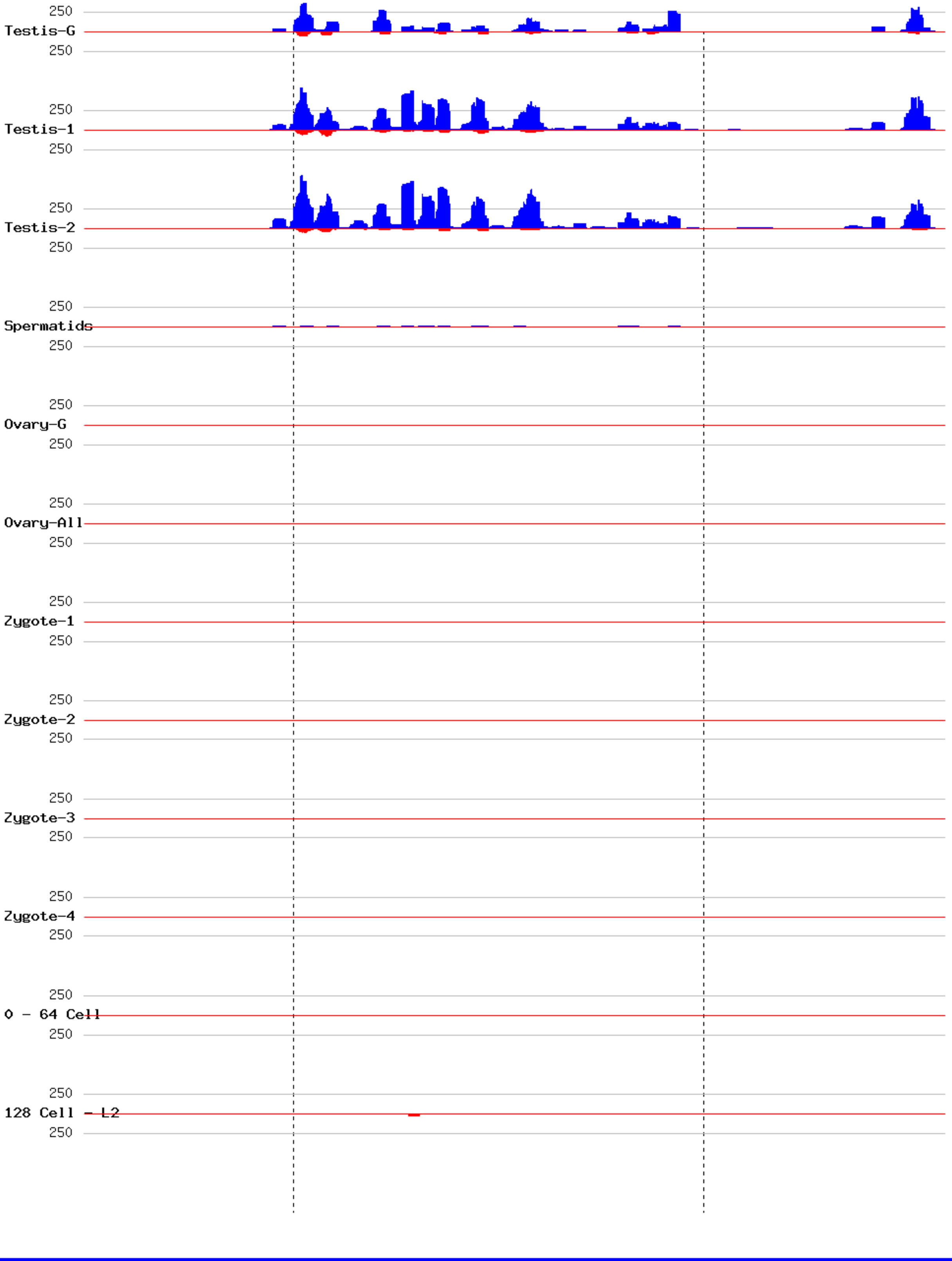
ASCF_4576_1768 CUT-1-like_cuticlin_protein 1768 bp



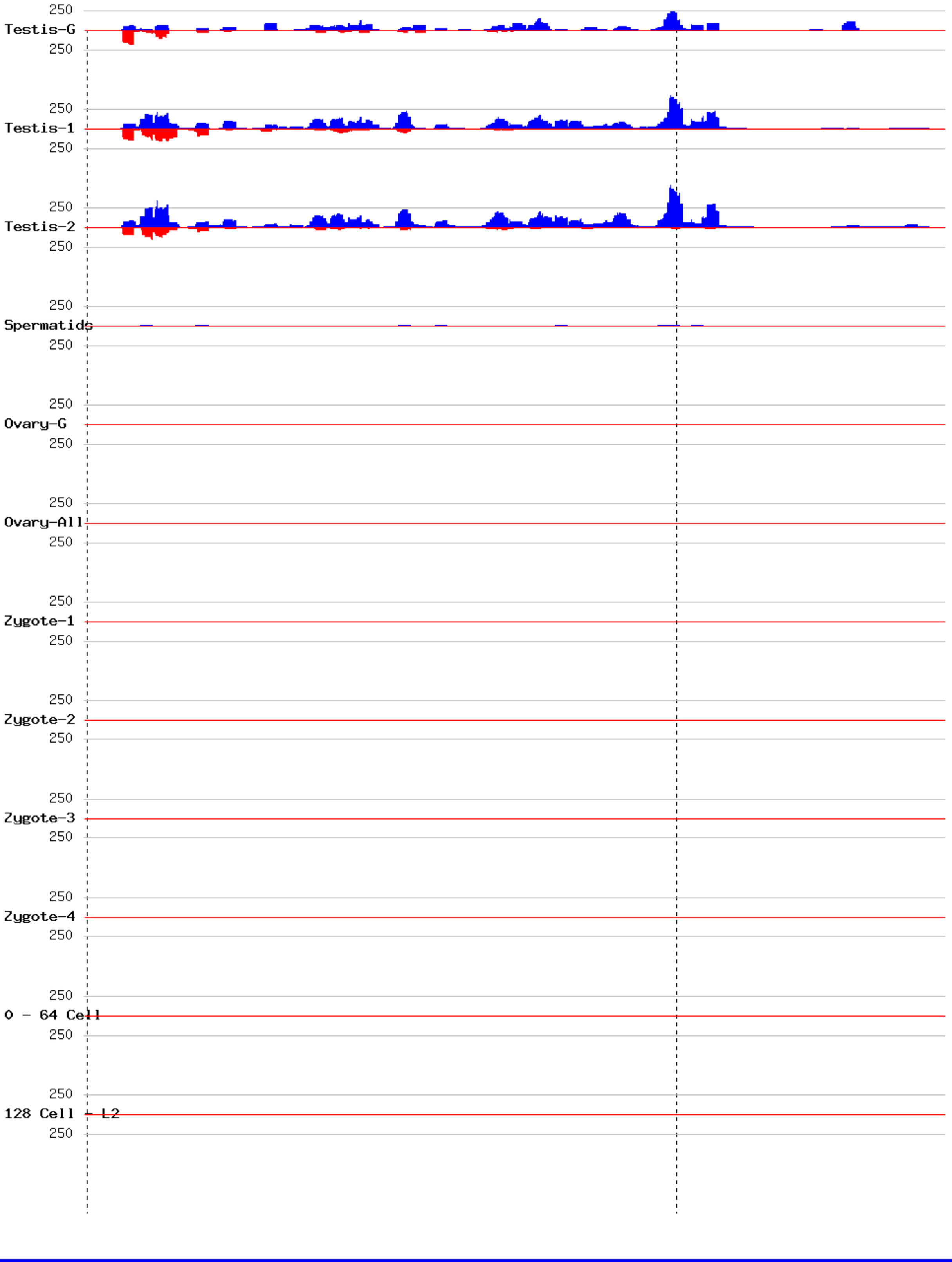
ASCF_4598_1763 Wound-induced_GSK-3-like_protein 1763 bp



ASCF_4648_1751 Serine/threonine-protein_phosphatase 1751 bp

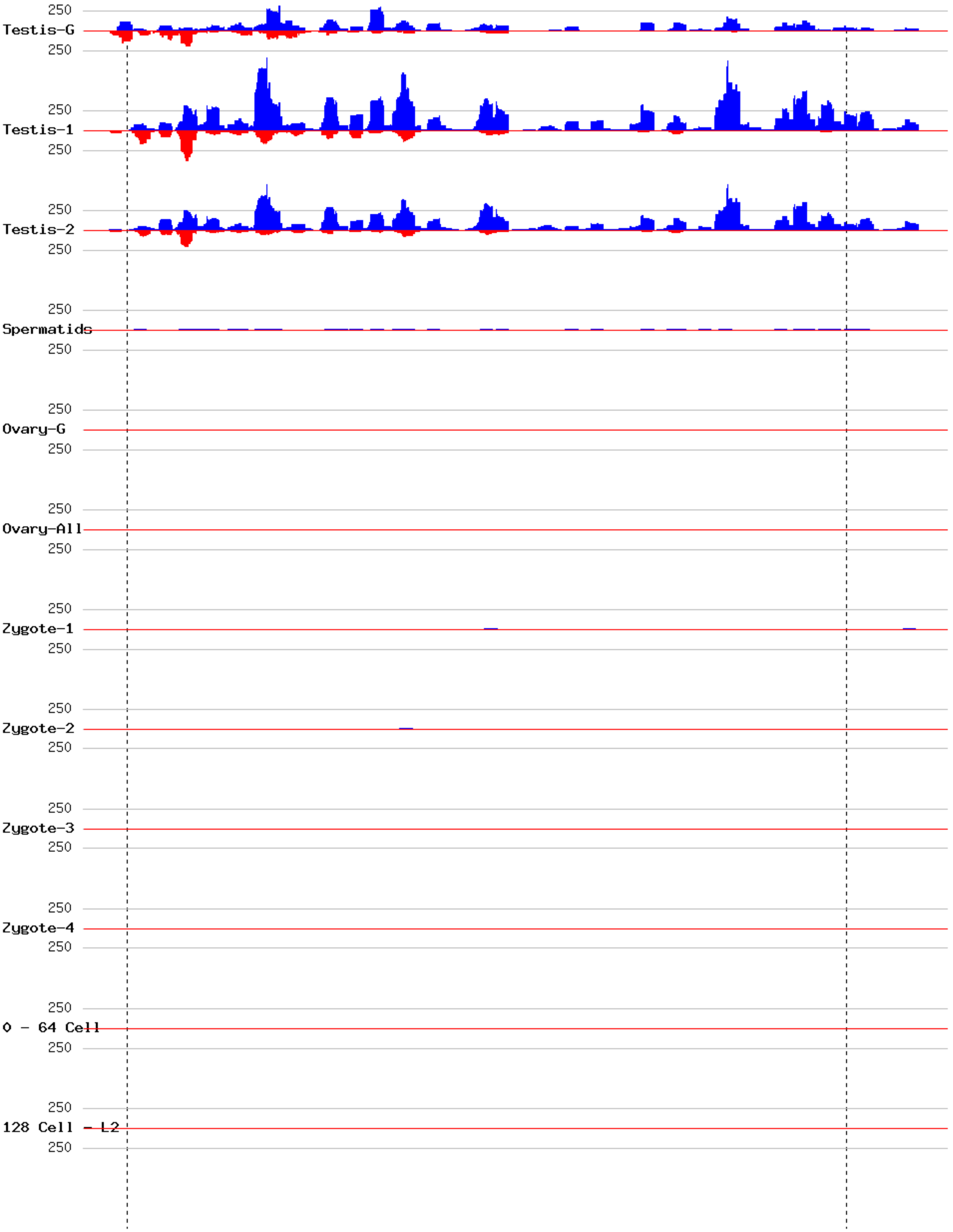


ASCF_4662_1747 Protein_kinase_domain_containing_protein 1747 bp



ASCF_4705_1735 Sugar_transporter_family_protein 1735 bp

ASCF_4717_1733 AN1-like_Zinc_finger_family_protein 1733 bp



ASCF_4743_1728 Hypothetical_protein 1728 bp

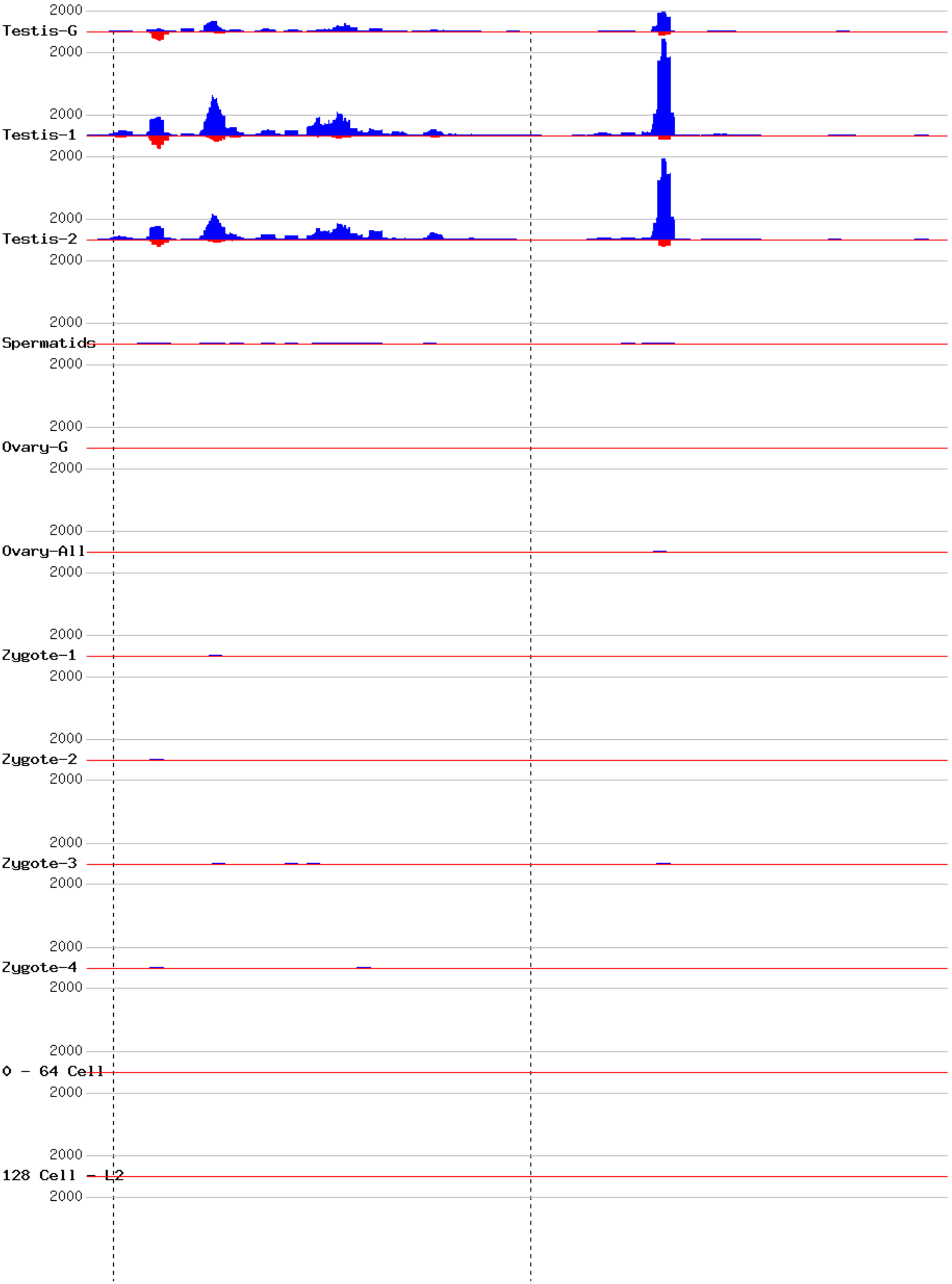
ASCF_4952_1676 PDZ_domain_containing_protein 1676 bp

ASCF_4977_1672 PDZ_domain_containing_protein 1672 bp

ASCF_5003_1665 Hypothetical_protein 1665 bp

ASCF_5012_1663 Hypothetical_protein 1663 bp

ASCF_5046_1654 PDZ_domain_containing_protein 1654 bp



ASCF_5050_1653 Hypothetical_protein 1653 bp

ASCF_5183_1625 Protein_kinase_domain_containing_protein 1625 bp

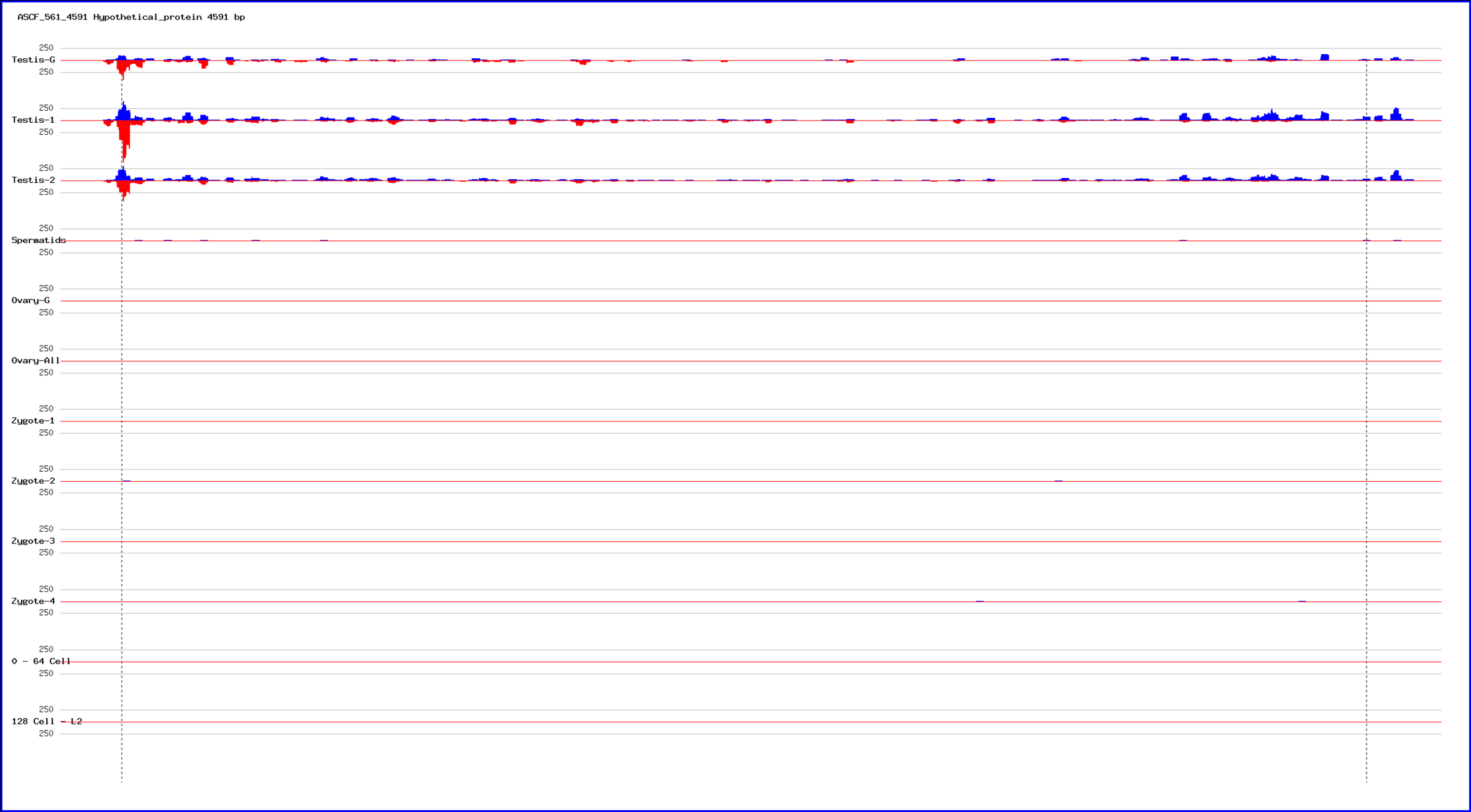
ASCF_5305_1596 Protein_kinase_domain_containing_protein 1596 bp

ASCF_5339_1583 PDZ_domain_containing_protein 1583 bp

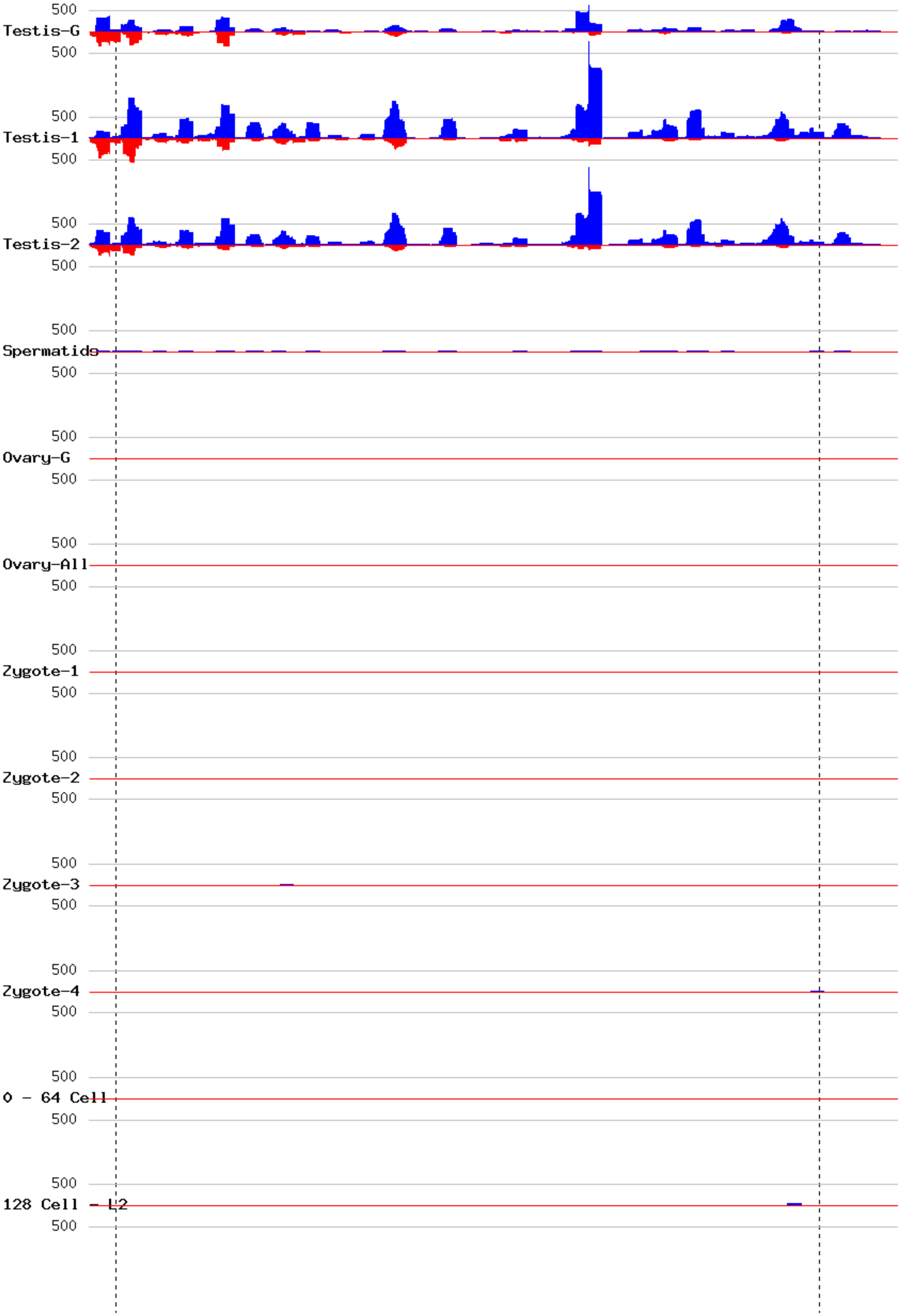
ASCF_5358_1579 Protein_kinase_domain_containing_protein 1579 bp

ASCF_5362_1578 Protein_kinase_domain_containing_protein 1578 bp

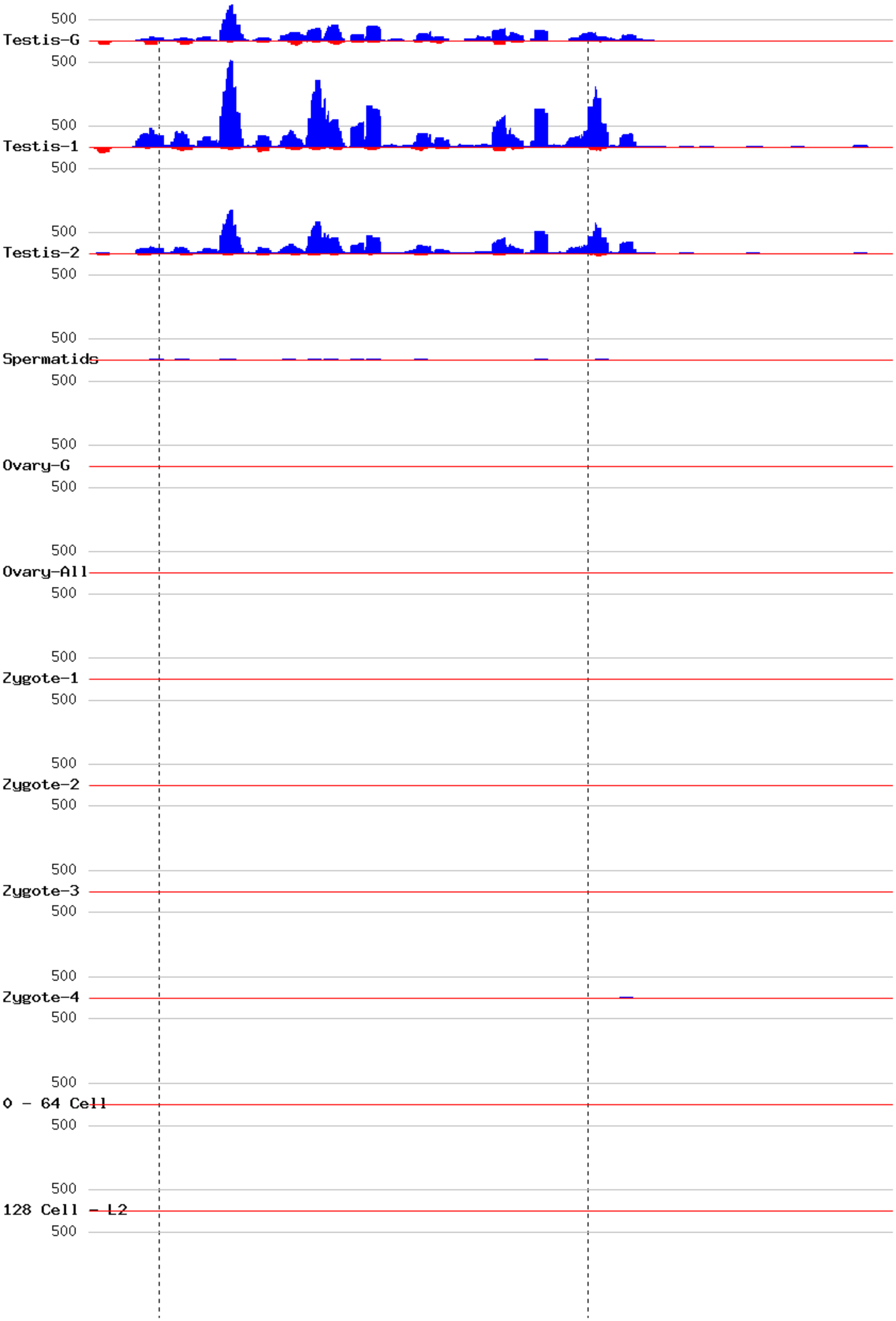
ASCF_5418_1563 Protein_kinase_domain_containing_protein 1563 bp


ASCF_561_4591 Hypothetical_protein 4591 bp
250
Testis-G
250
250
Testis-1
250
250
Testis-2
250
250
Spermatids
250
250
Ovary-G
250
250
Ovary-All
250
250
Zygote-1
250
250
Zygote-2
250
250
Zygote-3
250
250
Zygote-4
250
250
0 - 64 Cell
250
250
128 Cell - L2
250

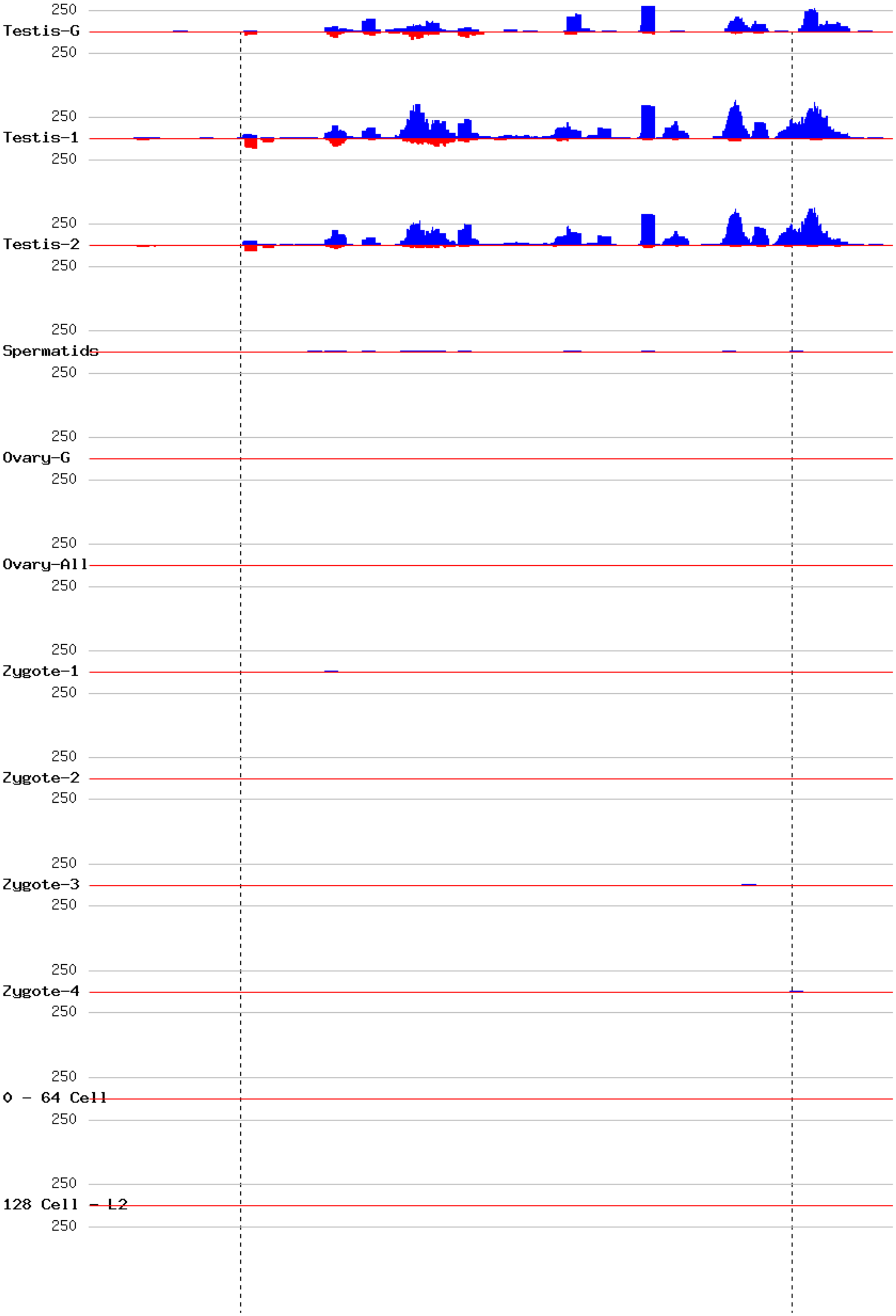
ASCF_5630_1514 Tyrosine_kinase 1514 bp



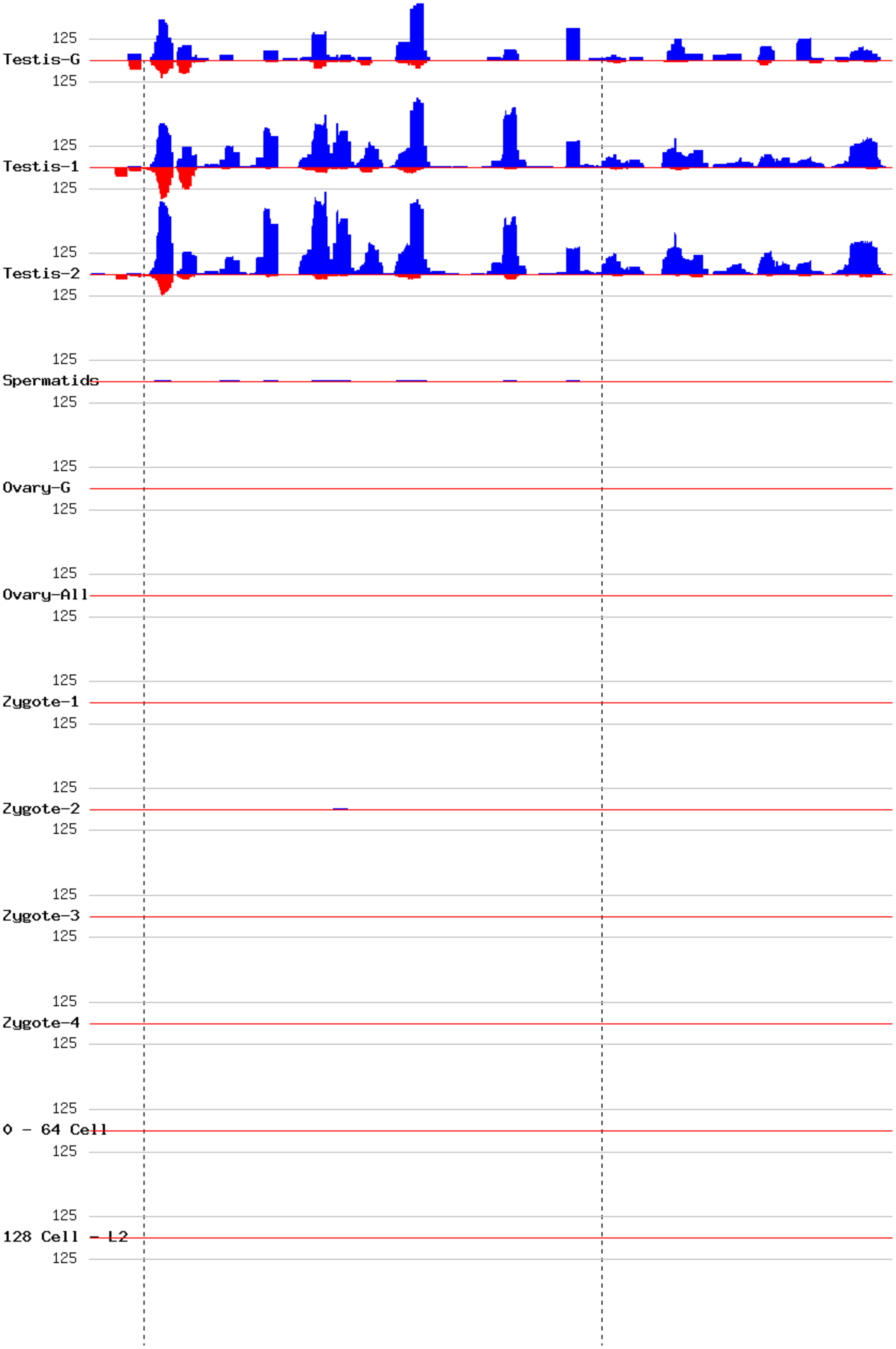
ASCF_5649_1510 Hypothetical_protein 1510 bp



ASCF_5653_1507 Protein_kinase_domain_containing_protein 1507 bp

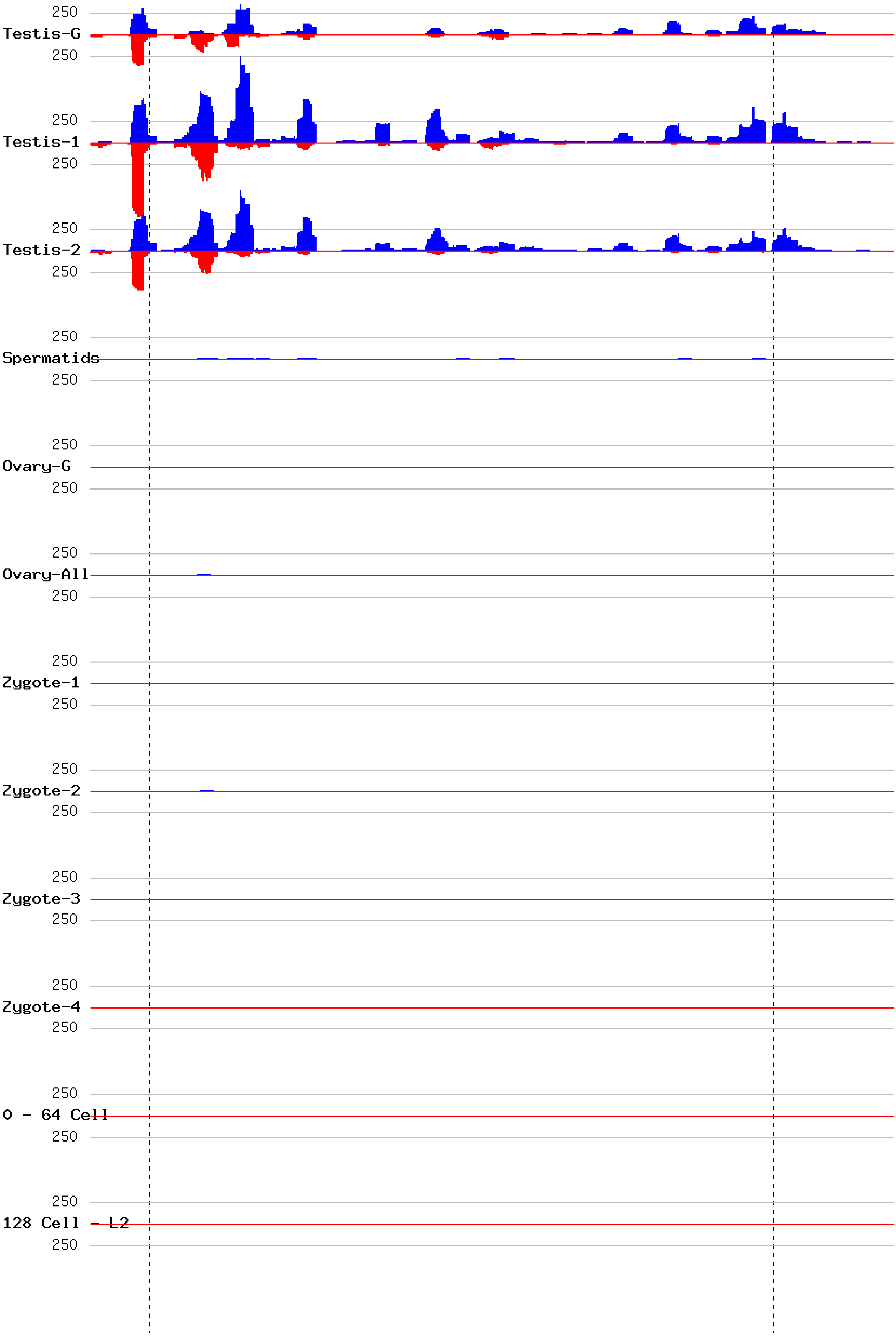


ASCF_5682_1500 Hypothetical_protein 1500 bp

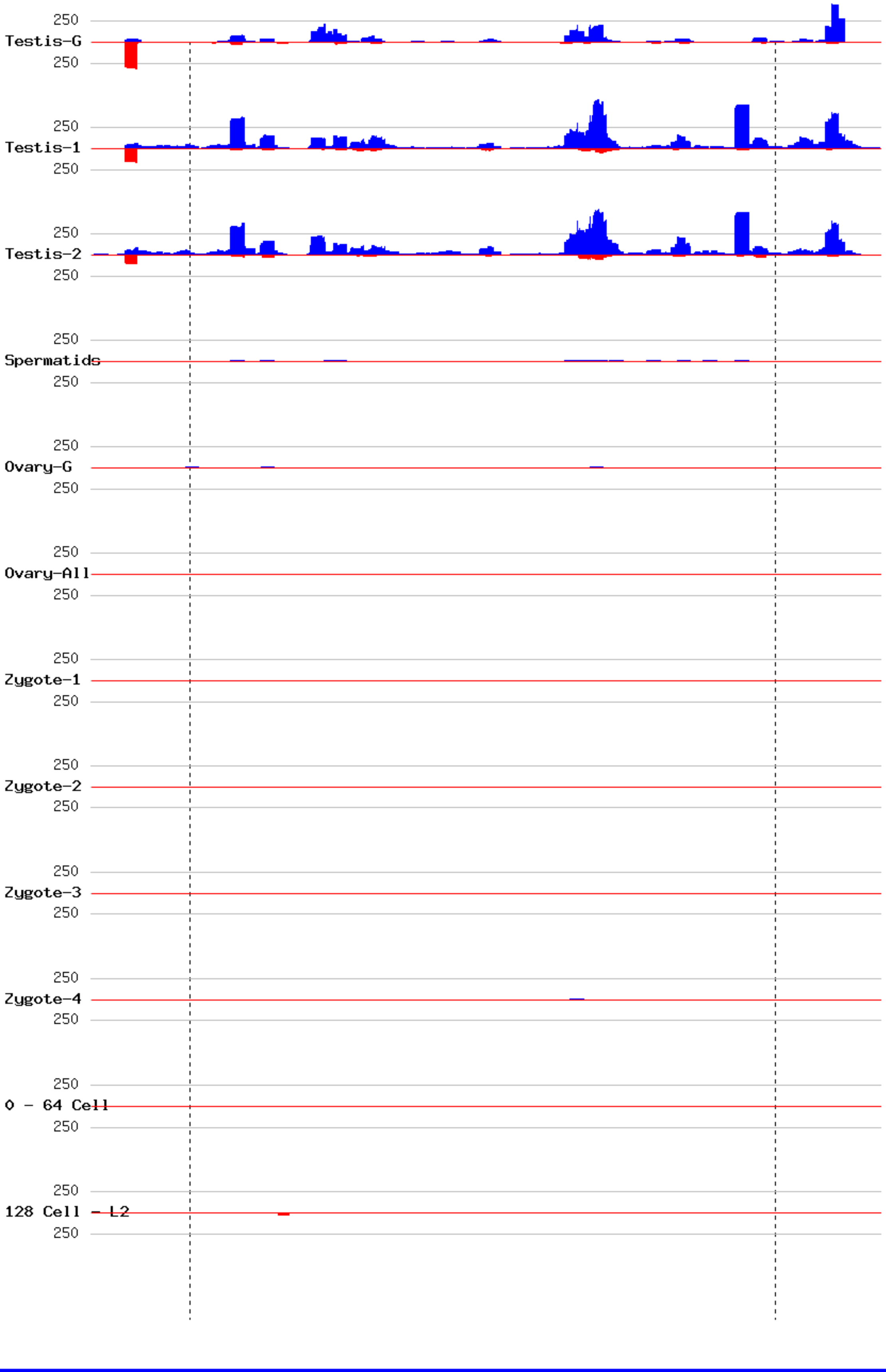


ASCF_5748_1486 Serine/threonine-protein_phosphatase 1486 bp

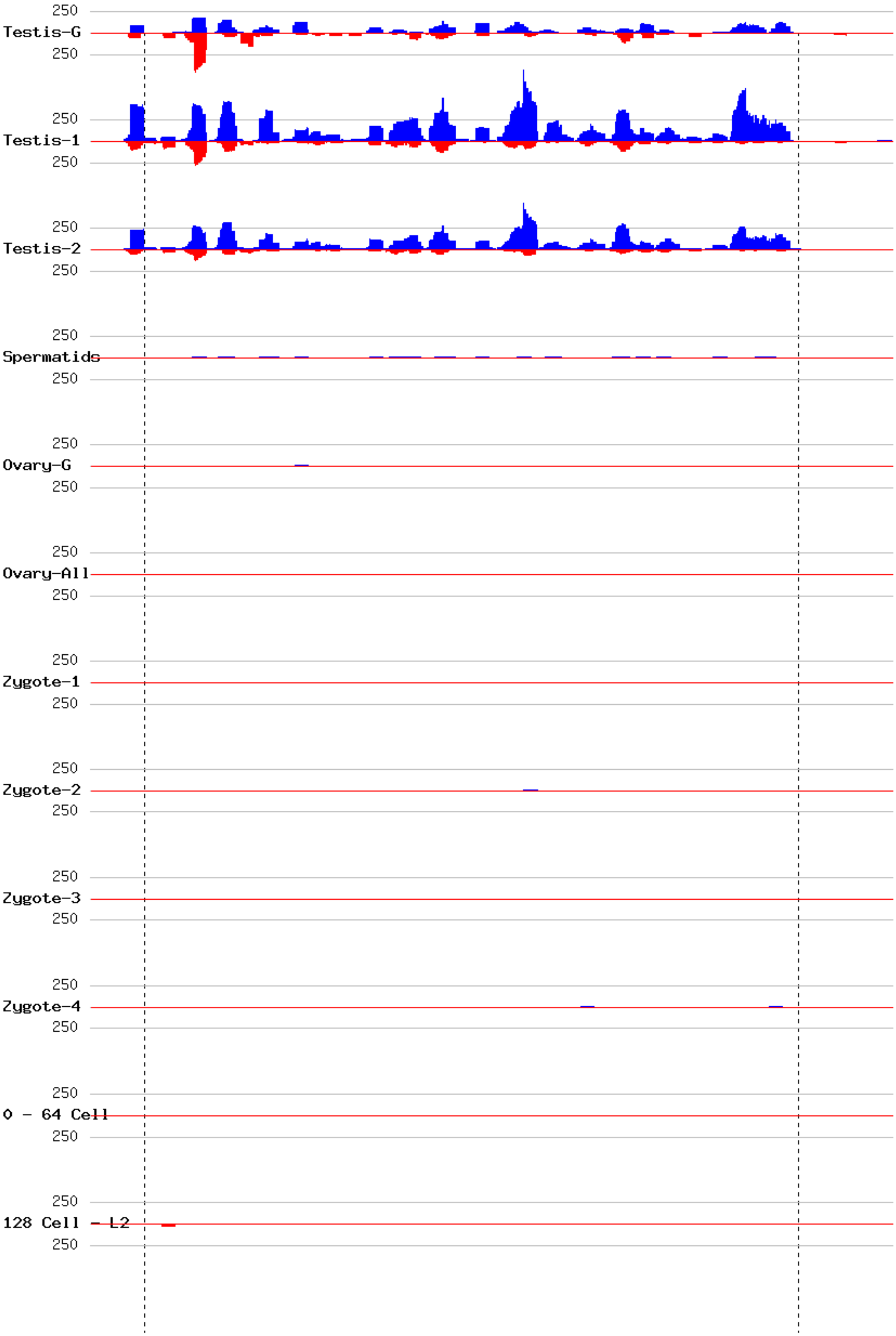
ASCF_5756_1486 Protein_kinase_domain_containing_protein 1486 bp



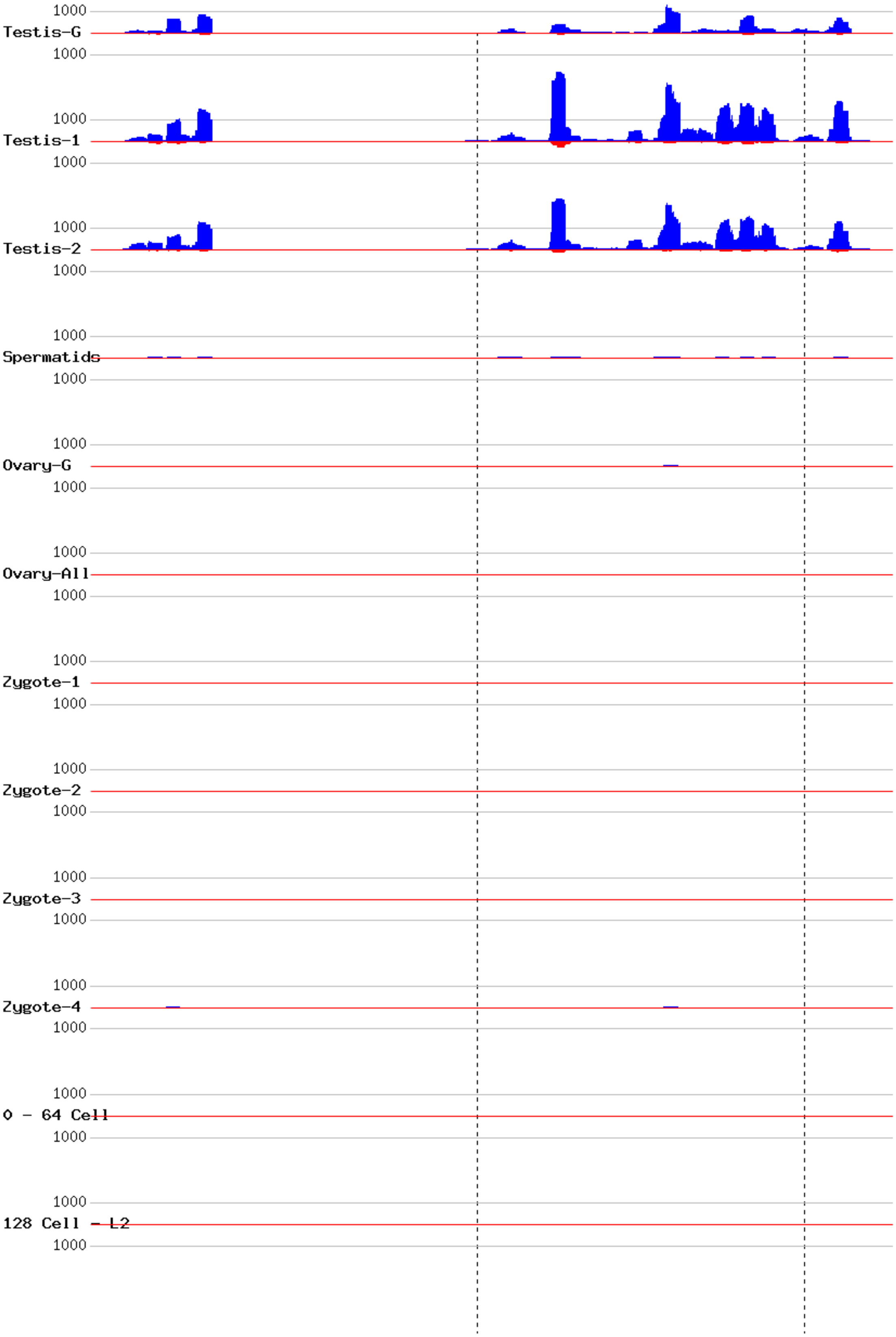
ASCF_5766_1484 Ceramide_cholinephosphotransferase_1 1484 bp



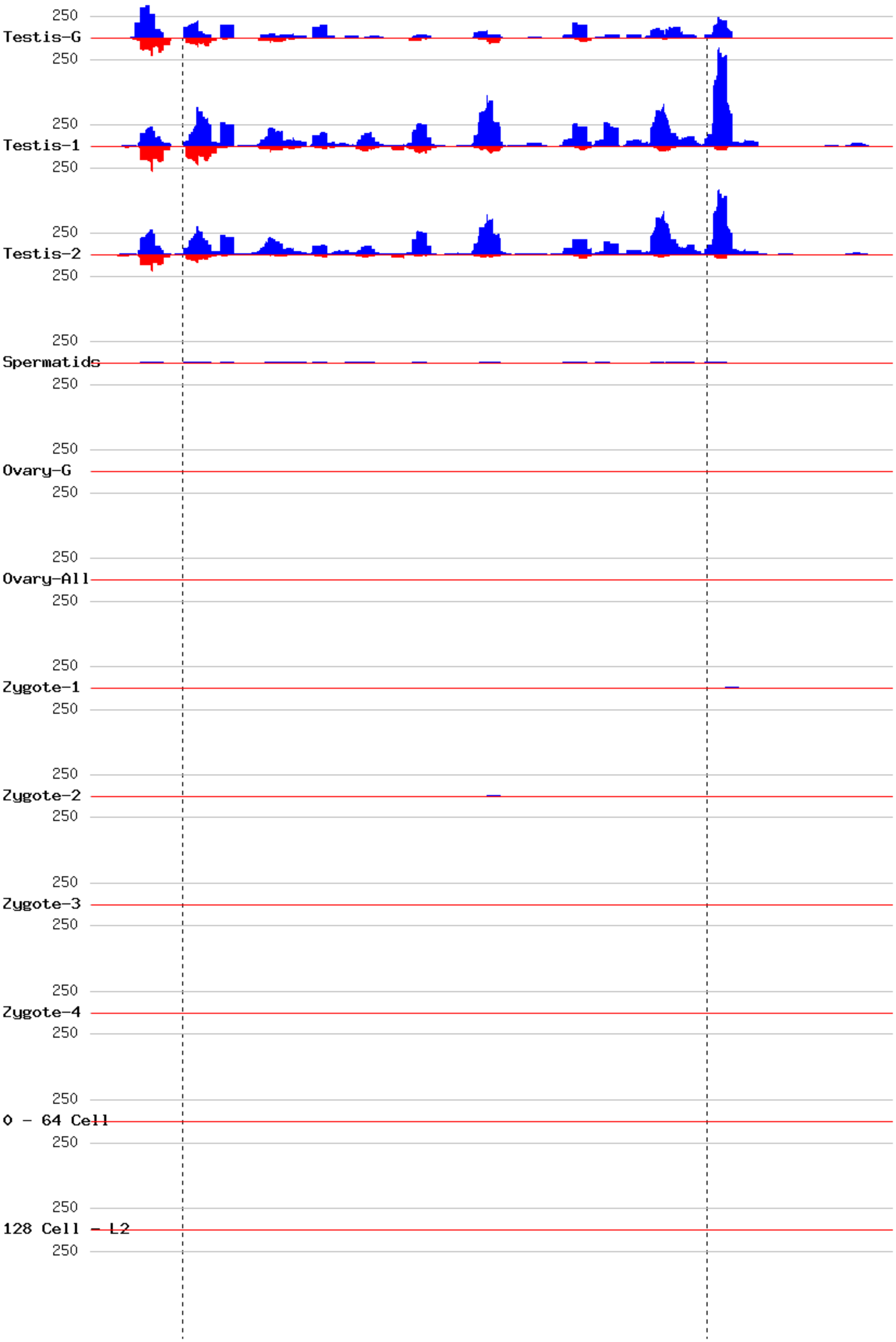
ASCF_5778_1482 Protein-tyrosine_phosphatase_containing_protein 1482 bp



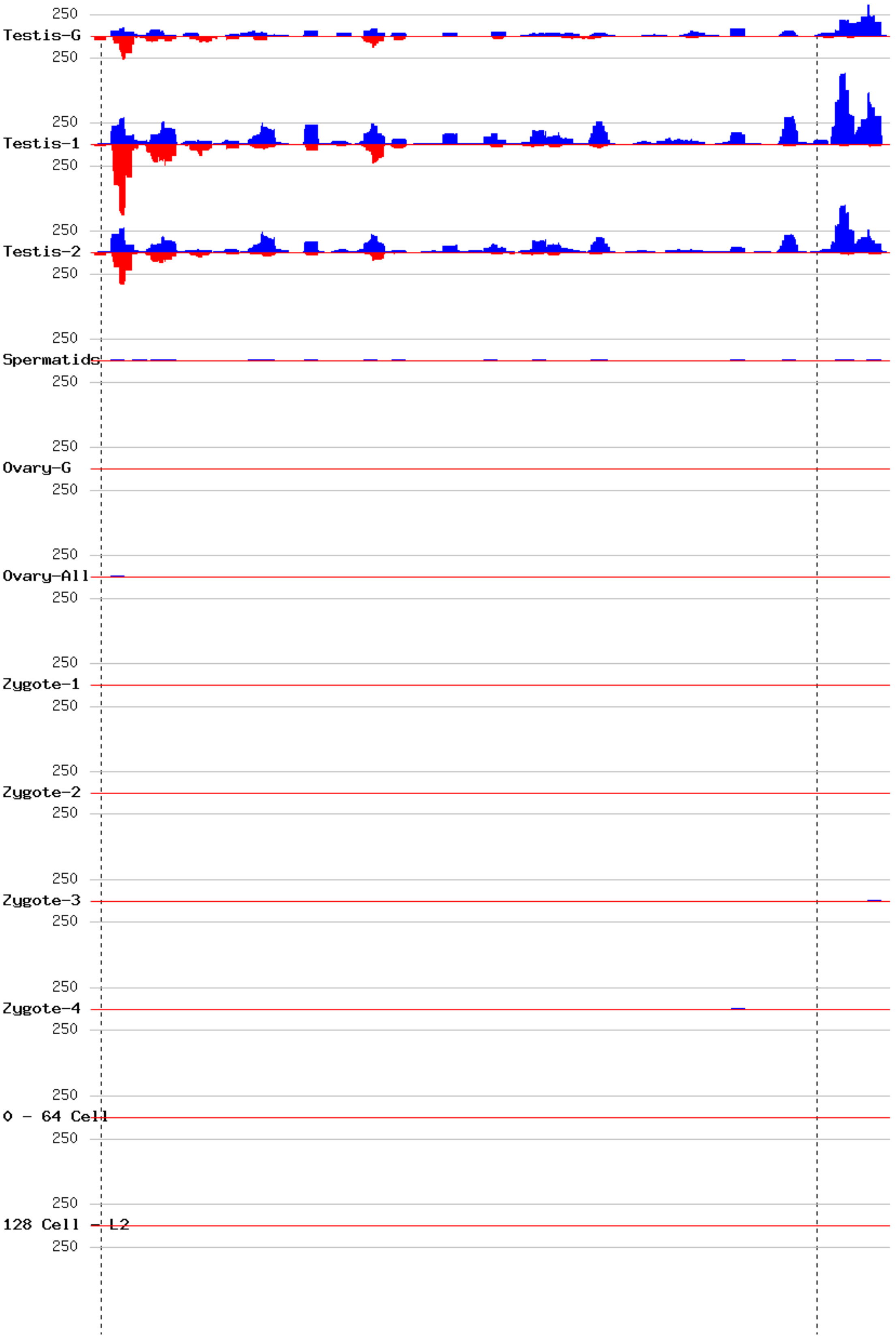
ASCF_5784_1480 Major_sperm_protein 1480 bp



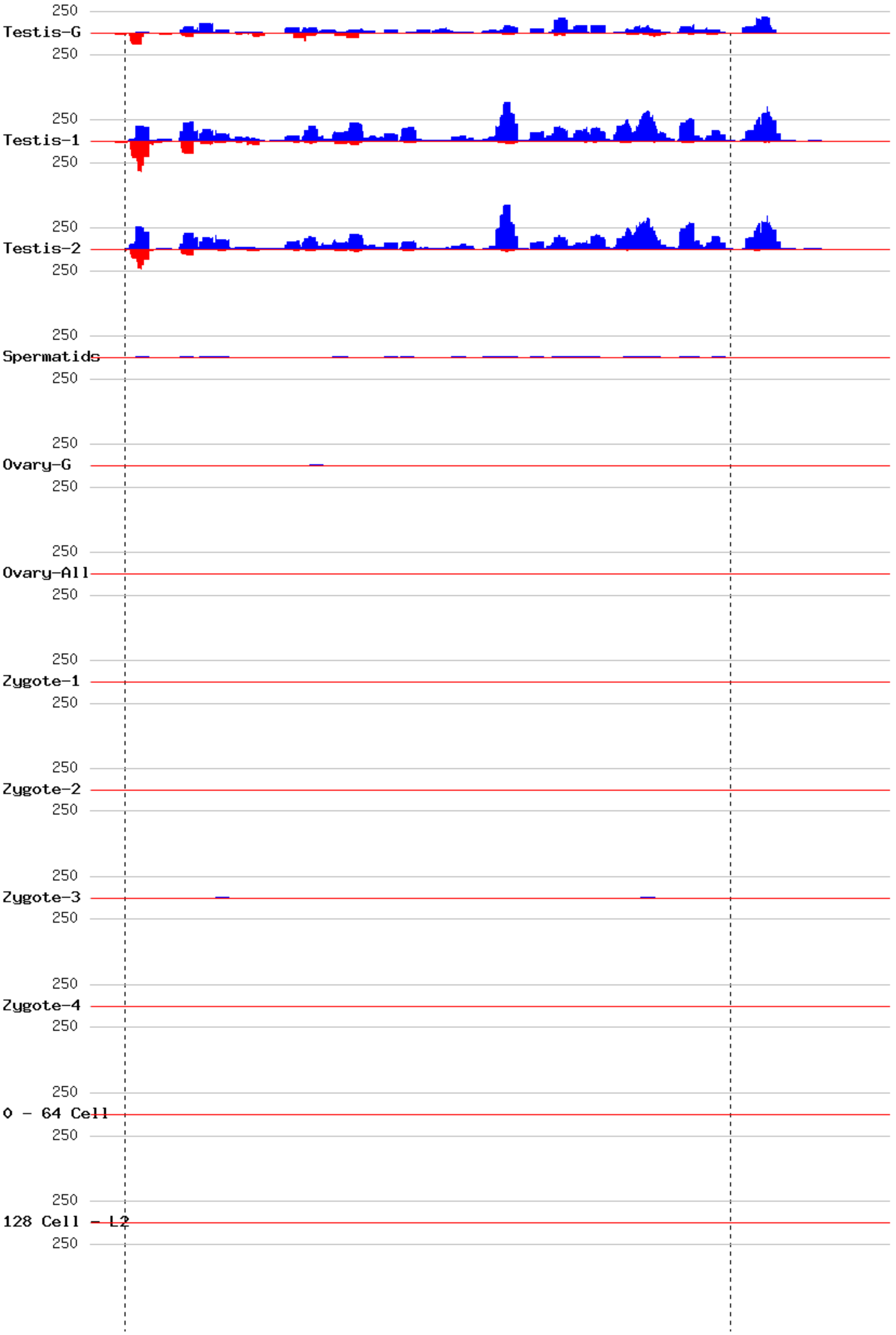
ASCF_5786_1480 Serine/threonine-protein_phosphatase 1480 bp



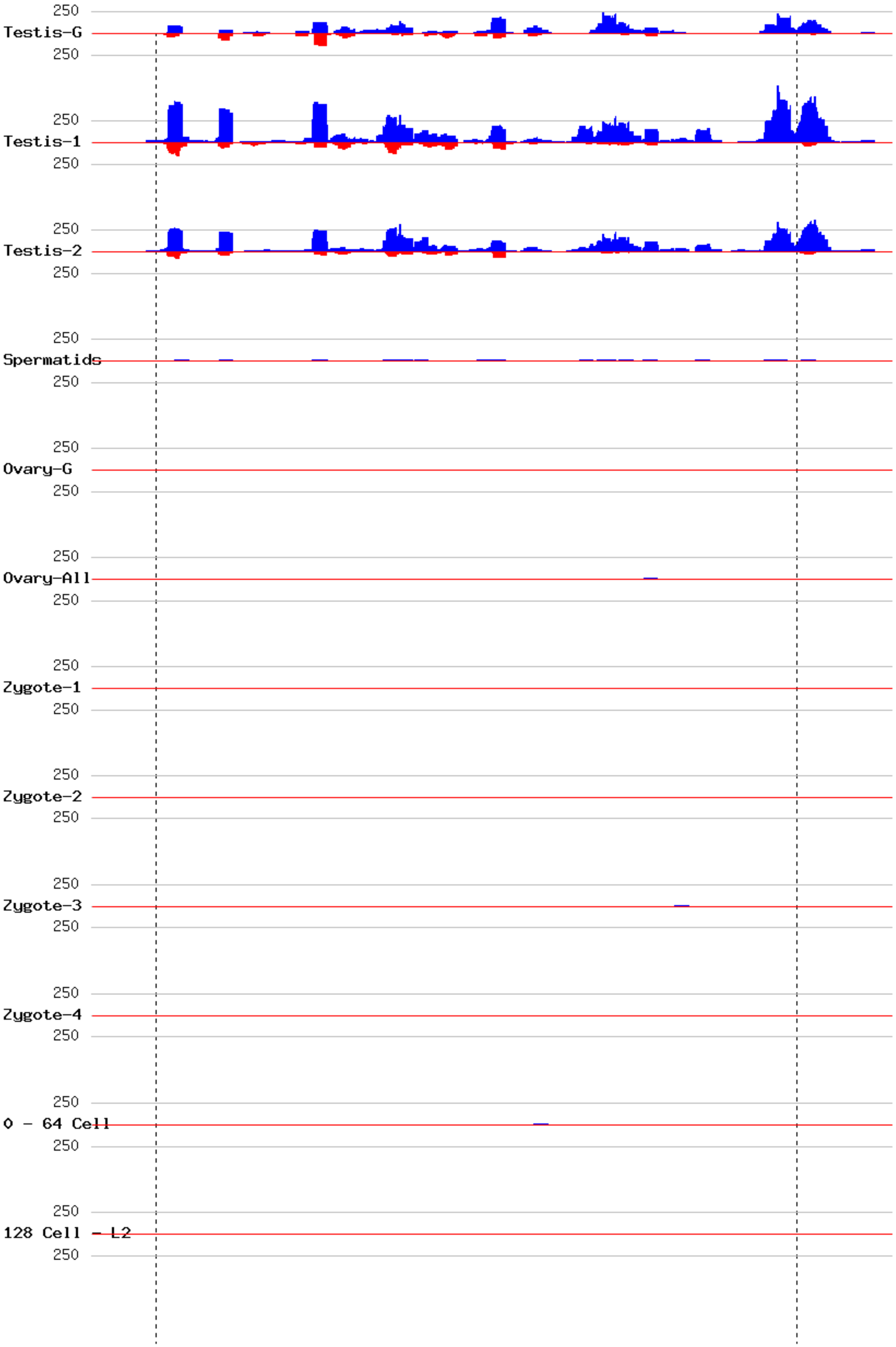
ASCF_5791_1479 Protein_kinase_domain_containing_protein 1479 bp



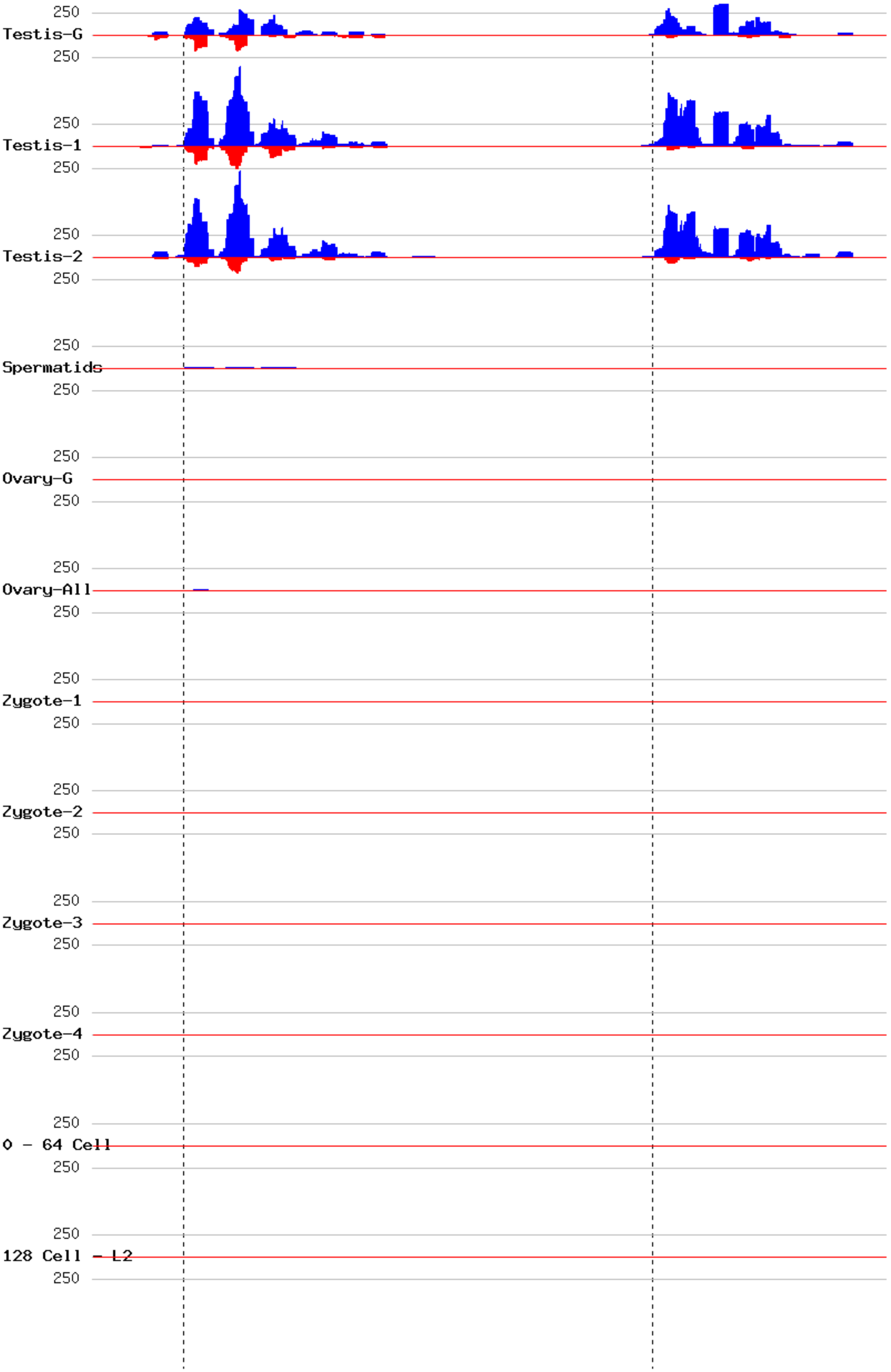
ASCF_5797_1478 Protein_kinase_domain_containing_protein 1478 bp



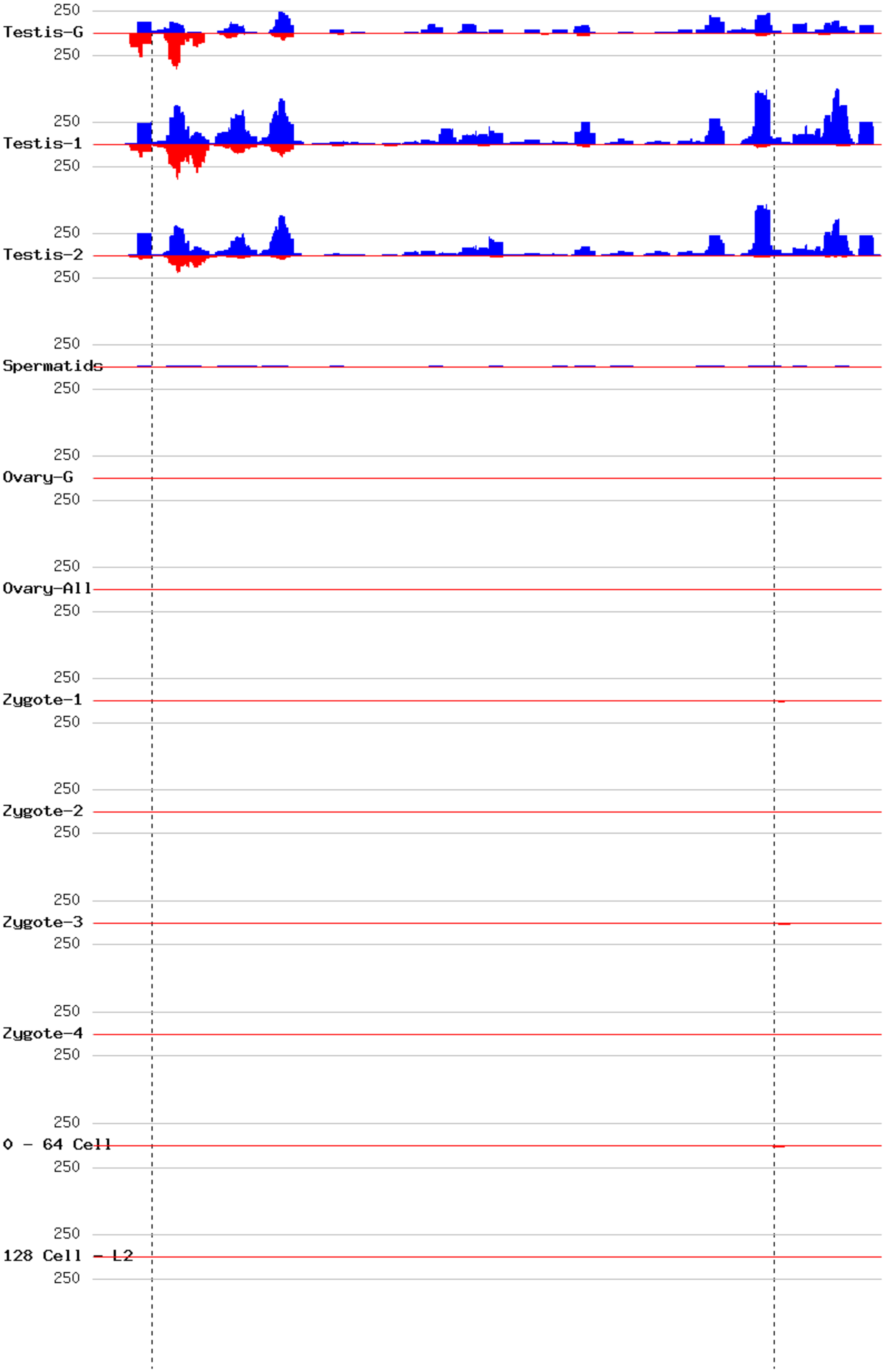
ASCF_5844_1467 Serine/Threonine_Kinases 1467 bp



ASCF_6008_1429 Major_sperm_protein 1429 bp



ASCF_6084_1416 Hypothetical_protein 1416 bp



ASCF_6085_1416 Hypothetical_protein 1416 bp

1000
Testis-G
1000

1000
Testis-1
1000

1000
Testis-2
1000

1000
Spermatids
1000

1000
Ovary-G
1000

1000
Ovary-All
1000

1000
Zygote-1
1000

1000
Zygote-2
1000

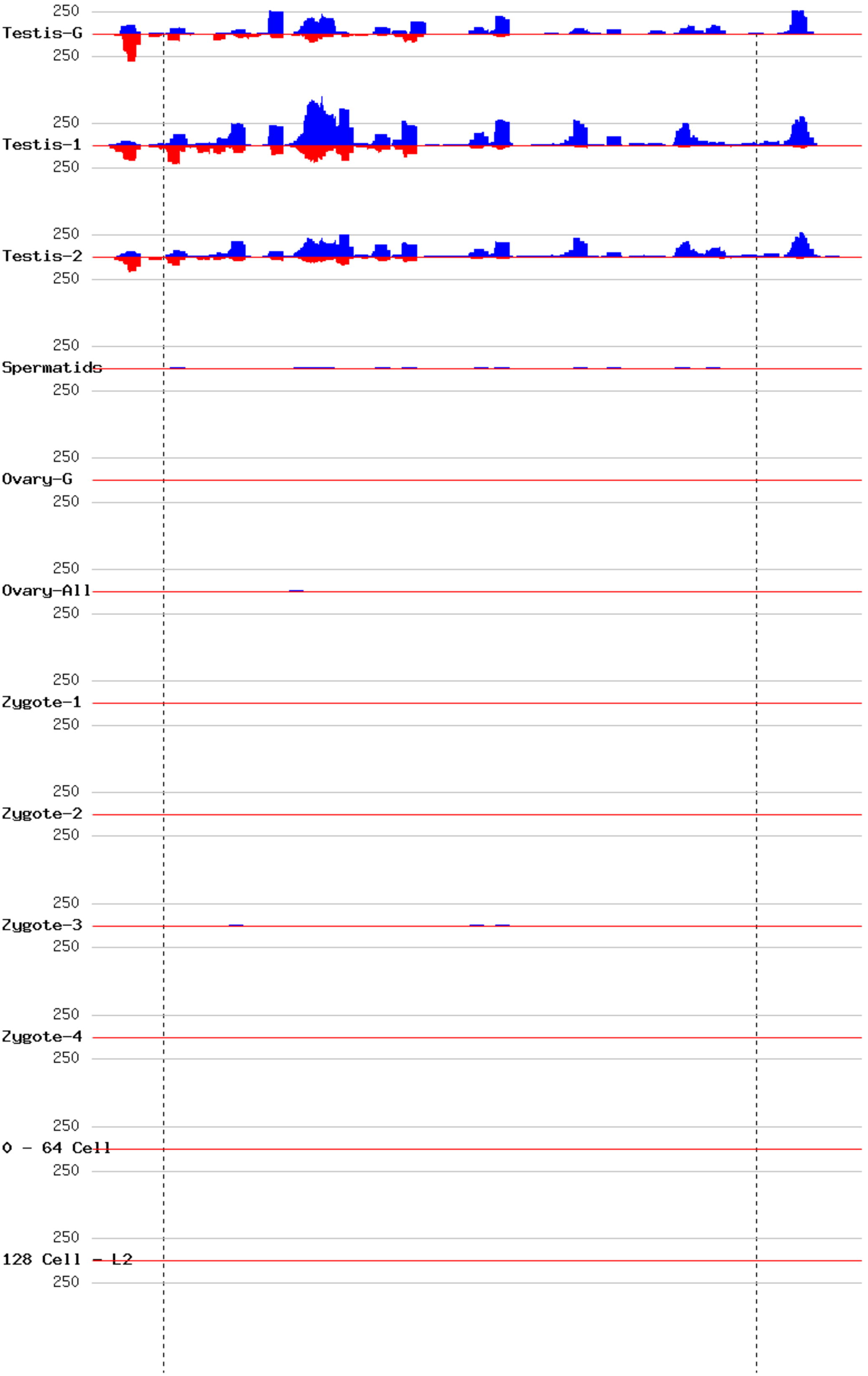
1000
Zygote-3
1000

1000
Zygote-4
1000

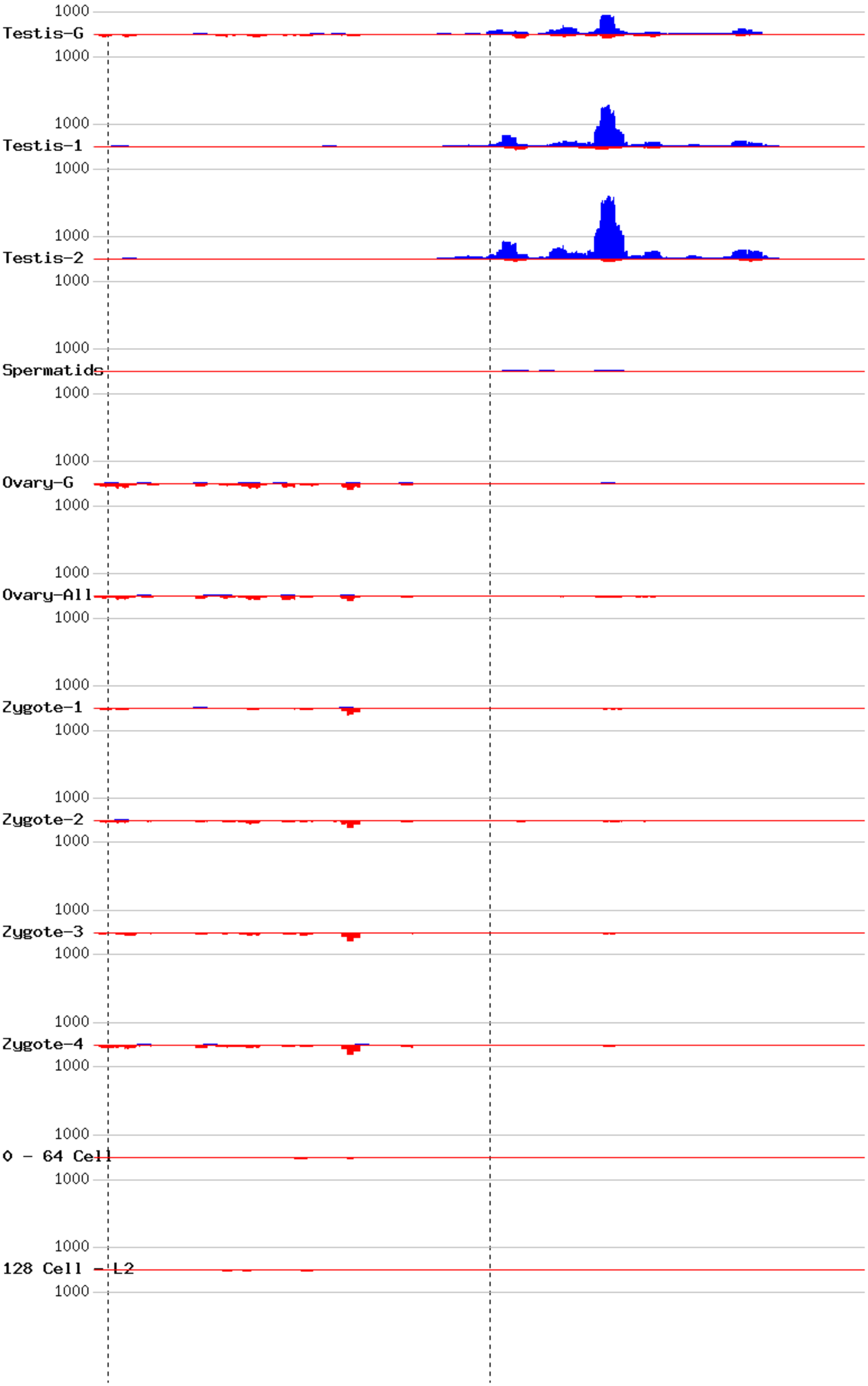
1000
0 - 64 Cell
1000

1000
128 Cell - L2
1000

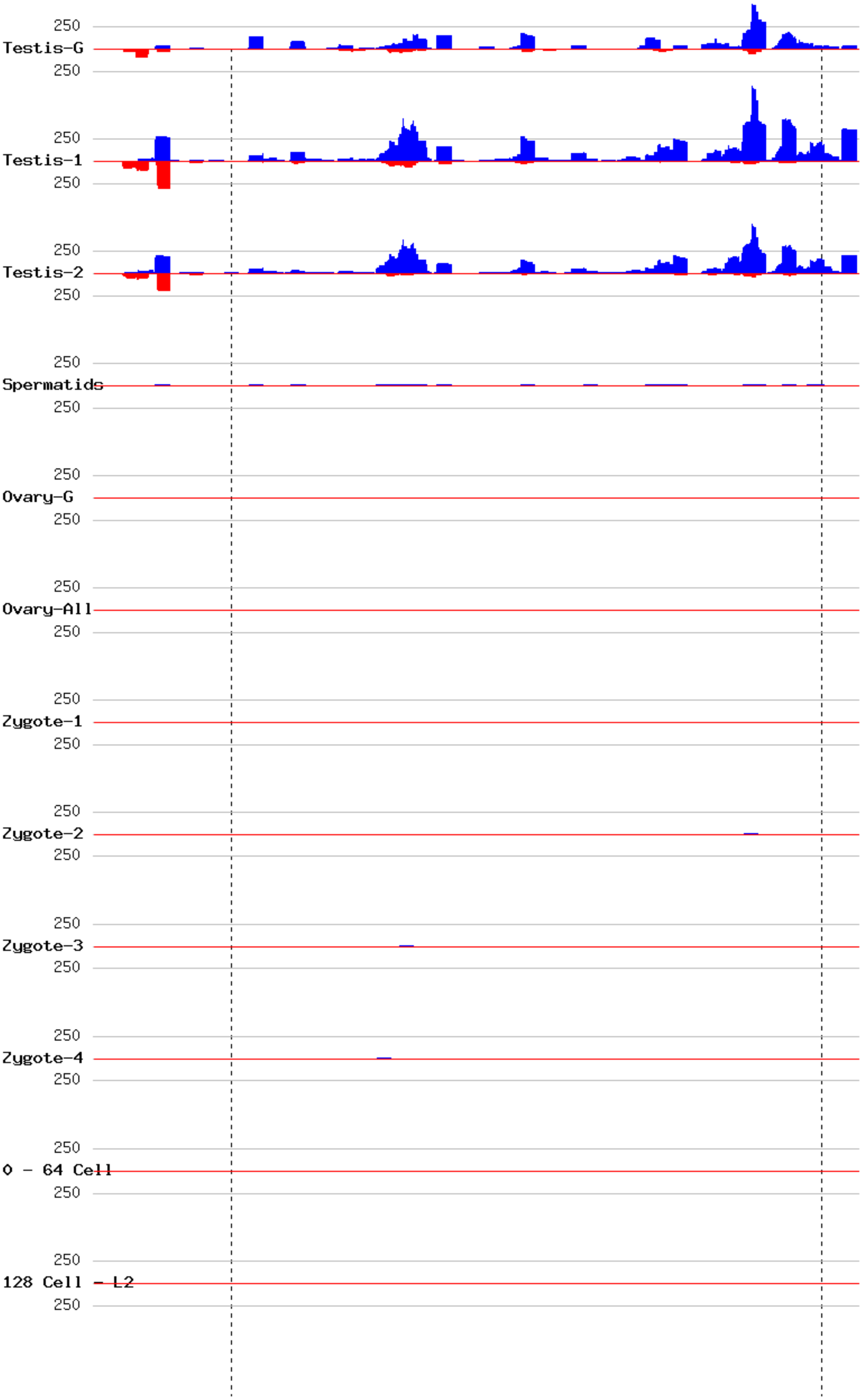
ASCF_6256_1381 Serine/threonine-protein_kinase 1381 bp



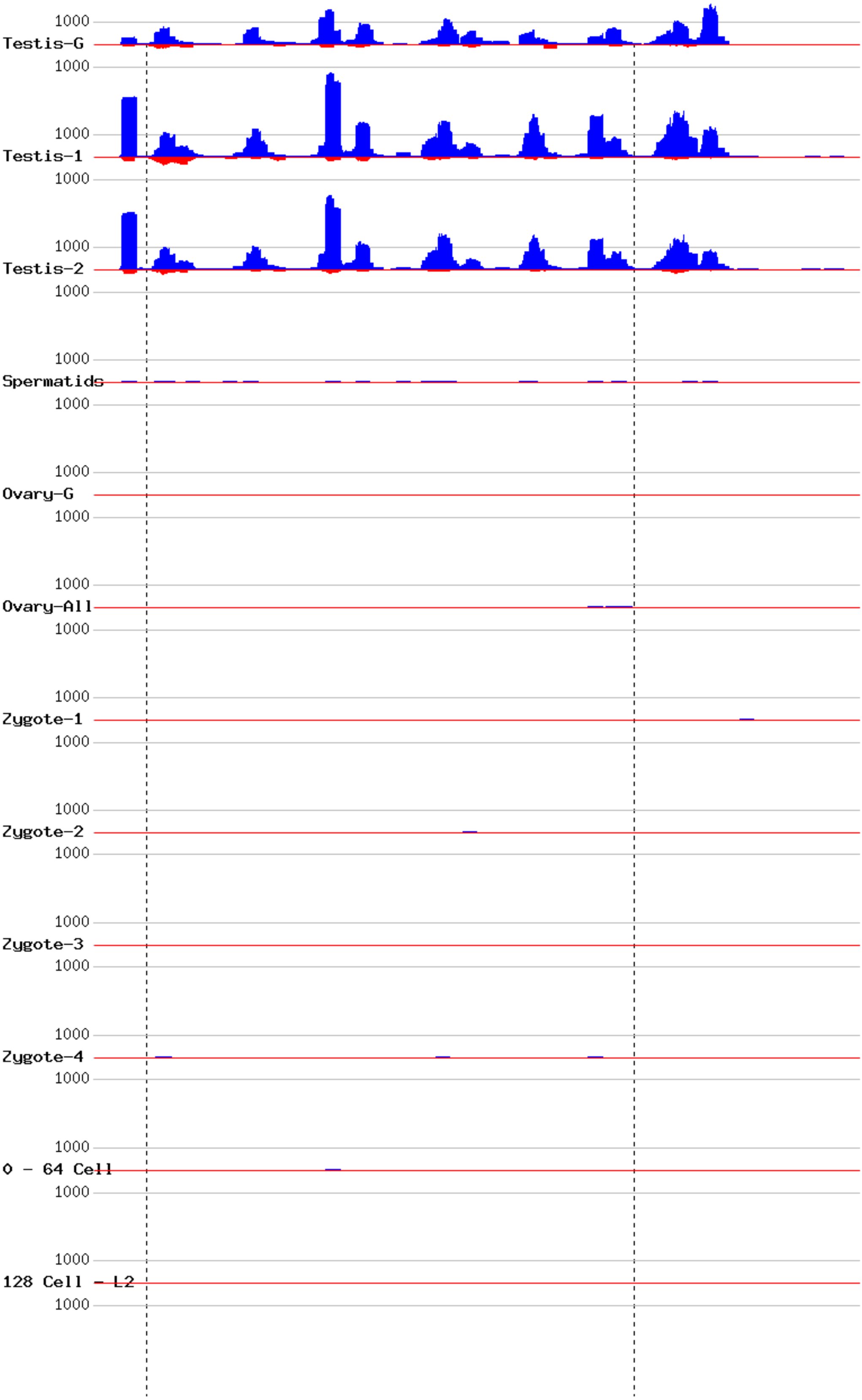
ASCF_6285_1373 Hypothetical_protein 1373 bp



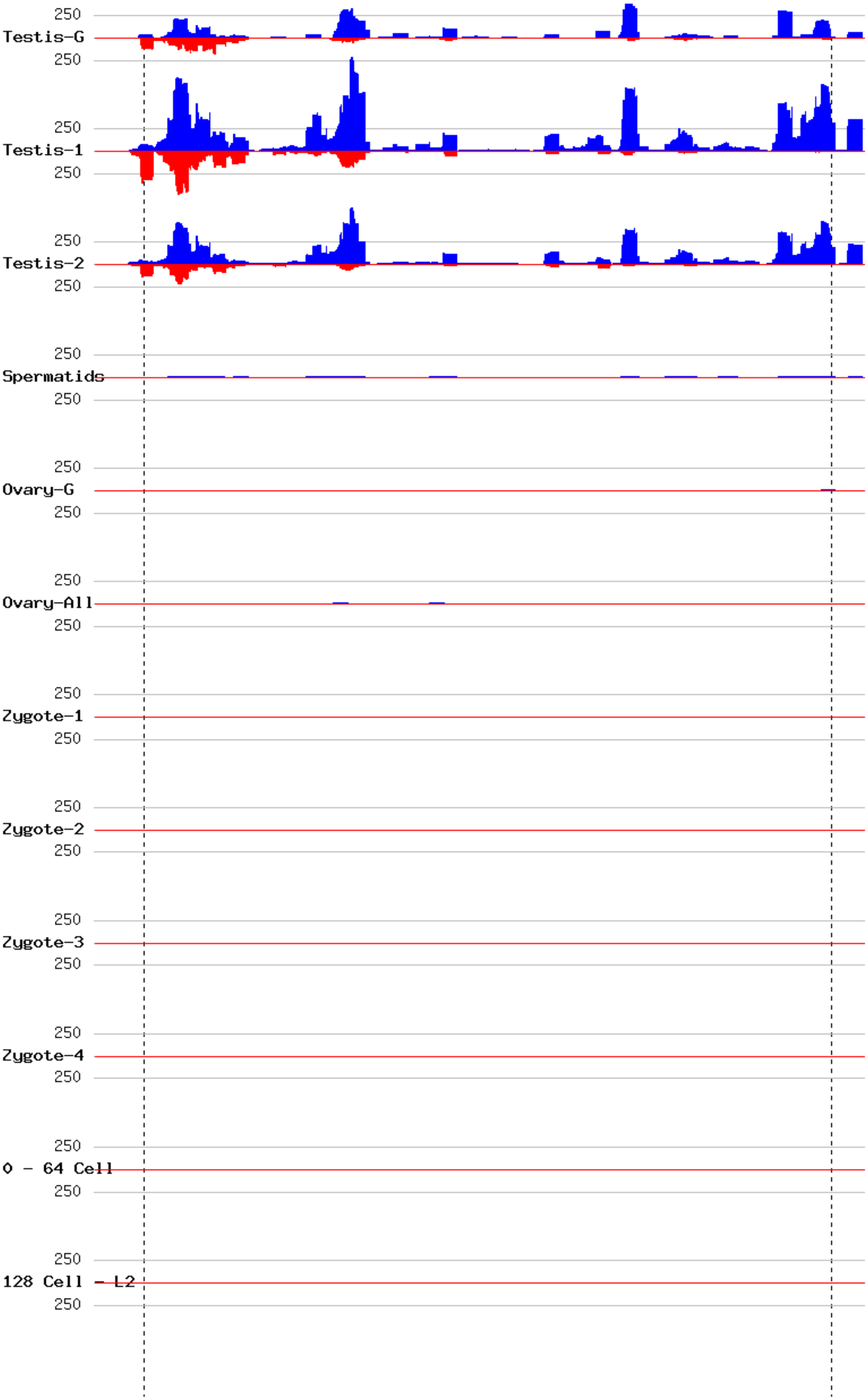
ASCF_6325_1365 Protein_kinase_domain_containing_protein 1365 bp



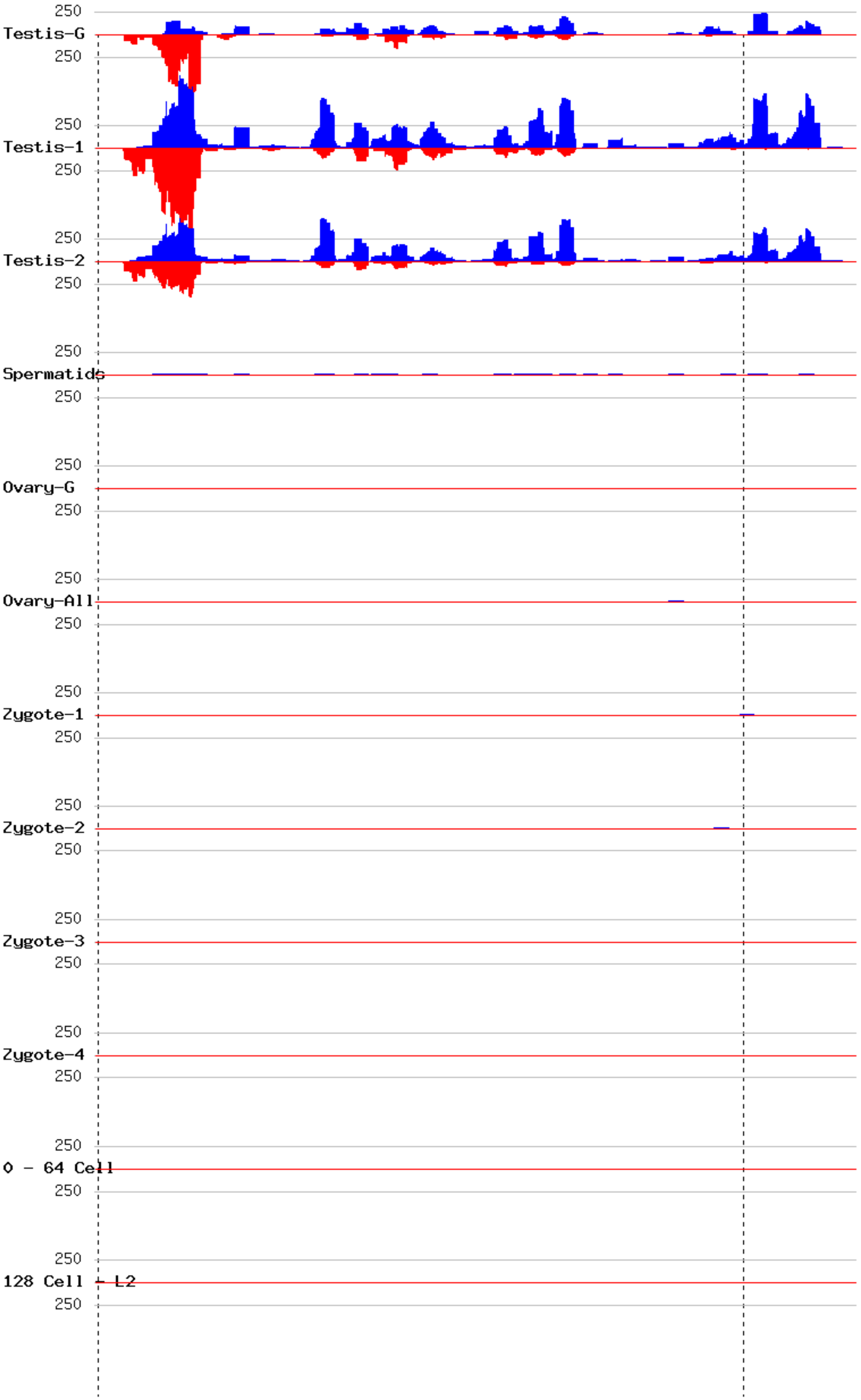
ASCF_6343_1361 Hypothetical_protein 1361 bp



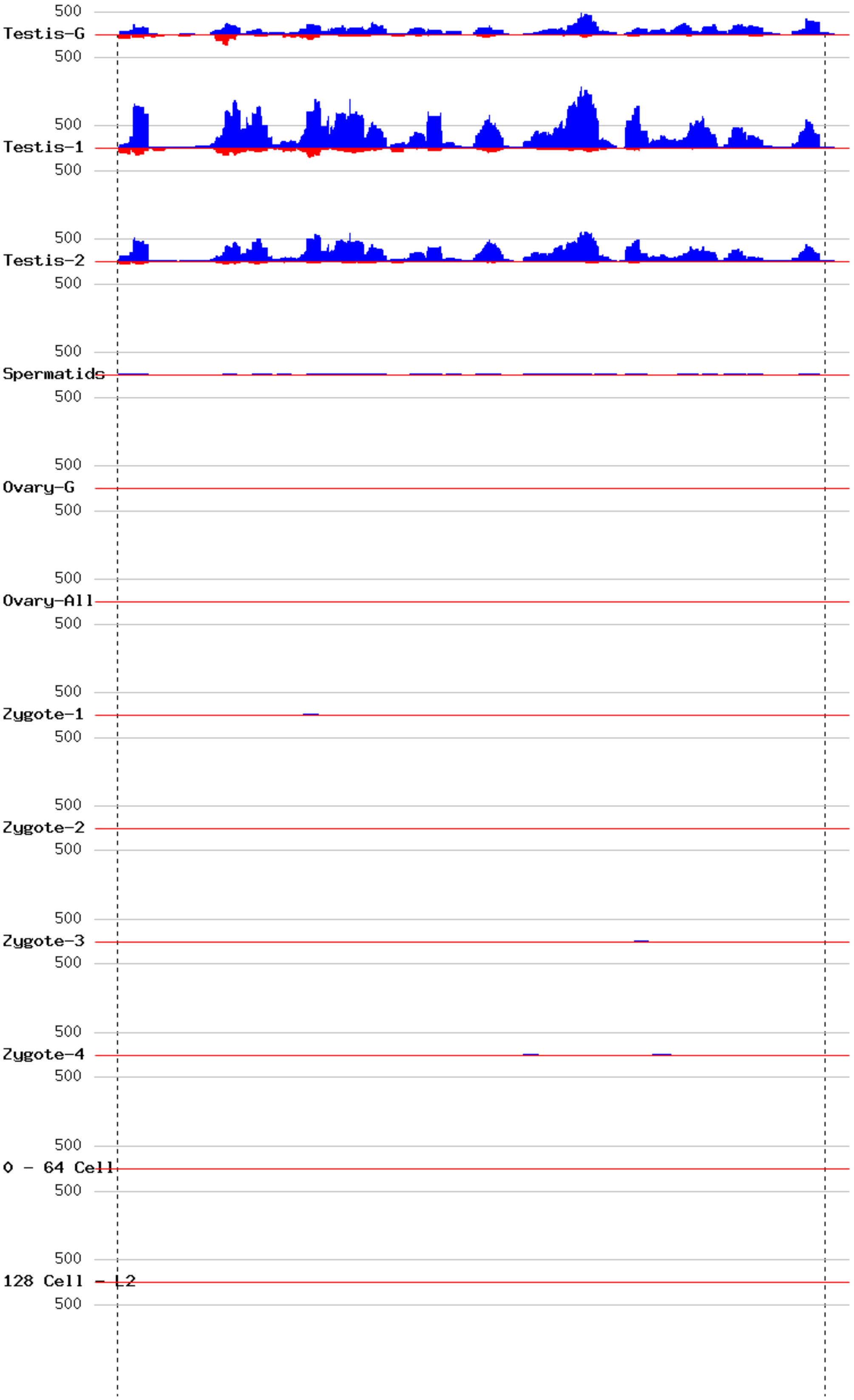
ASCF_6347_1360 Protein-tyrosine_phosphatase_containing_protein 1360 bp



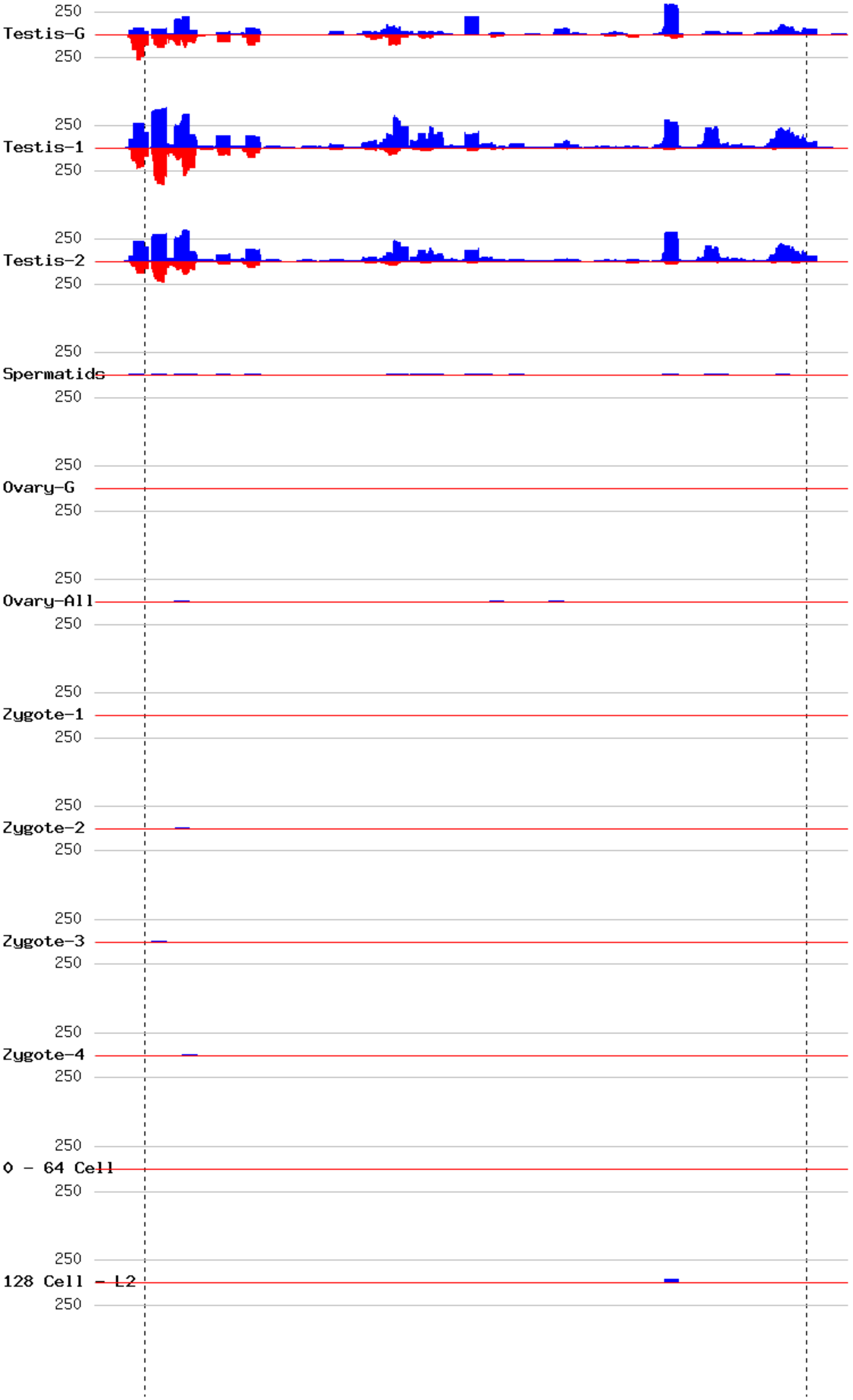
ASCF_6412_1343 Protein_kinase_domain_containing_protein 1343 bp



ASCF_6489_1330 Hypothetical_protein 1330 bp



ASCF_6501_1327 Serine/threonine-protein_phosphatase 1327 bp



ASCF_653_4338 Hypothetical_protein 4338 bp

500
Testis-G
500

500
Testis-1
500

500
Testis-2
500

500
Spermatids
500

500
Ovary-G
500

500
Ovary-All
500

500
Zygote-1
500

500
Zygote-2
500

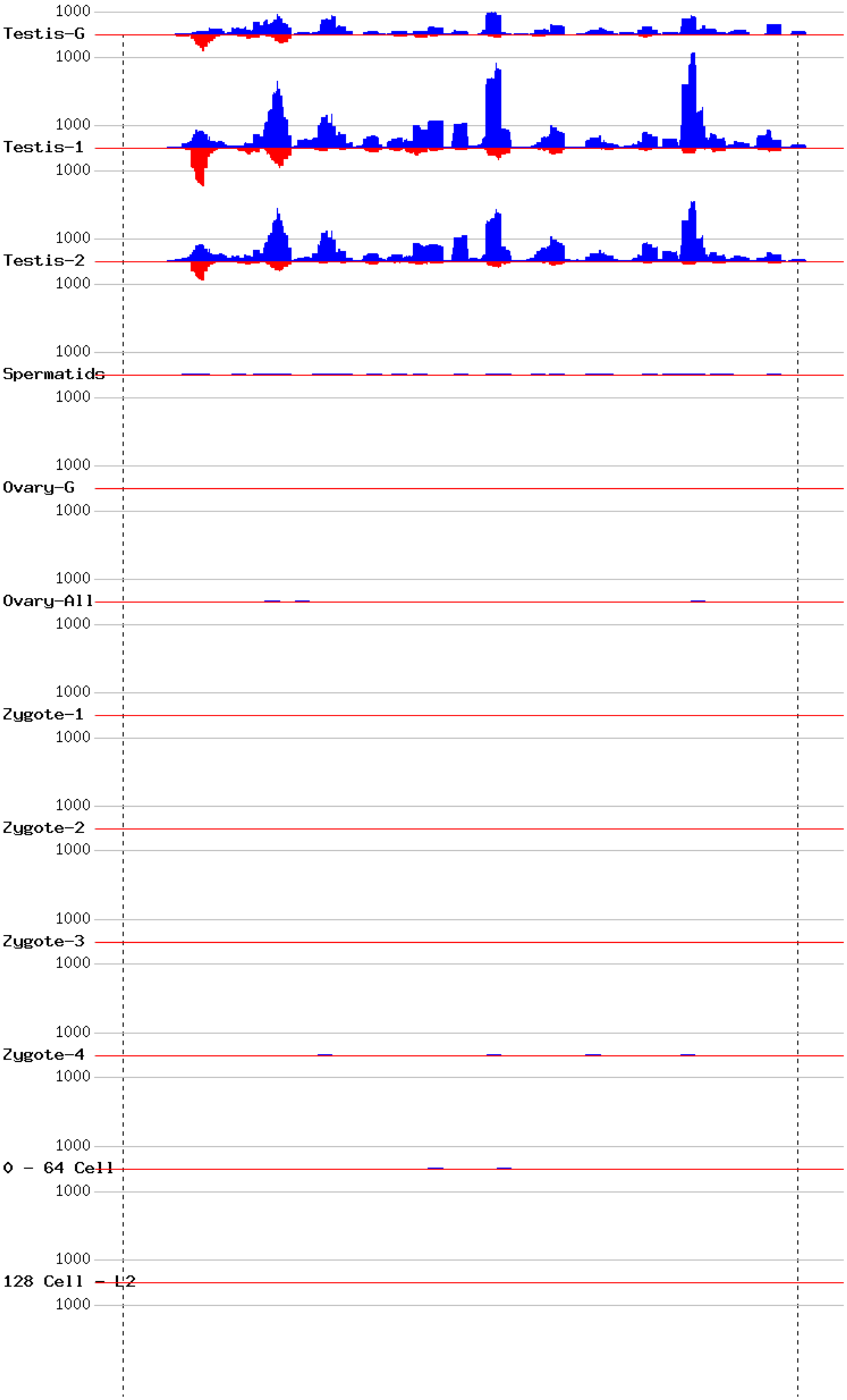
500
Zygote-3
500

500
Zygote-4
500

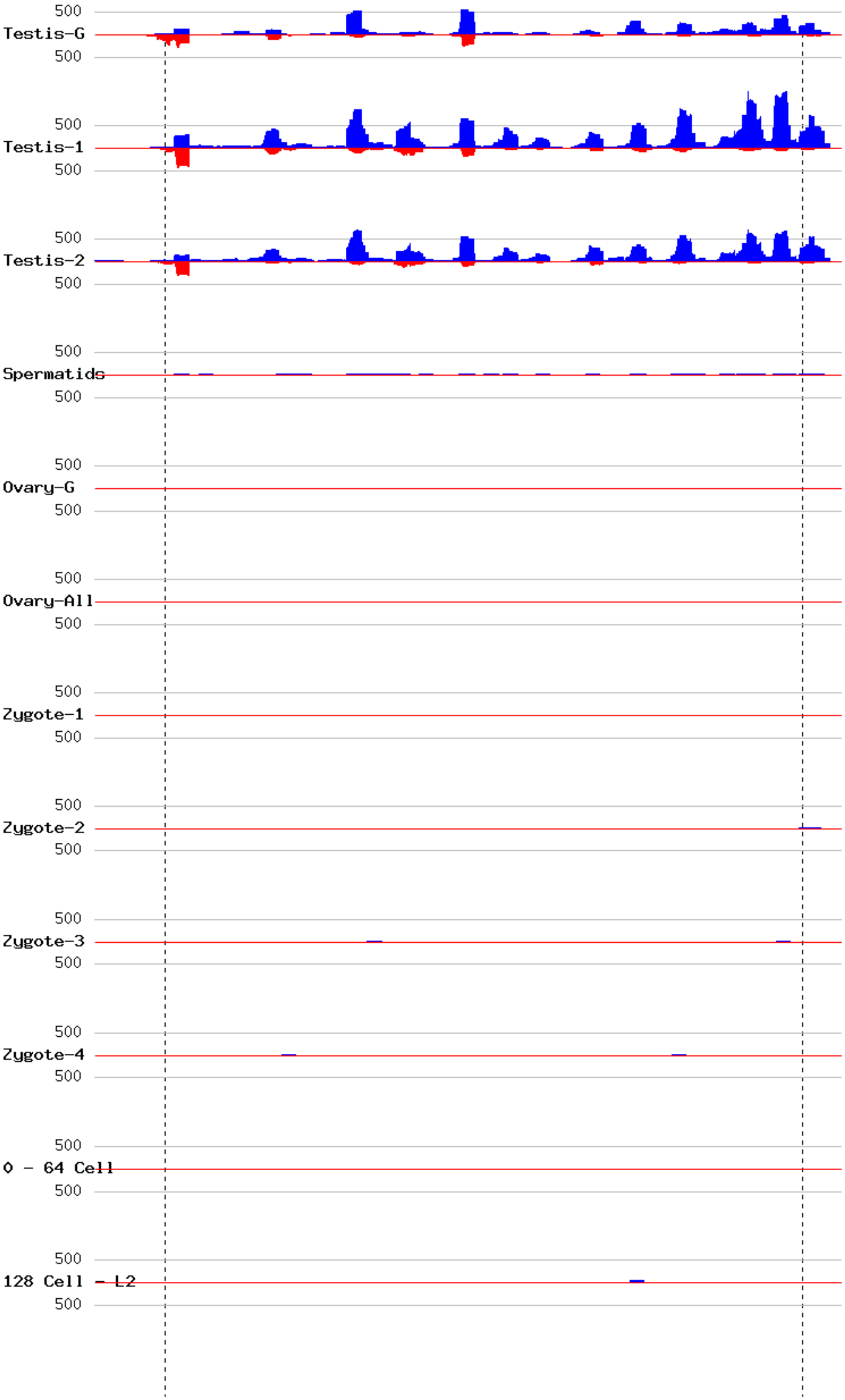
500
0 - 64 Cell
500

500
128 Cell - L2
500

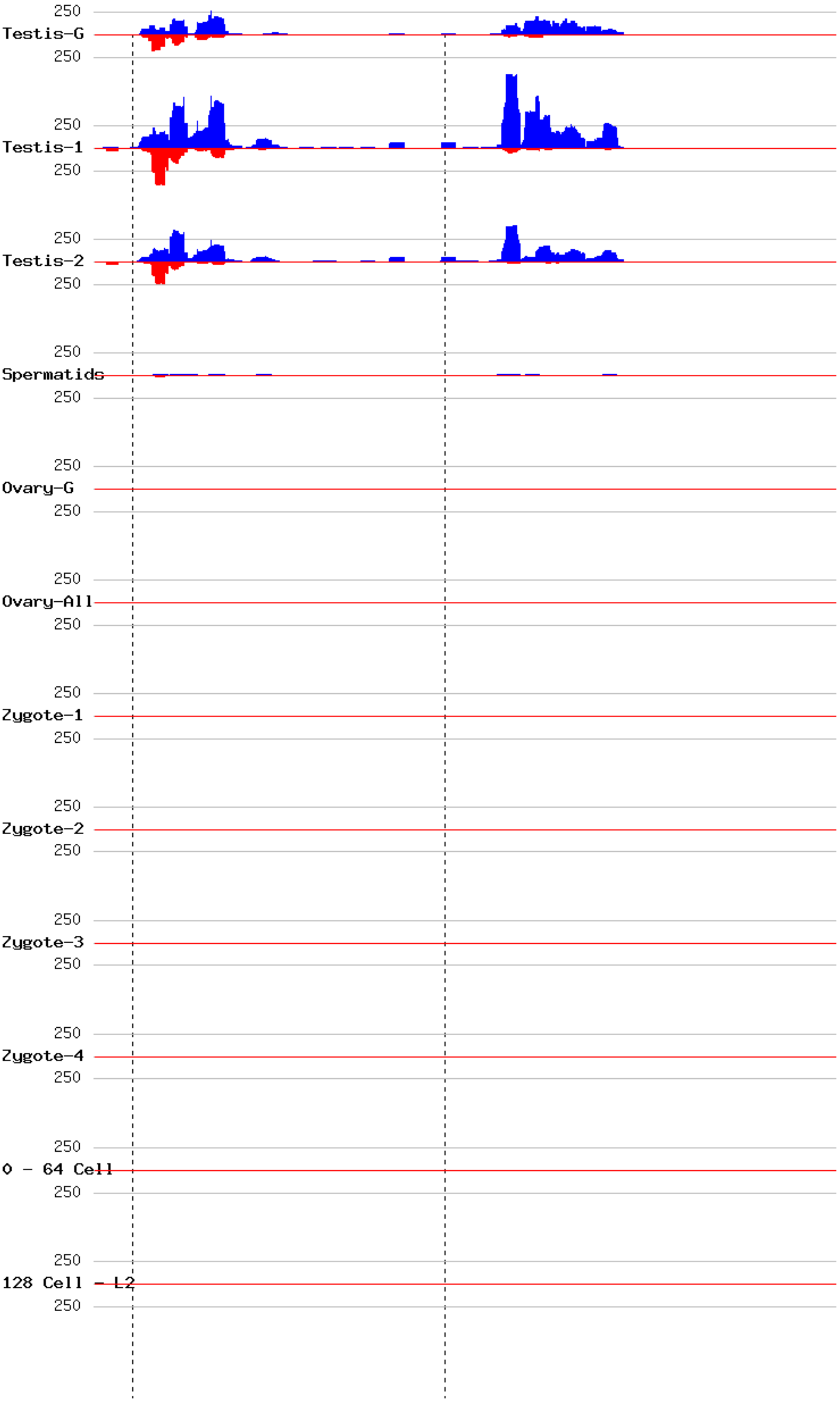
ASCF_6535_1321 MSP_fiber_protein_2b 1321 bp



ASCF_6551_1317 Protein-tyrosine_phosphatase_containing_protein 1317 bp



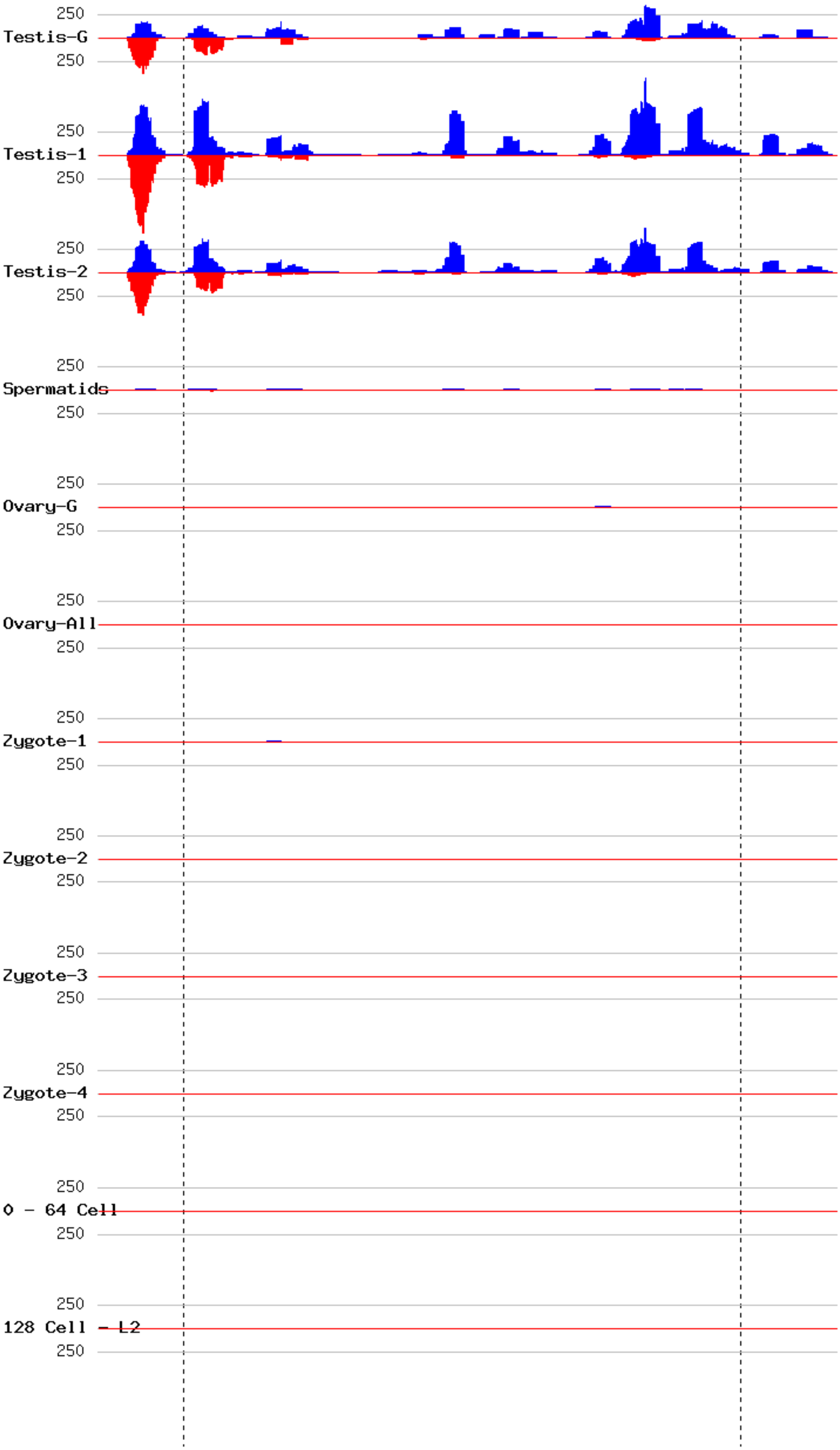
ASCF_6602_1307 Hypothetical_protein 1307 bp



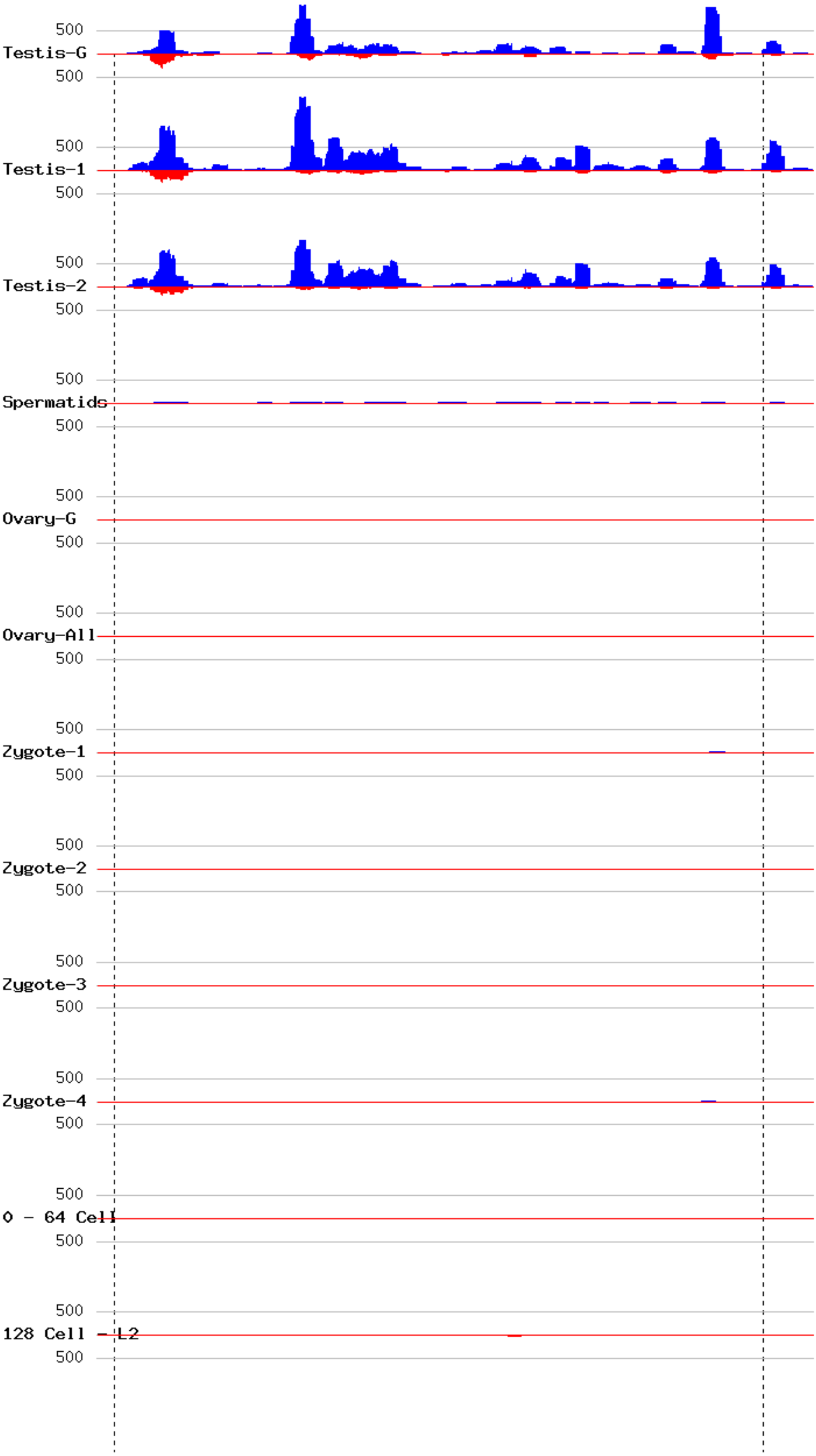
ASCF_6737_1277 Hypothetical_protein 1277 bp



ASCF_6816_1261 Protein_kinase_domain_containing_protein 1261 bp



ASCF_6942_1231 AN1-like_Zinc_finger_family_protein 1231 bp



ASCF_6950_1228 Major_sperm_protein 1228 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

250

ASCF_6975_1222 Serine/threonine-protein_phosphatase 1222 bp

250
Testis-G
250

250
Testis-1
250

250
Testis-2
250

250
Spermatids
250

250
Ovary-G
250

250
Ovary-All
250

250
Zygote-1
250

250
Zygote-2
250

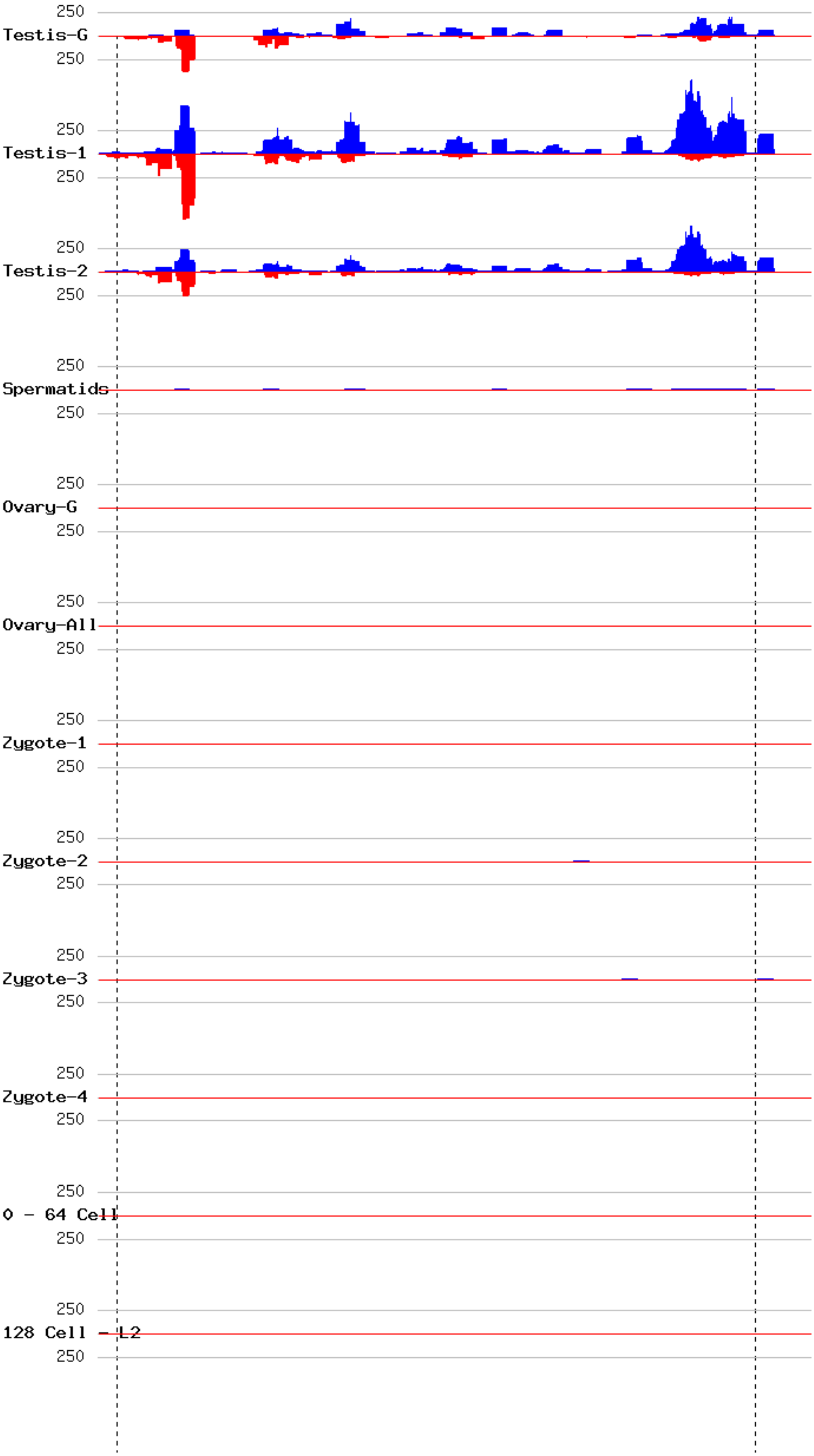
250
Zygote-3
250

250
Zygote-4
250

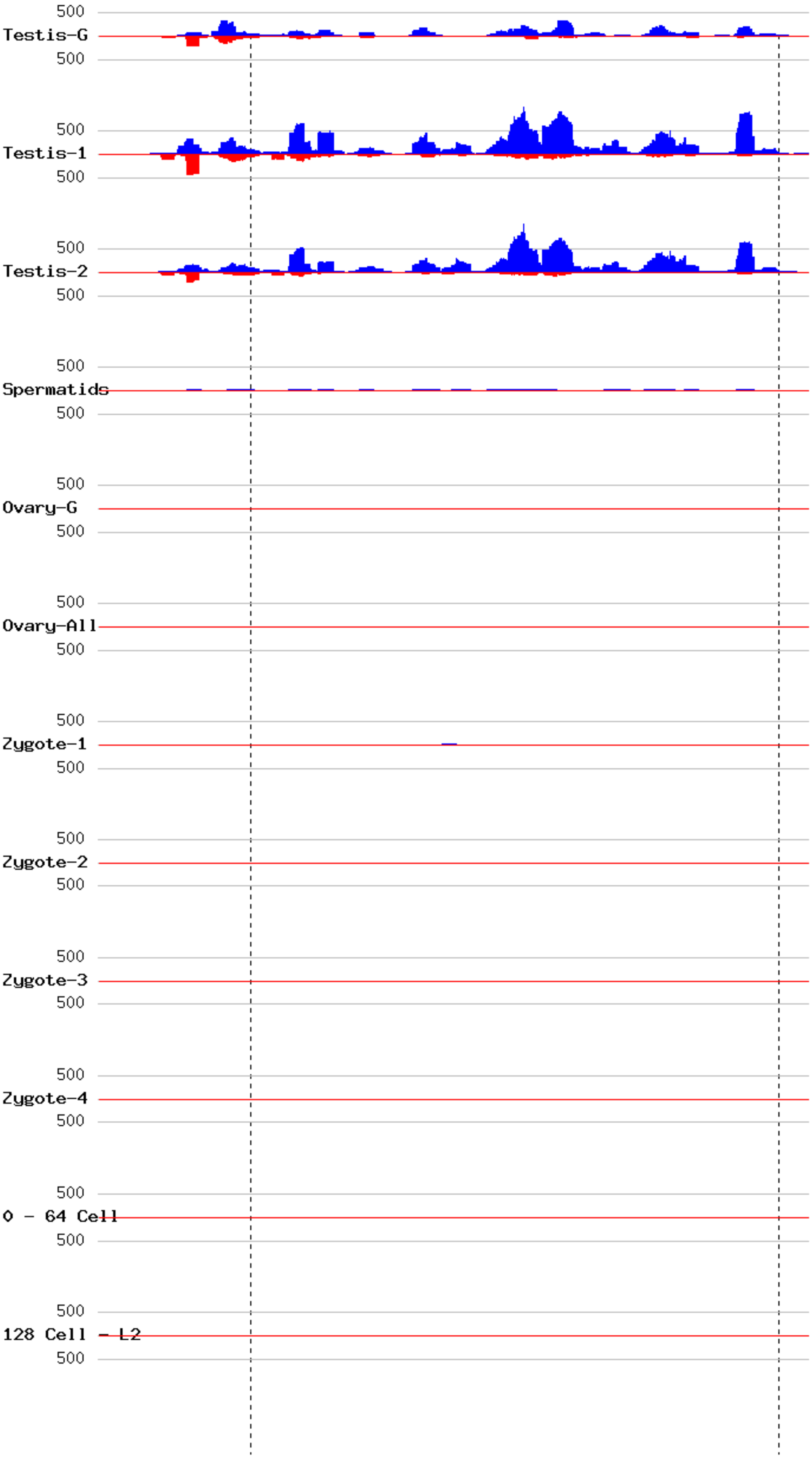
250
0 - 64 Cell
250

250
128 Cell - L2
250

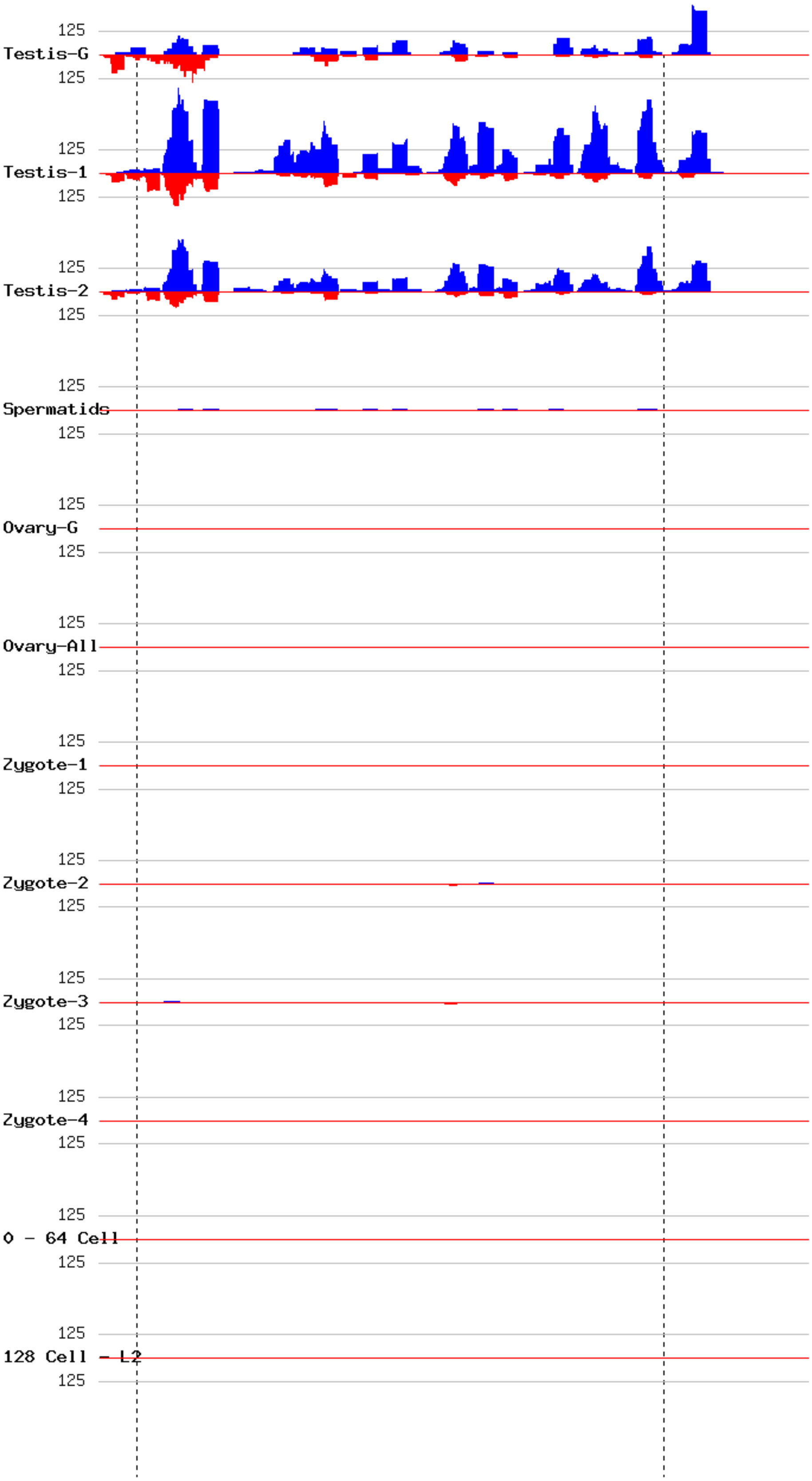
ASCF_7027_1208 Protein_kinase_domain_containing_protein 1208 bp



ASCF_7043_1203 Major_sperm_protein 1203 bp



ASCF_7061_1199 Hypothetical_protein 1199 bp



ASCF_7156_1178 Protein_kinase_domain_containing_protein 1178 bp

250
Testis-G
250

250
Testis-1
250

250
Testis-2
250

250
Spermatids
250

250
Ovary-G
250

250
Ovary-All
250

250
Zygote-1
250

250
Zygote-2
250

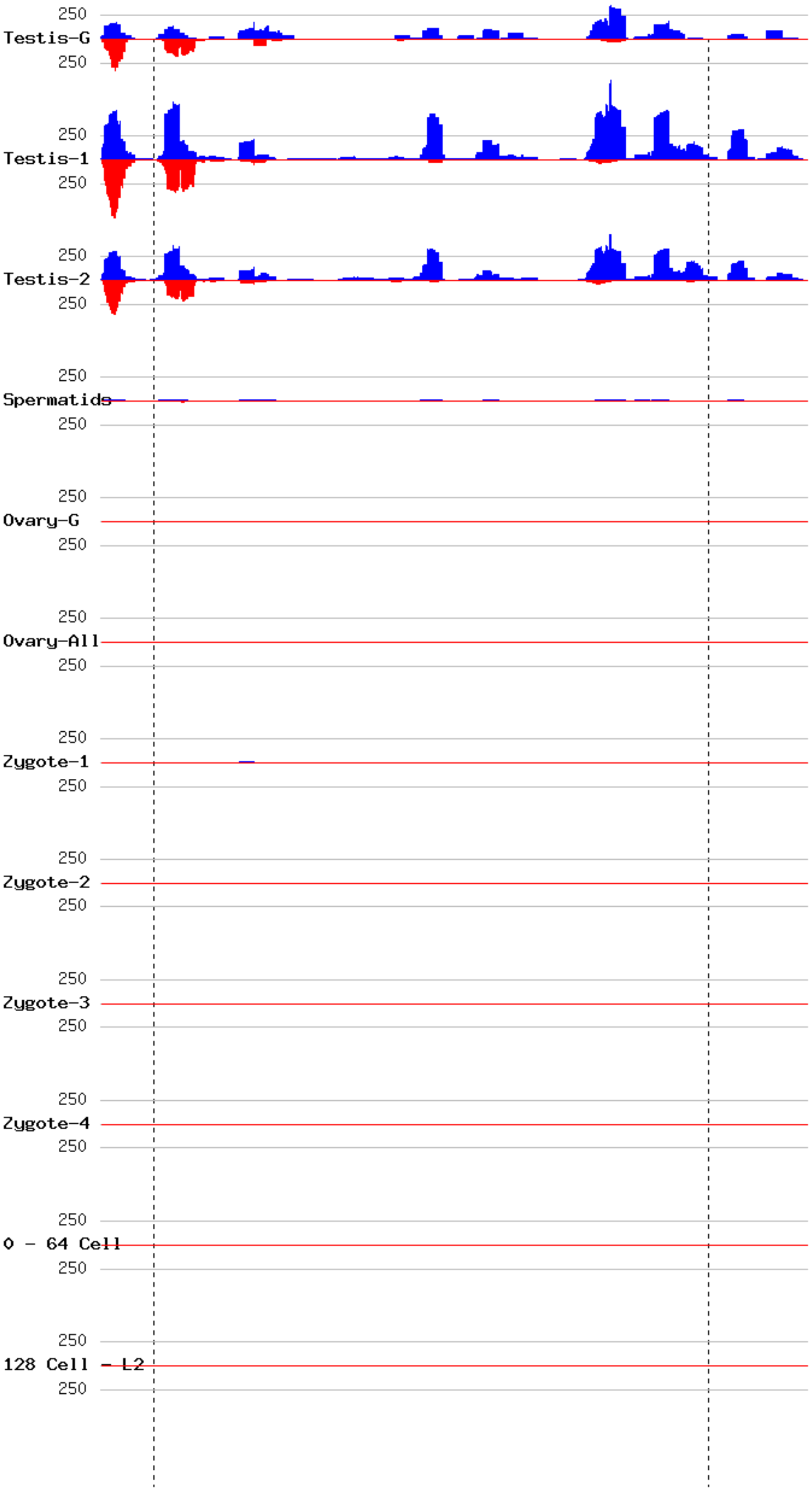
250
Zygote-3
250

250
Zygote-4
250

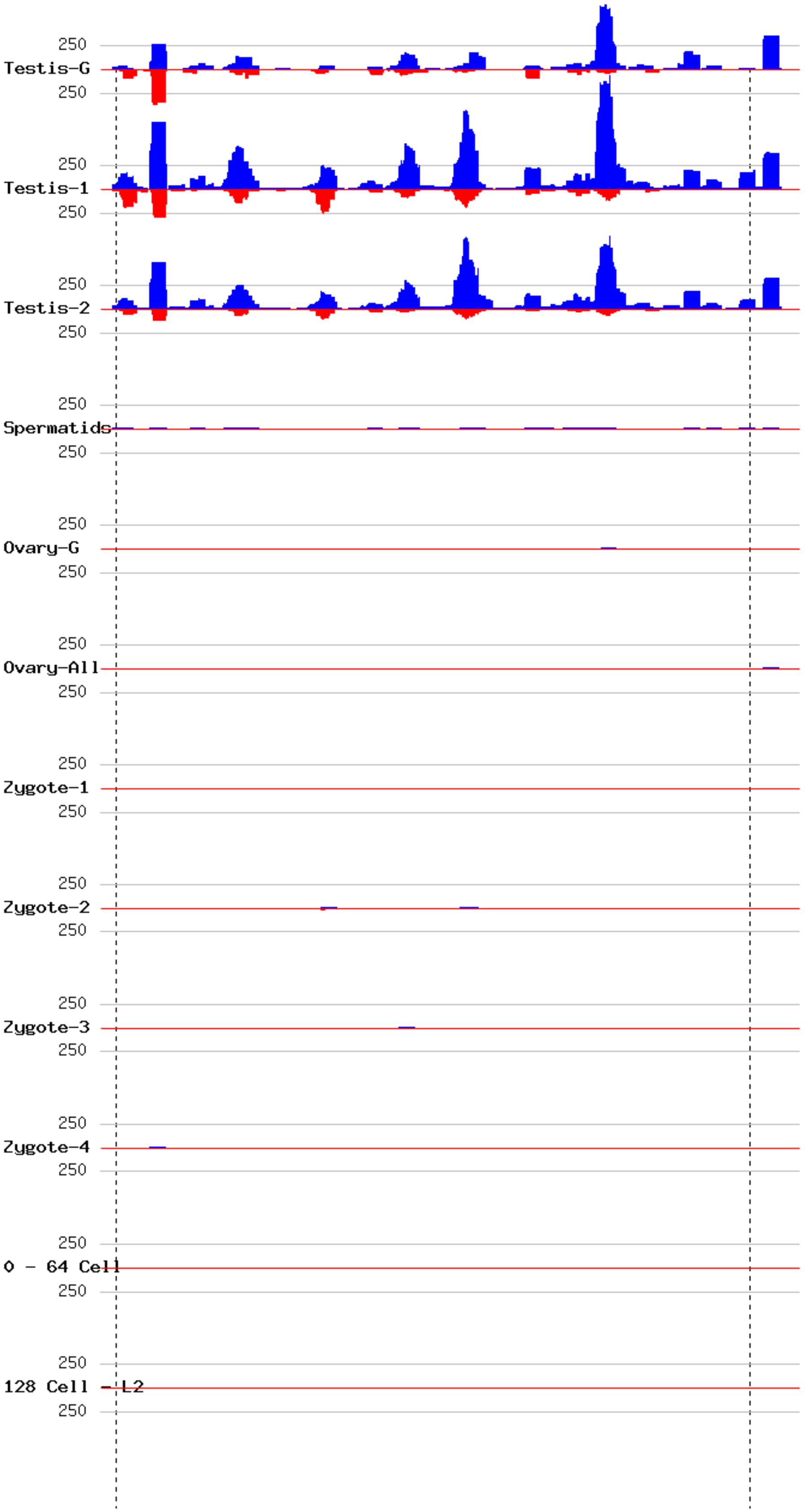
250
0 - 64 Cell
250

250
128 Cell - L2
250

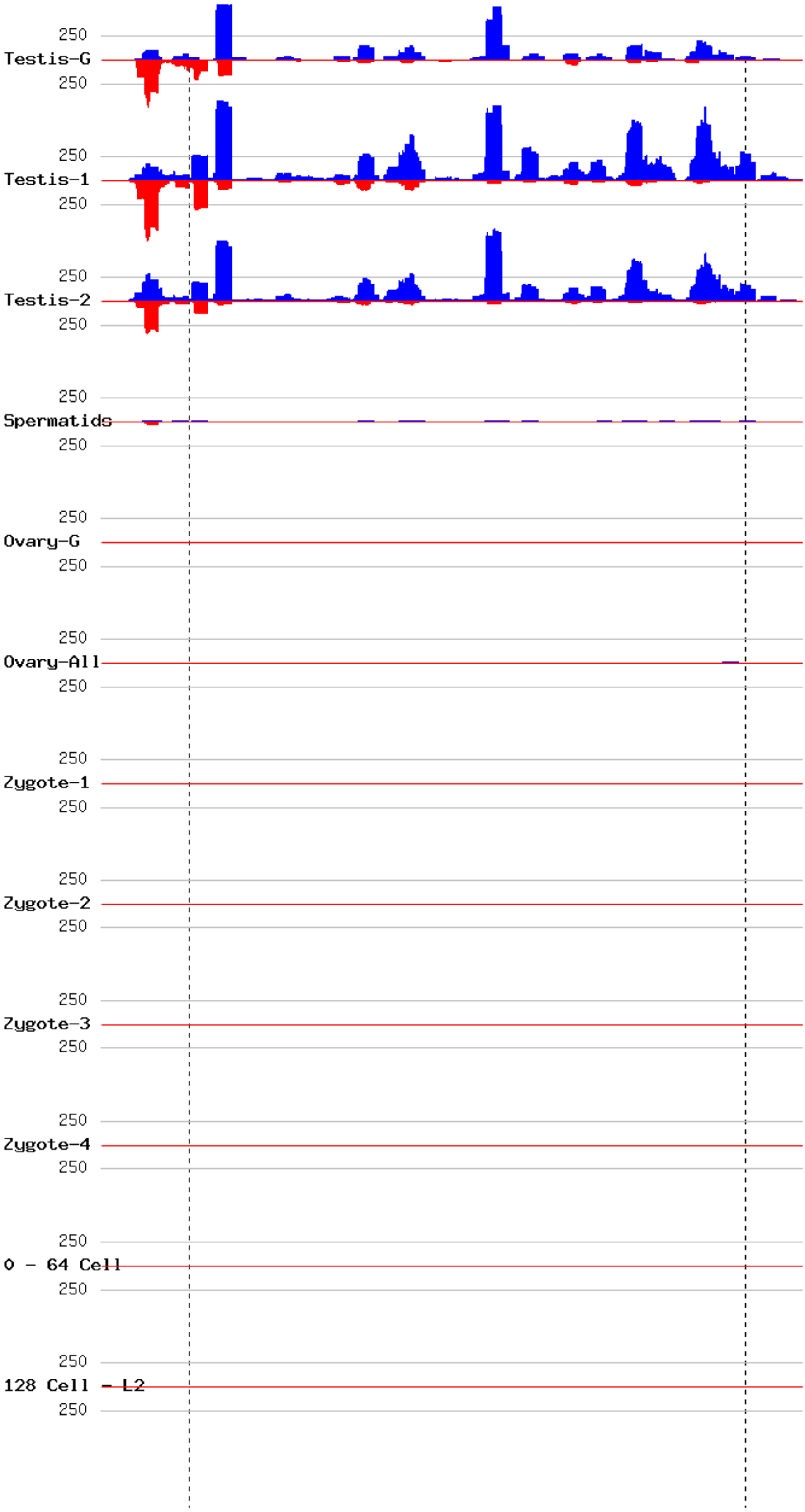
ASCF_7185_1173 Protein_kinase_domain_containing_protein 1173 bp



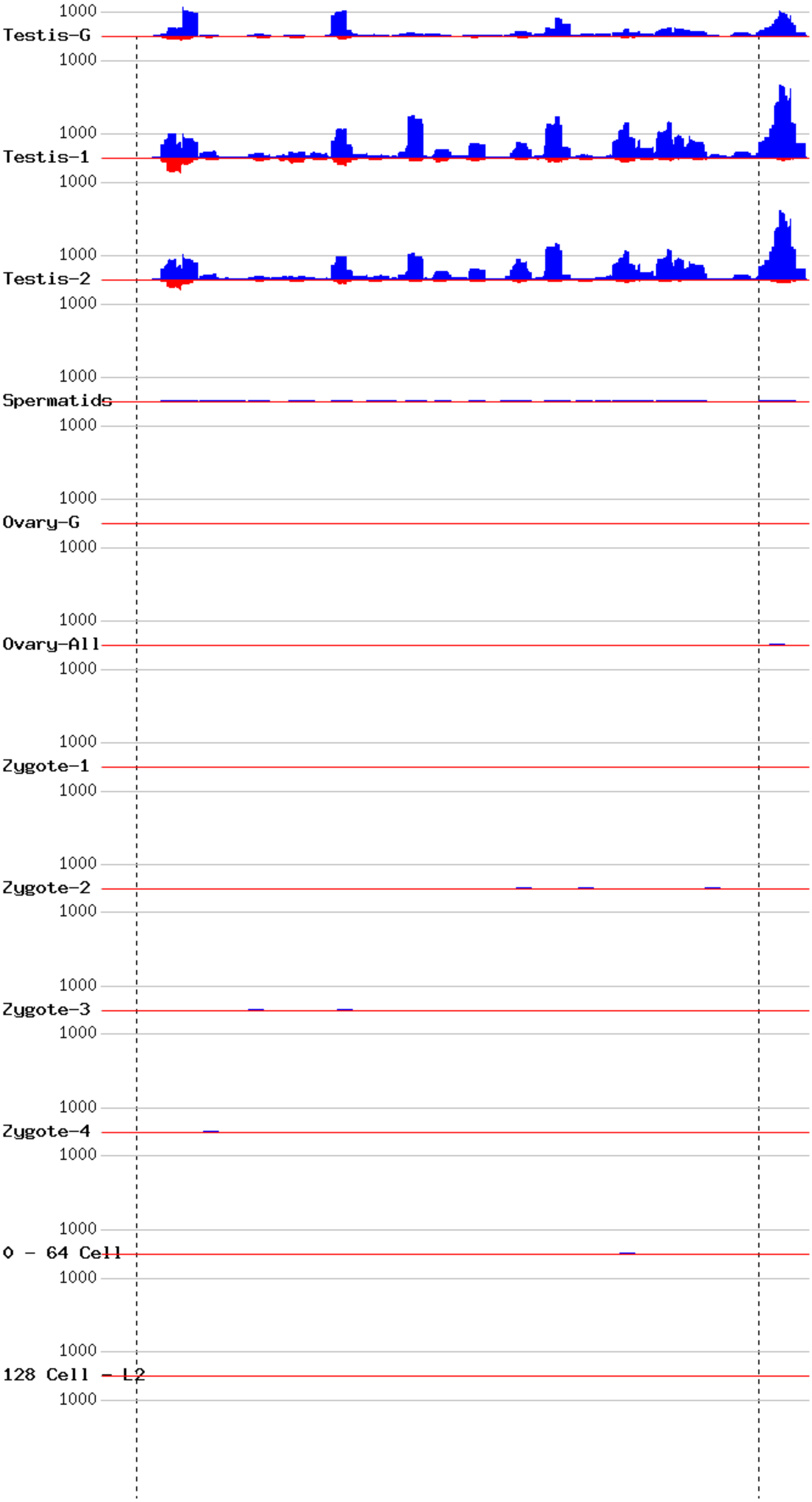
ASCF_7206_1167 Protein_kinase_domain_containing_protein 1167 bp



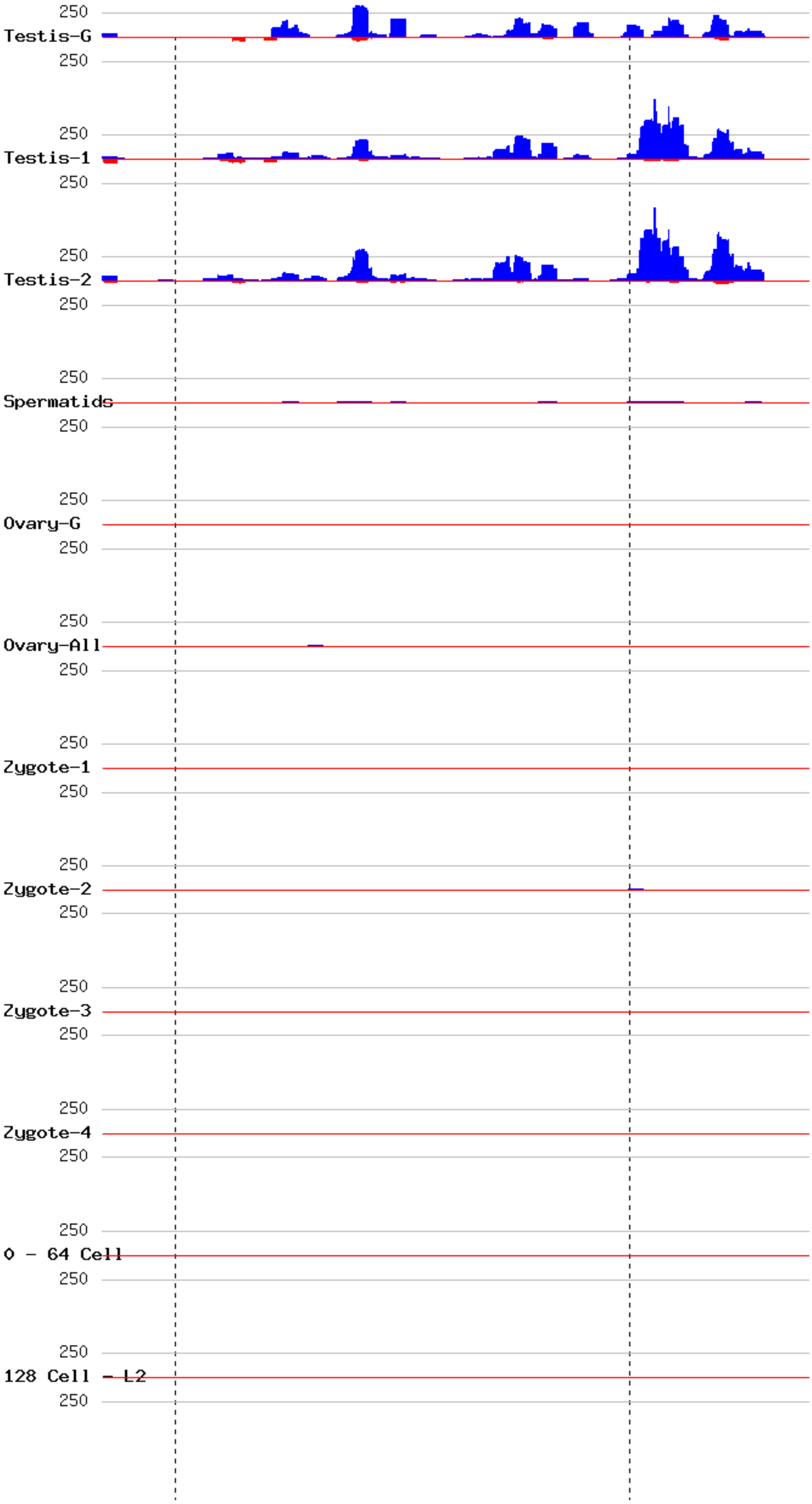
ASCF_7223_1163 Hypothetical_protein 1163 bp



ASCF_7229_1162 Protein-tyrosine_phosphatase_containing_protein 1162 bp



ASCF_7232_1161 Hypothetical_protein 1161 bp



ASCF_7287_1150 Major_sperm_protein 1150 bp

125
Testis-G
125

125
Testis-1
125

125
Testis-2
125

125
Spermatids
125

125
Ovary-G
125

125
Ovary-All
125

125
Zygote-1
125

125
Zygote-2
125

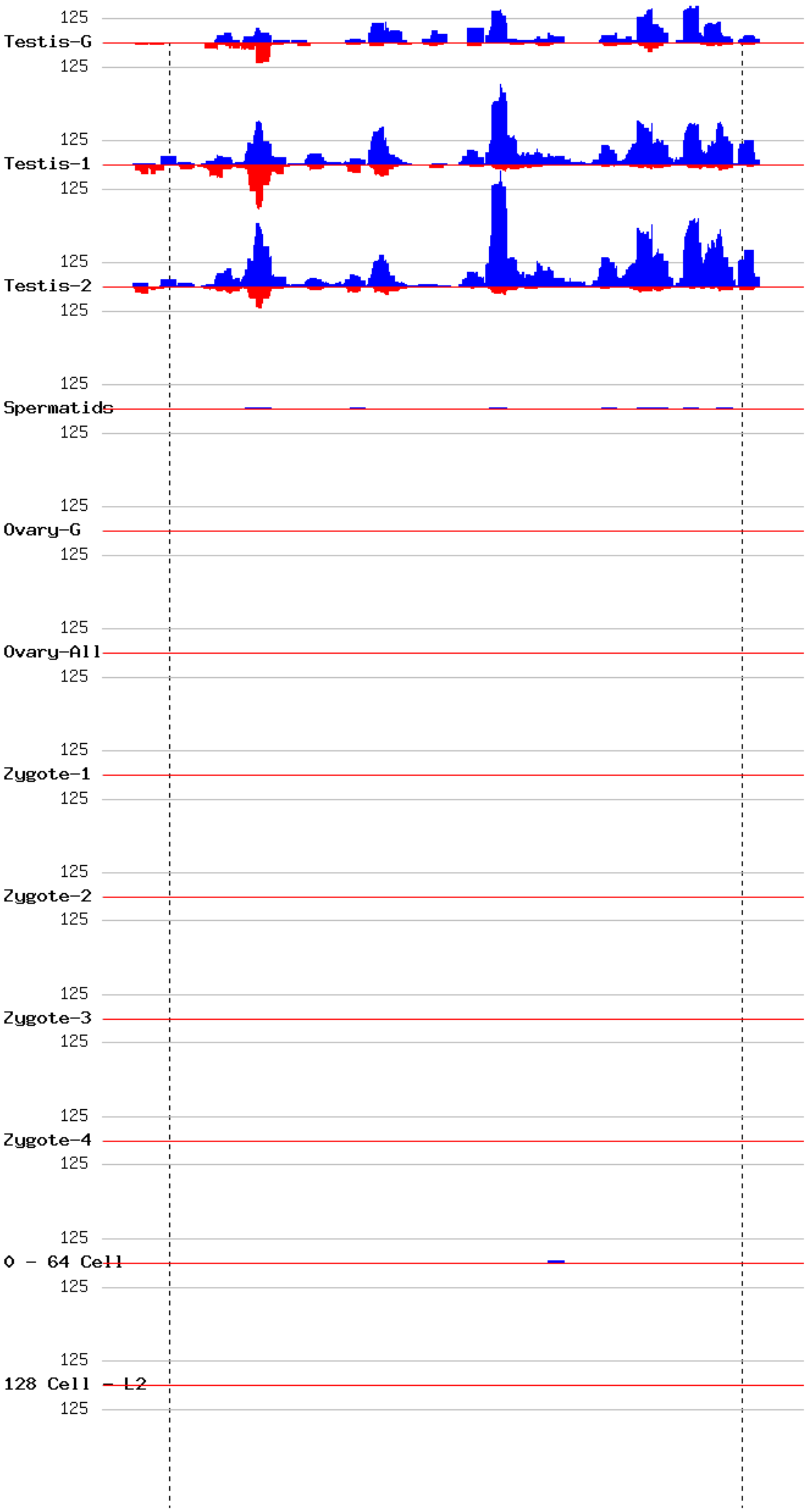
125
Zygote-3
125

125
Zygote-4
125

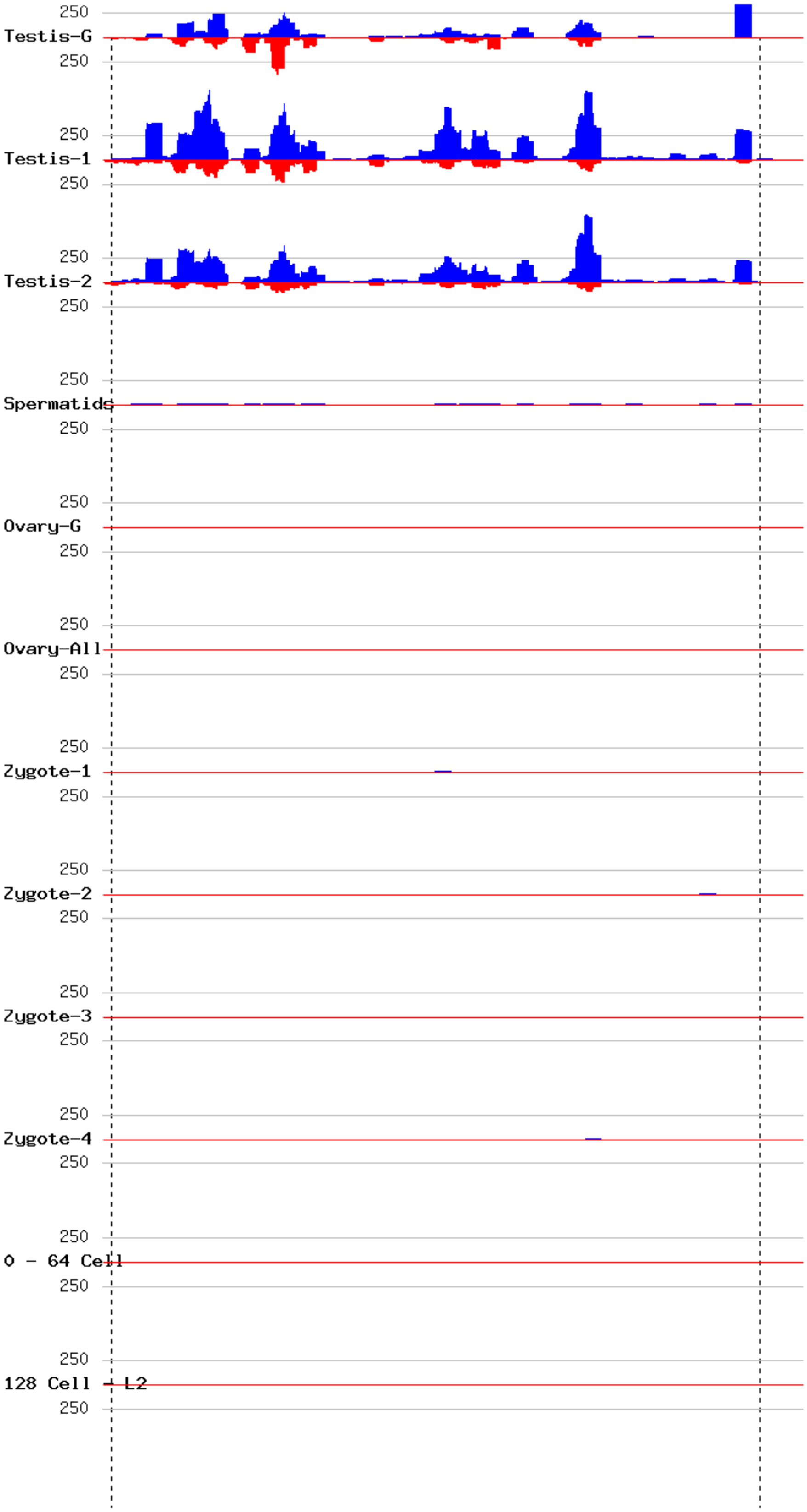
125
0 - 64 Cell
125

125
128 Cell - L2
125

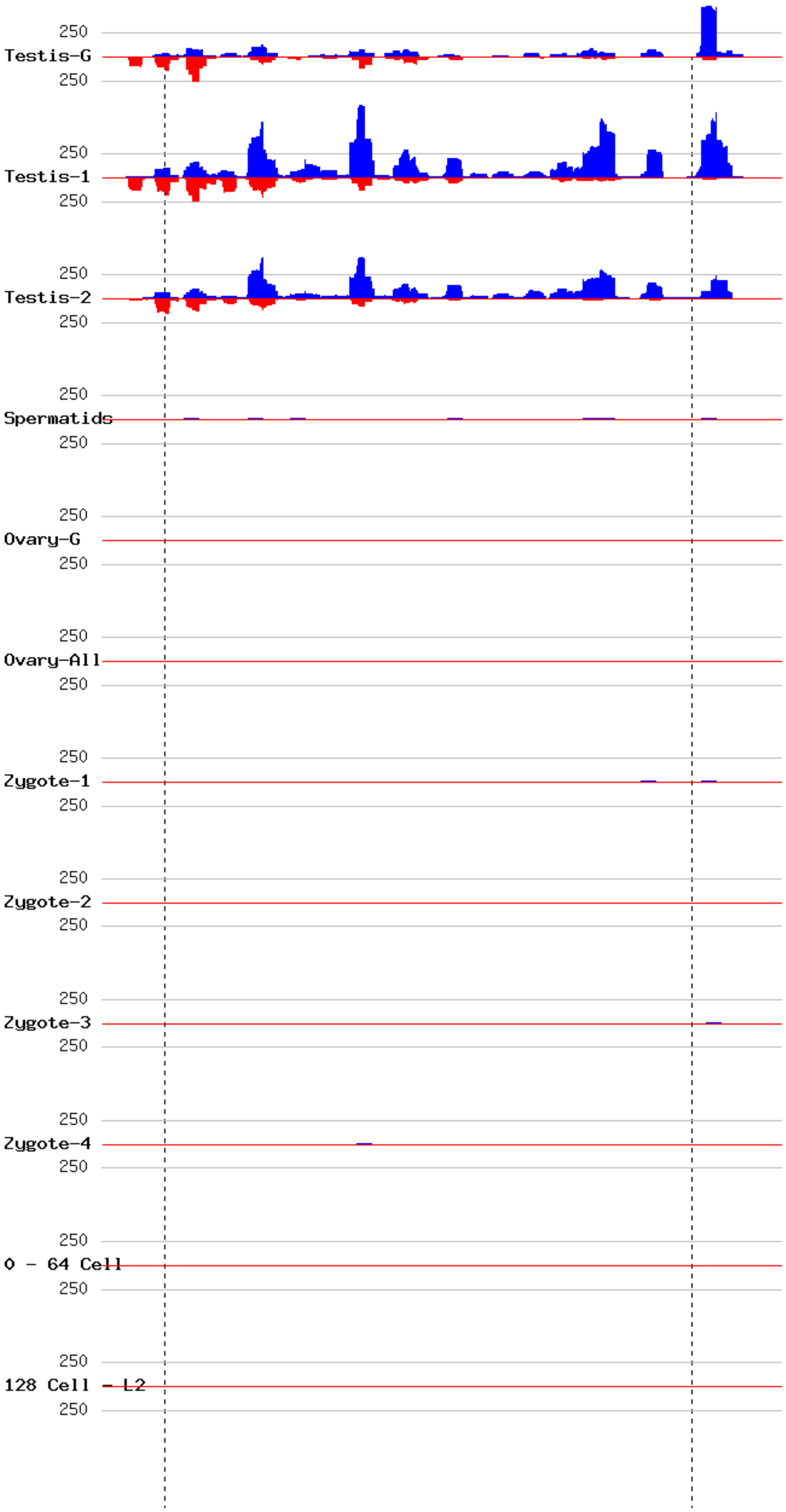
ASCF_7288_1149 Serine/threonine-protein_phosphatase 1149 bp



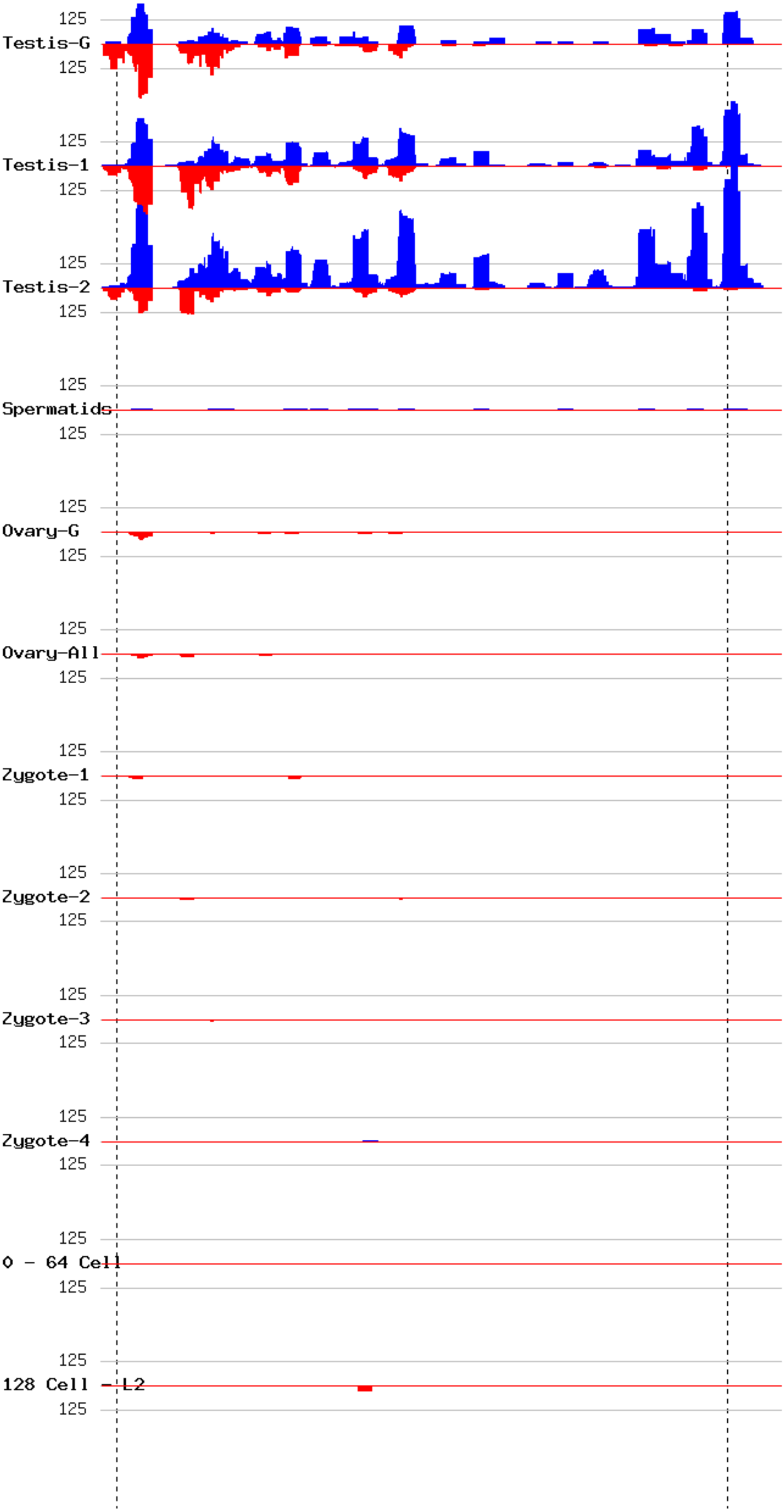
ASCF_7314_1142 Protein-tyrosine_phosphatase_containing_protein 1142 bp



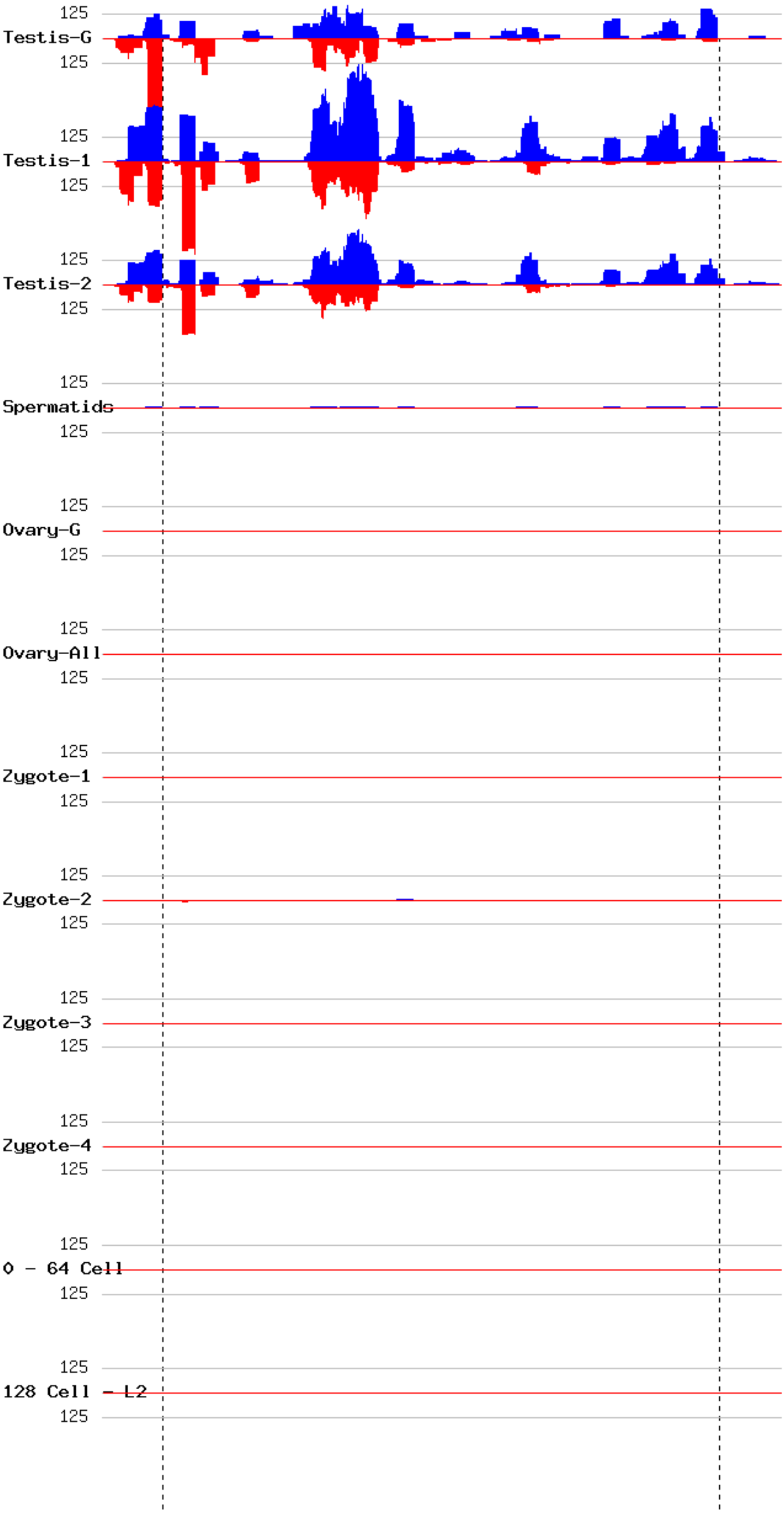
ASCF_7401_1124 Hypothetical_protein 1124 bp



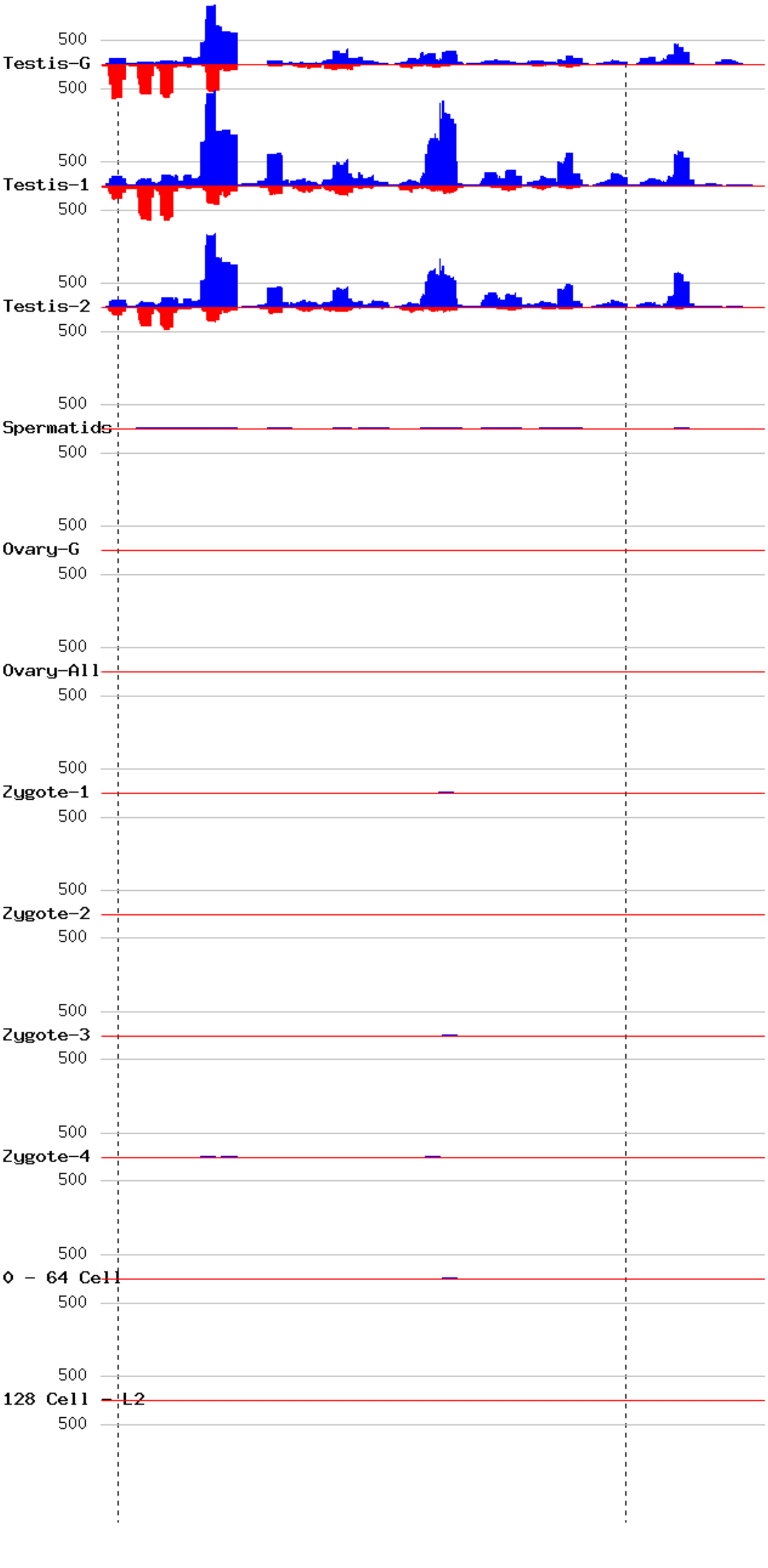
ASCF_7446_1116 Serine/threonine_protein_phosphatase 1116 bp



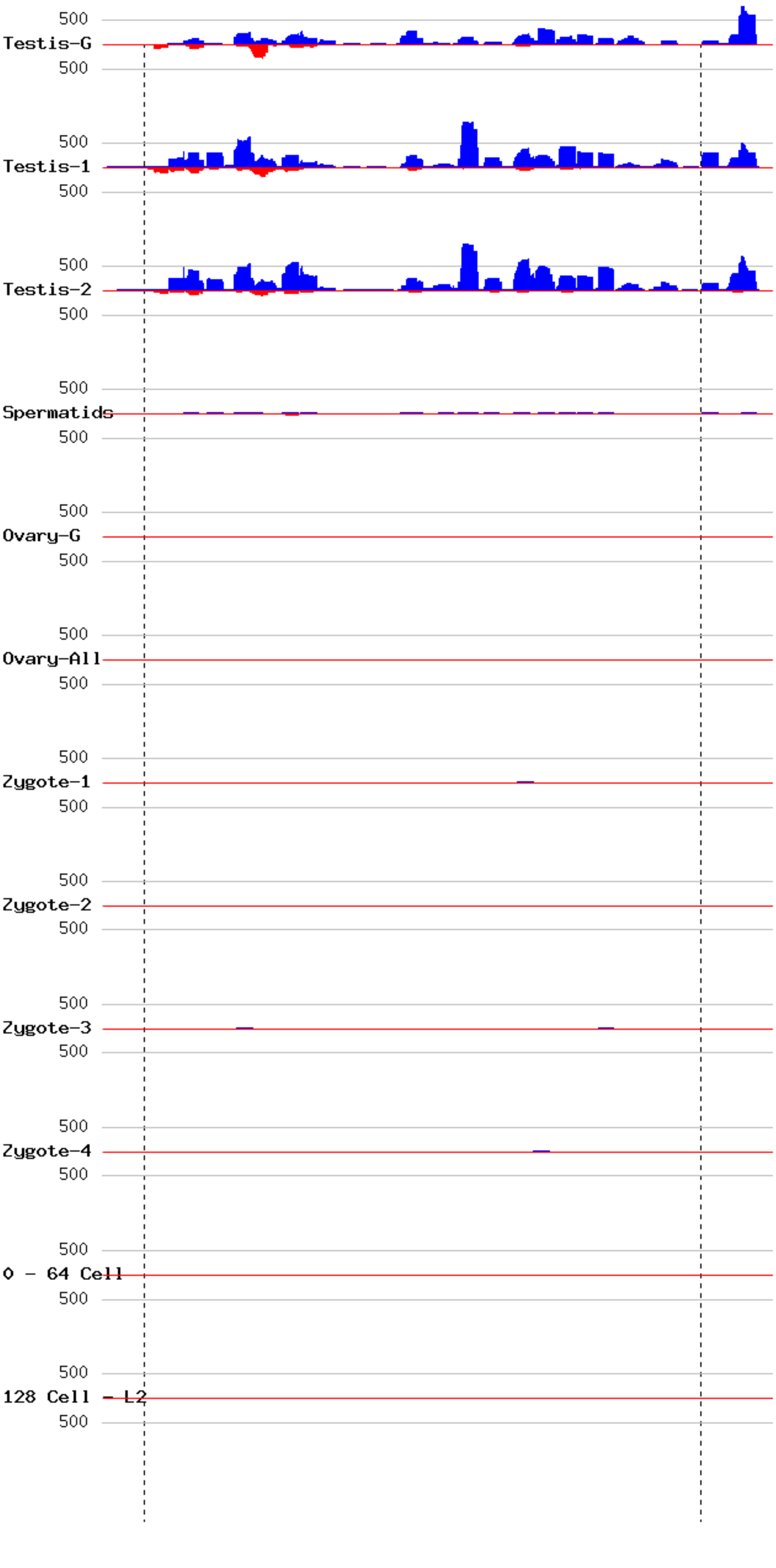
ASCF_7515_1102 Adenylate_kinase_isoenzyme_1 1102 bp



ASCF_7559_1093 Hypothetical_protein 1093 bp



ASCF_7581_1088 PDZ_domain_containing_protein 1088 bp

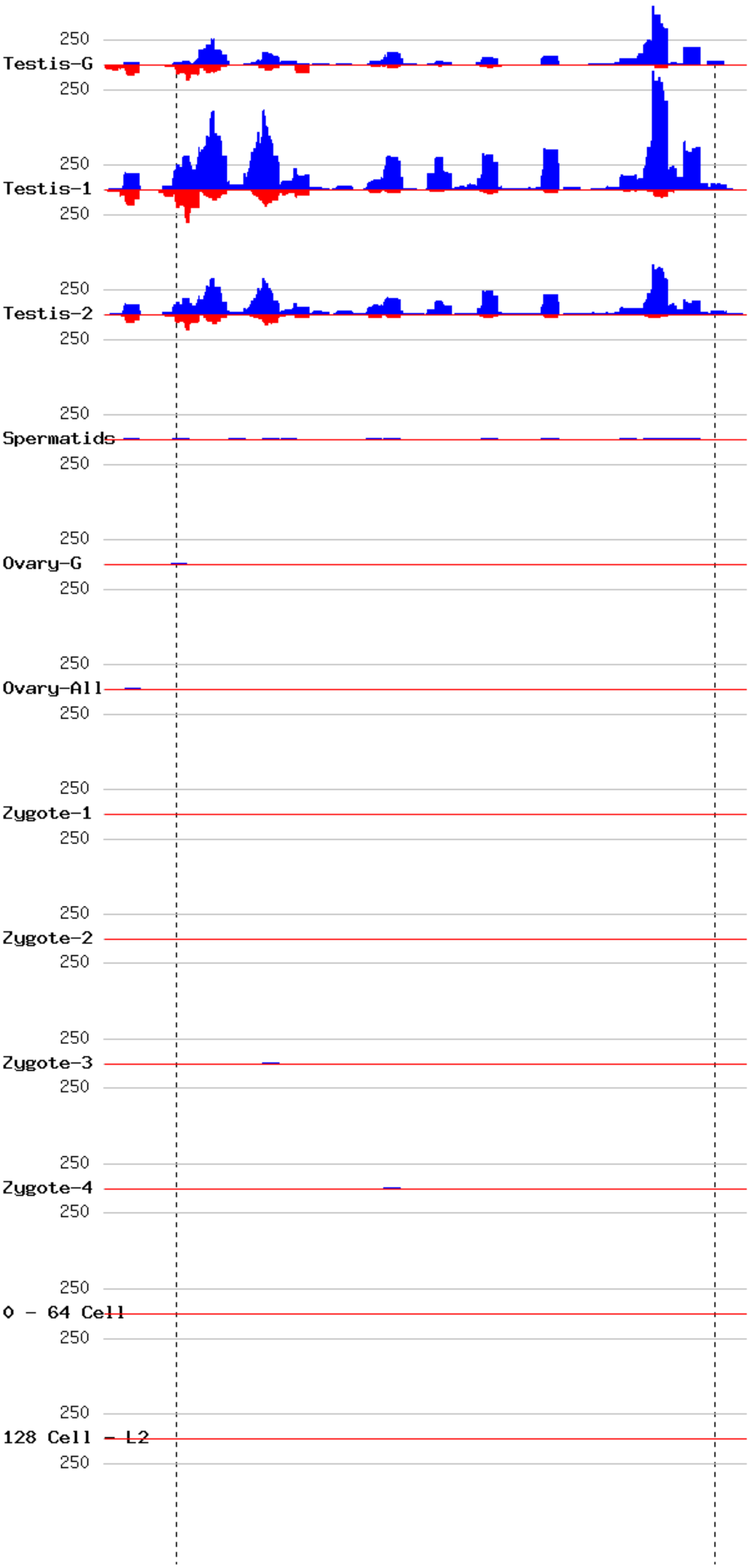


ASCF_7819_1033 Hypothetical_protein 1033 bp

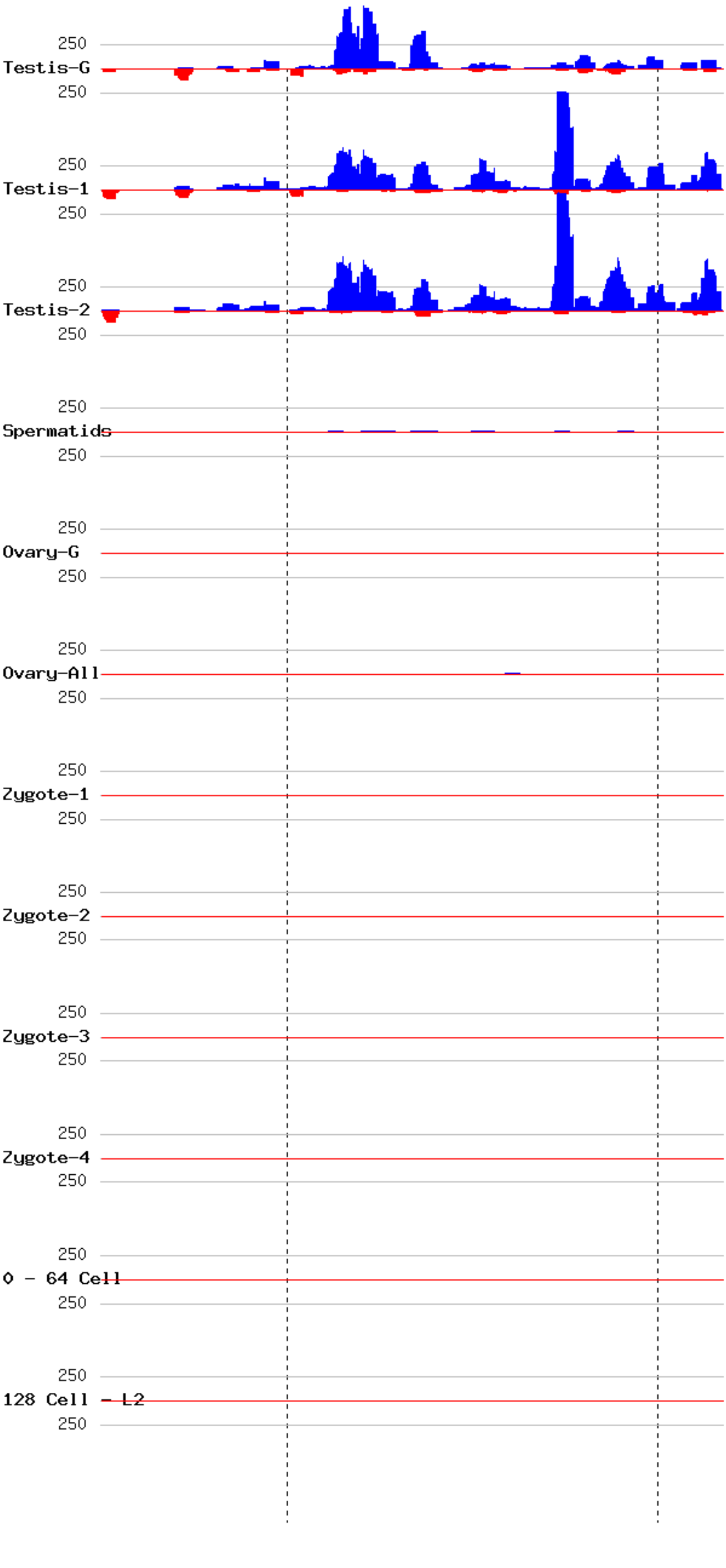
Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

500

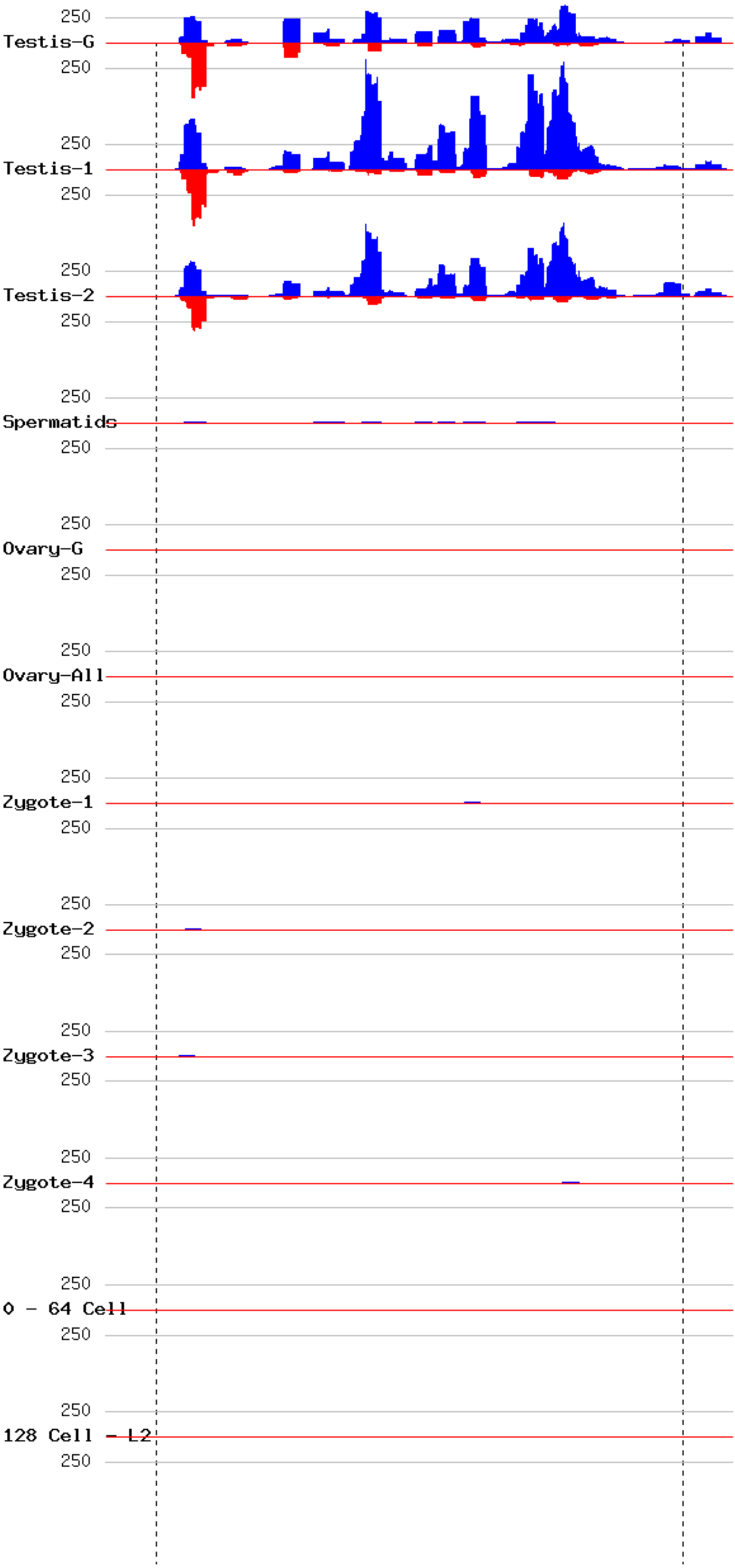
ASCF_7827_1029 Protein-tyrosine_phosphatase_containing_protein 1029 bp



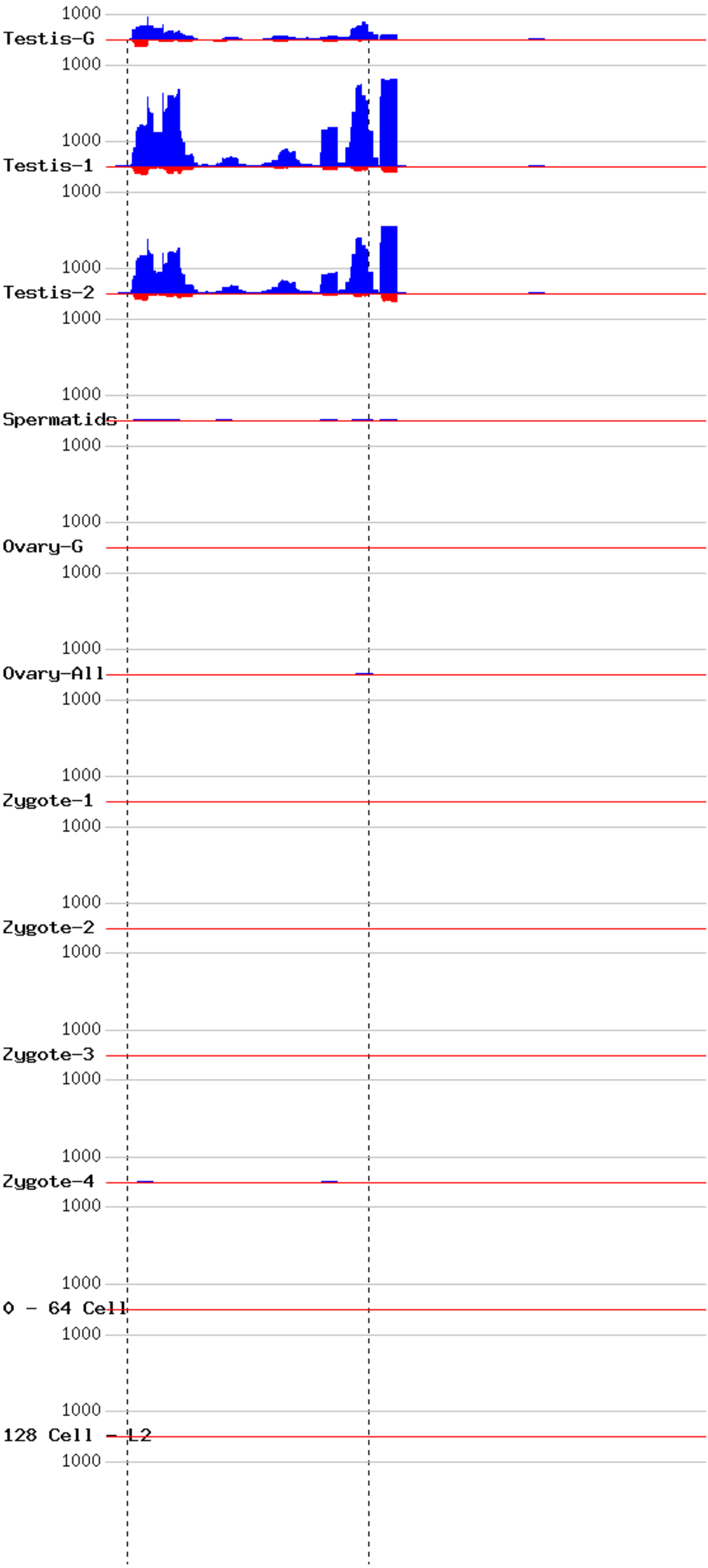
ASCF_7829_1029 Tau-tubulin_kinase 1029 bp



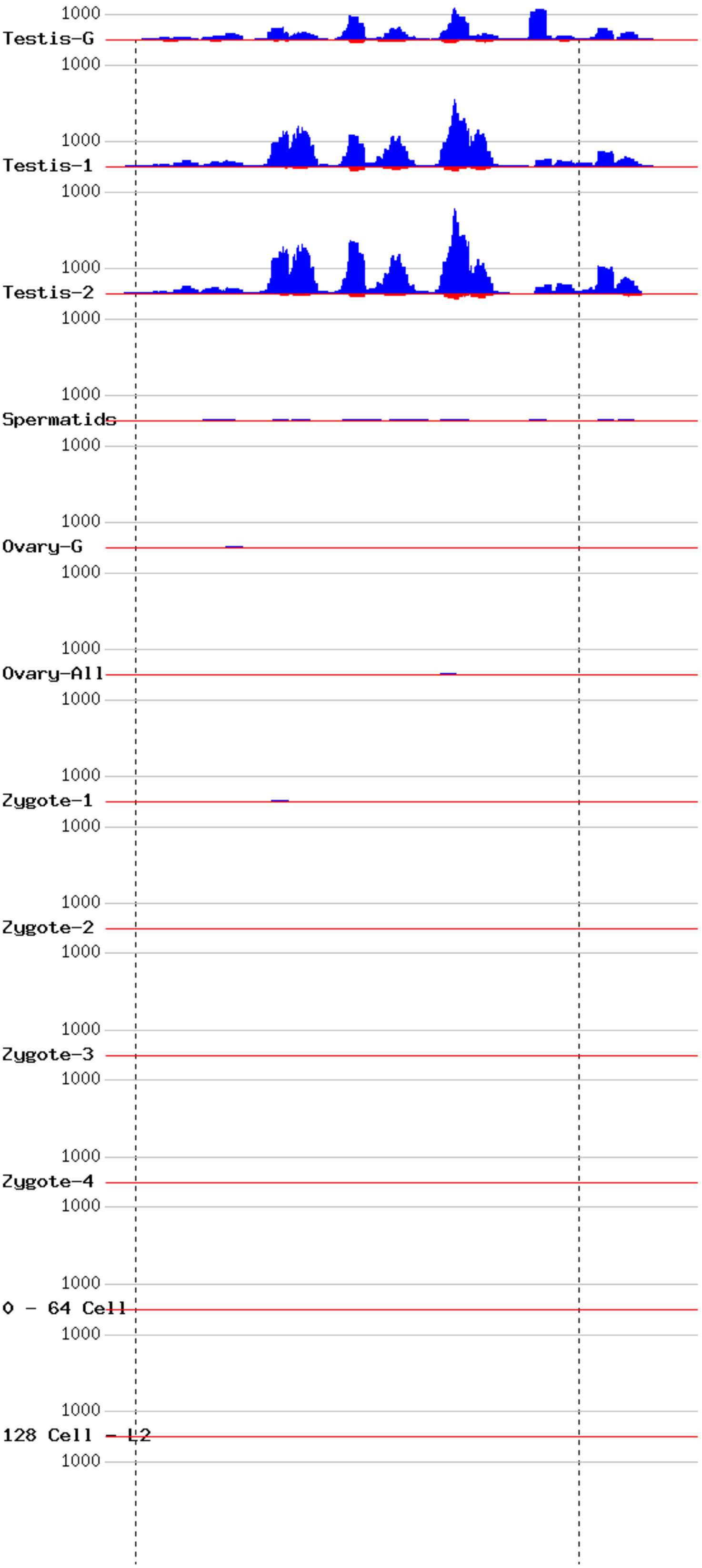
ASCF_8005_989 Major_sperm_protein 989 bp



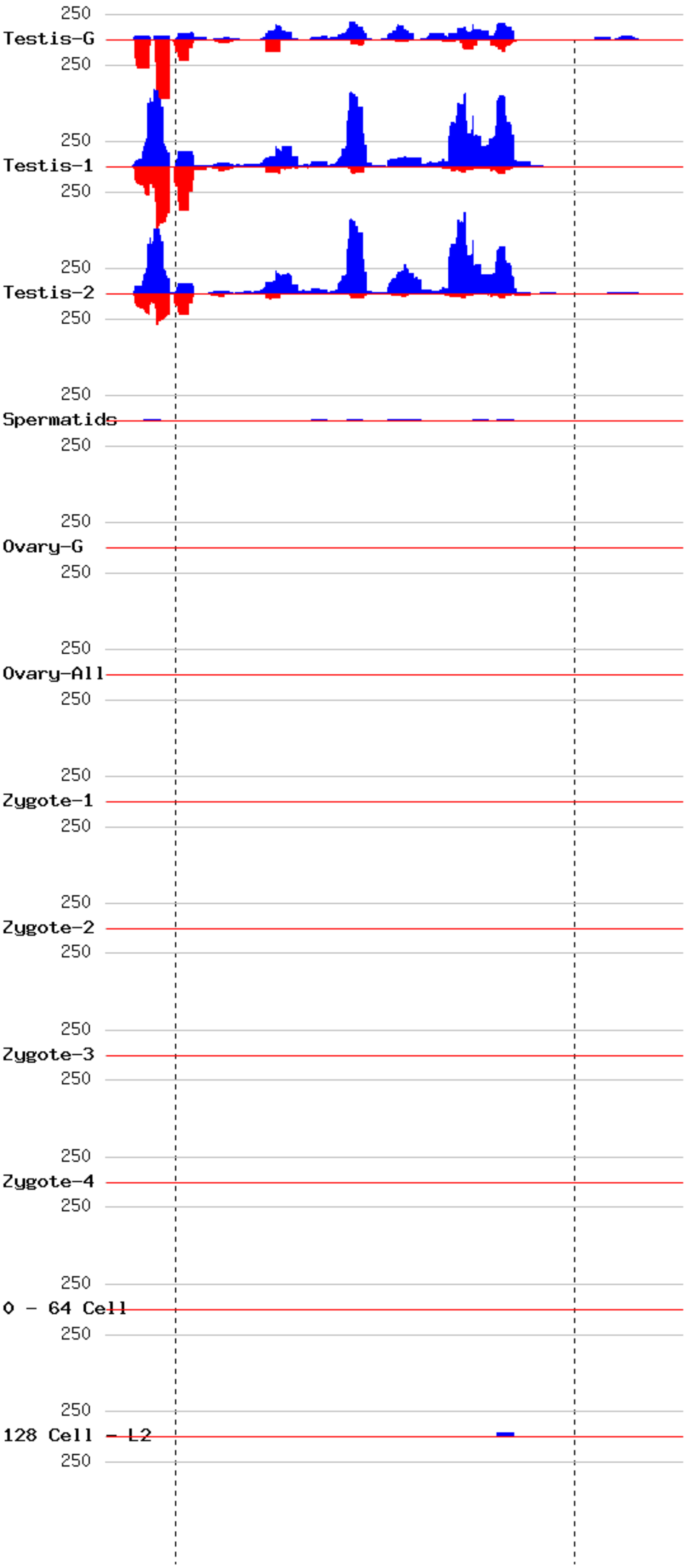
ASCF_8123_945 MSP_fiber_protein_alpha 945 bp



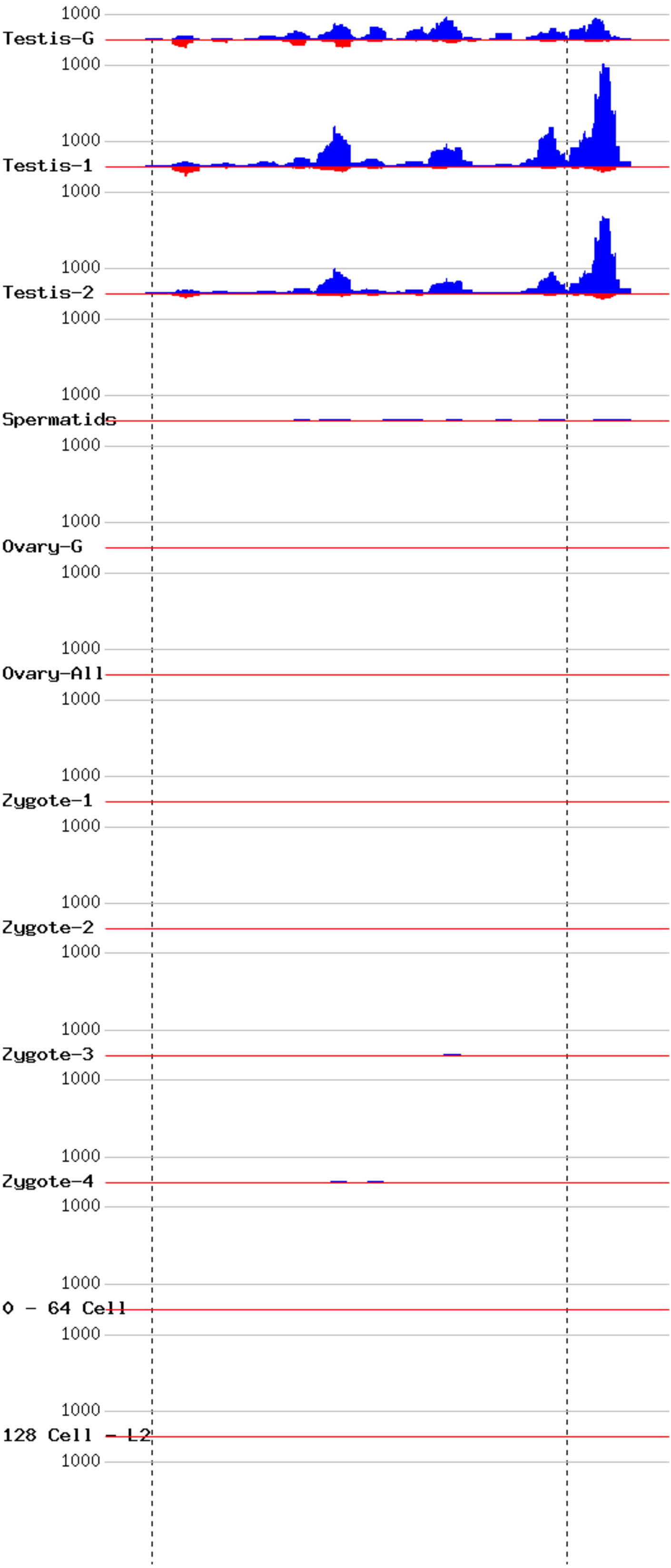
ASCF_8161_933 Hypothetical_protein 933 bp



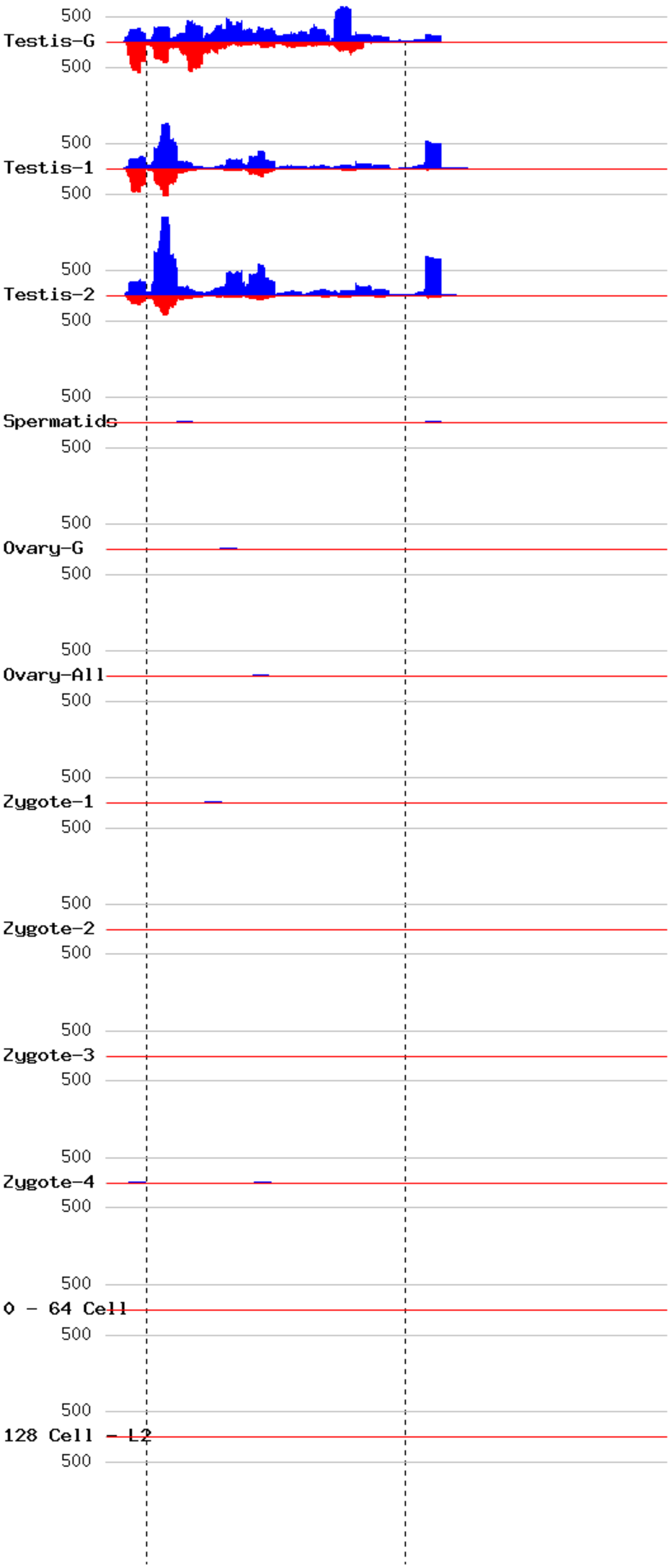
ASCF_8234_908 TB2/DP1_HVA22_family_protein 908 bp



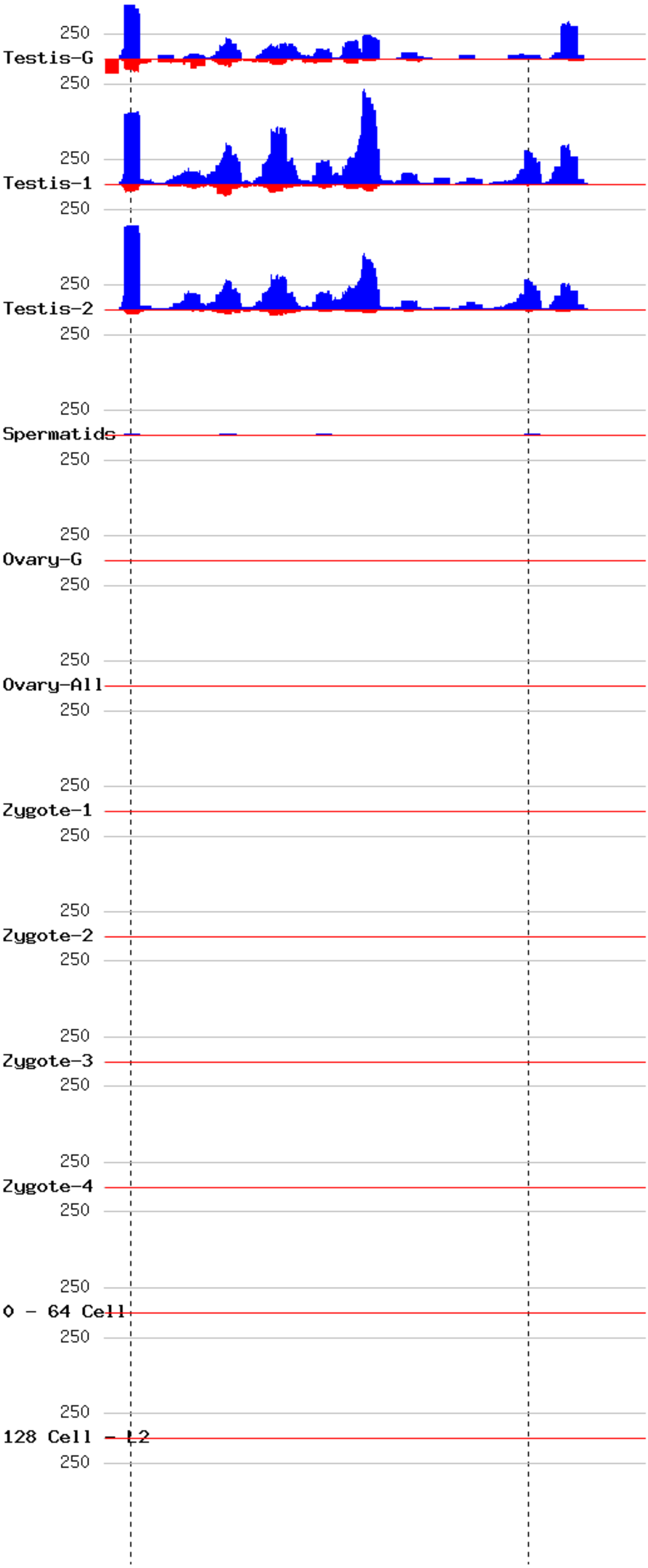
ASCF_8289_888 Hypothetical_protein 888 bp



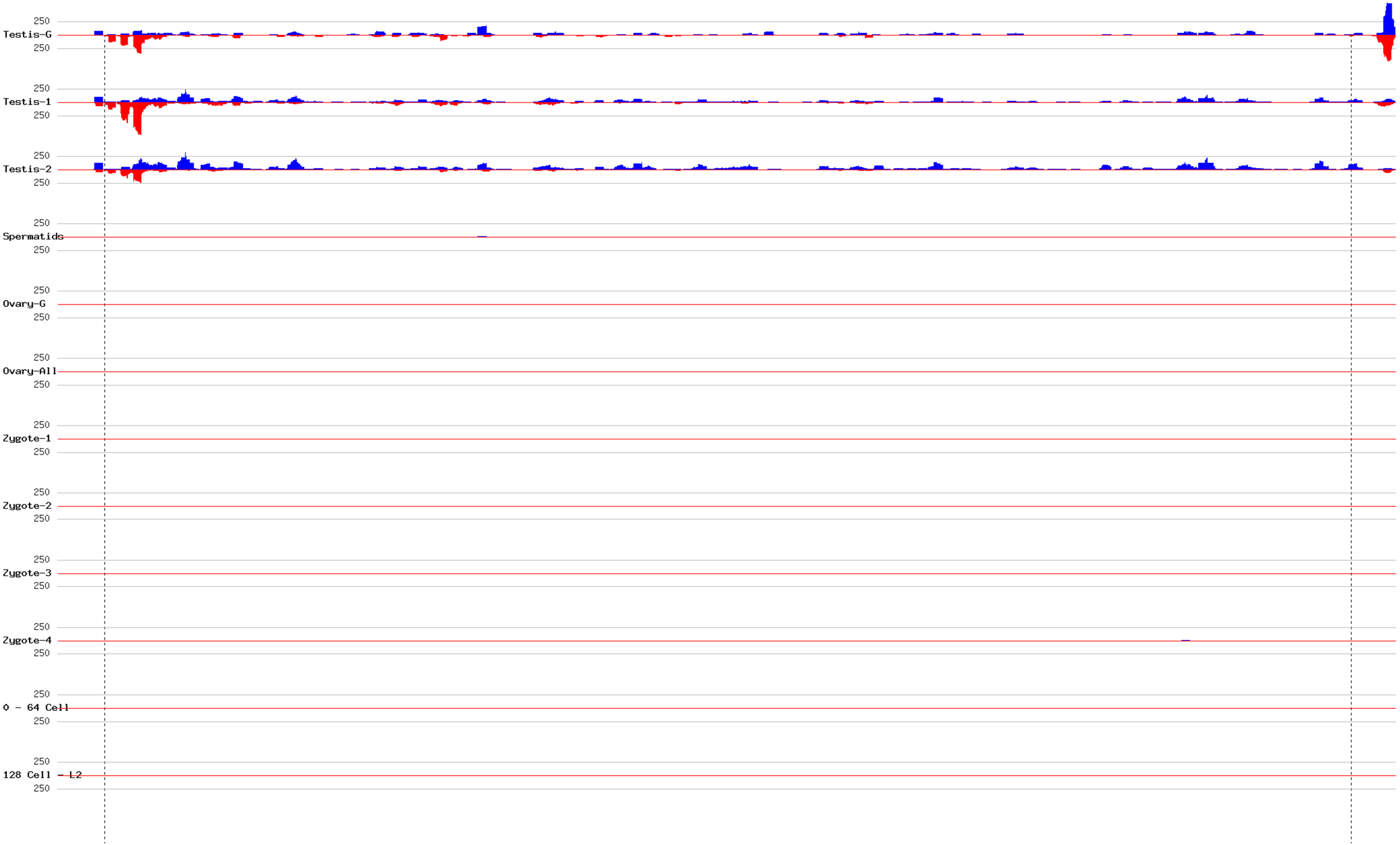
ASCF_8297_884 Hypothetical_protein 884 bp



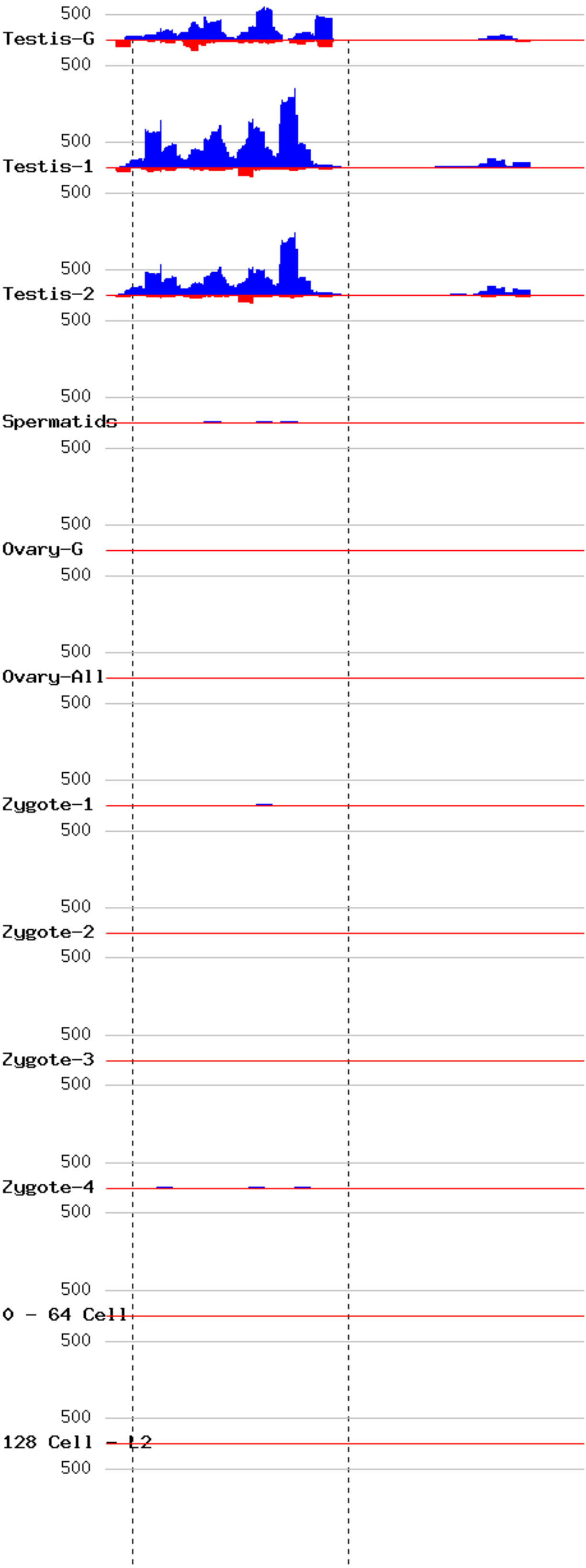
ASCF_8360_862 Hypothetical_protein 862 bp

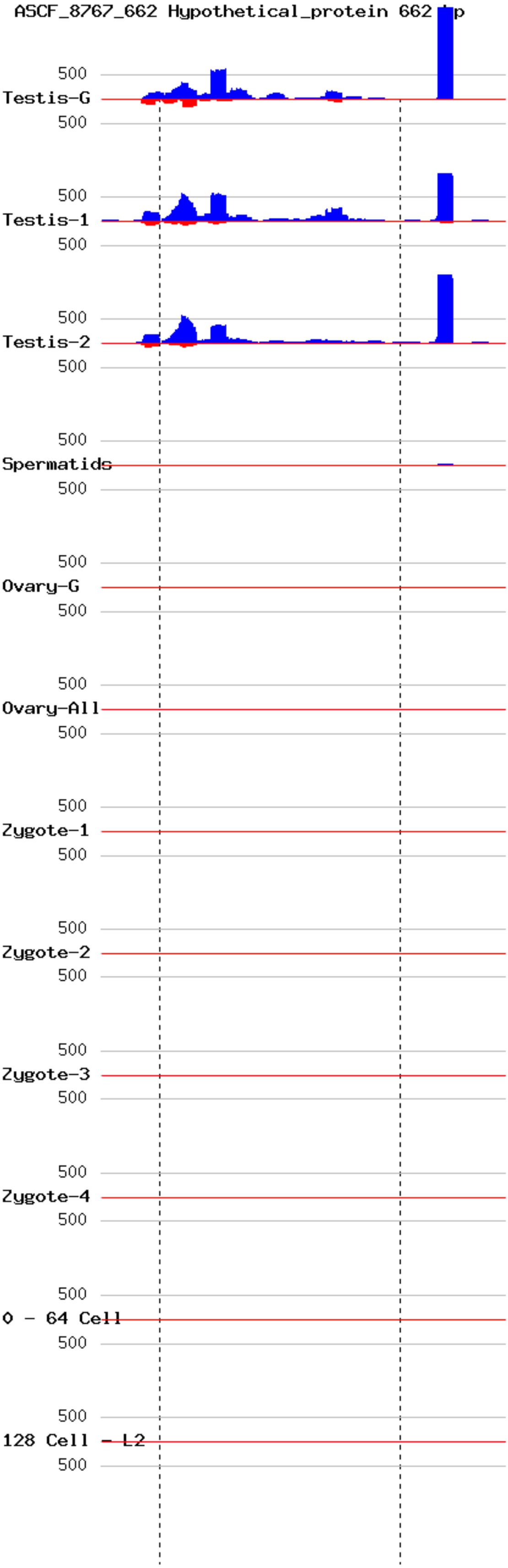


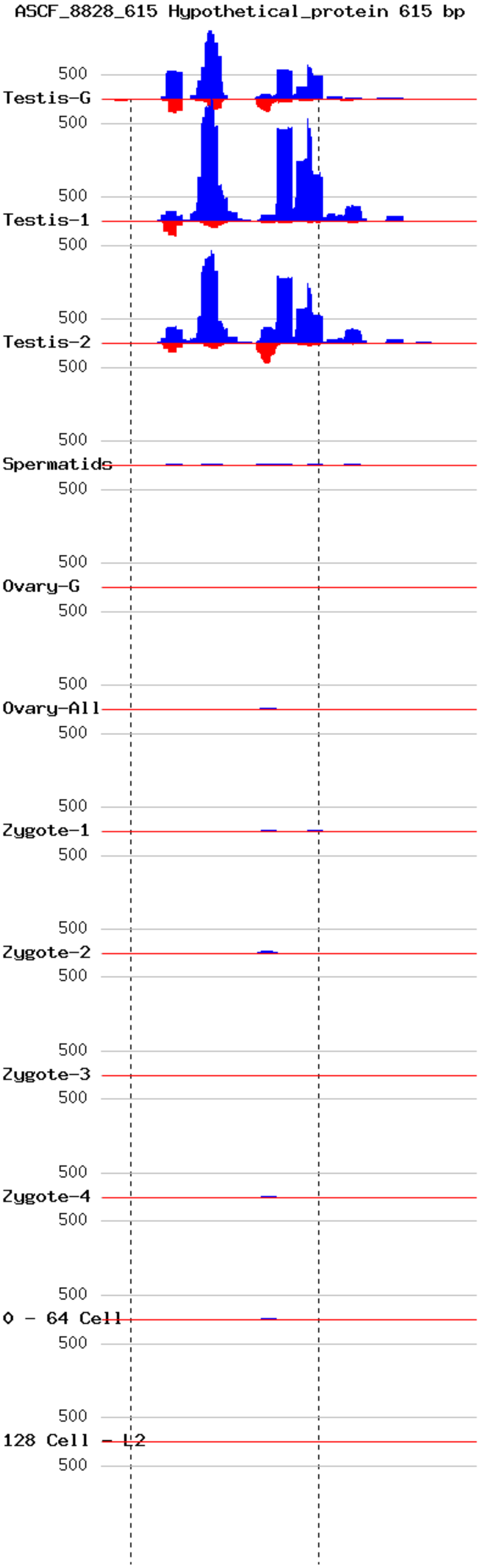
ASCF_848_3976 Myosin_or_motor_domain_containing_protein 3976 bp



ASCF_8593_749 Hypothetical_protein 749 bp



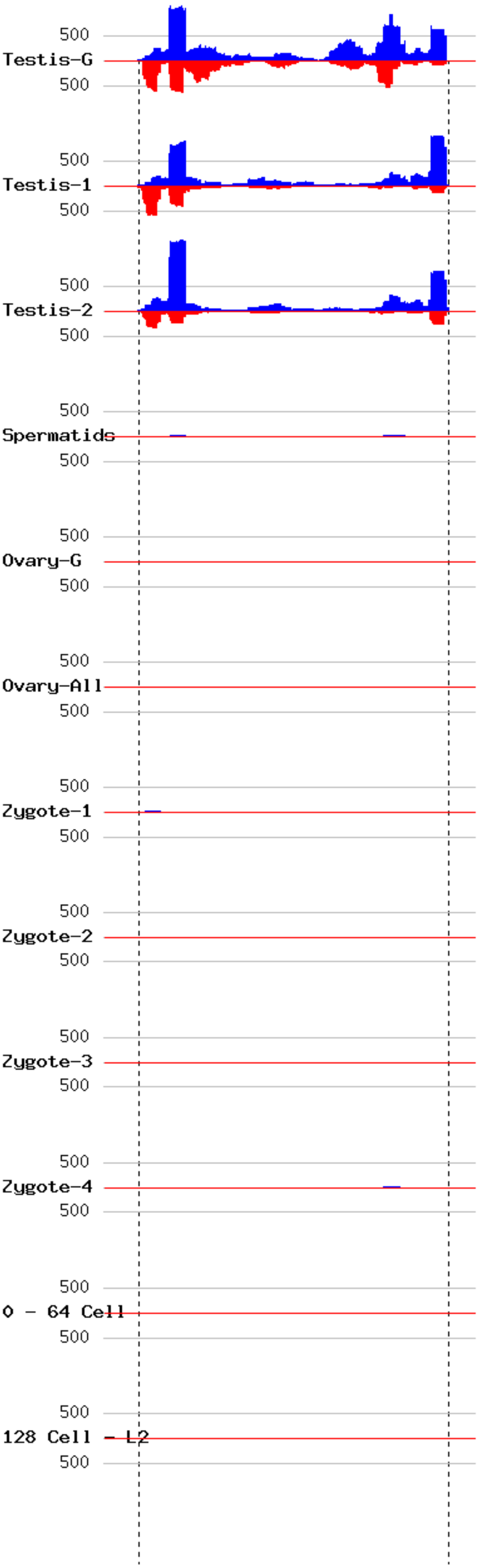

ASCF_8767_662 Hypothetical_protein 662 bp
500
Testis-G
500
500
Testis-1
500
500
Testis-2
500
500
Spermatids
500
500
Ovary-G
500
500
Ovary-All
500
500
Zygote-1
500
500
Zygote-2
500
500
Zygote-3
500
500
Zygote-4
500
500
0 - 64 Cell
500
500
128 Cell - L2
500


ASCF_8828_615 Hypothetical_protein 615 bp
500
Testis-G
500
500
Testis-1
500
500
Testis-2
500
500
Spermatids
500
500
Ovary-G
500
500
Ovary-All
500
500
Zygote-1
500
500
Zygote-2
500
500
Zygote-3
500
500
Zygote-4
500
500
0 - 64 Cell
500
500
128 Cell - L2
500

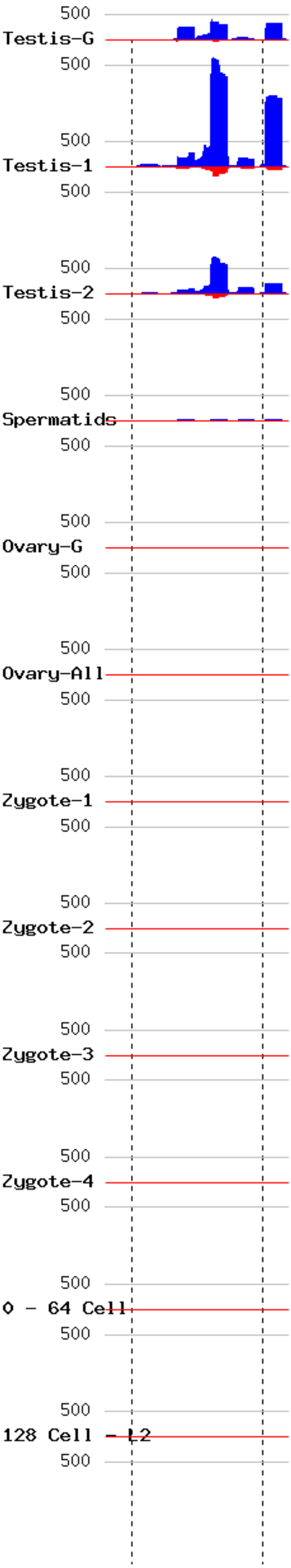
ASCF_8844_594 MSP_fiber_protein_beta 594 bp



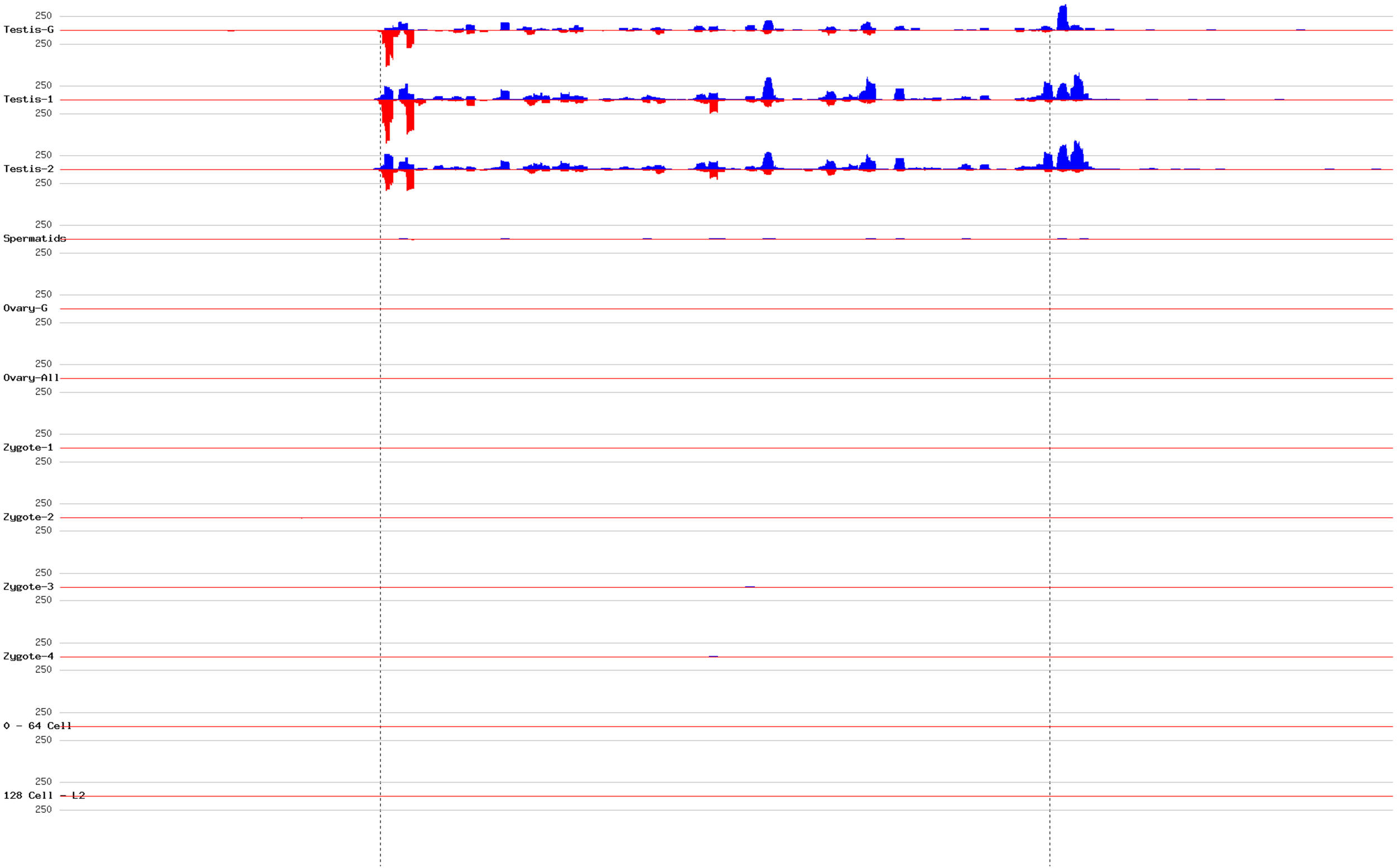
ASCF_8845_593 Hypothetical_protein 593 bp



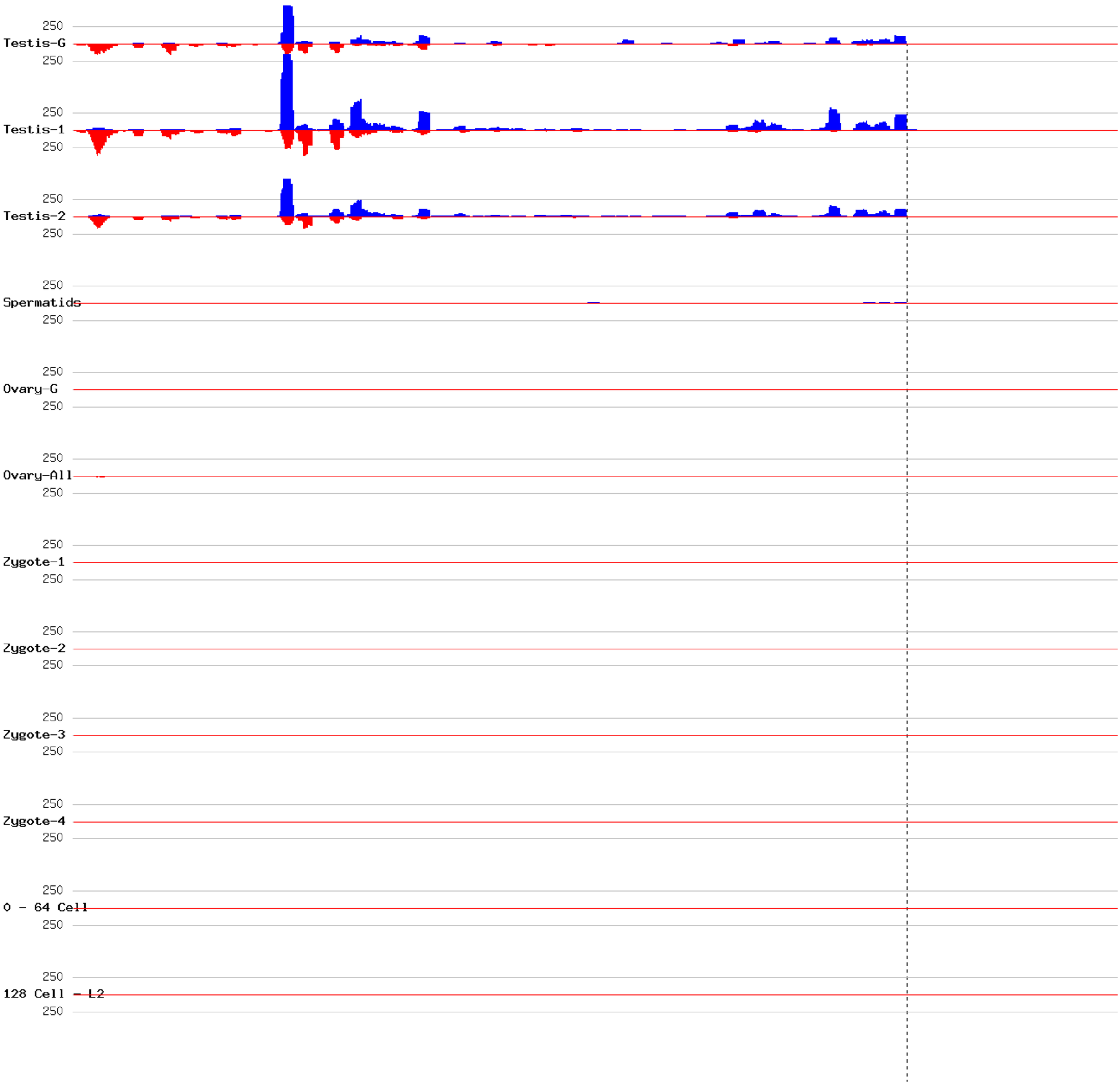
ASCF_8996_288 Major_sperm_pro



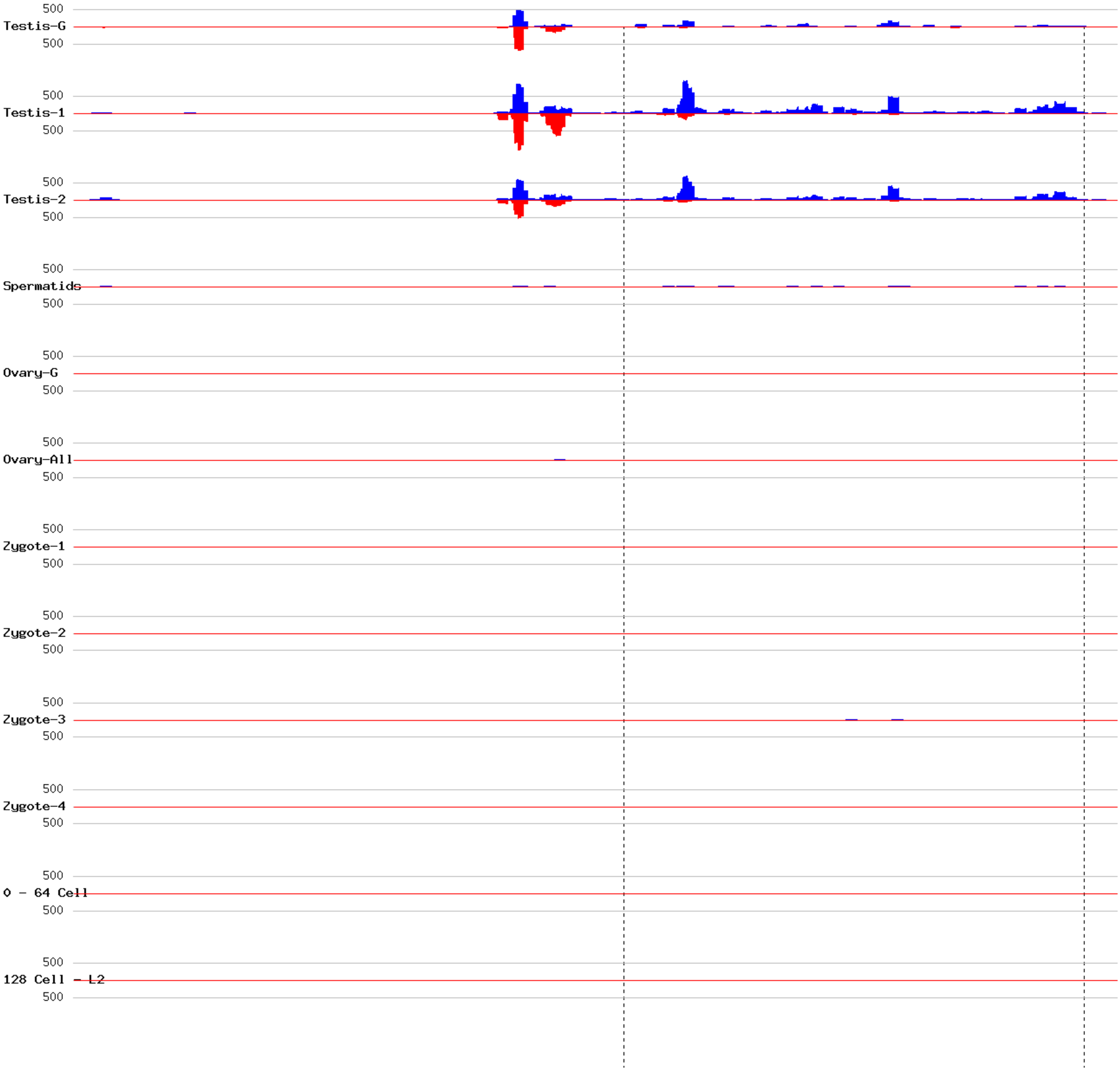
ASCF_937_3827 Phosphoenolpyruvate_carboxykinase 3827 bp



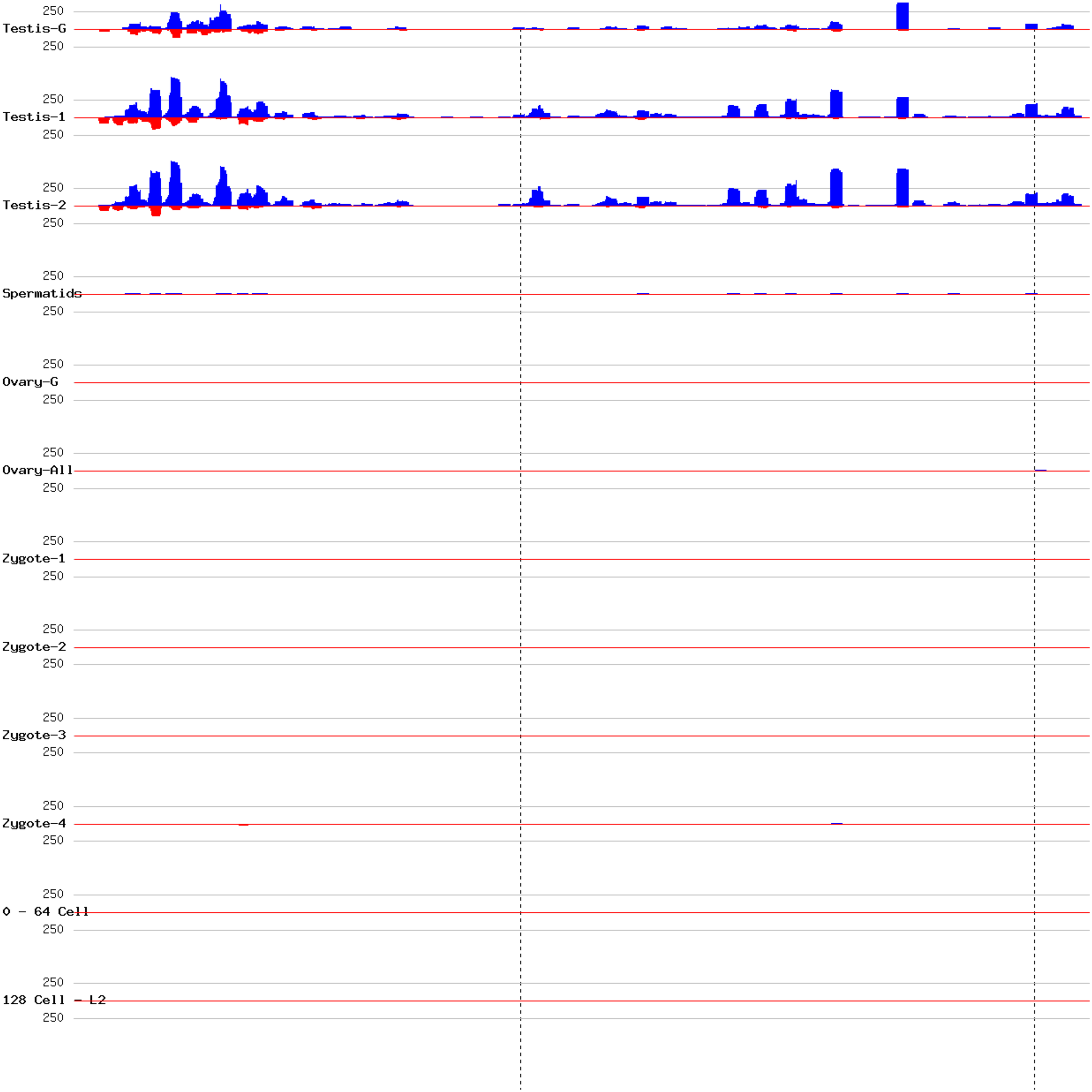
ASCP_1071_2414 2-oxoisovalerate_dehydrogenase_beta 2414 bp



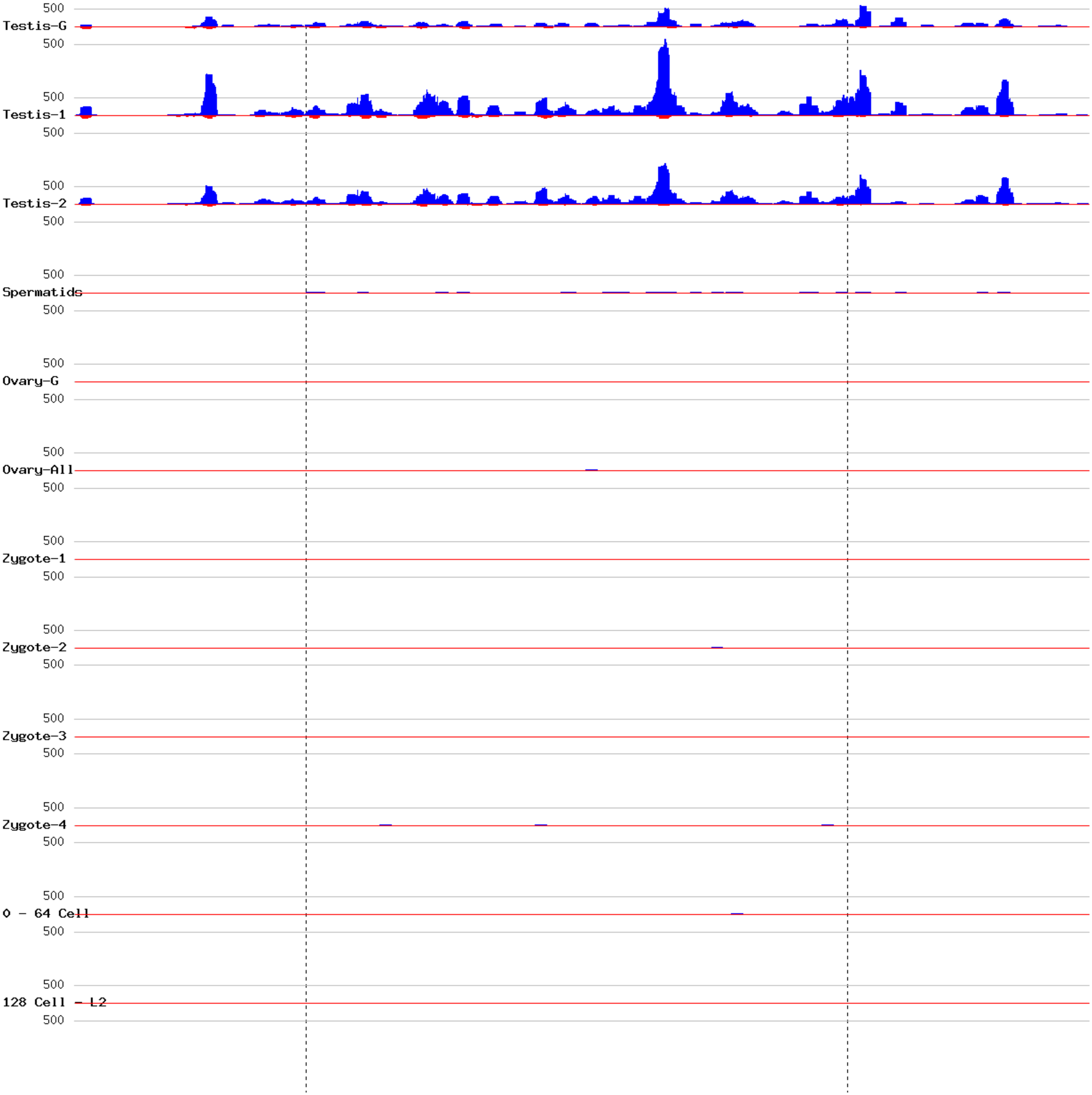
ASCP_1075_2408 Protein_kinase_domain_containing_protein 2408 bp



ASCP_1197_2300 Serine/threonine_protein_phosphatase_PP1 2300 bp

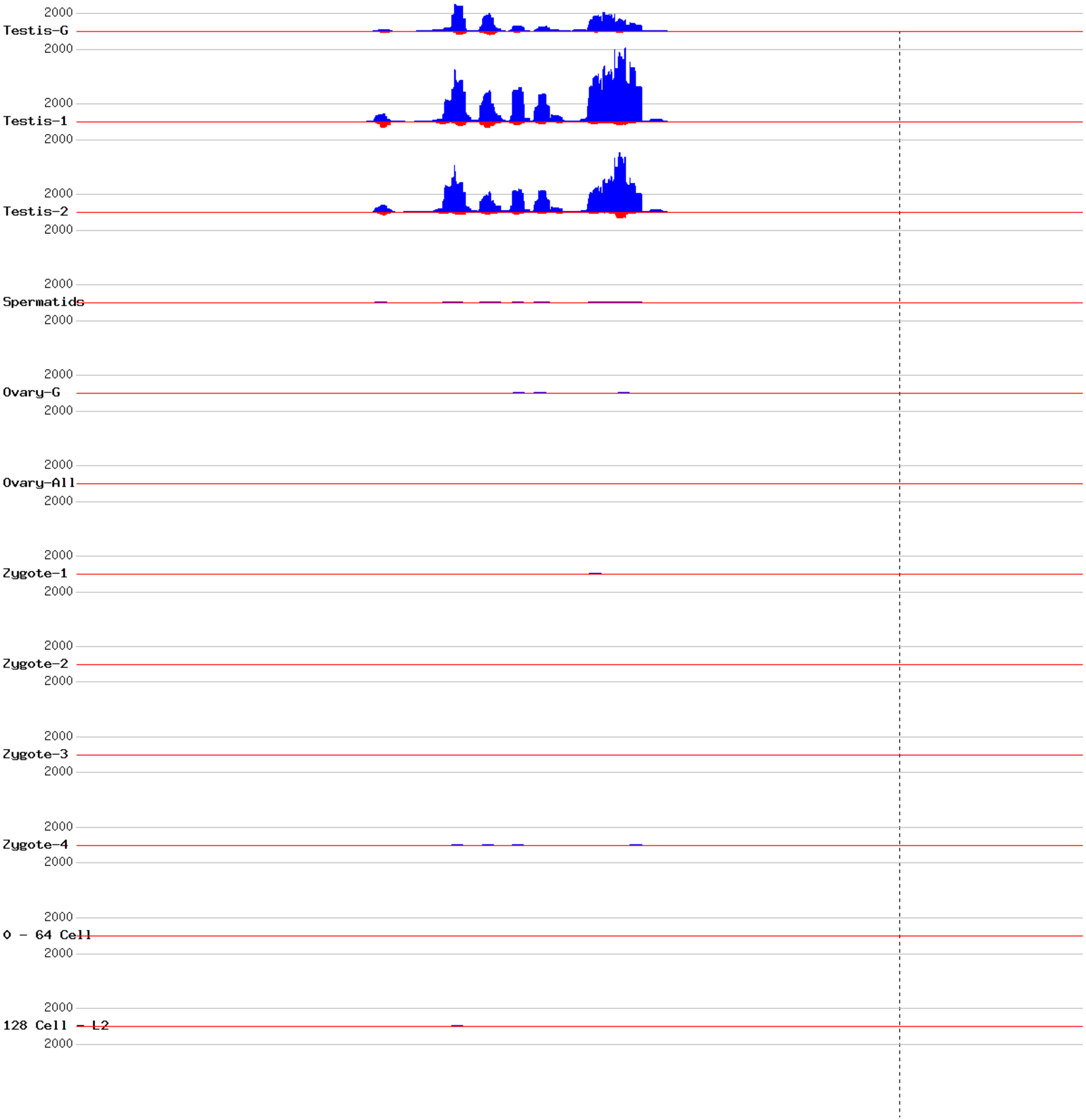


ASCP_1206_2286 Hypothetical_protein 2286 bp

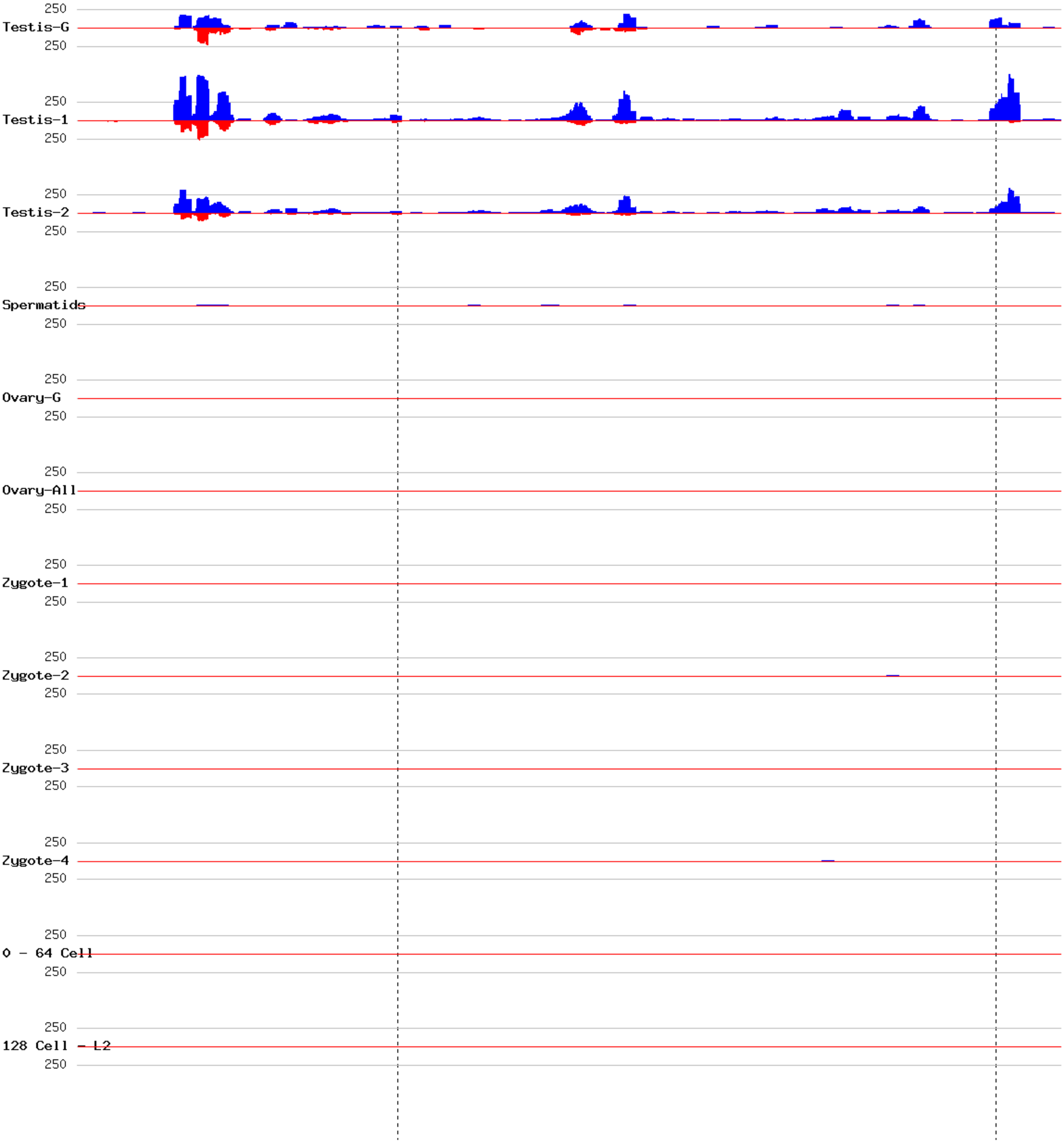


ASCP_1265_2224 Major_sperm_protein 2224 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2



ASCP_1367_2125 Hypothetical_protein 2125 bp



ASCP_1393_2102 Hypothetical_protein 2102 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

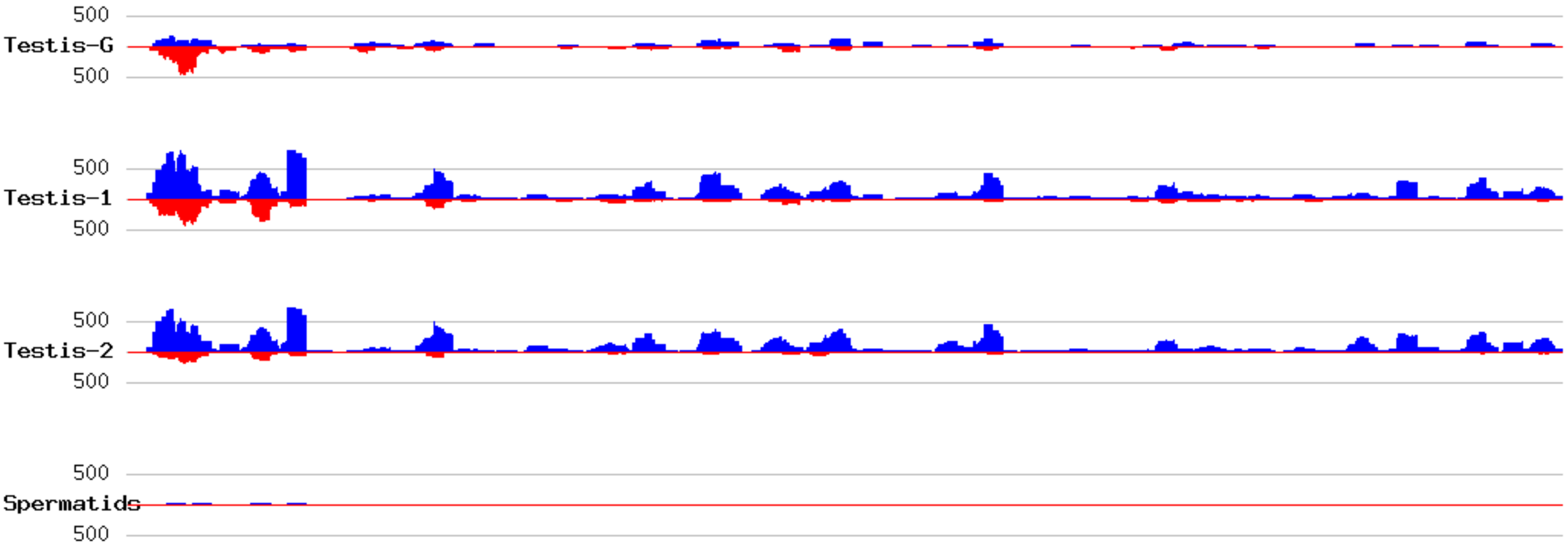
250

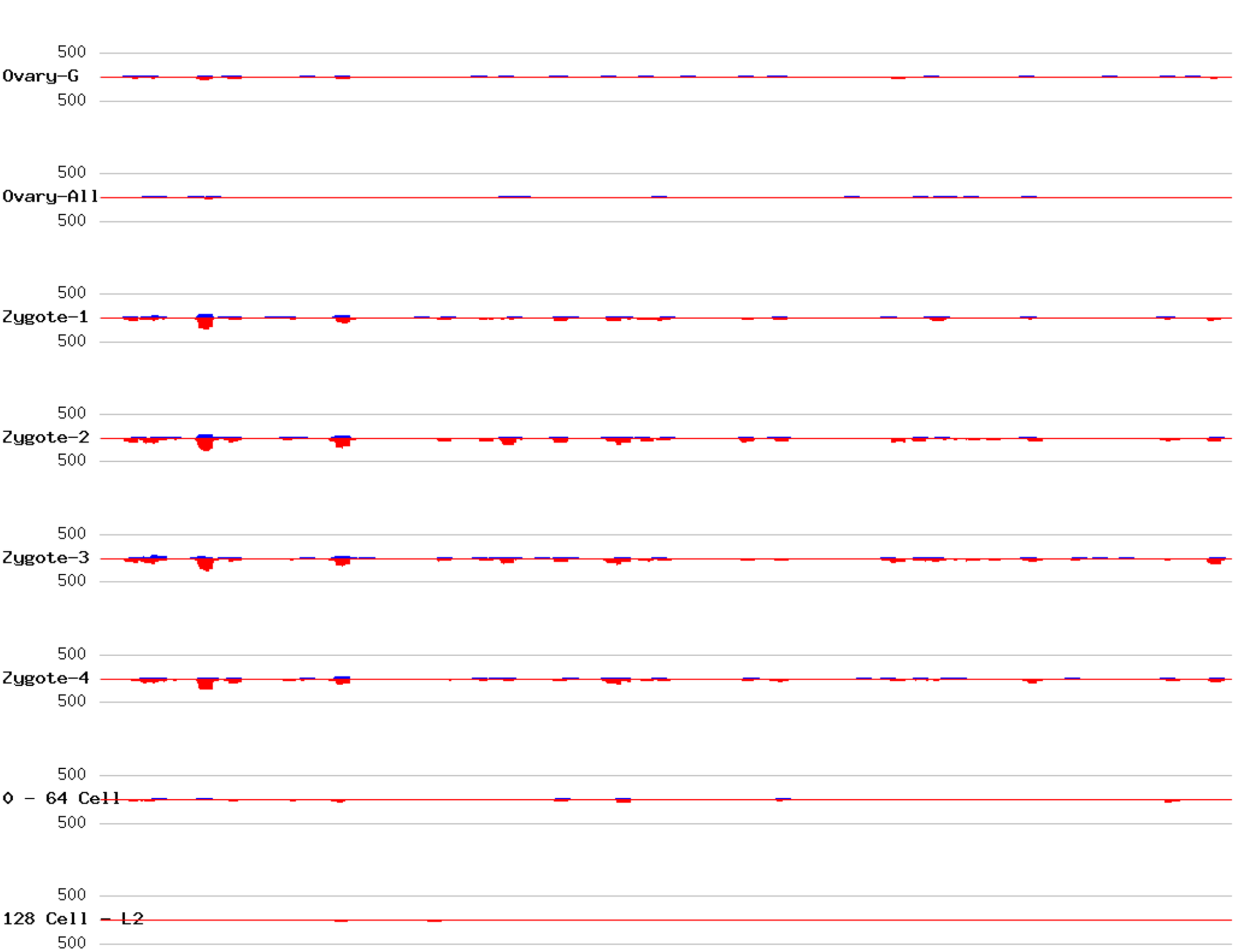
ASCP_1601_1925 Hypothetical_protein 1925 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

250

ASCP_1679_1878 Ubiquitin_family_member_protein 1878 bp

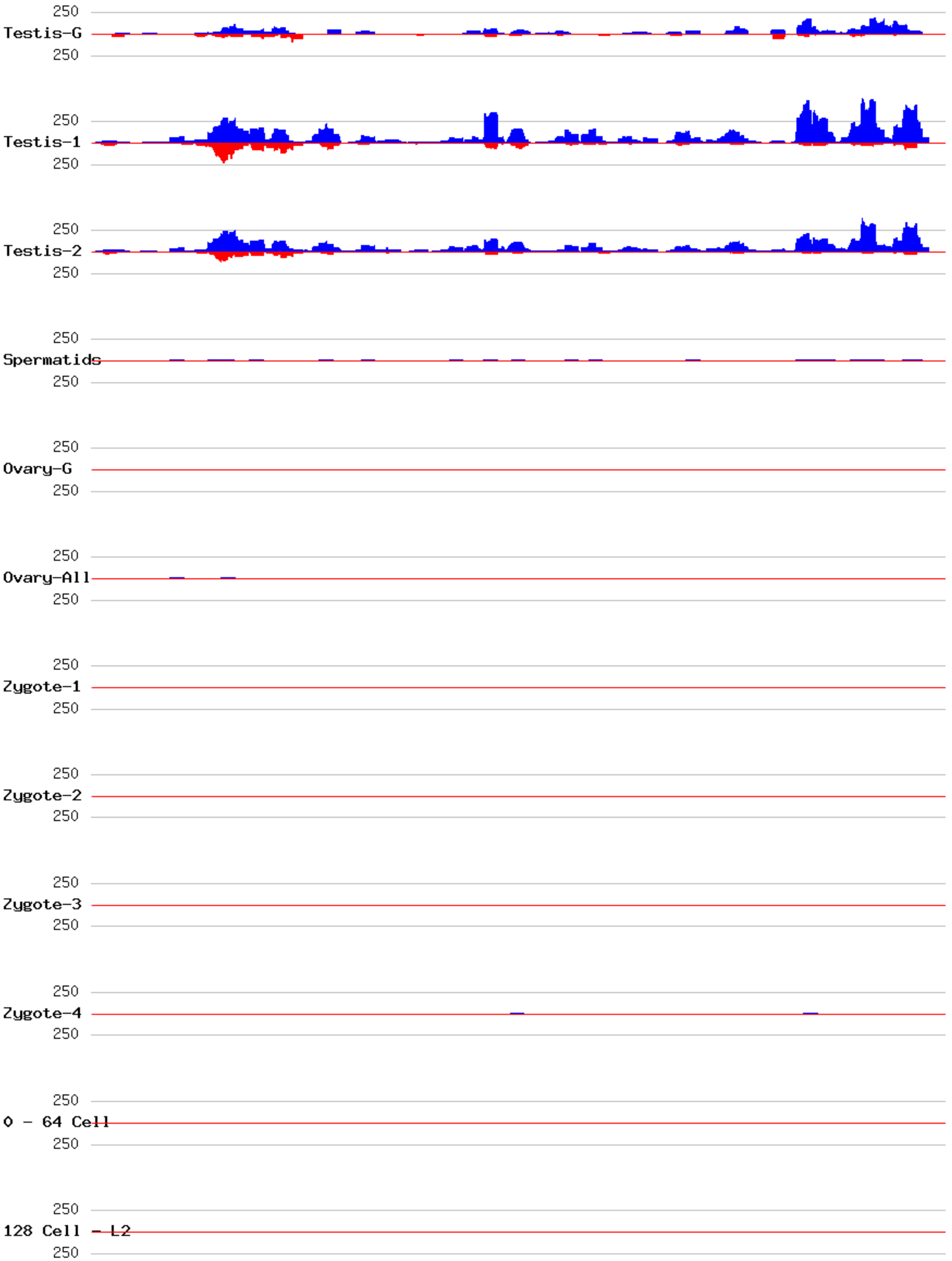




ASCP_1900_1718 Protein_kinase_domain_containing_protein 1718 bp

ASCP_2024_1645 Hypothetical_protein 1645 bp

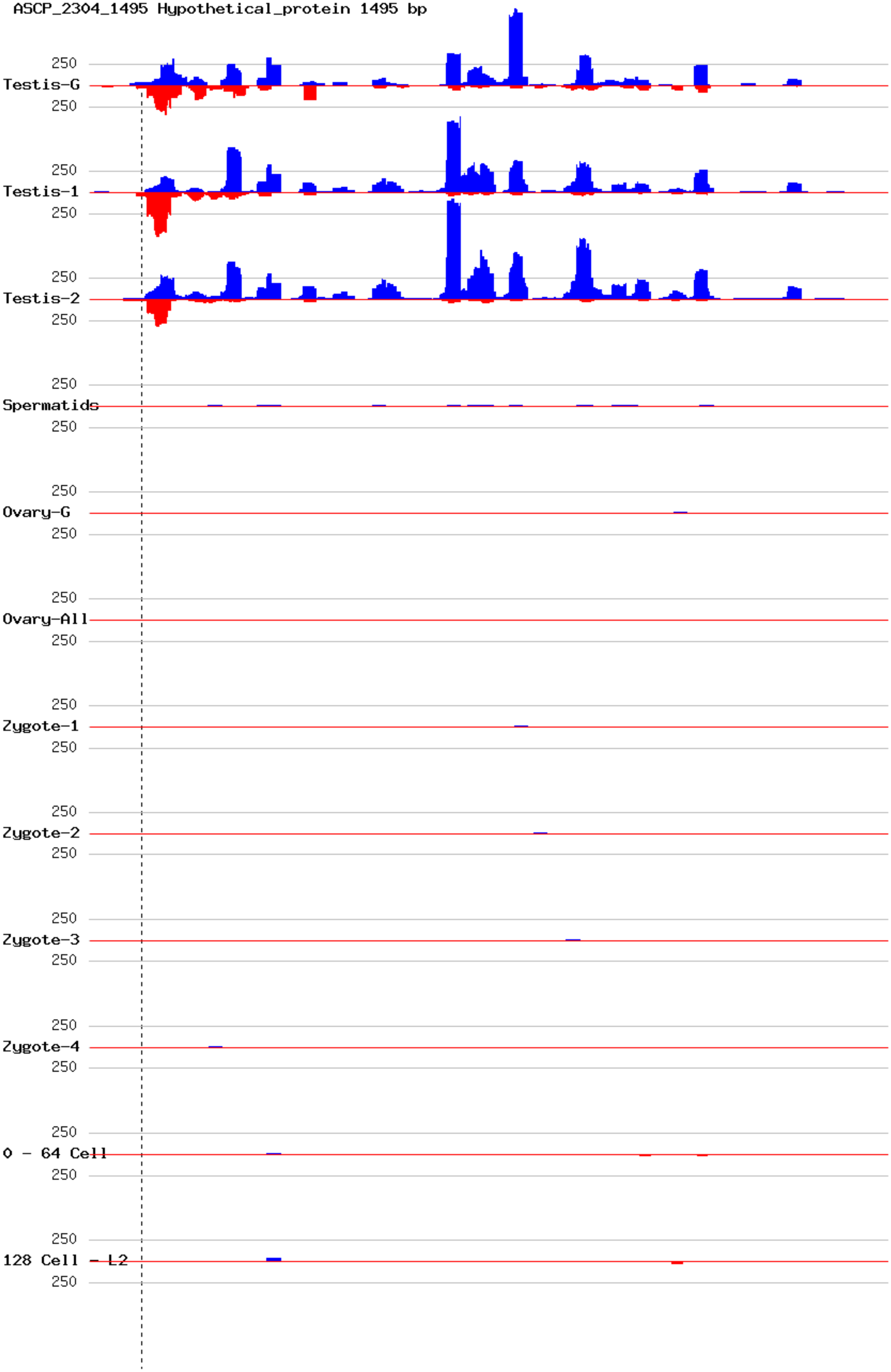
ASCP_2158_1569 Hypothetical_protein 1569 bp



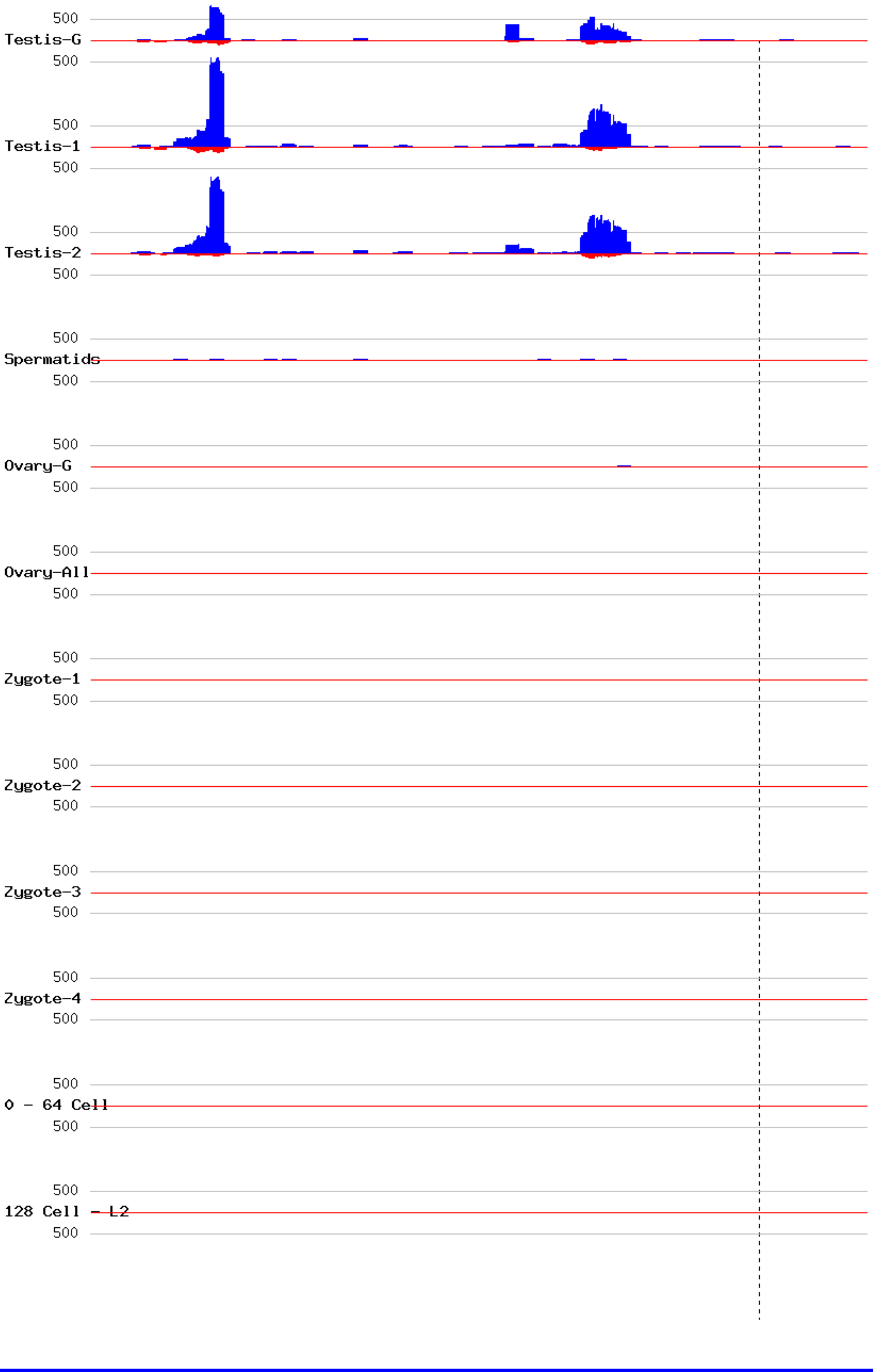
ASCP_2181_1558 Phosphoenolpyruvate_carboxykinase 1558 bp

ASCP_2244_1526 Hypothetical_protein 1526 bp

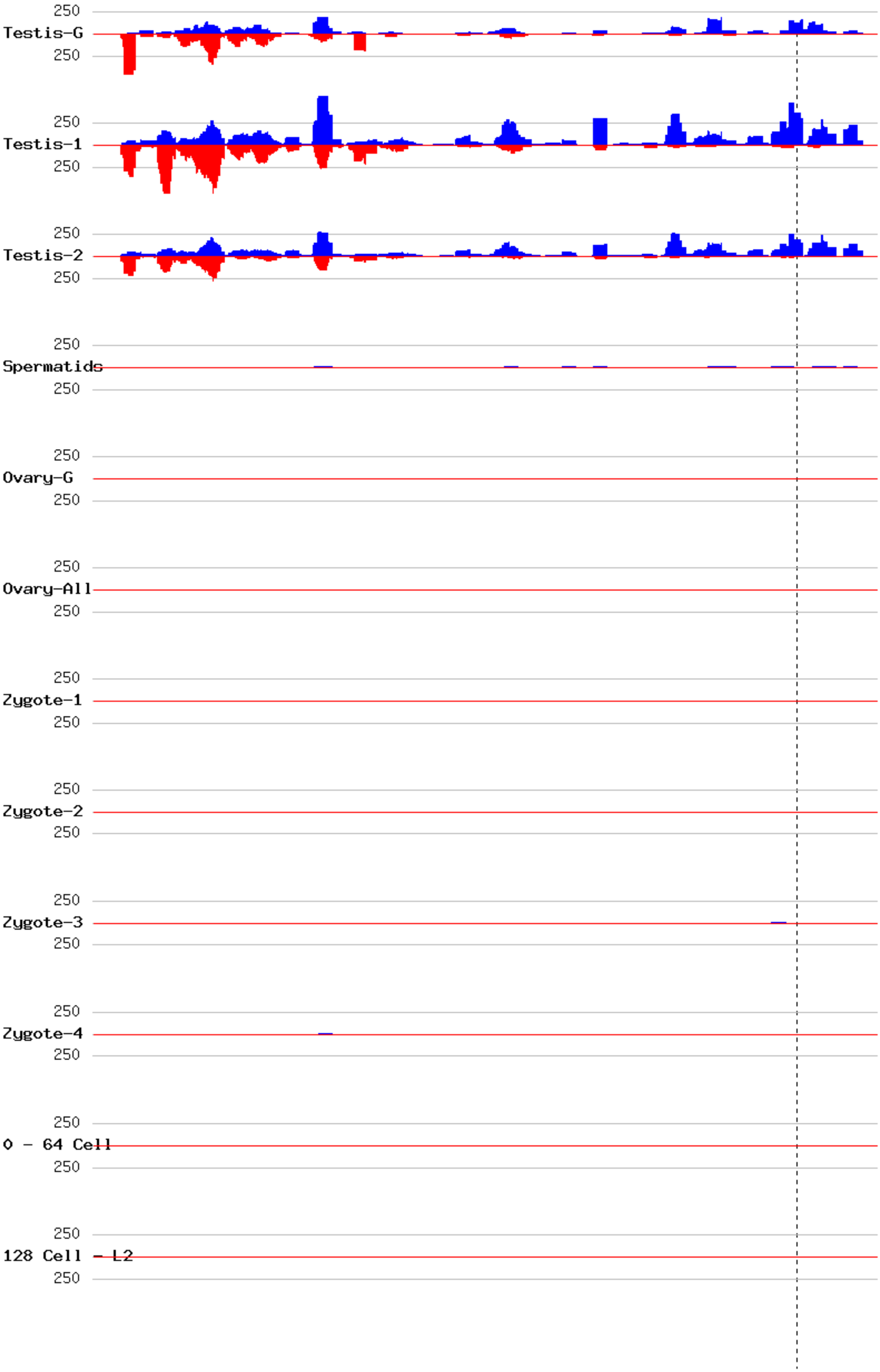
ASCP_2304_1495 Hypothetical_protein 1495 bp



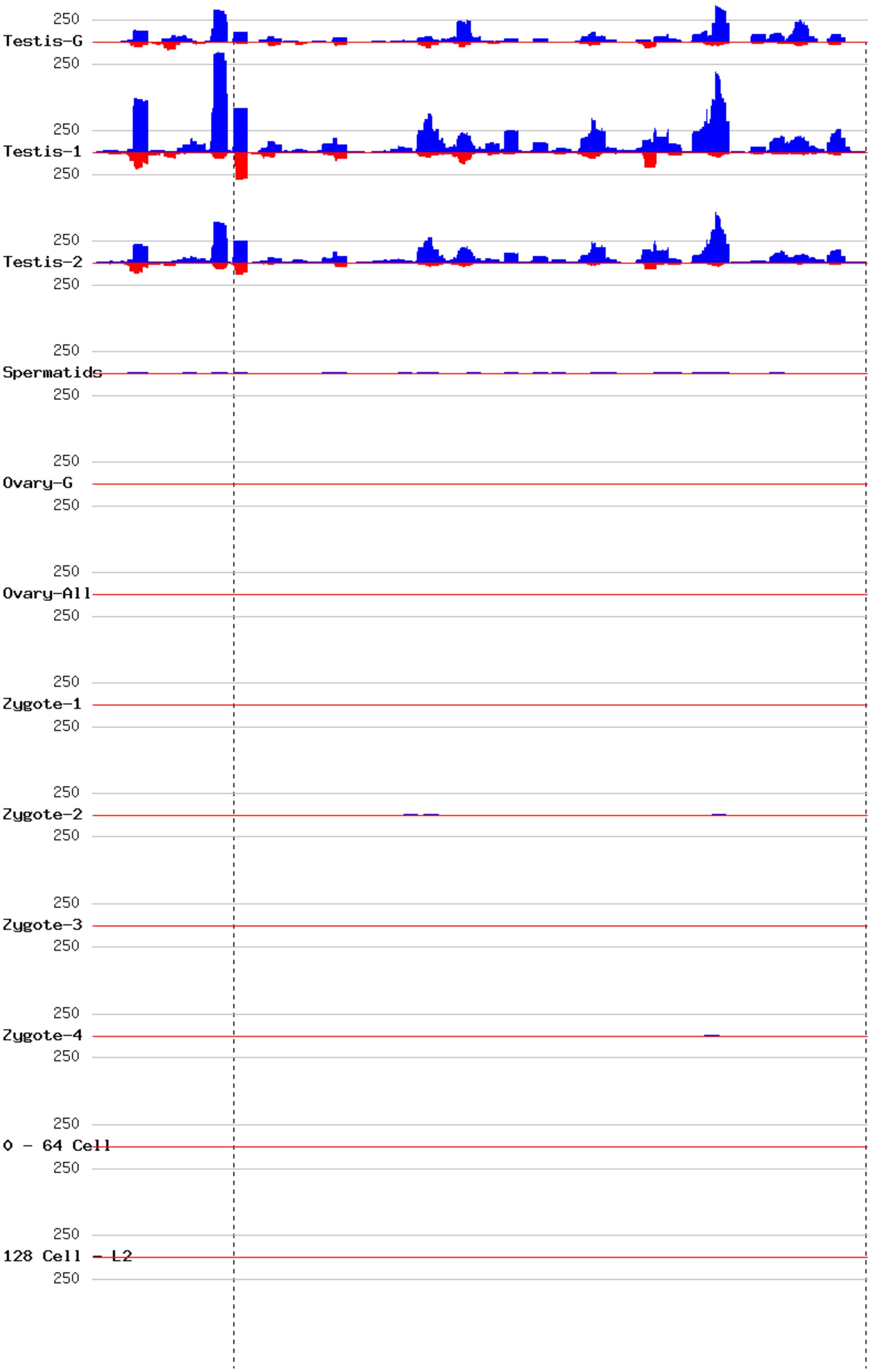
ASCP_2385_1458 Major_sperm_protein 1458 bp



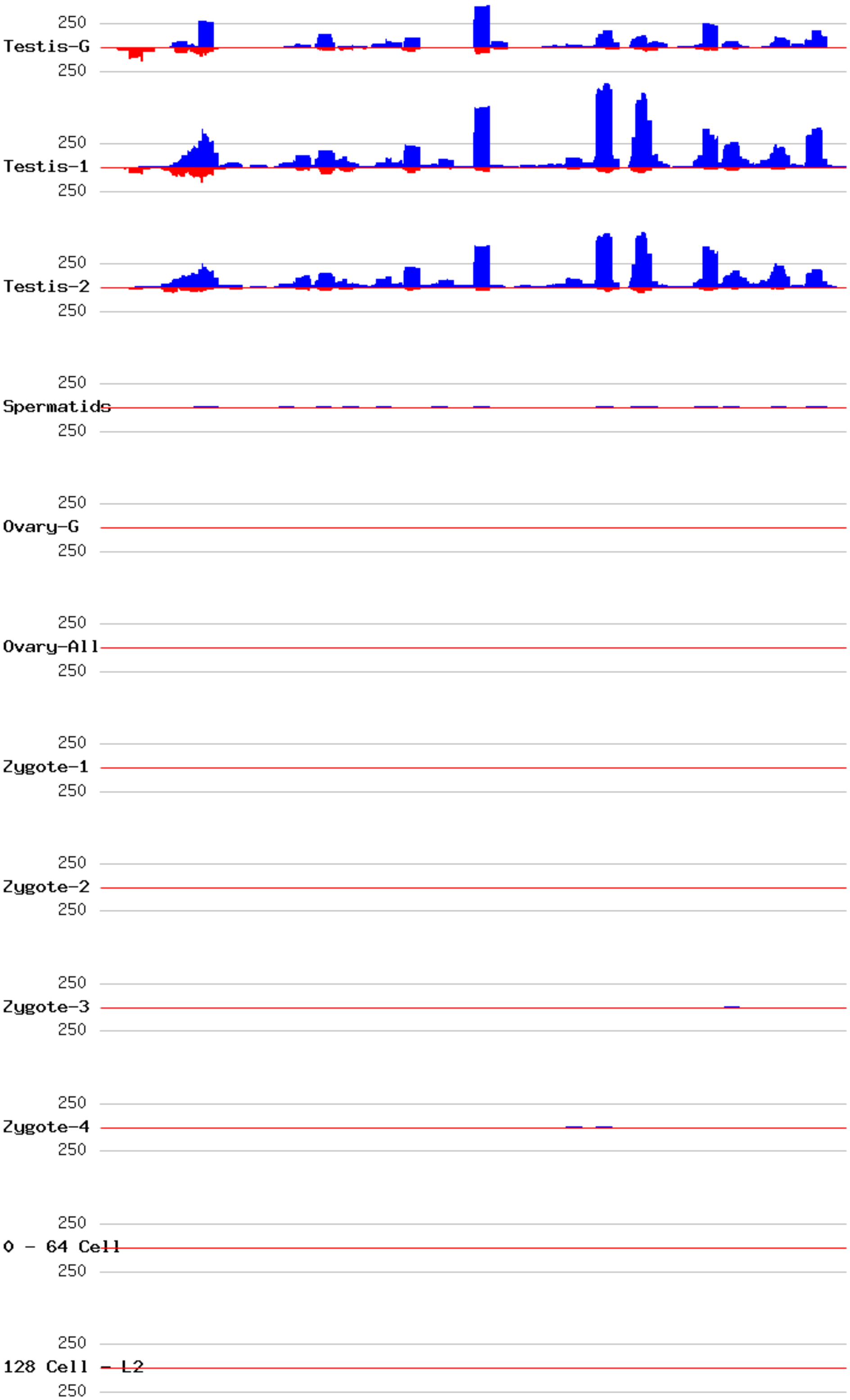
ASCP_2479_1411 Hypothetical_protein 1411 bp



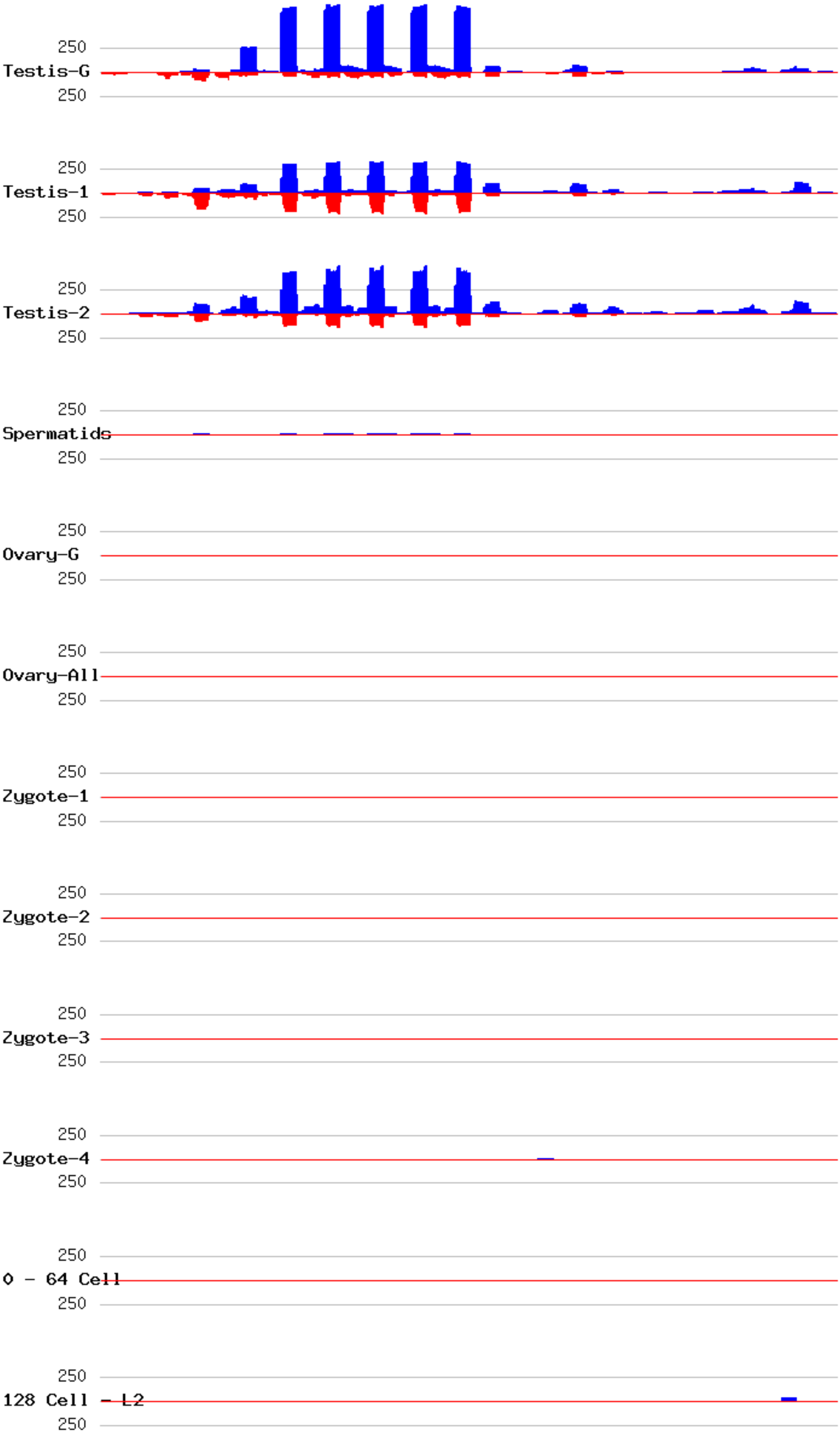
ASCP_2500_1402 Hypothetical_protein 1402 bp



ASCP_2938_1242 Protein_kinase_domain_containing_protein 1242 bp



ASCP_2999_1221 Sperm-specific_family_class_q_protein_2 1221 bp



ASCP_3048_1206 Tyrosine-protein_kinase 1206 bp

1000
Testis-G
1000

1000
Testis-1
1000

1000
Testis-2
1000

1000
Spermatids
1000

1000
Ovary-G
1000

1000
Ovary-All
1000

1000
Zygote-1
1000

1000
Zygote-2
1000

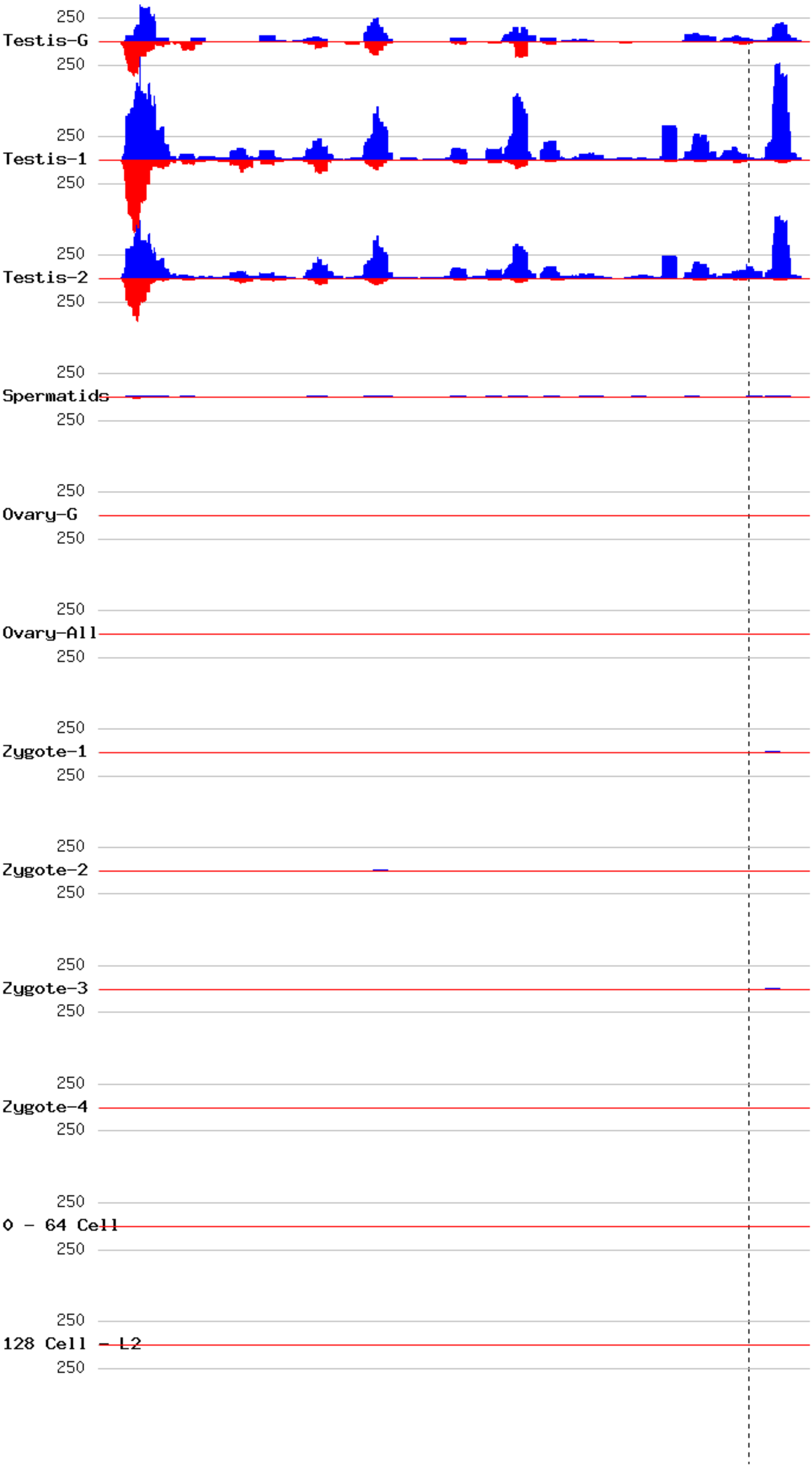
1000
Zygote-3
1000

1000
Zygote-4
1000

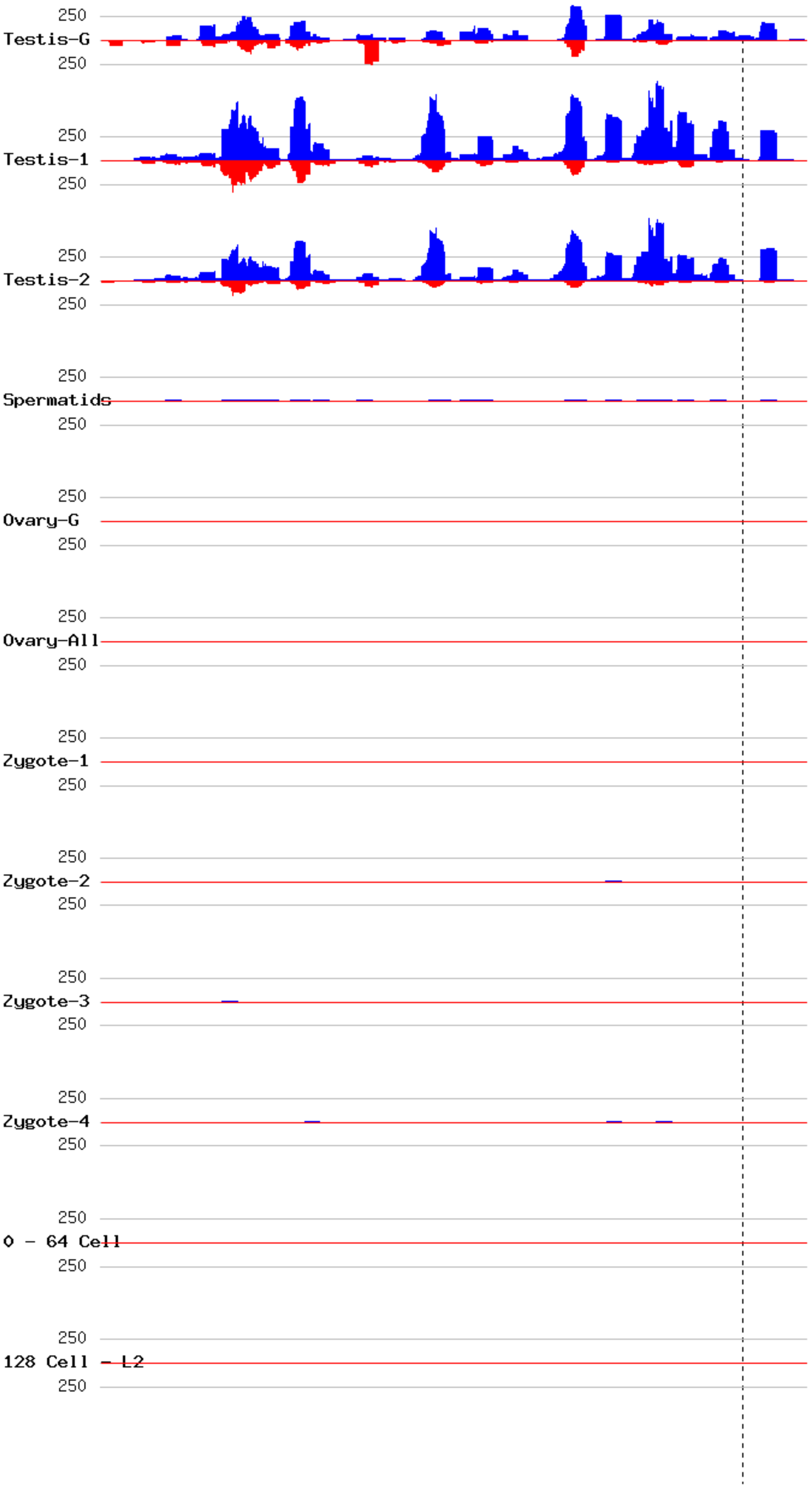
1000
0 - 64 Cell
1000

1000
128 Cell - L2
1000

ASCP_3065_1201 Protein_kinase_domain_containing_protein 1201 bp



ASCP_3160_1175 Protein-tyrosine_phosphatase_containing_protein 1175 bp

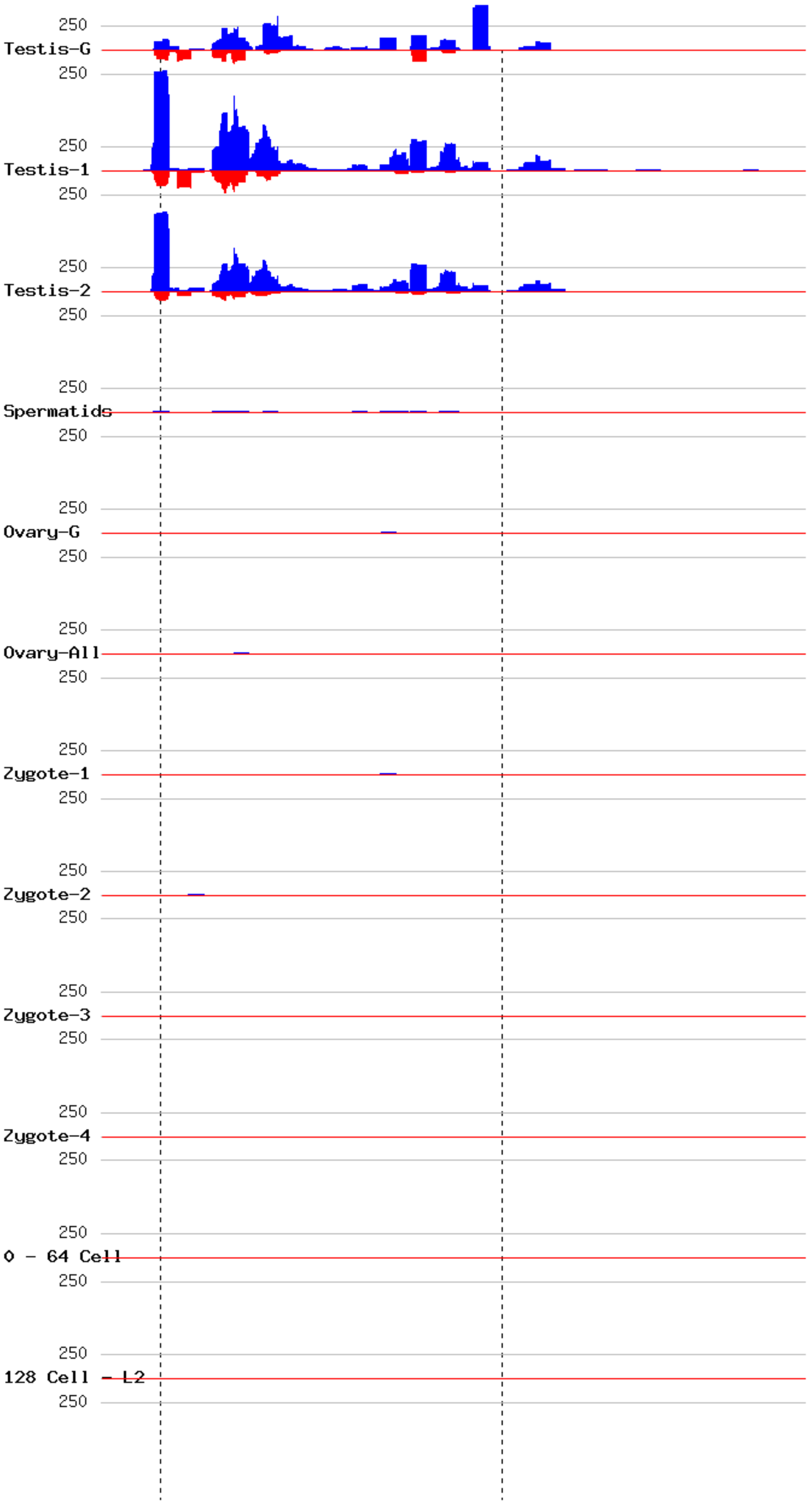


ASCP_3178_1169 Protein_kinase_domain_containing_protein 1169 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

250

ASCP_3188_1167 Hypothetical_protein 1167 bp

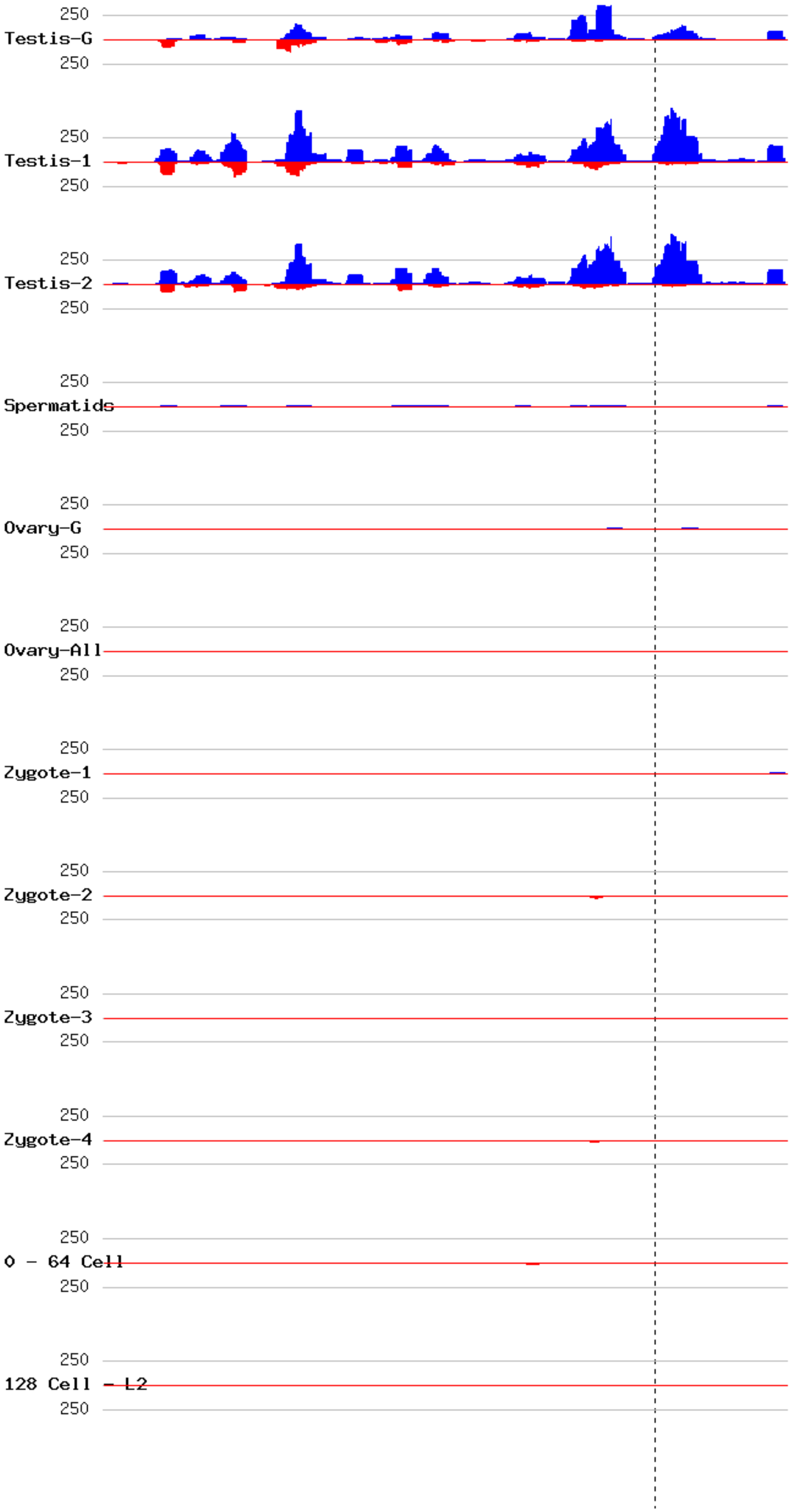


ASCP_3296_1138 Pyruvate dehydrogenase E1 component 1138 bp

Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

250

ASCP_3369_1118 TAG-164_protein 1118 bp

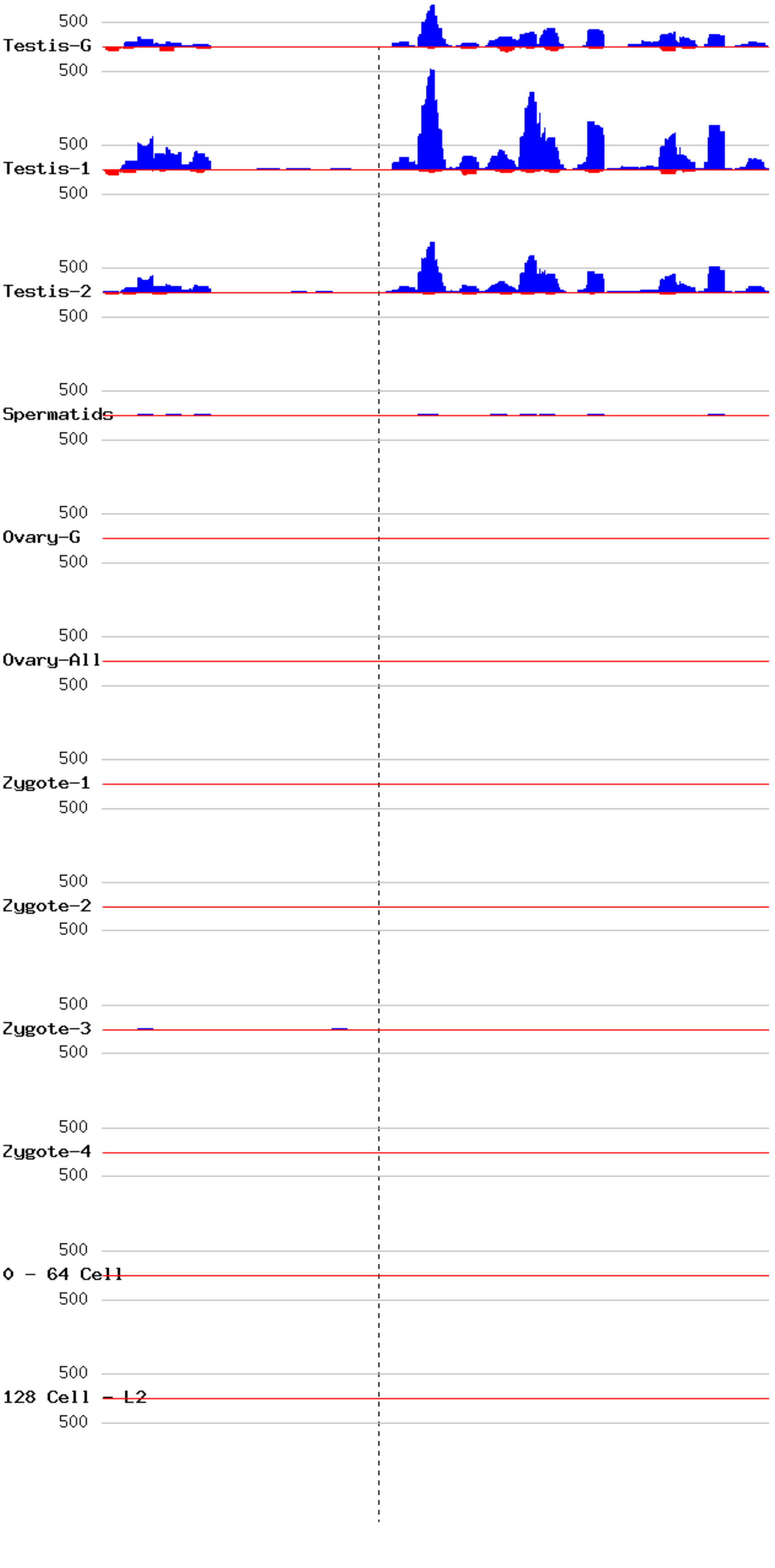


ASCP_3399_1110 Protein-tyrosine_phosphatase_containing_protein 1110 bp

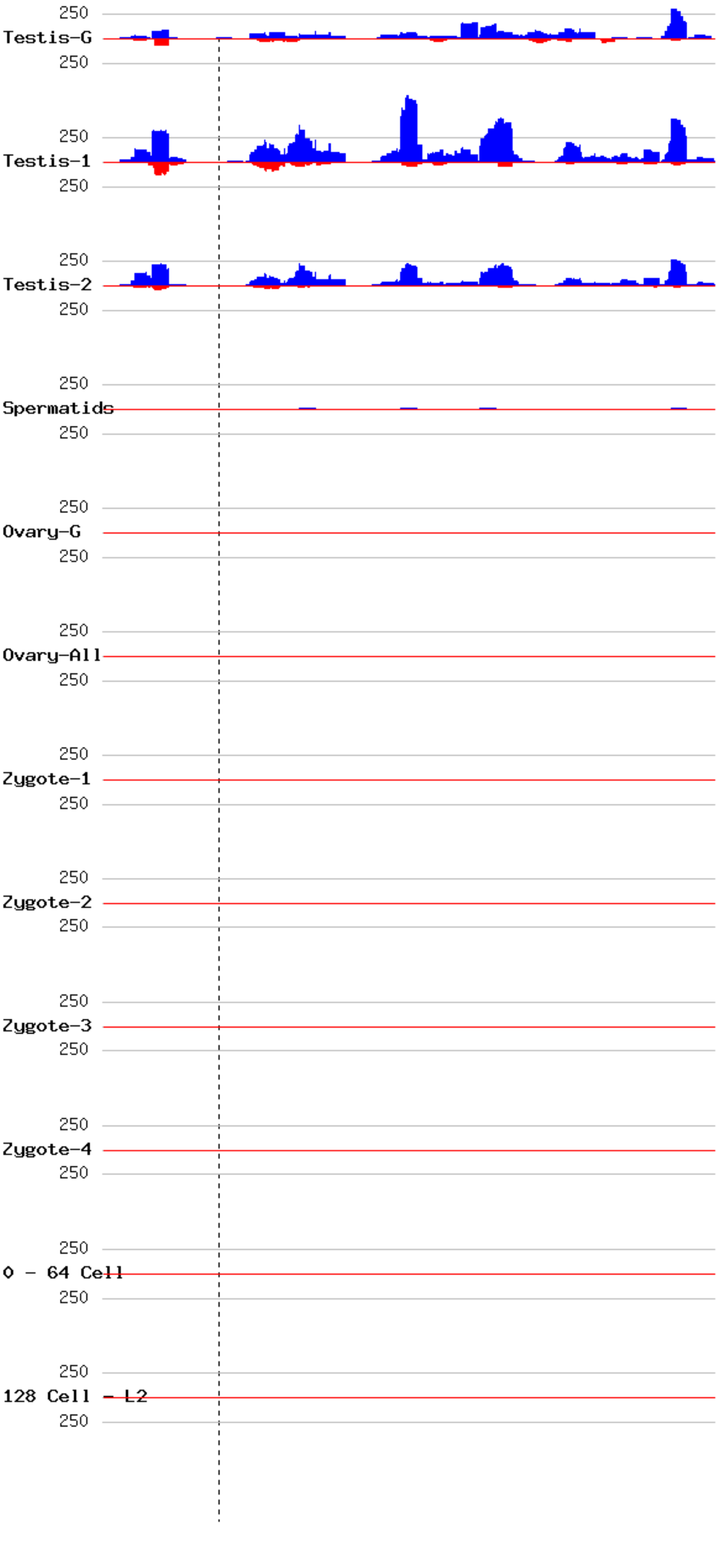
Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

500

ASCP_3507_1085 Hypothetical_protein 1085 bp



ASCP_3900_991 Fructose-bisphosphate_aldolase 991 bp



ASCP_393_3876 Hypothetical_protein 3876 bp

Testis-G
500
500

Testis-1
500
500

Testis-2
500
500

Spermatids
500
500

Ovary-G
500
500

Ovary-All
500
500

Zygote-1
500
500

Zygote-2
500
500

Zygote-3
500
500

Zygote-4
500
500

0 - 64 Cell
500
500

128 Cell - L2
500
500

ASCP_404_3847 RPN-10_protein 3847 bp

500
Testis-G
500

500
Testis-1
500

500
Testis-2
500

500
Spermatids
500

500
Ovary-G
500

500
Ovary-All
500

500
Zygote-1
500

500
Zygote-2
500

500
Zygote-3
500

500
Zygote-4
500

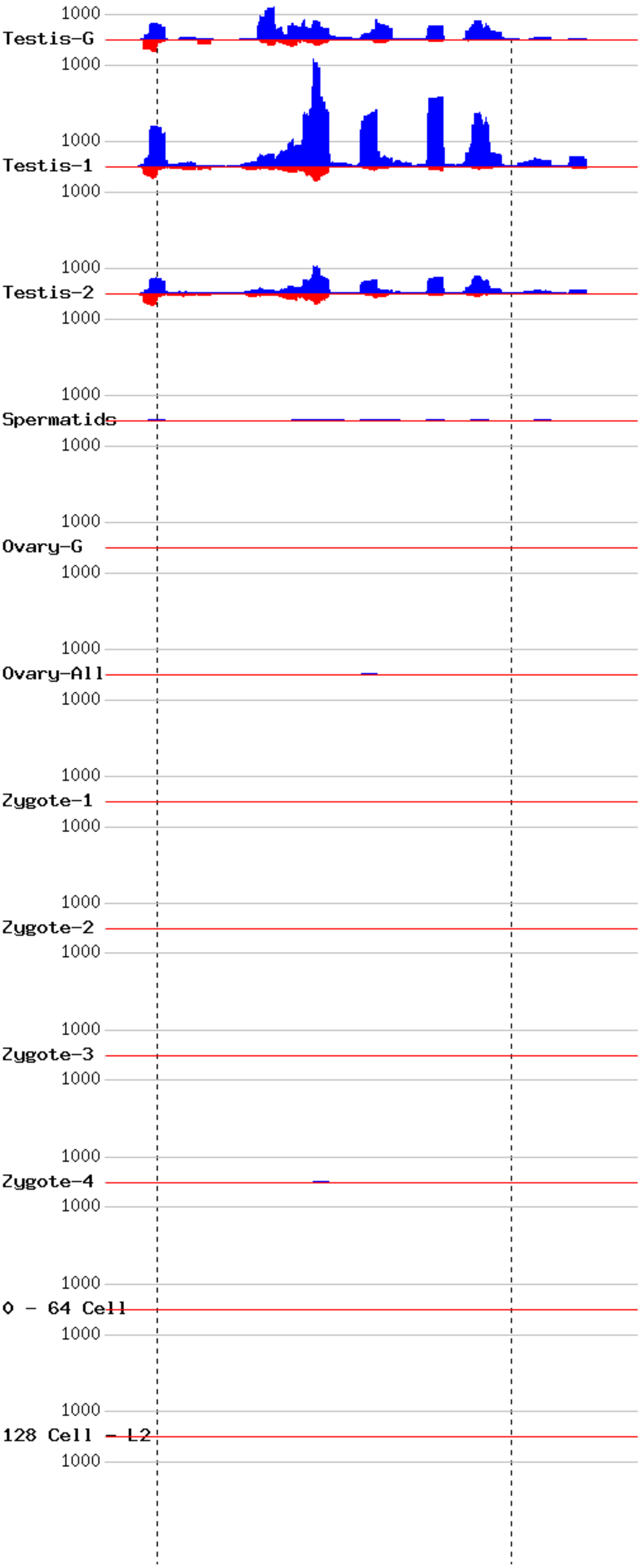
500
0 - 64 Cell
500

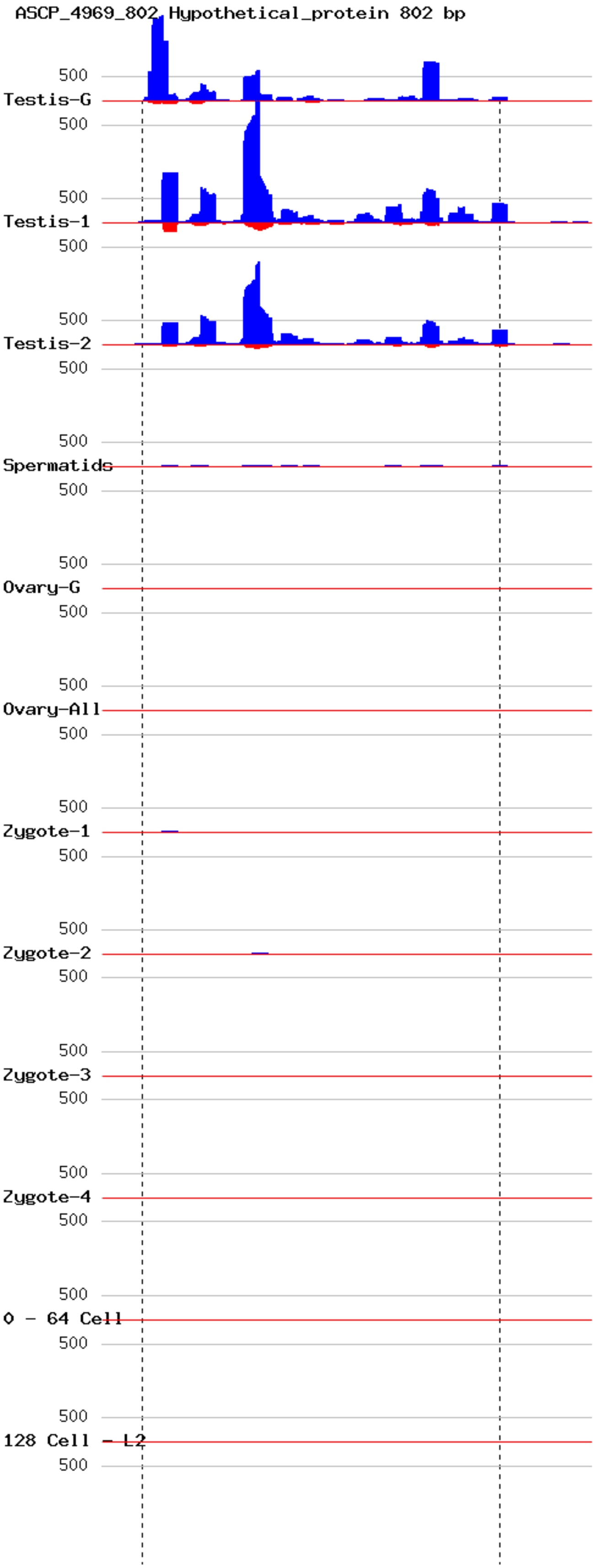
500
128 Cell - L2
500

ASCP_4197_930 Hypothetical_protein 930 bp

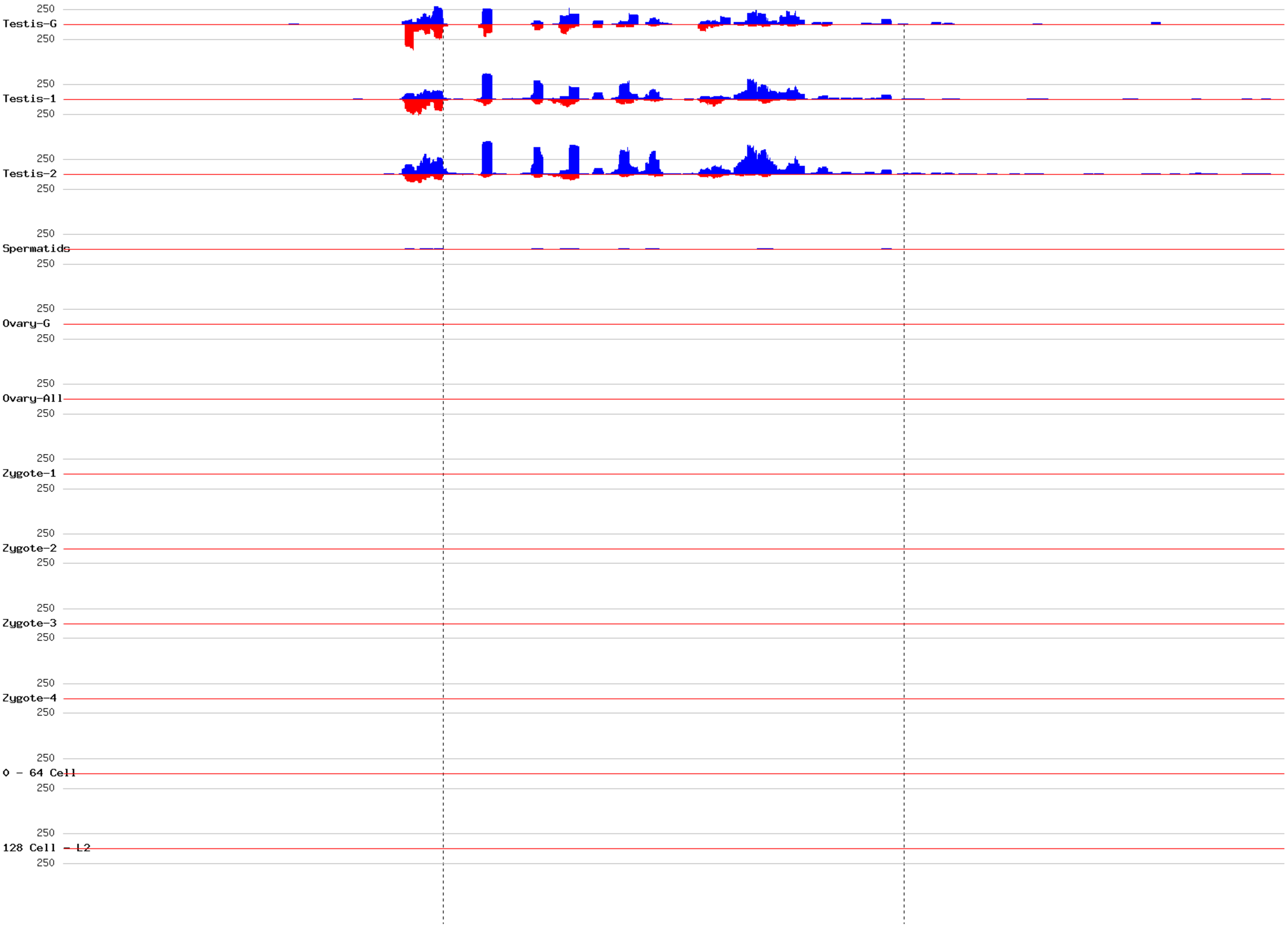
1000
Testis-G
1000
1000
Testis-1
1000
1000
Testis-2
1000
1000
Spermatids
1000
1000
Ovary-G
1000
1000
Ovary-All
1000
1000
Zygote-1
1000
1000
Zygote-2
1000
1000
Zygote-3
1000
1000
Zygote-4
1000
1000
0 - 64 Cell
1000
1000
128 Cell - L2
1000

ASCP_4707_838 Hypothetical_protein 838 bp

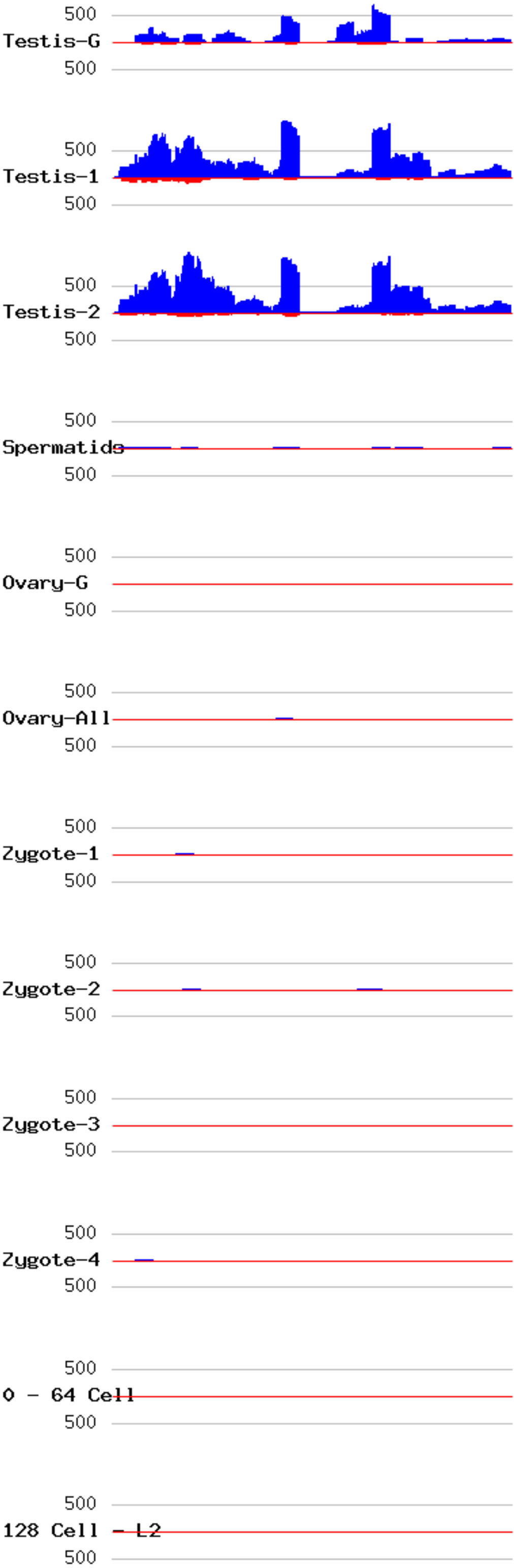



ASCP_4969_802 Hypothetical_protein 802 bp
500
Testis-G
500
500
Testis-1
500
500
Testis-2
500
500
Spermatids
500
500
Ovary-G
500
500
Ovary-All
500
500
Zygote-1
500
500
Zygote-2
500
500
Zygote-3
500
500
Zygote-4
500
500
0 - 64 Cell
500
500
128 Cell - L2
500

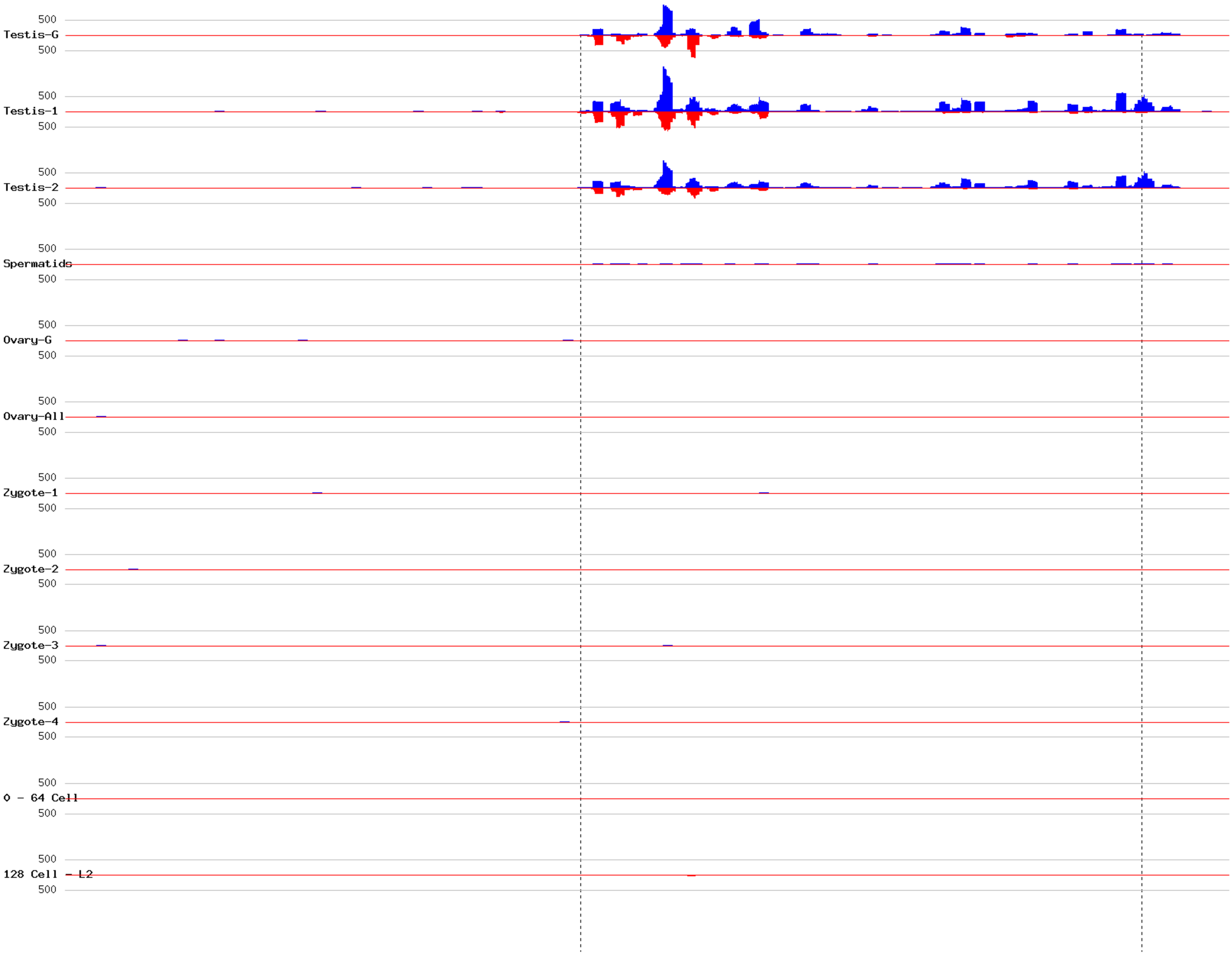
ASCP_603_3258 Protein_kinase_domain_containing_protein 3258 bp



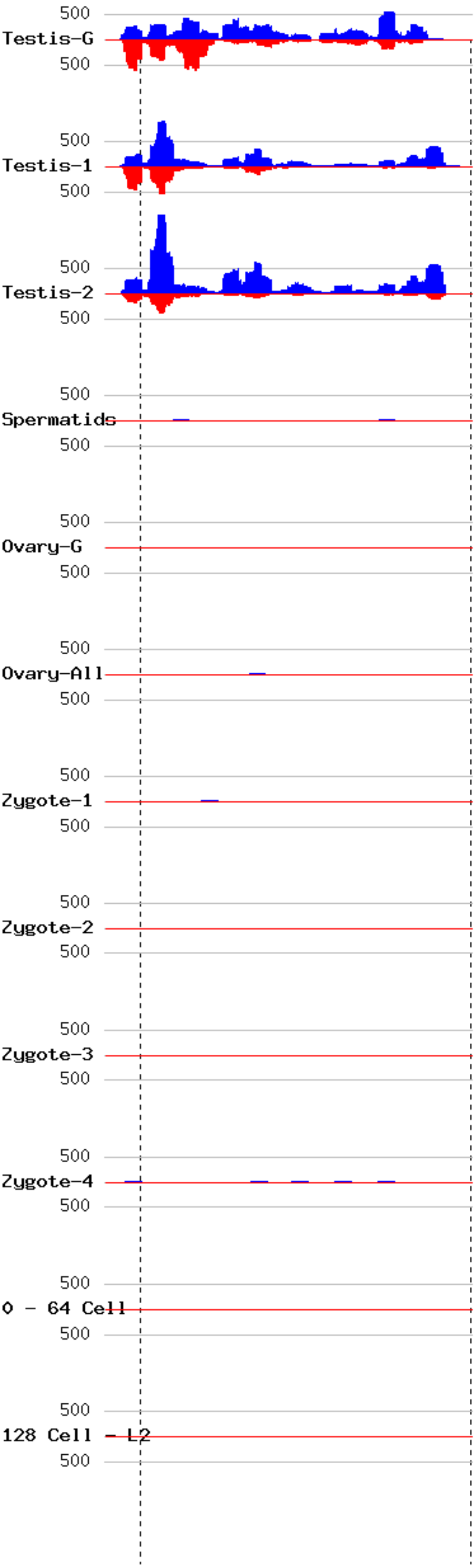
ASCP_6784_591 TB2/DP1_HVA22_family_protein 591



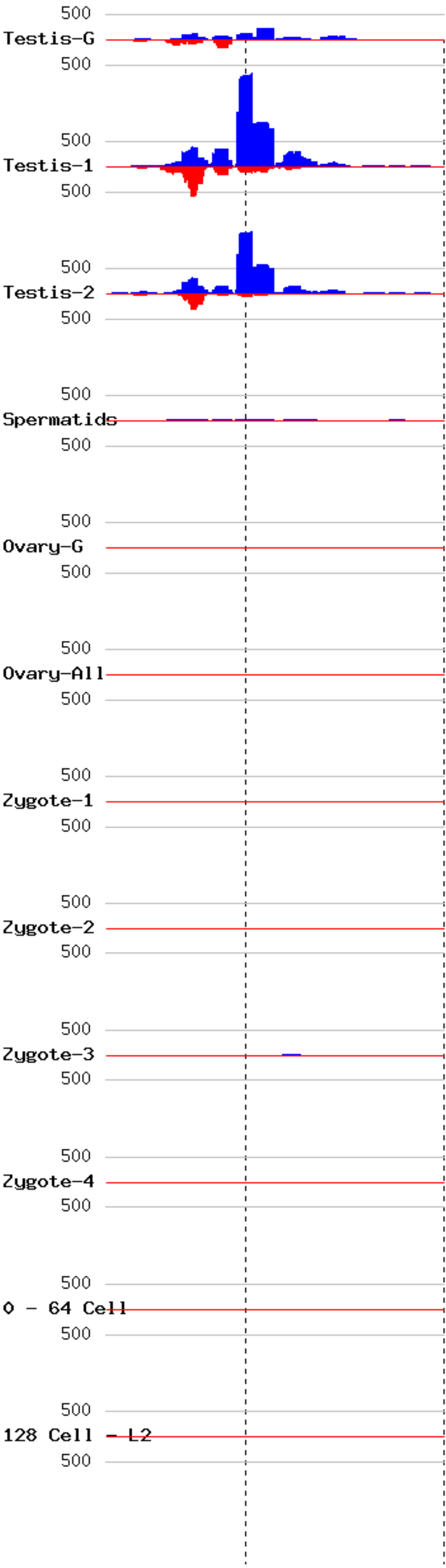
ASCP_690_3049 Tyrosine-protein_kinase_Fer 3049 bp



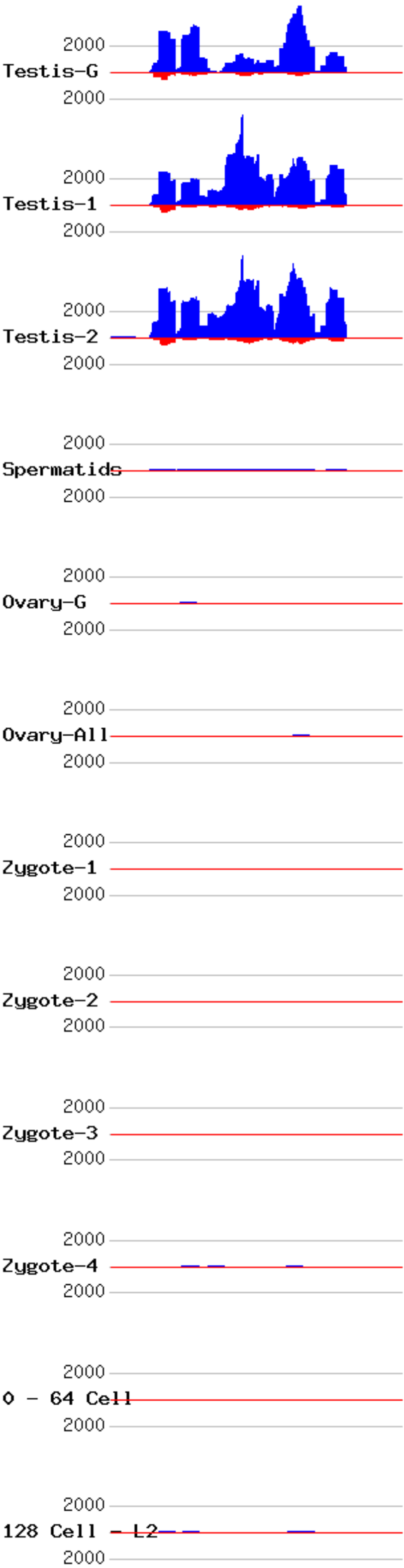
ASCP_6918_579 Hypothetical_protein 579 bp



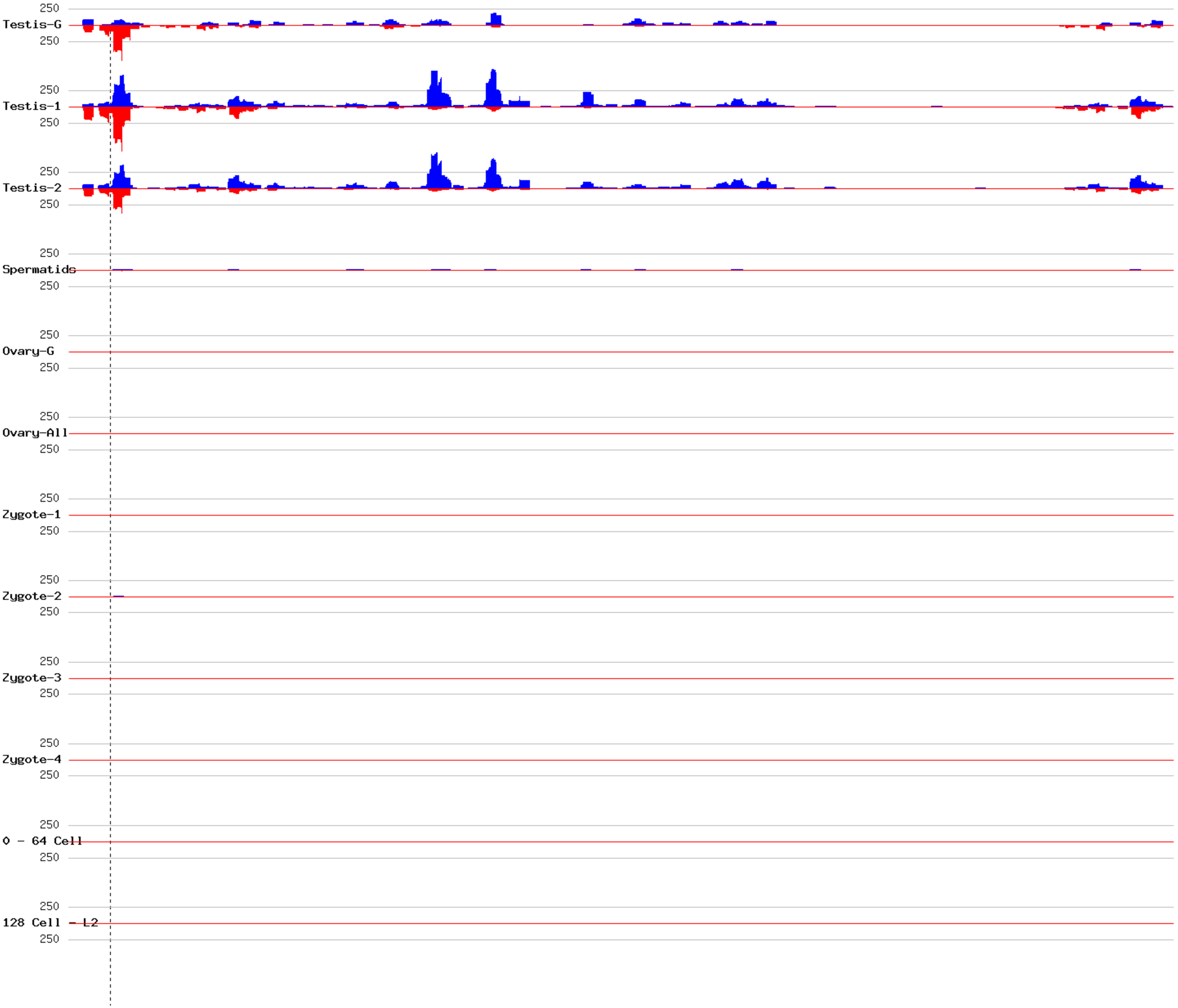
ASCP_7376_533 Protein-tyrosine_phosphatase_



ASCP_8247_440 Hypothetical_protein 440



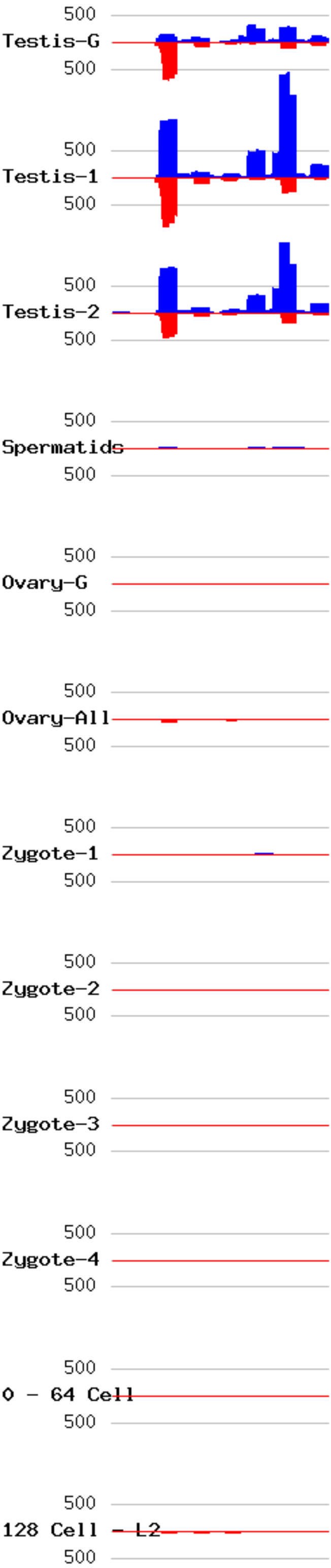
ASCP_871_2704 Protein_kinase_domain_containing_protein 2704 bp



ASCP_8747_383 Hypothetical_protein



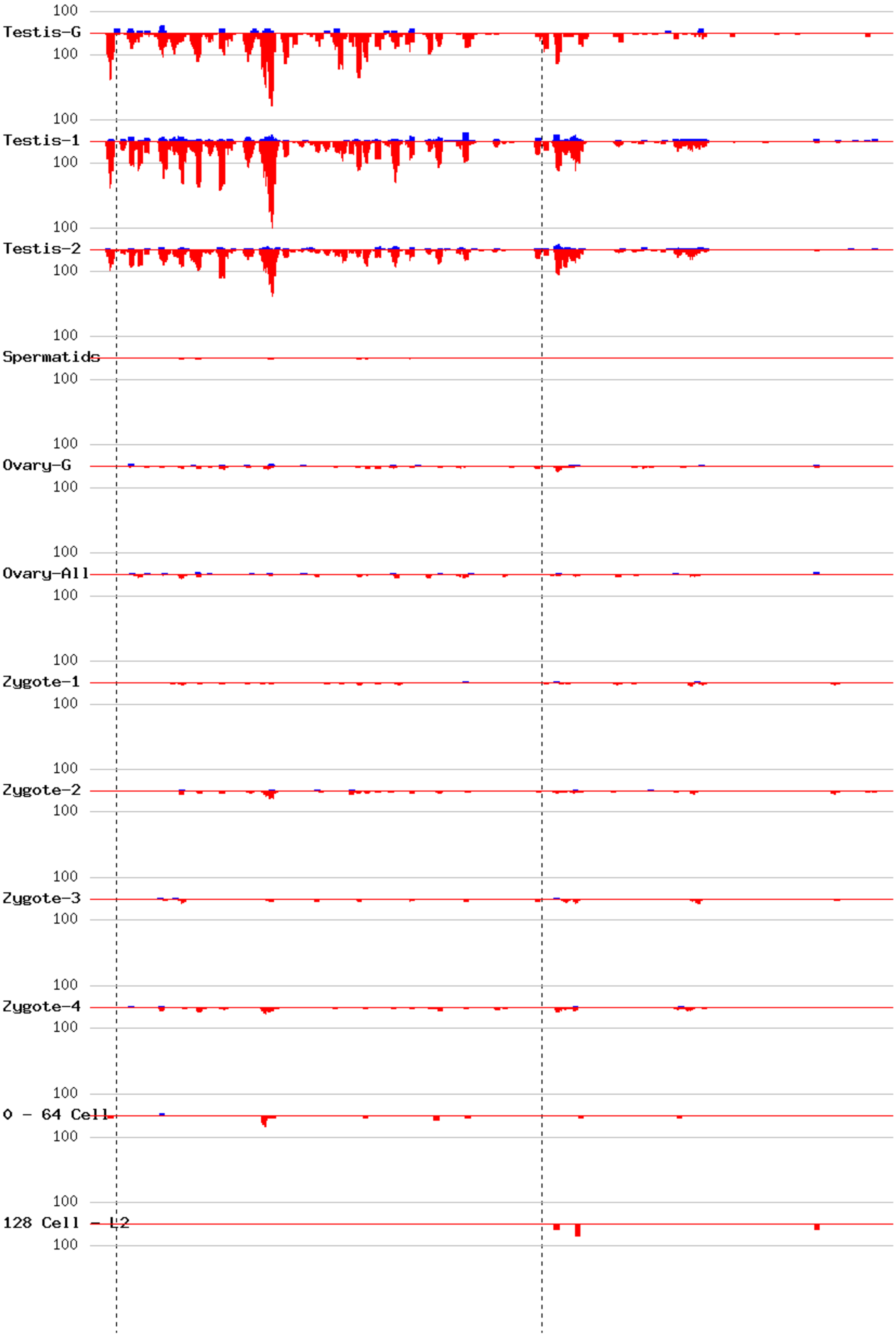
ASCP_9239_321 Major_sperm_prote



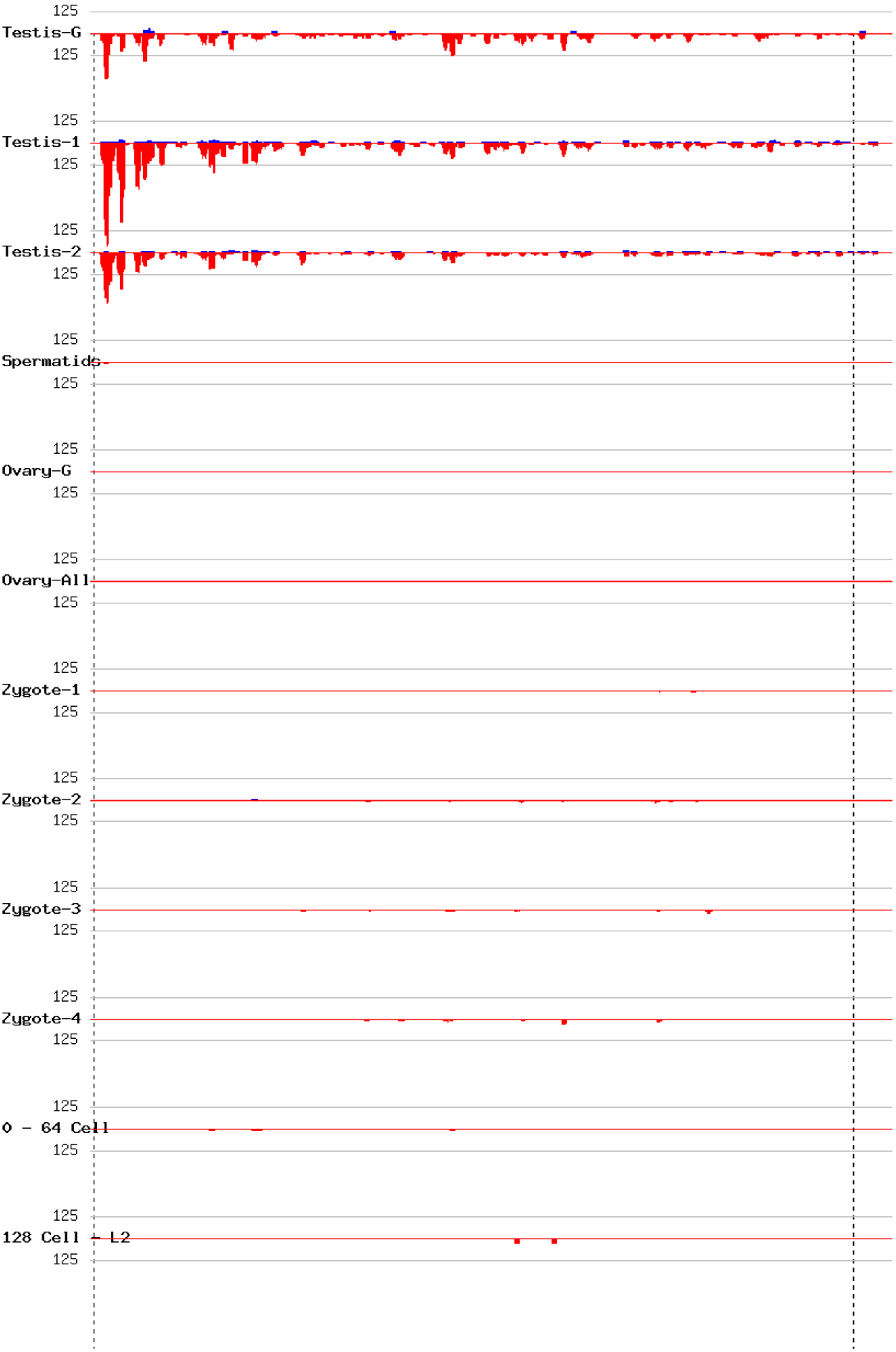
ASCF_1010_3730 Hypothetical_protein 3730 bp

ASCF_1021_3717 Hypothetical_protein 3717 bp

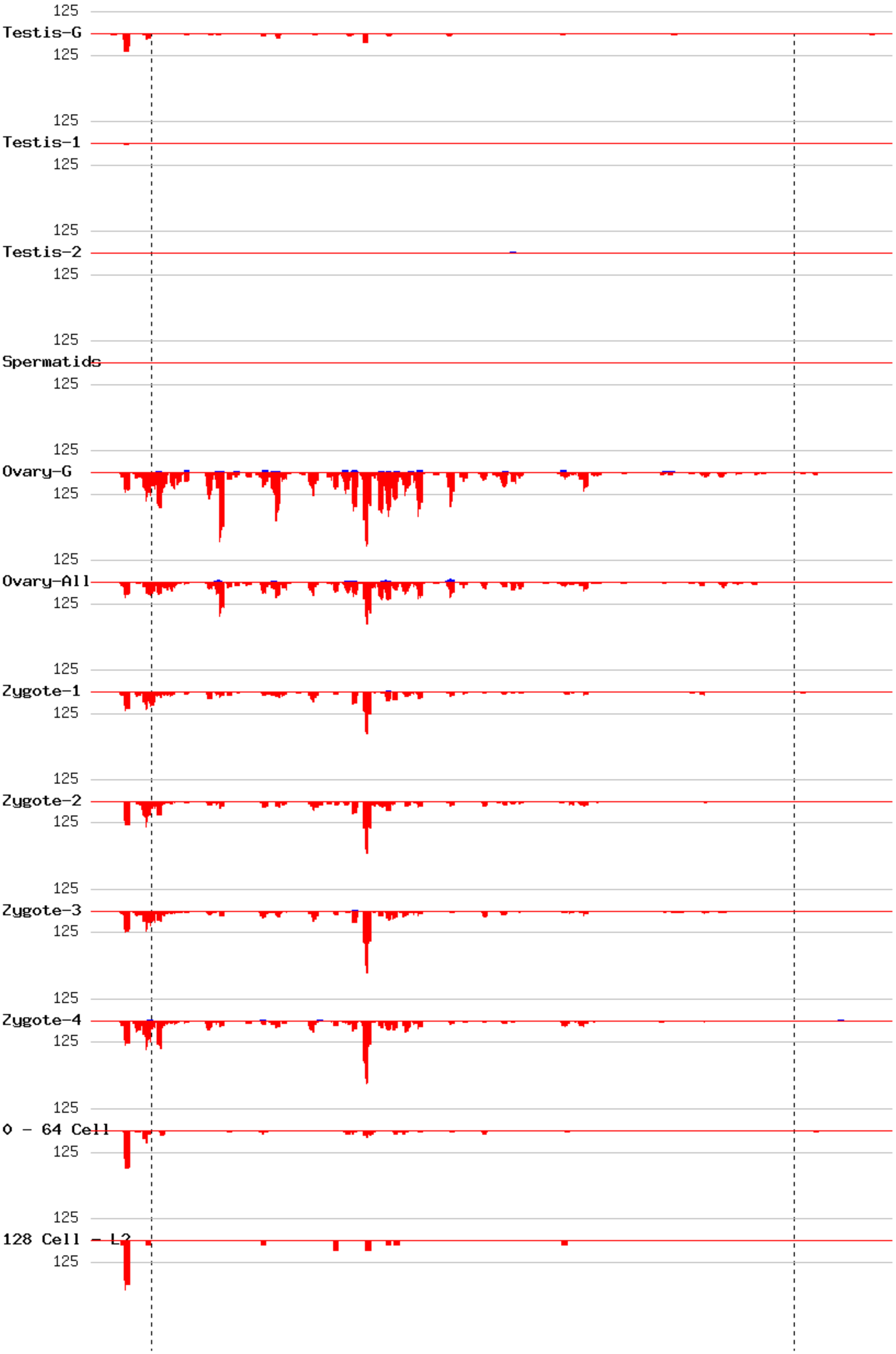
ASCF_1026_3709 Zinc_finger_C2H2_type_family_protein 3709 bp



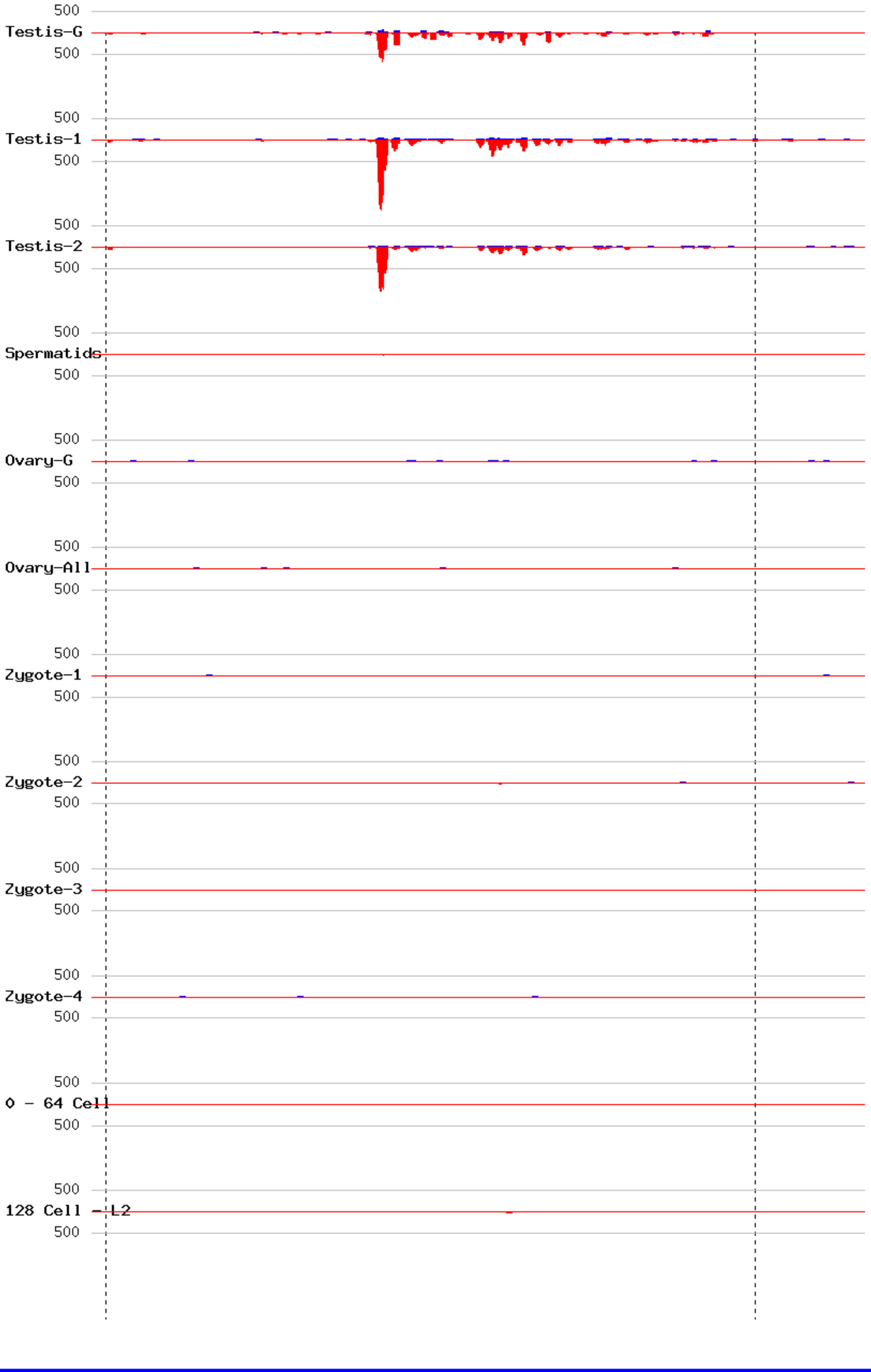
ASCF_1062_3656 Hypothetical_protein 3656 bp



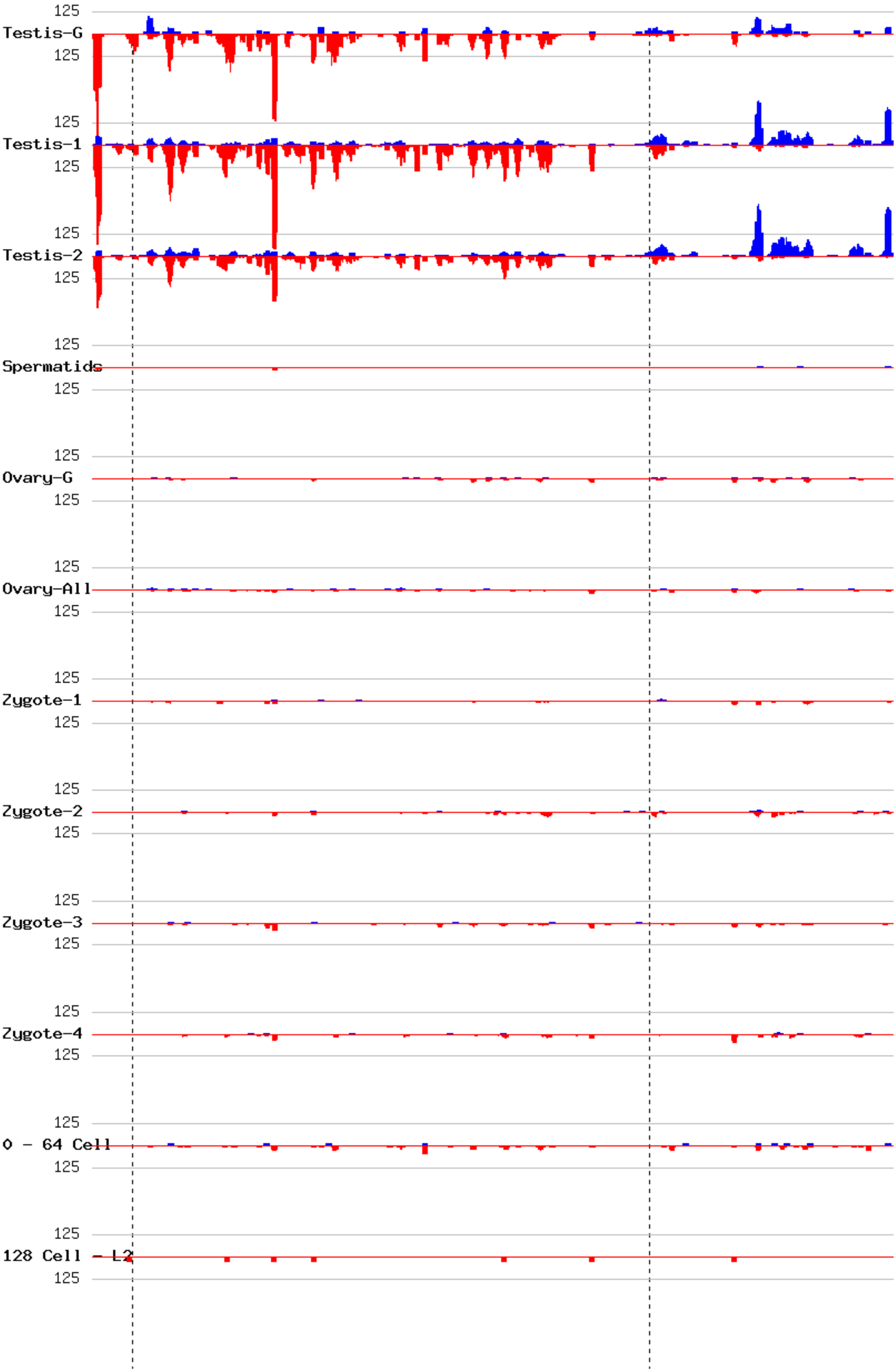
ASCF_1066_3652 Hypothetical_protein 3652 bp



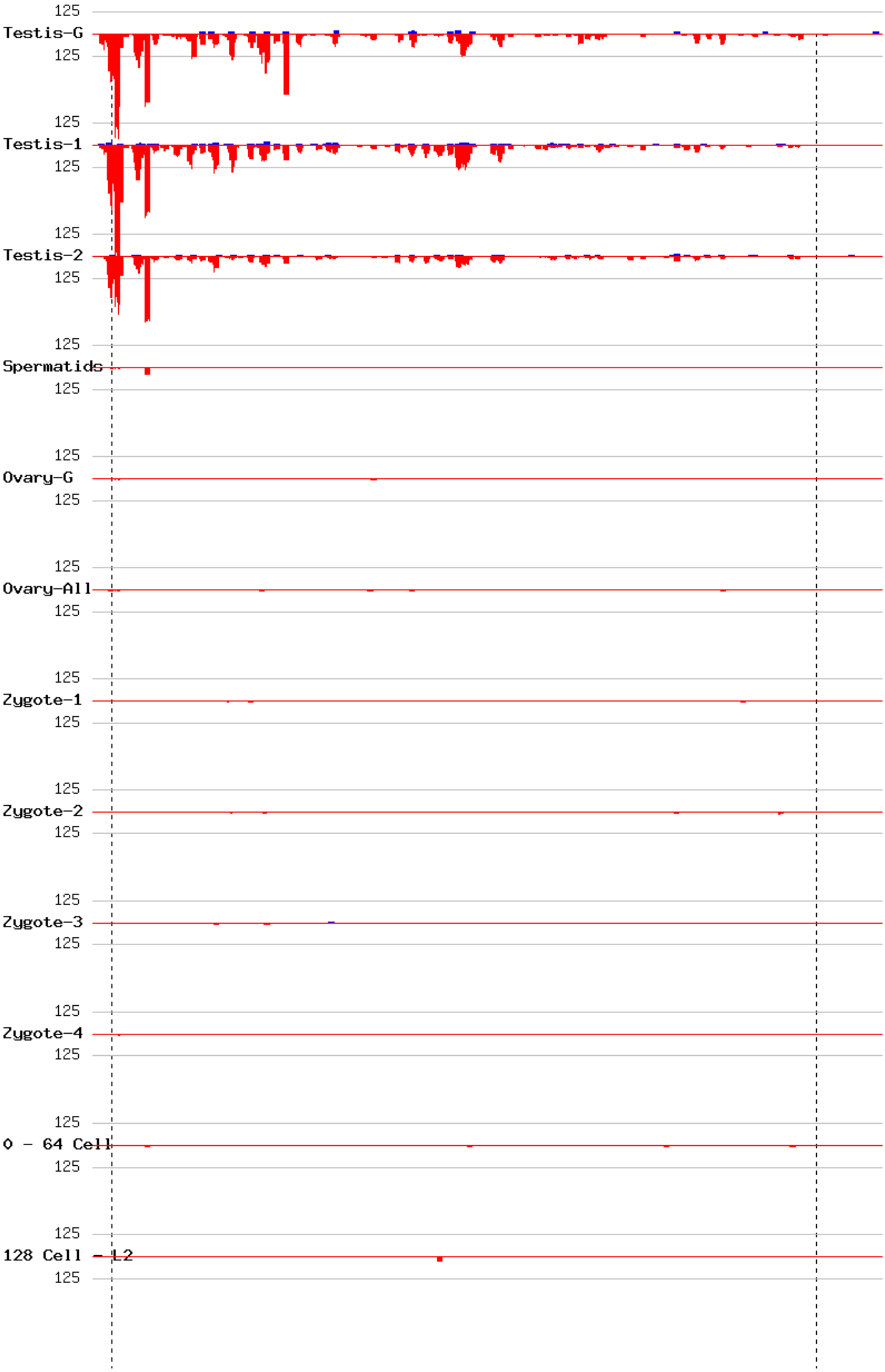
ASCF_1109_3609 Hypothetical_protein 3609 bp



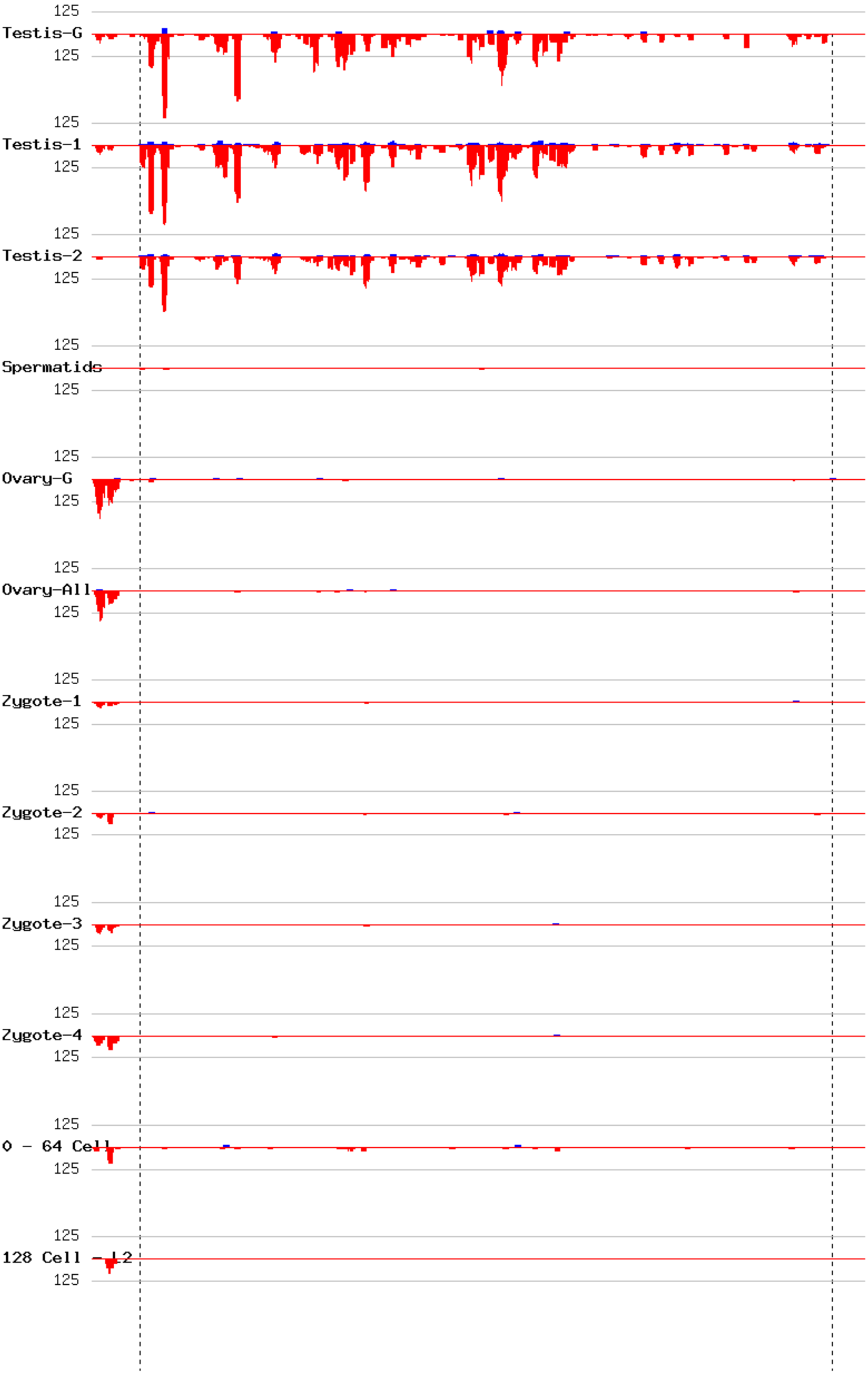
ASCF_1117_3604 RNA_binding_protein 3604 bp



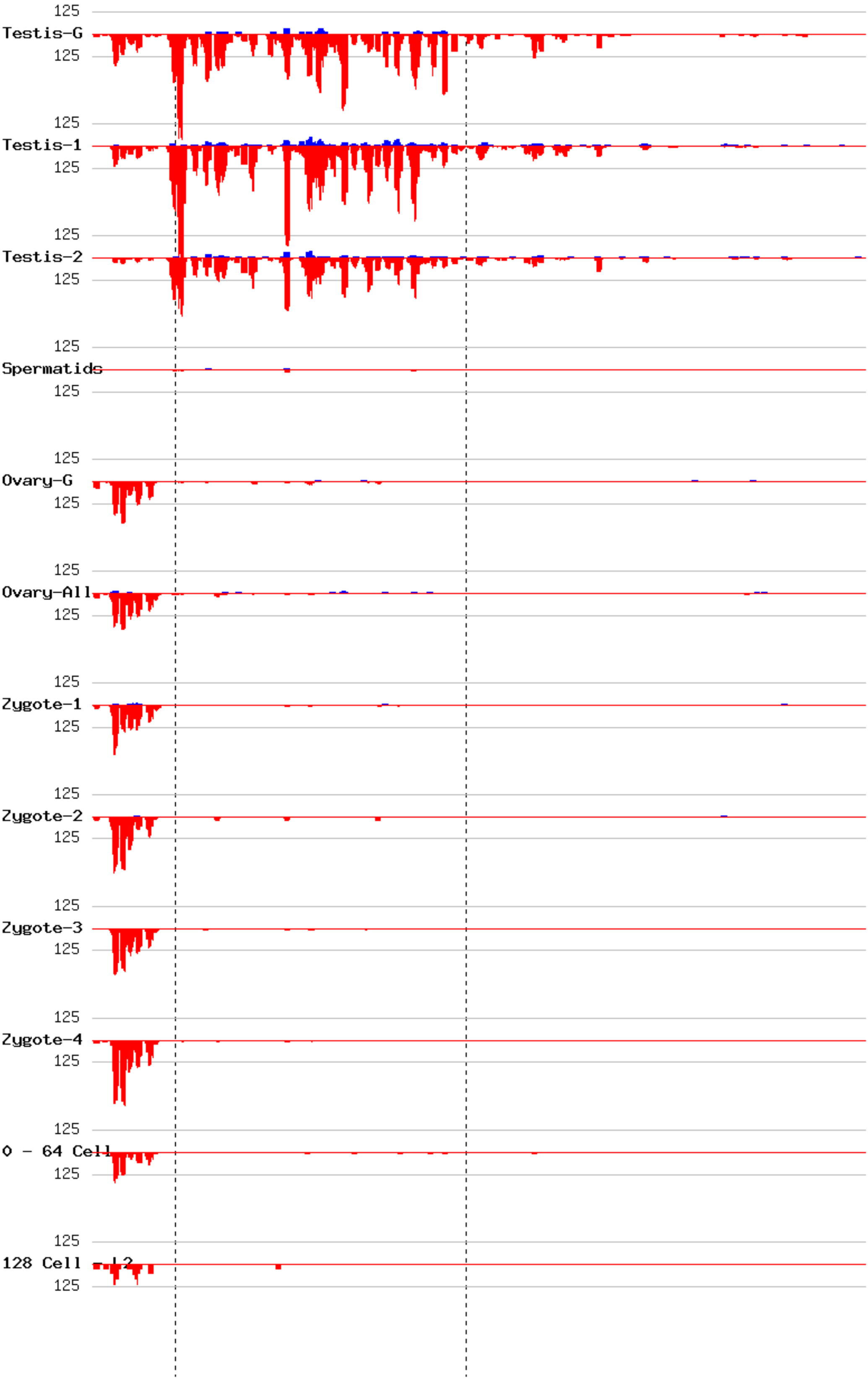
ASCF_1171_3550 Patched_related_family_protein_5 3550 bp



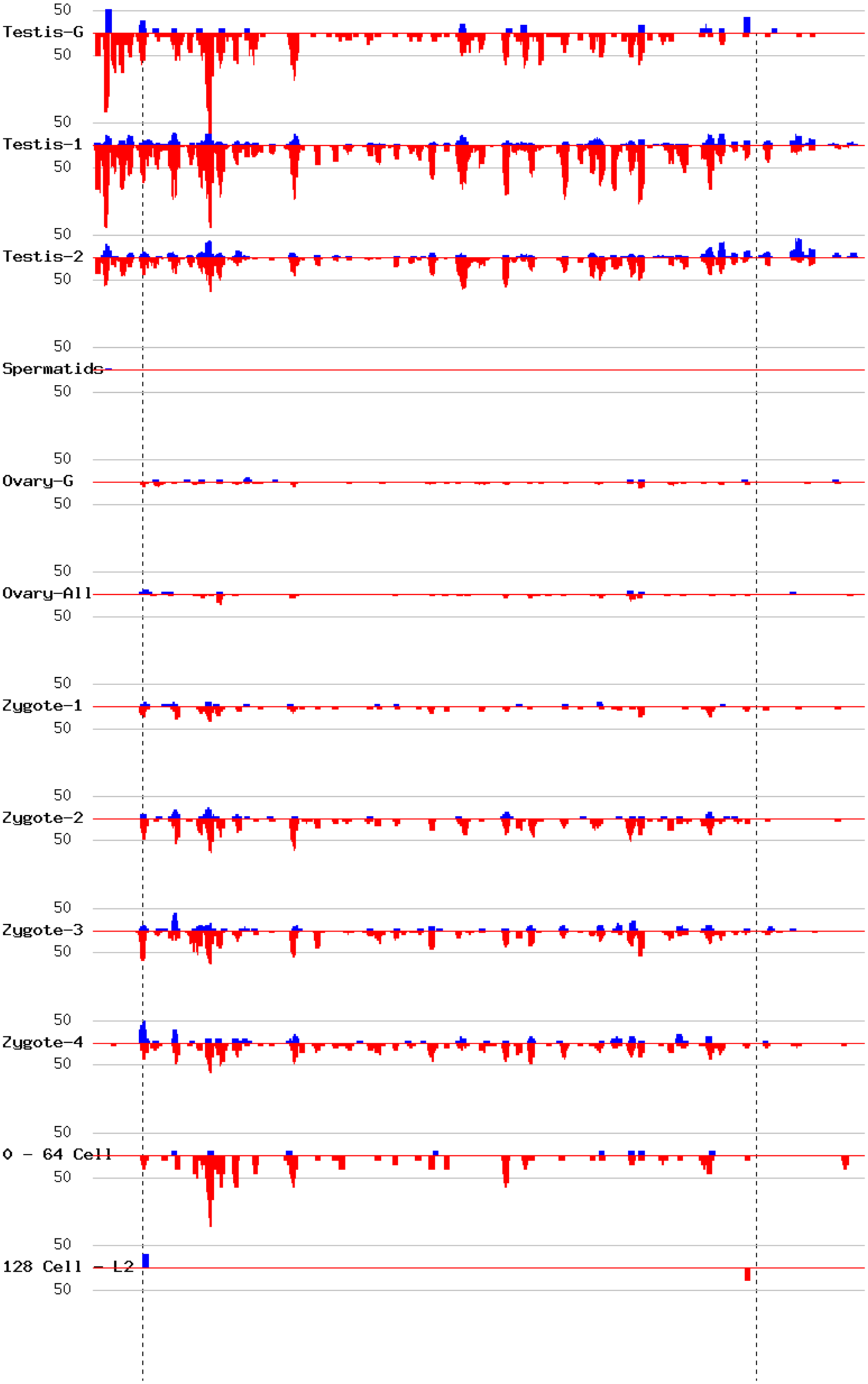
ASCF_1247_3473 Kinesin_motor_domain_containing_protein 3473 bp



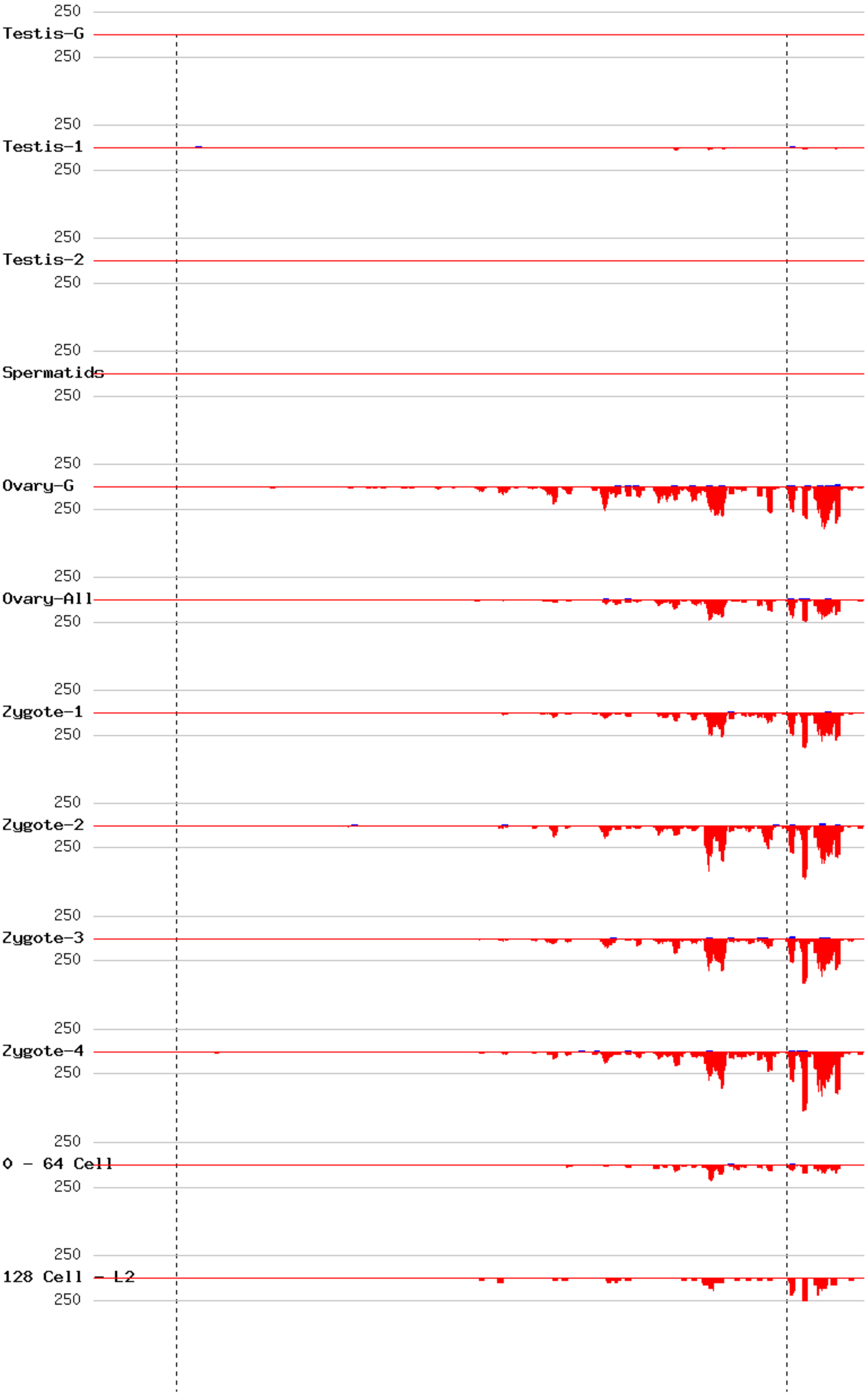
ASCF_1262_3459 Conserved_germline_helicase_protein_1 3459 bp



ASCF_1278_3439 Hypothetical_protein 3439 bp



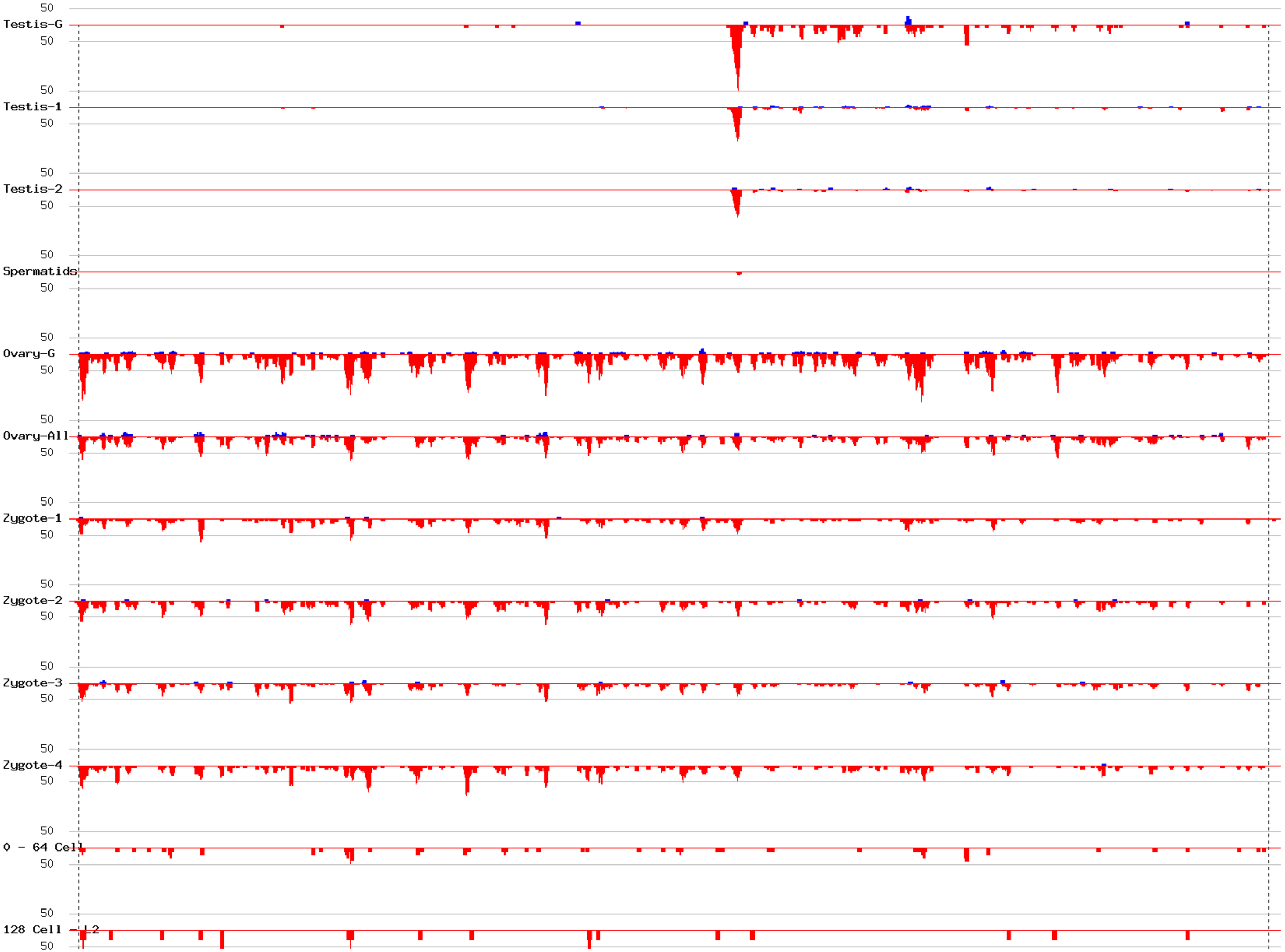
ASCF_1313_3405 Hypothetical_protein 3405 bp



ASCF_134_7365 SET_domain_containing_protein 7365 bp

100
Testis-G
100
100
Testis-1
100
100
Testis-2
100
100
Spermatids
100
100
Ovary-G
100
100
Ovary-All
100
100
Zygote-1
100
100
Zygote-2
100
100
Zygote-3
100
100
Zygote-4
100
100
0 - 64 Cell
100
100
128 Cell - L2
100

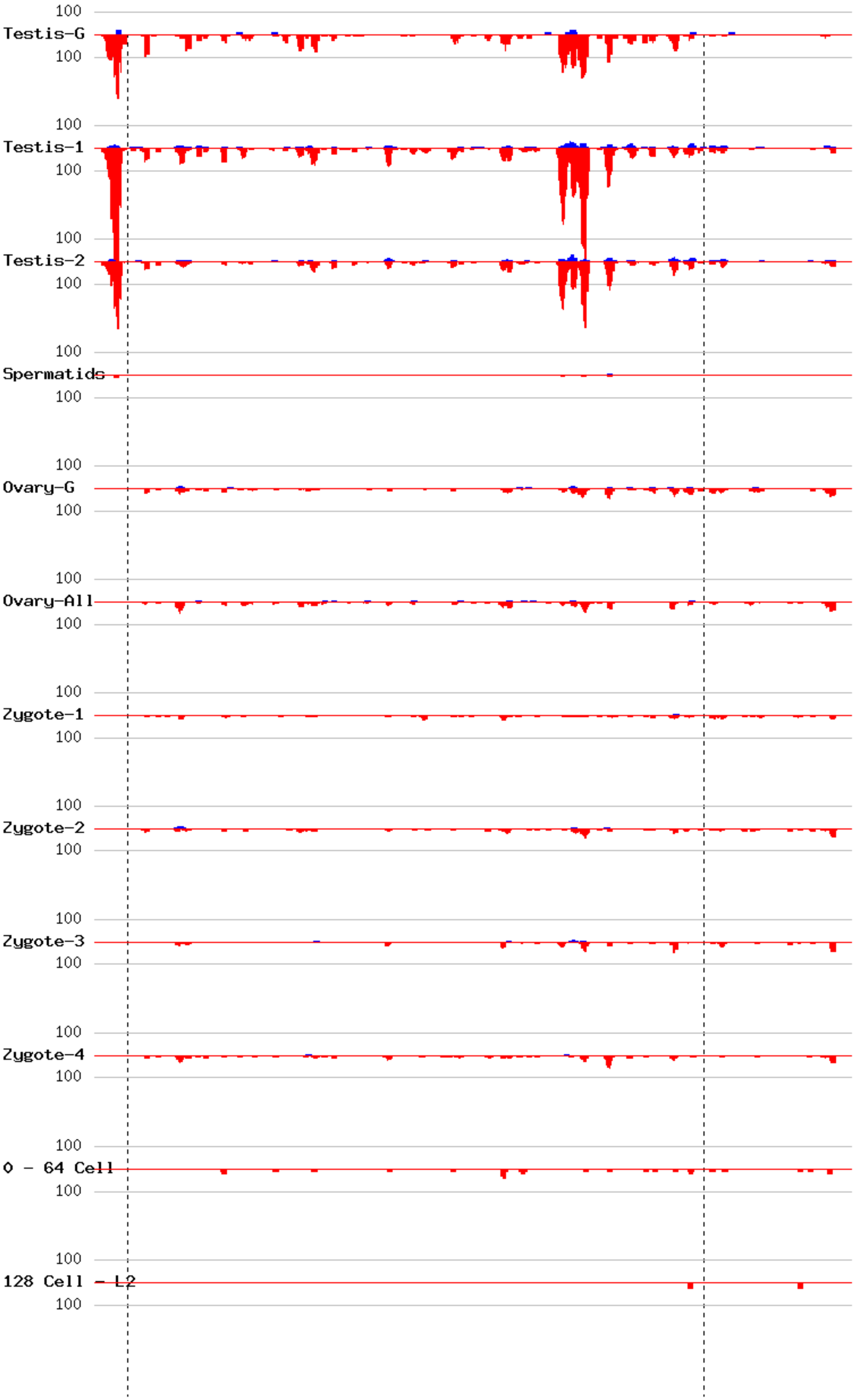
ASCF_135_7359 Neurofibromatosis_type_1 7359 bp



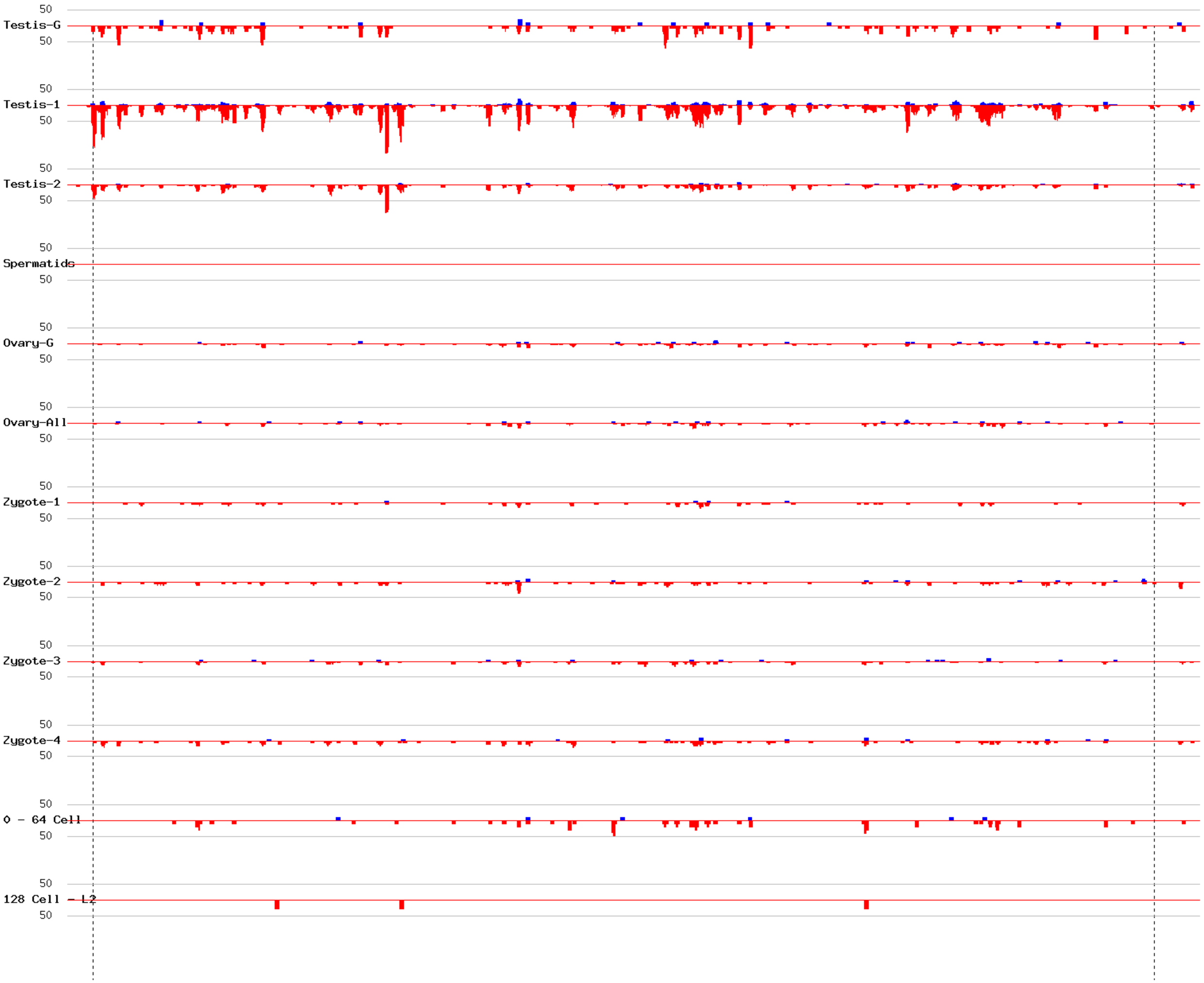
ASCF_136_7355 Protein_kinase_domain_containing_protein 7355 bp

125
Testis-G
125
125
Testis-1
125
125
Testis-2
125
125
Spermatids
125
125
Ovary-G
125
125
Ovary-All
125
125
Zygote-1
125
125
Zygote-2
125
125
Zygote-3
125
125
Zygote-4
125
125
0 - 64 Cell
125
125
128 Cell - L2
125

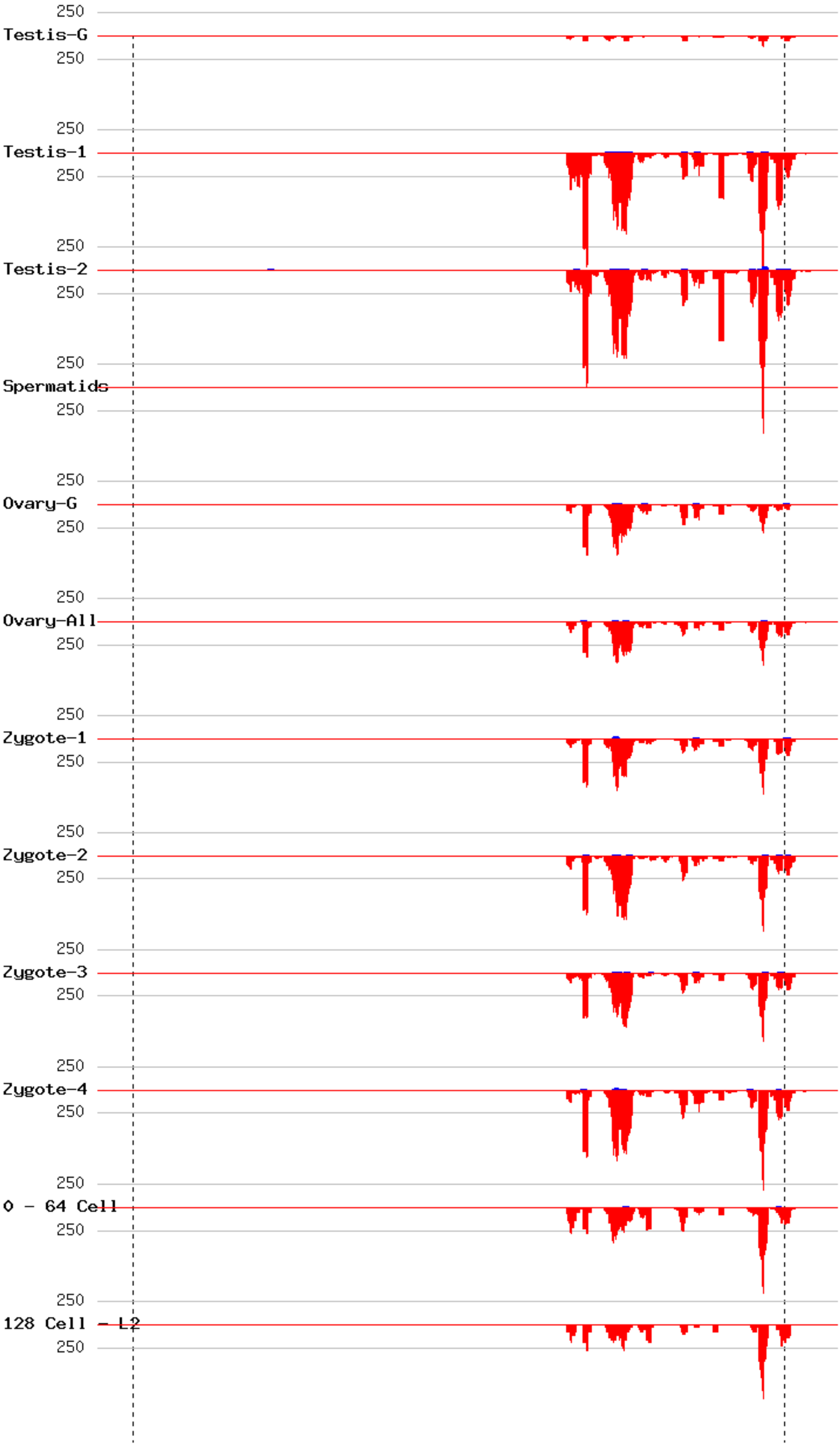
ASCF_1370_3337 Hypothetical_protein 3337 bp



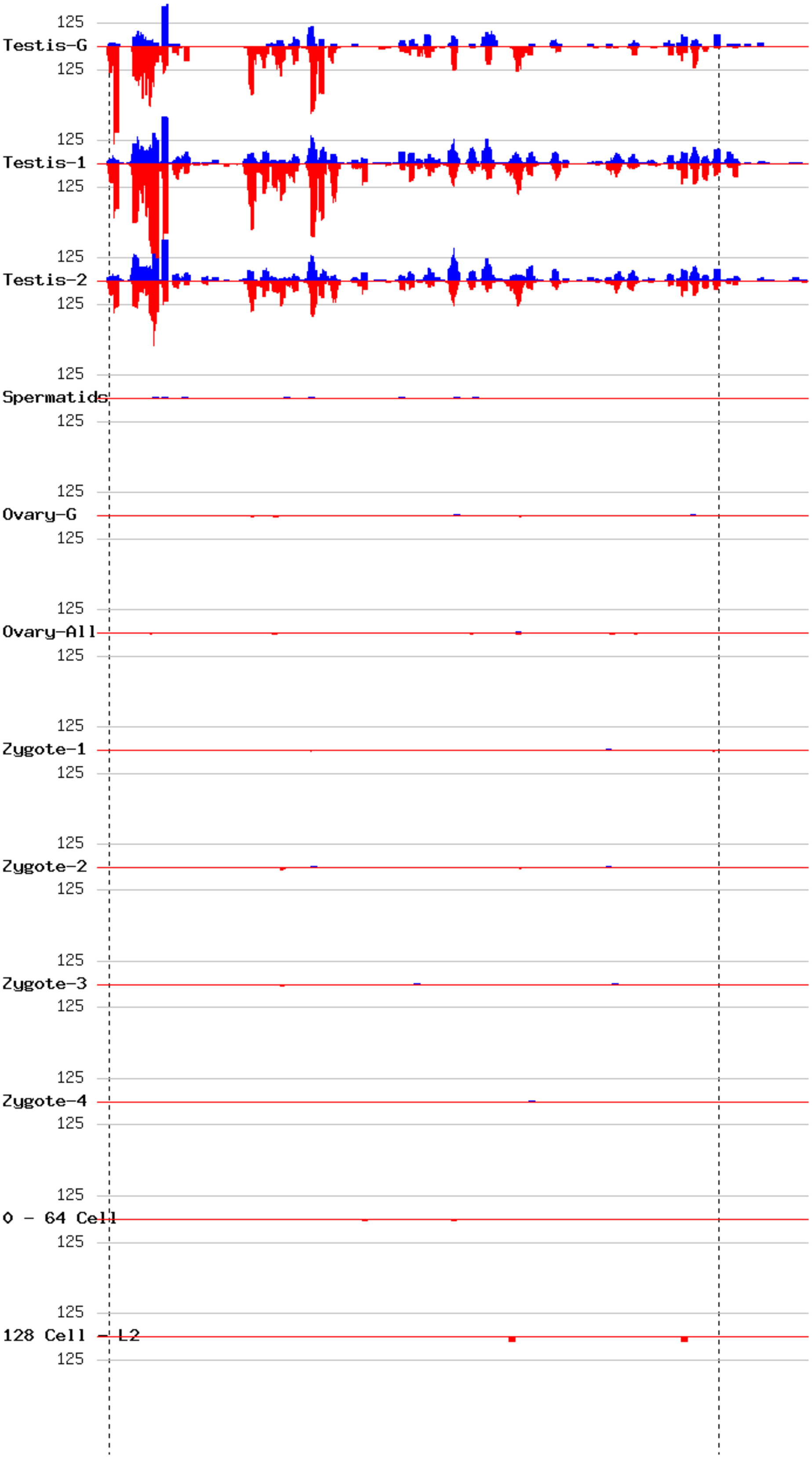
ASCF_153_7128 Hypothetical_protein 7128 bp



ASCF_1555_3157 Polypeptide_N-acetylgalactosaminyltransferase 3157 bp



ASCF_1705_3033 Sulfate_permease_family_protein_6 3033 bp



ASCF_1715_3023 Hypothetical_protein 3023 bp

125
Testis-G
125

125
Testis-1
125

125
Testis-2
125

125
Spermatids
125

125
Ovary-G
125

125
Ovary-All
125

125
Zygote-1
125

125
Zygote-2
125

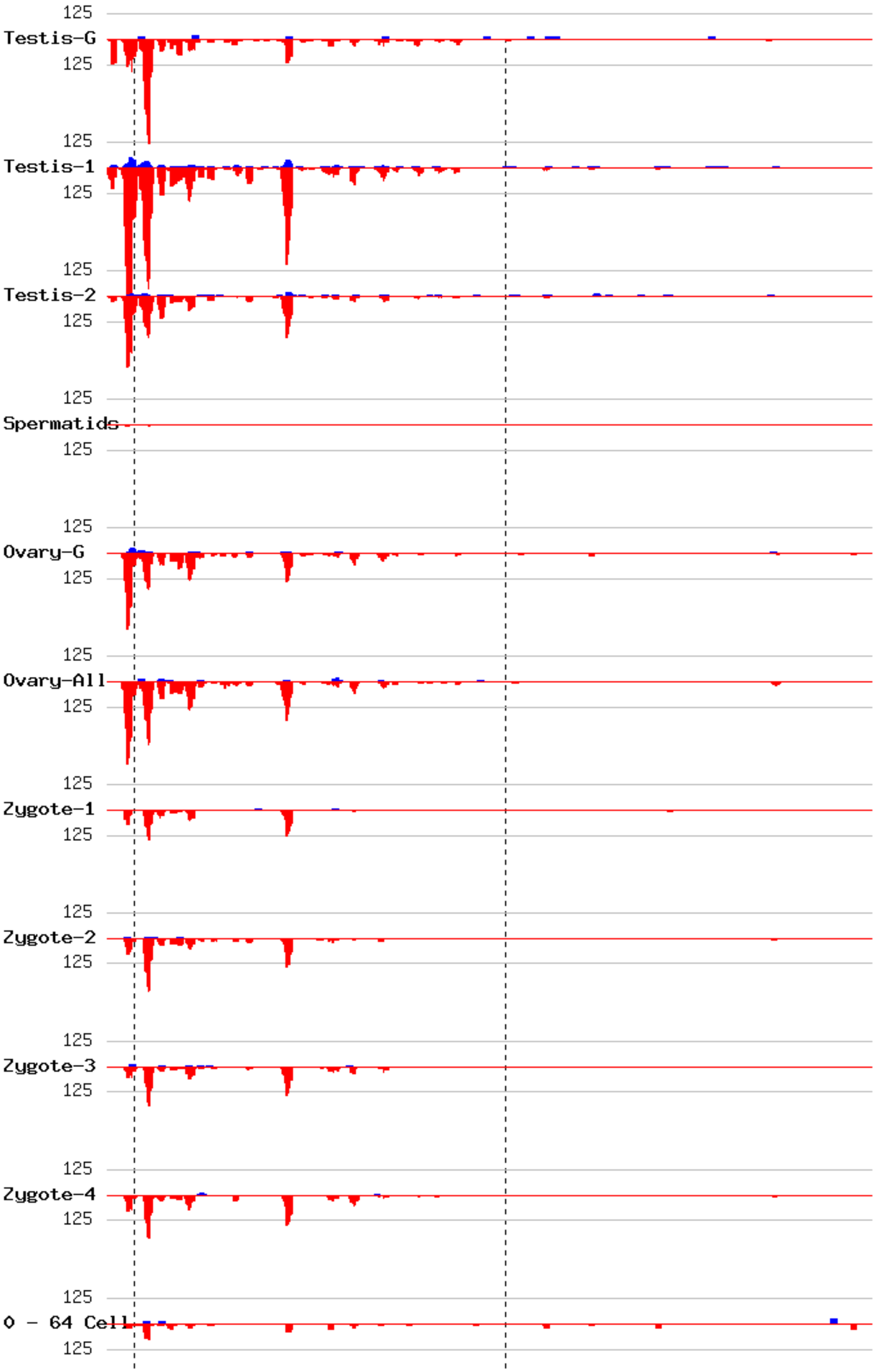
125
Zygote-3
125

125
Zygote-4
125

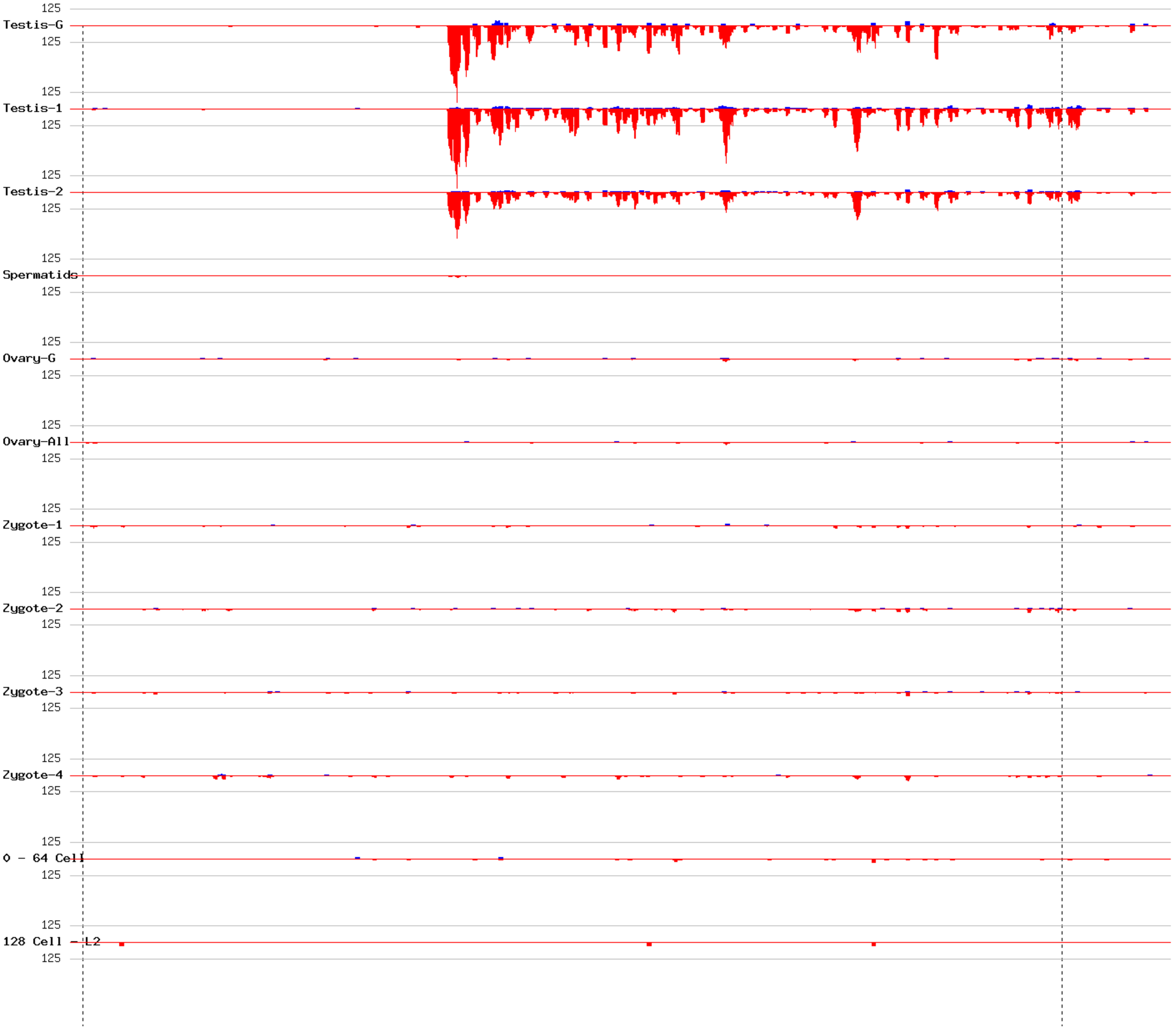
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125

125
128 Cell - L2
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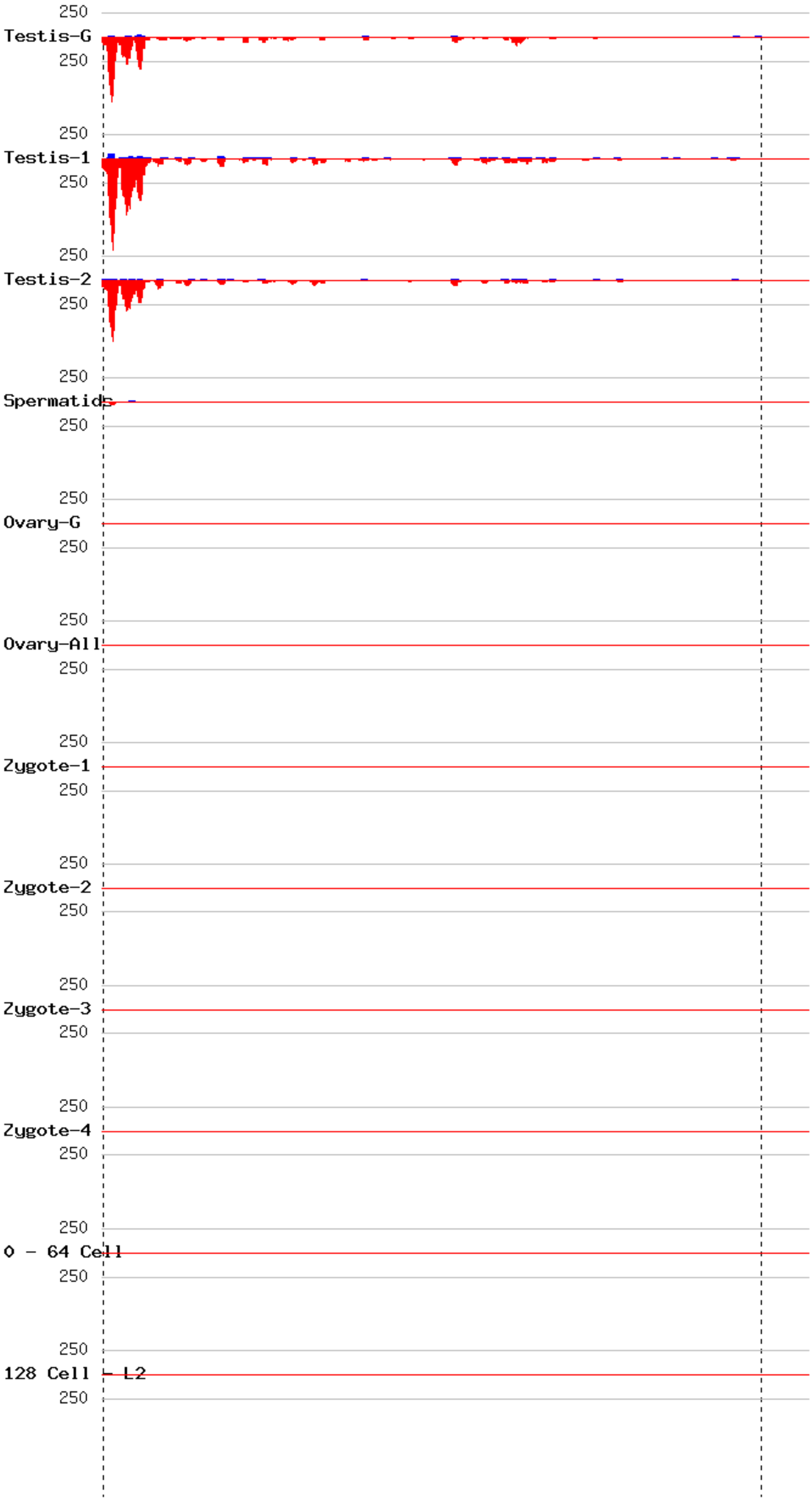
ASCF_1783_2975 SH3_domain-binding_protein 2975 bp



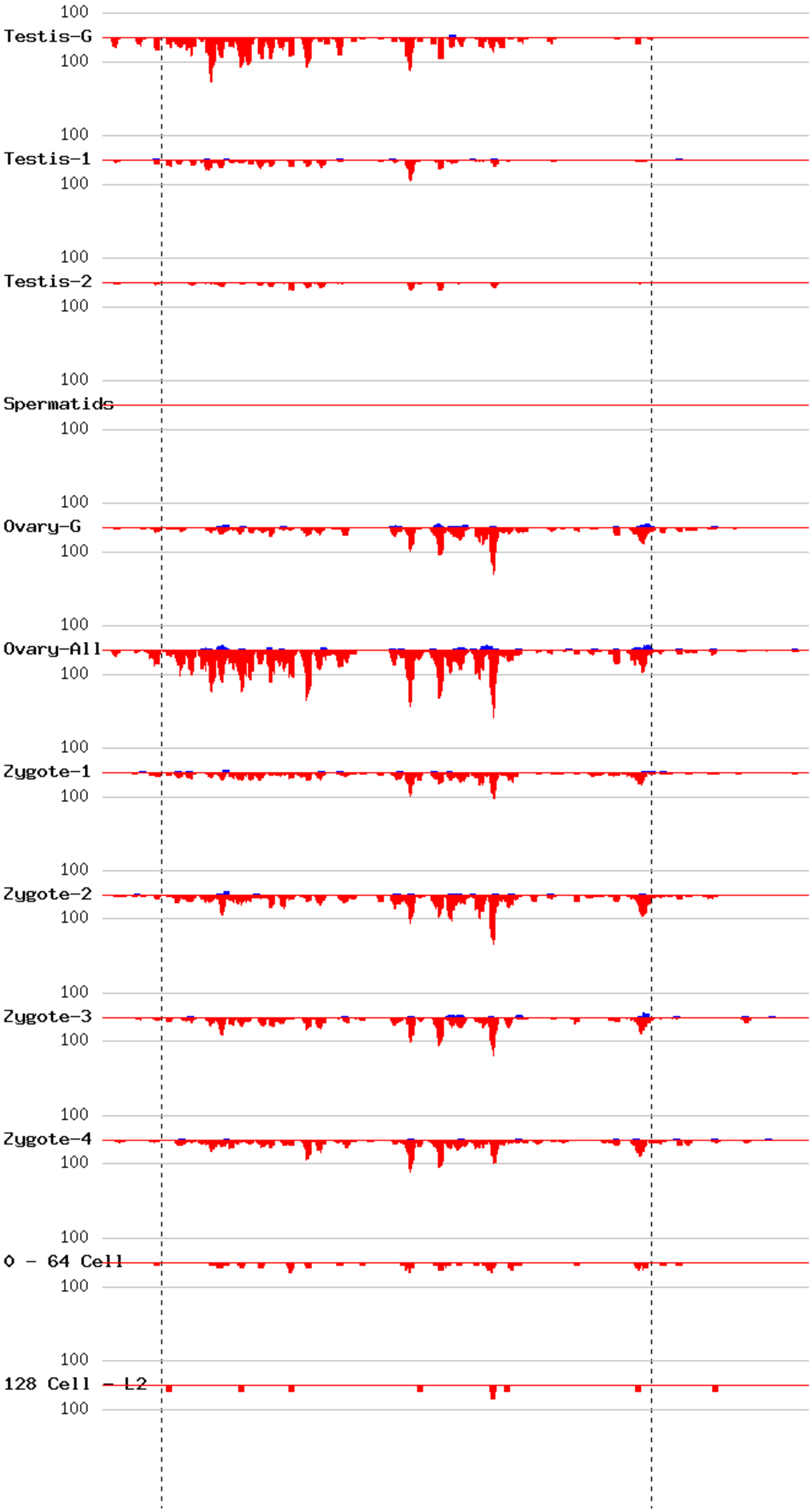
ASCF_188_6600 Hypothetical_protein 6600 bp



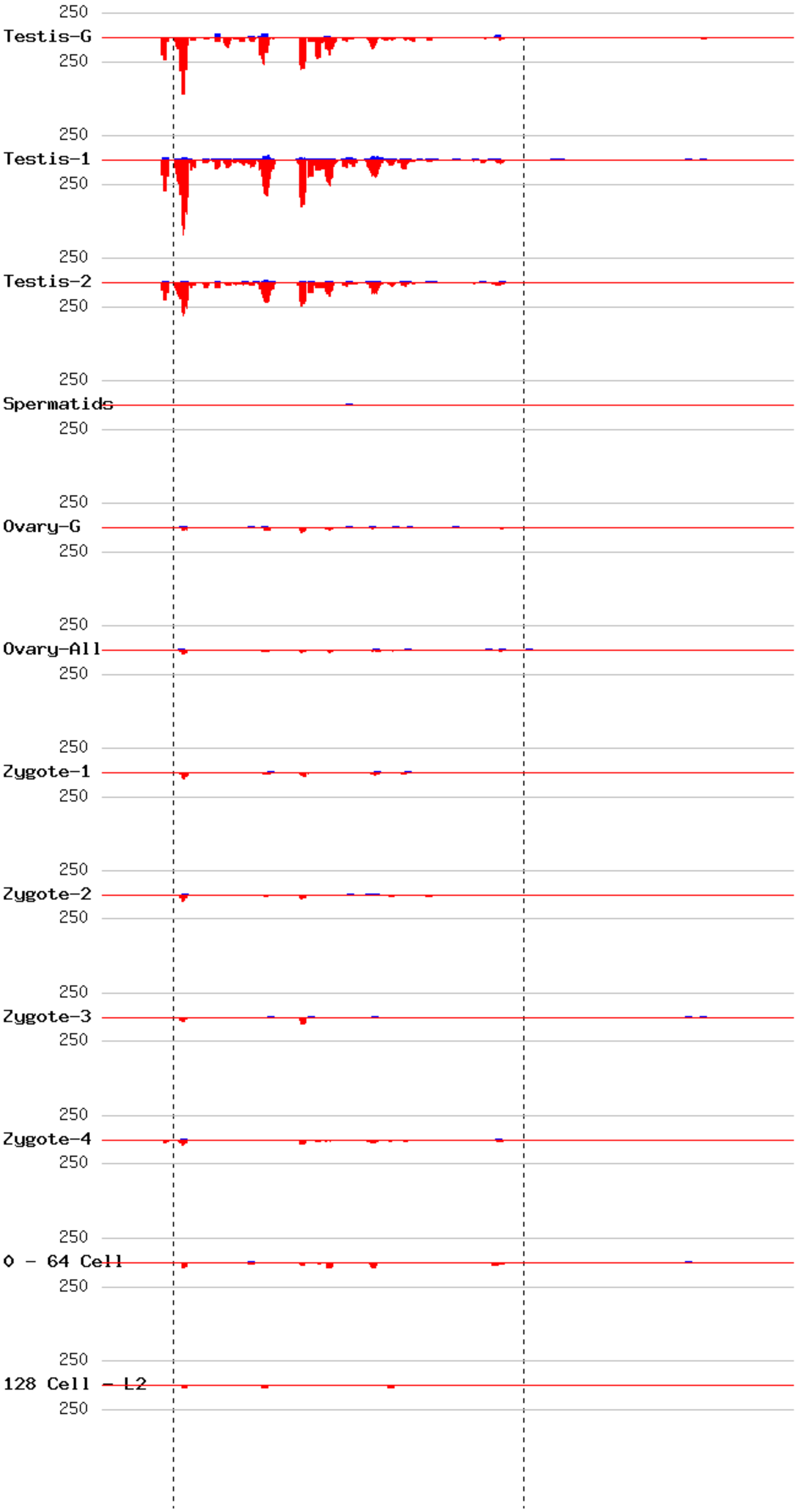
ASCF_1881_2906 Hypothetical_protein 2906 bp



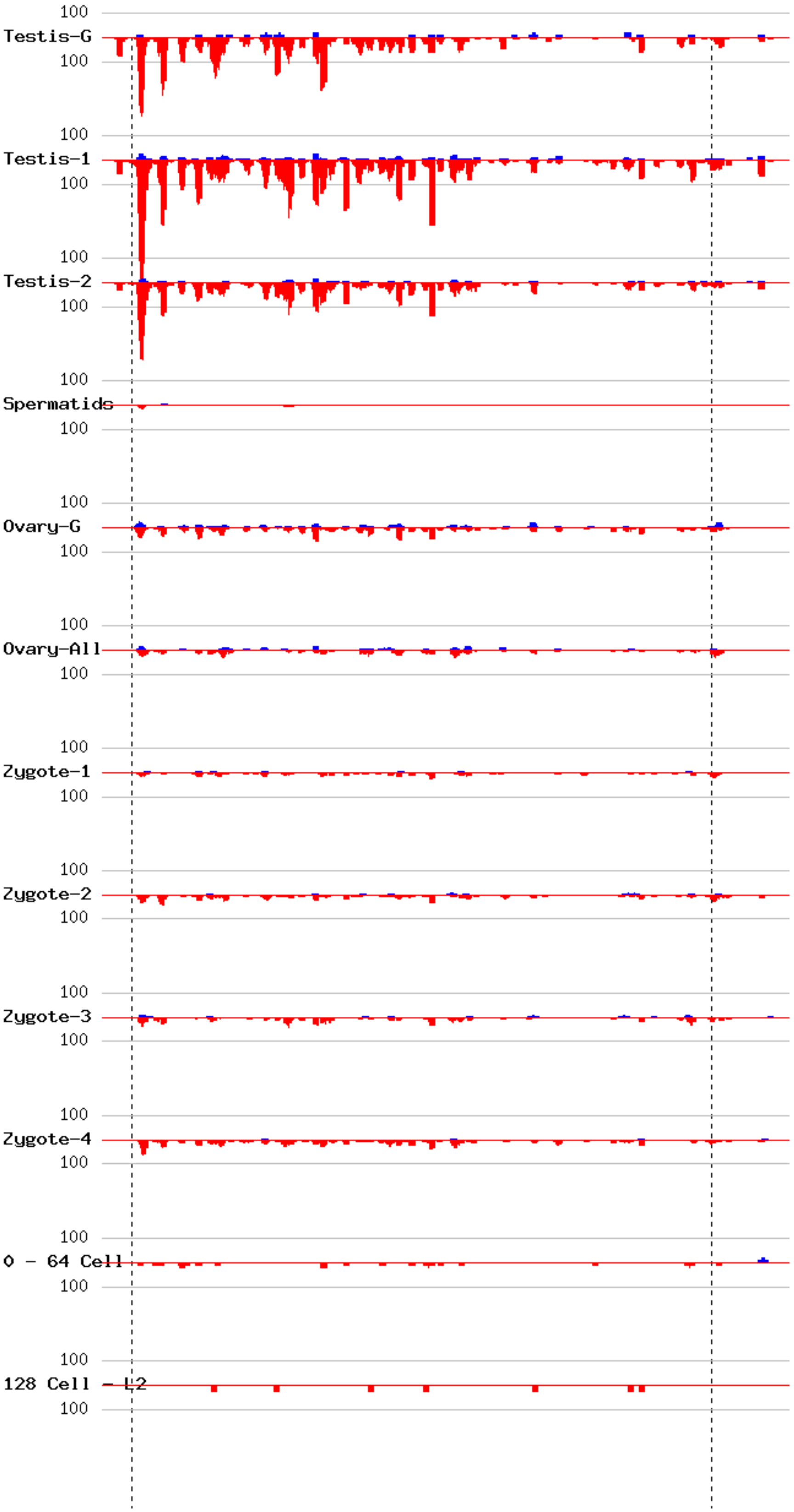
ASCF_1918_2880 Hypothetical_protein 2880 bp



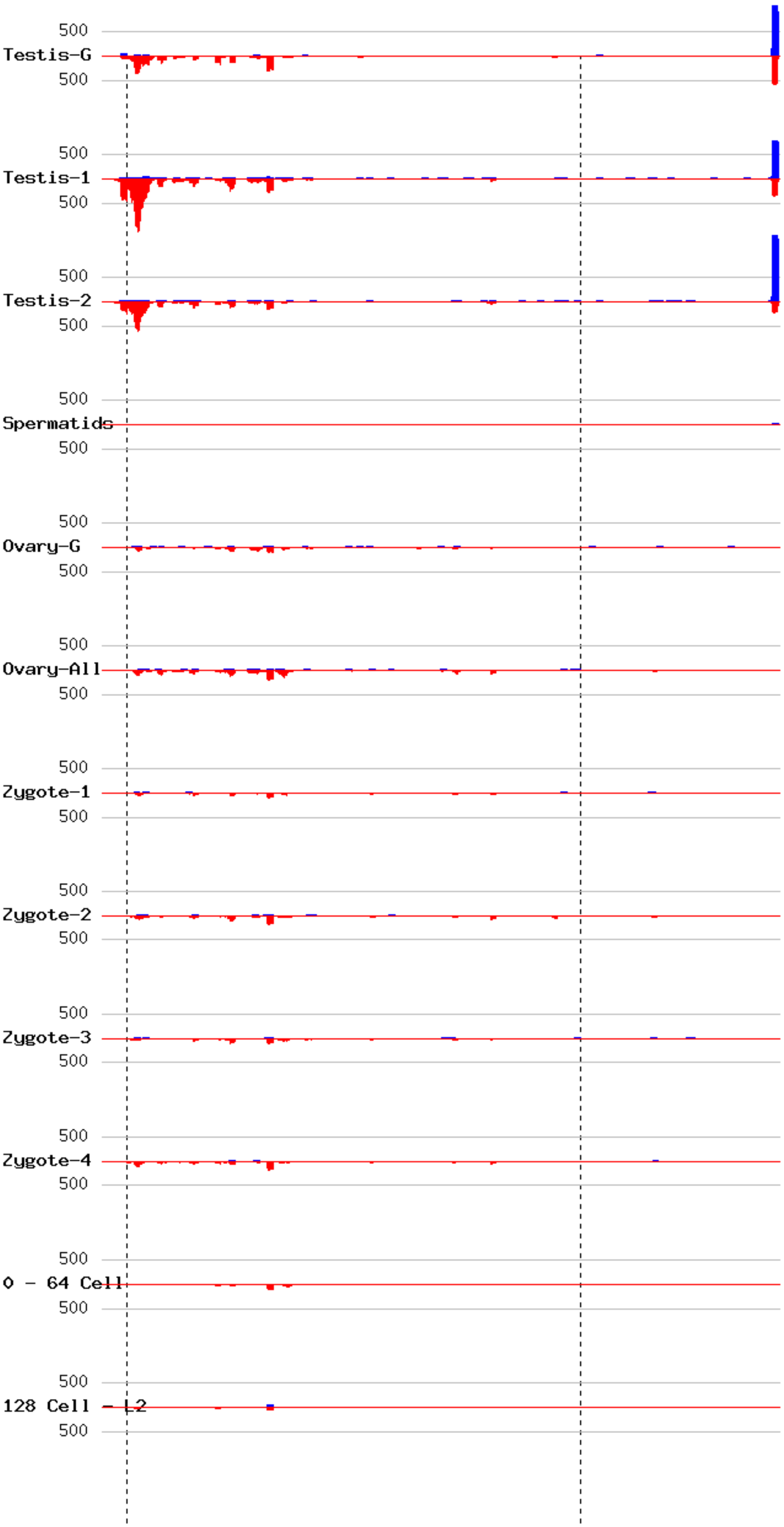
ASCF_2011_2823 LMBR1-like_conserved_region_family_protein 2823 bp



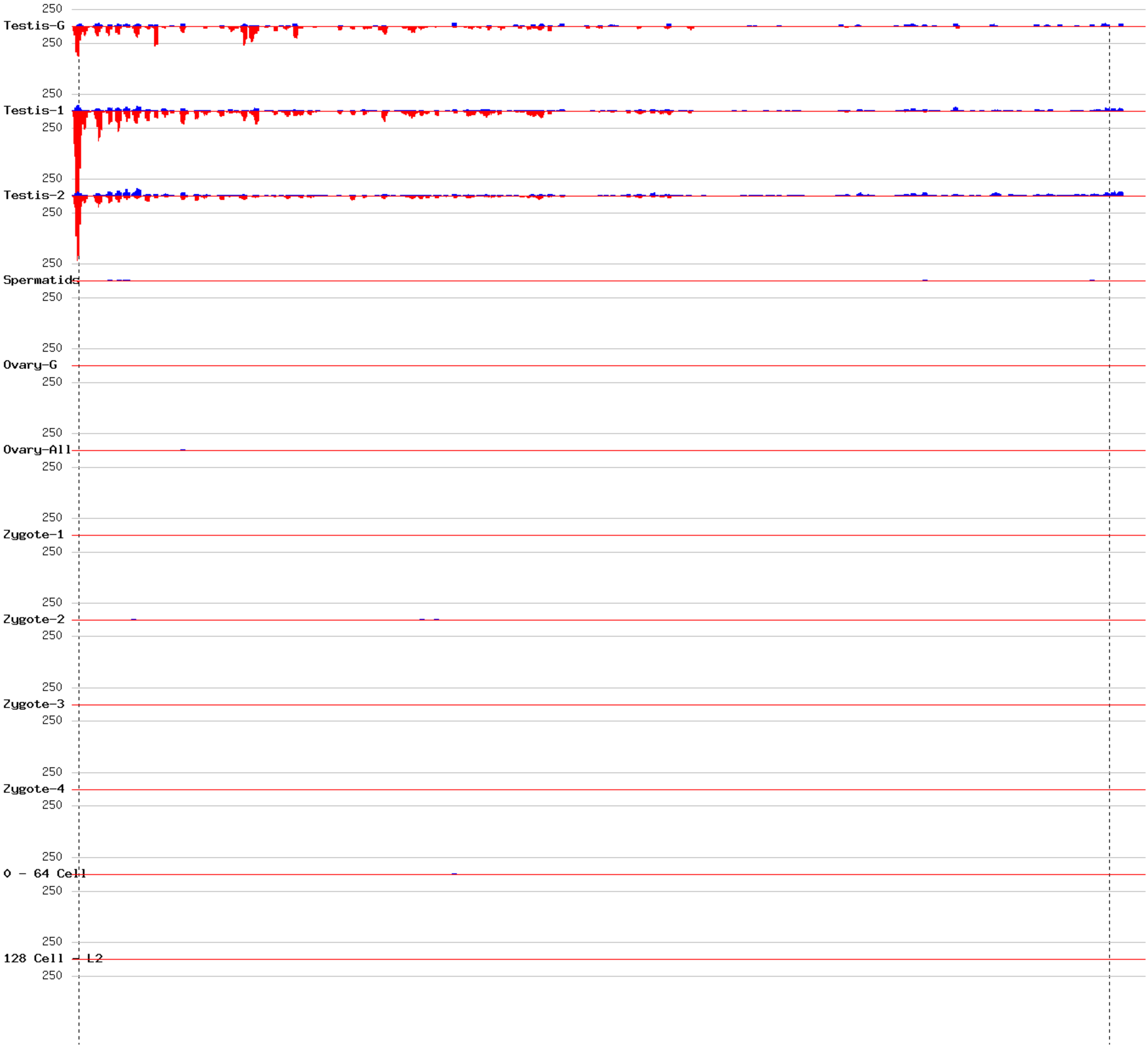
ASCF_2047_2800 Nanos_homolog_2 2800 bp



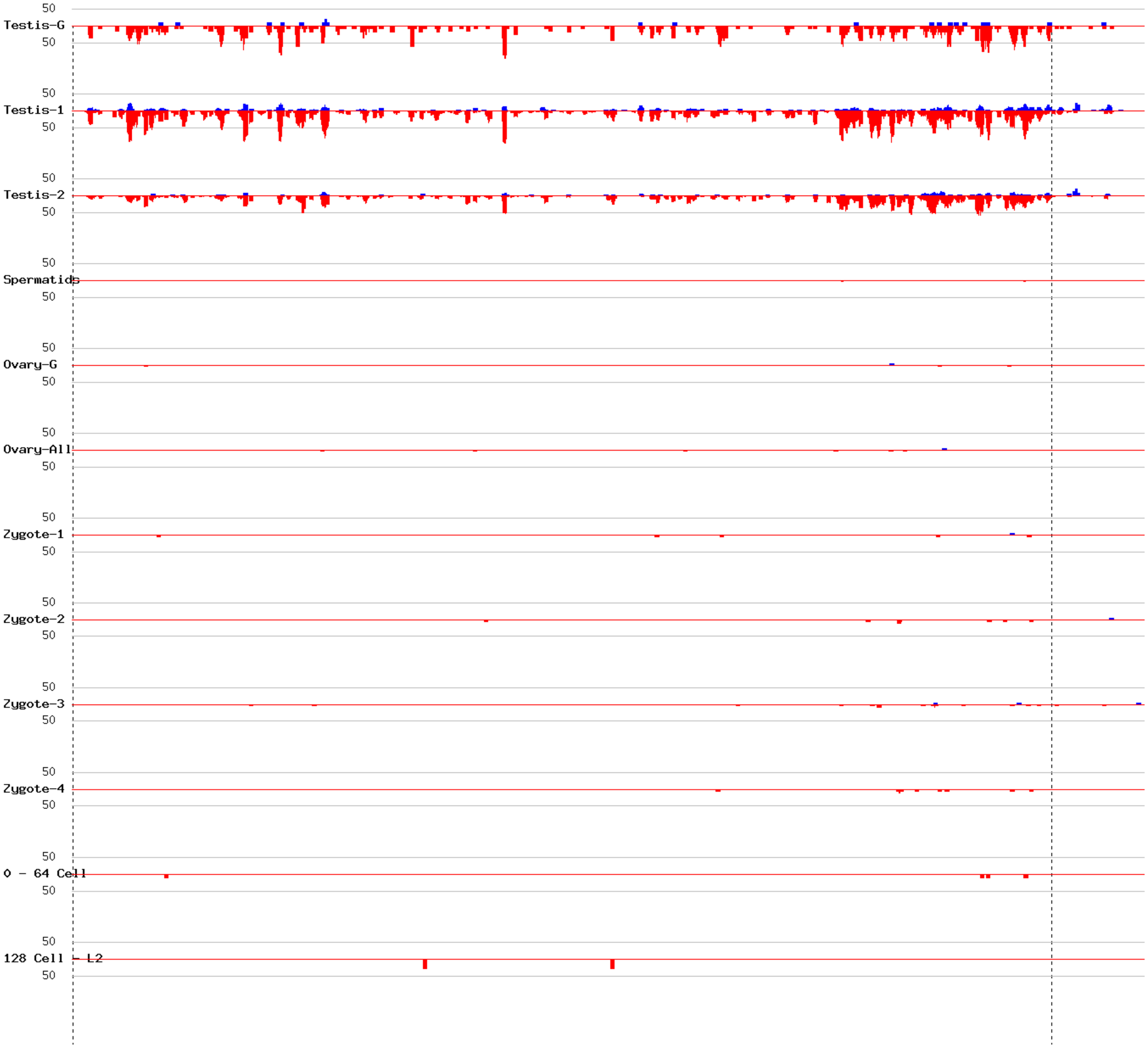
ASCF_2096_2756 HEC/Ndc80p_family_protein 2756 bp



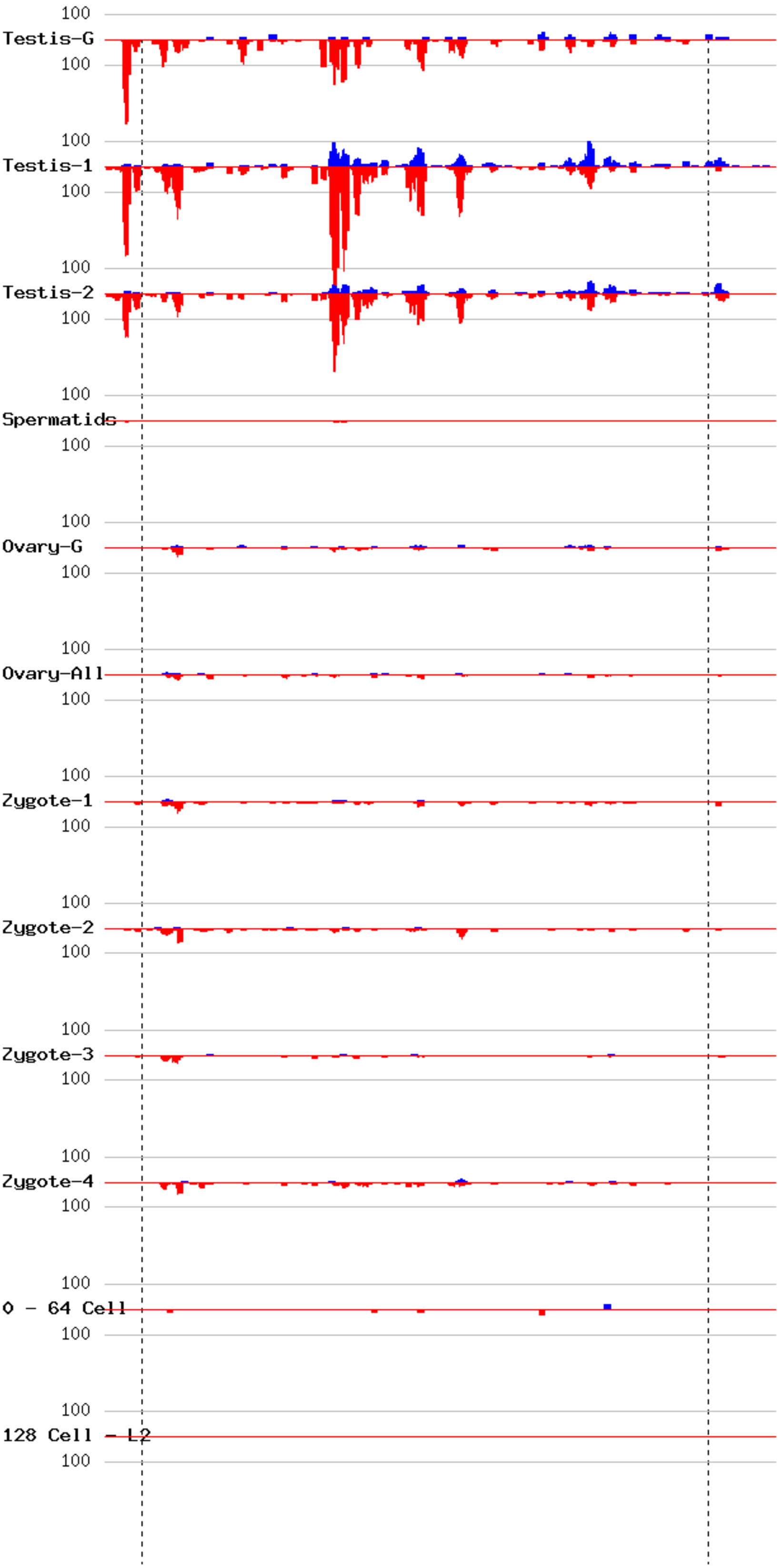
ASCF_220_6325 Hypothetical_protein 6325 bp



ASCF_221_6321 DNA-directed_RNA_polymerase 6321 bp



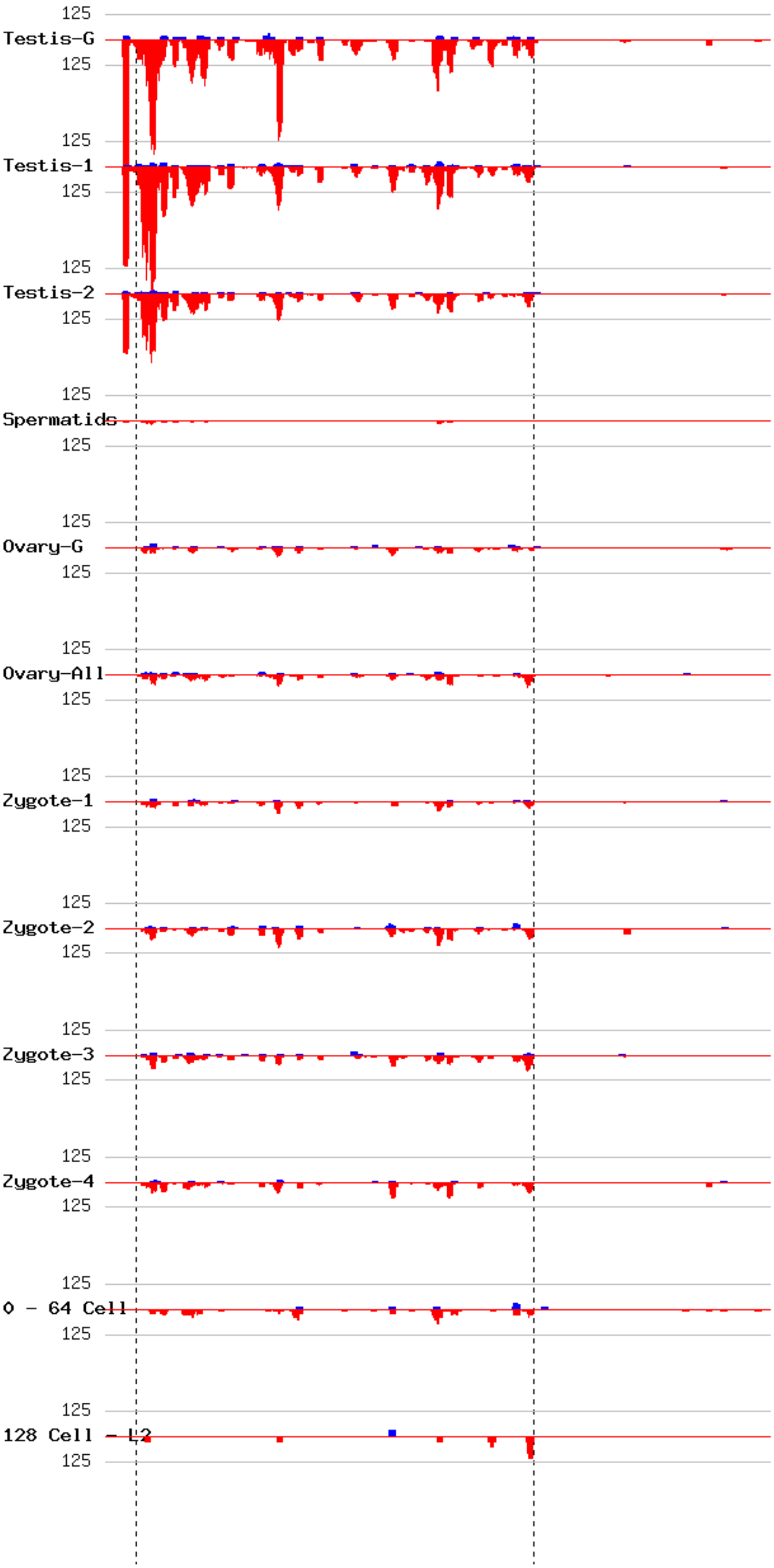
ASCF_2303_2643 Hypothetical_protein 2643 bp



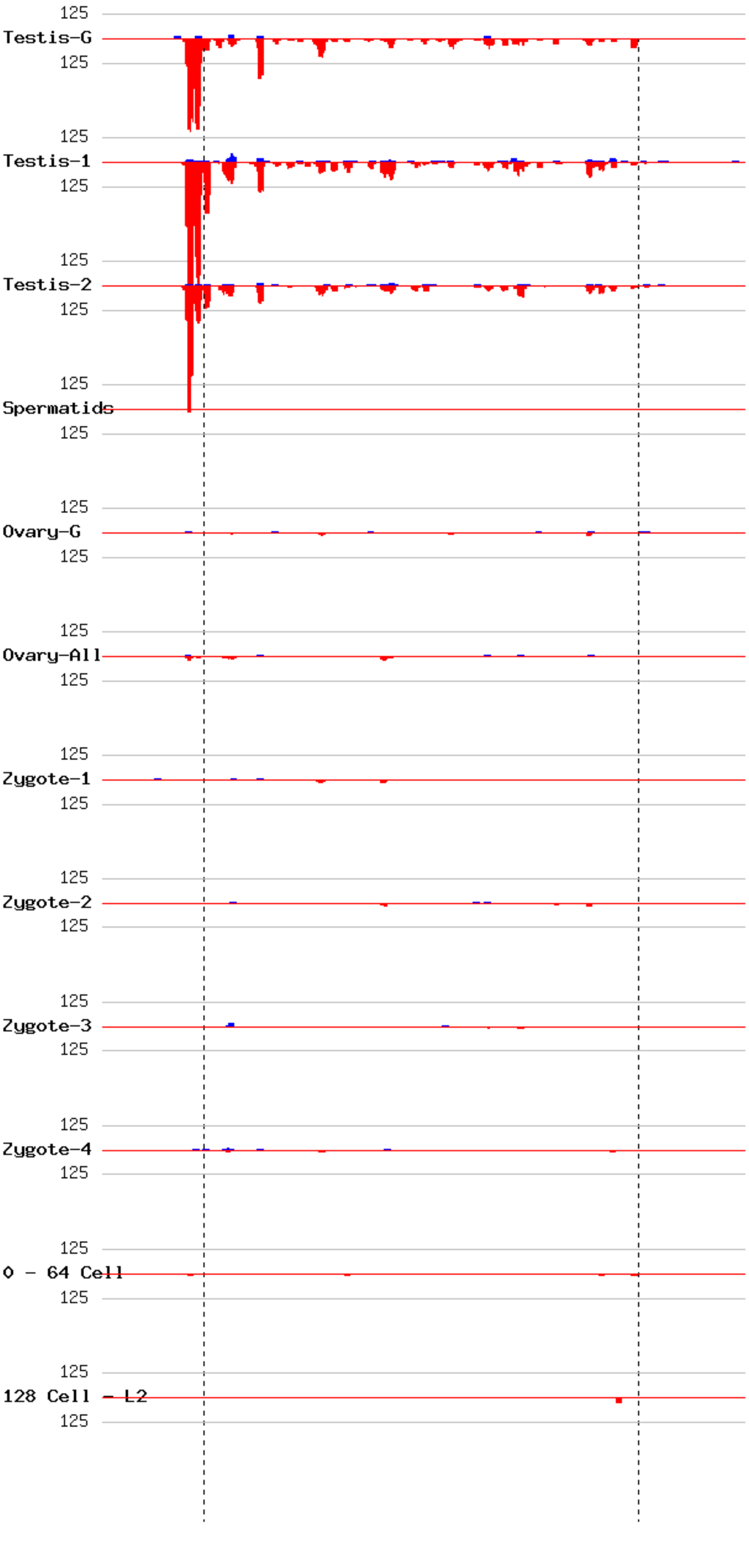
ASCF_2327_2630 Hypothetical_protein 2630 bp

100
Testis-G
100
100
Testis-1
100
100
Testis-2
100
100
Spermatids
100
100
Ovary-G
100
100
Ovary-All
100
100
Zygote-1
100
100
Zygote-2
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0 - 64 Cell
100
100
128 Cell - L2
100

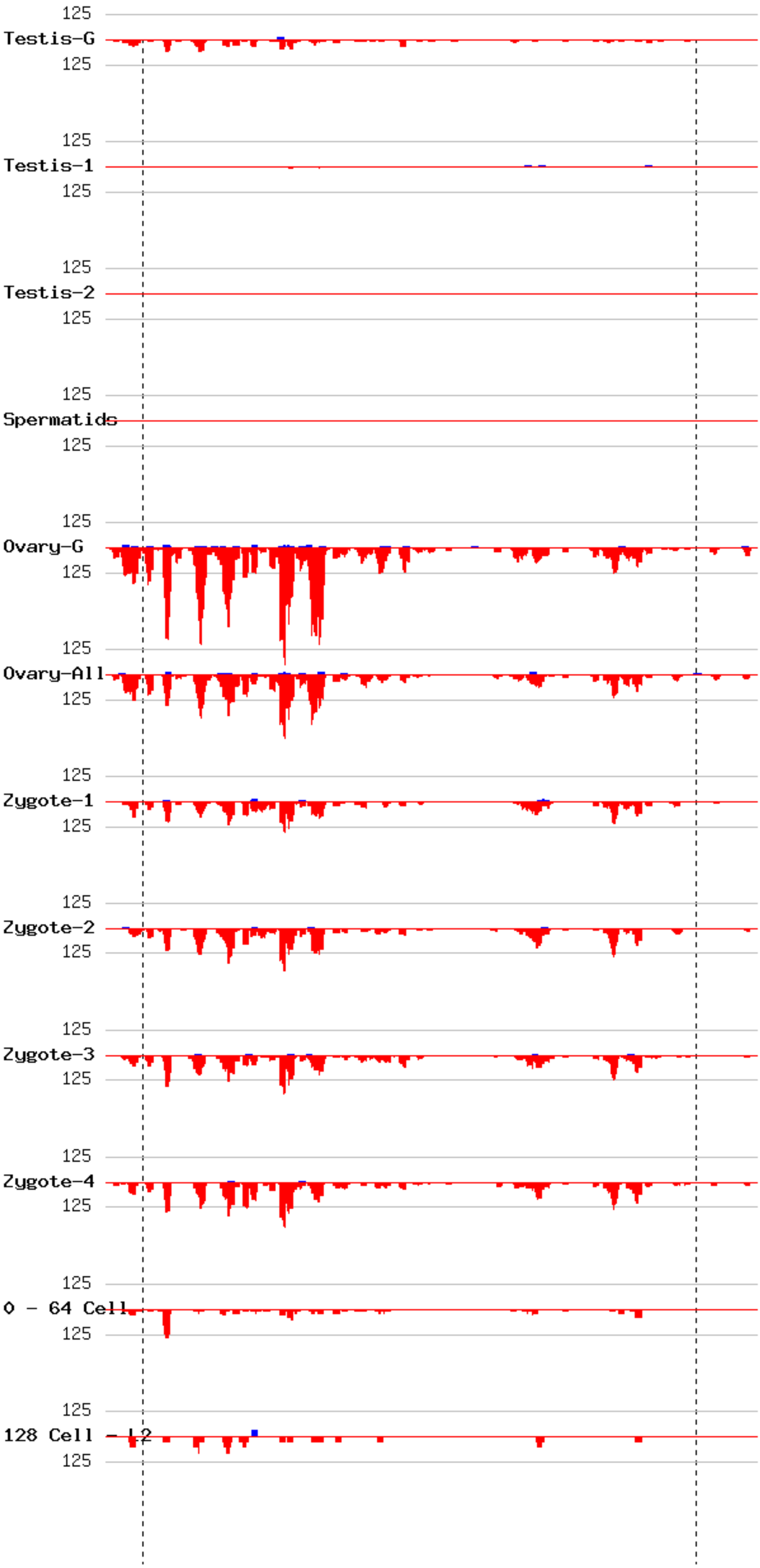
ASCF_2346_2617 Fizzy-related_protein 2617 bp



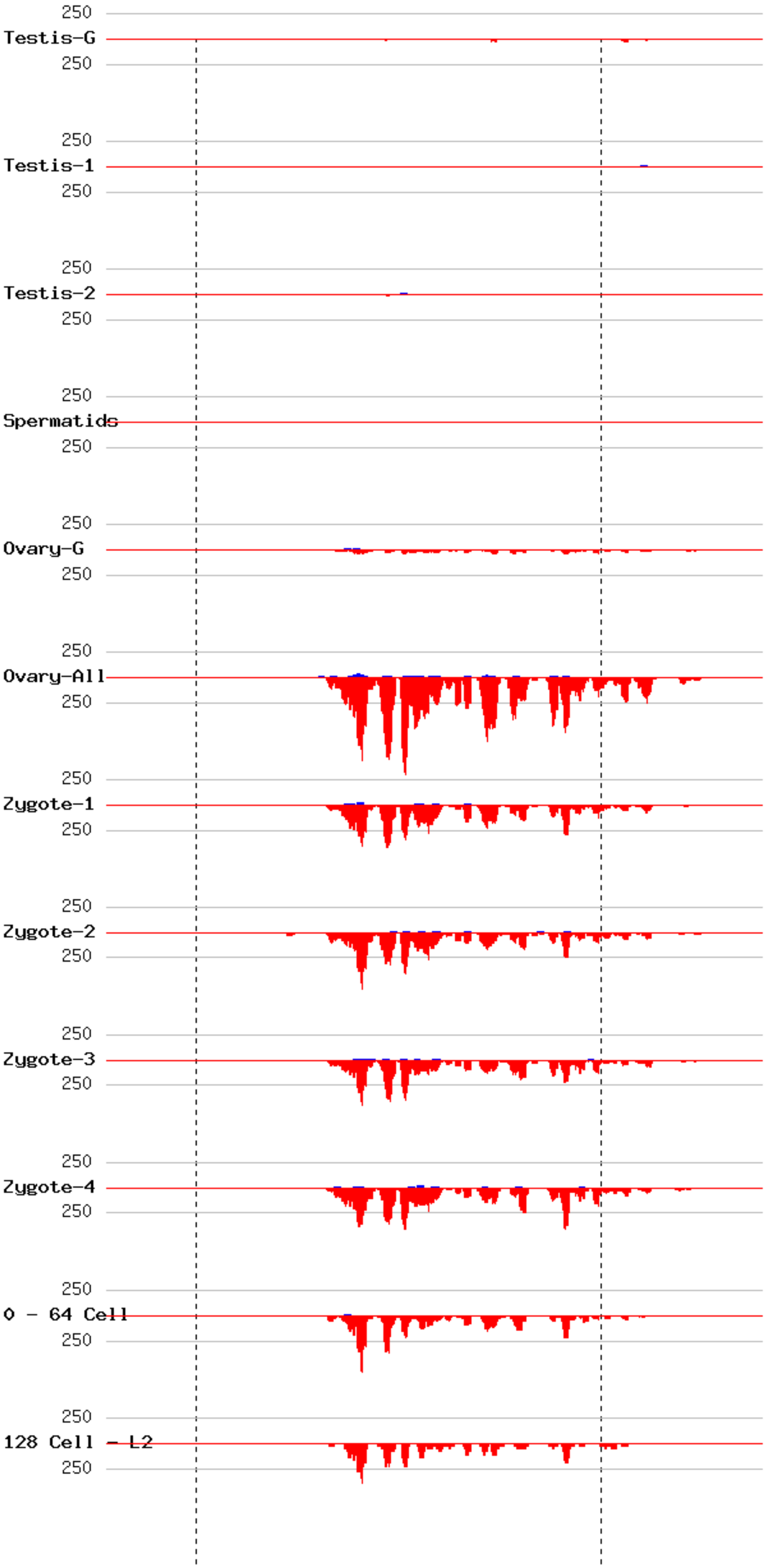
ASCF_2372_2603 Kelch_motif_family_protein 2603 bp



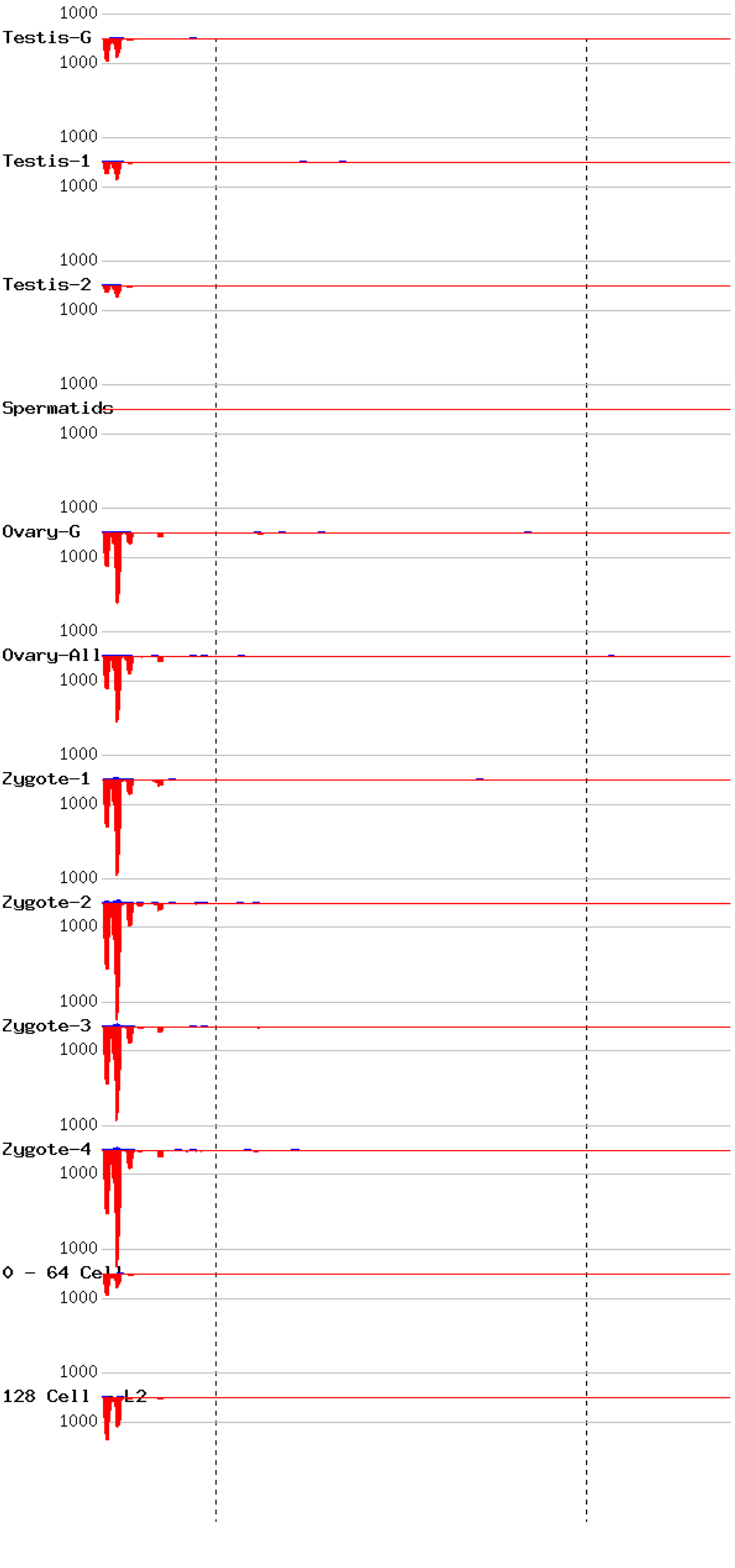
ASCF_2429_2569 Hypothetical_protein 2569 bp



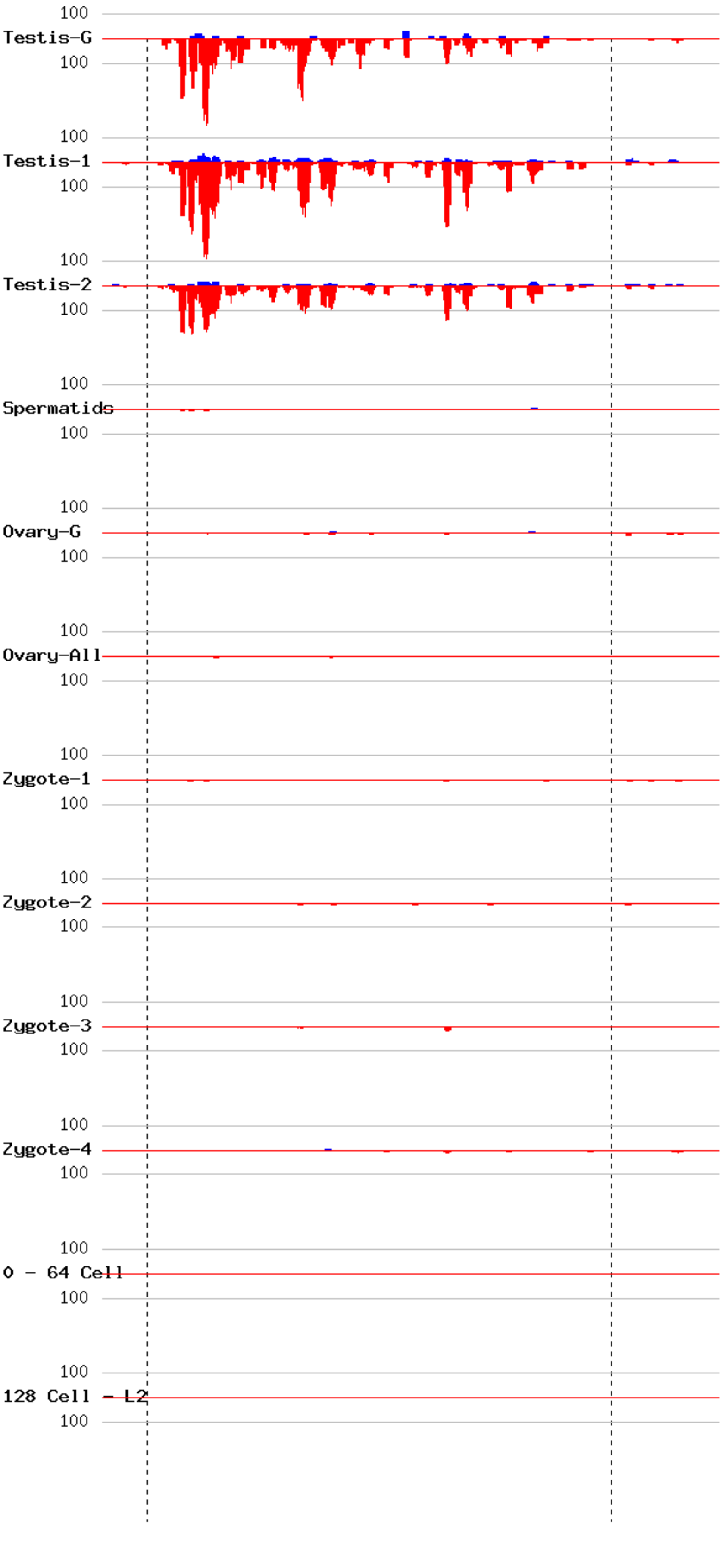
ASCF_2432_2567 Nuclear_hormone_receptor_family_member_nhr-25 2567 bp



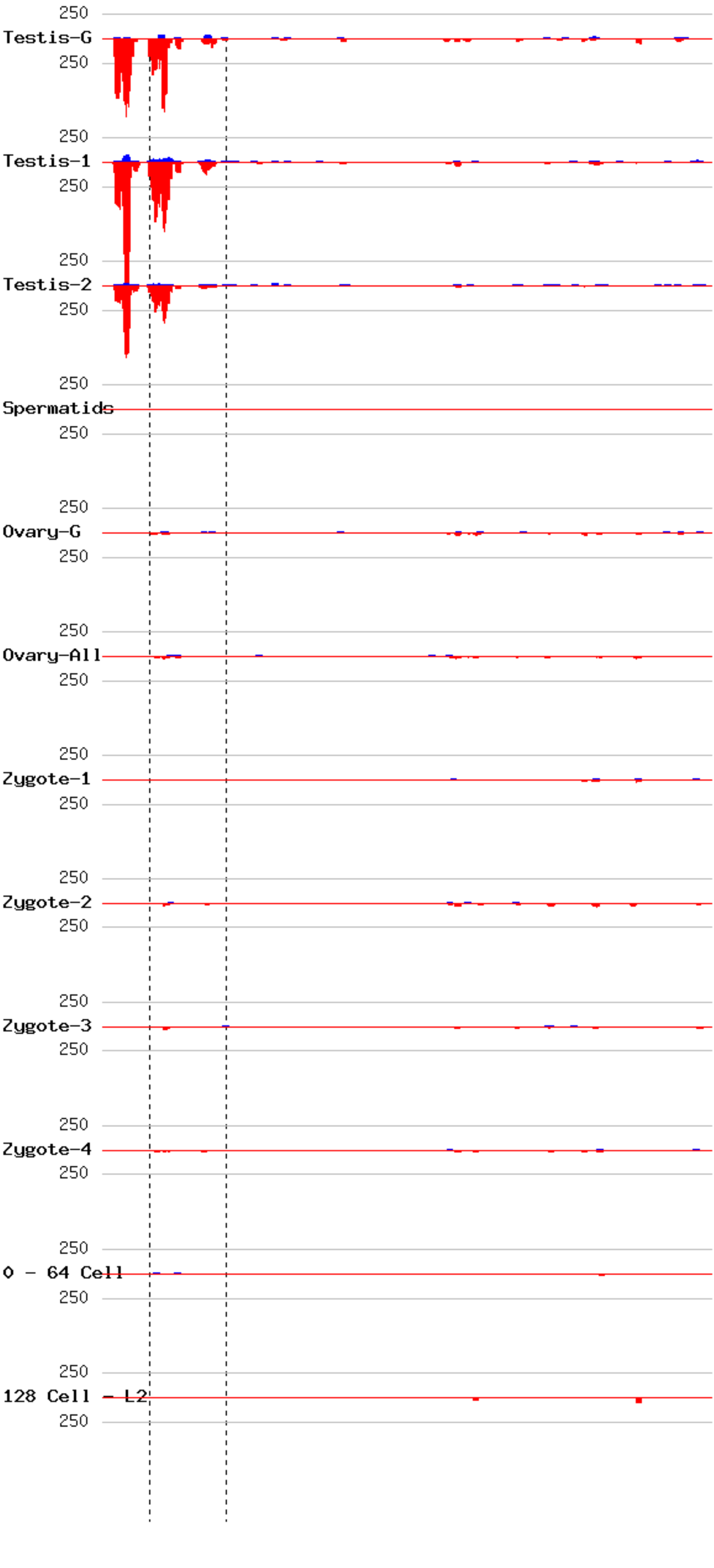
ASCF_2478_2541 Hypothetical_protein 2541 bp



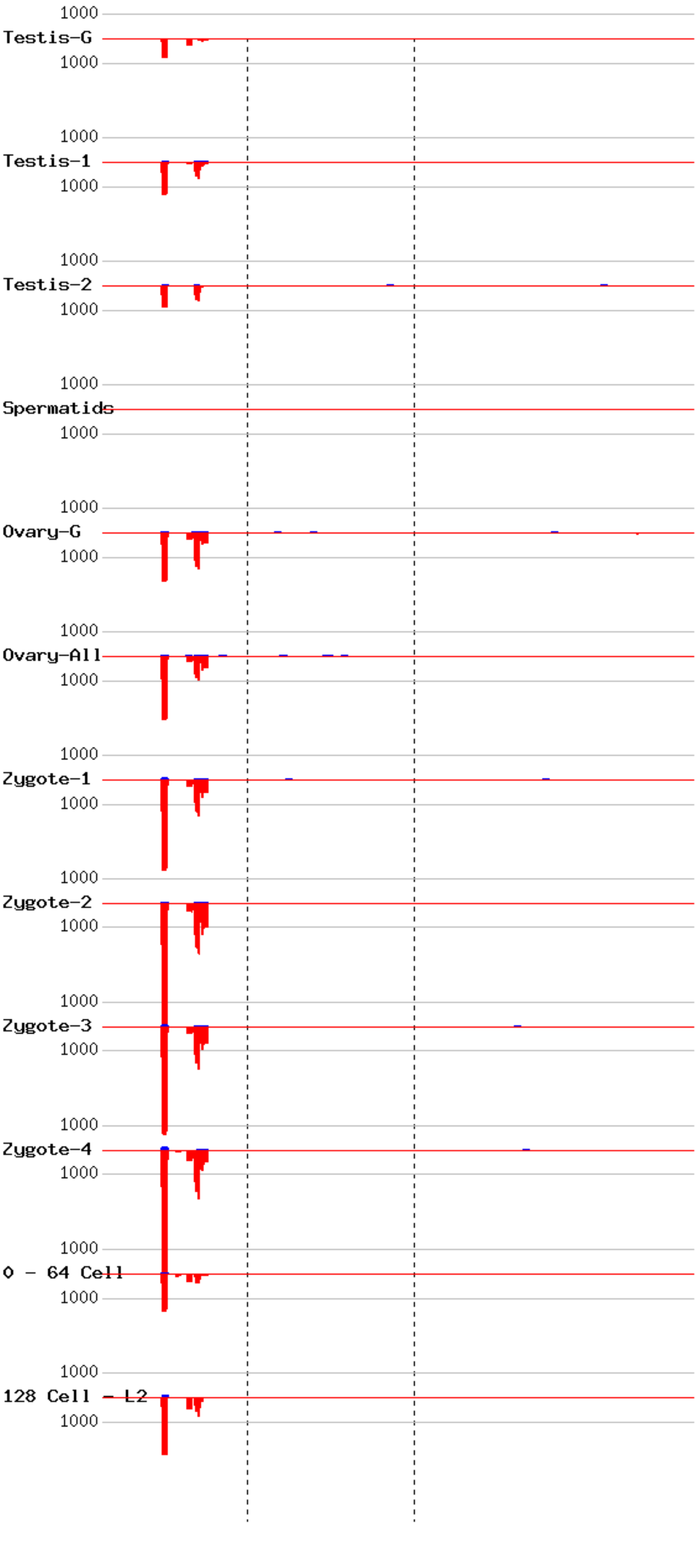
ASCF_2564_2499 Protein_phosphatase_PP2A_regulatory_subunit 2499 bp



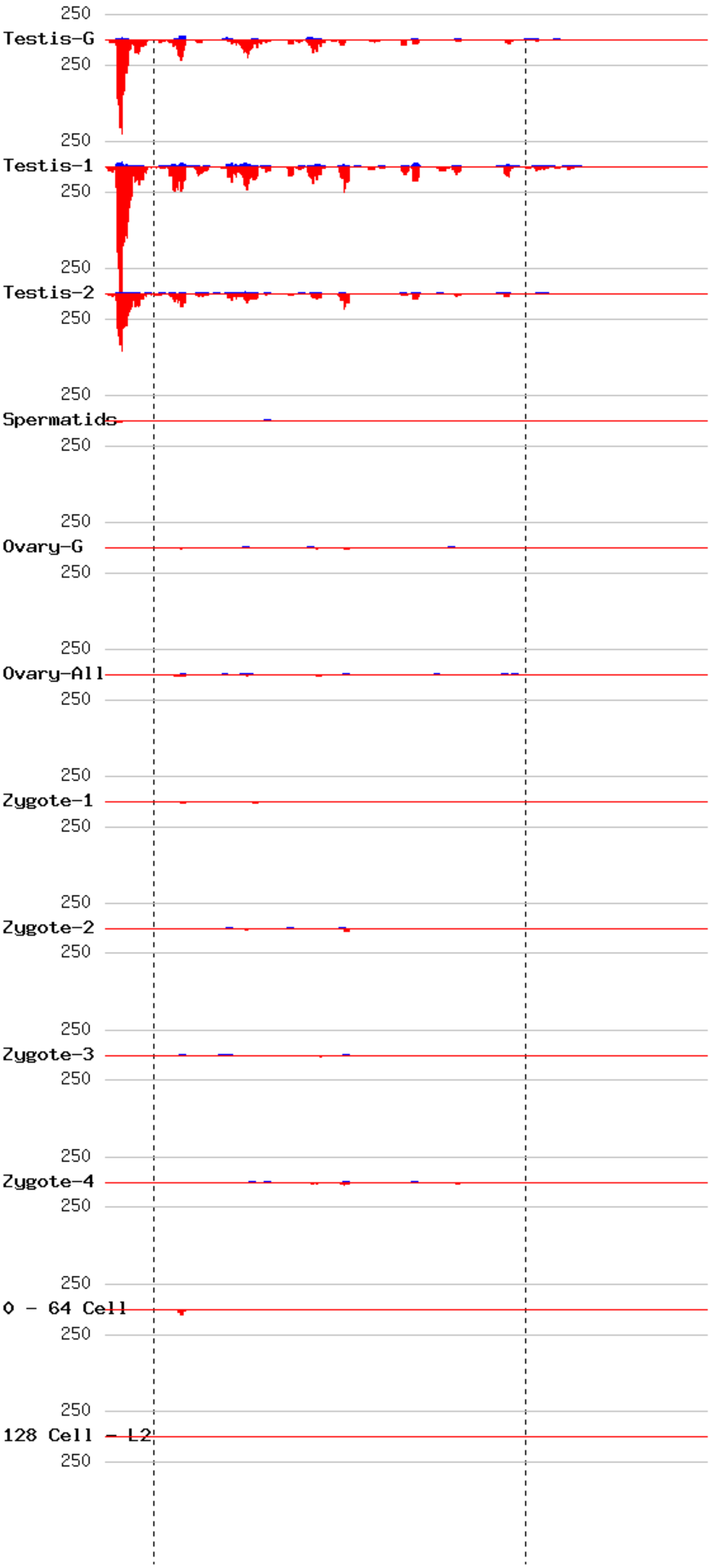
ASCF_2628_2468 Hypothetical_protein 2468 bp



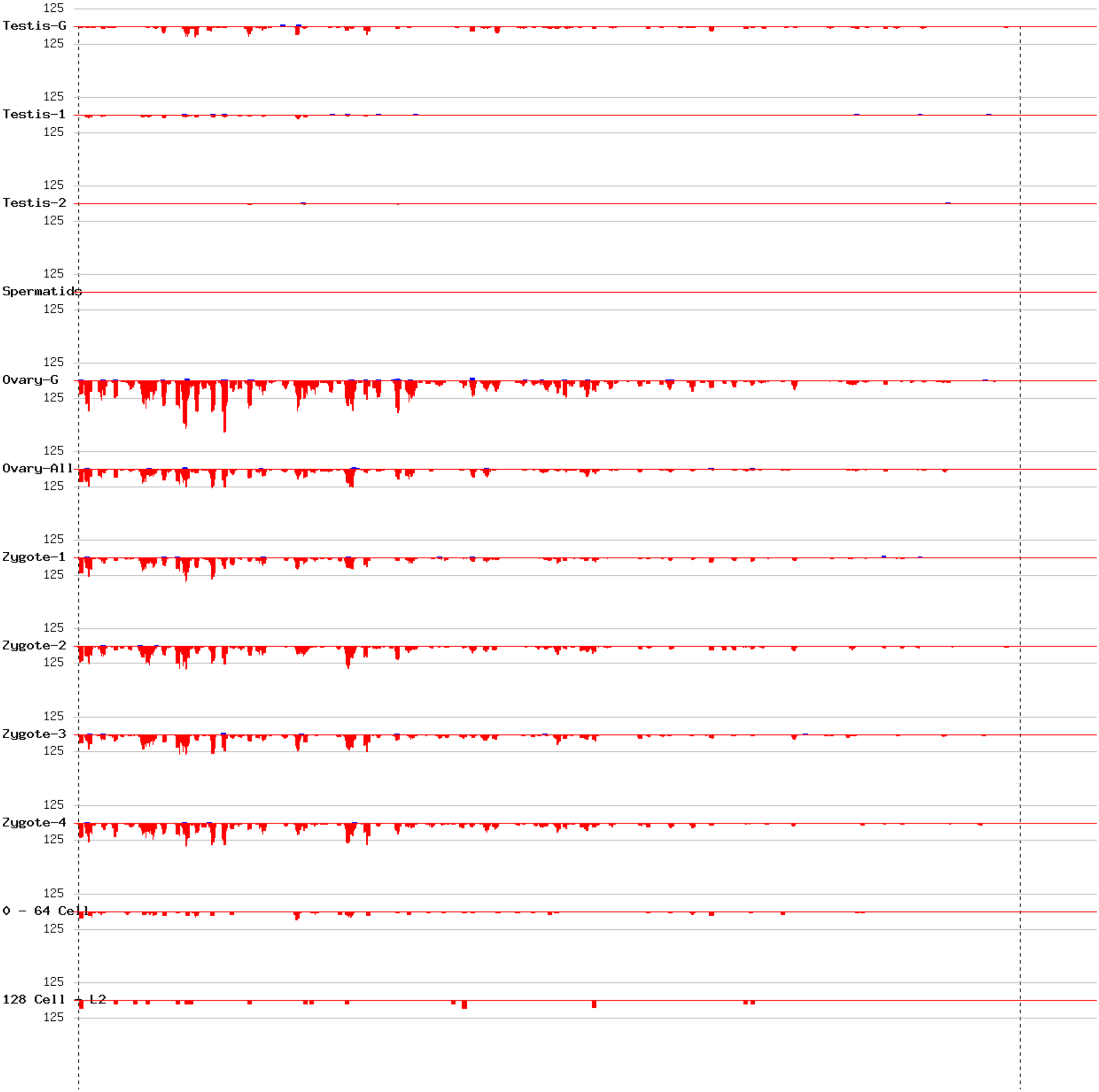
ASCF_2805_2390 Hypothetical_protein 2390 bp



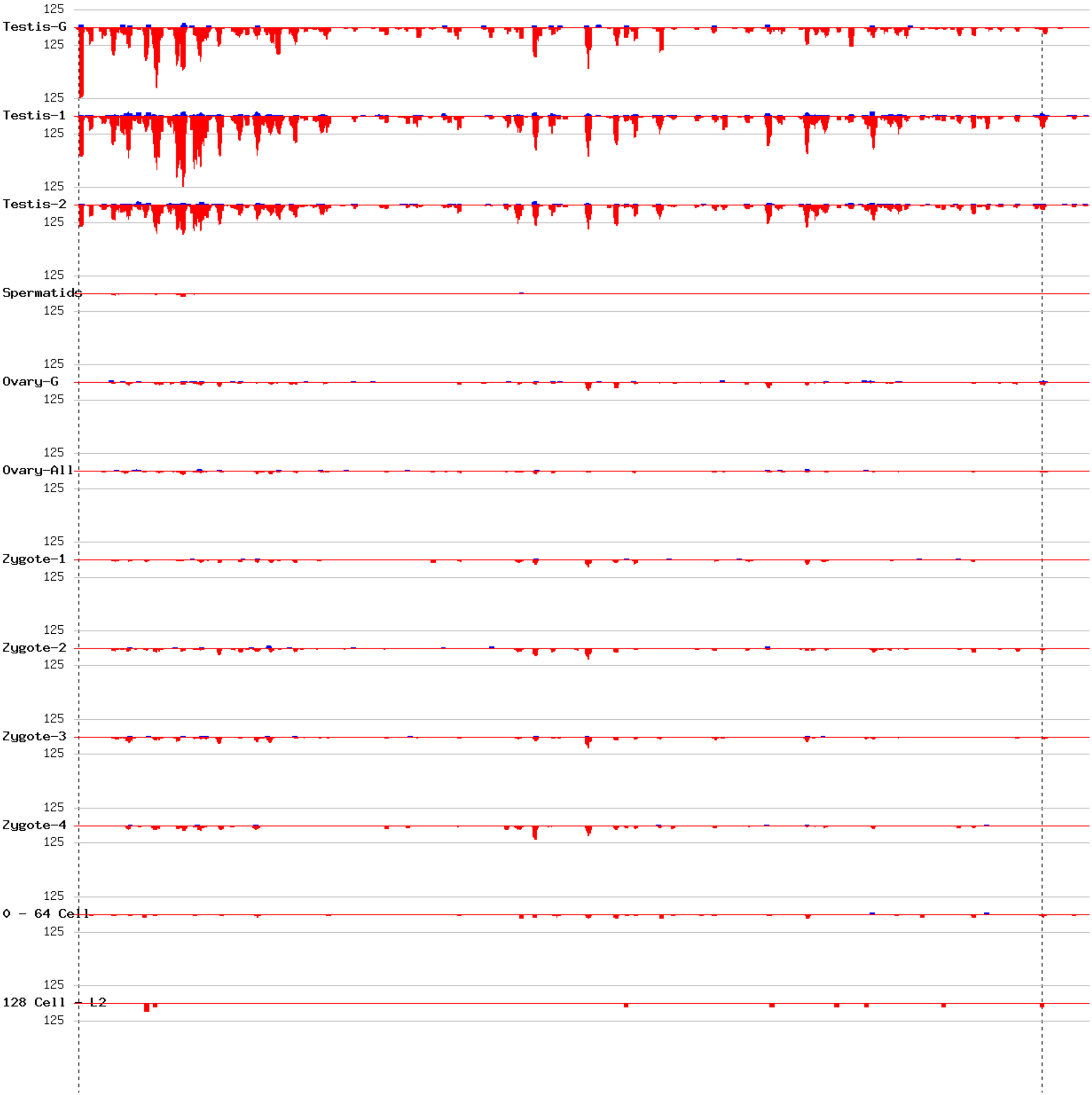
ASCF_2858_2370 WD-repeat_protein_22 2370 bp



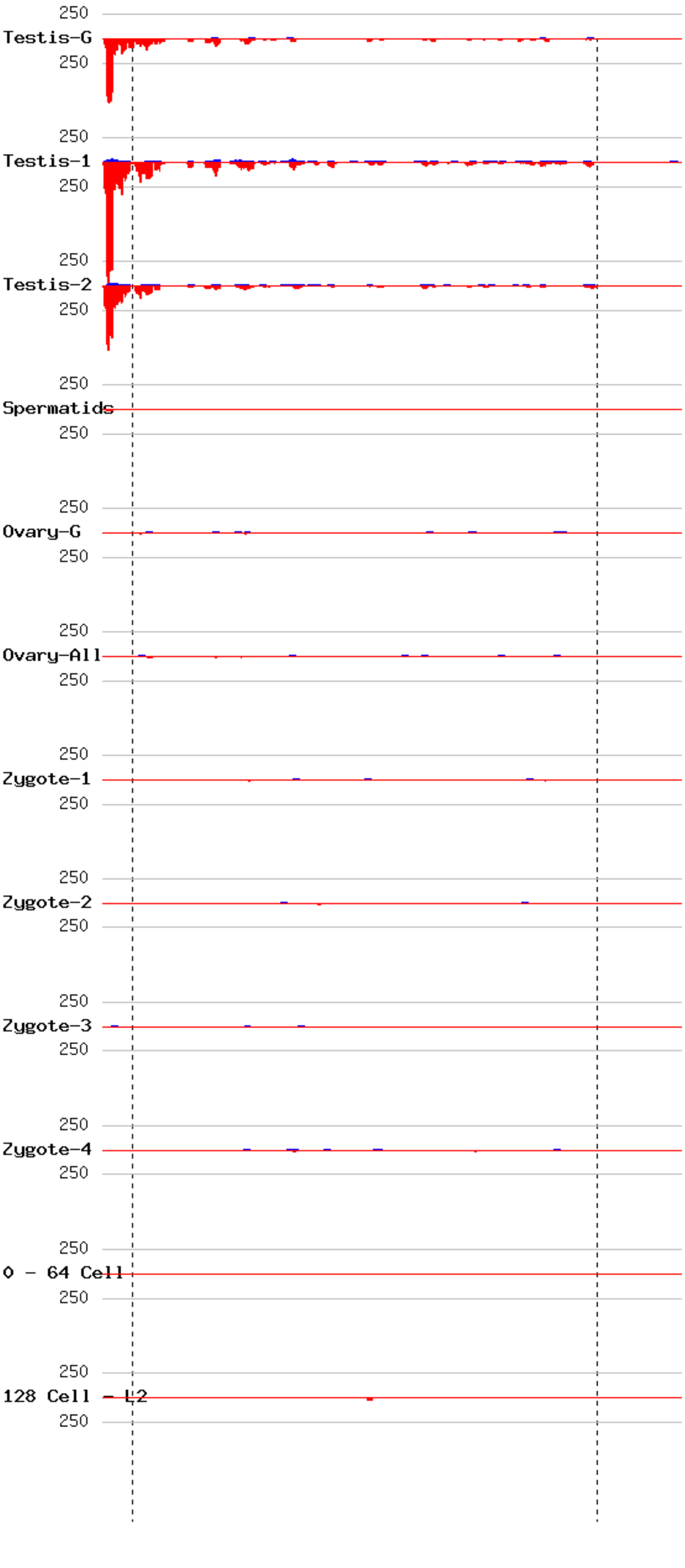
ASCF_286_5773 Hypothetical_protein 5773 bp



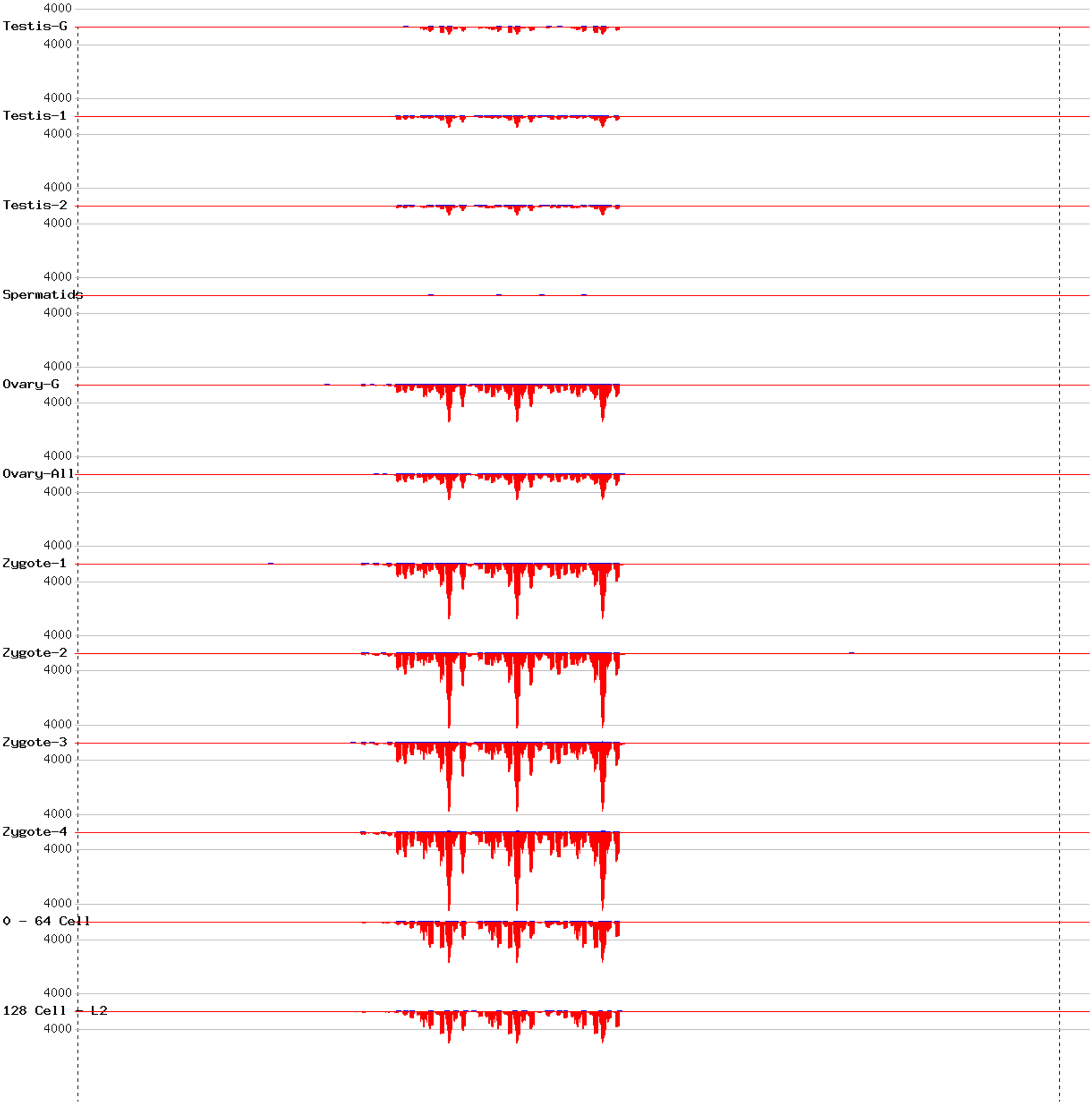
ASCF_292_5721 Notch_signaling_pathway_homolog_protein 5721 bp



ASCF_2923_2342 Hypothetical_protein 2342 bp

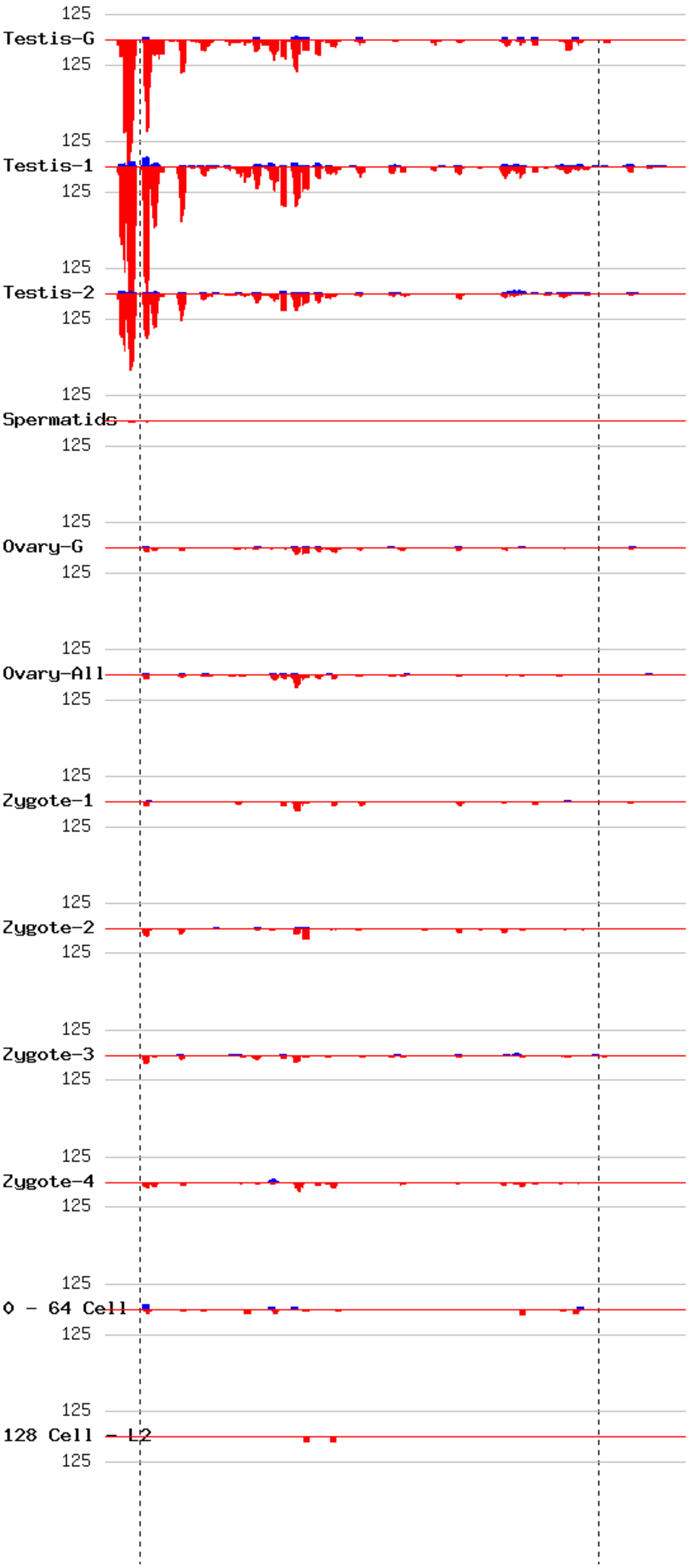


ASCF_299_5666 Hypothetical_protein 5666 bp

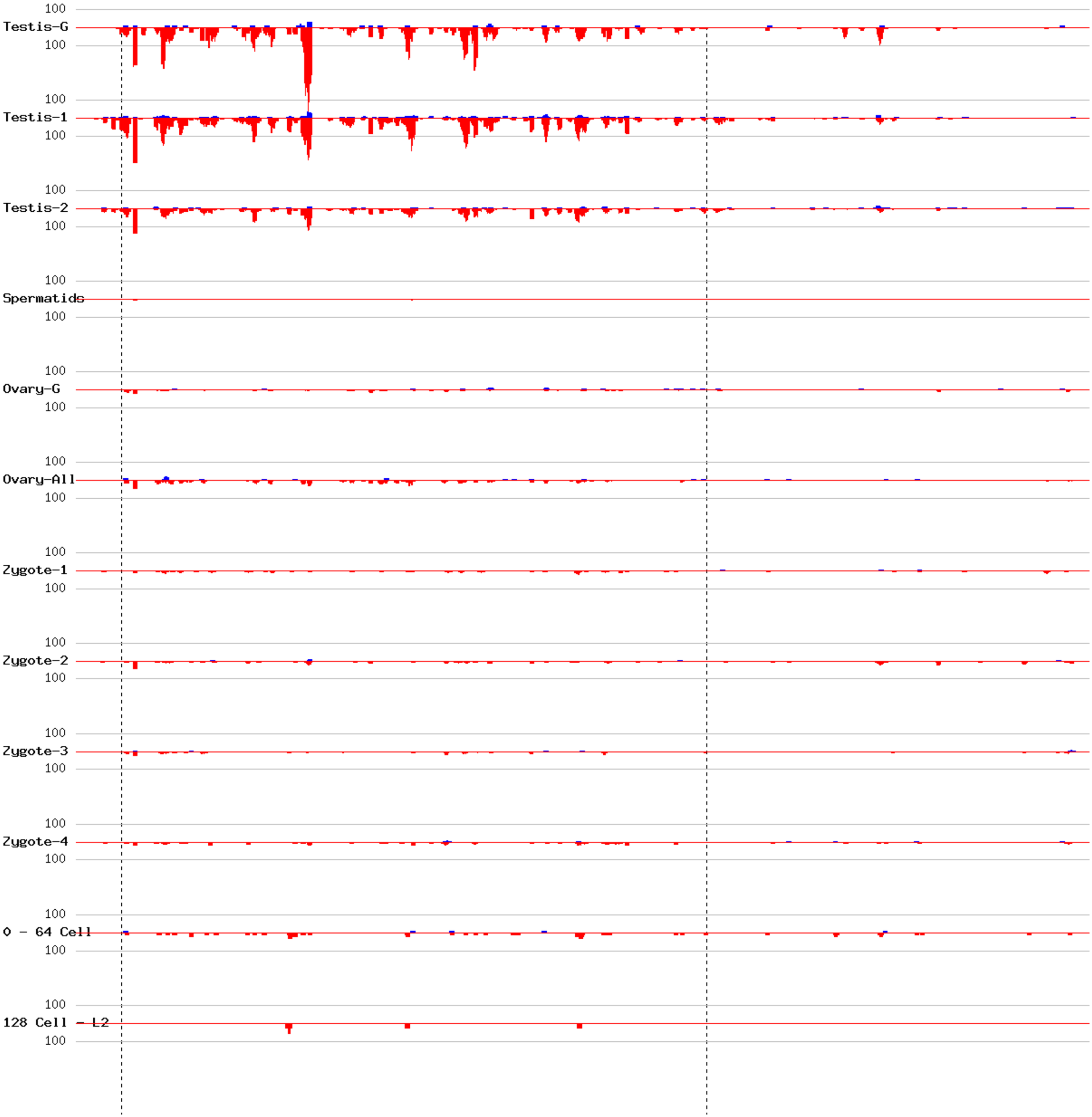



ASCF_3_20236 Hypothetical_protein 20236 bp
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Testis-G
1000
1000
Testis-1
1000
1000
Testis-2
1000
1000
Spermatids
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Ovary-G
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1000
Ovary-All
1000
1000
Zygote-1
1000
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1000
1000
128 Cell - 4
1000

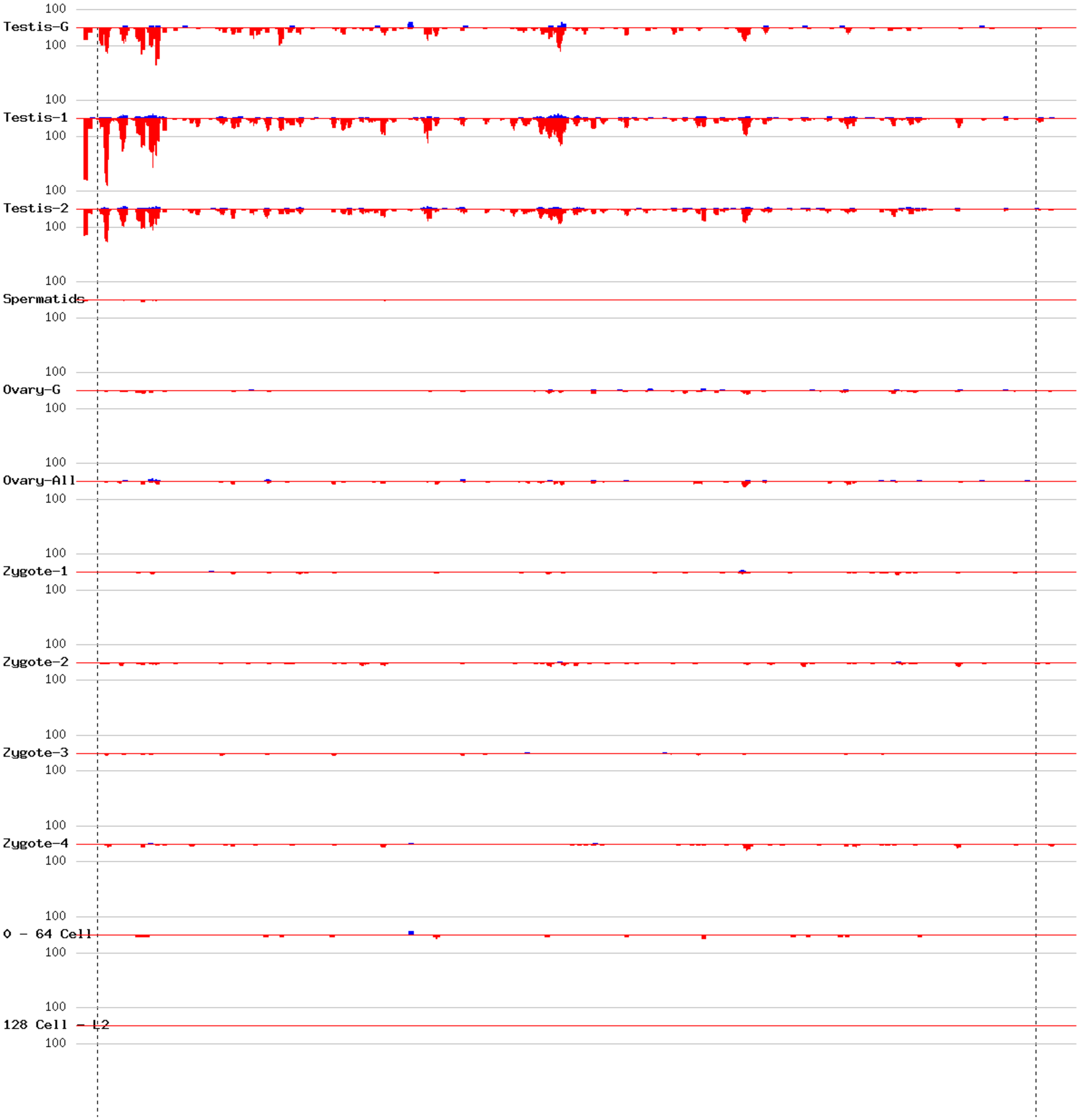
ASCF_3068_2283 Hypothetical_protein 2283 bp



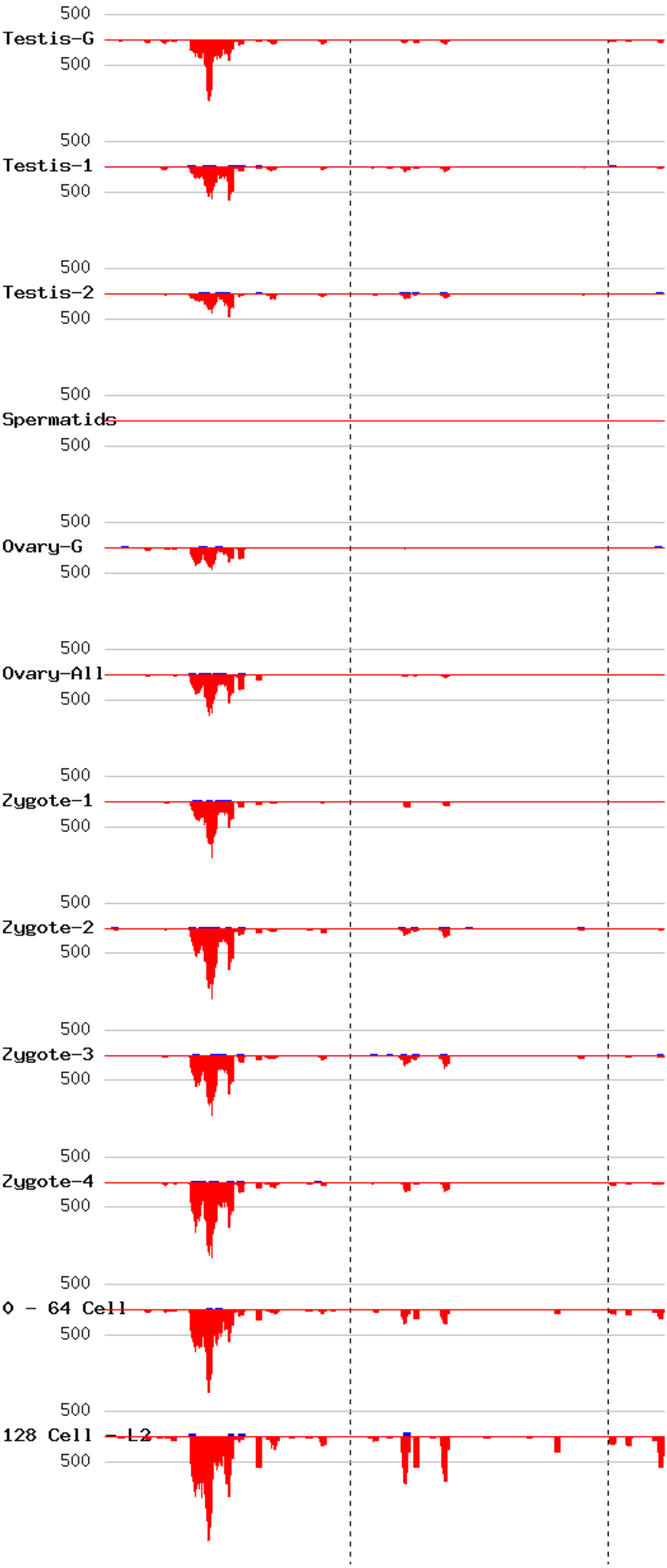
ASCF_310_5590 PH_domain_containing_protein 5590 bp



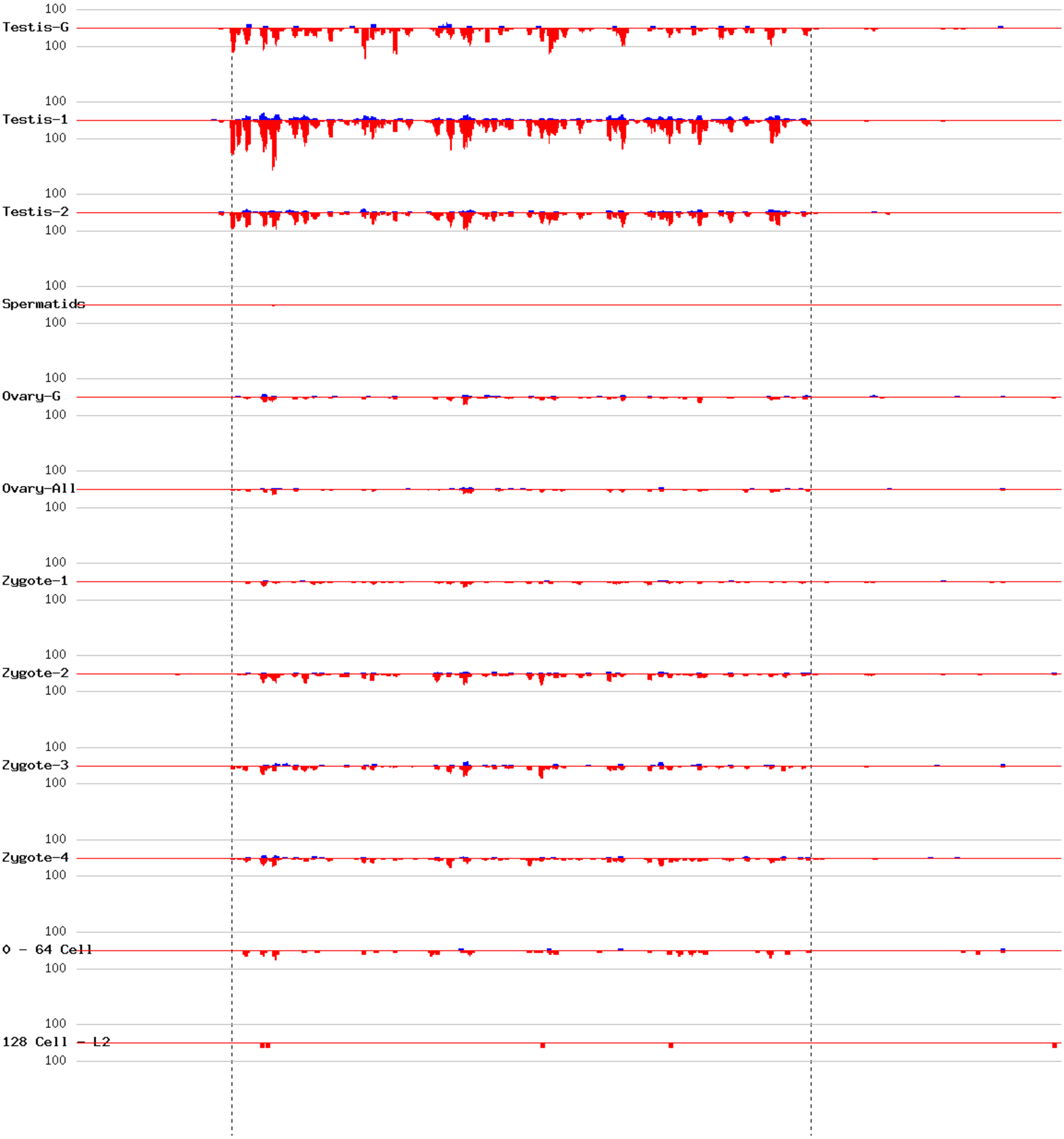
ASCF_321_5508 Bromodomain_containing_protein 5508 bp



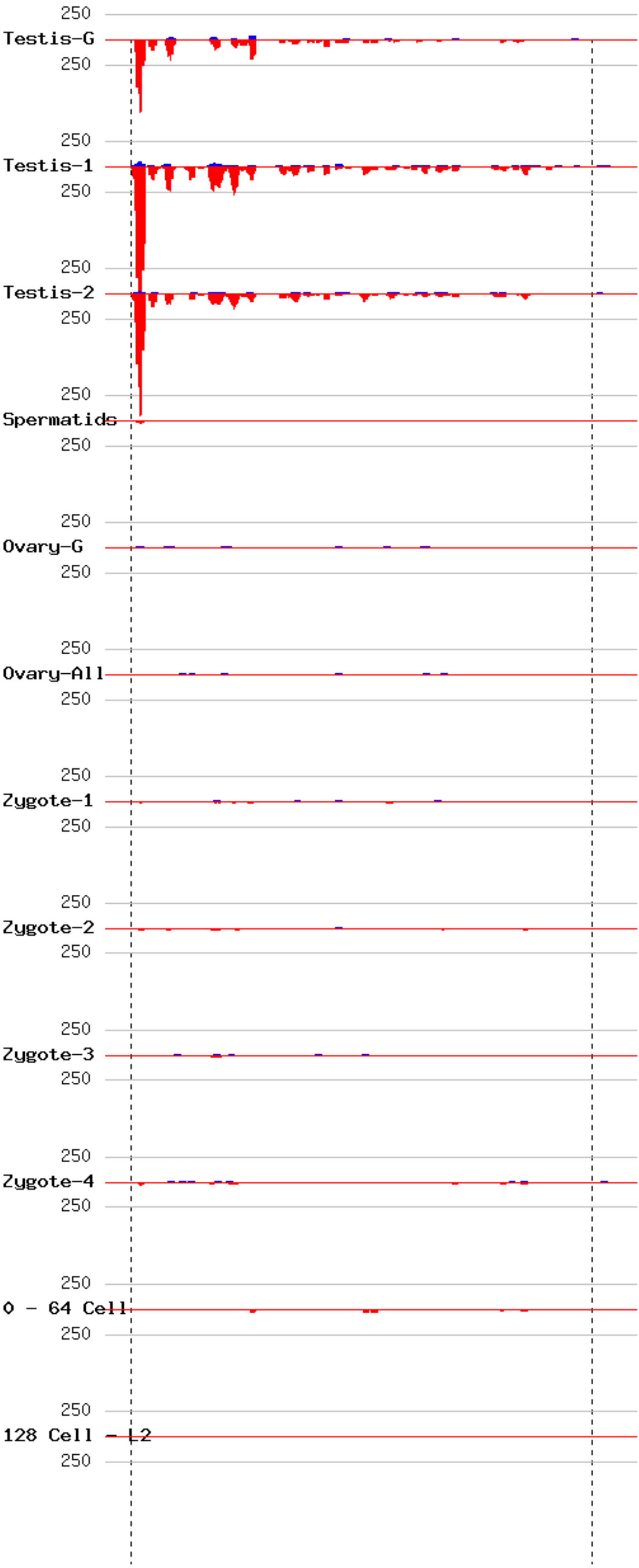
ASCF_3277_2202 Hypothetical_protein 2202 bp



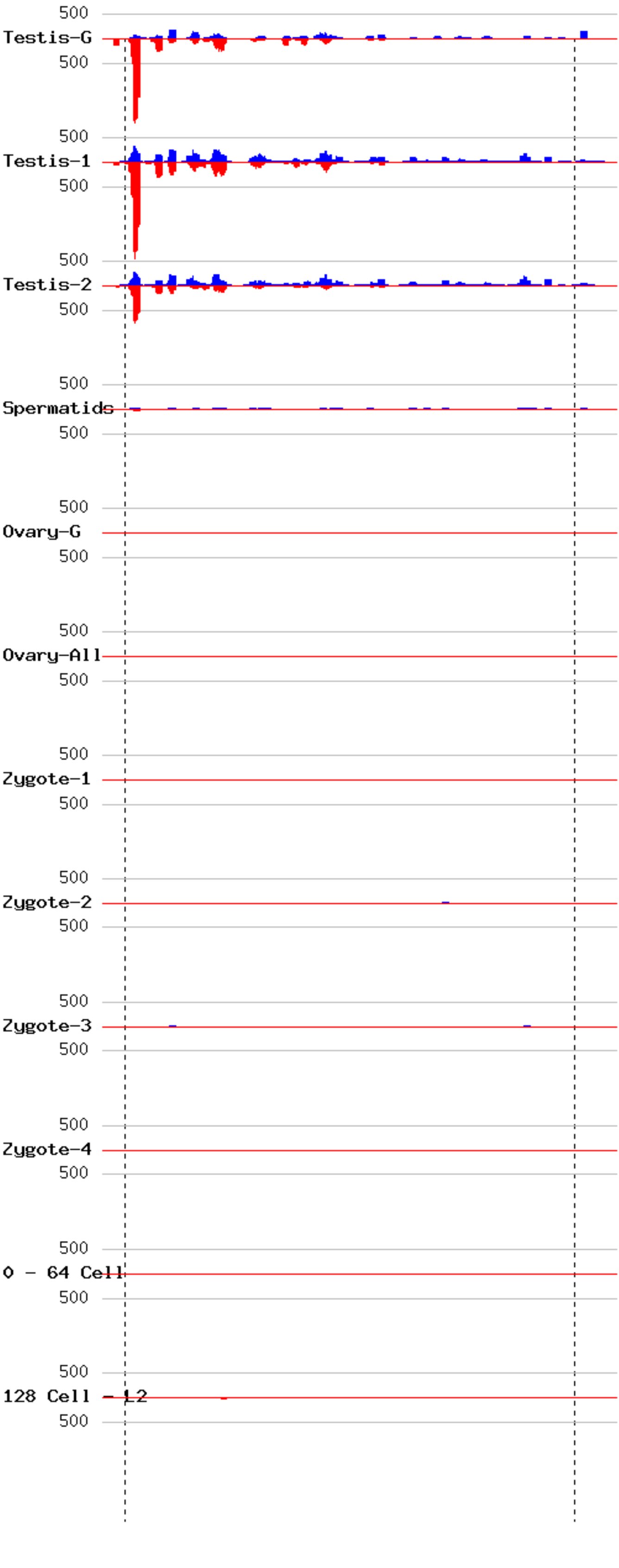
ASCF_351_5338 Chromosome-Segregation_and_RNAi_deficient_Argonaute 5338 bp



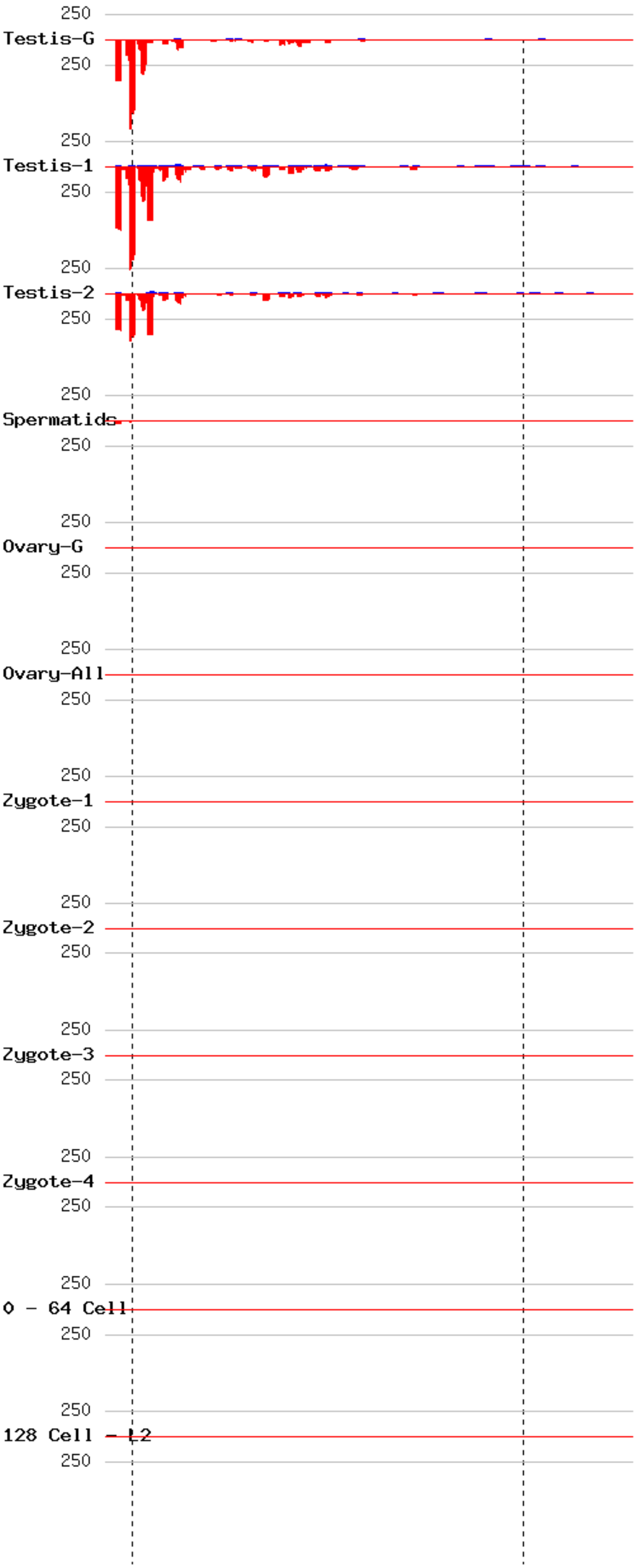
ASCF_3561_2090 Hypothetical_protein 2090 bp



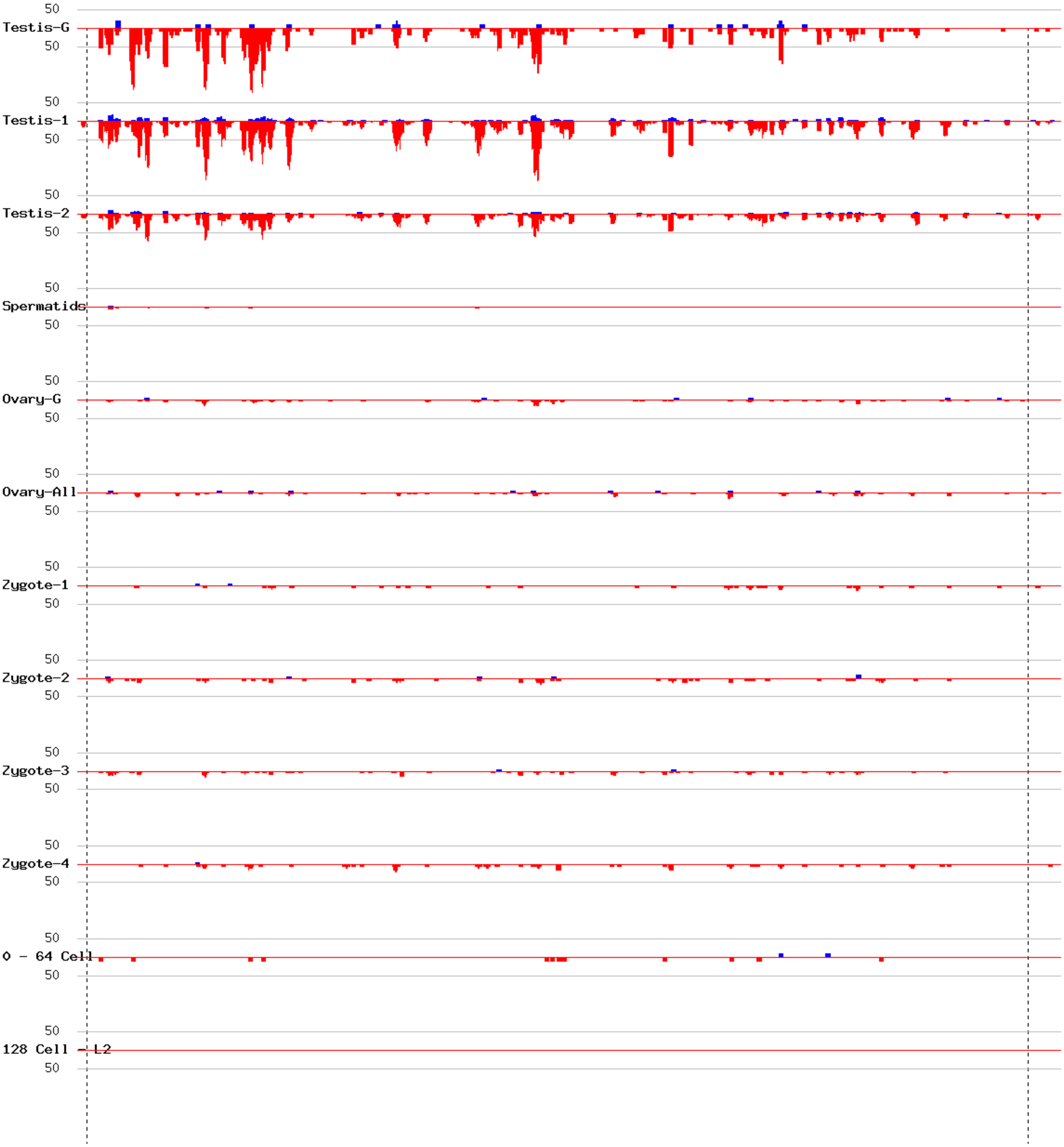
ASCF_3580_2082 Hypothetical_protein 2082 bp



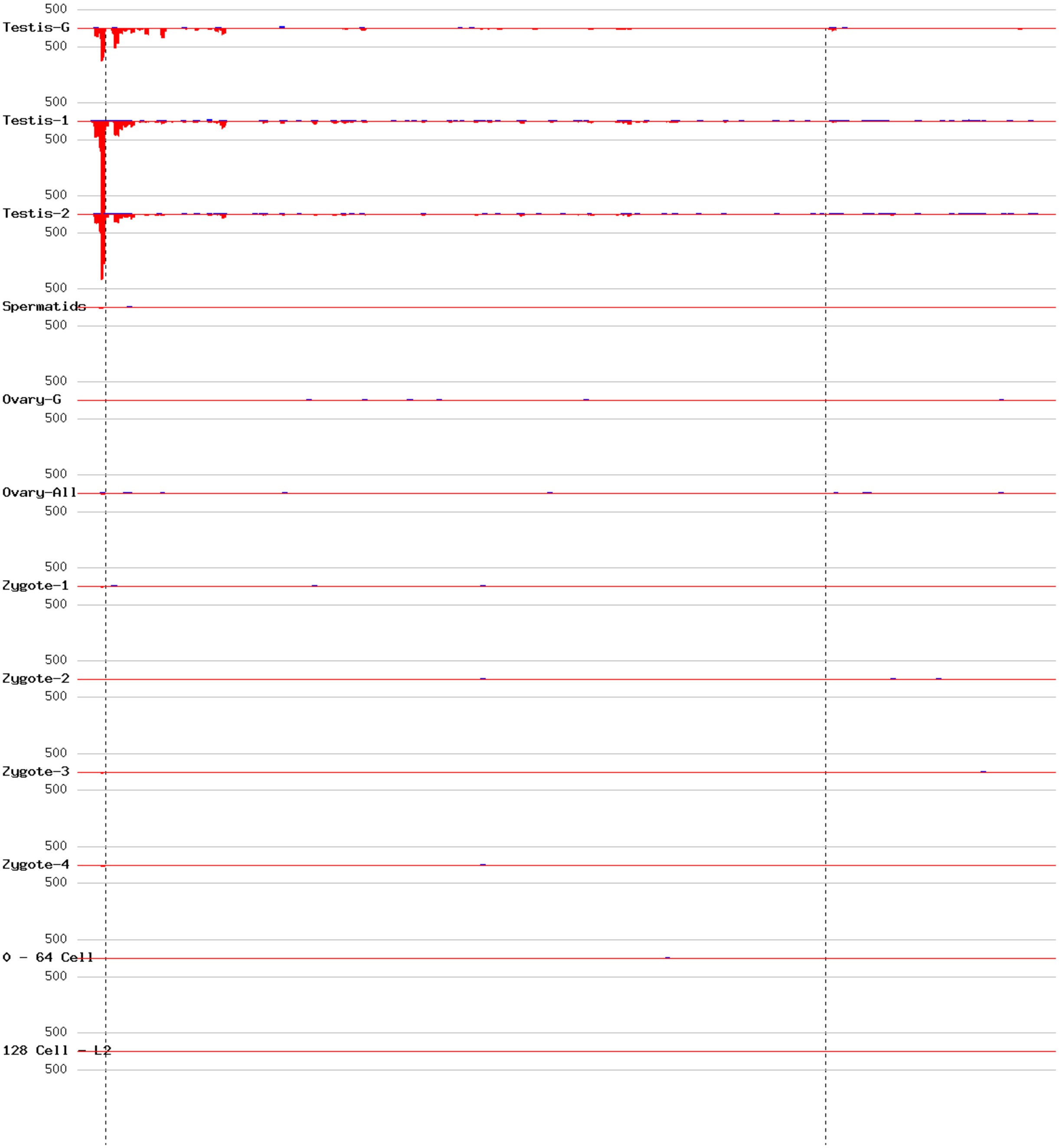
ASCF_3596_2077 Hypothetical_protein 2077 bp



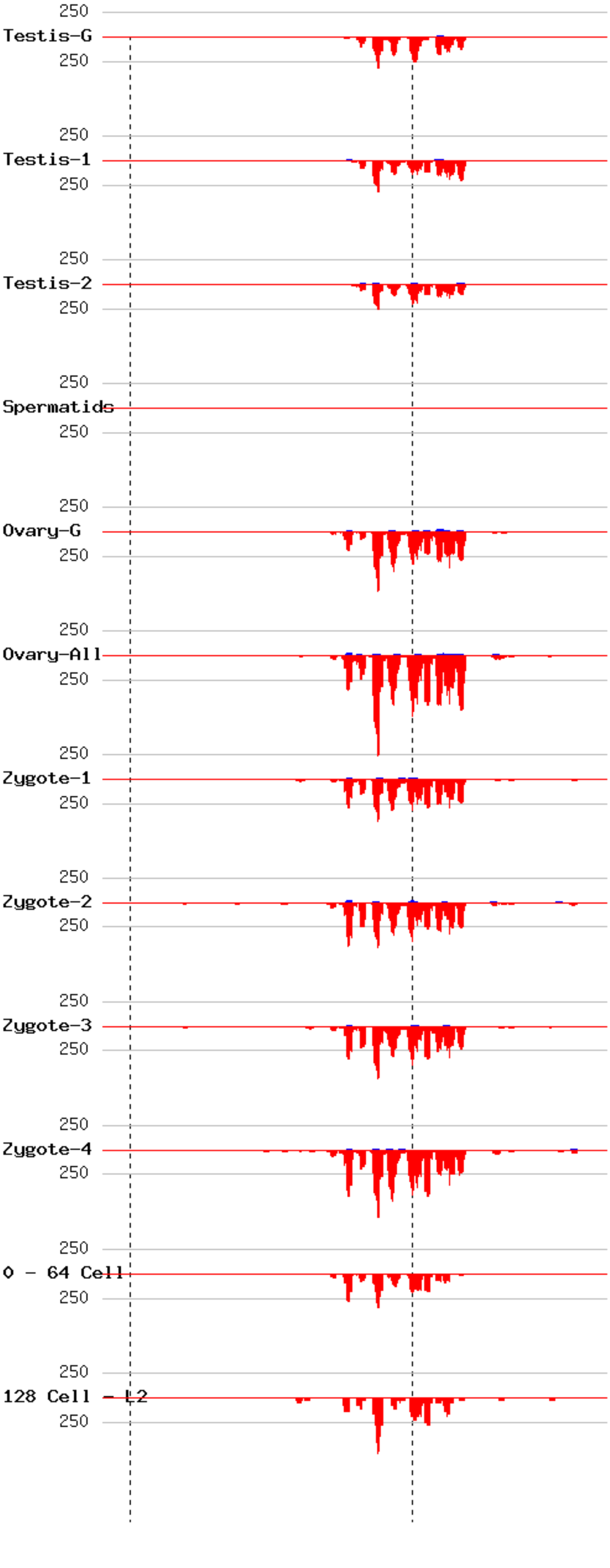
ASCF_365_5293 Hypothetical_protein 5293 bp



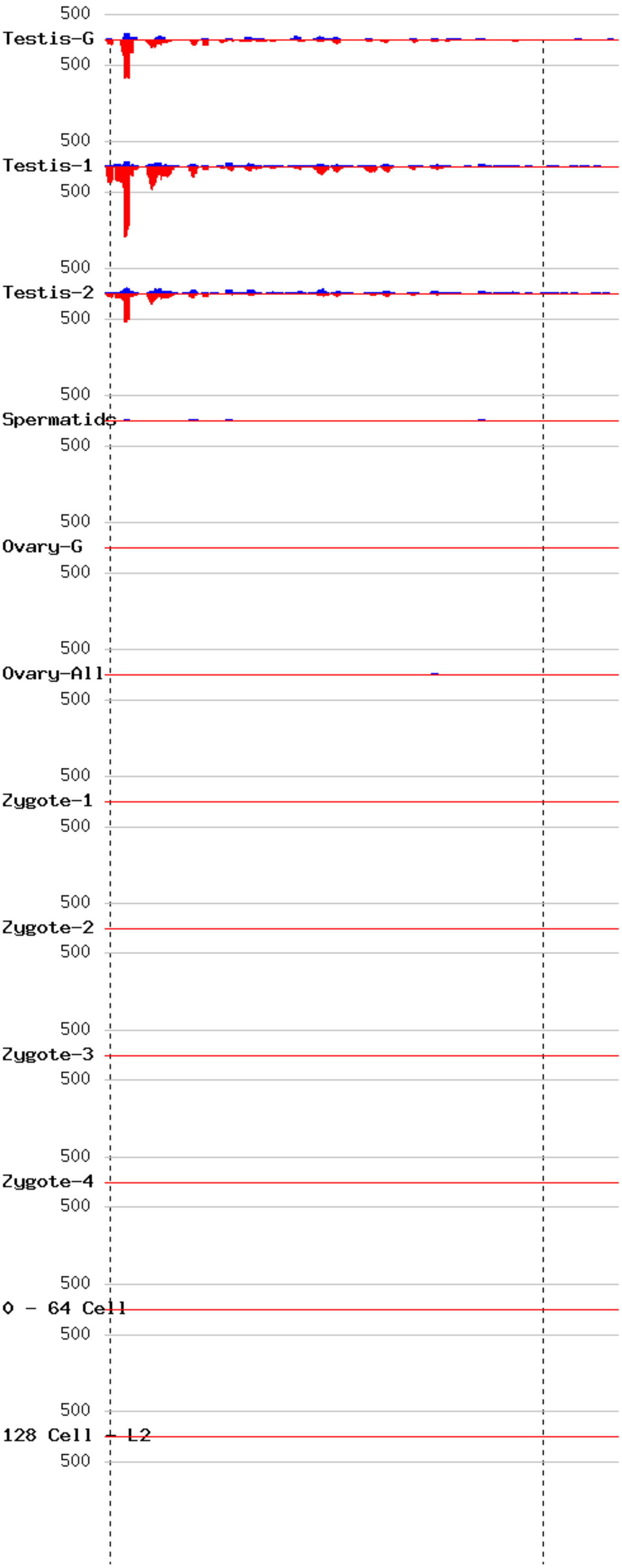
ASCF_368_5258 Phospholipase_C_beta_4 5258 bp



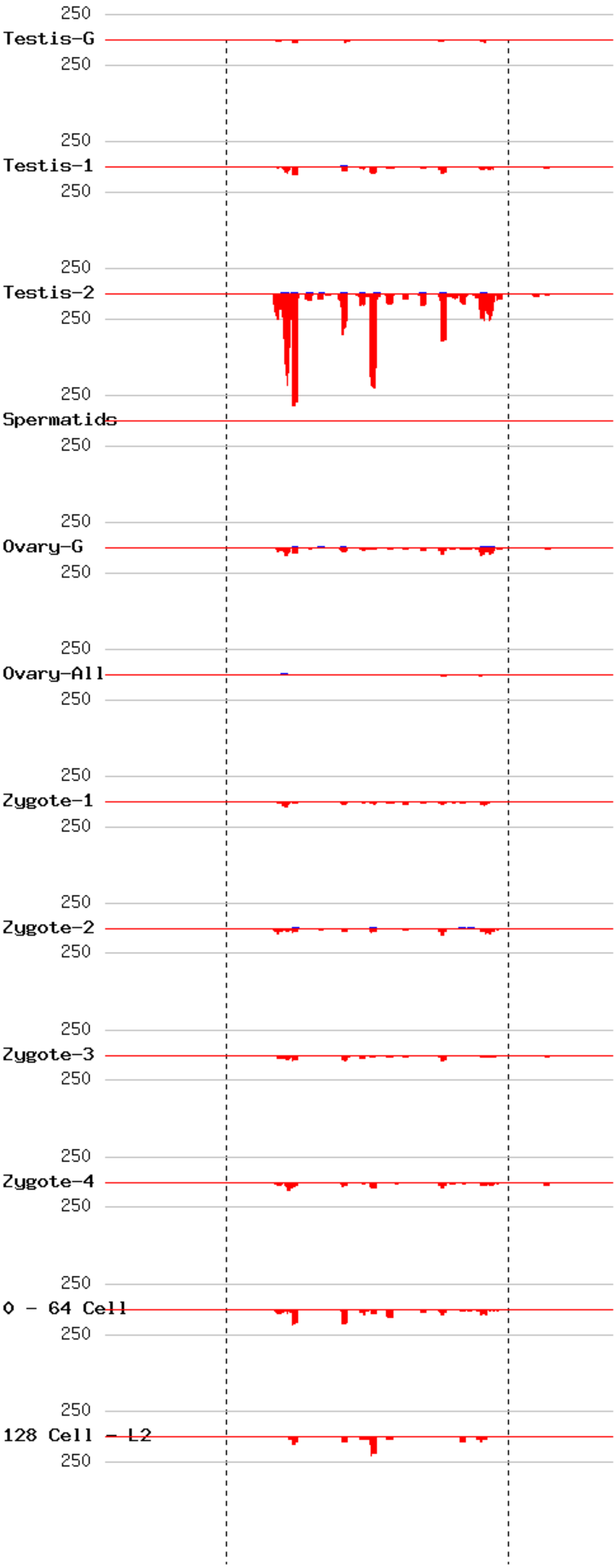
ASCF_3717_2035 Calponin_homolog_OV9M 2035 bp



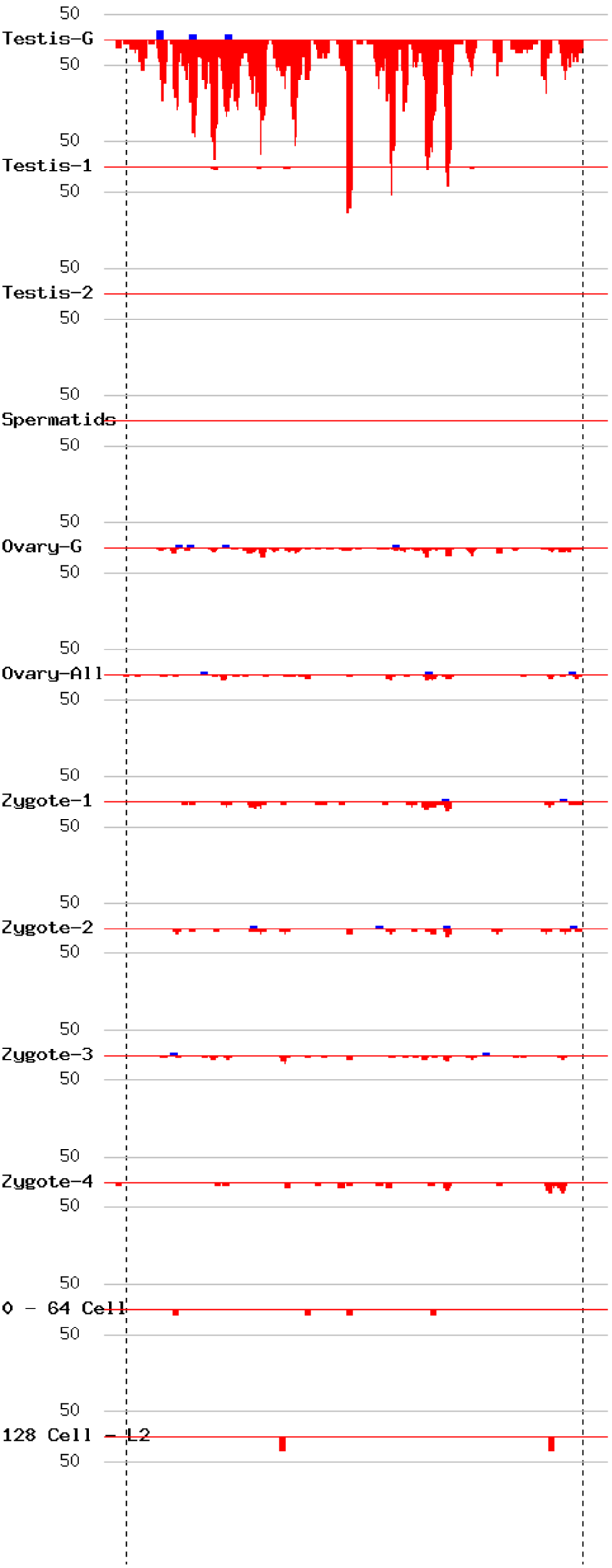
ASCF_3762_2021 Hypothetical_protein 2021 bp



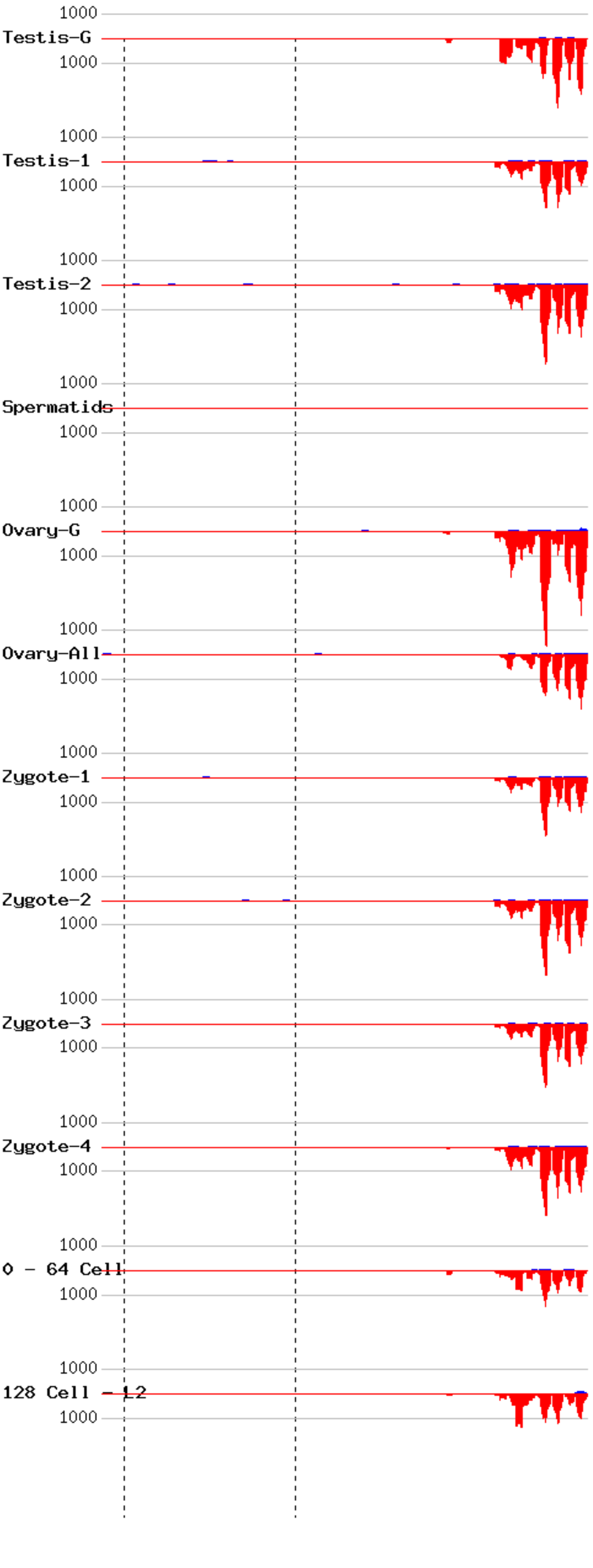
ASCF_3832_1997 Collagen_protein_107 1997 bp



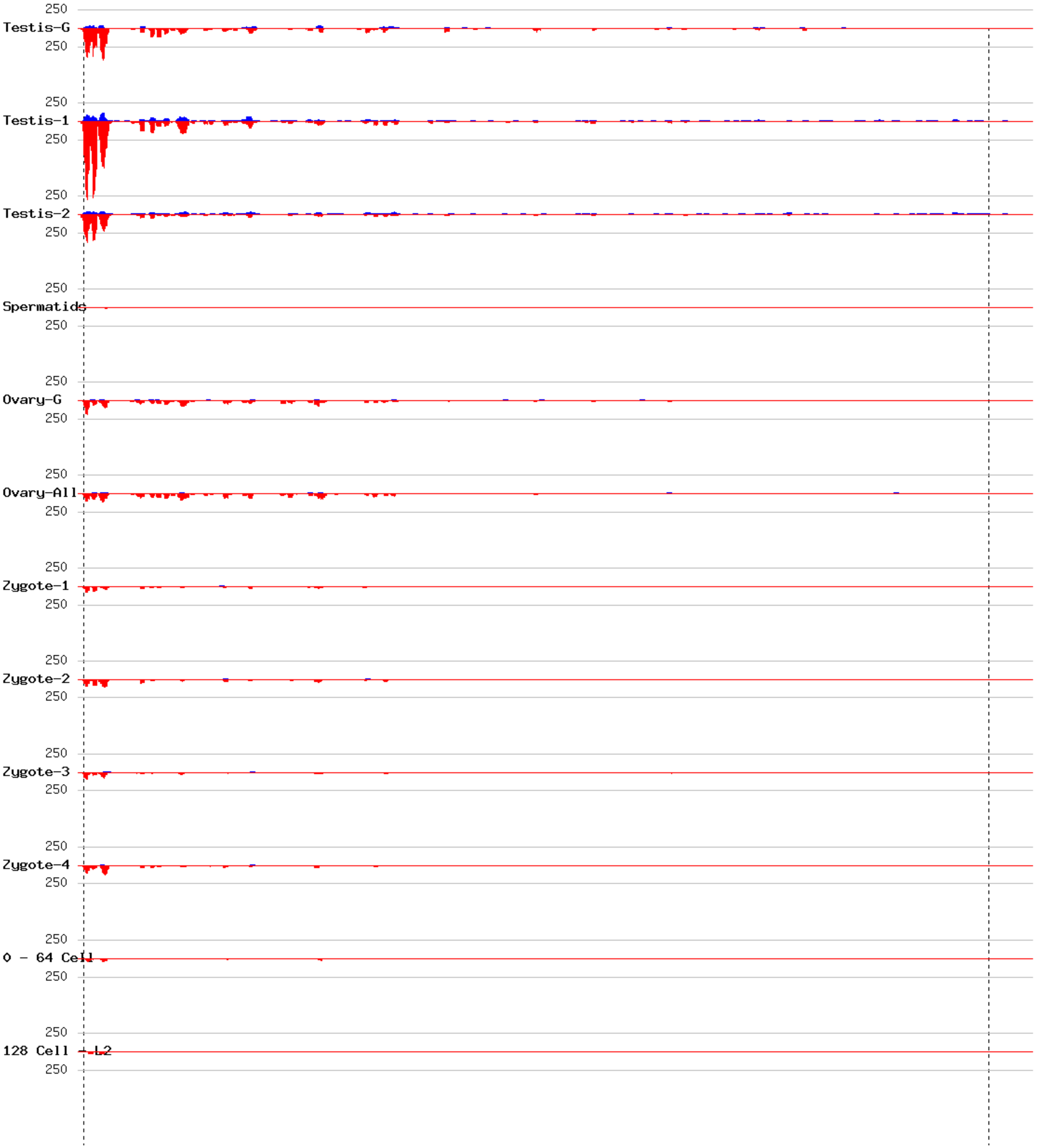
ASCF_3866_1984 Hypothetical_protein 1984 bp



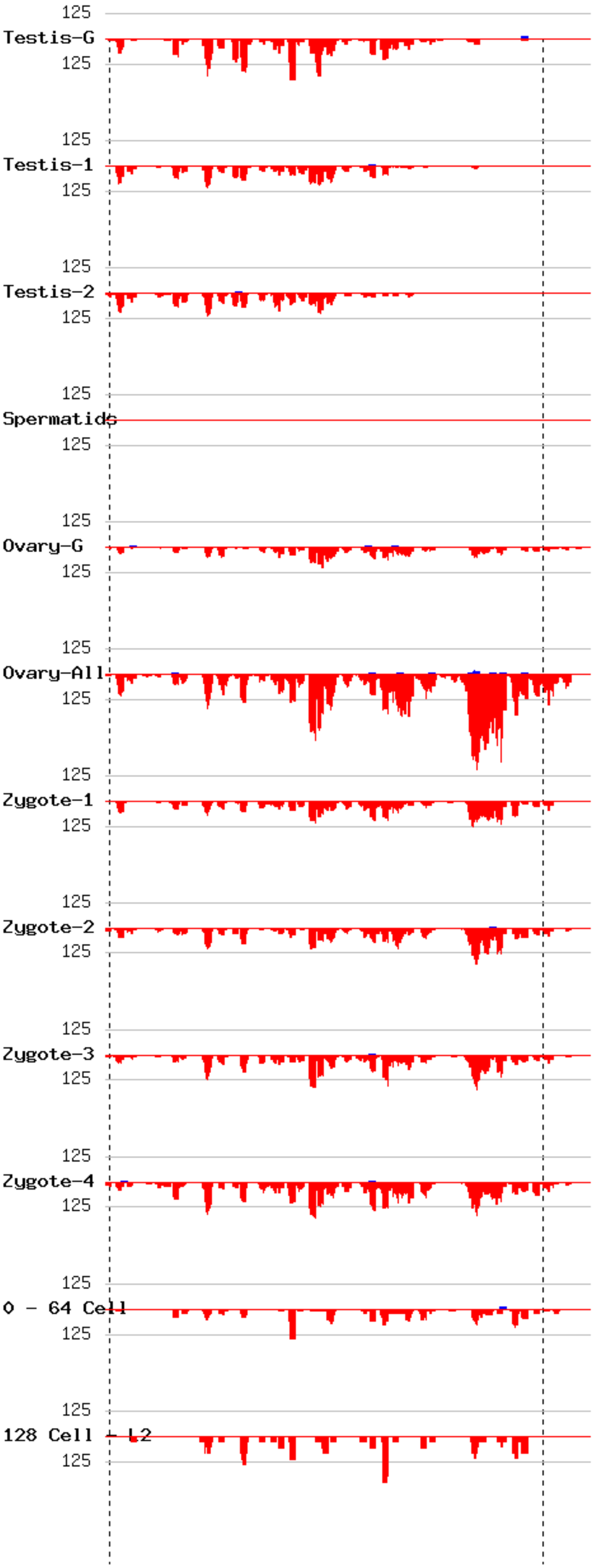
ASCF_3899_1974 MMAB-1_protein 1974 bp



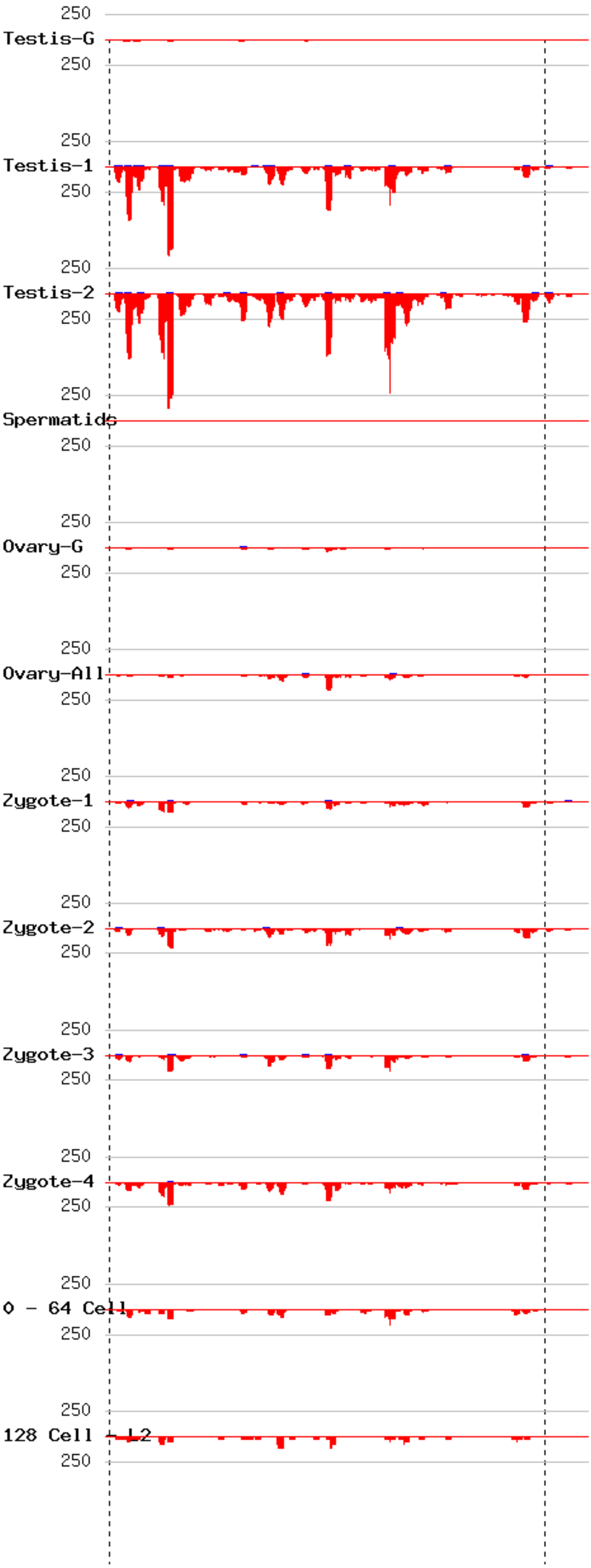
ASCF_406_5130 Hypothetical_protein 5130 bp



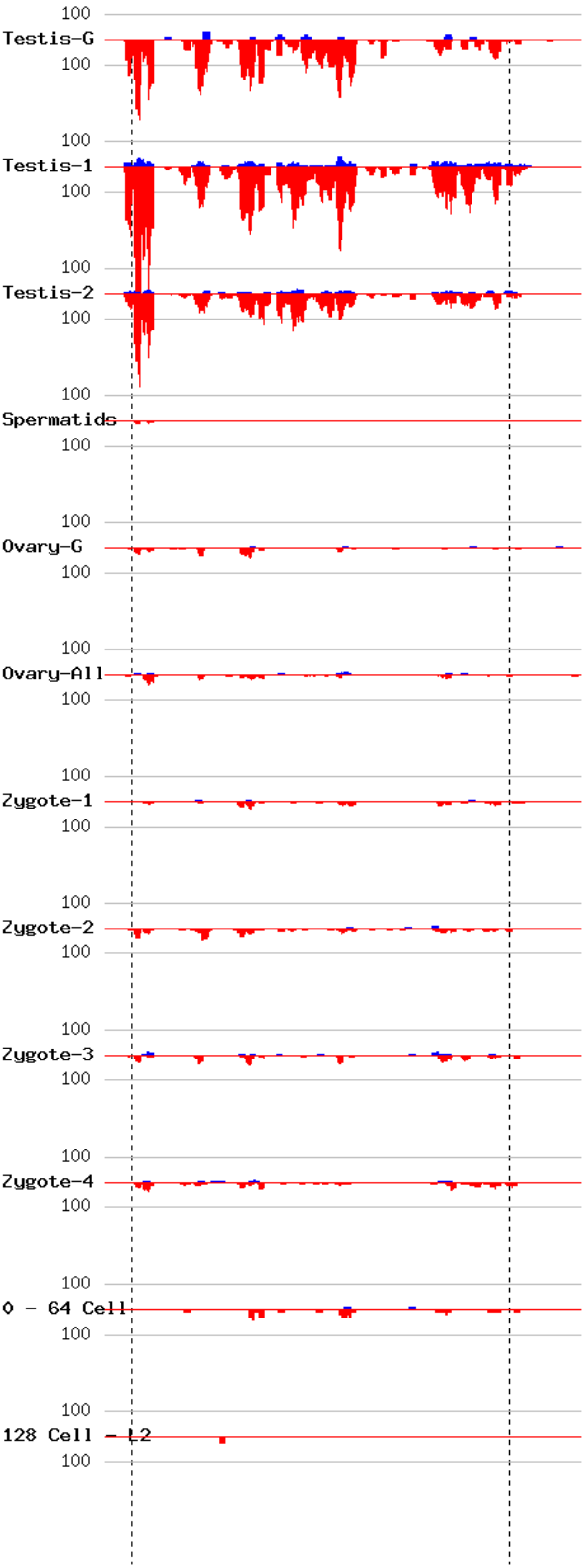
ASCF_4108_1908 Hypothetical_protein 1908 bp



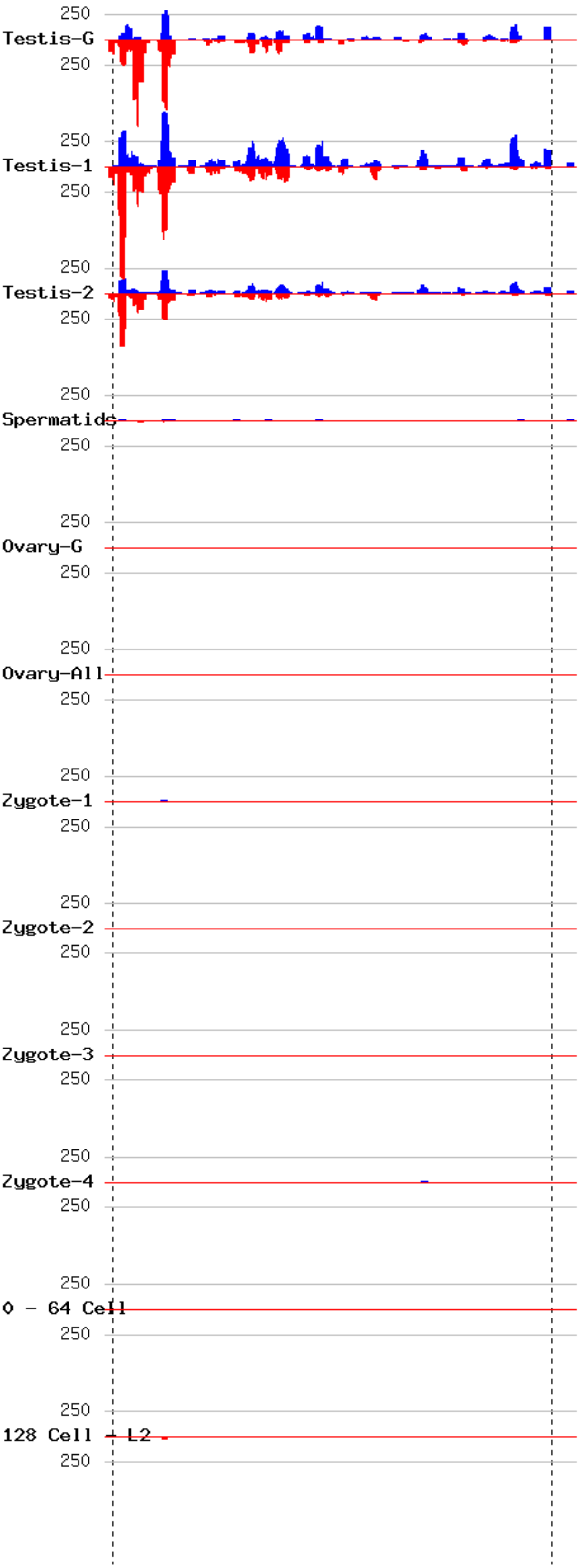
ASCF_4137_1900 Cuticle_collagen 1900 bp



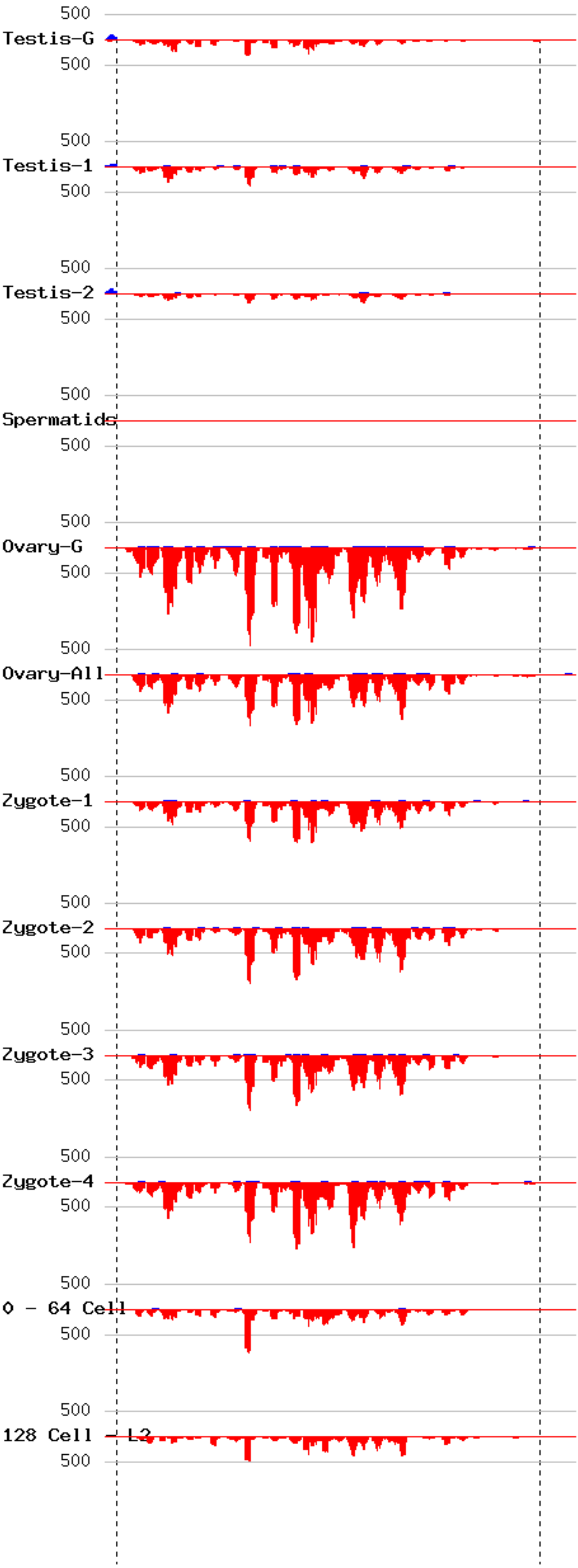
ASCF_4218_1873 TSC-22/dip/bun_family_protein 1873 bp



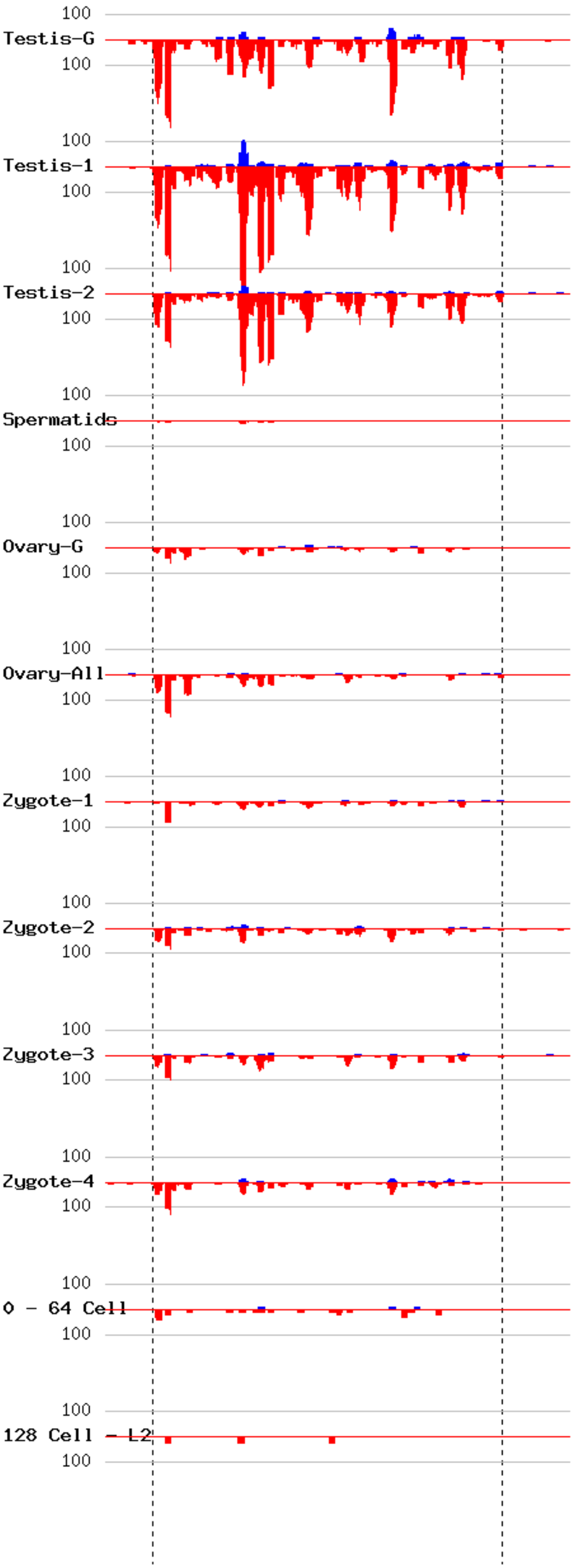
ASCF_4283_1855 Hypothetical_protein 1855 bp



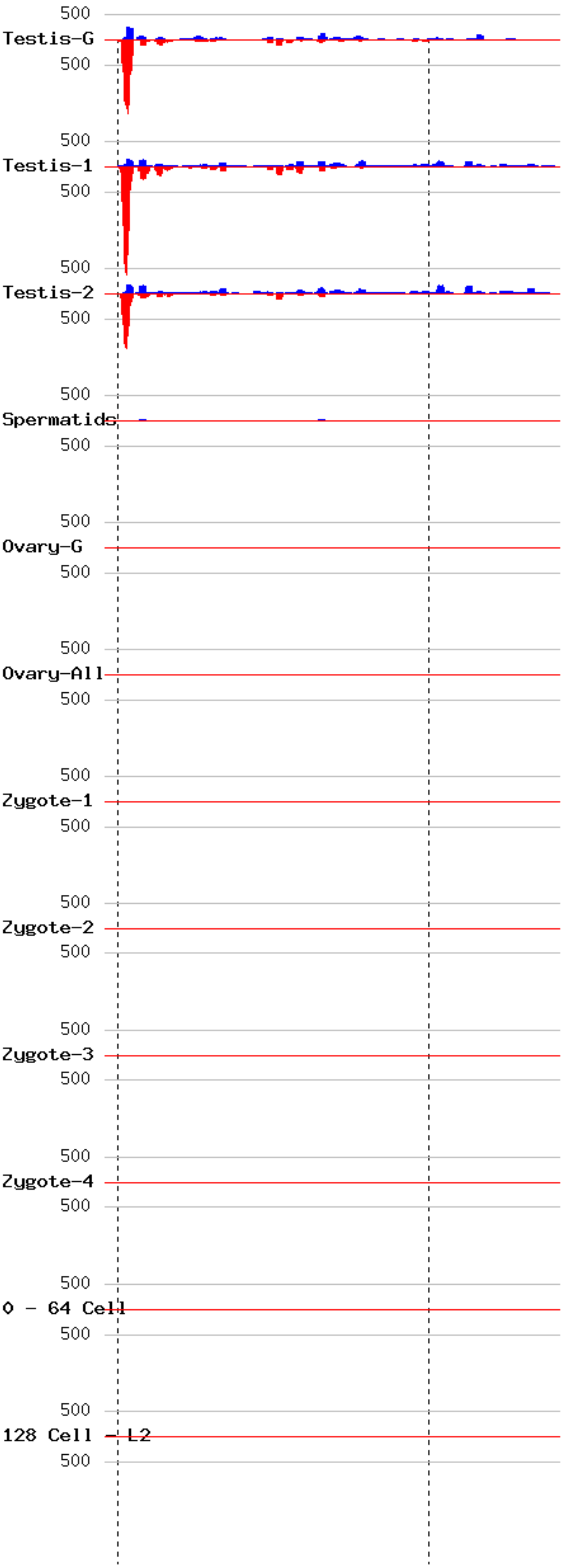
ASCF_4287_1854 Hypothetical_protein 1854 bp



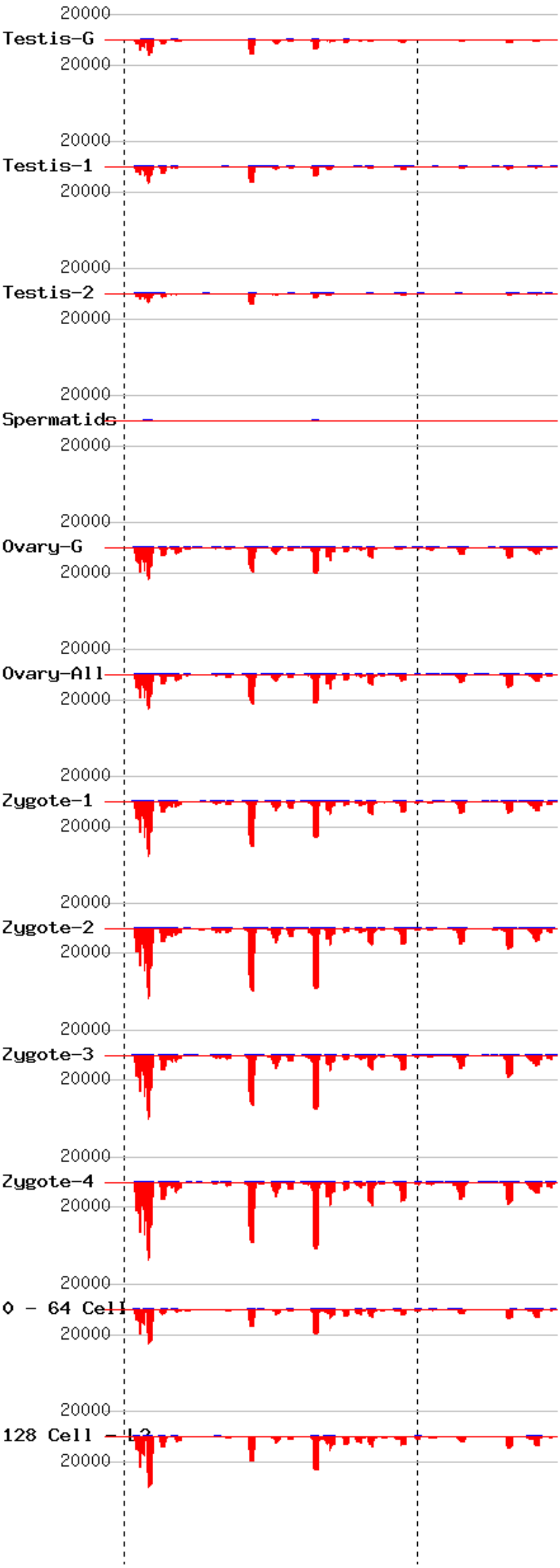
ASCF_4381_1827 Hypothetical_protein 1827 bp



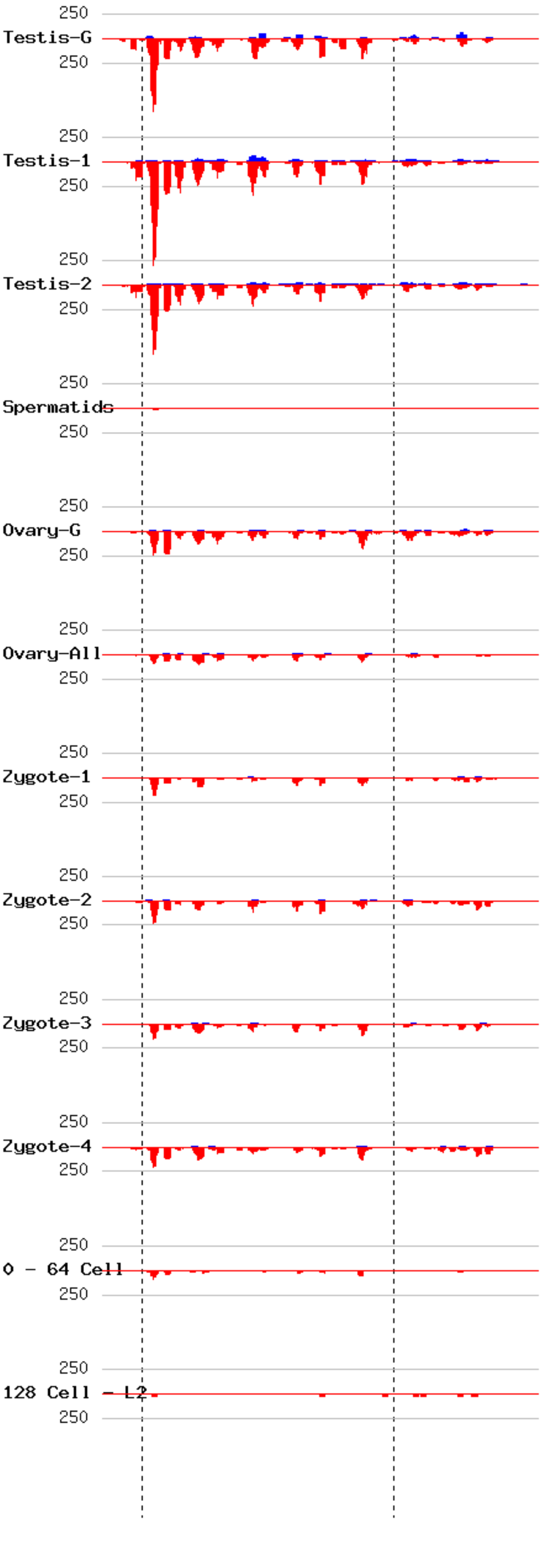
ASCF_4485_1794 Protein_kinase_domain_containing_prote

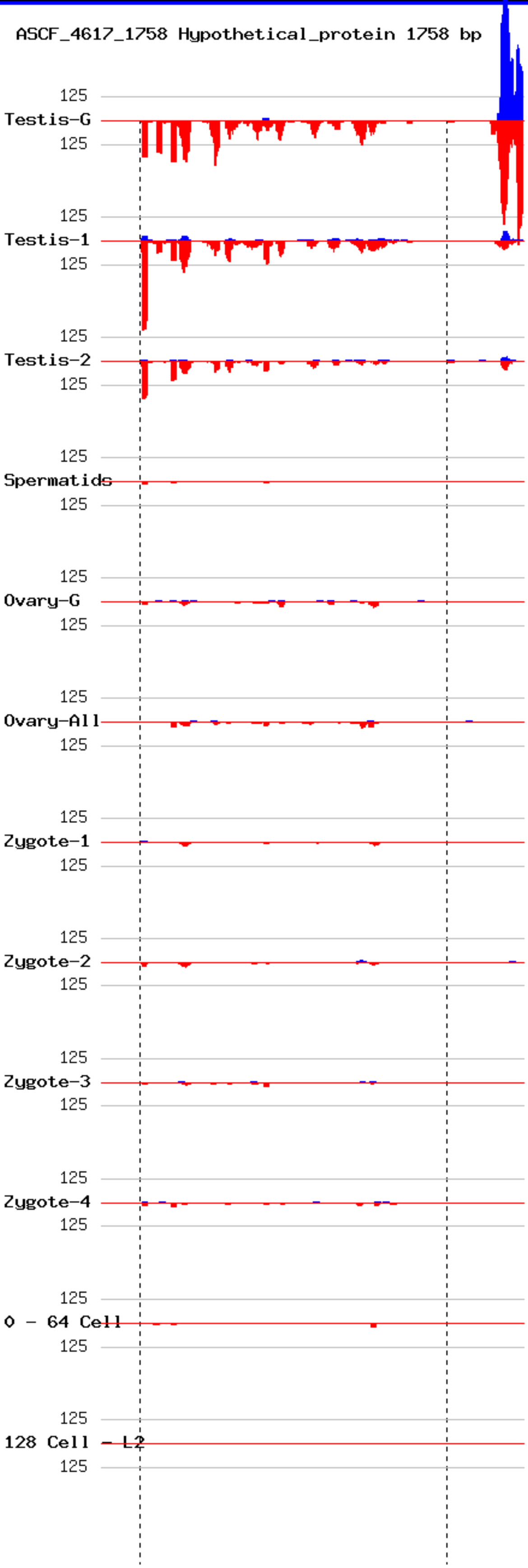


ASCF_4512_1784 Hypothetical_protein 1784 bp

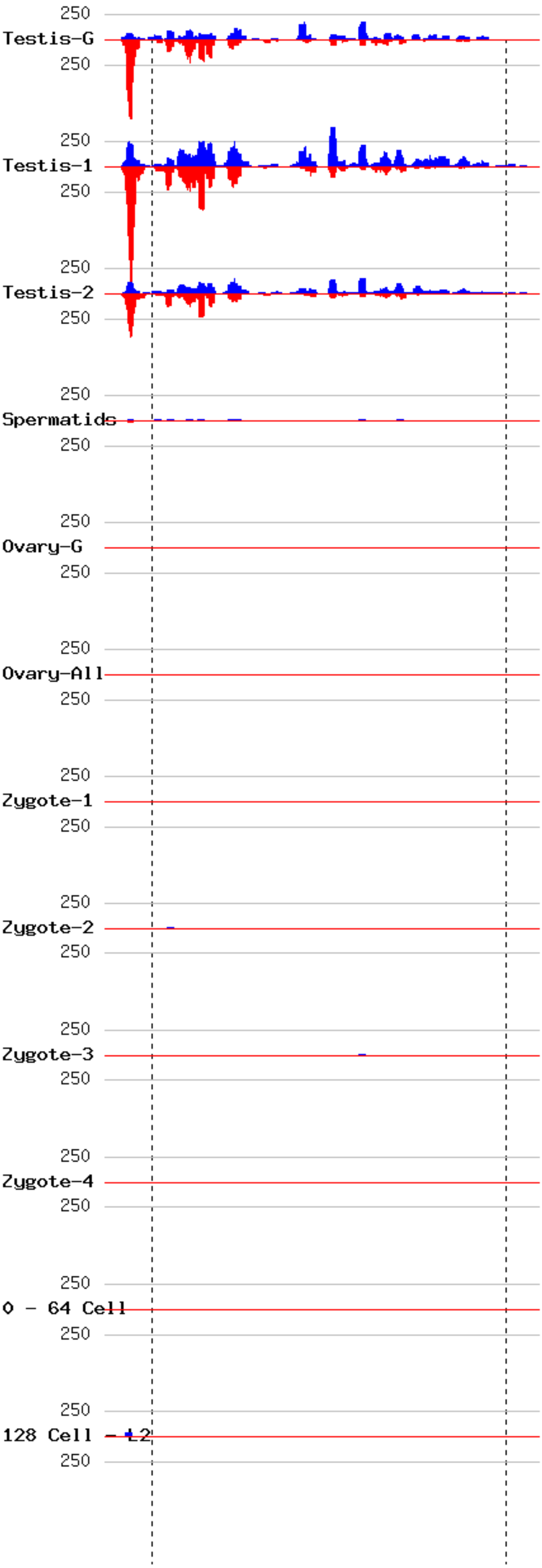


ASCF_4583_1766 Glyceraldehyde-3-phosphate_dehydrogena

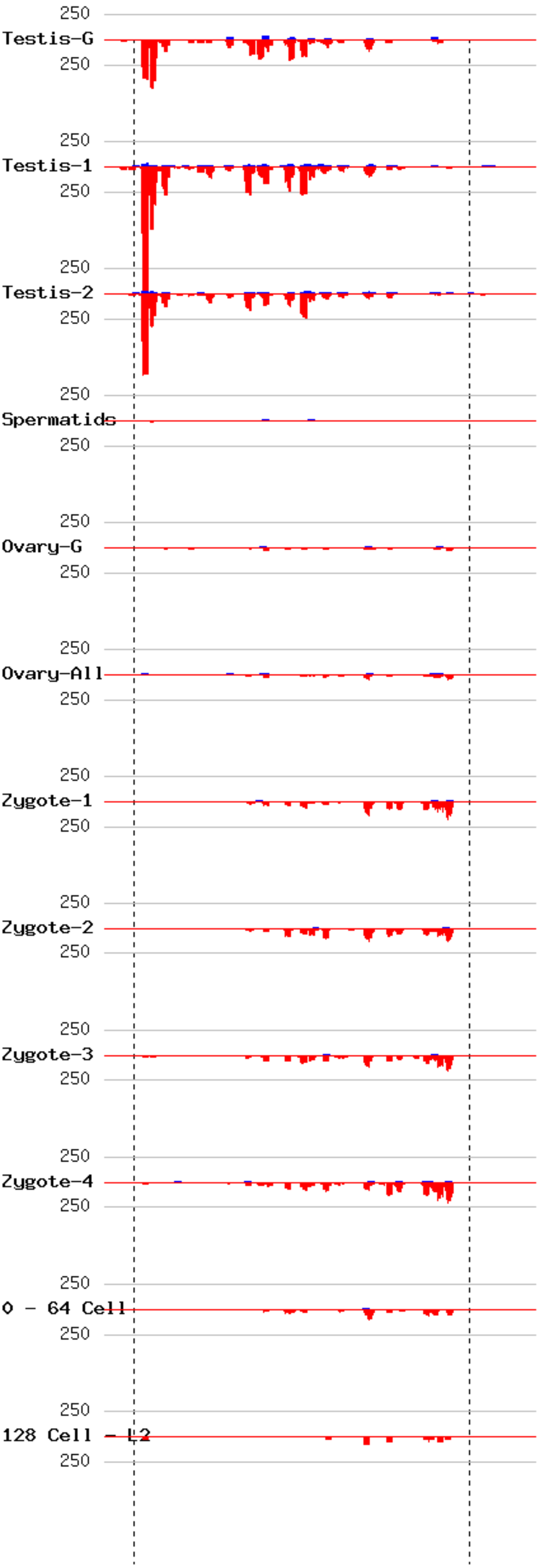


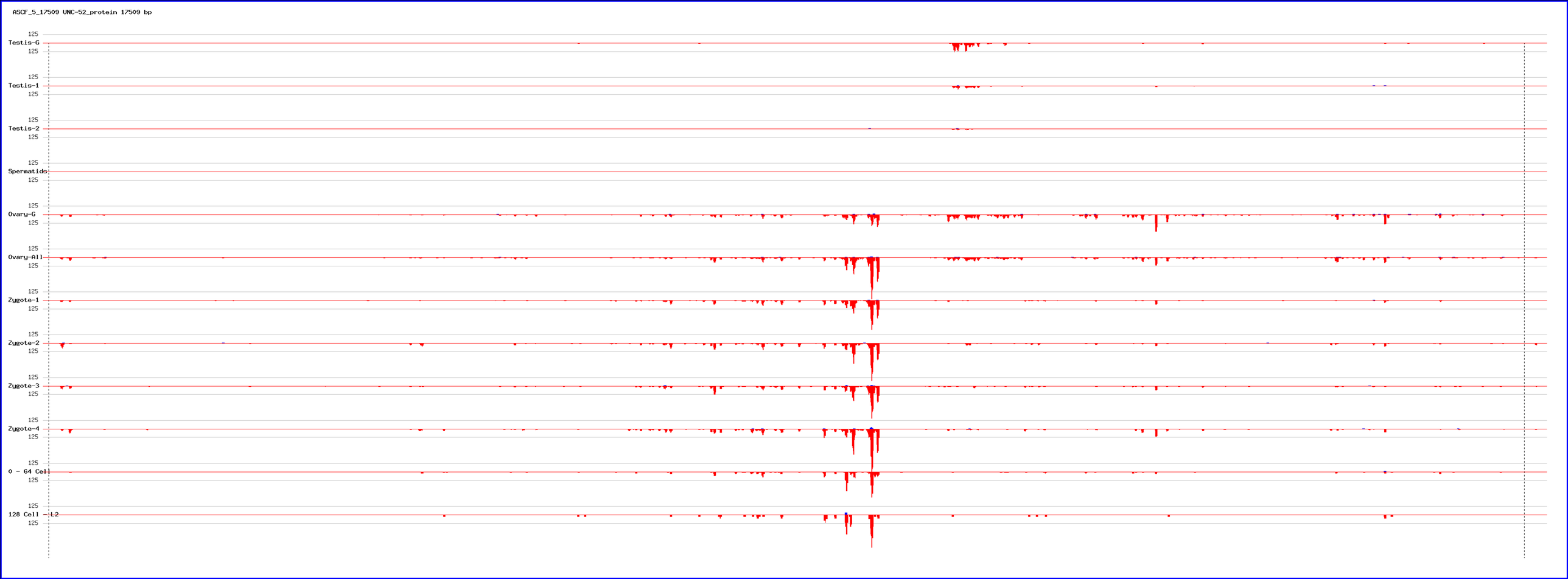

ASCF_4617_1758 Hypothetical_protein 1758 bp
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Testis-G
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Testis-1
125
125
Testis-2
125
125
Spermatids
125
125
Ovary-G
125
125
Ovary-All
125
125
Zygote-1
125
125
Zygote-2
125
125
Zygote-3
125
125
Zygote-4
125
125
0 - 64 Cell
125
125
128 Cell - L2
125

ASCF_4806_1713 Hypothetical_protein 1713 bp

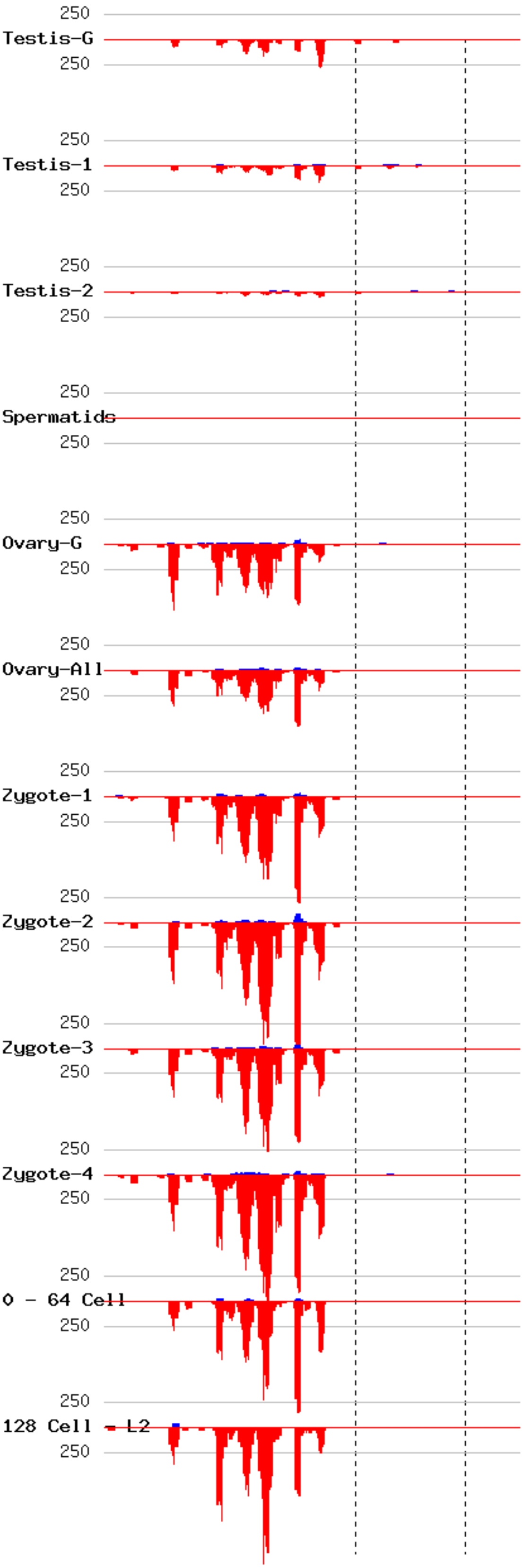


ASCF_4859_1699 Leucine_Rich_Repeat_family_protein 1

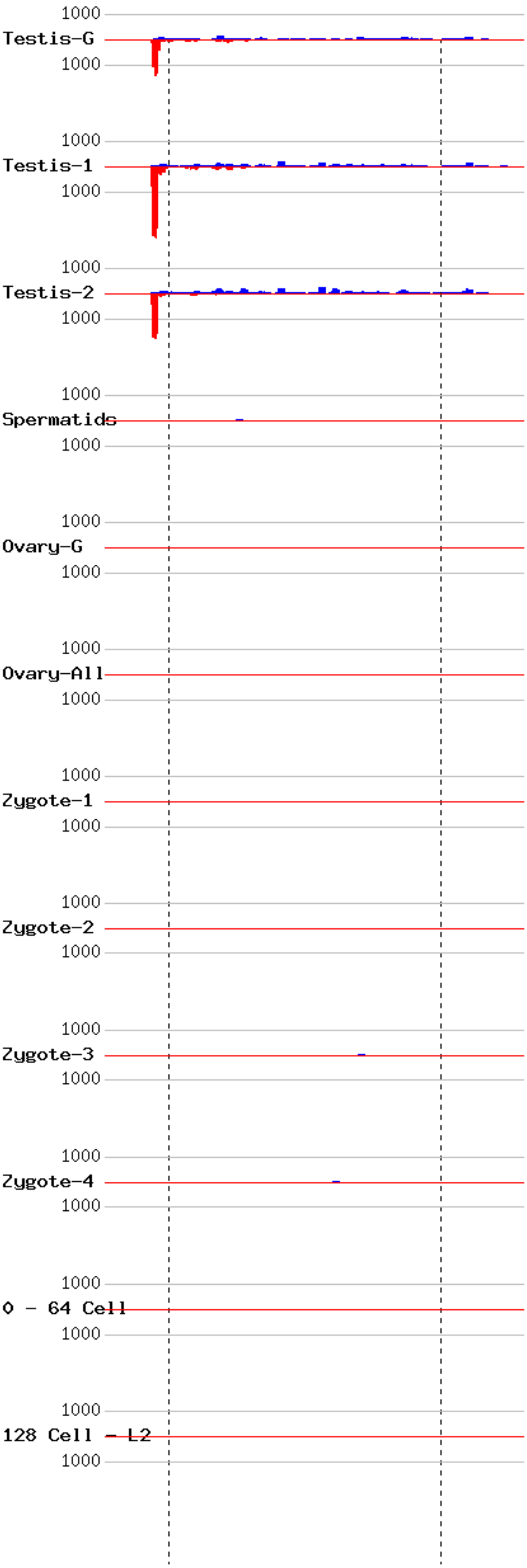



ASCF_5_17509 UNC-52_protein 17509 bp
125
Testis-G
125
125
Testis-1
125
125
Testis-2
125
125
Spermatids
125
125
Ovary-G
125
125
Ovary-All
125
125
Zygote-1
125
125
Zygote-2
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125
Zygote-3
125
125
Zygote-4
125
125
0 - 64 Cell
125
125
128 Cell - L2
125

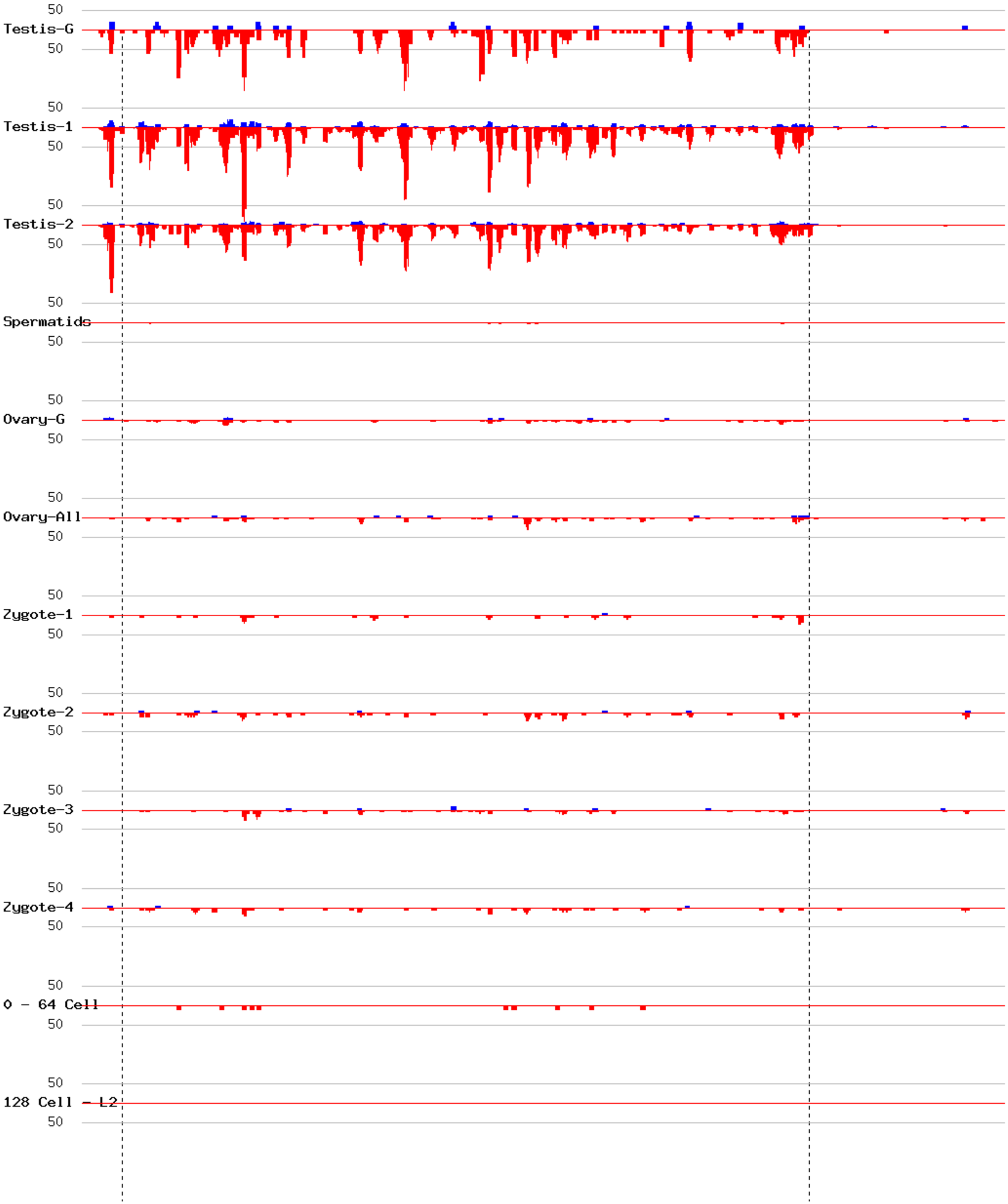
ASCF_5073_1647 40S_ribosomal_protein_S16 1647 bp



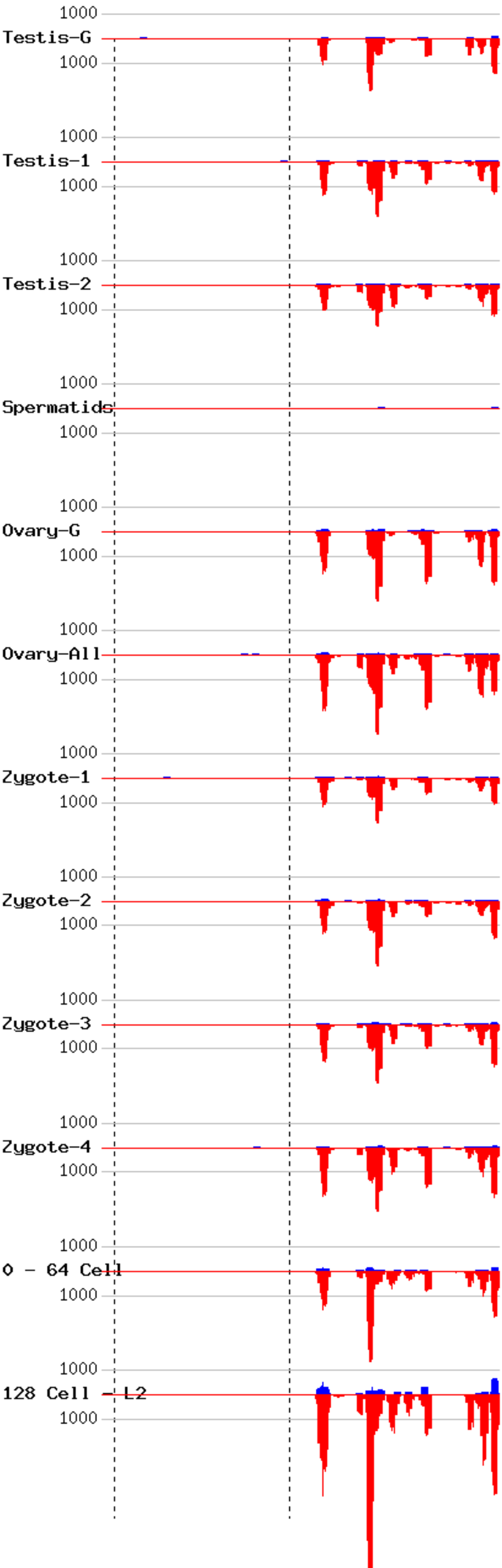
ASCF_5091_1645 Serine/threonine-protein_phosphatas



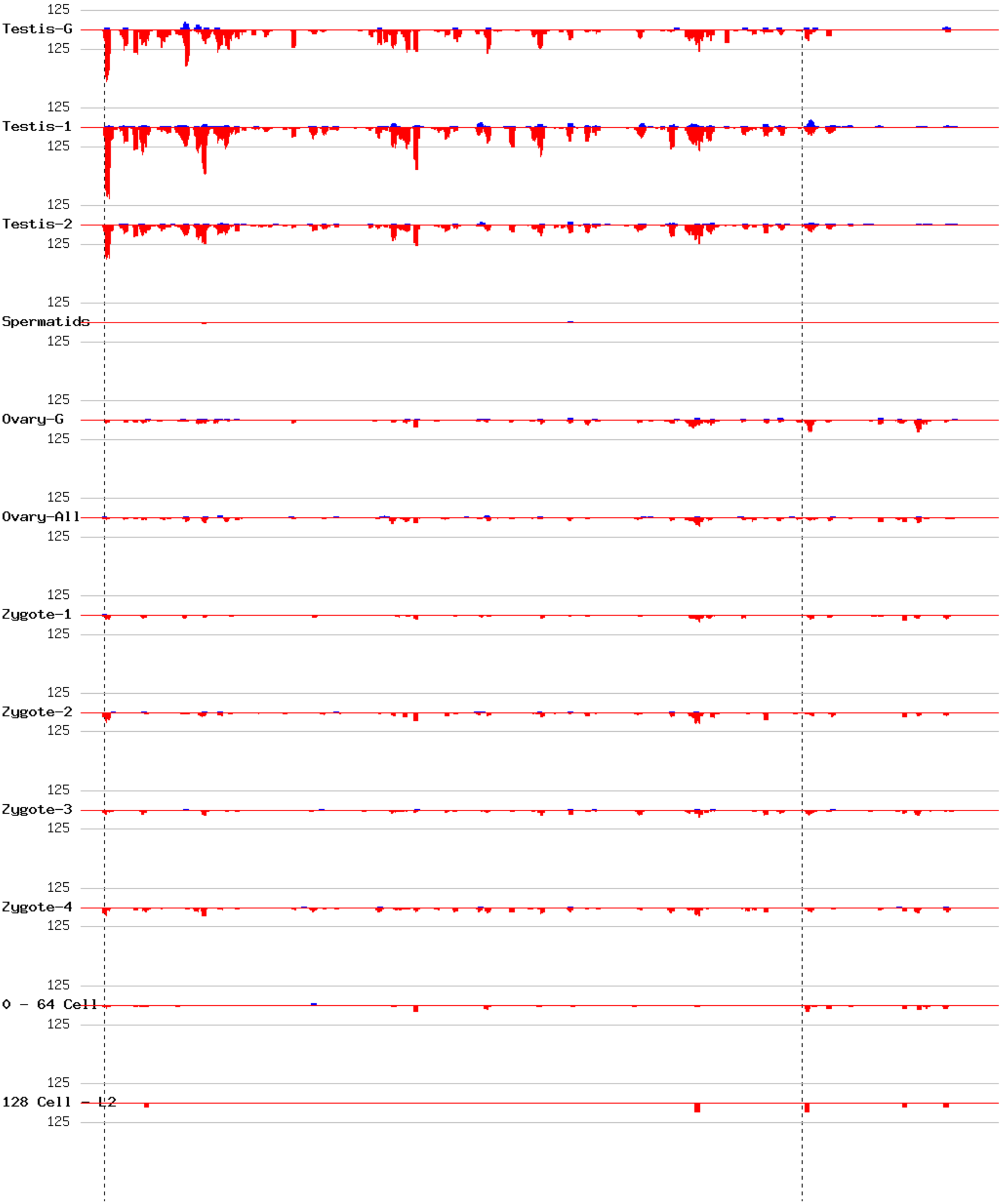
ASCF_517_4727 DNA-directed_RNA_polymerase 4727 bp



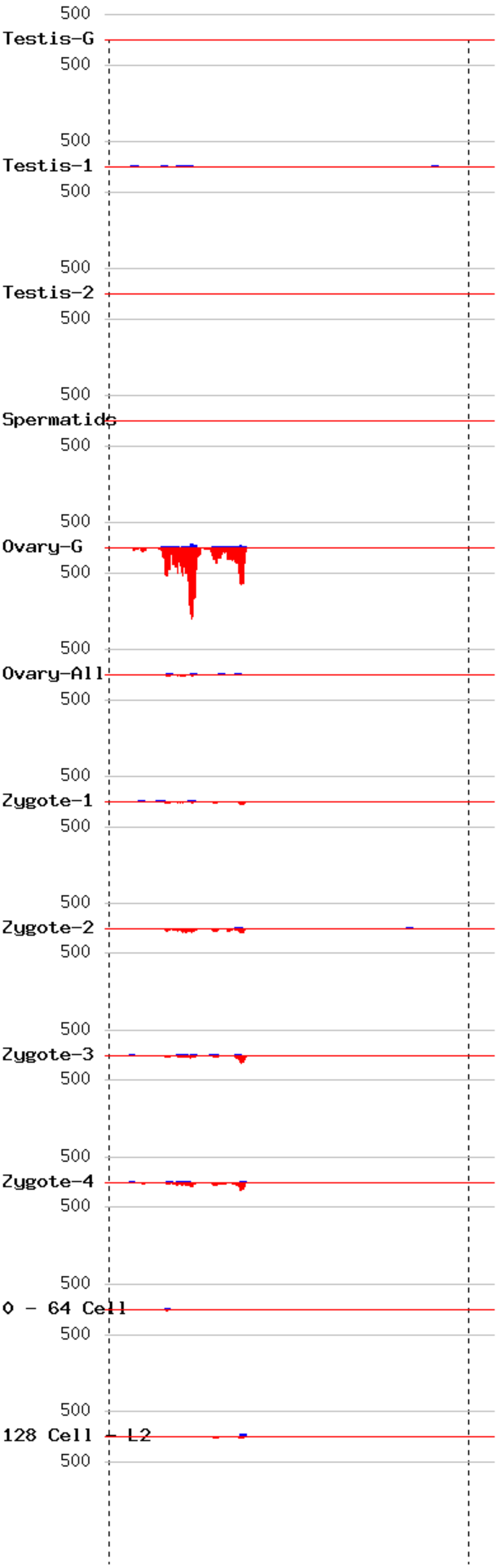
ASCF_5254_1611 SET_domain_containing_protein 1611



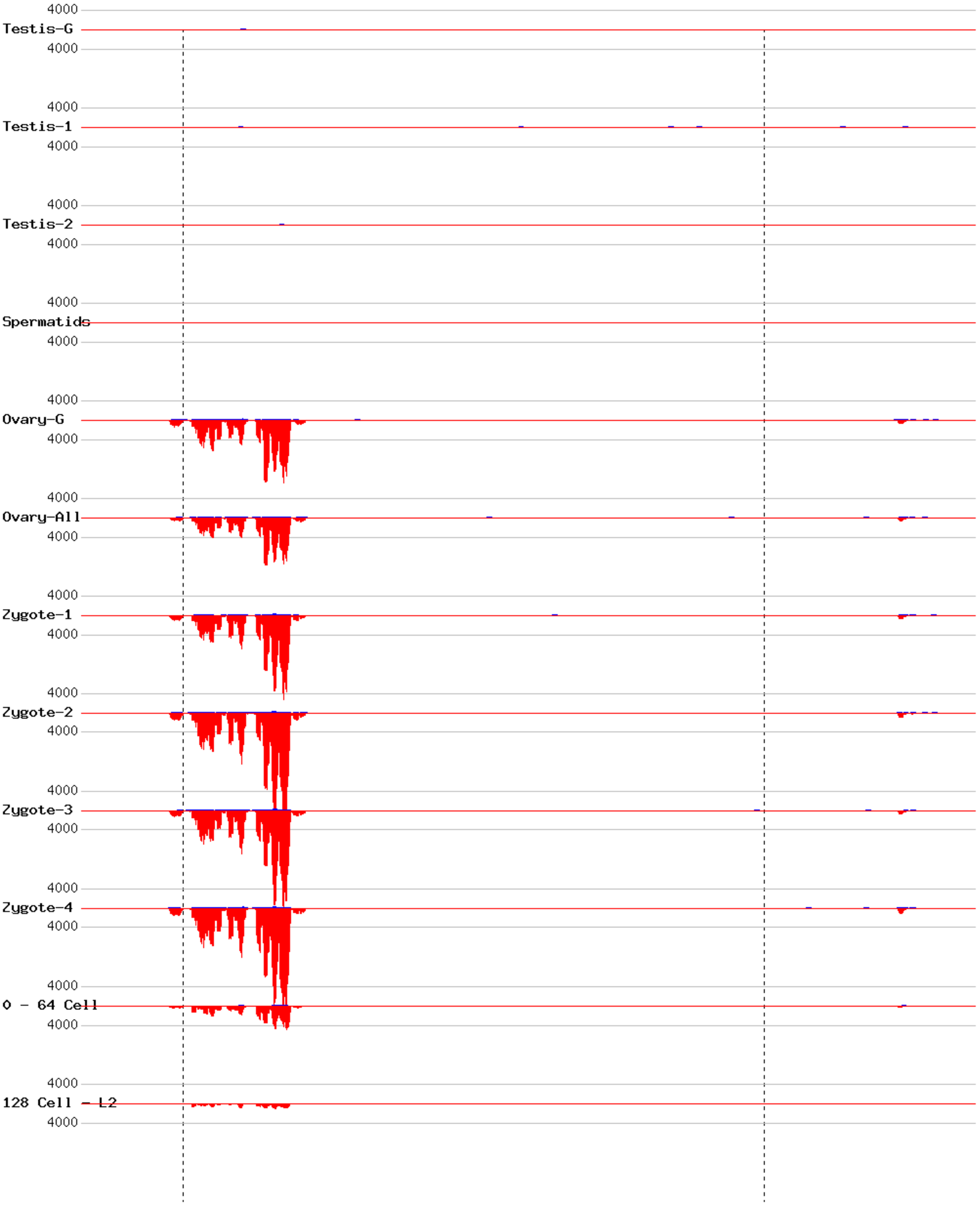
ASCF_529_4701 RNB-like_protein 4701 bp



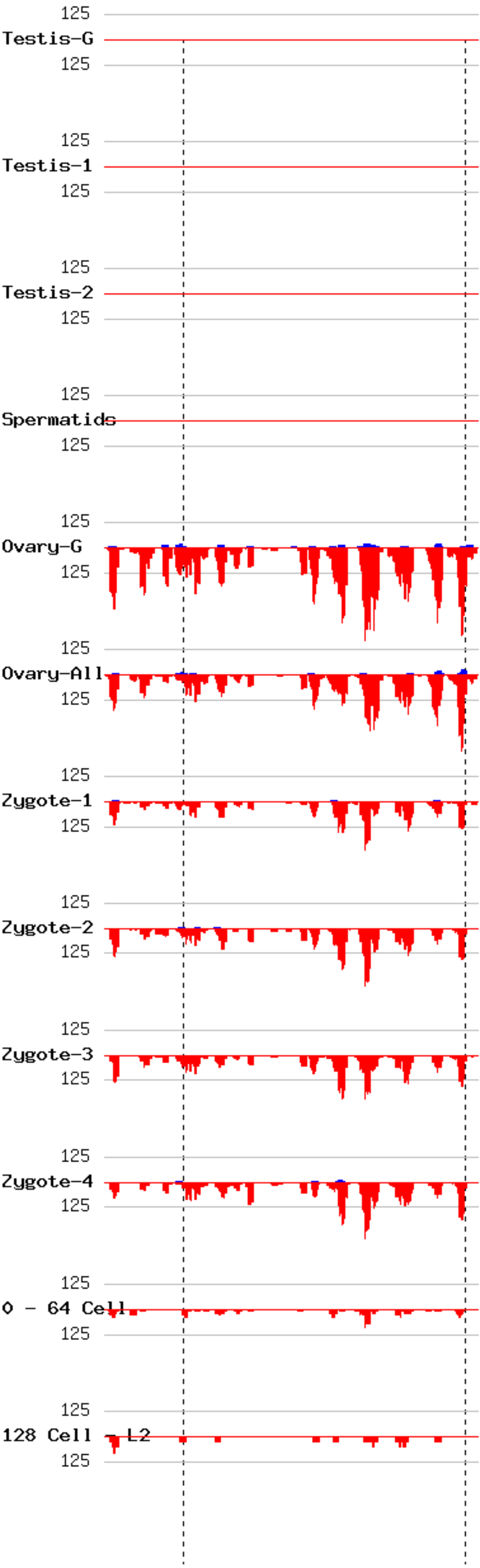
ASCF_5548_1533 Histone_H3 1533 bp



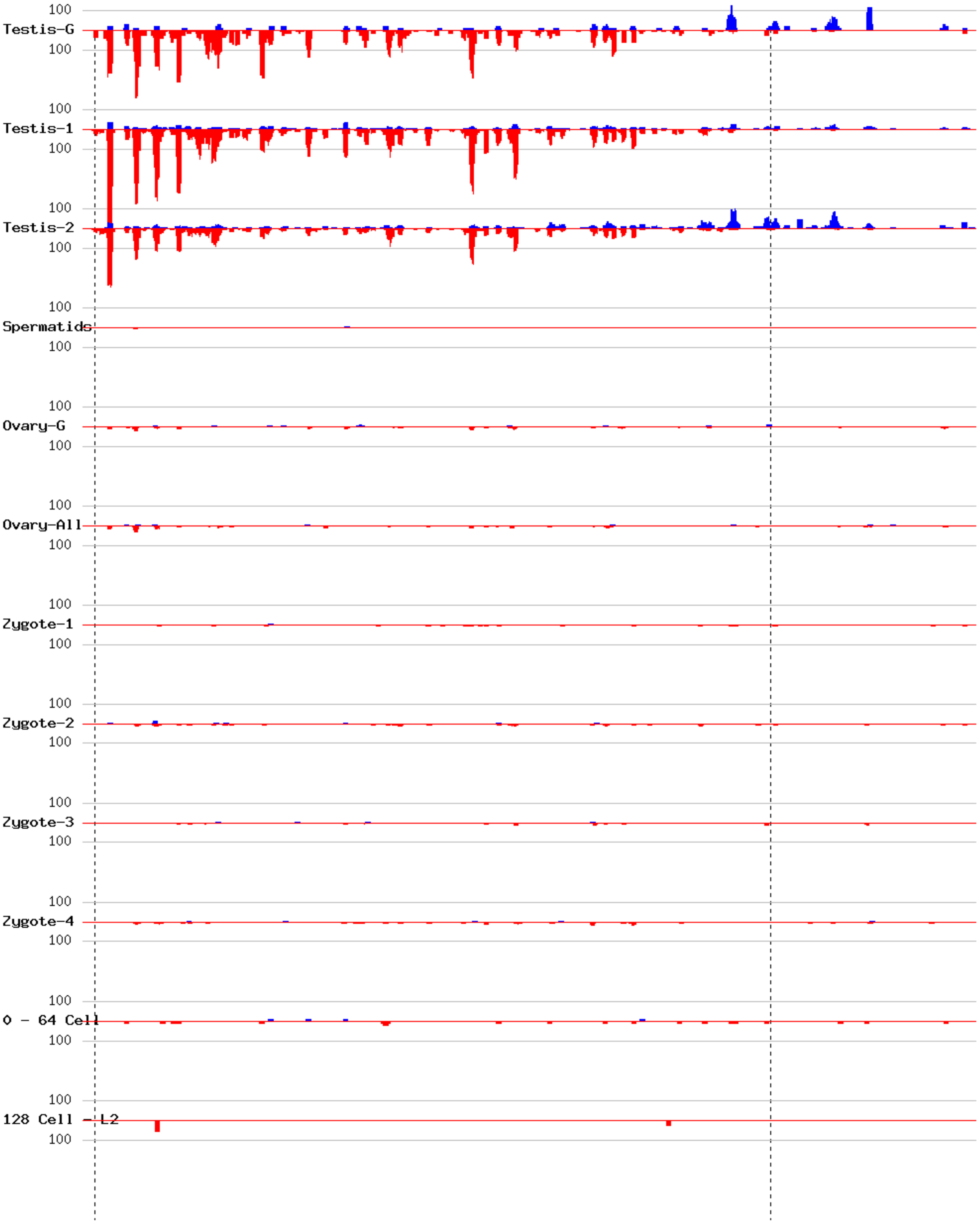
ASCF_564_4579 Hypothetical_protein 4579 bp



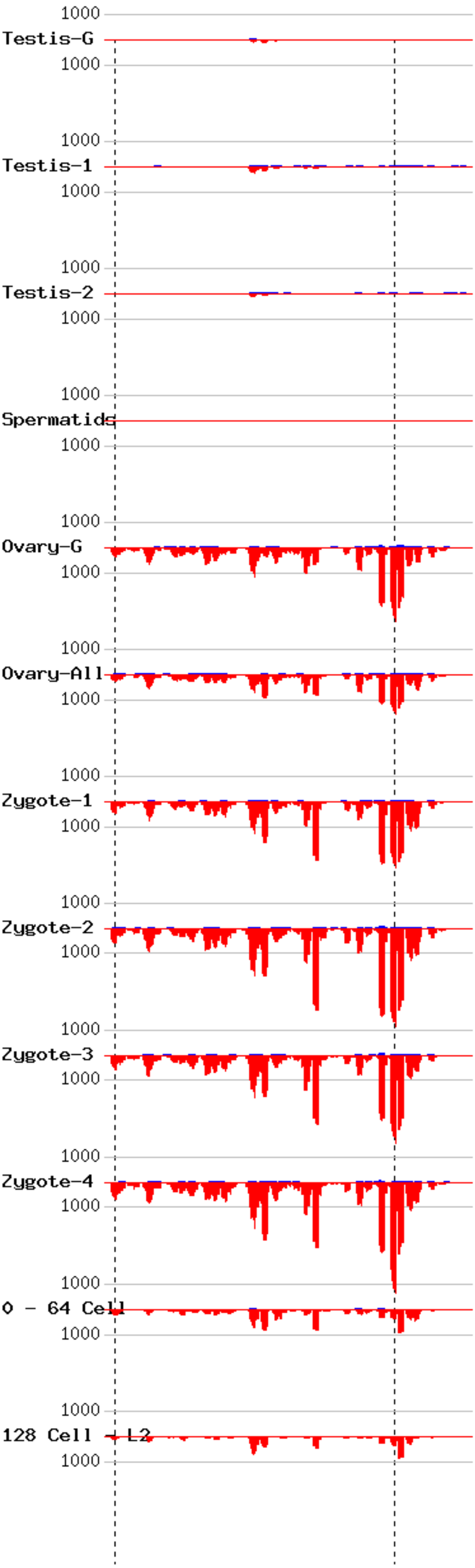
ASCF_5821_1472 Protein_phosphatase 1472 bp



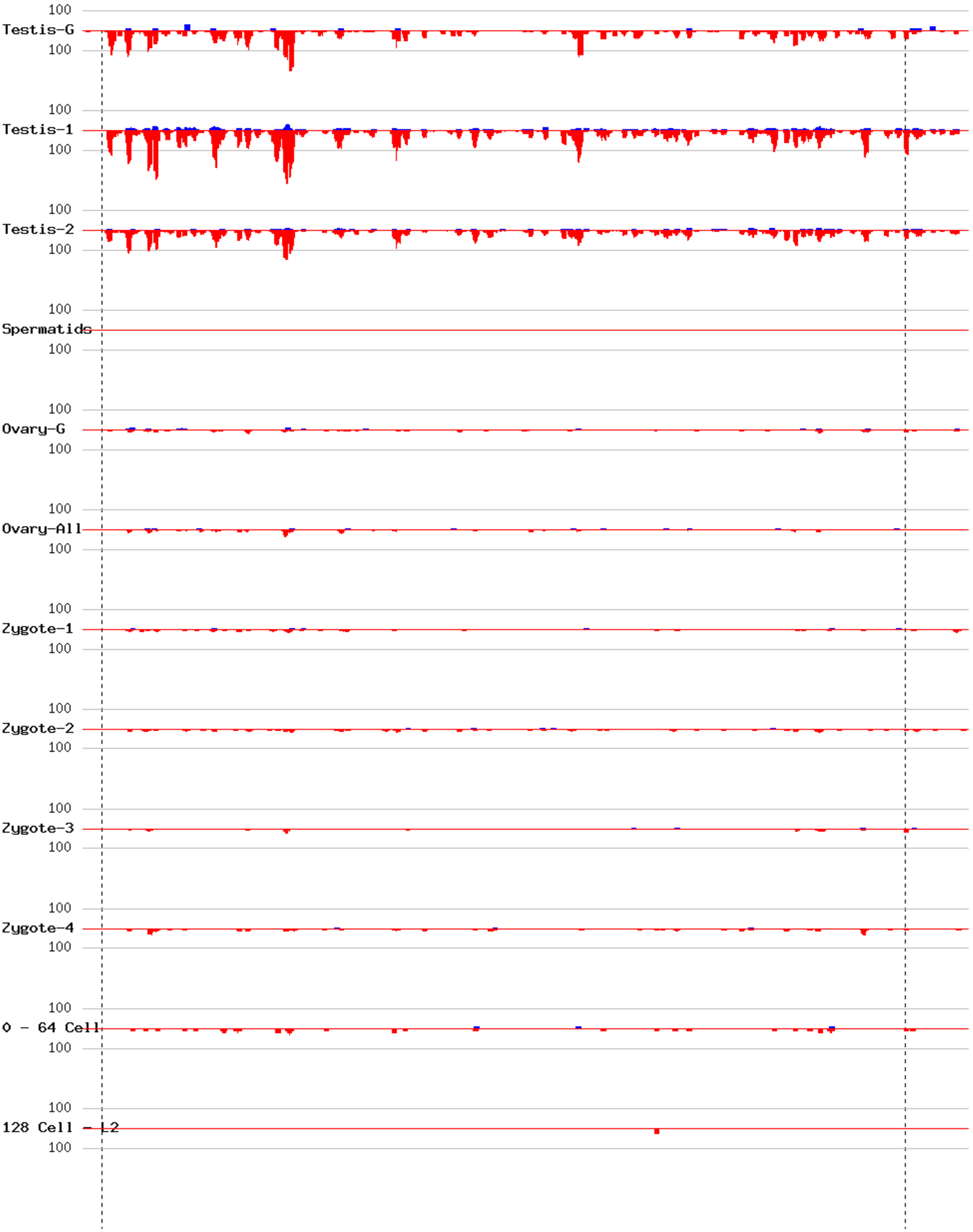
ASCF_588_4506 Hypothetical_protein 4506 bp



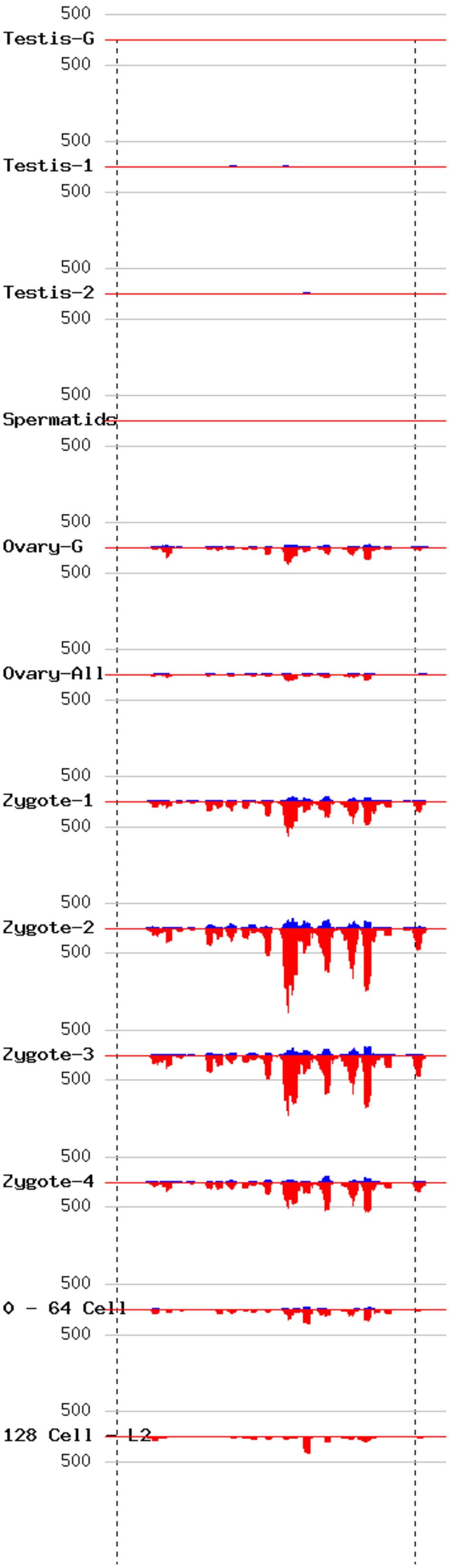
ASCF_5922_1448 BZIP_transcription_factor_fami



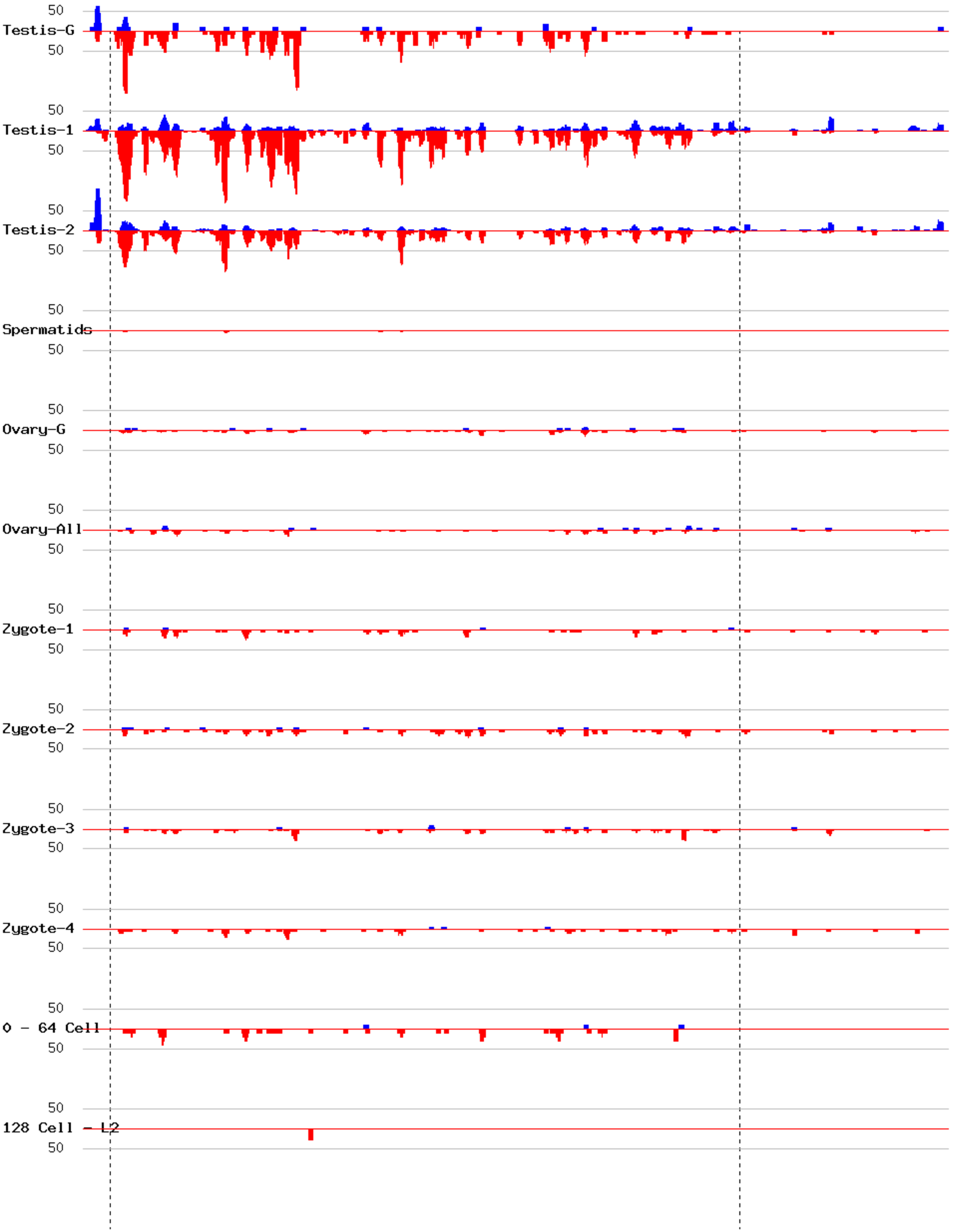
ASCF_619_4438 Hypothetical_protein 4438 bp



ASCF_6433_1340 Chitin_binding_protein 1340

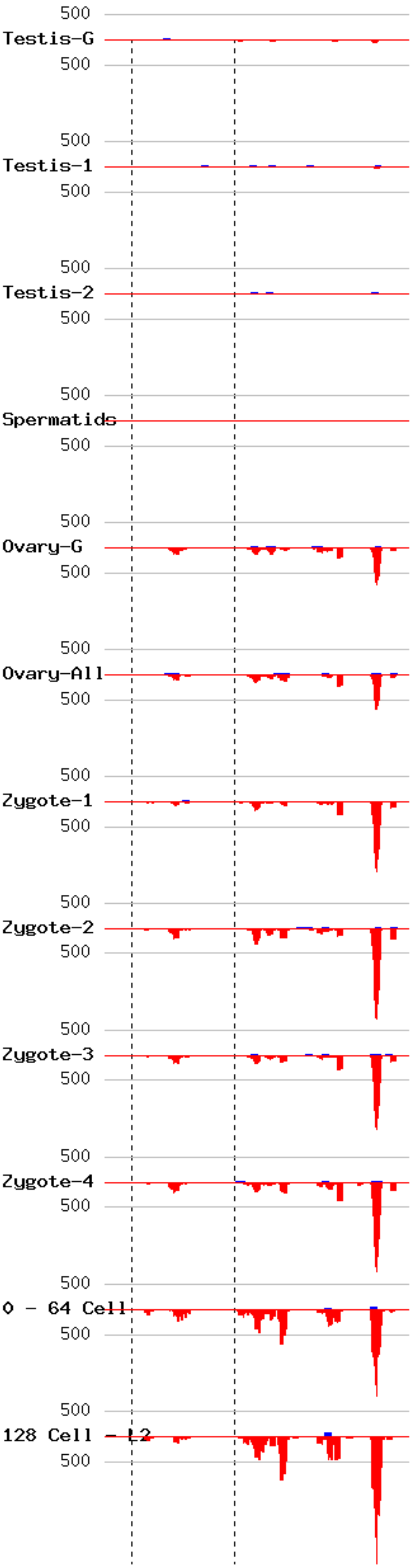


ASCF_652_4339 Ubiquitin_carboxyl-terminal_hydrolase 4339 bp

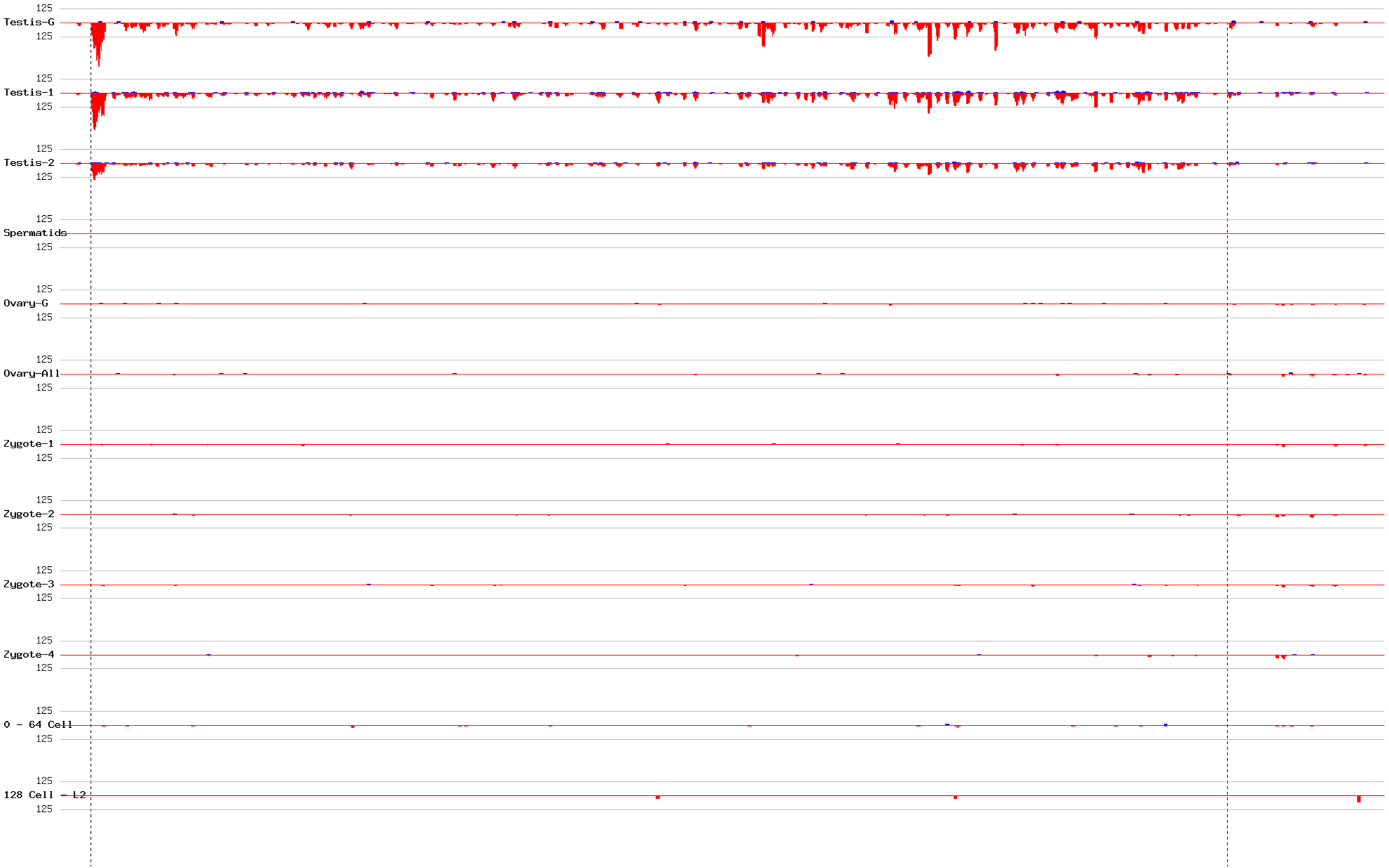


ASCF_665_4307 Hypothetical_protein 4307 bp

ASCF_7080_1196 Spindle_and_centromere-as

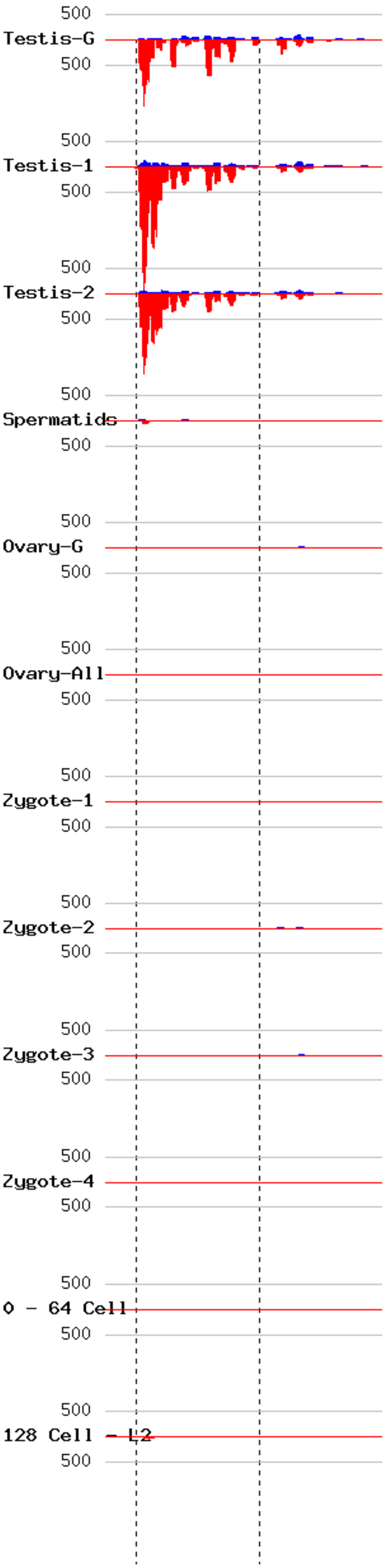


ASCF_71_9416 CCR4-Not_complex_component 9416 bp

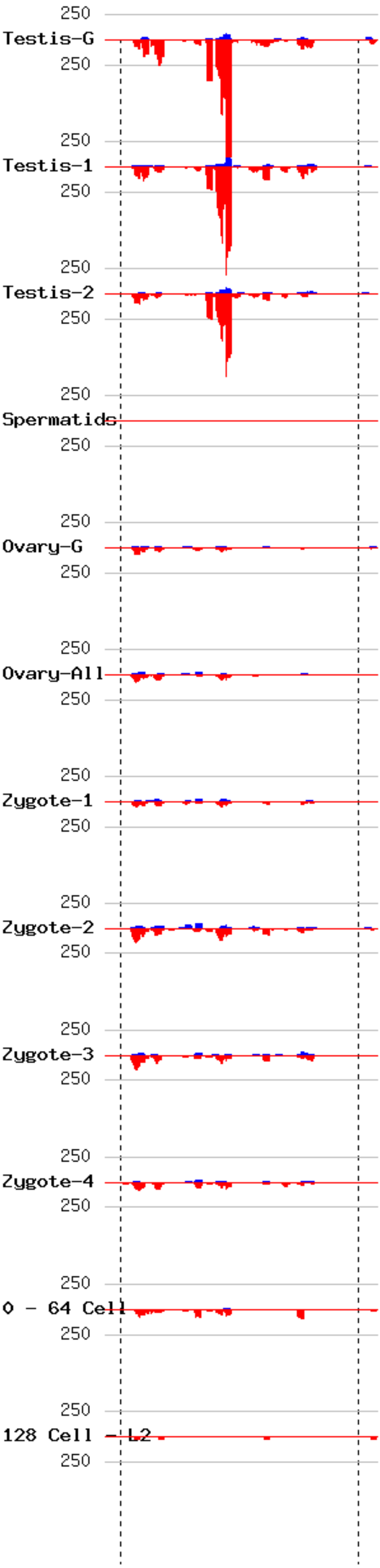


ASCF_729_4160 Exonuclease_family_protein 4160 bp

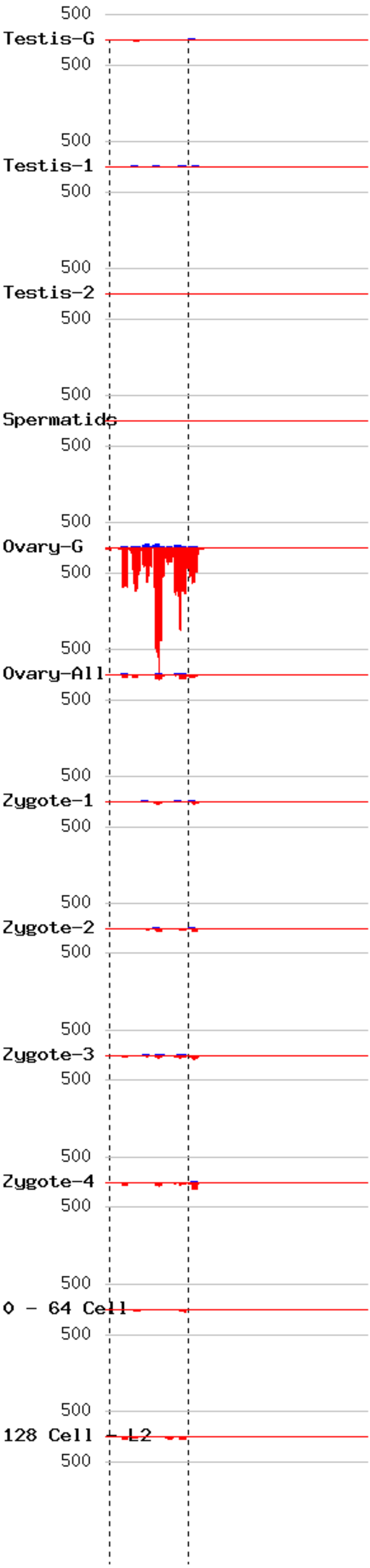
ASCF_7582_1088 Eukaryotic_translation



ASCF_7656_1070 Hypothetical_protein 1



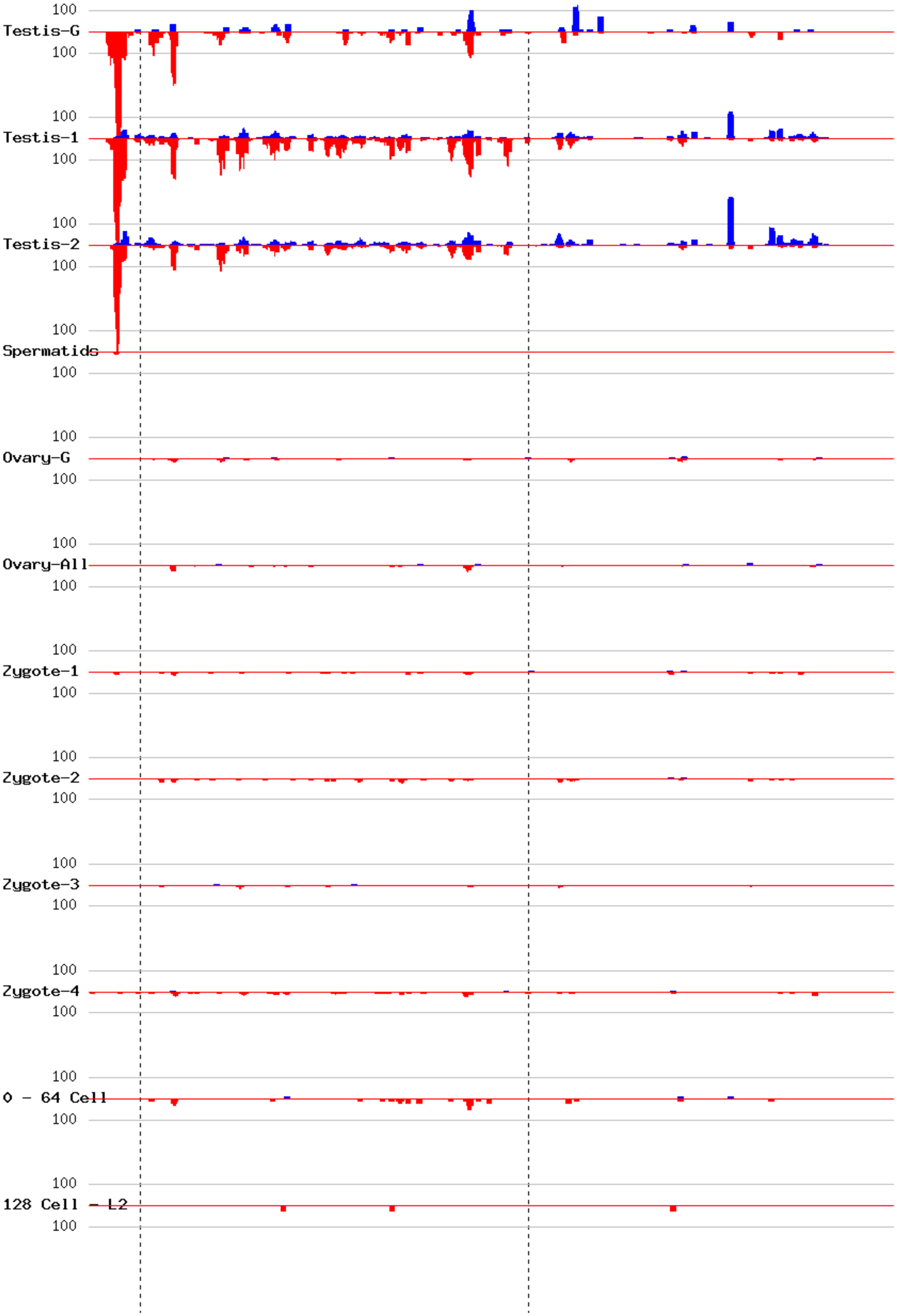
ASCF_7825_1030 Histone_H4 1030 bp



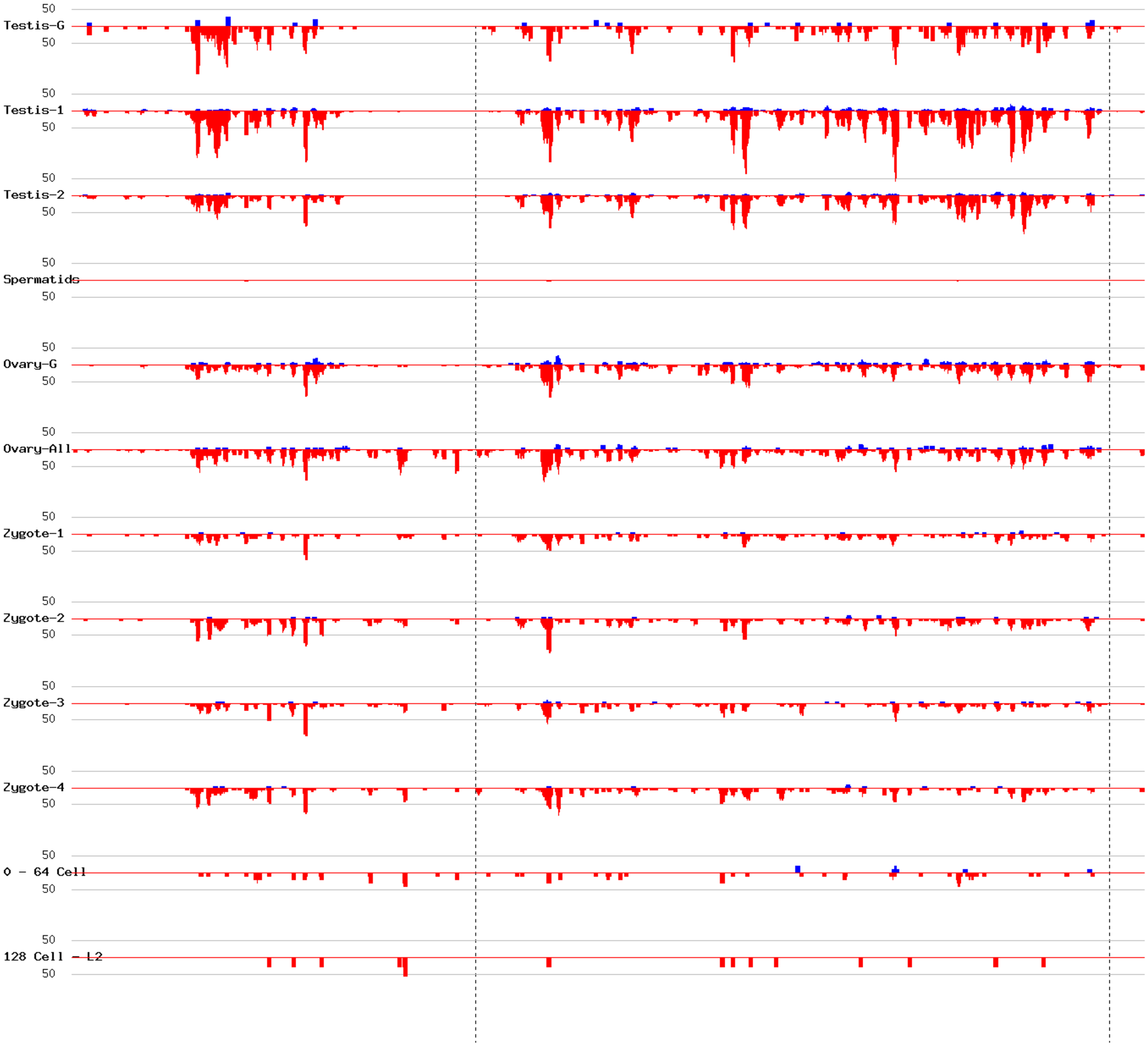
ASCF_847_3979 Nuclear_RNAi_Defective_3_Argonaute 3979 bp

ASCF_980_3775 Hypothetical_protein 3775 bp

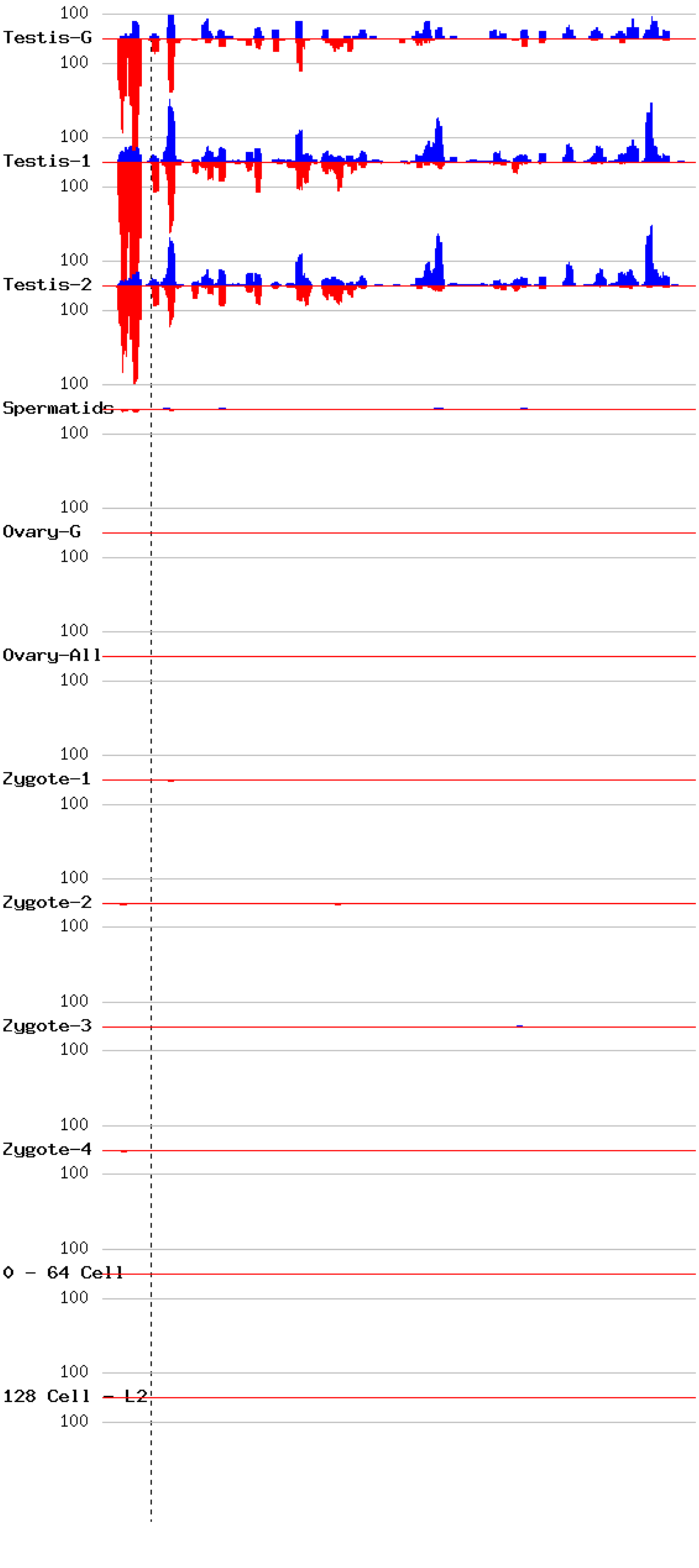
ASCF_982_3773 Tu_GTP_binding_domain_containing_protein 3773 bp



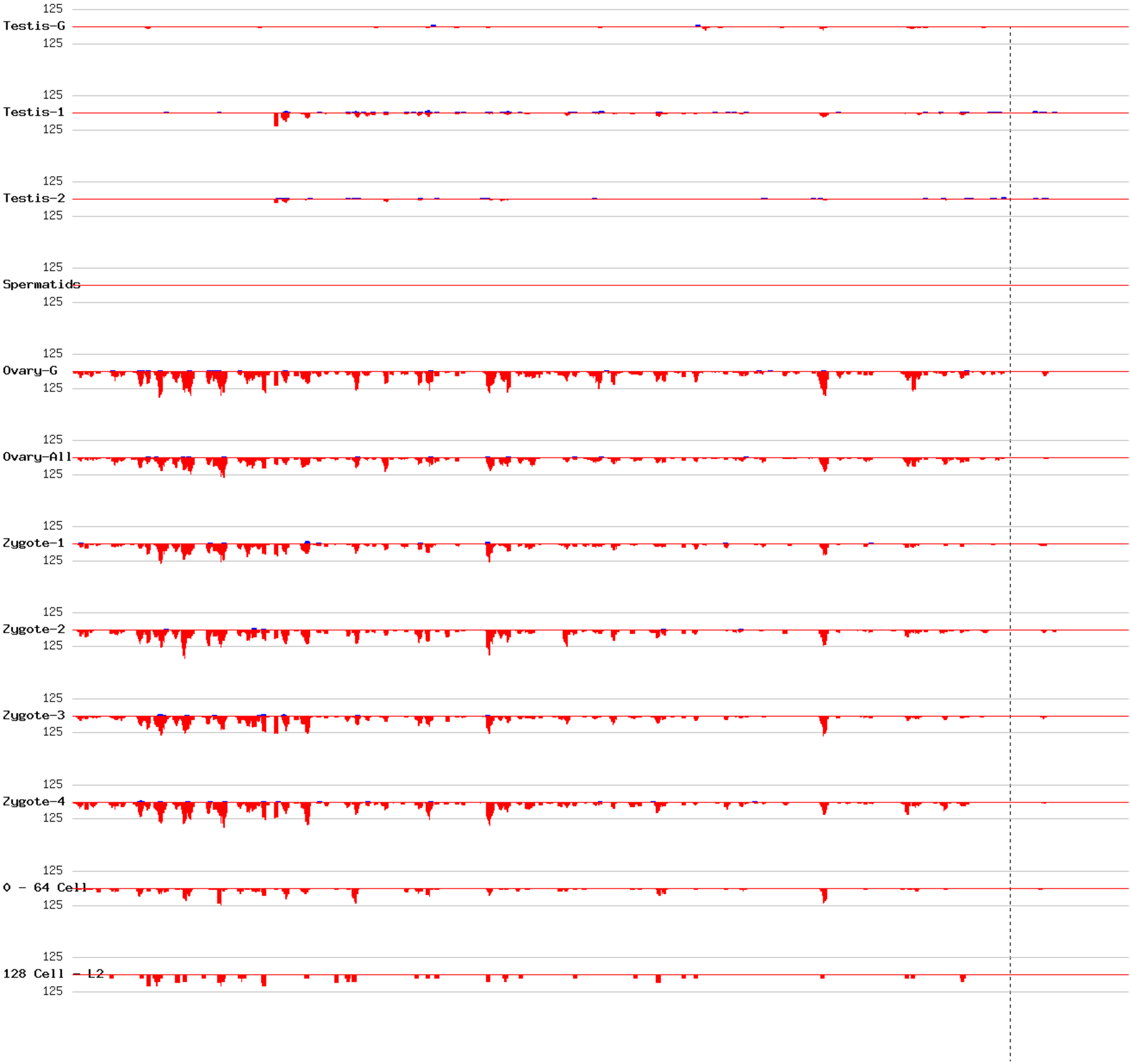
ASCP_105_6337 PAP/25A_associated_domain_containing_protein 6337 bp



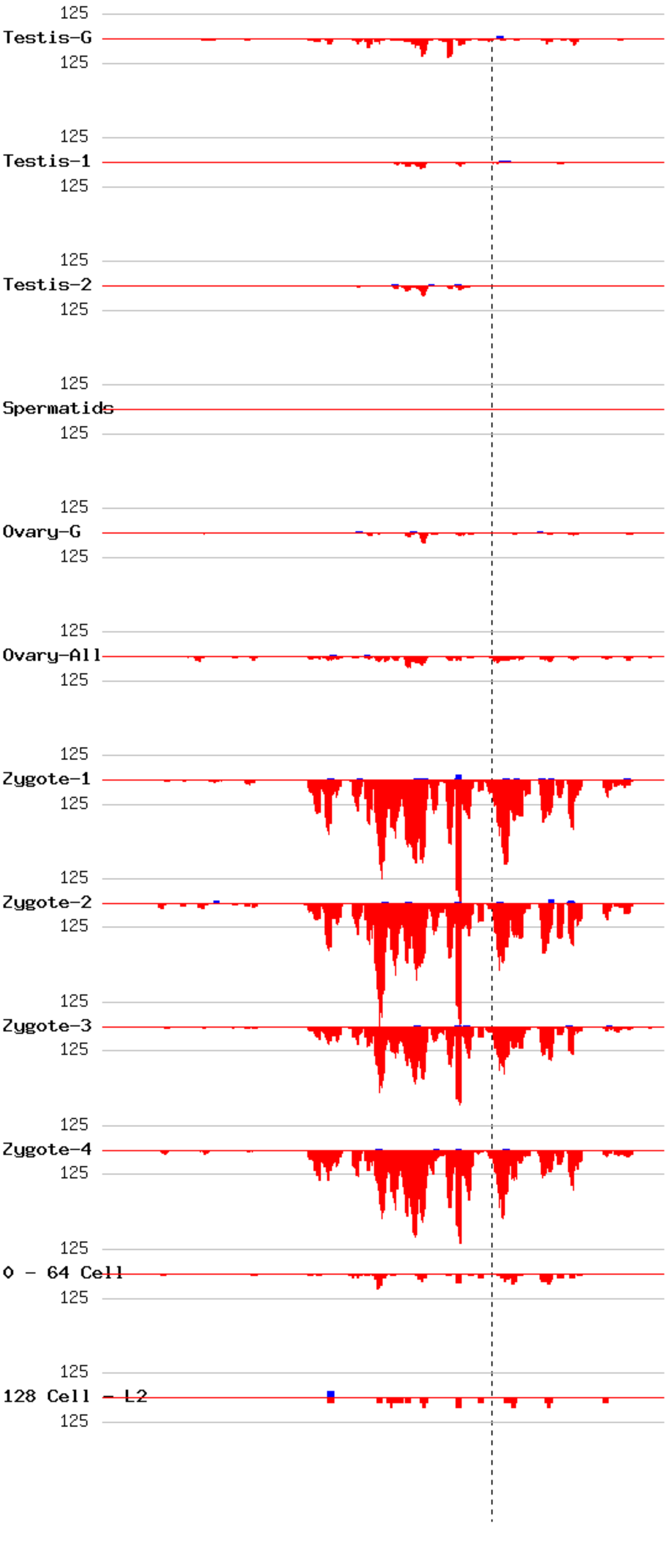
ASCP_1088_2398 Hypothetical_protein 2398 bp



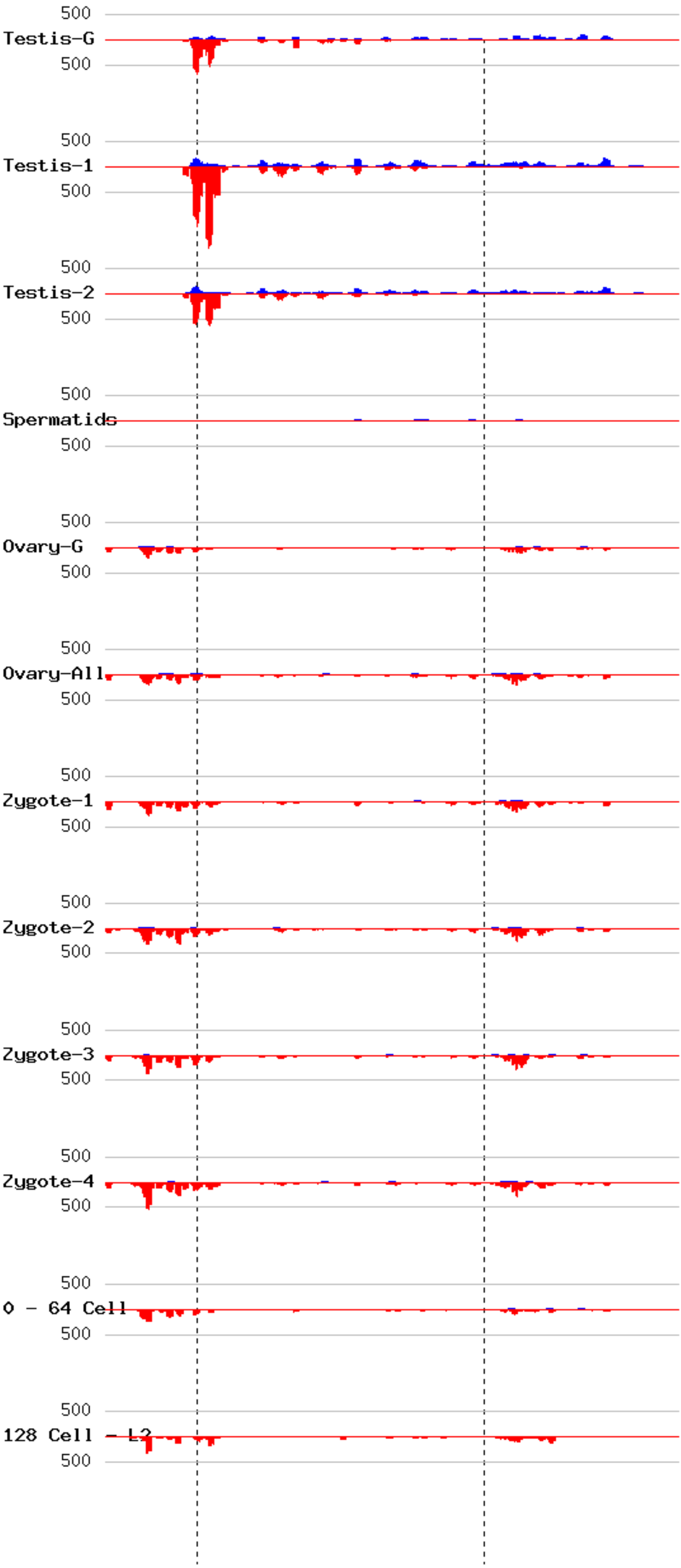
ASCP_118_6128 Protein_kinase_domain_containing_protein 6128 bp



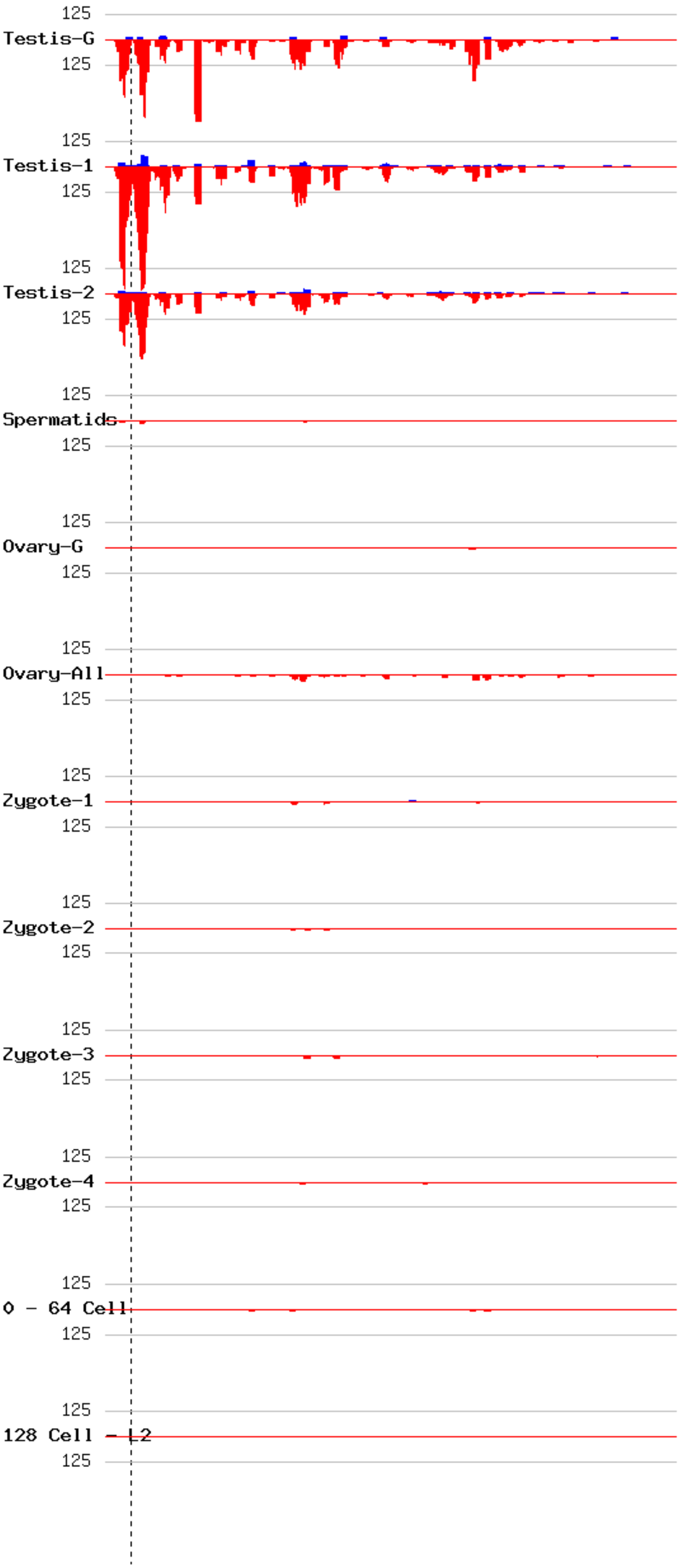
ASCP_1222_2273 Transcription_factor_Mef2c_protein 2273 bp



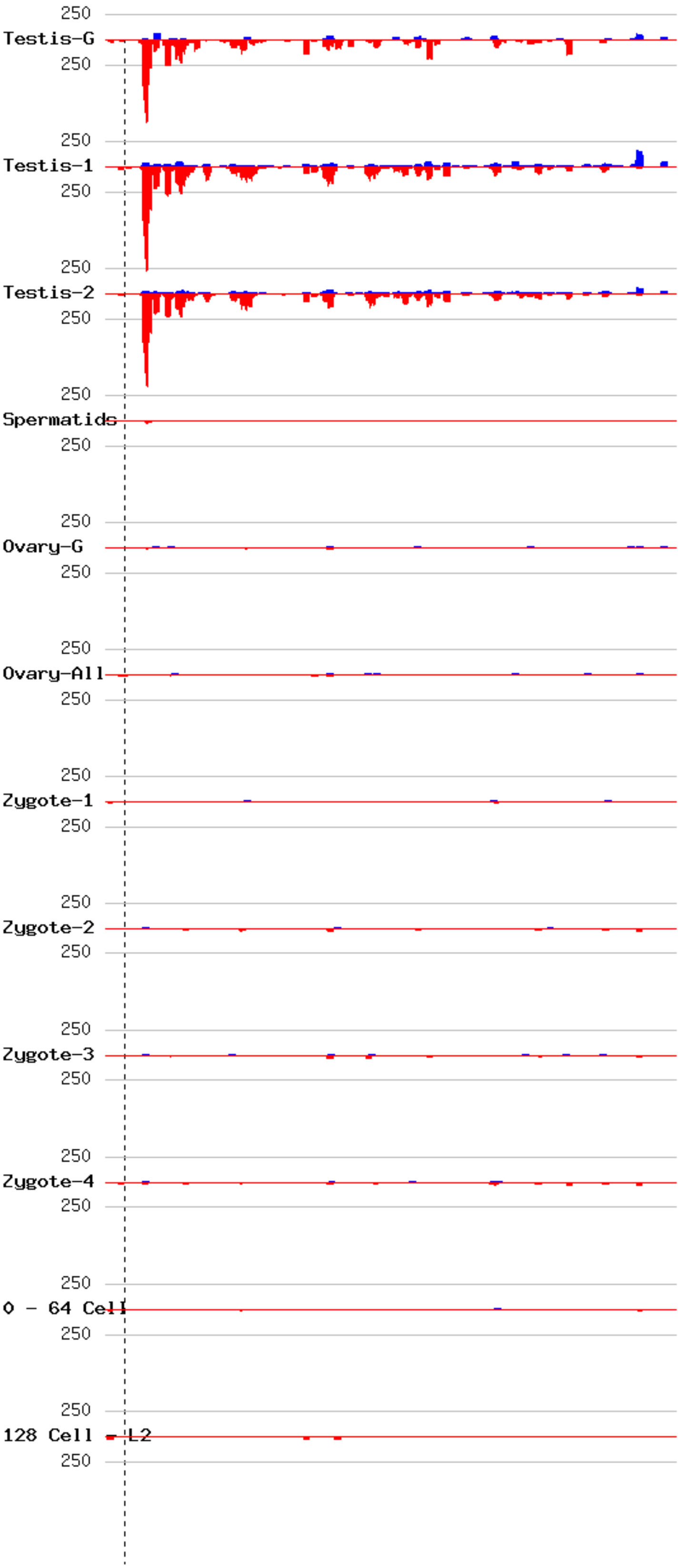
ASCP_1237_2256 Hypothetical_protein 2256 bp



ASCP_1244_2247 Hypothetical_protein 2247 bp

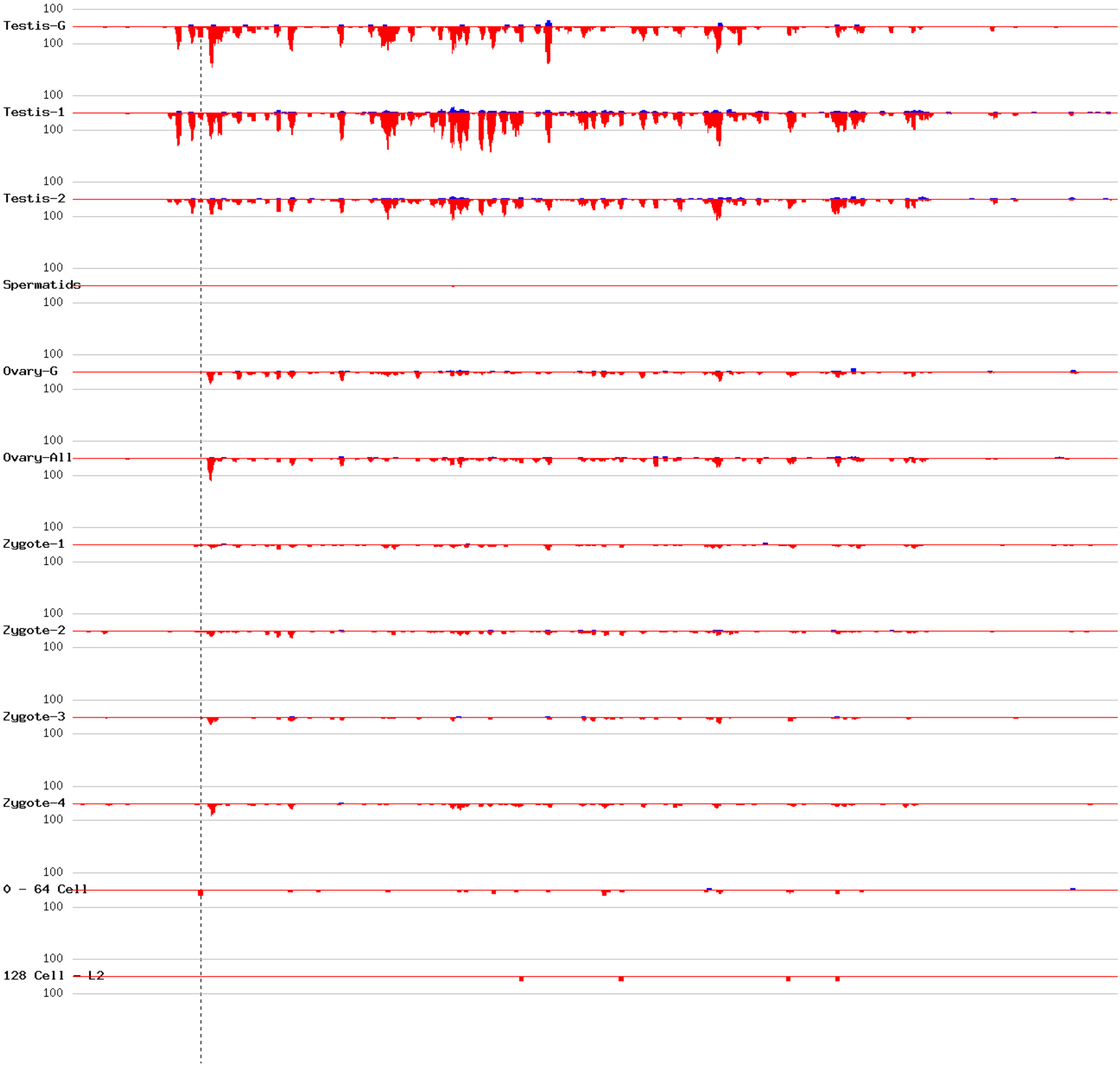


ASCP_1245_2247 Cytoplasmic_polyadenylation_element_binding_prot

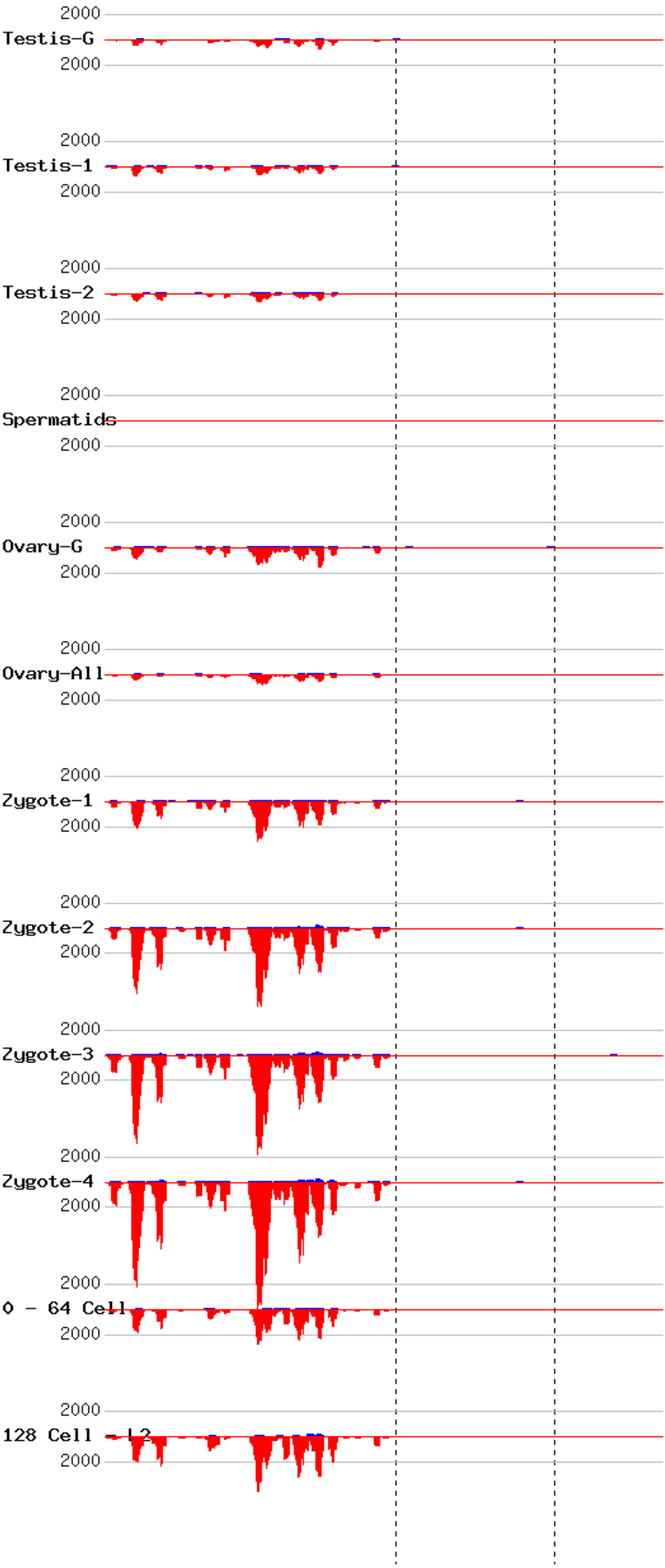


ASCP_126_6046 KH_domain_containing_protein 6046 bp

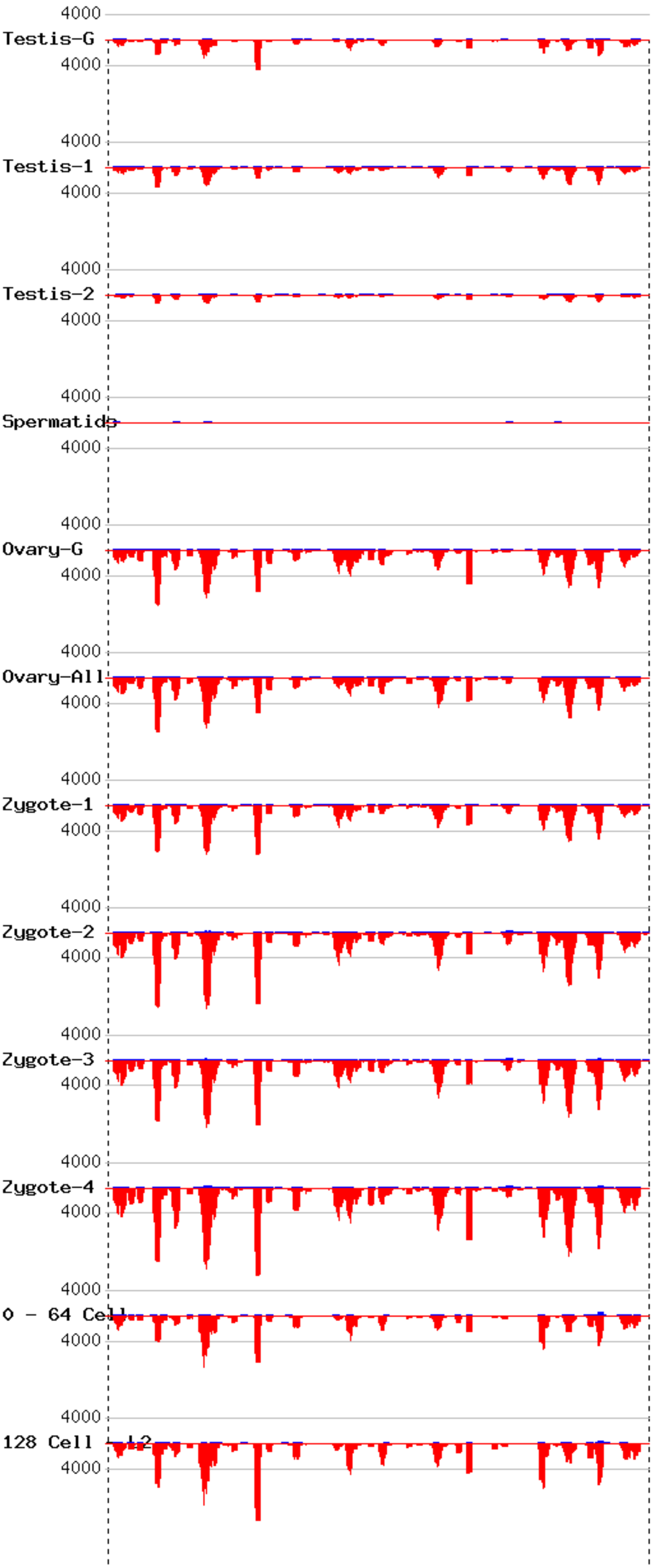
Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2

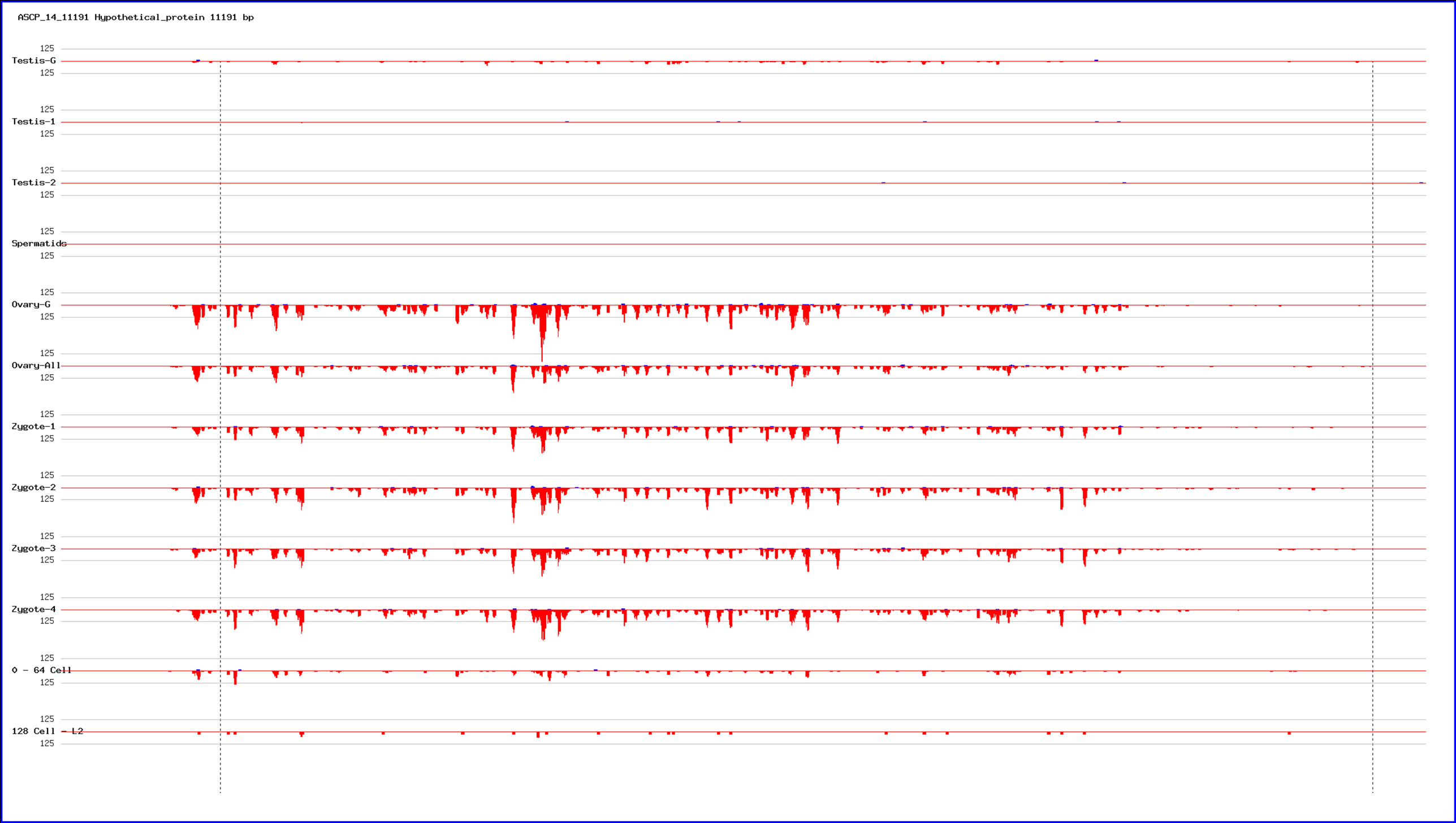


ASCP_1293_2196 MRPL-41_protein 2196 bp

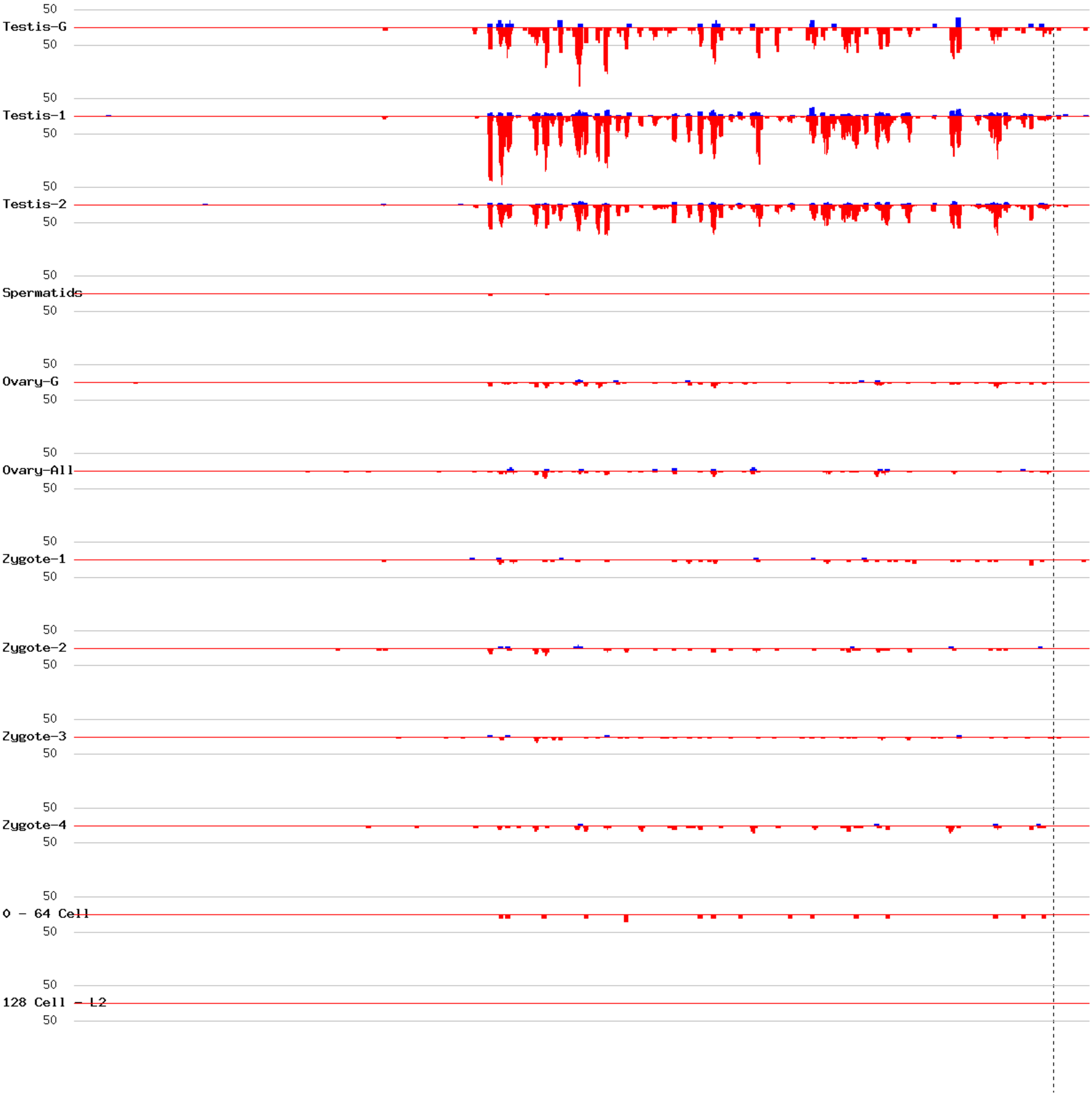


ASCP_1361_2132 Hypothetical_protein 2132 bp

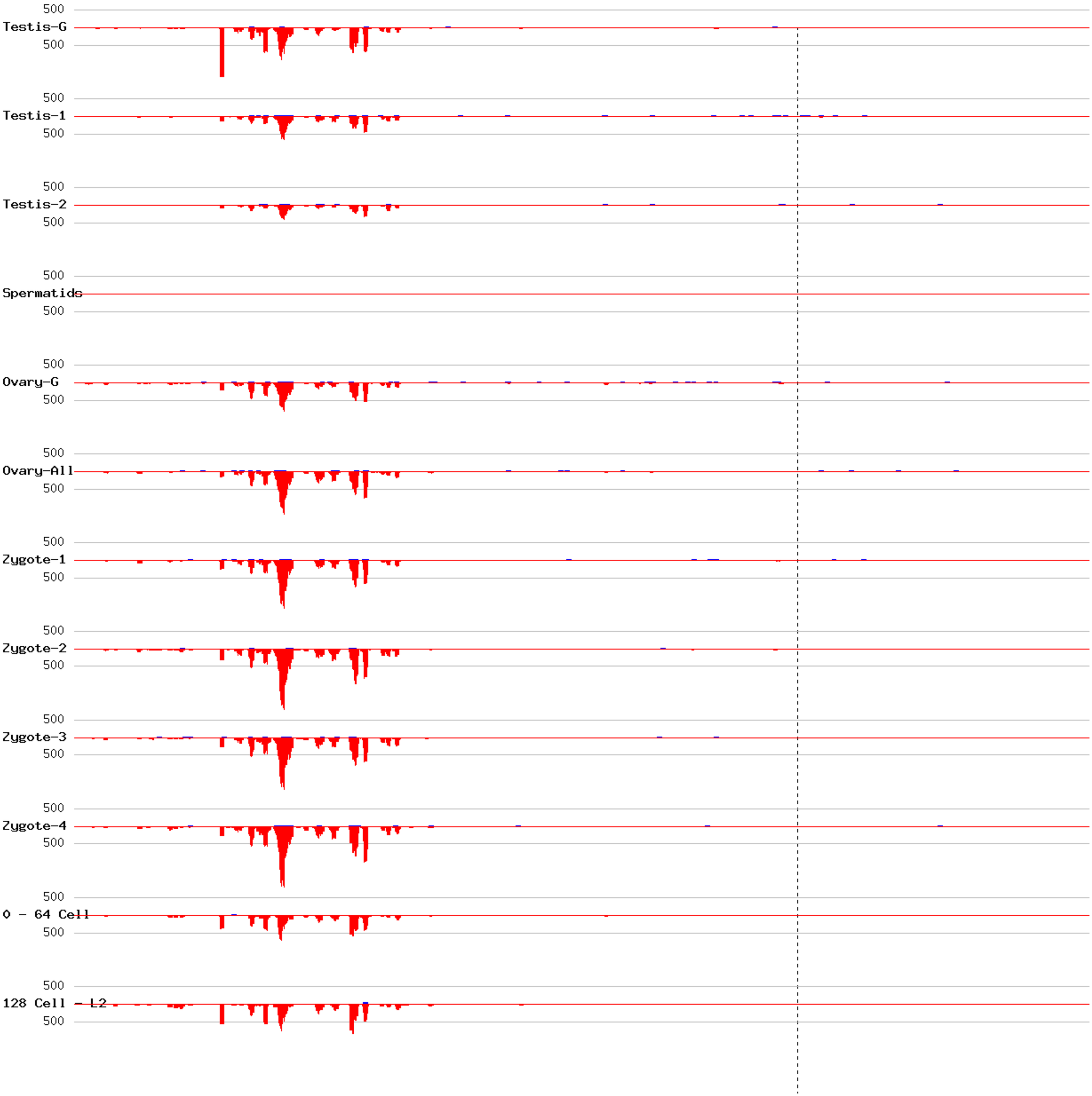



ASCP_14_11191 Hypothetical_protein 11191 bp
125
Testis-G
125
125
Testis-1
125
125
Testis-2
125
125
Spermatids
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Ovary-G
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125
Ovary-All
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125
Zygote-1
125
125
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Zygote-4
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0 - 64 Cell
125
125
128 Cell - L2
125

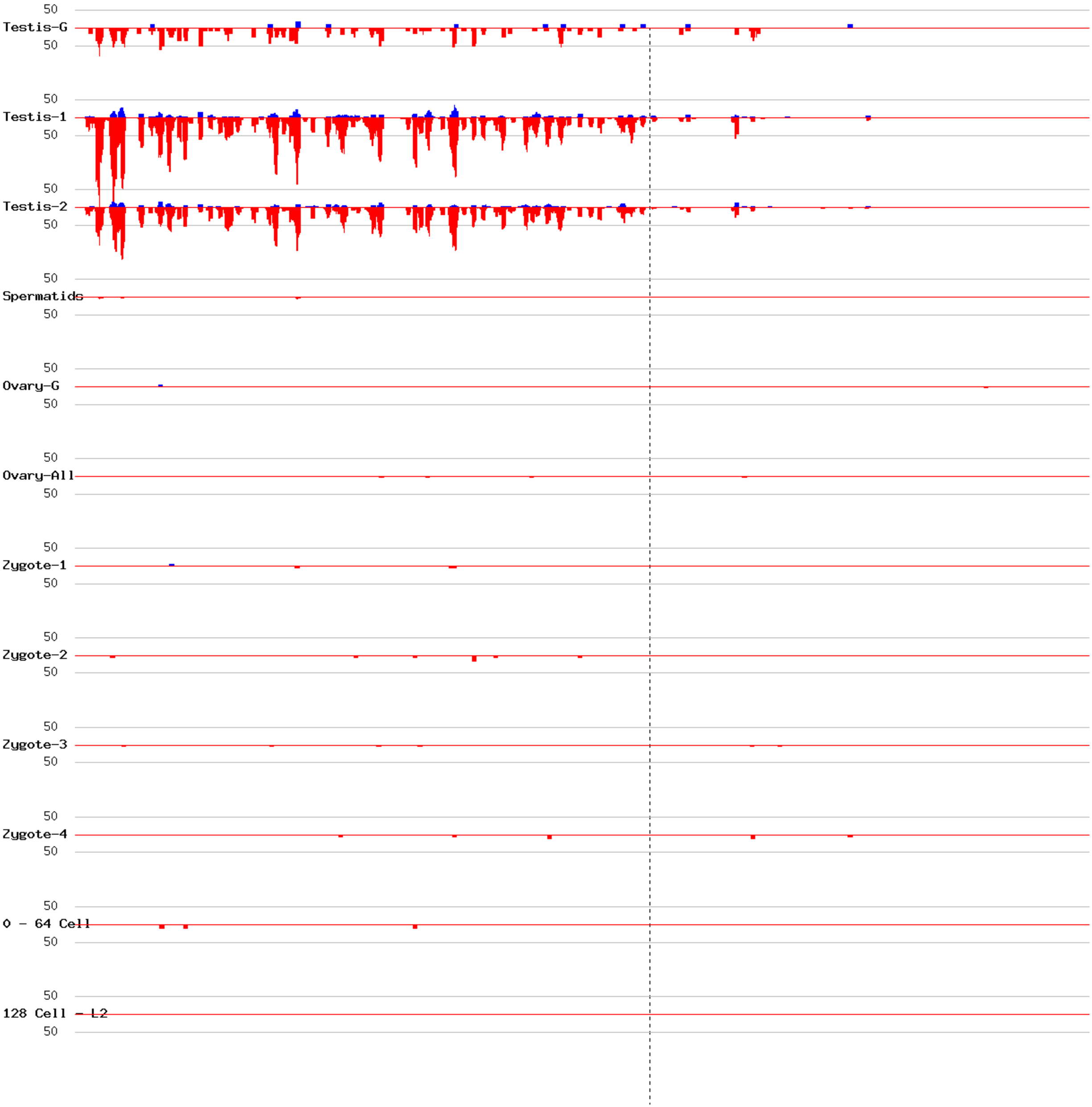
ASCP_145_5722 Membrane-associated_protein_gex-3 5722 bp



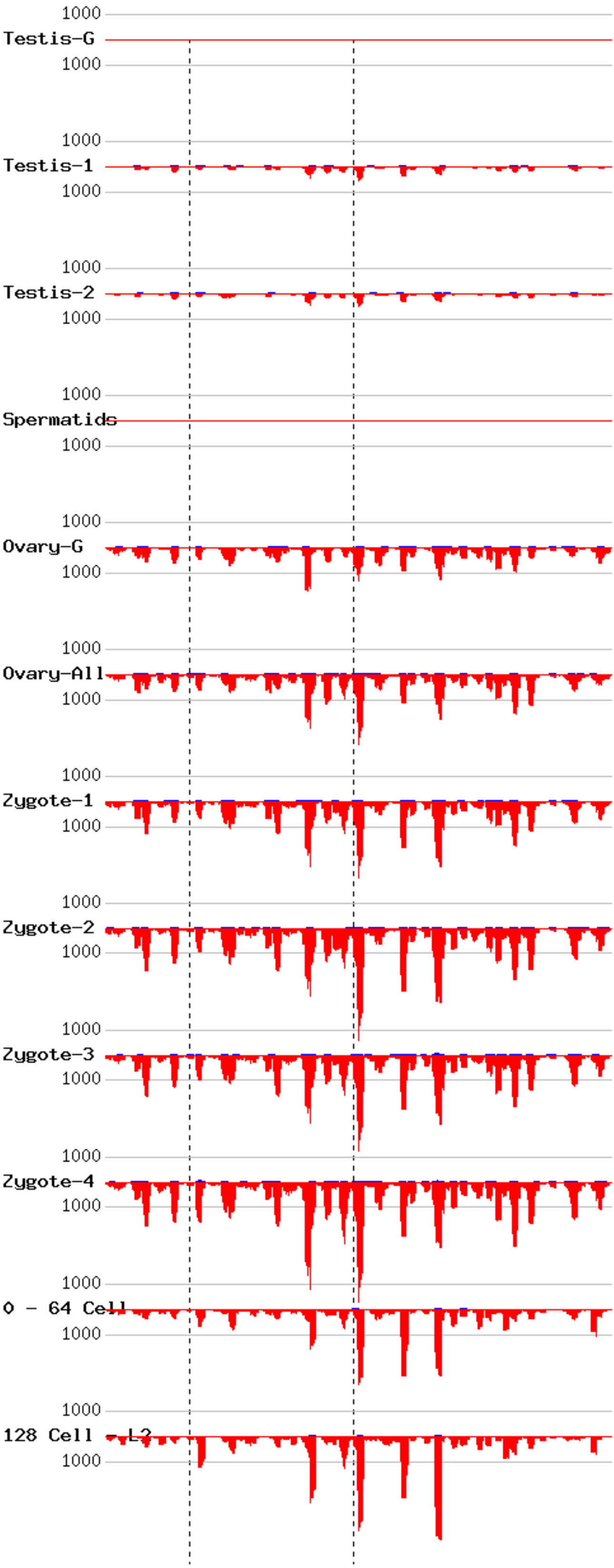
ASCP_147_5711 Hypothetical_protein 5711 bp



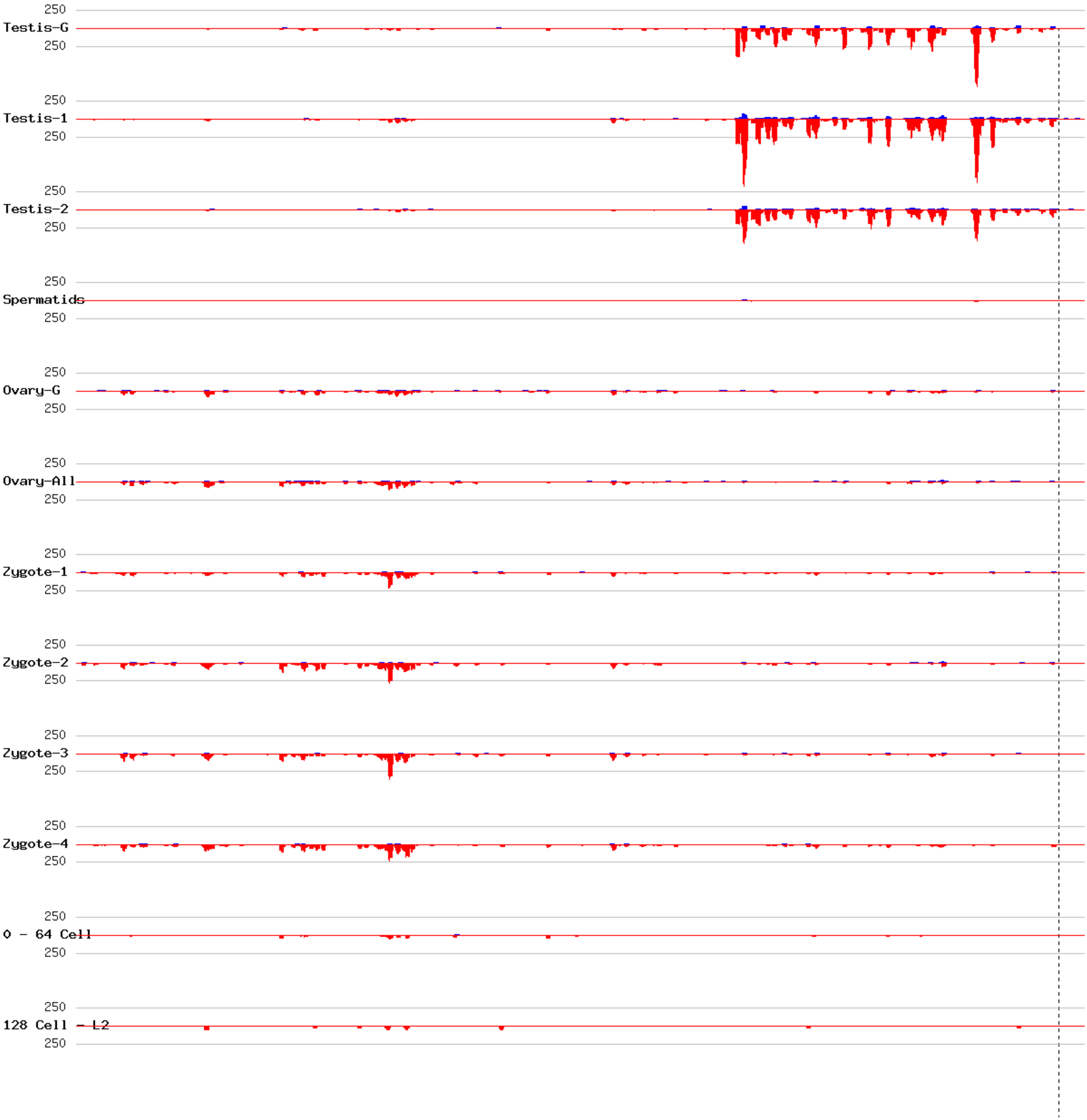
ASCP_152_5655 2-oxoglutarate_dehydrogenase_E1_component 5655 bp



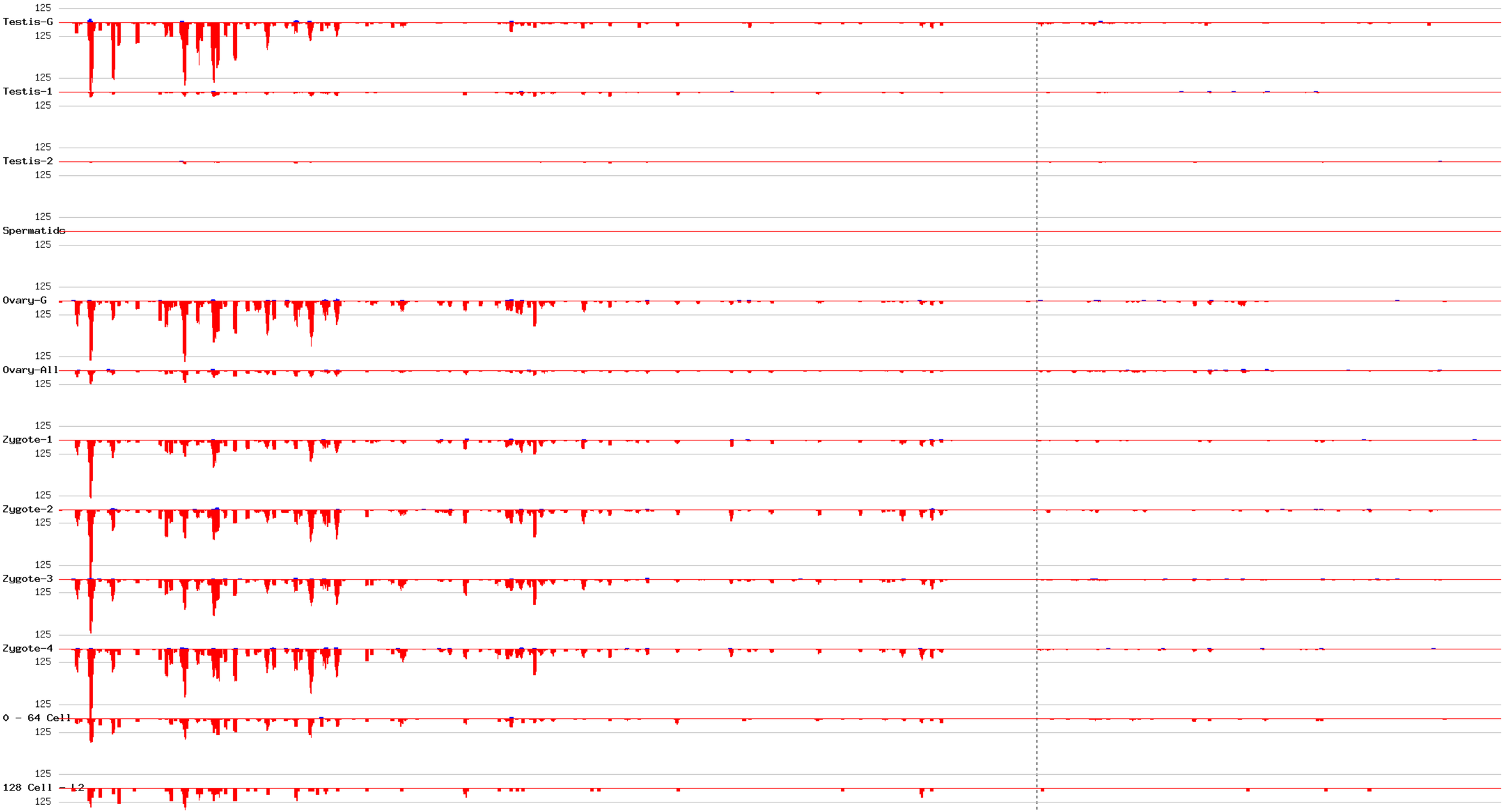
ASCP_1524_1992 Kinesin_K39 1992 bp



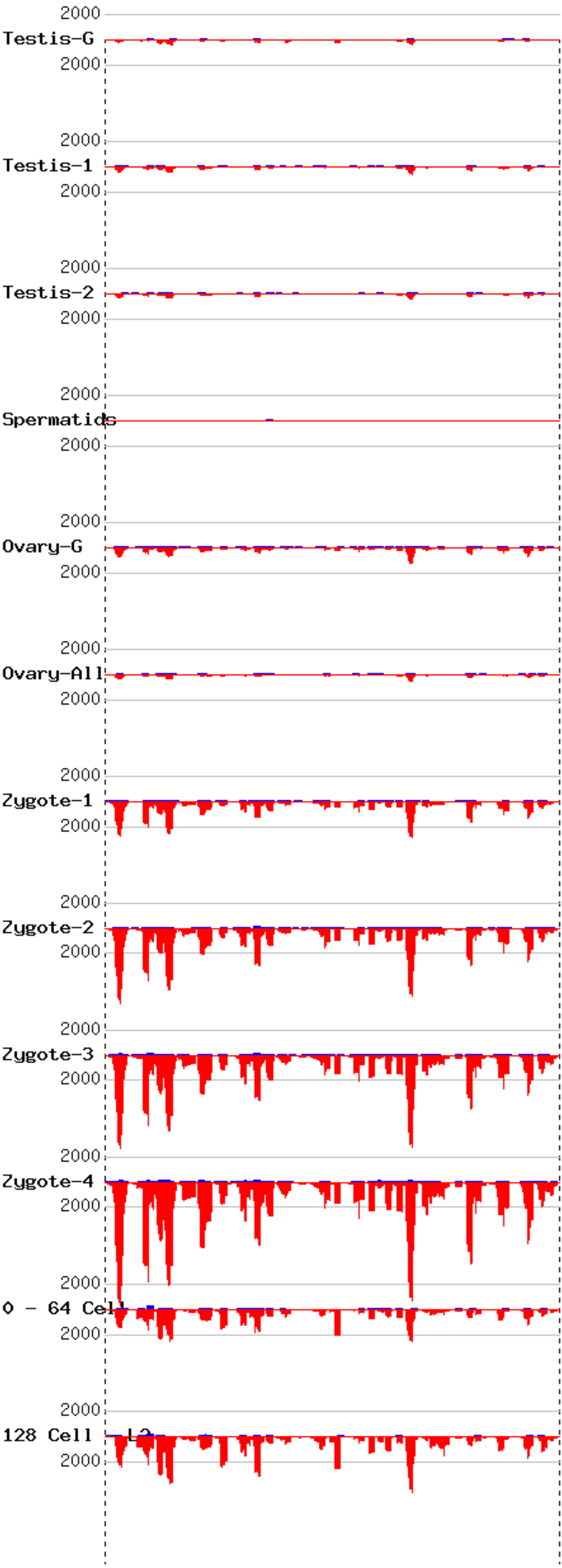
ASCP_158_5555 Hypothetical_protein 5555 bp



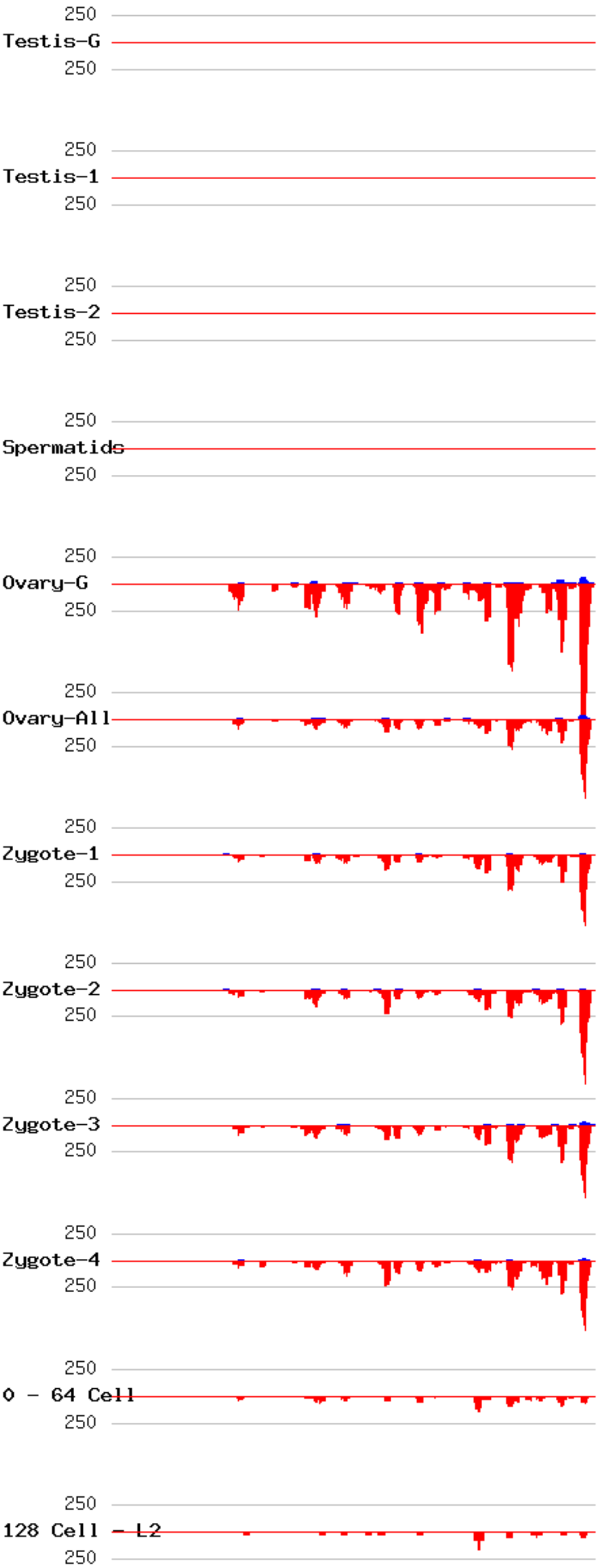
ASCP_17_10353 Hypothetical_protein 10353 bp



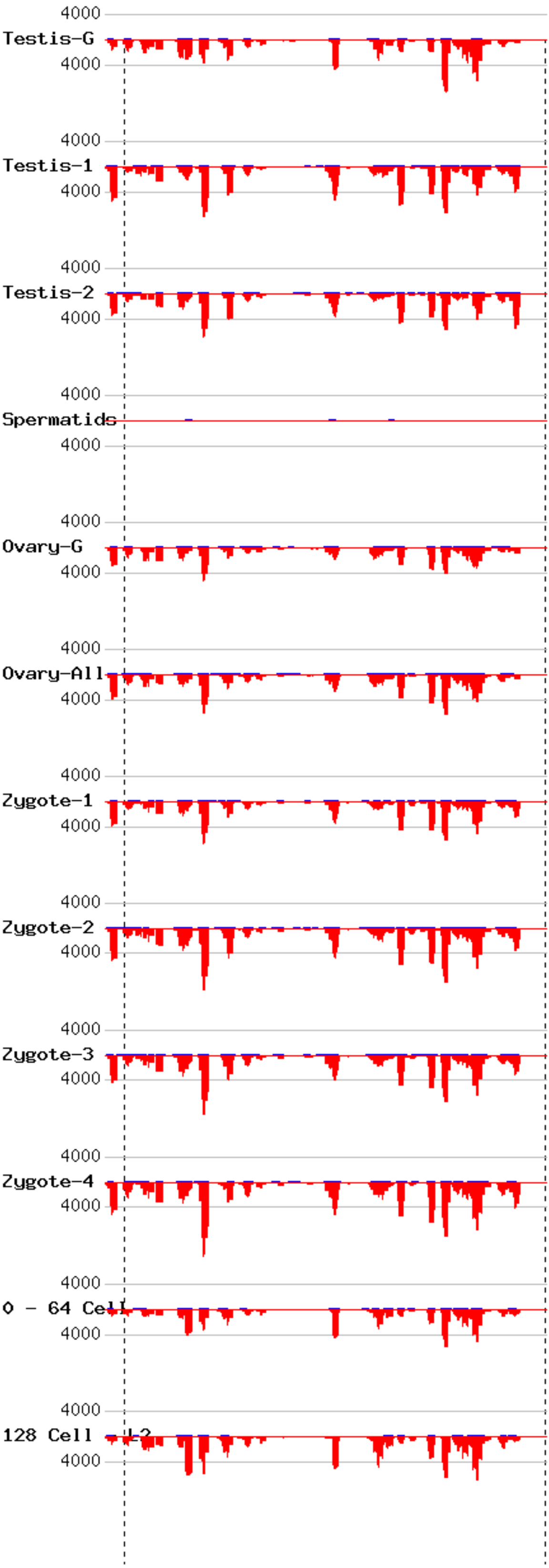
ASCP_1786_1792 Hypothetical_protein 1792 bp



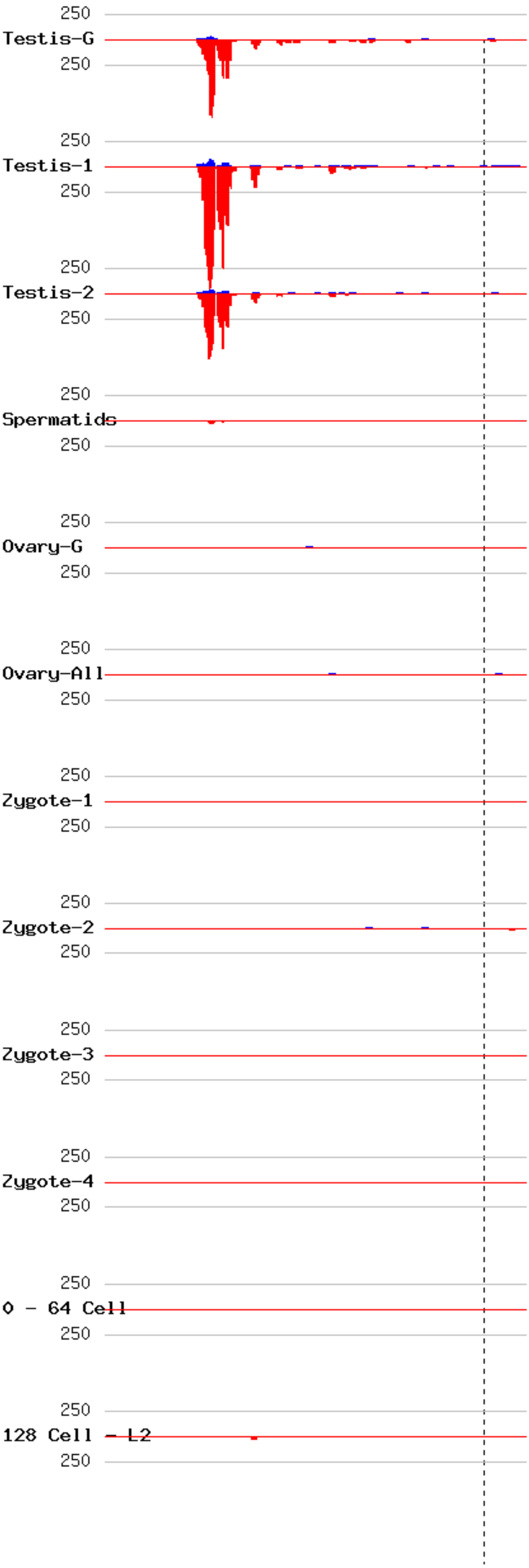
ASCP_1800_1782 Glutamate_dehydrogenase 1782 bp



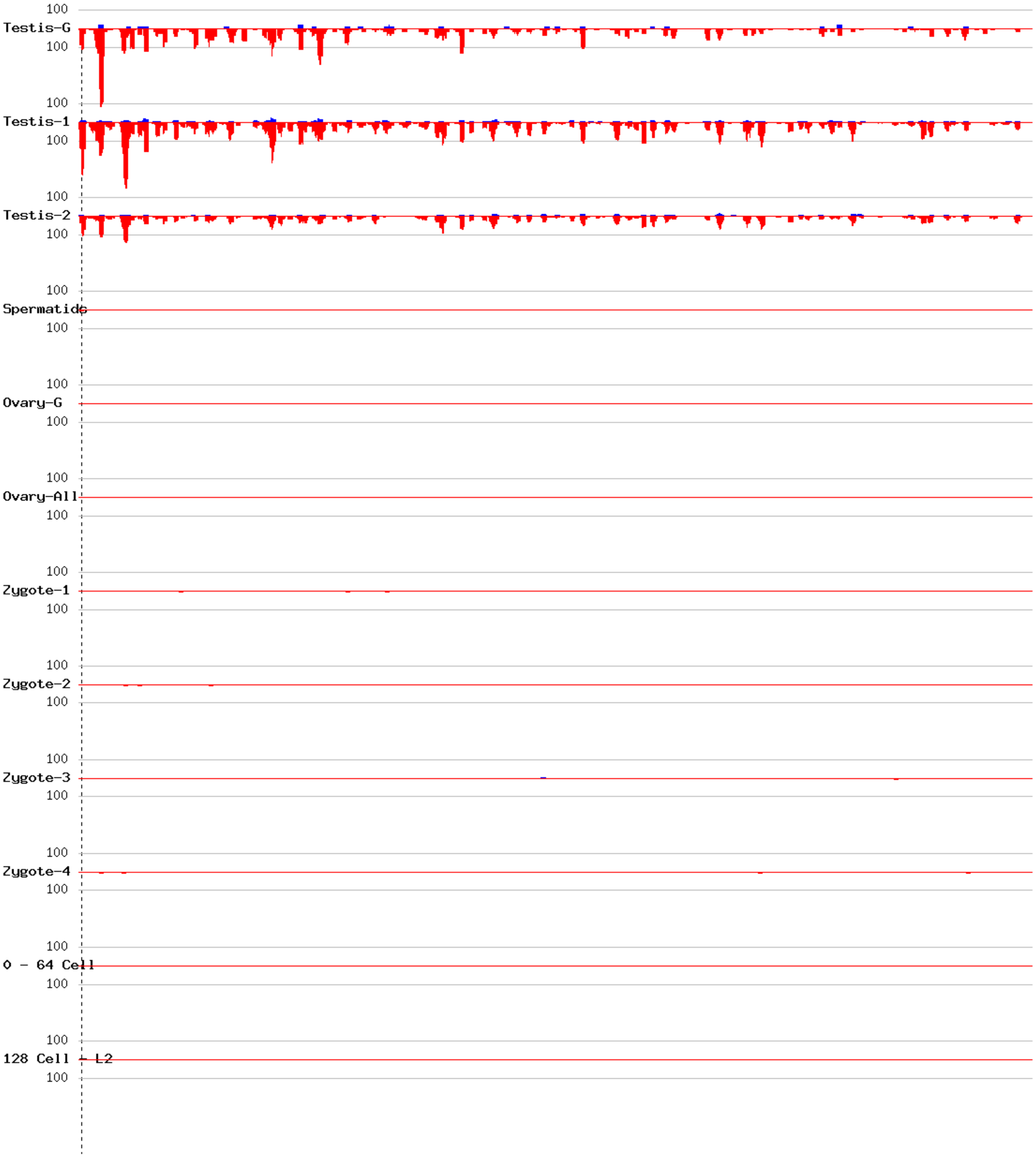
ASCP_1871_1738 Hypothetical_protein 1738 bp



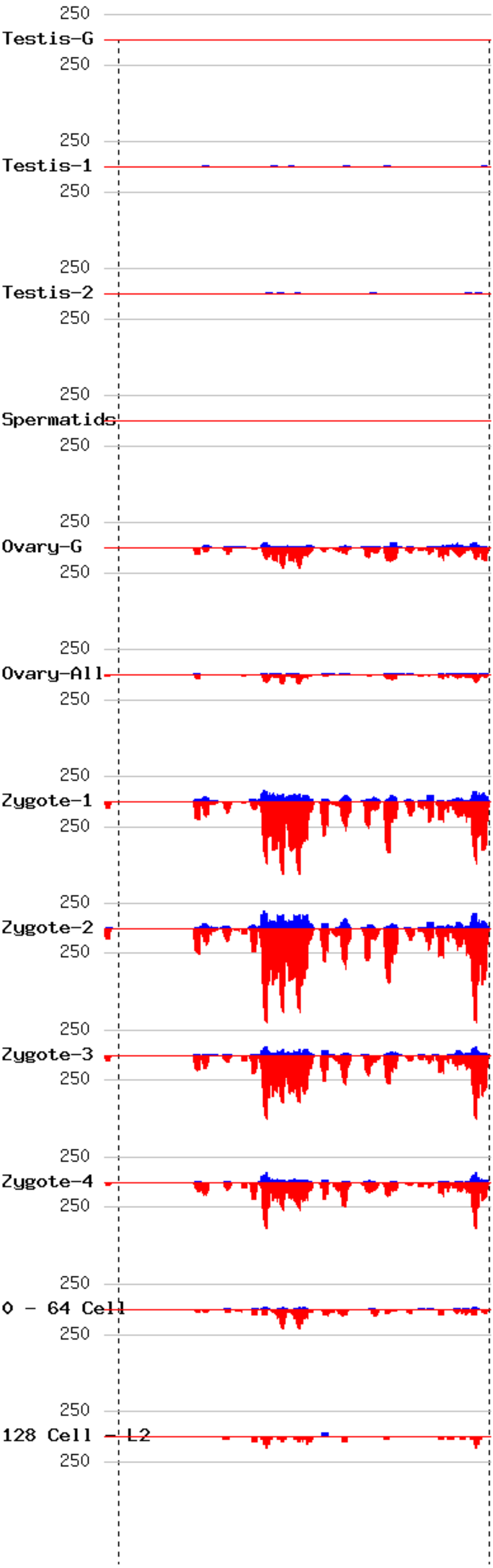
ASCP_1994_1659 Homeobox_domain_containing_protein



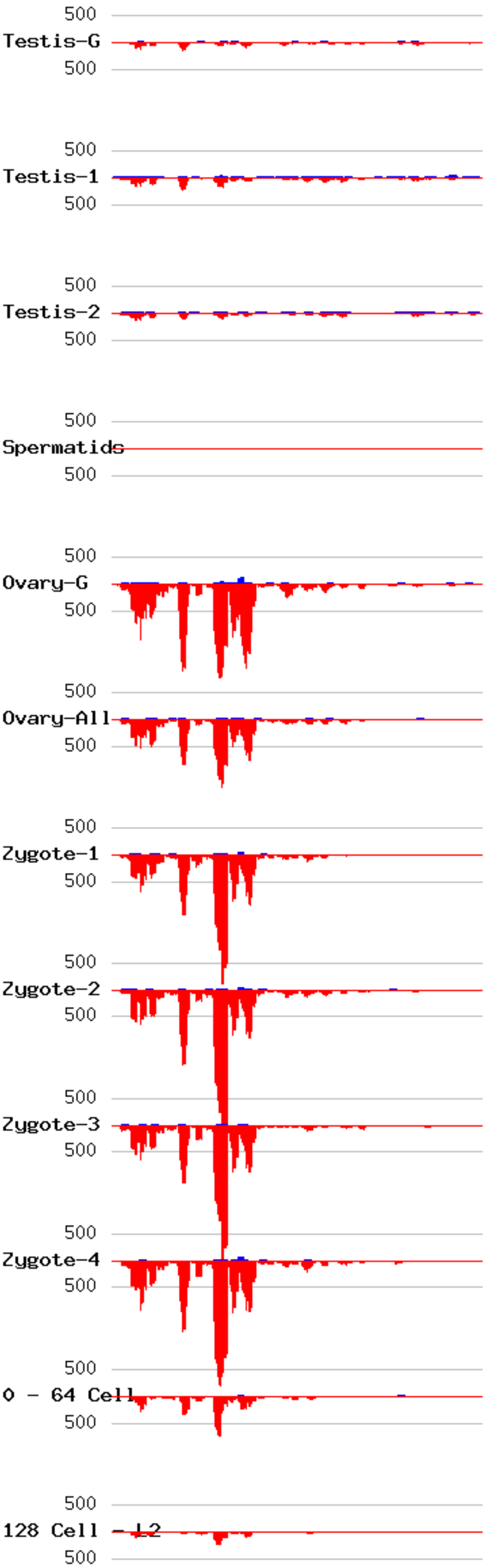
ASCP_205_5089 Hypothetical_protein 5089 bp



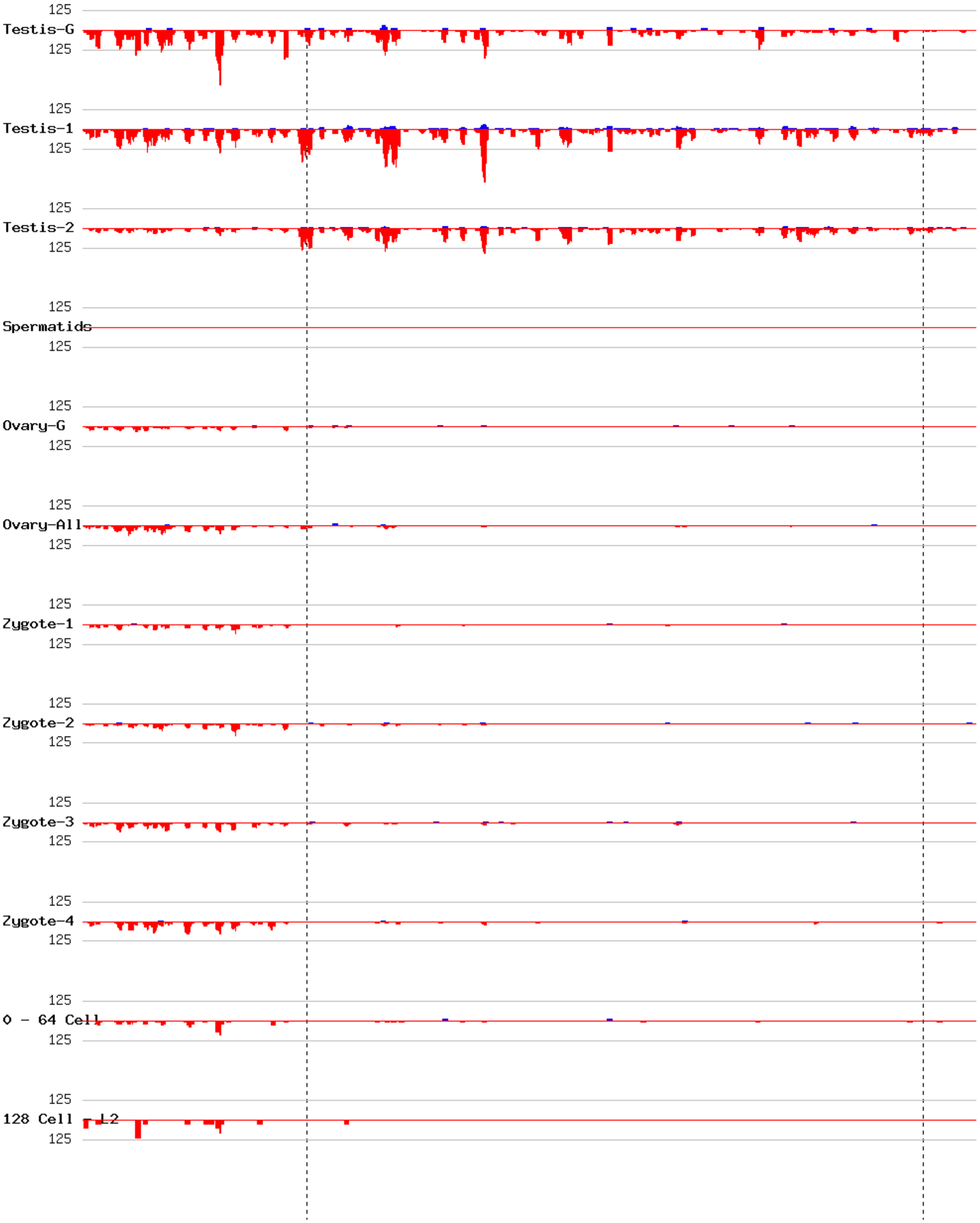
ASCP_2254_1520 Chitin_binding_protein 1520 bp



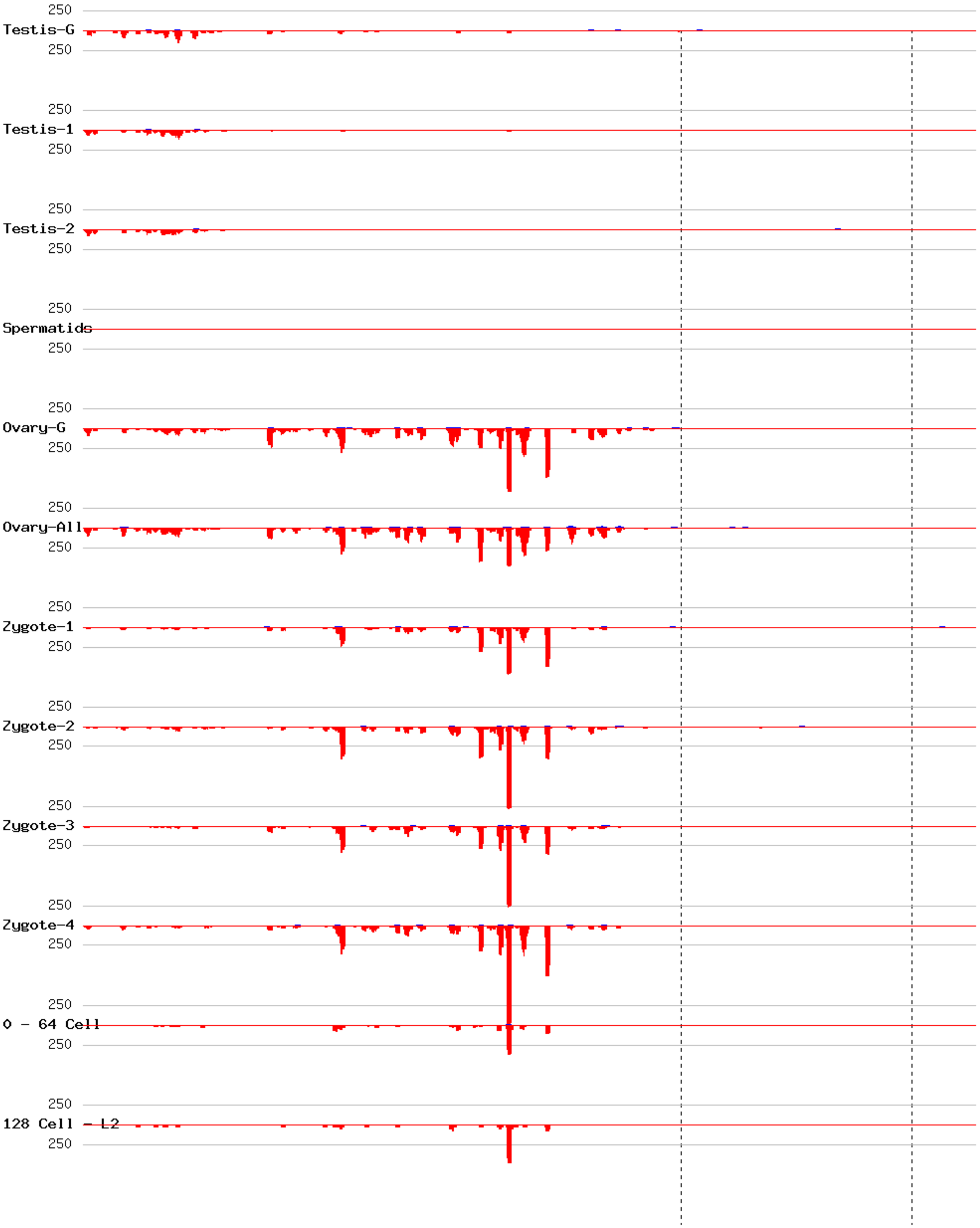
ASCP_2585_1365 Hypothetical_protein 1365 bp



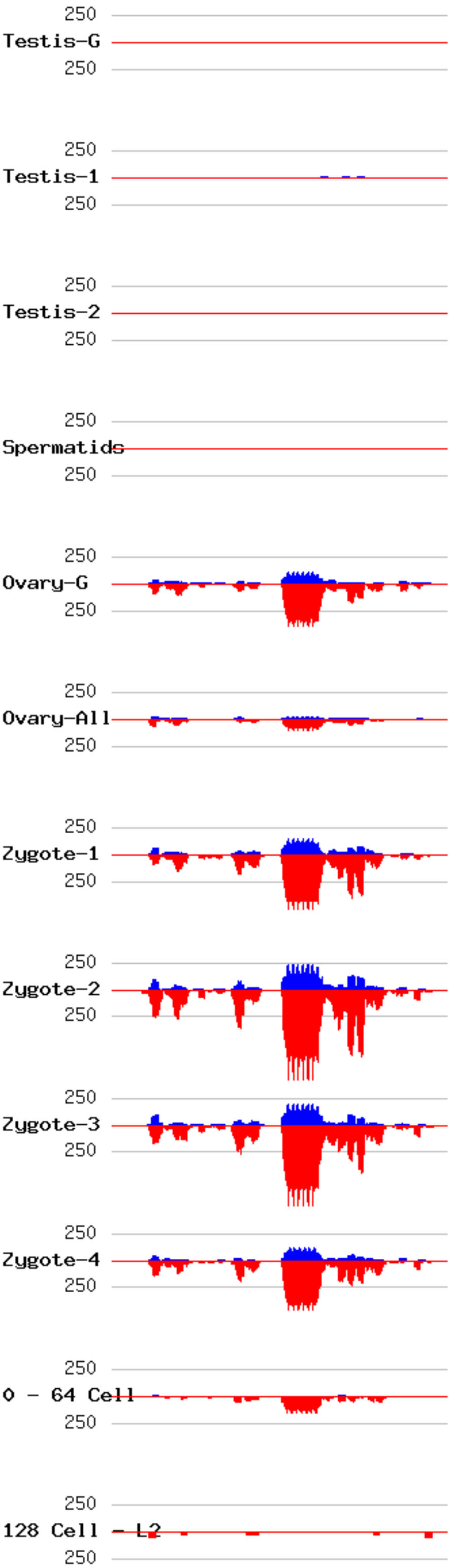
ASCP_280_4507 Ankyrin_repeat_domain_protein 4507 bp



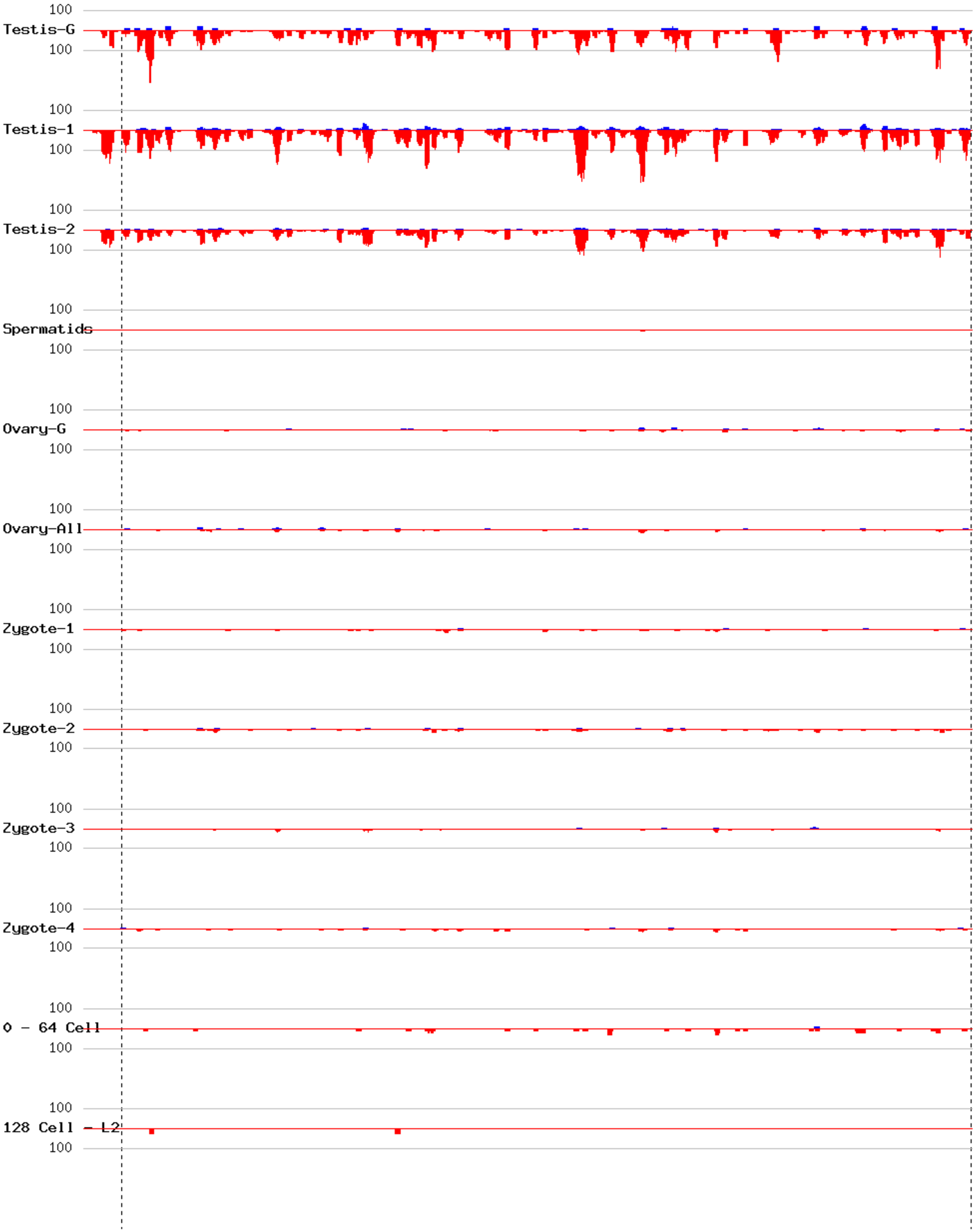
ASCP_287_4489 Pseudouridylate_synthase 4489 bp



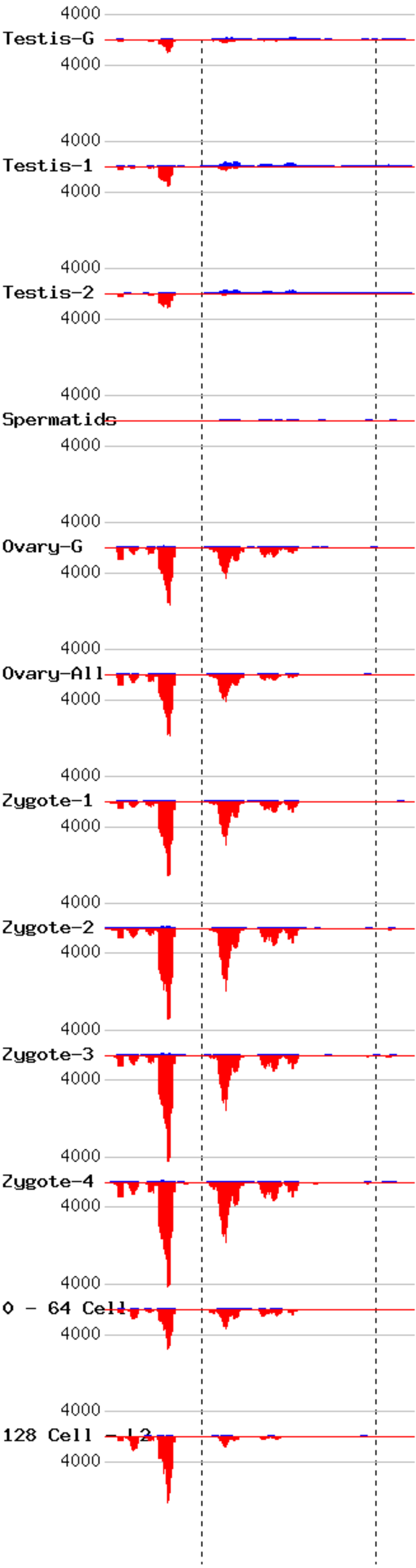
ASCP_2945_1239 Chitin_binding_protein 123



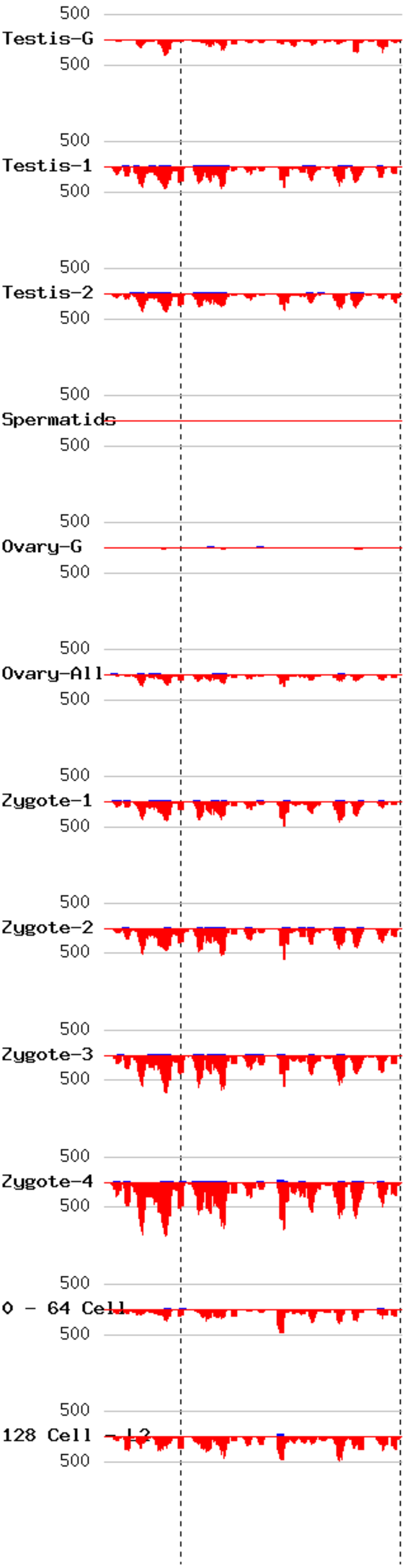
ASCP_295_4450 La_domain_containing_protein 4450 bp



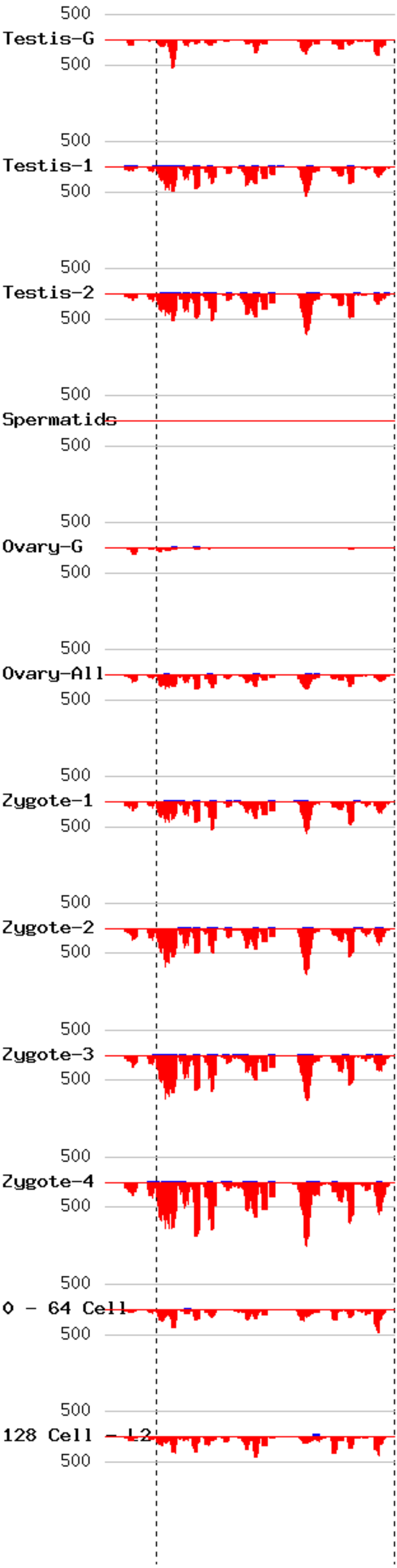
ASCP_3020_1215 Hypothetical_protein 1215



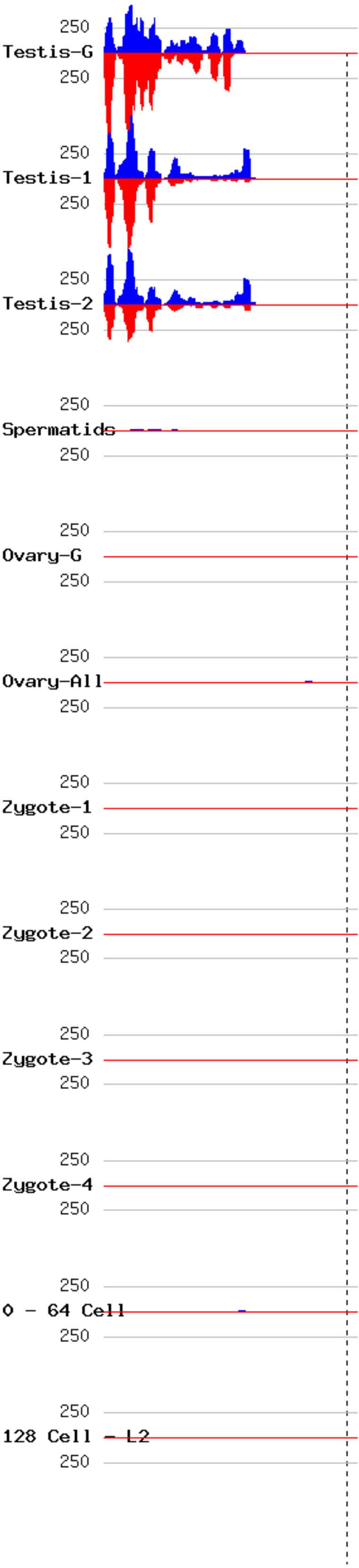
ASCP_3173_1172 Integrase_core_domain_co



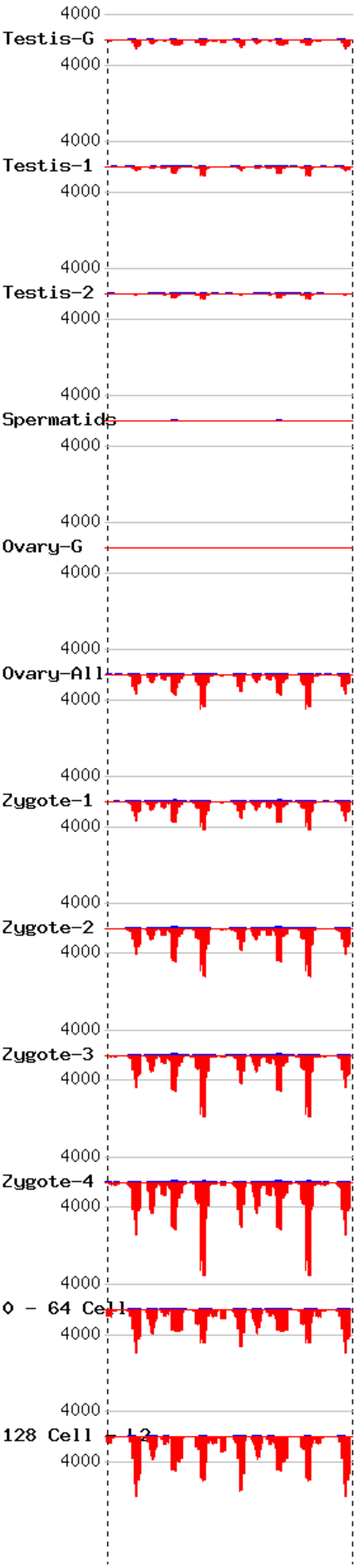
ASCP_3294_1138 Hypothetical_protein 11



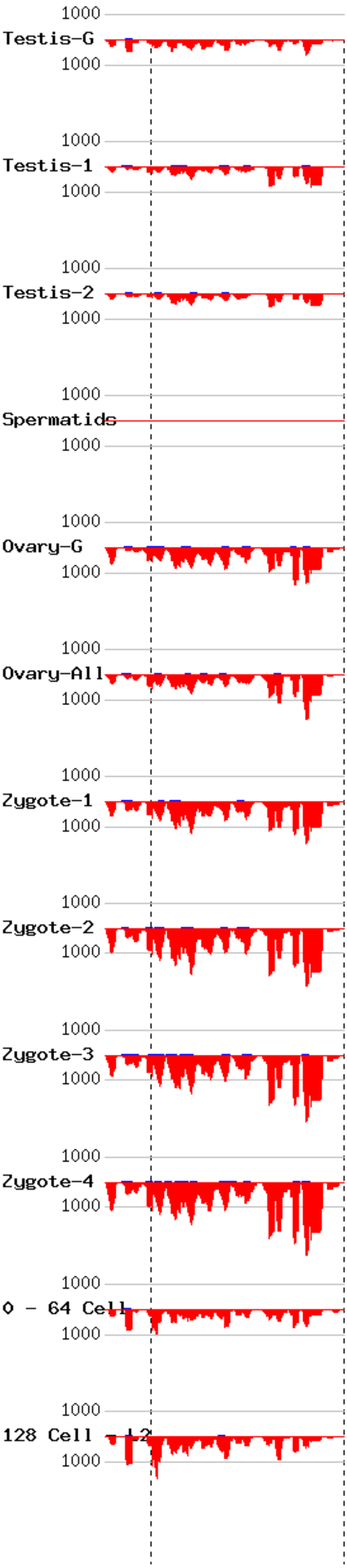
ASCP_3810_1009 Hypothetical_protein



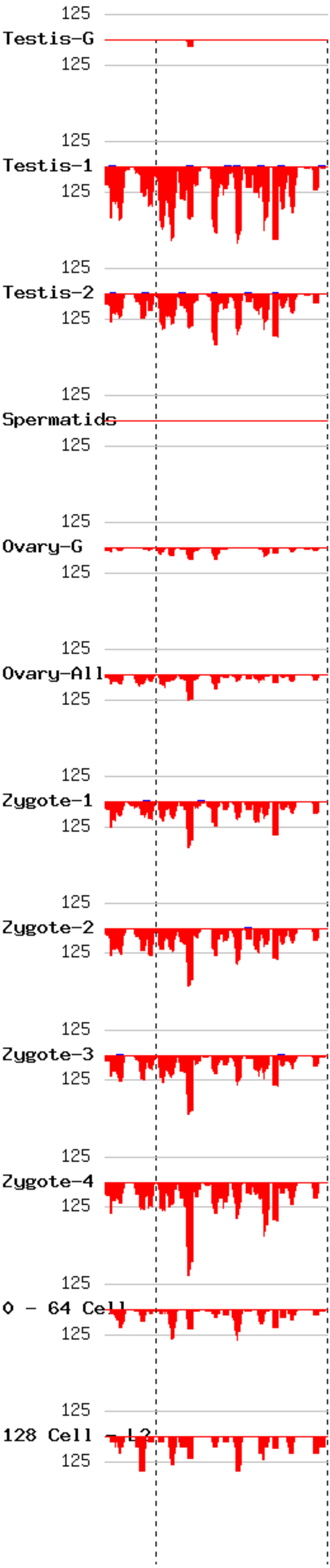
ASCP_3954_979 I-connectin 979 bp



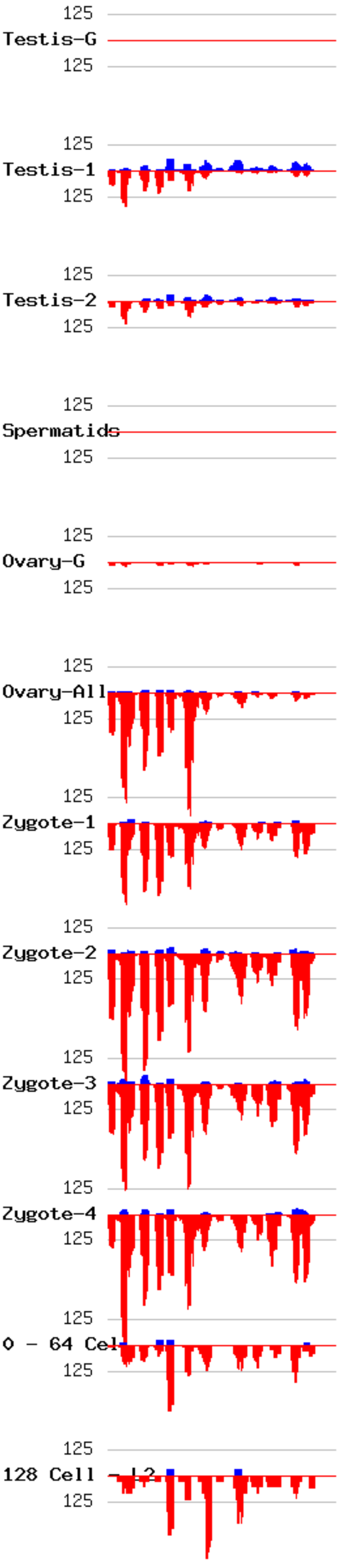
ASCP_4127_943 Hypothetical_protein



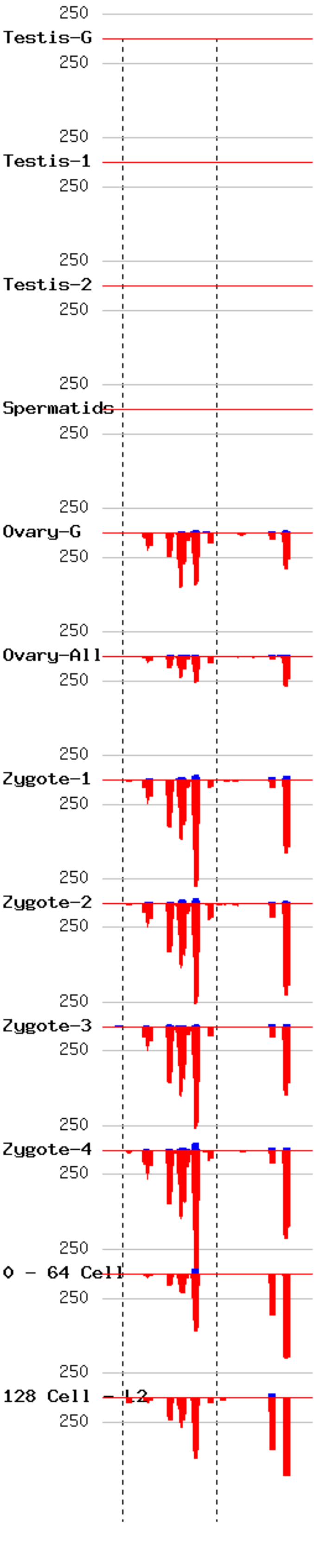
ASCP_4460_876 Gag-Pol_polyprotein



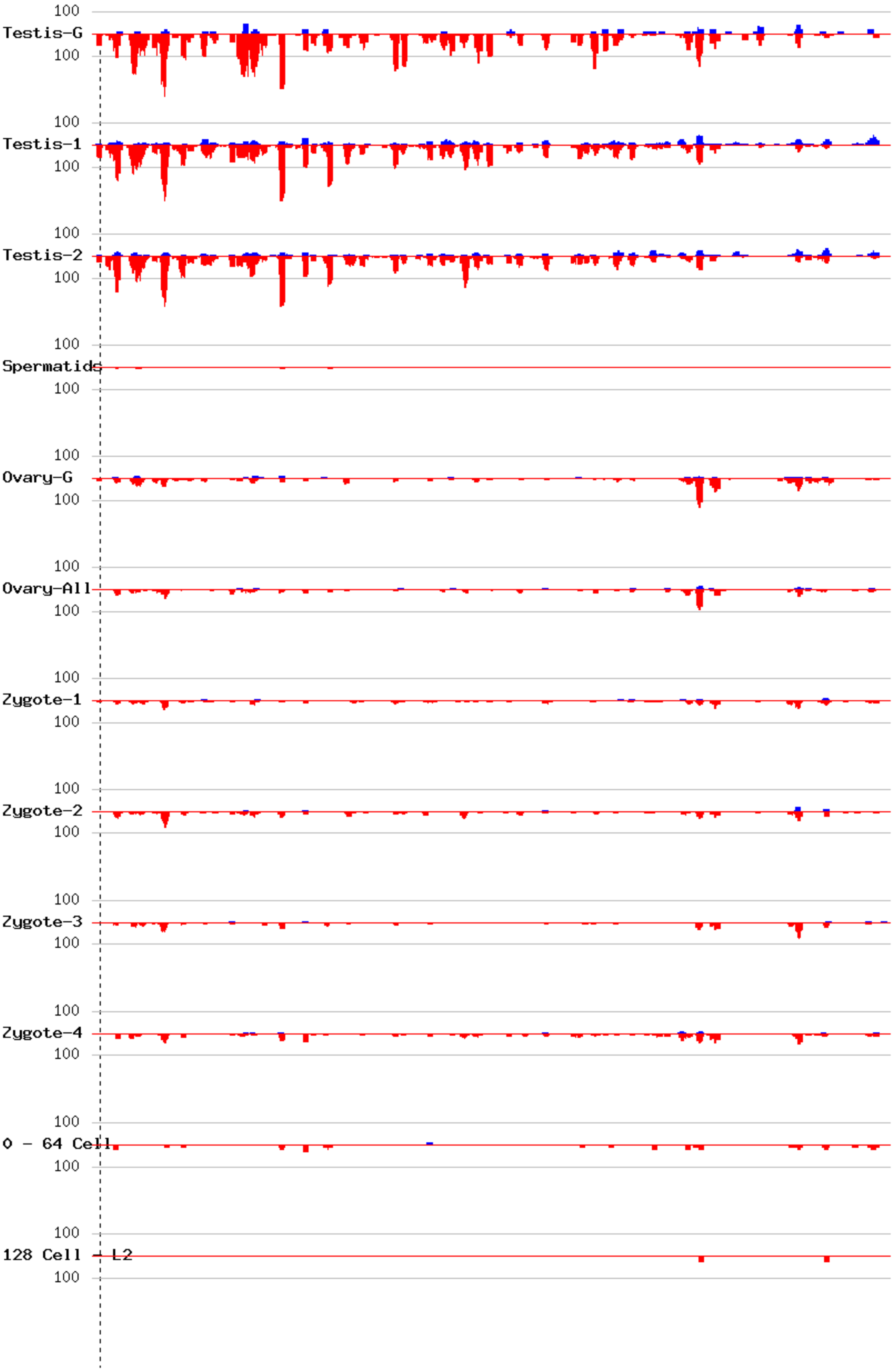
ASCP_4478_873 RNA-dependent_RNA_p



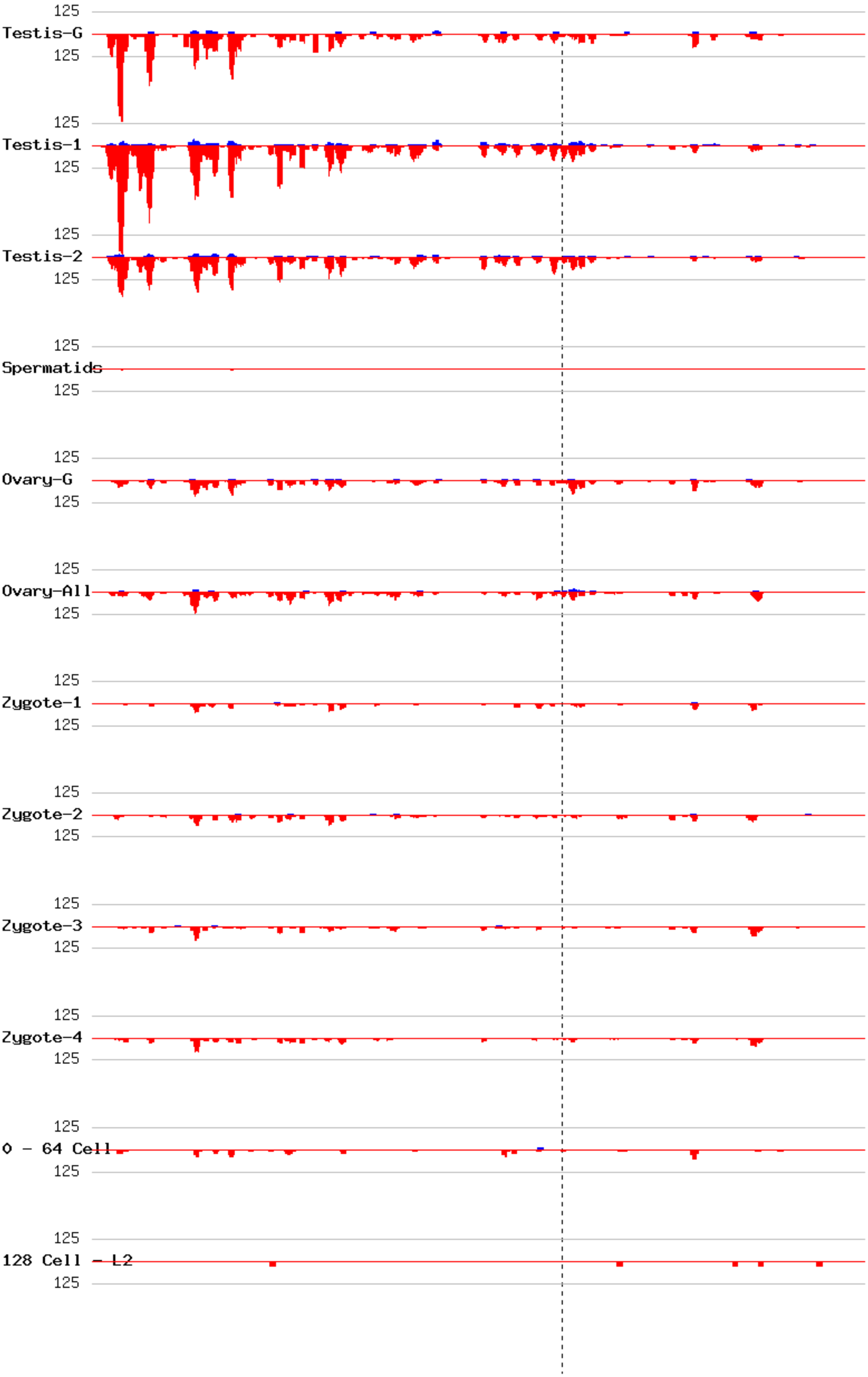
ASCP_4630_849 Hypothetical_prote



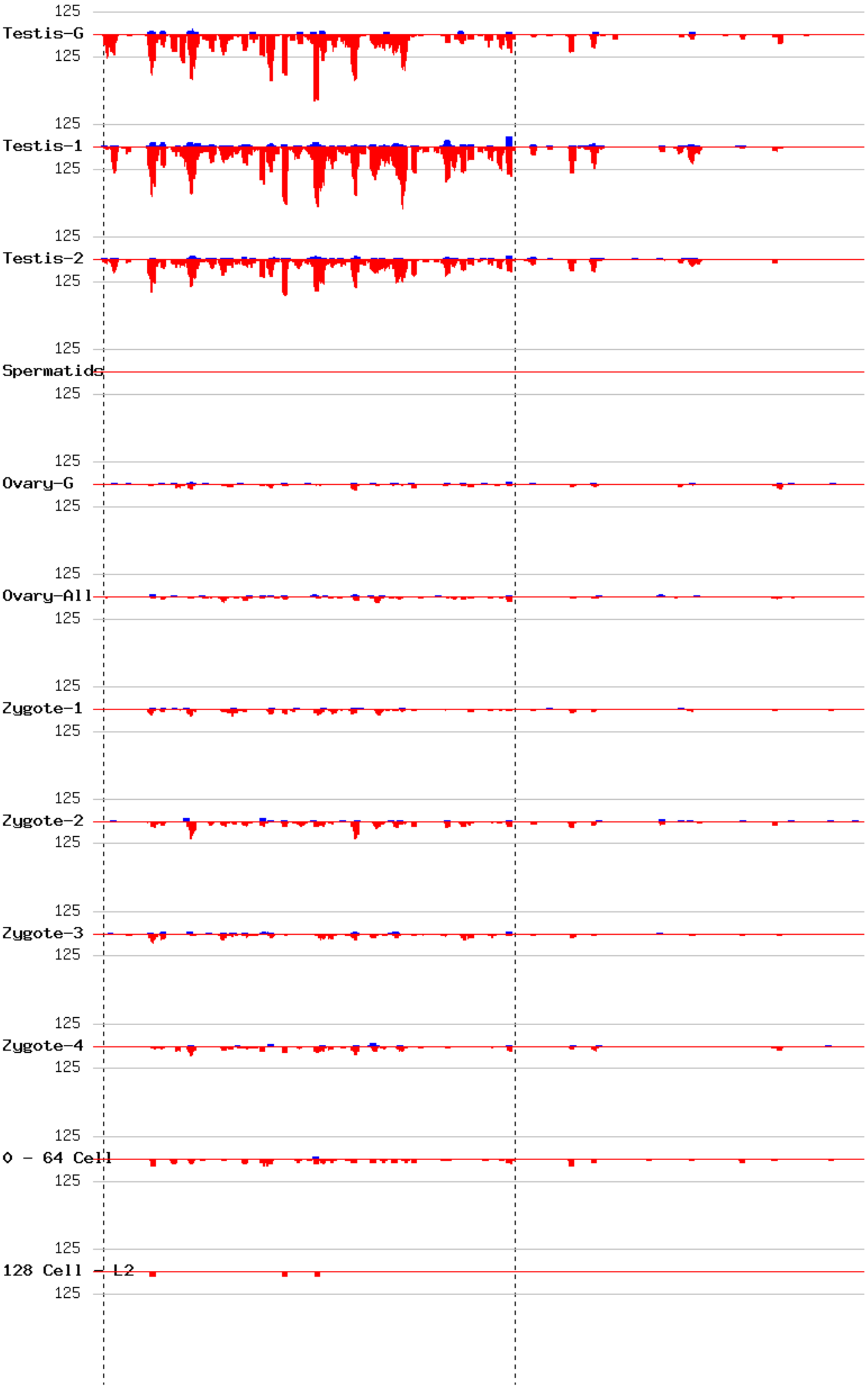
ASCP_473_3592 Hypothetical_protein 3592 bp



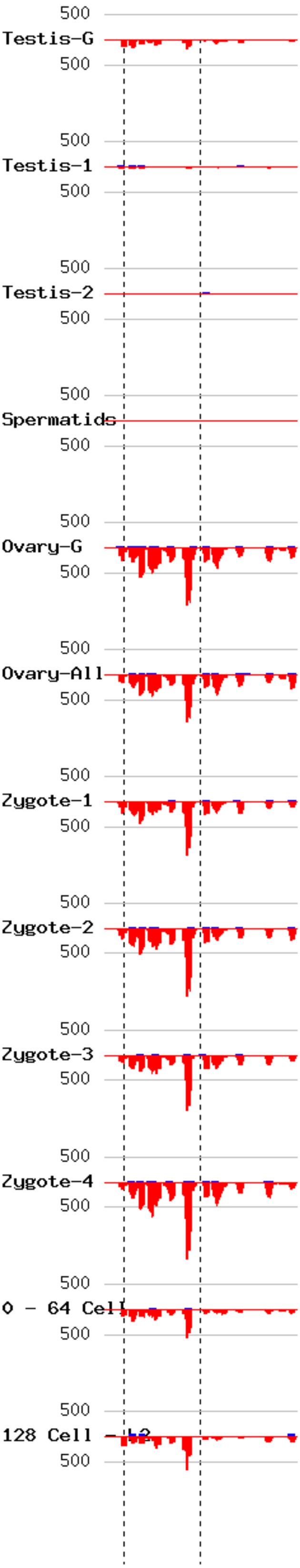
ASCP_513_3461 ATP-dependent_RNA_helicase_An3 3461 bp



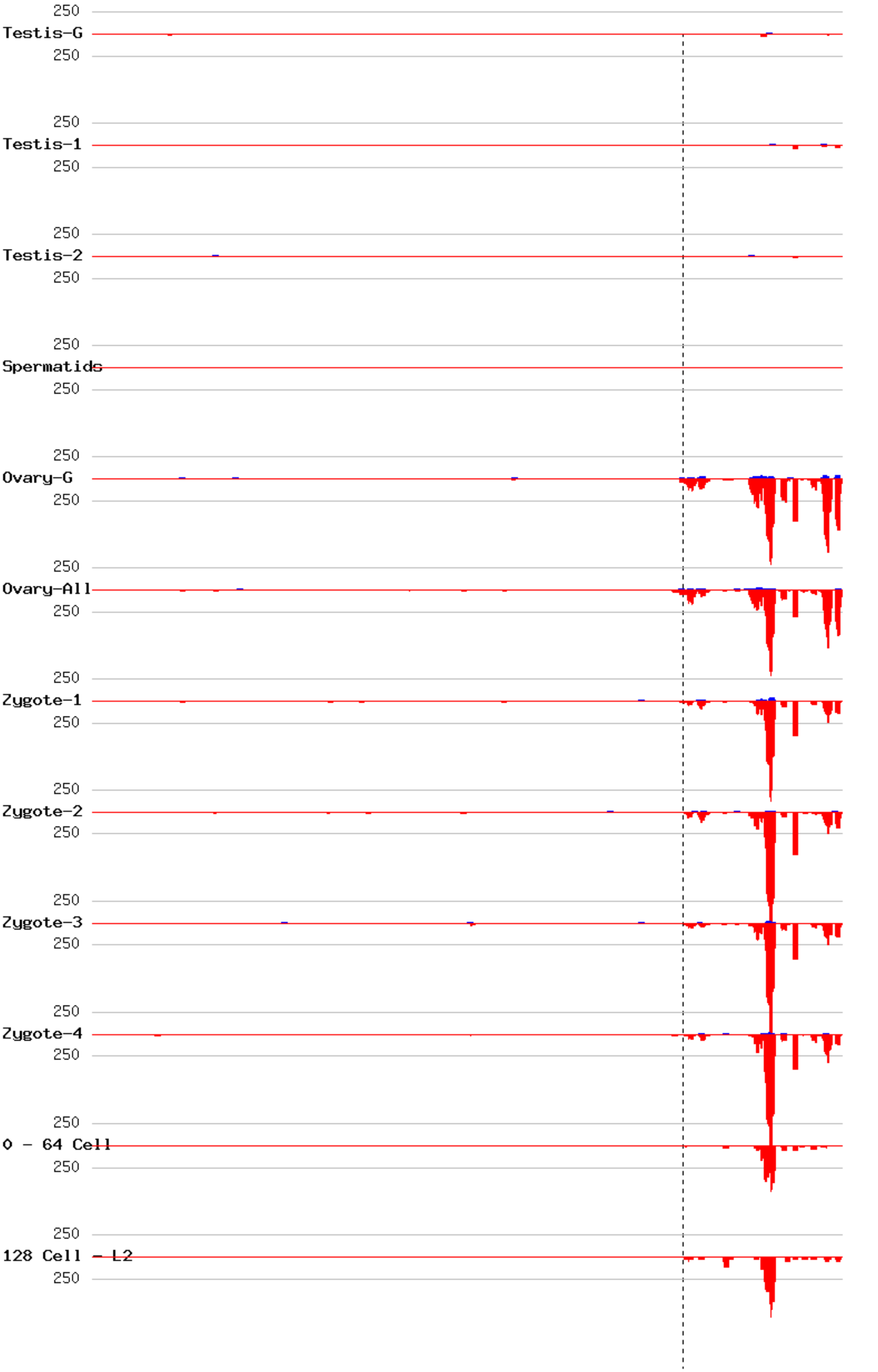
ASCP_528_3426 Hypothetical_protein 3426 bp



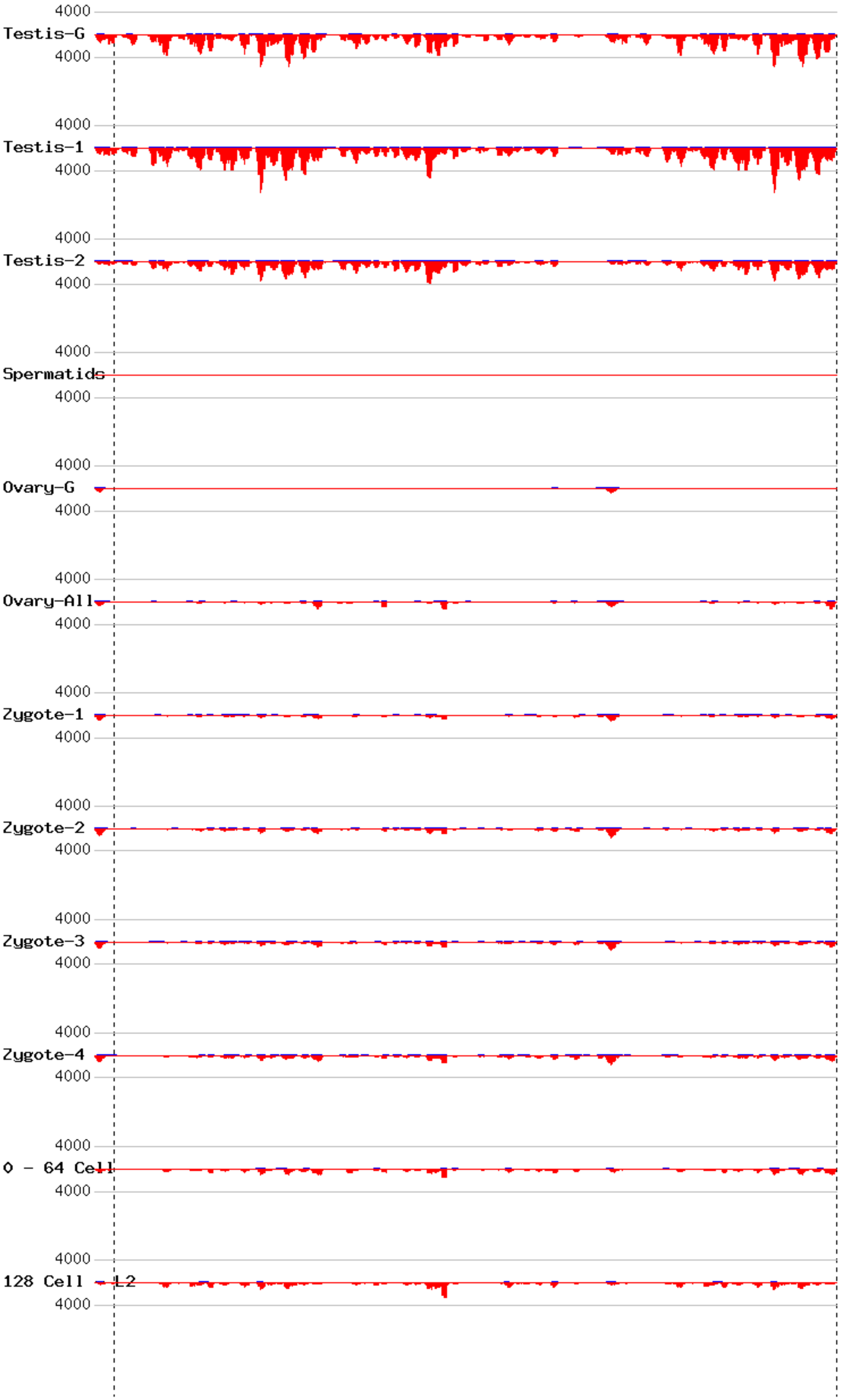
ASCP_5311_758 TPR_Domain_conta



ASCP_550_3371 Niemann-Pick_C1_protein 3371 bp

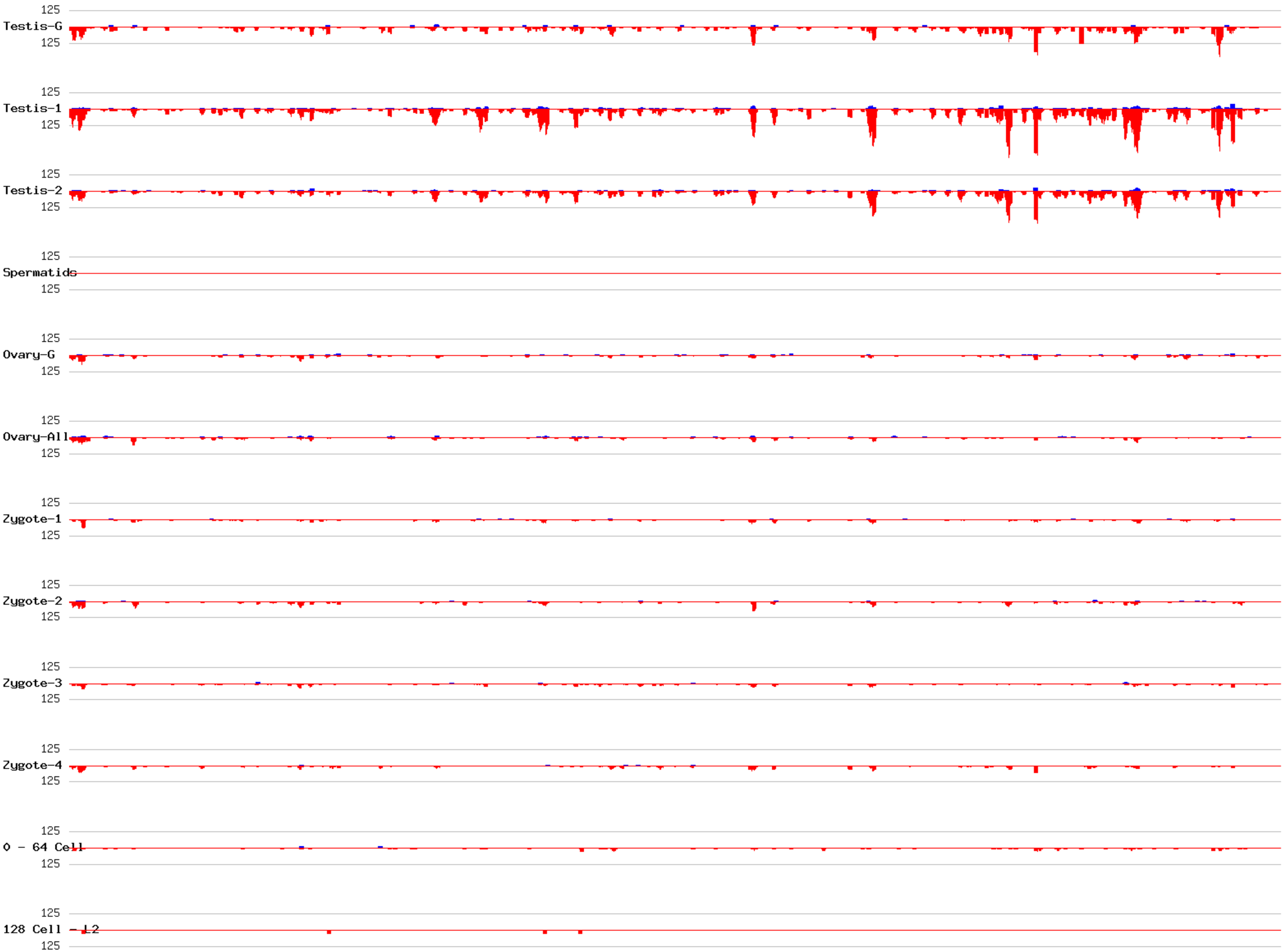


ASCP_596_3271 Hypothetical_protein 3271 bp

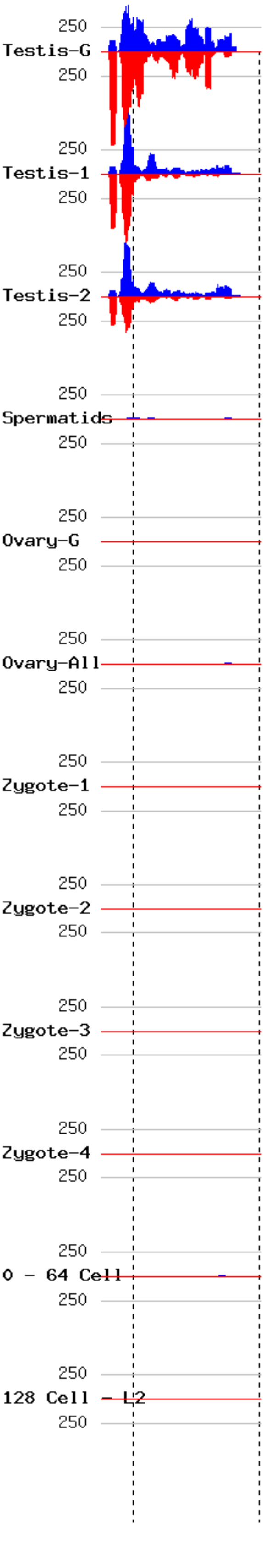


ASCP_62_7377 Zinc_finger_C2H2_type_family_protein 7377 bp

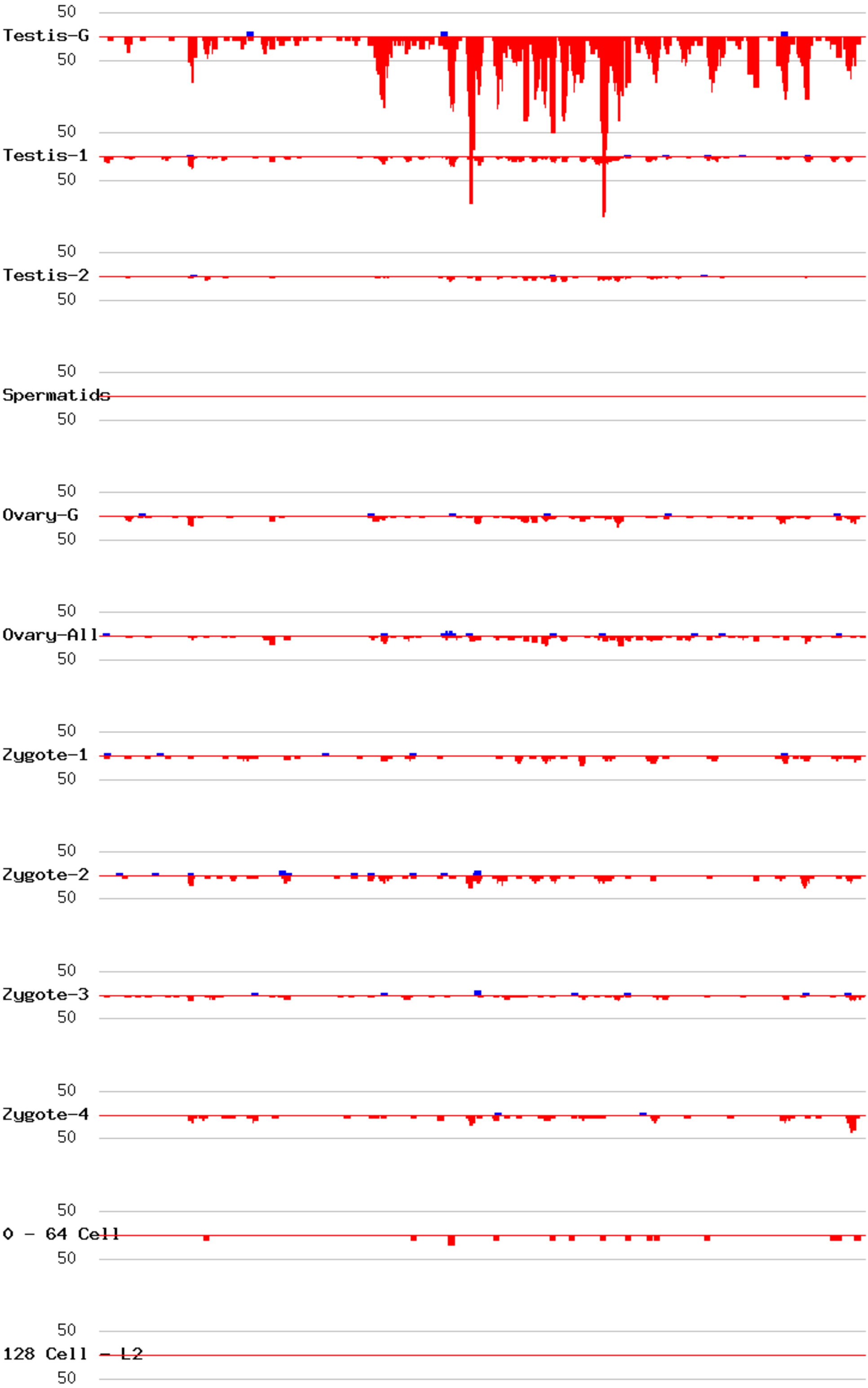
Testis-G
Testis-1
Testis-2
Spermatids
Ovary-G
Ovary-All
Zygote-1
Zygote-2
Zygote-3
Zygote-4
0 - 64 Cell
128 Cell - L2



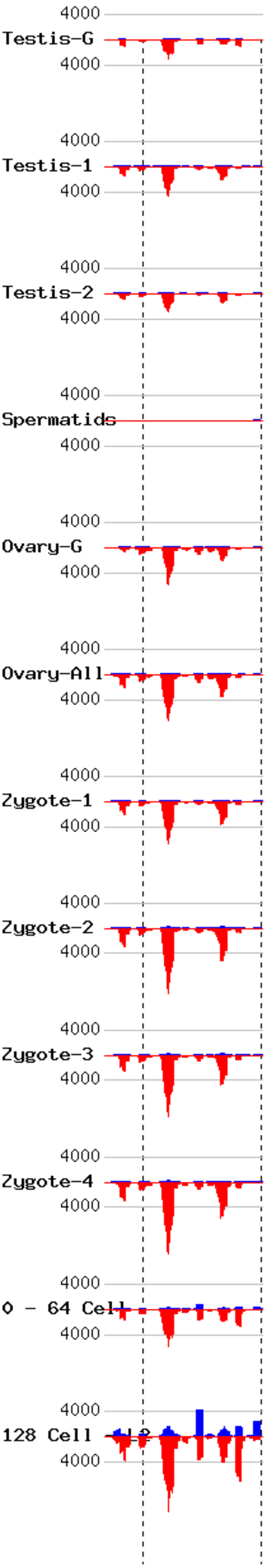
ASCP_6229_650 Hypothetical_p



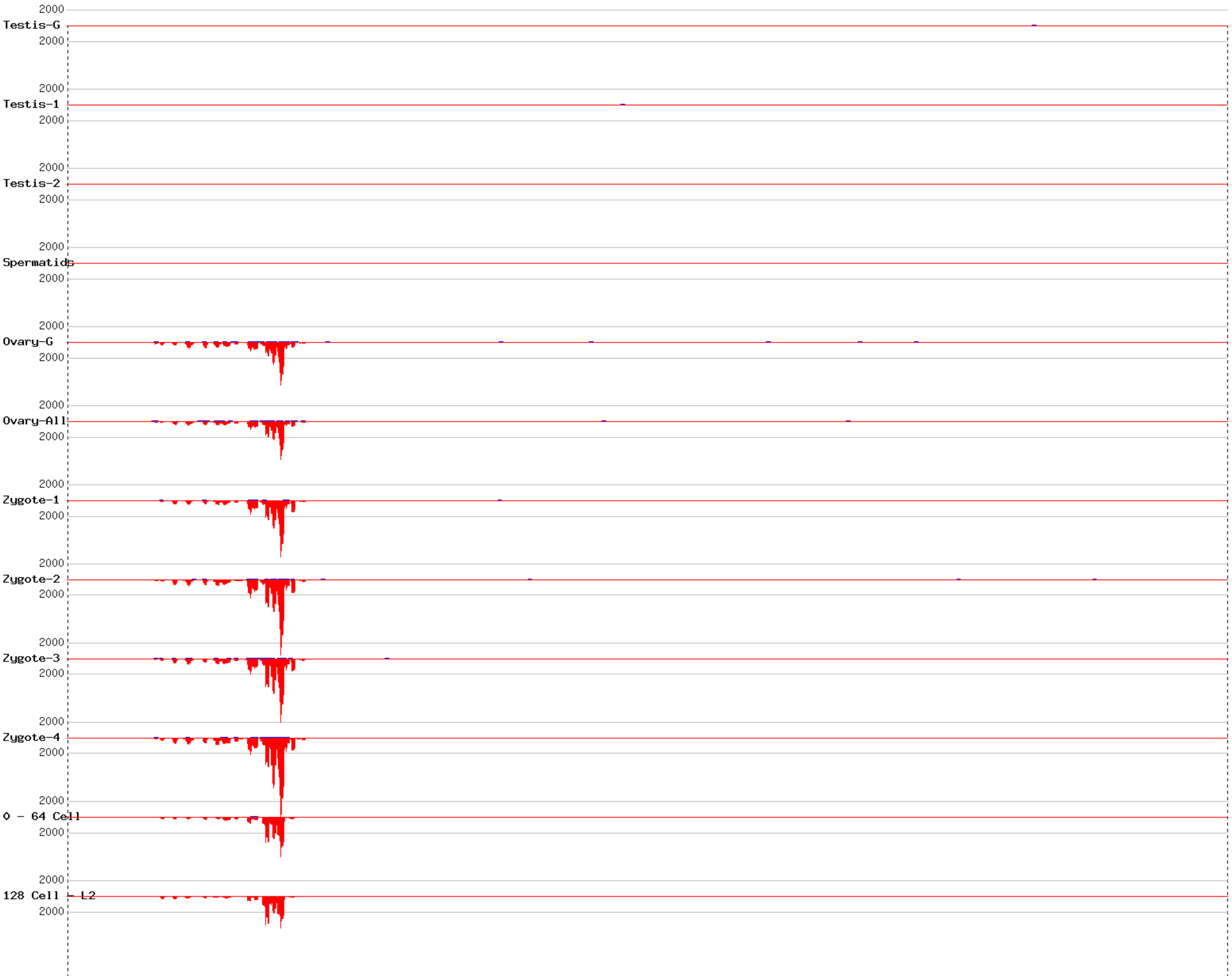
ASCP_623_3198 Hypothetical_protein 3198 bp



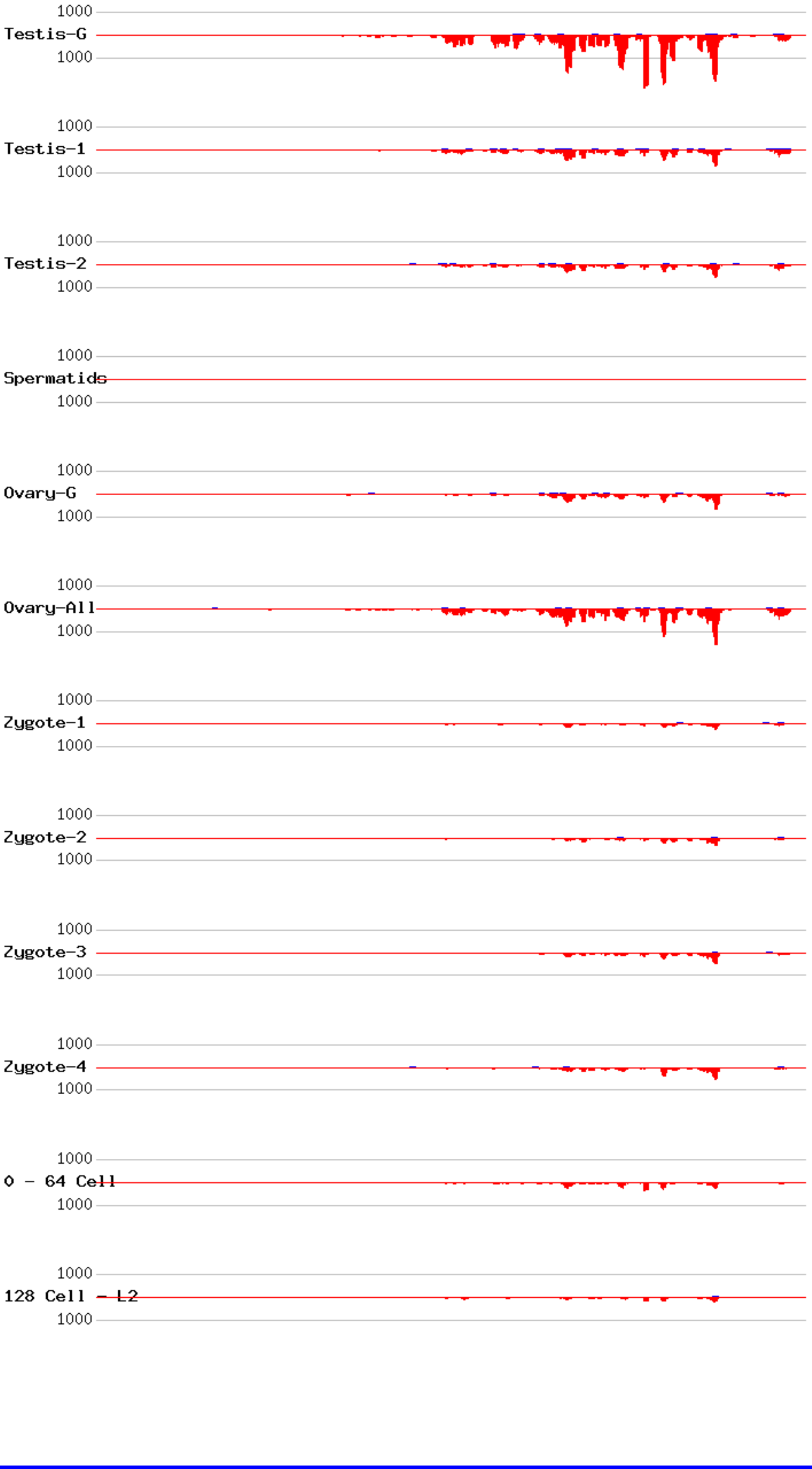
ASCP_6473_622 Gag_protein 6



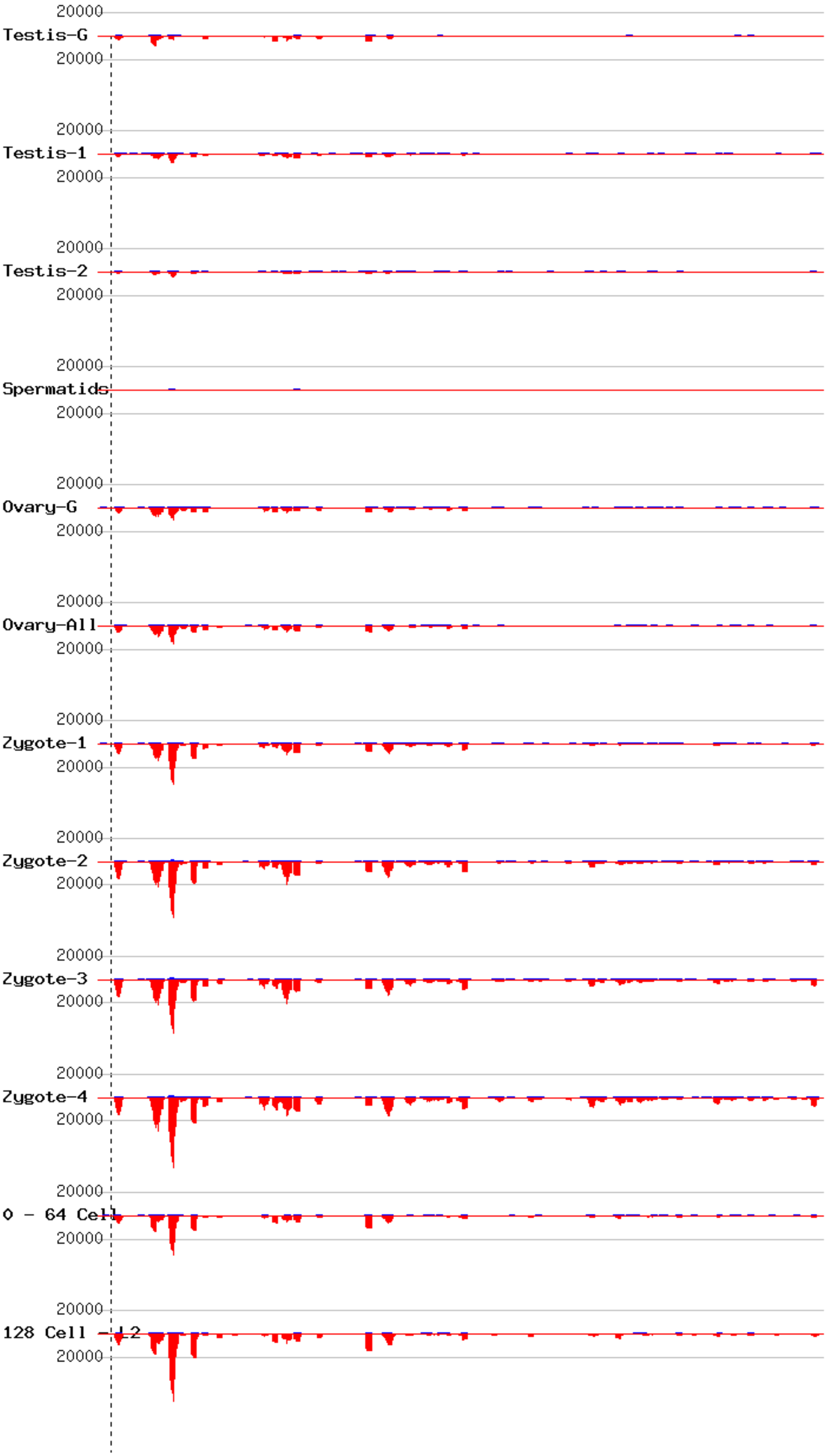
ASCP_66_7339 Hypothetical_protein 7339 bp



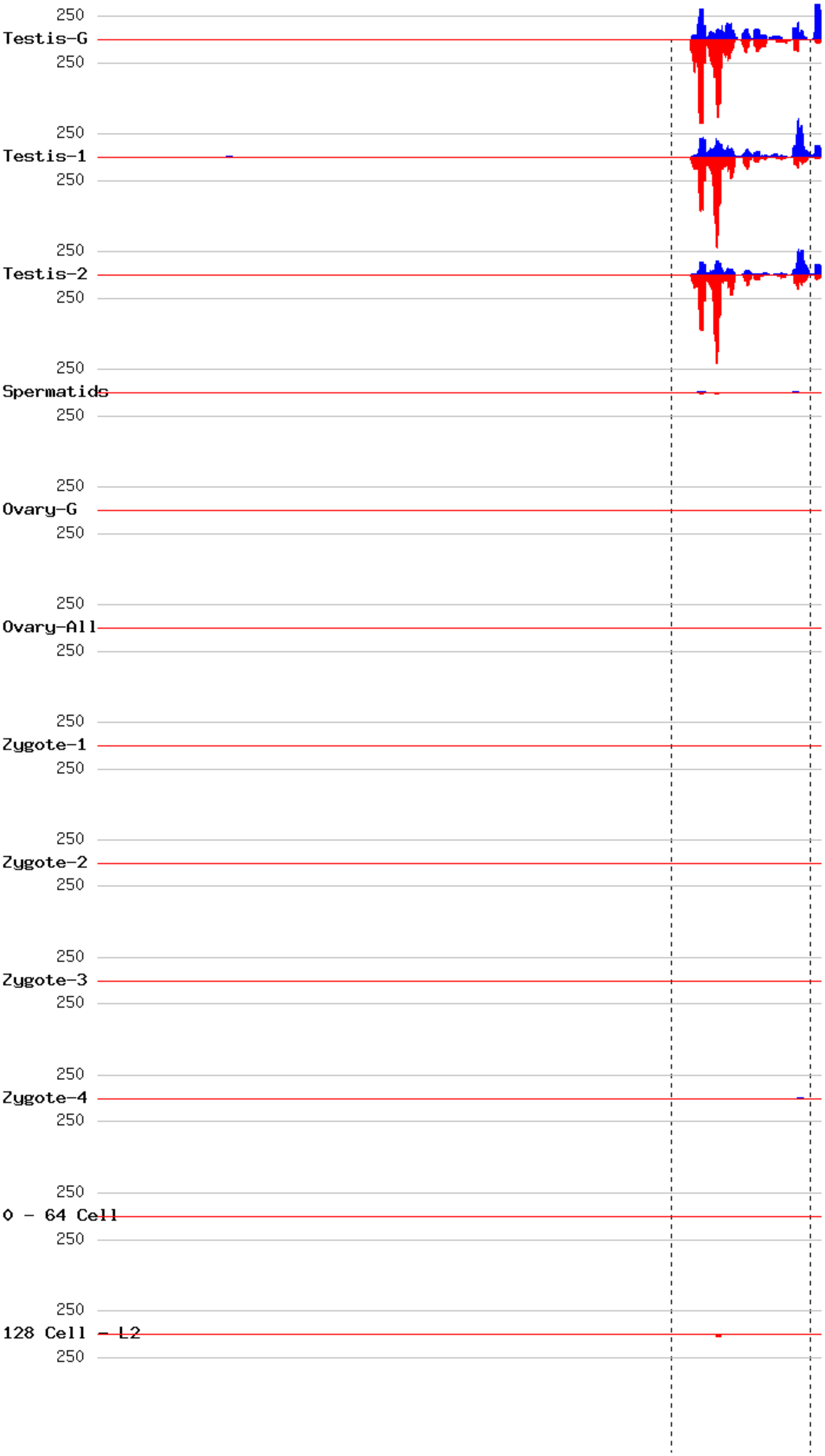
ASCP_667_3090 Vinculin 3090 bp



ASCP_674_3075 Hypothetical_protein 3075 bp



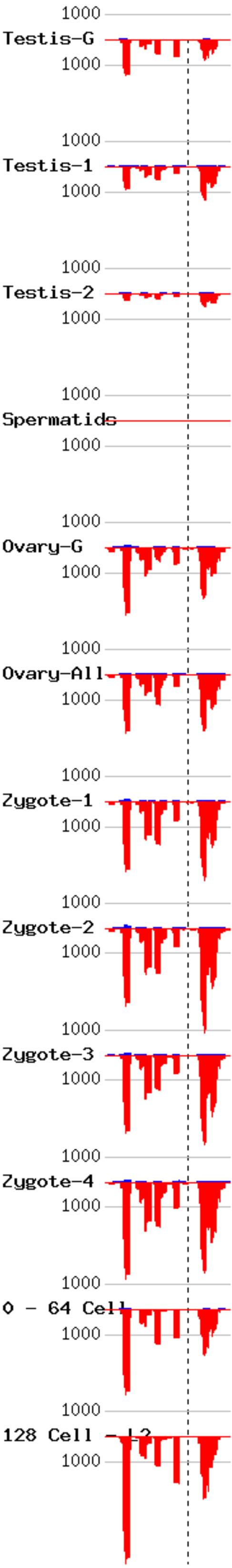
ASCP_679_3071 Hypothetical_protein 3071 bp



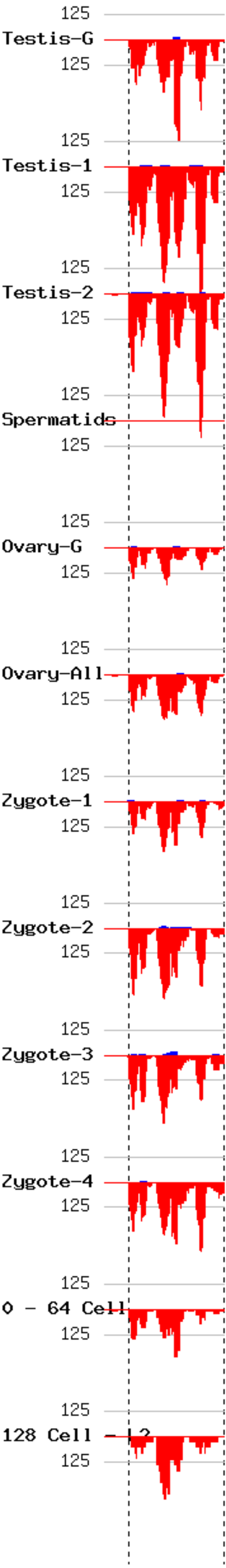
ASCP_713_3004 Zinc_finger_domain_containing_protein 3004 bp



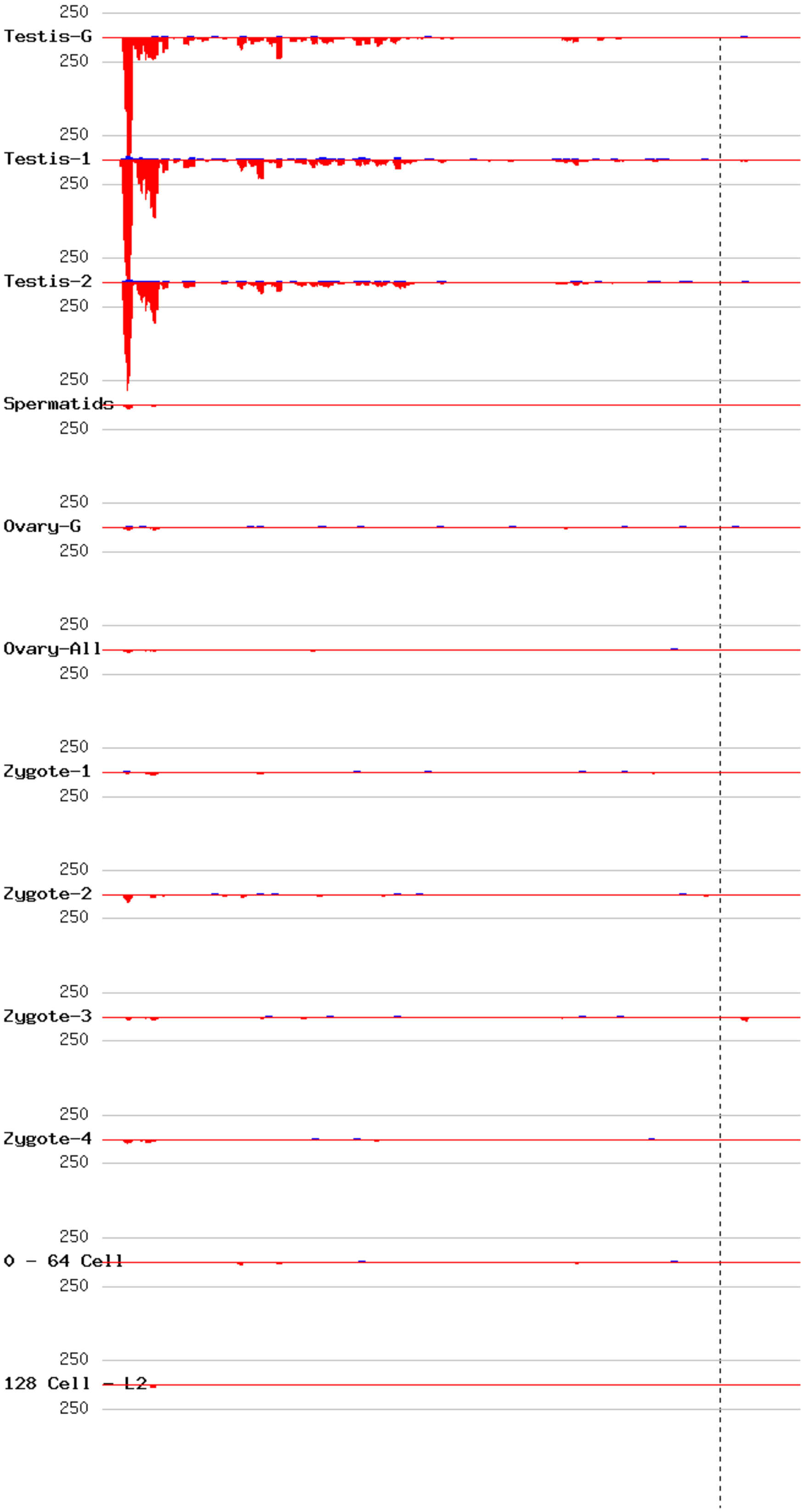
ASCP_7740_494 Hypothetic



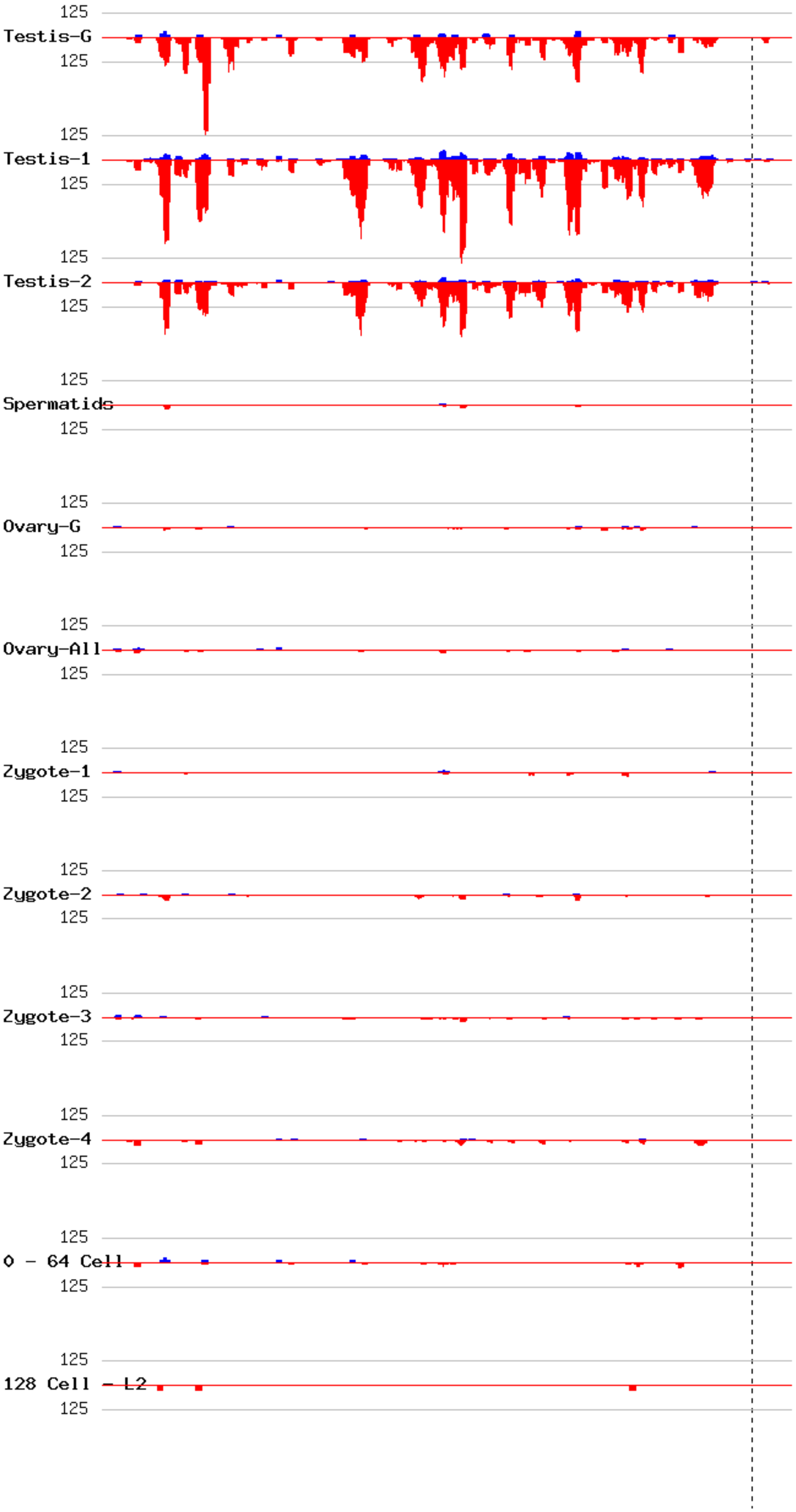
ASCP_7921_474 Gag-pol_po



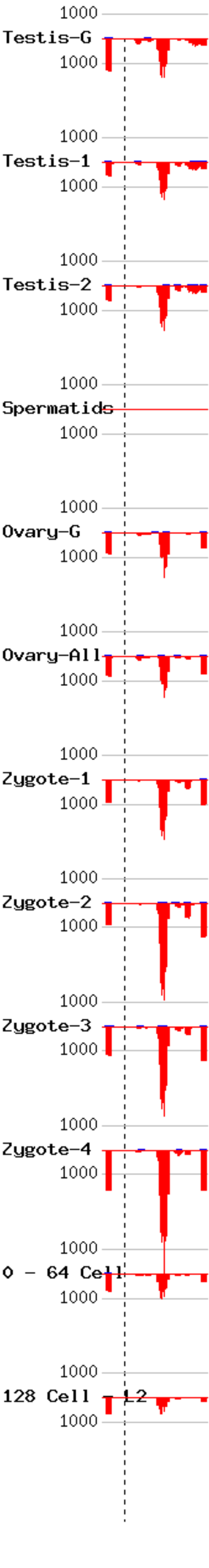
ASCP_796_2848 Hypothetical_protein 2848 bp

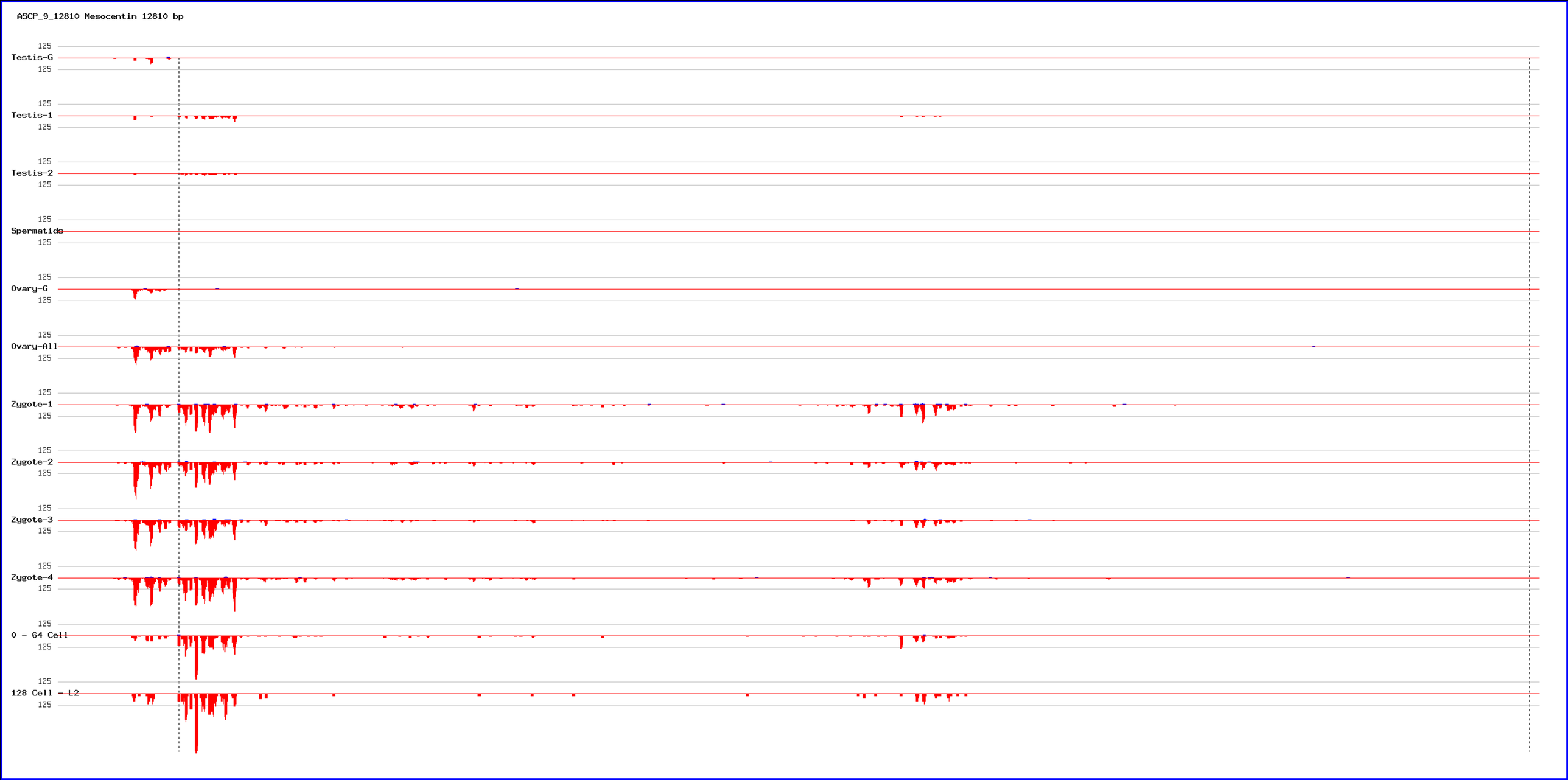


ASCP_812_2813 ENT_domain_containing_protein 2813 bp

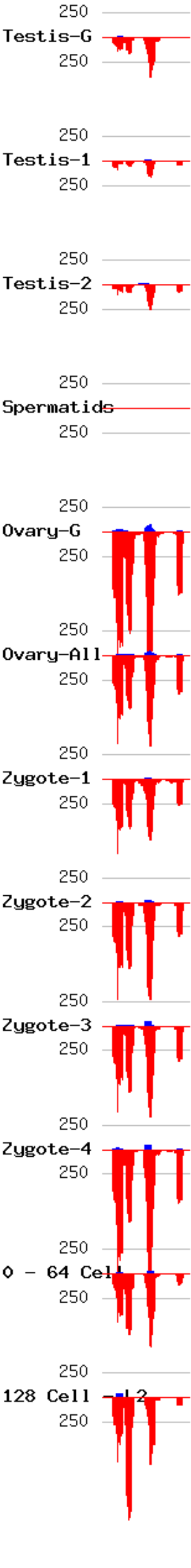


ASCP_8384_426 Reverse_t

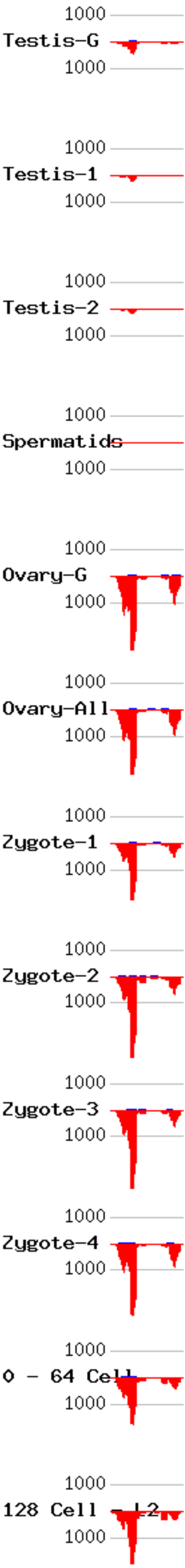



ASCP_9_12810 Mesocentin 12810 bp
125
Testis-G
125
125
Testis-1
125
125
Testis-2
125
125
Spermatids
125
125
Ovary-G
125
125
Ovary-All
125
125
Zygote-1
125
125
Zygote-2
125
125
Zygote-3
125
125
Zygote-4
125
125
0 - 64 Cell
125
125
128 Cell - L2
125

ASCP_9008_351 Collage



ASCP_9476_270 Colla



ASCP_95_6516 Hypothetical_protein 6516 bp

1000
Testis-G
1000

1000
Testis-1
1000

1000
Testis-2
1000

1000
Spermatids
1000

1000
Ovary-G
1000

1000
Ovary-All
1000

1000
Zygote-1
1000

1000
Zygote-2
1000

1000
Zygote-3
1000

1000
Zygote-4
1000

1000
0 - 64 Cell
1000

1000
128 Cell - L2
1000

ASCP_971_2550 Hypothetical_protein 2550 bp

250
Testis-G
250

250
Testis-1
250

250
Testis-2
250

250
Spermatids
250

250
Ovary-G
250

250
Ovary-All
250

250
Zygote-1
250

250
Zygote-2
250

250
Zygote-3
250

250
Zygote-4
250

250
0 - 64 Cell
250

250
128 Cell - L2
250