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DR. LUKAS WISGRILL (Orcid ID : 0000-0001-9833-9499)
PROF. HARRI ALENIUS (Orcid ID : 0000-0003-0106-8923)

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Microbial and transcriptional differences elucidate atopic dermatitis heterogeneity across skin sites

Noora Ottman[*1], Mauricio Barrientos-Somarribas[*2], Nanna Fyhrquist[1,3], Helen Alexander[4], Lukas Wisgrill[5], Peter Olah[7,8], Sophia Tsoka[9], Dario Greco[10,11,12], Francesca Levi-Schaffer[13], Vassili Soumelis[14,15], Jens M. Schröder[16], Juha Kere[17,18], Frank O. Nestle[19], Jonathan Barker[20], Annamari Ranki[21], Antti Lauerma[21], Bernhard Homey[7], Björn Andersson[#2], Harri Alenius[#%1,3]

* Equal contribution
Equal contribution

Corresponding author: Harri Alenius
Address: IMM, Box 210, 171 77 Stockholm, Sweden;
email: harri.alenius@ki.se; phone: +46 70 757 6176.

Author affiliations:

[1] Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden
[2] Department of Cell and Molecular Biology, Karolinska Institutet, Stockholm, Sweden
[3] Human Microbiome Research Program, University of Helsinki, Helsinki, Finland

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[4] St John's Institute of Dermatology, Guy's and St Thomas' NHS Foundation Trust and King's College London, London, UK
[5] Division of Neonatology, Pediatric Intensive Care and Neuropediatrics, Medical University of Vienna, Vienna, Austria
[7] Department of Dermatology, University Hospital Duesseldorf, Duesseldorf, Germany.
[8] Department of Dermatology, Venereology and Oncodermatology, University of Pécs, Pécs, Hungary.
[9] Department of Informatics, Faculty of Natural and Mathematical Sciences, King's College London, London, UK.
[10] Faculty of Medicine and Life Sciences, University of Tampere, Tampere 33520, Finland.
[11] Institute of Biomedical Technology, University of Tampere, Tampere, Finland.
[12] Institute of Biotechnology, University of Helsinki, Helsinki, Finland.
[13] Pharmacology Unit, School of Pharmacy, The Institute for Drug Research, Faculty of Medicine, The Hebrew University of Jerusalem, Jerusalem, Israel.
[14] Institut Curie, 26 rue d'Ulm, 75248 Paris, France.
[15] INSERM, U932, Paris, France.
[16] Department of Dermatology, University Hospital Schleswig-Holstein, Kiel, Germany.
[17] Department of Biosciences and Nutrition, Karolinska Institutet, Stockholm, Sweden.
[18] School of Basic and Medical Biosciences, King's College London, London, UK.
[19] Cutaneous Medicine Unit, St. John's Institute of Dermatology and Biomedical Research Centre, Faculty of Life Sciences and Medicine, King's College London, London, UK.
[20] St John's Institute of Dermatology, Division of Genetics and Molecular Medicine, Faculty of Life Sciences and Medicine, Kings College London, London SE1 9RT, UK.
[21] Department of Dermatology, Allergology and Venereology, University of Helsinki and Helsinki University Hospital, Inflammation Centre, Helsinki, Finland.

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Abstract

It is well established that different sites in healthy human skin are colonized by distinct microbial communities due to different physiological conditions. However, few studies have explored microbial heterogeneity between skin sites in diseased skin, such as atopic dermatitis (AD) lesions. To address this issue, we carried out deep analysis of the microbiome and transcriptome in the skin of a large cohort of AD patients and healthy volunteers, comparing two physiologically different sites: upper back and posterior thigh. Microbiome samples and biopsies were obtained from both lesional and non-lesional skin to identify changes related to the disease process. Transcriptome analysis revealed distinct disease-related gene expression profiles depending on anatomical location, with keratinization dominating the transcriptomic signatures in posterior thigh, and lipid metabolism in the upper back. Moreover, we show that relative abundance of *Staphylococcus aureus* is associated with disease severity in the posterior thigh, but not in the upper back. Our results suggest that AD may select for similar microbes in different anatomical locations – an 'AD-like microbiome', but distinct microbial dynamics can still be observed when comparing posterior thigh to upper back. This study highlights the importance of considering the variability across skin sites when studying the development of skin inflammation.

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Introduction

Skin forms a life-sustaining interface between the human body and the environment, and recent research reveals the importance of cutaneous microbial communities in health and disease. The healthy skin microbiota varies widely between individuals and changes with age, gender, genetic variation, health status and living environment[1-3]. It is also clear that the skin microbiota is not one single community, but a collection of commensal communities where each community adapts to and modulates the physiological and immunological environment of the sites they inhabit[4]. Typically, the healthy human skin microbiome is mostly stable within an individual over time[5]. The maintenance of skin homeostasis relies on a finely tuned balance between the host and its microbes at each site, and a disruption of this balance likely contributes to inflammatory skin diseases such as atopic dermatitis (AD)[6, 7].

AD is a highly heterogenous disease characterized by chronic itchy rashes, inflammation and frequent skin infections, and it is currently the most common chronic inflammatory skin disease in industrialized countries[8]. AD lesions can extend from the typical sites of predilection, such as body folds, to most skin surfaces[8], and manifestations vary extensively by age, severity, age of onset [9] and ethnicity [10]. However, at present, the precise mechanisms driving the onset and course of AD are insufficiently understood and the optimal type and time-point for intervention are unknown[11]. Investigating the role of the microbiome and its interaction with the skin in AD will likely reveal important clues regarding disease mechanisms and improved biomarkers to stratify patients into disease subtypes. This will also stimulate future research on innovative treatments directed at endotype components[12].

We and others have reported previously that the AD skin microbiota is perturbed, including a decrease in microbial diversity in comparison to healthy subjects[13, 14]. In many cases, *Staphylococcus aureus* colonizes the skin, with a prevalence of 70 % on lesional skin and 39% on non-lesional skin of AD patients according to culture-based methods[15]. Culture-independent studies have shown that the relative abundance of staphylococci, *S. aureus* and *S. epidermidis* in particular, positively correlates with AD severity during flares[14, 16]. A recent culture-based study supported these findings by demonstrating that AD patients colonized with *S. aureus* have more severe disease symptoms as well as a greater degree of type 2 immune deviation and barrier

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disruption compared to patients not colonized with *S. aureus*[17]. From the host perspective, several studies of the human skin transcriptome have found an induction of type 2 immune pathways, and disturbances in lipid metabolism and barrier function[18-27]. However, most of these studies have been limited by small sample sizes[22, 26, 27]. Our recent study combined analyses of the skin microbiota and host transcriptome analyses from the same subjects with a greater sample number to elucidate microbe-host interactions in AD [13].

Only a few microbiome and transcriptome studies have explored AD heterogeneity between skin sites. Most studies have focused on a single site or pooled samples from different body sites for statistical analyses. Since the anatomical location is known to be a strong determinant of the microbial composition in healthy individuals [28], local skin physiology could determine the role of the microbiota in AD in a skin-site dependent fashion. A recent study analyzed the effect of different skin sites and their physiological properties such as lipid profile at the microbiome level in patients with AD [29]. Epidermal lipid composition correlated strongly with bacterial diversity and composition at AD predilection sites. Higher levels of long-chain unsaturated fatty acids were found to be associated with increased abundance of the lipophilic Propionibacteria and Corynebacteria [29].

In the present study, we aimed to further explore the interaction between host and skin microbiome in AD by examining two physiologically distinct body sites: posterior thigh and upper back. The skin microbiota was determined using 16S rRNA gene sequencing, and the host transcriptome by DNA microarrays. Integration of these results revealed site-specific characteristics of AD pathophysiology which have relevance for understanding both disease mechanisms and treatment targets.

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Methods

Subject recruitment and sampling

Adult patients (18-83 years) with moderate-to-severe chronic AD (SCORAD score > 25, n=91), as well as healthy volunteers (n=126) were recruited to the study. Microbiome skin swab samples and skin biopsies were obtained from areas with active disease in the upper back or posterior thigh (from above poplitea to bottom of buttocks) in AD patients. Healthy volunteers were sampled in corresponding skin areas. All clinical procedures were approved by the appropriate local Institutional Review Boards (UH, Dnro 91/13/03/00/2011; HHU, 3647/2011; KINGS, 11/H0802/6) and all subjects provided written informed consent before participation. A detailed description of the recruitment and sampling is available in Fyhrquist *et al* 2019[13]. **Figure E1** in the supplementary material describes the patient and control numbers, sample numbers per anatomical location, and study method used. All Affymetrix analysed samples are matched with the 16S analysed samples.

16S amplicon processing and data analysis

Library preparation and sequence preprocessing were performed as described in Fyhrquist *et al* 2019[13]. Briefly, DNA was extracted from the microbiome samples, barcoded, regions V3-V4 amplified using primers 341F/805R, and sequenced with 454 FLX titanium. Sequences were preprocessed with Qiime, and operational taxonomic units (OTUs) were picked at 99.3% identity.

Alpha diversity measures were calculated with vegan package in R [30], tested with Mann Whitney U test and FDR corrected with Benjamini Hochberg (BH). Beta diversity was calculated using the Bray-Curtis dissimilarity and ordination was performed with PCoA and UMAP. Permanova test for differences within groups was implemented with the adonis function from the vegan R package. Differential abundance testing of clades was carried out using ANCOM from the python scikit-bio skbio.stats.composition.ancom package version 0.4.2 [31]. The test was run with default parameters and 'holm-bonferroni' multiple comparisons correction. All analyses should be interpreted as exploratory.

Microarray data processing and data analysis

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Total RNA was extracted from skin tissue samples using the RNeasy Fibrous Tissue Mini kit (Qiagen), amplified according to Affymetrix protocols, and hybridized to array plates.

Normalization, batch correction and differential analysis was performed in the eUTOPIA[32] platform (https://github.com/Greco-Lab/eUTOPIA). In short, the affymetrix arrays were normalized and technical batch effects originating from sample preparation were removed (SVA-package with Combat function). For identification of differentially expressed genes, a linear model (R package Limma) was fitted to the data (using age, gender, clinical center as covariates), and pairwise comparisons were done using the empirical Bayes method. Transcriptomes were defined based on a fold change of 1.5 or greater and a Benjamini-Hochberg adjusted p-value less than 0.05.

Network analysis was generated using the INfORM[33] (https://github.com/Greco-Lab/INfORMhttps://github.com/Greco-Lab/INfORM) by Greco Lab with default parameters. Functional enrichment analyses were performed using web-based tools Enrichr (http://amp.pharm.mssm.edu/Enrichr/) and the PANTHER Gene Ontology version 13.1 and the Ingenuity Pathway Analysis by Qiagen. Heatmaps were generated with Perseus.

Association with severity

Association between AD severity and *S. aureus* abundance was performed using the Spearman correlation. Two measures of severity were used: 1) objective SCORAD as a measure of global AD severity, and 2) local SCORAD, a study specific measure of severity of the sampled lesions, based on the objective SCORAD criteria (see Fyhrquist et a. 2019[13]).

Leukocyte deconvolution and module detection

To evaluate the relative cell fraction of involved leukocyte subsets in all studied skin sites, the CIBERSORT (CS) algorithm was used to estimate cell proportions of 22 individual immune cells utilizing the "L22" validated gene signature matrix [34]. Estimations are based on 1000 permutations. No significance filter has been applied to the estimated cell fractions to include all samples for further analysis (Figure E11).

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Weighted Gene Co-Expression Analysis (WGCNA) was used to integrate the relation of relative abundance of *S. aureus* and *S. epidermidis* as well as estimated cell fraction of the CS algorithm in lesional skin of the posterior thigh [35]. The parameters used were minCorKME = 0.5 and minKMEtoStay = 0.3 and minModuleSize = 50, resulting in a total of 15 modules. Generated module eigengenes were correlated with microbial and cellular traits of interest (Figure E12). Modules with a correlation coefficient > 0.5 and p-value < 0.001 were further analyzed for gene enrichment and pathway analysis using clusterProfiler [36].

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Results

Differences in microbial dynamics of AD skin between thigh and upper back are characterized by *S. aureus*

The skin microbiota of both AD patients (n = 84) and healthy subjects (n = 117) was dominated by the phyla Firmicutes, Proteobacteria, Actinobacteria and Bacteroidetes (Fig. 1a) as expected [37]. Of these, Firmicutes and Proteobacteria showed differences in abundance between the clinical groups (ANCOM [31]analysis). Firmicutes were increased in both AD lesional and non-lesional skin compared to healthy controls, while Proteobacteria were decreased in AD lesional samples compared to both non-lesional and controls (Fig. E1).

At the genus level, *Staphylococcus* was the most common genus observed in AD samples, with *S. aureus* as the most prevalent species (Fig. 1b). *S. aureus* (OTU 883806) showed significant differential abundance between the groups. *S. aureus* was increased in AD lesions and non-lesional samples compared to controls (Fig. E2) and it was differentially abundant between AD and healthy controls in the thigh samples (n = 45), but the evidence in back samples was inconclusive (n = 39) (Fig. E3).

To investigate the skin site differences further, we determined the microbial alpha diversity (in this case the Shannon index), which measures species richness and distribution within a population (Fig. 2a). In posterior thigh, the alpha diversity was progressively reduced from healthy skin to non-lesional AD skin and further to lesional AD skin. A closer look at the microbial composition of the samples suggested that a gradual increase of *S. aureus* from healthy person to non-lesional AD and further to lesional AD skin is an important driver of the reduction in alpha diversity. In contrast, alpha diversity did not differ between any of the studied groups in upper back samples. Of note, microbial diversity was lower in healthy back compared to healthy posterior thigh (n = 92, Fig E4a), consistent with previous studies[38]. We obtained similar results by using the Simpson index (Fig. E4b,c). It should be noted, however, that low number of samples from the back of healthy control (n=13) subjects limits the power of the microbiome analysis.

Analysis of beta diversity, measuring the degree of similarity between sample groups, was also carried out. AD lesional and non-lesional samples from both skin sites were found to form an AD sample cluster, while the thigh healthy skin cluster showed some overlap with AD samples, and

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upper back healthy controls formed a more separate group (Fig. 2b). These results indicated that there is an 'AD-like microbiome' which is skin-site independent.

Further analysis revealed additional skin-site specific dynamics in AD, as indicated by the alpha diversity measures (Fig. 2b and Fig. E5). In thigh samples, healthy, non-lesional and lesional samples formed clear but partially overlapping clusters. *S. aureus* and *Staphylococcus* spp. were found to be differentially abundant between the three conditions (Fig. E3a). In contrast, upper back healthy samples formed a separate cluster from the corresponding AD samples, but the lesional and non-lesional samples clustered more closely than the corresponding thigh samples. Two OTUs, labelled as *Herbaspirillum* spp. and *Curvibacter* spp., were differentially abundant in upper back AD compared to controls, but these have been identified as common kit contaminants[39, 40] (Fig. E3b). We also identified a group of samples with a distinct bacterial profile. These samples contained OTUs from the Burkholderiaceae, Enterobacteriaceae, Microbacteriaceae and Oxalobacteraceae families, with *Cryocola* spp. and *Halomonas phoceae* as the most abundant taxa (Fig. E6).

The non-lesional skin transcriptome in AD differs from that of healthy skin, and is strongly influenced by anatomical site

To identify skin processes altered in AD in the two sampled anatomical locations, we compared the transcriptional profile of non-lesional AD skin with healthy controls. In posterior thigh, 108 genes (Table E2) were differentially expressed (fold change (FC) > 1.5, adj. p-value < 0.05) between non-lesional AD and healthy skin samples, while the same comparison in upper back resulted in 371 (Table E4) differentially expressed genes (DEGs) (Fig. E7).

Analysis of the identified gene signatures for functional enrichment based on gene ontology (GO) categories revealed clear differences between the anatomical locations. Non-lesional AD in posterior thigh showed an enrichment in biological processes related to cornification and epidermal cell differentiation, as well as lymphocyte chemotaxis, compared to healthy thigh controls (Fig. 3a). In upper back, the same comparison revealed mainly the enrichment of lipid, small molecule, cofactor and organic acid metabolism, lacking any immune components (Fig. 3b). Ingenuity Pathway Analysis (IPA) suggested that functions related to inflammatory responses, cellular movement and immune cell trafficking were activated in thigh non-lesional AD sites in

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comparison to healthy control samples (Fig. 3c). In contrast, in non-lesional AD sites in upper back, small-molecule biochemistry and lipid metabolism were strongly down-regulated compared to control samples (Fig 3d).

Lesional AD skin is characterized by increased Th2-type immune responses regardless of the anatomical location

The skin transcriptional profiles of lesional and non-lesional sites of AD patients were also compared. We found 709 DEGs (Table E1) between thigh lesional and non-lesional samples, whereas 328 genes (Table E3) were found to differ in expression between back lesional and non-lesional samples (Fig E7). Functional characterization of the differentially expressed genes using IPA revealed that many of the same pathways (e.g. *Th2 pathway*, *MIF regulation of innate immunity*, *Leukocyte extravasation signaling*) were activated in lesional sites in both anatomical regions. However, there were also important differences between the two different sites (Fig 4a, b). In posterior thigh, the *Th1 pathway* and *iCOS-iCOSL signaling in T helper cells* were among the most significantly activated pathways (Fig 4a). In the upper back, *LXR/RXR activation*, involved in the regulation of lipid metabolism and inflammation, was strongly suppressed in the lesional sites in comparison to non-lesional skin (Fig. 4b).

IPA analysis of cellular and molecular functions of DEGs between lesional and non-lesional AD samples also showed a high degree of similarity between thigh and back (Fig. 4c, d). In both sites, functions associated with *Cellular movement*, *Immune cell trafficking*, *Cell-to-cell signaling and interaction*, and *Hematological system function* were the most significantly enriched.

Transcriptional differences between thigh and back are defined by major variations in lipid metabolism

To understand the molecular basis behind the physiological differences between posterior thigh and upper back, we compared the gene expression across these sites for both AD patients and healthy controls. We found 117 genes, that were differentially expressed between thigh and upper back in all three clinical conditions (Table E6), ie. non-lesional and lesional AD and healthy controls. (Fig. 5a). Functions such as long-chain fatty acid metabolism and unsaturated fatty acid biosynthesis were highly enriched in upper back samples compared to posterior thigh, regardless

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of the clinical condition (Fig. 5b). Furthermore, the metabolism of linoleic, alpha-linolenic and arachidonic acid was also induced in upper back samples.

Association between *S. aureus* abundance and disease severity is dependent on the skin site

As several previous studies have linked *S. aureus* abundance in lesional and non-lesional skin to AD severity [14, 16, 17, 41], we examined whether this association was present in the two different skin sites. In our dataset, the abundance of *S. aureus* in both thigh lesional and non-lesional samples correlated positively with the objective SCORAD (as a measure of global AD severity), whereas no such correlation was found in either sample type in upper back samples (Fig. 6a). Similar results were obtained when assessing the correlation between *S. aureus* and sample specific local severity measures (Fig. E8).

A closer inspection of the association between *S. aureus* and objective SCORAD levels revealed that severe lesions (objective SCORAD > 40) in the thigh region are more often densely colonized by *S. aureus*, as opposed to severe lesions in the upper back region. In Fig. 6b, thigh and back lesional samples were partitioned into three groups based on the relative abundance of *S. aureus*: samples with 1 % or less *S. aureus* were labelled 'absent', samples with 80 % or more *S. aureus* were labelled 'high', and the samples in between were labelled 'mid'.

The abundance of *S. aureus* in posterior thigh associates with keratinization and circadian rhythm regulating genes

To investigate links between *S. aureus* colonization and transcriptional profiles in lesional skin samples, we compared gene expression profiles between thigh lesional samples which were abundantly colonized by S. *aureus* (referred as *S. aureus* 'high' samples), and those lacking *S. aureus* (referred as *S. aureus* 'absent' samples). This resulted in the identification of 99 DEGs (Table E5), which clearly separated the samples into two categories based on hierarchical clustering analyses (Fig. 7a). Functional enrichment analyses revealed overrepresentations of biological processes such as keratinization and epidermal cell differentiation, as well as circadian regulation of gene expression (Fig. 7b). IPA analysis further identified *Circadian rhythm signaling* as the most significantly enriched pathway in this set of genes (Fig 7c). Inference of networks based on the level of co-expression, importance and centrality of the genes, supported these

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findings further, revealing three clusters, enriched for keratinization, circadian regulation of gene expression, and cell division, respectively (Fig. E9).

We looked further into the specific genes regulating circadian rhythms, and observed that in lesional thigh samples, four genes (*BHLHE41*, *CIART*, *NR1D1*, *PER1*) were negatively correlated with objective SCORAD, while *NOCT* was positively correlated (Fig. 7d). Moreover, genes related to keratinocyte differentiation were negatively correlated with objective SCORAD (Fig. E10). Using the same approach comparing lesional and non-lesional samples in the upper back region, did not reveal any significant associations between the abundance of *S. aureus* and severity. To conclude, our results show links between disease severity, the expression of disease relevant genes, and the abundance of *S. aureus*, but in a site-specific manner.

Modular immune responses in lesional skin of the posterior thigh are associated with *S. aureus* and *S. epidermidis* abundancies

The relative abundances of *S. aureus* and *S. epidermidis* were inversely correlated ($R = -0.52$; $p<0.001$) in lesional skin in the posterior thigh area. To assess the transcriptional impact of these microbes and their relation on lesional skin, we employed leukocyte deconvolution as well as weighted gene co-expression analysis (WGCNA) to detect associated modules within this specific skin site. First, we sought to identify major leukocyte changes within the affected skin using a transcriptome-wide leukocyte deconvolution algorithm. Lesional skin exhibited major changes in leukocyte composition, with significantly higher proportions of dendritic cells (resting & activated) and macrophages as well as significantly lower resting mast cells and activated natural killer cells compared to non-lesional skin and healthy controls (Fig. E11). Thus, the microbial relation and estimated relative cell fractions were further used as traits in the WGCNA. Hence, we identified 2 modules associated with the relation of relative abundance of *S. aureus* and *S. epidermidis*; 1 positively (tan module, further referred as *S. aureus* module (SAMod)) and 1 negatively (brown module, further referred as *S. epidermidis* module (SEMod)) correlating module (Figure 8a). The SAMod displayed enrichment for extracellular matrix organization, complement activation, angiogenesis and leukocyte migration. Additionally, KEGG pathway enrichment identified *S. aureus* infection and complement & coagulation cascades as highly enriched terms. However, this module was not highly correlating ($p<0.001$) with any immune cell type. In contrast, SEMod exhibited GO BP enrichment for fat cell differentiation and epidermis

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development. Intriguingly, this module was highly associated with the estimated mast cell fractions (Figure 8 b/c).

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Discussion

Our study highlights the importance of the ecological skin niches in defining microbe-host interaction, and this needs to be taken into account when studying AD etiology and progression. By analyzing a large cohort of AD patients and healthy controls and focusing on two anatomical locations; the upper back and posterior thigh, we were able to show that although AD selects for similar microbes across anatomical locations – an 'AD-like microbiome', microbial dynamics in AD differ significantly between the different sites. Moreover, we show that the abundance of *S. aureus* is associated with disease severity only in the posterior thigh region, and not in the upper back region. Transcriptome analysis revealed distinct disease-related processes depending on the anatomical location, with keratinization playing a major role in posterior thigh, and lipid metabolism dominating in the back, suggesting possible links between the skin microenvironment and microbial dynamics. Thus, our results emphasize the concept of ecological niches that define microbe-host interaction in AD: the host transcriptome defines the ecological niche (sebaceous gland-rich versus – poor, lipid-production) and the niche defines the existence and coexistence of microbes.

Reduced microbial diversity is usually associated with AD, but we observed such a decrease only in posterior thigh, and similar discrepancies exist in the literature[14, 42, 43]. Our results suggest the existence of an *'AD-like microbiome',* consistent with Baurecht 2018[29]: the disease exhibits an environment that is enriched in a particular *Staphylococcus-rich* microbial community in the different skin sites independent of the influence of local physiology. The AD-like microbiome model helps to explain why alpha diversity is not always decreased; the less diverse healthy sites like 'upper back' can transition to an 'AD-like' state without a visible change in their alpha diversity metrics. Upper back lesions showed somewhat higher diversity than thigh lesions in these patients. A possible explanation for this could be that the thigh lesions were more severe on average. We also observed that the effect of the disease for selecting microbes is particularly strong in lesions, but it can also be observed in non-lesional skin.

The availability of transcriptome data from the very same skin sites that had been sampled for the microbiota, allowed us to examine host processes that could explain differences in the skin physiology of the different sites and the disease conditions. Lipid metabolism constituted the main difference between thigh and back in the transcriptome analysis, and perturbations to lipid

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metabolism genes were observed in both skin sites between healthy controls and non-lesional skin. We speculate that this may have major implications on microbial colonization in AD skin, and consequently on the disease manifestations. Two studies have suggested a connection between epidermal lipid composition and bacterial community composition [44]. Here, linoleic, alpha-linolenic and arachidonic acid metabolism were shown to be stimulated in the back and these molecules have been shown to have antimicrobial activity, and may selectively inhibit certain groups of bacteria such as *Staphylococcus*[45]. It has also been shown that certain strains of *S. aureus* have evolved intrinsic defense mechanisms to cope with these fatty acids[46-48].

Keratinocyte differentiation, which we found to be dysregulated in AD, contributes to skin barrier function[49]. In our data, keratinocyte differentiation and related biological processes showed differences between non-lesional skin and healthy control skin in thigh samples, and between thigh and back in AD. Furthermore, inflammatory responses were activated in non-lesional thigh skin compared to healthy control skin, which was not seen in the upper back samples. These results indicate that while there are differences between non-lesional and healthy control skin in both of the skin sites, non-lesional thigh skin shows signs of subclinical inflammation and an increased susceptibility to lesions, as reflected in the clinical predilection. Previous transcriptome studies have identified alterations in the expression of epidermal cornification genes on AD lesional and non-lesional skin but did not report which skin sites were sampled[20, 21].

In lesional skin, genes associated with inflammation were differentially expressed in skin of both body sites when compared to non-lesional skin of AD patients. Well-described type 2 inflammation pathway genes such as *IL4R*, C-C motif chemokine receptor type 4 (*CCR4*), and C-C motif chemokine 22 (*CCL22*) were upregulated in both lesional thigh and back in comparison with non-lesional skin. These genes were not differentially expressed in non-lesional AD samples compared to healthy control samples. Activation of the Th2 pathway has been previously reported in acute AD lesions[23], and more recently in a subgroup of AD patients characterized as type 2-high endotype, exhibiting a more severe form of the disease[26]. While AD is currently recognized as a multifactorial, heterogenous disease with different immune subsets, Th2-responses do play an important role in both acute lesions and chronic disease states[50].

Despite the reduction in inter-skin site variability driven by the disease, the detected differences in transcriptomes across the sites in both non-lesional and lesional sites could help explain the

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observed skin-site specific microbial dynamics in AD, which have been reported also for other skin diseases like psoriasis[51]. In particular, we see an increase of *S. aureus* abundance from non-lesional skin to lesional skin in thigh, which is not observed in upper back. Additionally, we show that the previously described positive association between *S. aureus* and disease severity (measured by SCORAD)[52] is observed only in posterior thigh, but not in the upper back region. We obtained comparable results when considering a lesion-specific measure of severity. Similar results were obtained by Kong et al. in antecubital and popliteal creases (moist), as well as volar forearm (dry), but not in nasal sites (moist and *S. aureus* rich)[14]. This raises questions regarding the presence and role of different *S. aureus* strains in AD, such as whether specific *S. aureus* strains actively contribute to an increase in severity, and whether certain strains preferentially colonize specific locations. These results stress the need to further explore the role of skin site variability as a crucial part of the experimental design in studies of AD and other skin diseases.

In our study, thigh lesional samples with high *S. aureus* levels had a distinct skin transcriptome profile compared to samples with low *S. aureus*. In particular, genes related to keratinization and circadian rhythm were differentially expressed between the sample groups. Keratinization relates to disruptions in the skin barrier, as noted above, whereas circadian rhythm influences cutaneous blood flow as well as epidermal barrier function. While it has been proposed that circadian rhythm plays a role in AD pathogenesis, the mechanistic evidence for this is still scarce[53], especially with regards to the relevance of circadian gene expression in the skin. However, there are studies linking circadian genes to psoriasis-like skin inflammation[44, 54]. Furthermore, pruritus and scratching, which are integral parts of the AD, could lead to sleep disruption and in turn may also influence genes which are regulated by circadian rhythm [55]. Further research is required to determine the significance of circadian rhythm genes in the pathogenesis of AD.

The relative abundance of *S. aureus* and *S. epidermidis* displayed an inverse correlation in lesional skin of the posterior thigh. Relative abundance of *S. aureus*, but not that of *S. epidermidis*, was also positively correlated with disease severity. In line with this, patients with severe AD have been reported to be colonized more dominantly by *S. aureus* strains whereas patients with milder disease demonstrate more *S. epidermidis* in skin flares[16]. To explore possible interaction between *S. aureus* and *S. epidermidis*, skin cell types and gene expression profiles on lesional thigh skin, we employed leukocyte deconvolution as well as WGCNA co-expression analysis. We identified two co-expression modules correlating positively with the *S. aureus* and *S. epidermidis*

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abundances. The *S. aureus* associated module displayed enrichment of *extracellular matrix organization* and *leukocyte migration*, but this module could not be assigned to any specific immune cell type. On the contrary, the *S. epidermidis* associated expression module exhibited enrichment of *epidermis development* and was highly associated with estimated mast cell proportions in the skin. Considering the inverse relationship between *S. aureus* and *S. epidermidis* abundances in lesional skin sites, these results suggest that *S. epidermidis* might play a role in mast cell function which in turn may have also an impact on milder disease severity compared to *S. aureus* dominated skin flares.

We have utilized in this study a large patient cohort that includes samples from body sites representing two different ecological microenvironments: dry and sebaceous. This dataset allowed us to examine the influence of epidermal surface lipids on microbial colonization and gene expression on the skin, and identify features that are common for the disease regardless of site. The present study also included a larger number of samples than most previous studies focusing on the effect of skin microbiota composition and host transcriptome on AD pathophysiology. Further studies with shotgun metagenomics are warranted to further elucidate the functional role of microbes in the disease.

In conclusion, these findings suggest that in AD, the skin microbiota interacts through local, host driven mechanisms, forming different ecological niches and thereby distinct microbe-host interactions, which should be taken into account when considering treatment options. Moreover, we propose that increased lipid metabolism in sebaceous areas may be a contributing factor to decreased *S. aureus* colonization through the production of antimicrobial lipids.

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Author contributions

Conceptualization: HA, BA, NO, MB-S; Resources: JB, BH, AL, AR; Methodology: JK, LW, BA, VS, MB-S, NO, NF; Formal Analysis: HA, NO, MB-S, LW, BA; Visualization, HA, NO, MB-S, LW; Writing – Original Draft: HA, BA, NO, MB-S; Writing – Review & Editing: NO, MB-S, NF, HeA, LW, PO, ST, DG, FL-S, VS, JMS, JK, FON, JB, AR, AL, BH, BA, HA; Equal contribution: NO, MB-S; Project Administration: HA

Conflict of interest statement

Dr. Ottman reports grants from BIOMAP IMI2 821511, during the conduct of the study; Dr. Barrientos-Somarribas has nothing to disclose; Dr. Fyhrquist has nothing to disclose; Dr. Alexander has nothing to disclose; Dr. Wisgrill has nothing to disclose; Dr. Olah has nothing to disclose; Dr. Tsoka has nothing to disclose; Dr. Greco has nothing to disclose; Dr. Levi-Schaffer

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has nothing to disclose; Dr. Soumelis has nothing to disclose; Dr. Schröder has nothing to disclose; Dr. Kere has nothing to disclose; Dr. Nestle reports other from Sanofi, outside the submitted work; Dr. Barker has nothing to disclose; Dr. Ranki reports grants from EU FP7/2007-2013, during the conduct of the study; Dr. Lauerma reports grants from Orion Corporation, outside the submitted work; Dr. Homey reports grants from EU-MAARS, grants from EU-BIOMAP, grants from DFG-FOR2690-HO 2092/7-1, during the conduct of the study; grants and personal fees from Galderma, personal fees from Abbvie, personal fees from Janssen, personal fees from Sanofi/Regeneron, personal fees from Leo Pharmaceuticals, outside the submitted work; Dr. Andersson has nothing to disclose; Dr. Alenius reports grants from BIOMAP IMI2 821511, during the conduct of the study.

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Figure legends

Figure 1. Microbial composition of the samples. a) Phyla-level barplot, highlighting the 4 most prevalent phyla: Firmicutes, Bacteroidetes, Actinobacteria and Proteobacteria. b) OTU-level barplot of relative abundances, highlighting *S. aureus* and *Staphylococcus spp.* which were differentially abundant between groups by ANCOM analysis. *C. acnes* and *S. epidermidis* are included for reference.

Figure 2. Alpha and beta diversity of skin samples. a) Shannon diversity index of lesional, nonlesional and healthy control samples divided by skin site. Significant differences between groups were found in thigh (Kruskal-Wallis, $p<0.001$) but not in upper back ($p > 0.05$). b) UMAP-based ordination of the samples using Bray-Curtis dissimilarity. Thigh and upper back samples were ordinated together; the visualization was split into two identical axes to highlight the site=specific dynamics. Other visualizations of the same ordination can be seen in Figure E5.

Figure 3. Gene ontology-based analysis of functional enrichment in a) thigh non-lesional (n=41) vs control sites (n=99), and b) back non-lesional (n=36) vs control sites (n=13). Downstream Effects Analysis in IPA was used to visualize, via color-coded heatmaps, putative biological and disease trends in c) thigh non-lesional vs control sites, and d) back non-lesional vs control sites. The color intensity of the squares in the heatmaps reflects the strength of the absolute z-score for predictions (orange = positive, blue = negative). The size of the squares reflects the B-H adjusted p-values.

Figure 4. Ingenuity canonic pathway analysis (IPA) of differentially expressed genes between a) lesional (n=43) and non lesional (n=41) samples in thigh and b) lesional (n=37) and non lesional (n=36) samples in back. Top molecular and cellular functions (IPA) between c) thigh lesional and non-lesional samples, and d) back lesional and non-lesional samples.

Figure 5. Analysis of differentially expressed genes in thigh vs back contrast. a) Venn diagram summarizing the differentially expressed genes between thigh and upper back on the different sample types: lesional AD, non lesional AD and healthy controls. b) Gene Ontology enrichment analysis of the 117 genes differentially expressed in all three conditions.

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Figure 6. S. aureus – objective SCORAD association. a) Measure of AD severity (objective SCORAD as a measure of global AD severity) correlates (Spearman) with *S. aureus* relative abundance in lesional (n=45; rho=0.57) and nonlesional (n=45; rho=0.53) skin from the thigh but the association is not observed in the back (n=40). b) Dividing samples high (> 80%) mid (1% to 80%) and absent (< 1%) *S. aureus* abundance, reveals that individuals with severe AD are more likely to have *S. aureus*-dominated thigh lesions with respect to moderate AD patients, while no difference in *S. aureus* colonization trends for lesions is observed for upper back between severe and moderate patients.

Figure 7. a) Heatmap of DEGs in *S. aureus* 'high' (n=19) vs 'absent' (n=12) contrast in lesional thigh samples. b) GO analysis of functional enrichment of DEGs in *S. aureus* 'high' vs 'absent' contrast in biological processes. c) Enrichment of canonical pathways in IPA analysis of DEGs in *S. aureus* 'high' vs 'absent' contrast. d) Correlation of circadian regulation associated genes with disease severity SCORAD (n=43).

Figure 8. Co-expression networks identify response modules of posterior thigh lesional skin associated with relative abundances of *S. aureus* and *S. epidermidis*. Weighted gene co-expression analysis (WGCNA) was used to determine modules associated with the relation of relative abundances of *S. aureus* and *S. epidermidis*. Furthermore, the leukocyte deconvolution algorithm Cibersort (CS) was applied on transcriptomics data to estimate the relative cell fractions within the affected skin to link modules towards cell fractions. Modules with a correlation coefficient > 0.5 and a p-value < 0.001 of the phenotypic trait "Relation SA vs. SE" were further analyzed. Two modules were associated with the relation of the relative abundance of *S. aureus* and *S. epidermidis*: 1 positively (referred as *S. aureus* module (SAMod)) and 1 negatively (referred as *S. epidermidis* module (SEMod)) correlating module a). SEMod was also positively associated to estimated mast cell fraction a). ClusterProfiler was used for GO biological processes b) and KEGG pathway c) enrichment.

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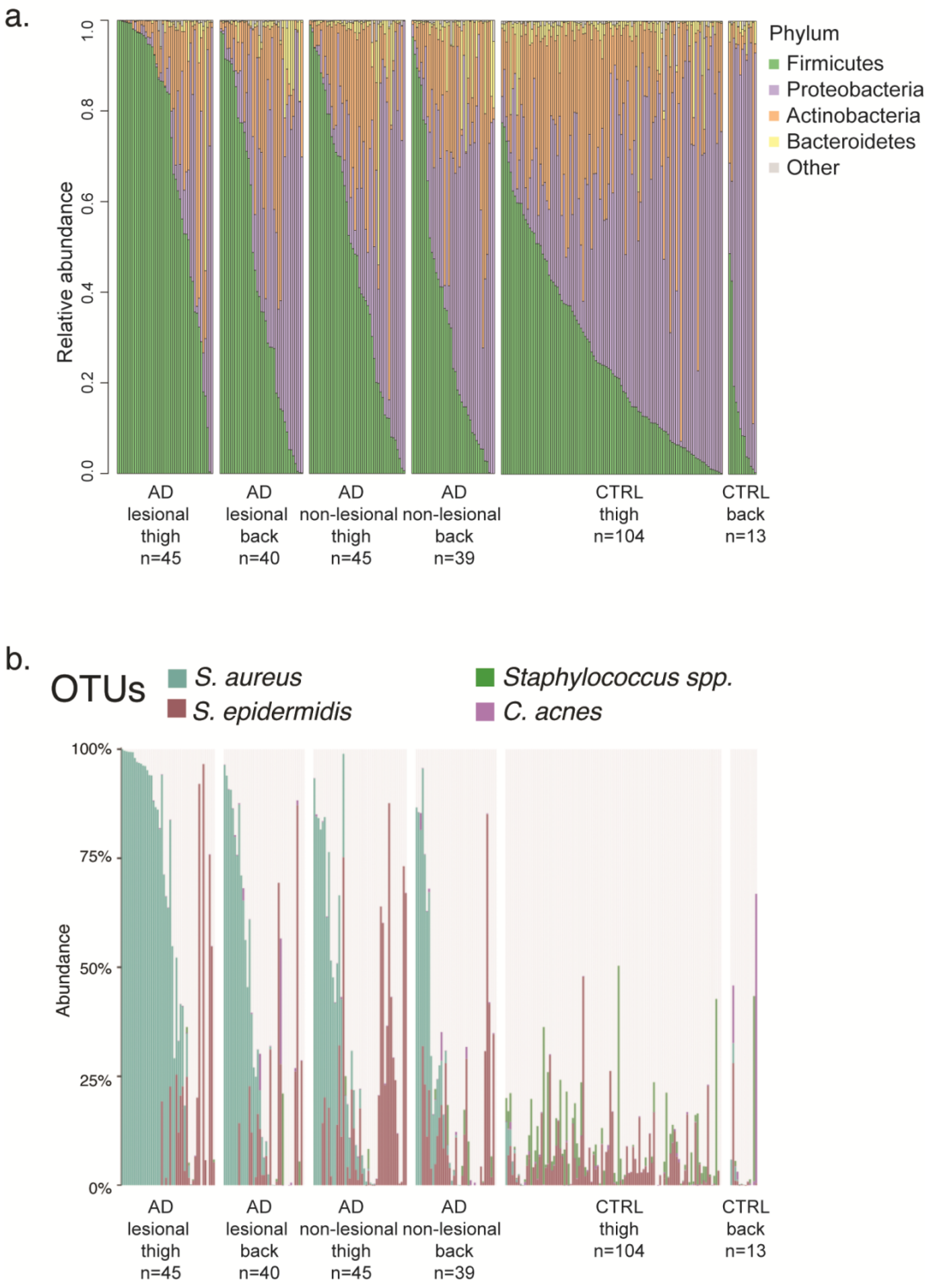


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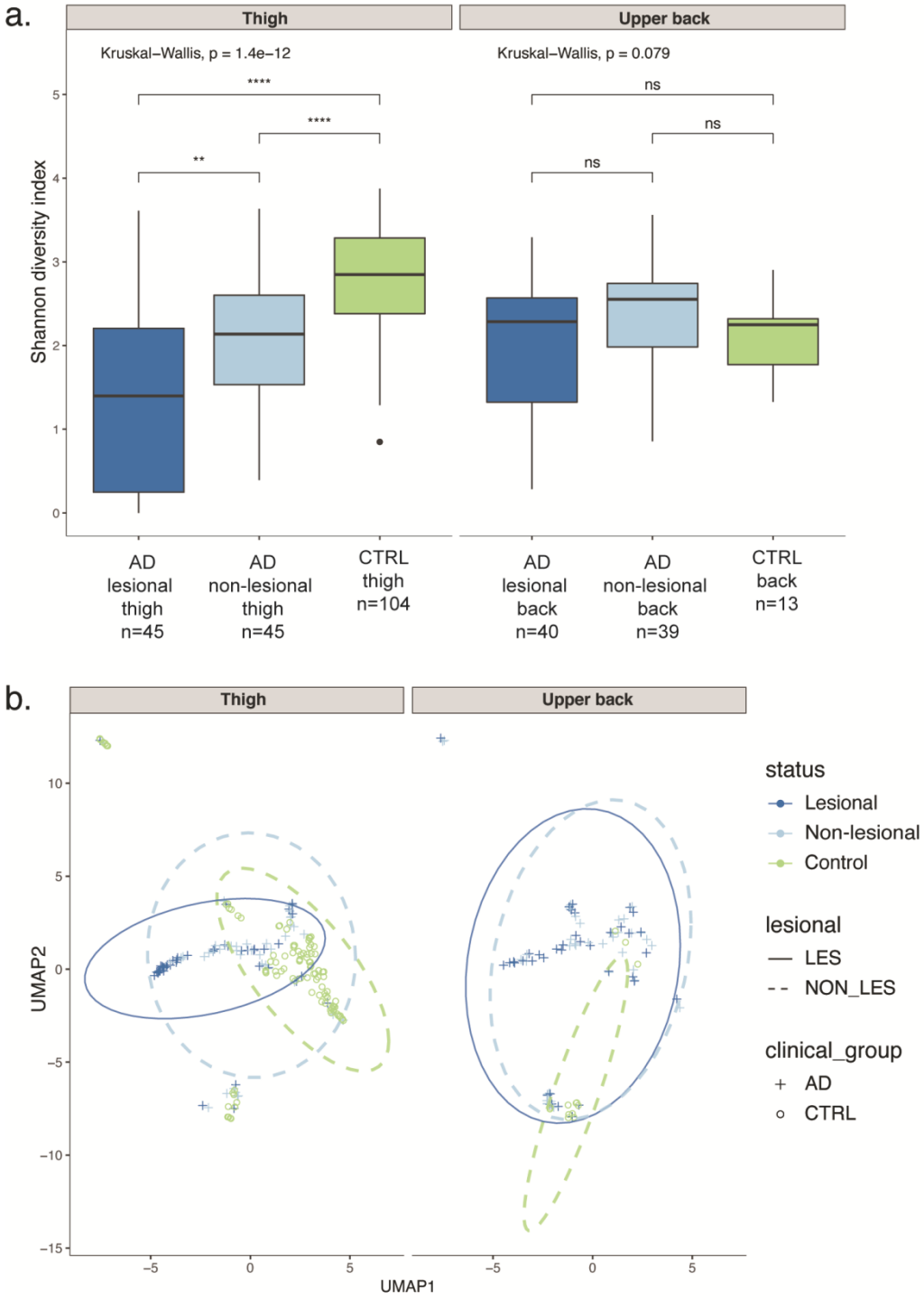


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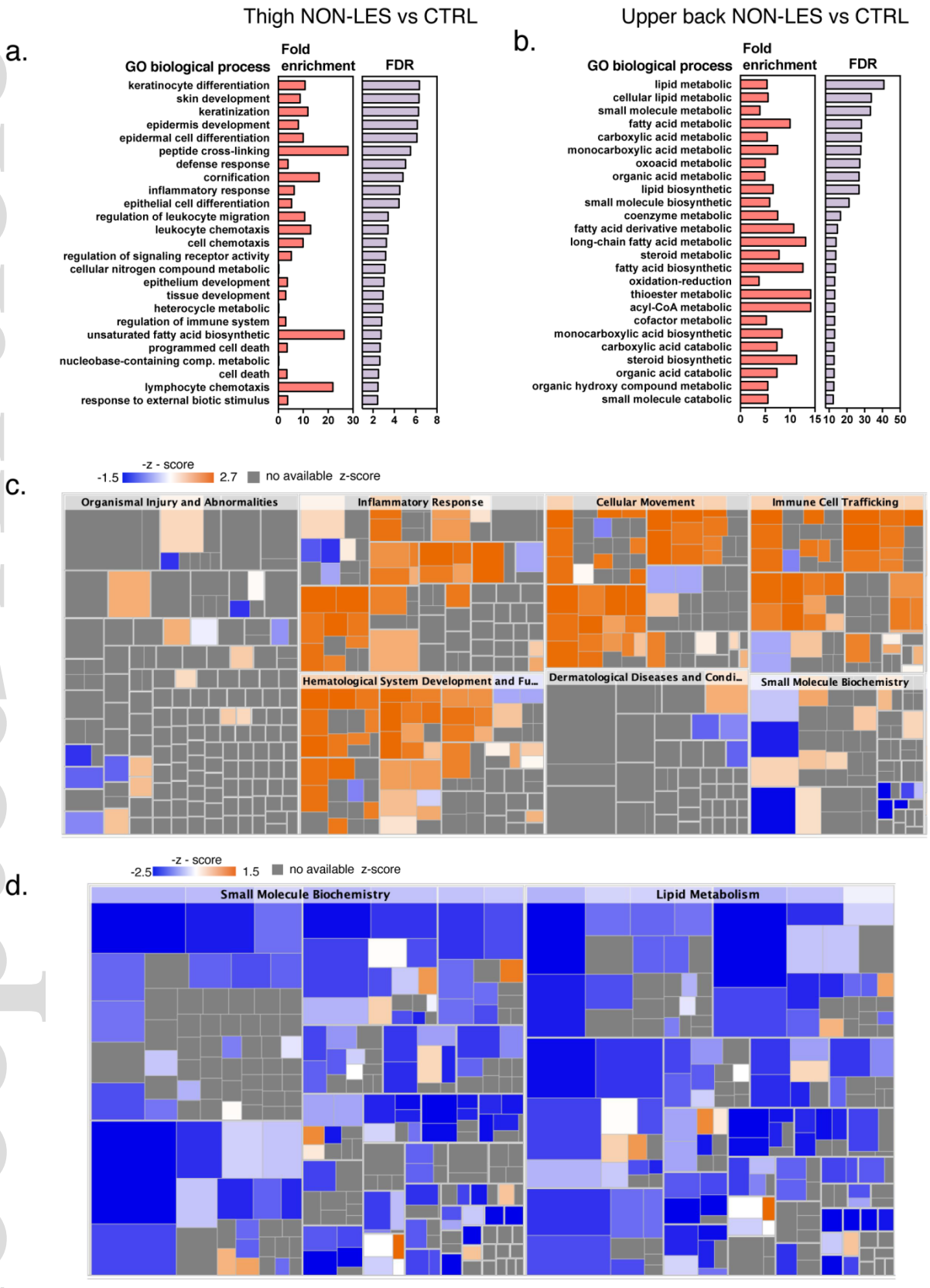


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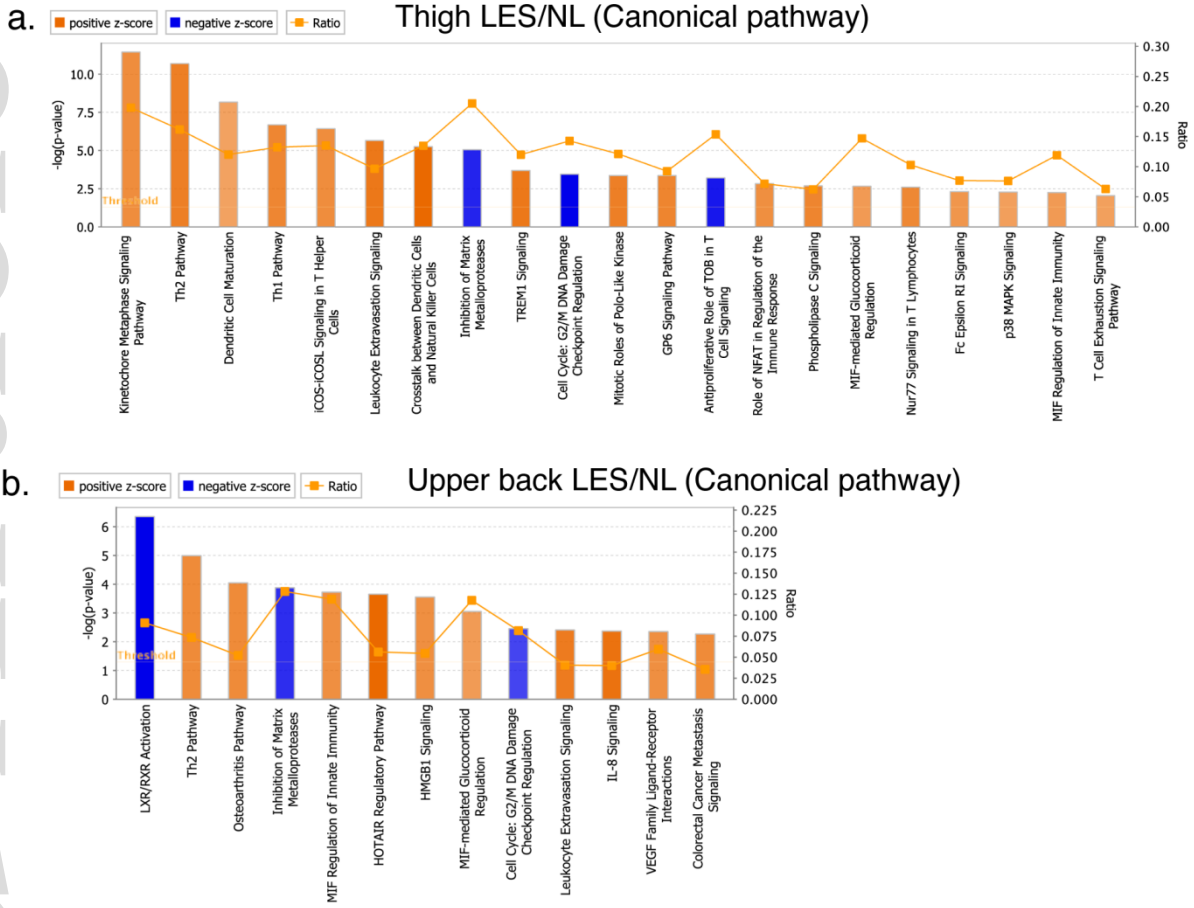
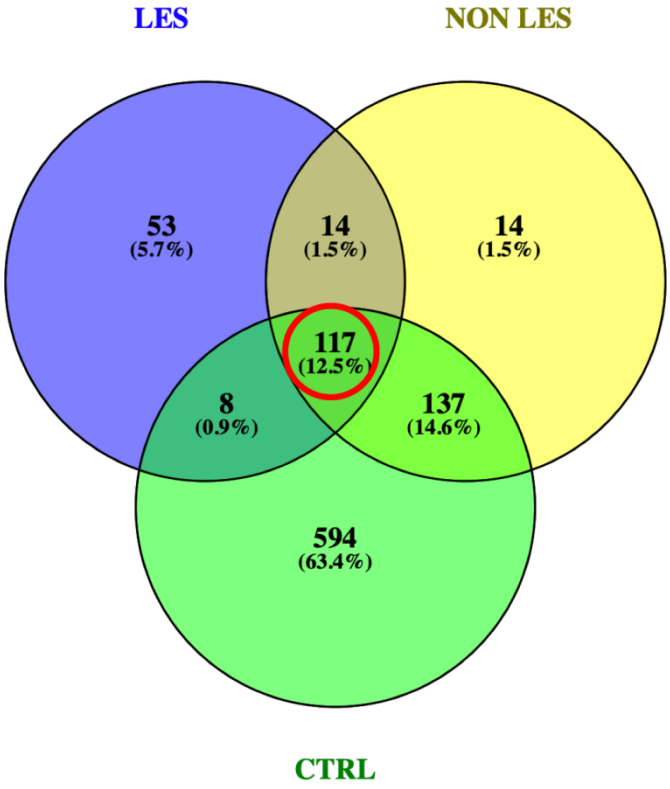


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a.



b.

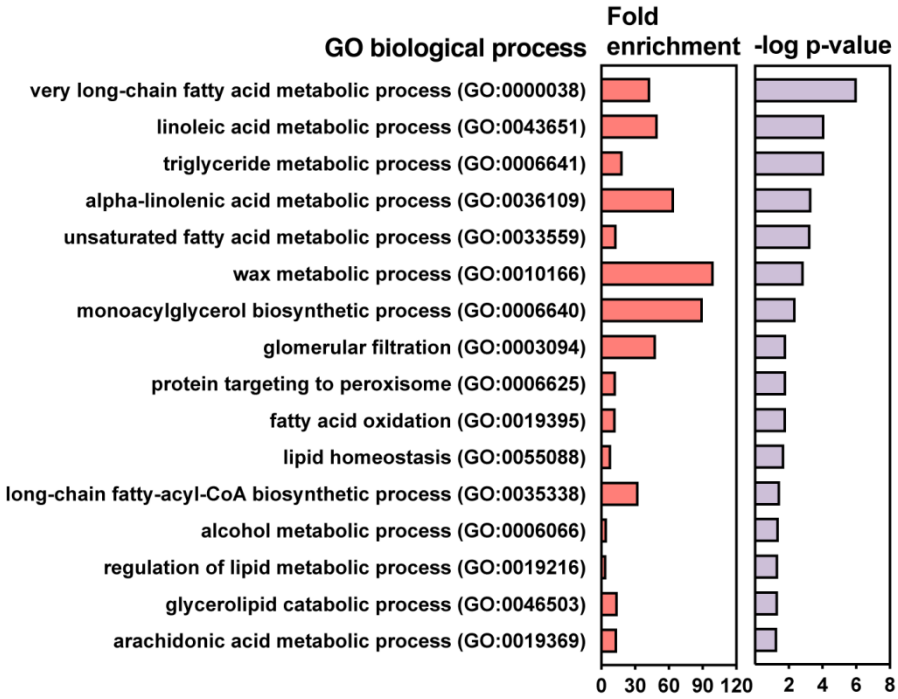


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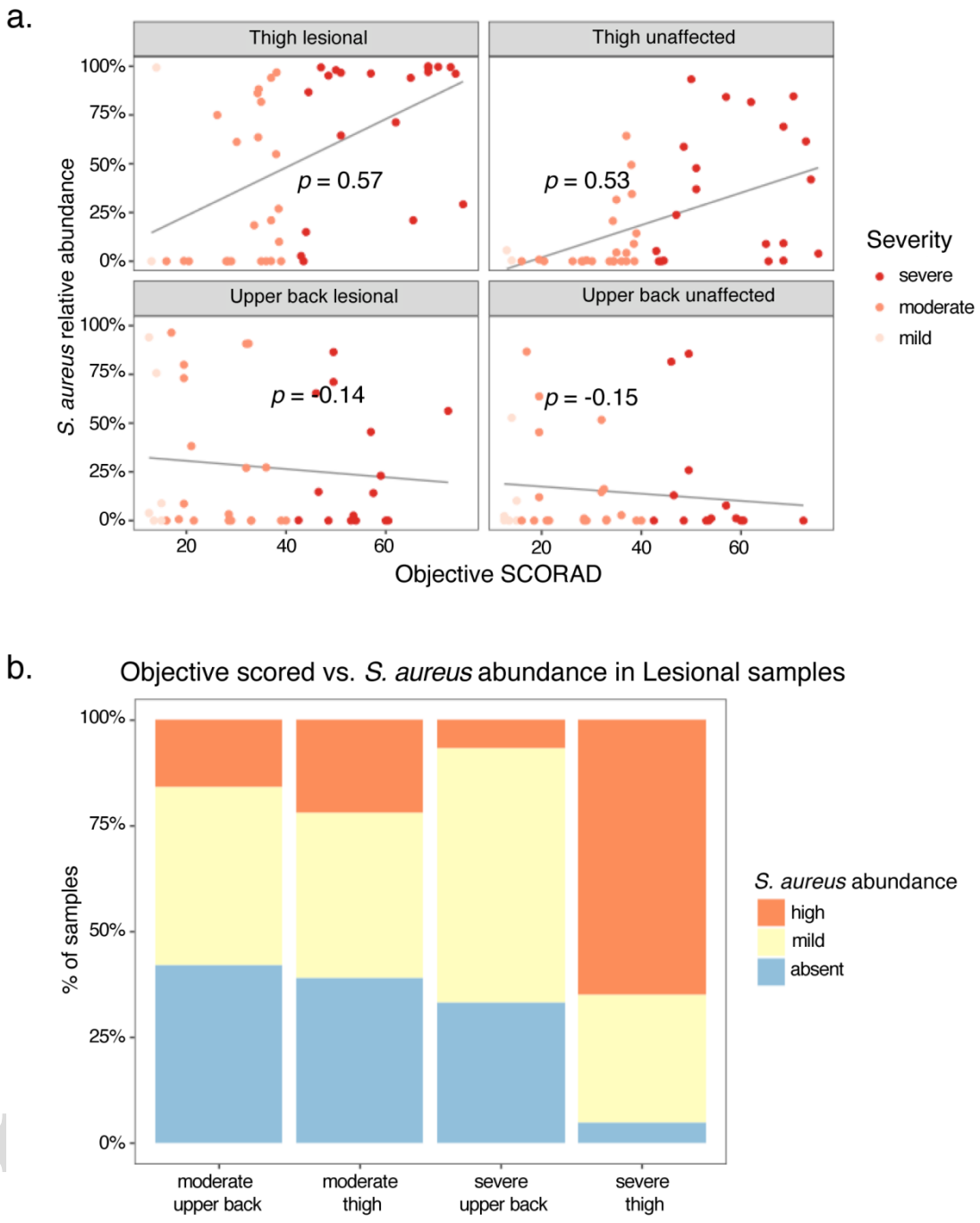


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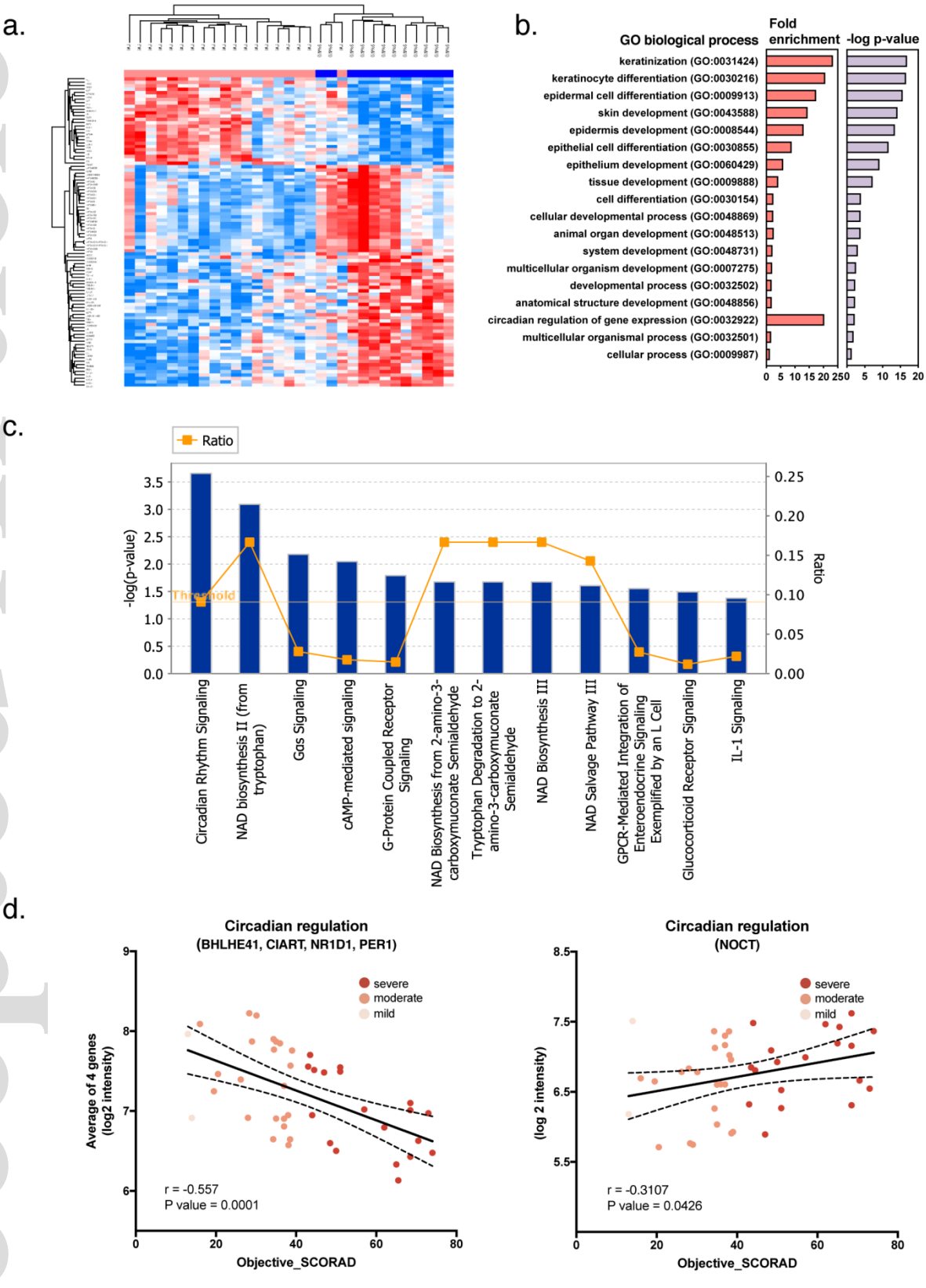


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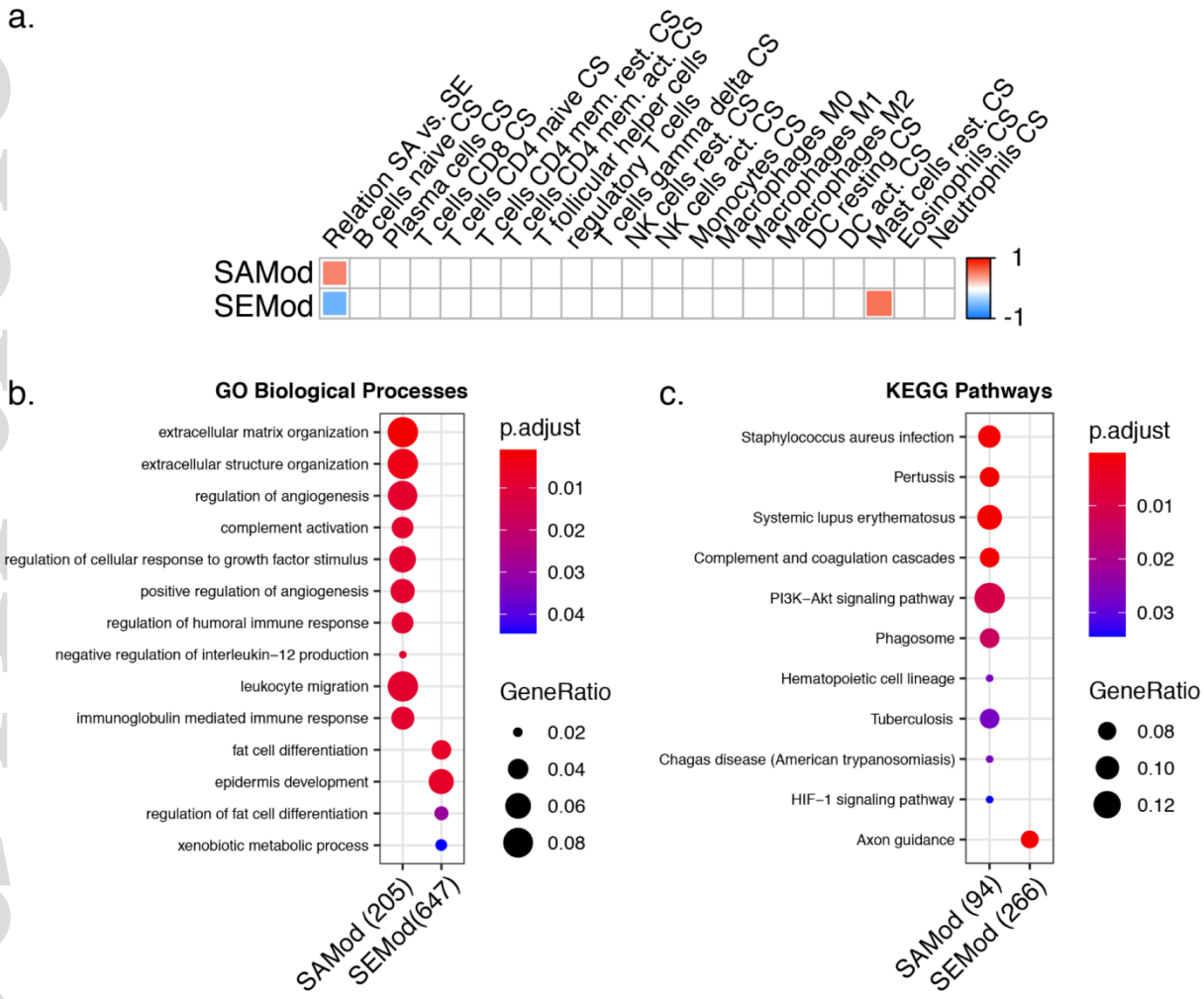
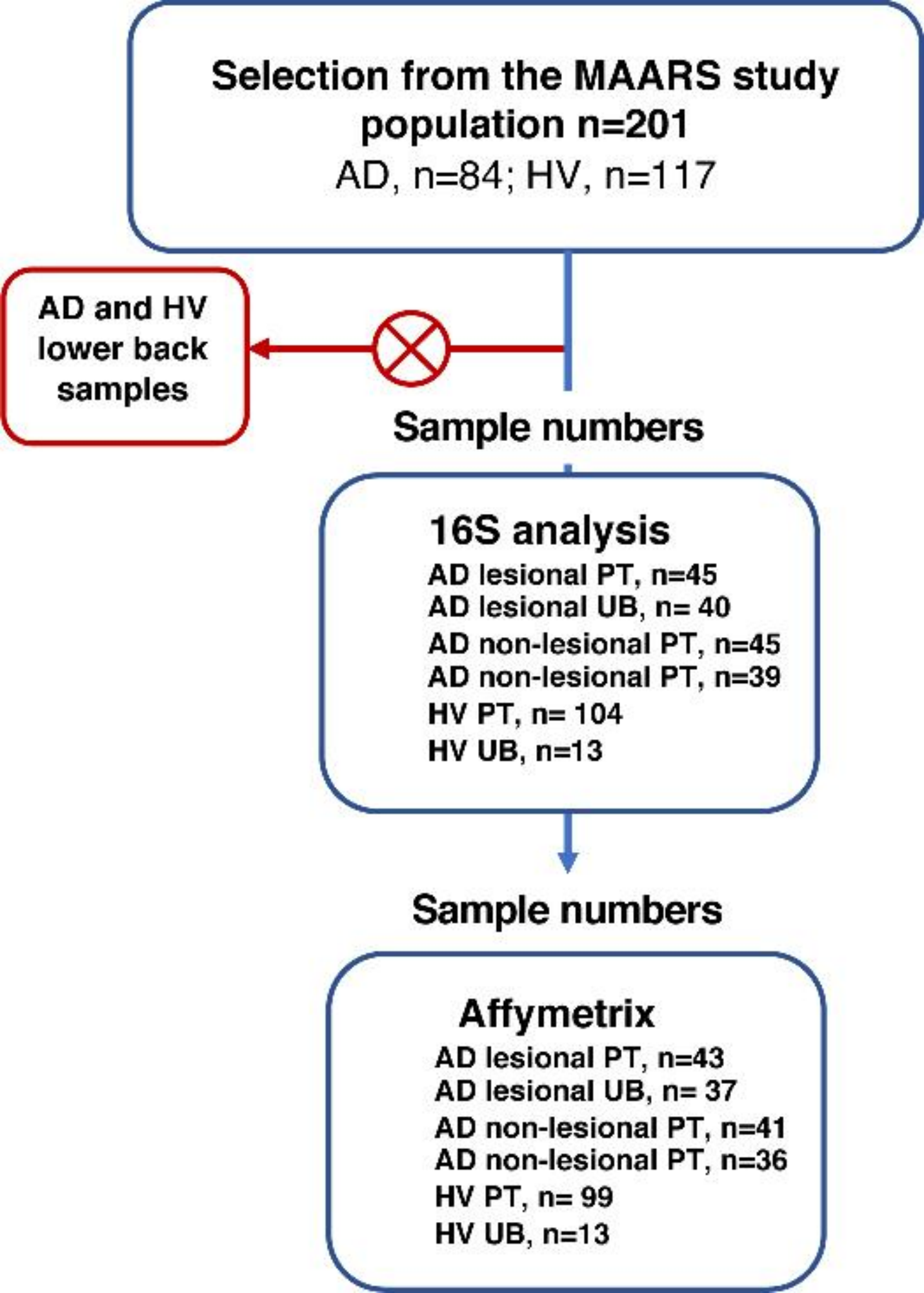
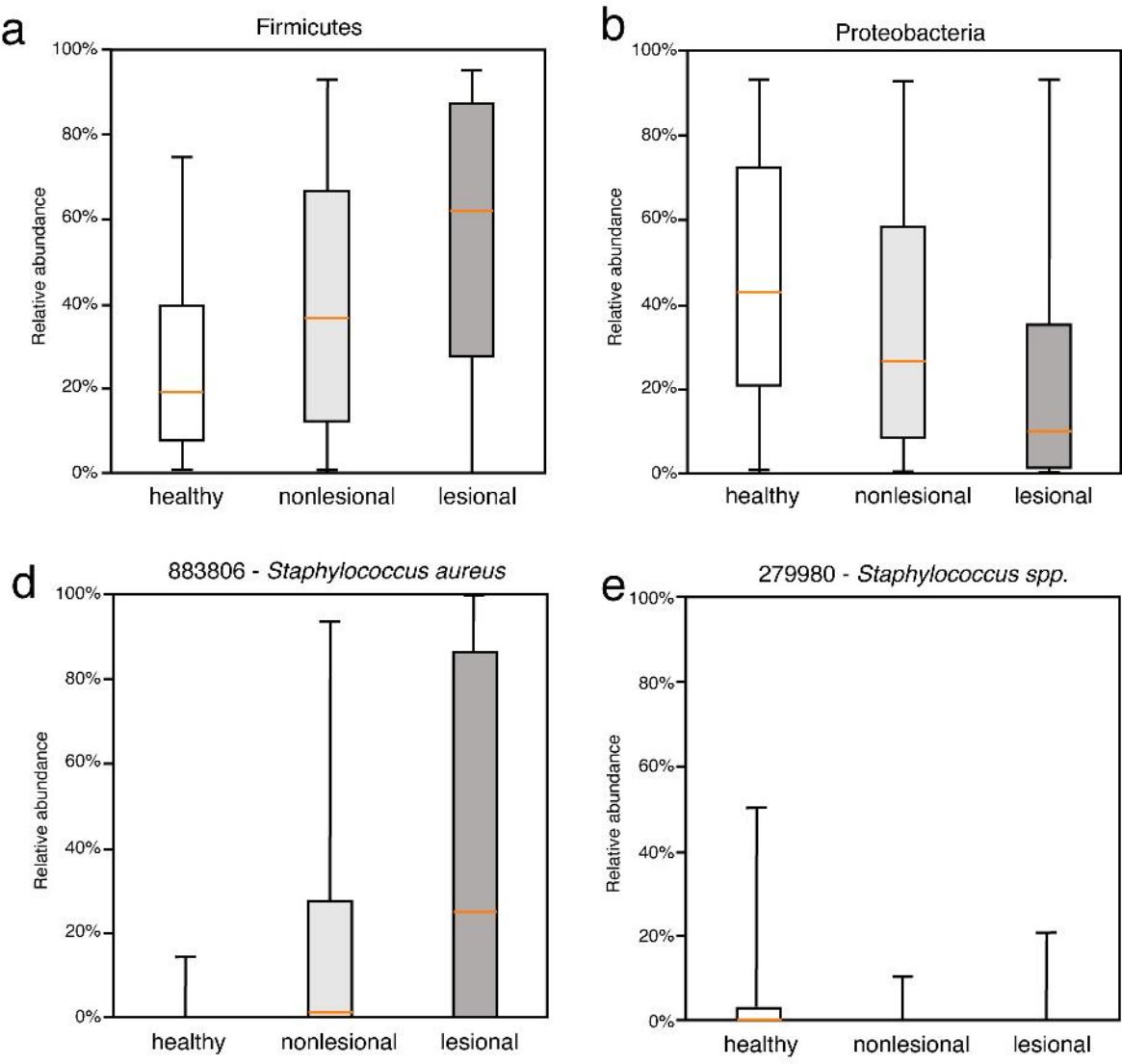
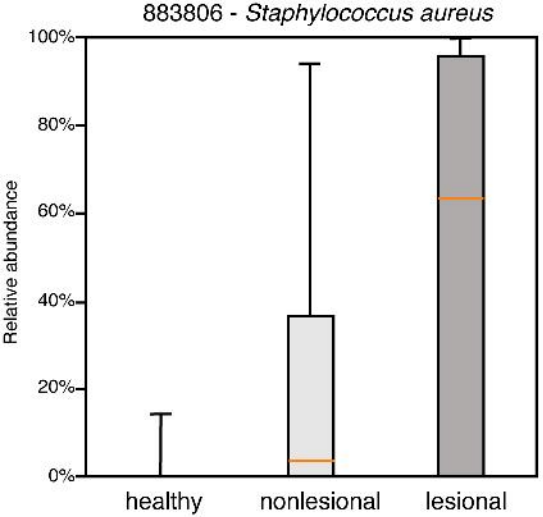


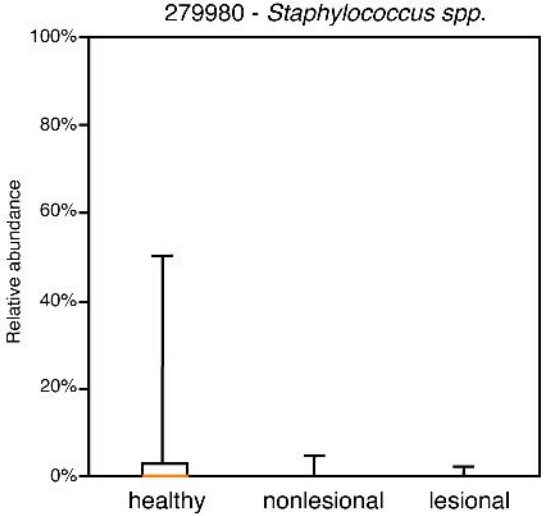
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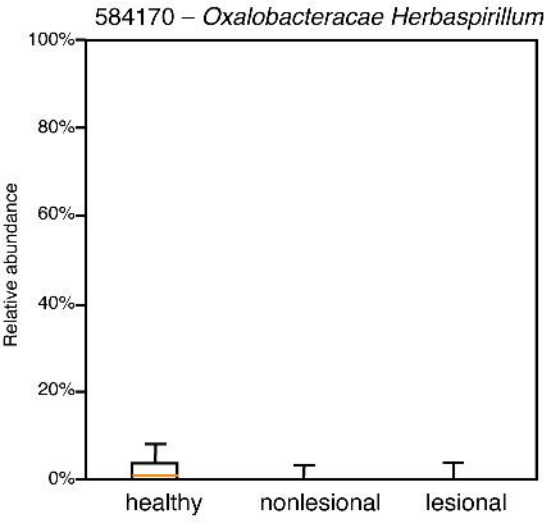
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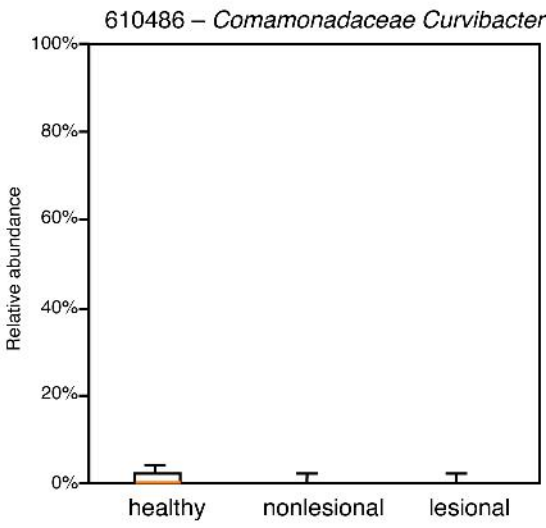

Selection from the MAARS study population n=201
AD, n=84; HV, n=117
AD and HV lower back samples
Sample numbers
16S analysis
AD lesional PT, n=45
AD lesional UB, n= 40
AD non-lesional PT, n=45
AD non-lesional PT, n=39
HV PT, n= 104
HV UB, n=13
Sample numbers
Affymetrix
AD lesional PT, n=43
AD lesional UB, n= 37
AD non-lesional PT, n=41
AD non-lesional PT, n=36
HV PT, n= 99
HV UB, n=13

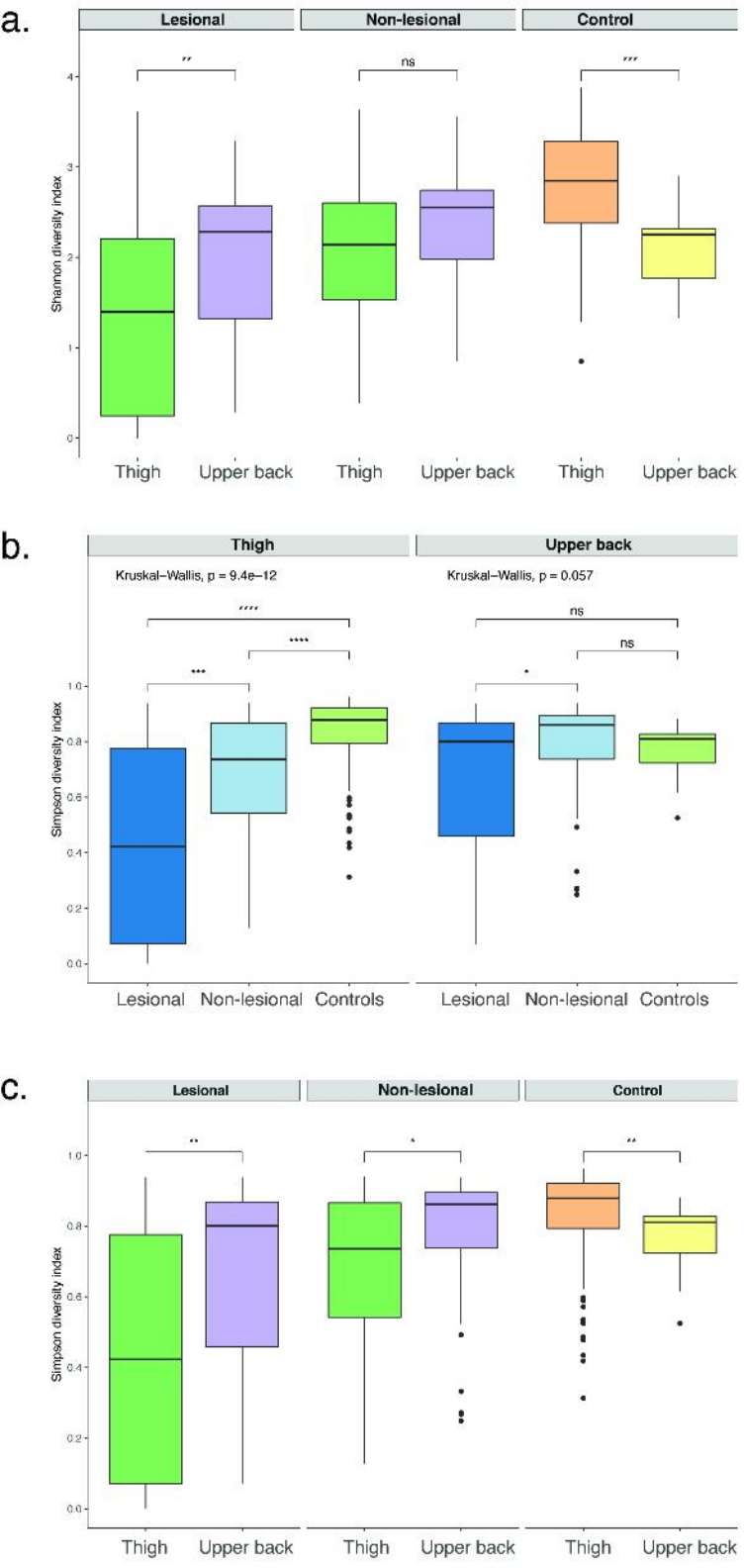

a
Firmicutes
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional
b
Proteobacteria
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional
d
883806 - Staphylococcus aureus
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional
e
279980 - Staphylococcus spp.
100%
80%
60%
40%
20%
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Relative abundance
healthy
nonlesional
lesional


883806 - Staphylococcus aureus
100%
80%
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40%
20%
0%
Relative abundance
healthy
nonlesional
lesional

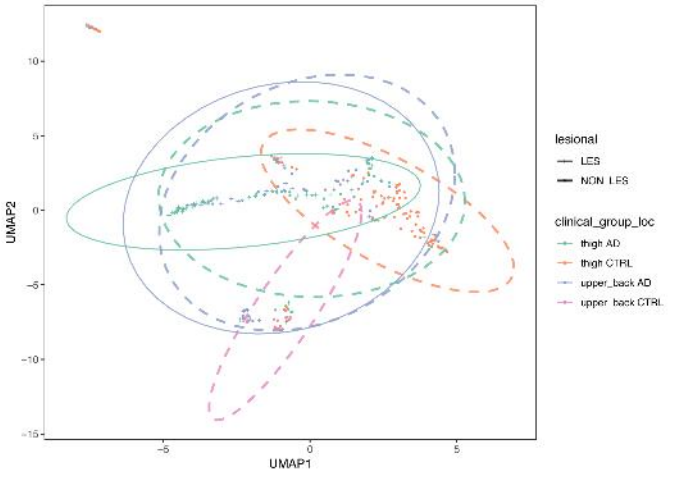

279980 - Staphylococcus spp.
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional


584170 – Oxalobacteraceae Herbaspirillum
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional

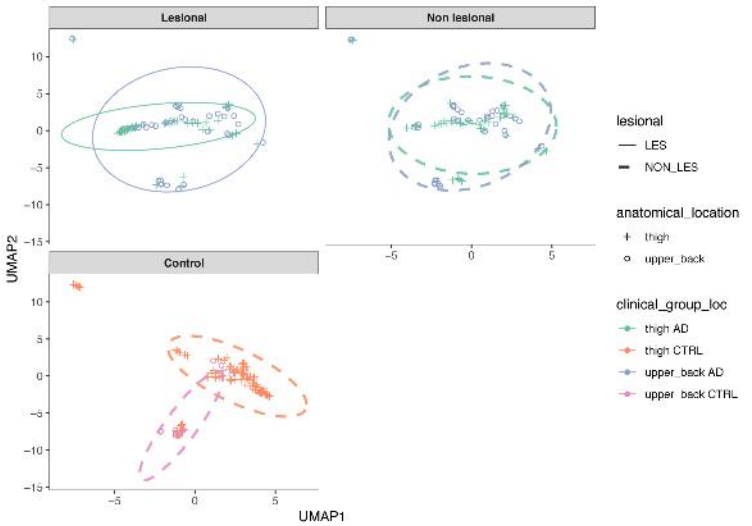

610486 – Comamonadaceae Curvibacter
100%
80%
60%
40%
20%
0%
Relative abundance
healthy
nonlesional
lesional


a.
Lesional
Non-lesional
Control
Shannon diversity index
ns
Thigh
Upper back
b.
Thigh
Upper back
Kruskal–Wallis, p = 9.4e−12
Kruskal–Wallis, p = 0.057
Simpson diversity index
Lesional
Non-lesional
Controls
c.
Lesional
Non-lesional
Control
Simpson diversity index
Thigh
Upper back

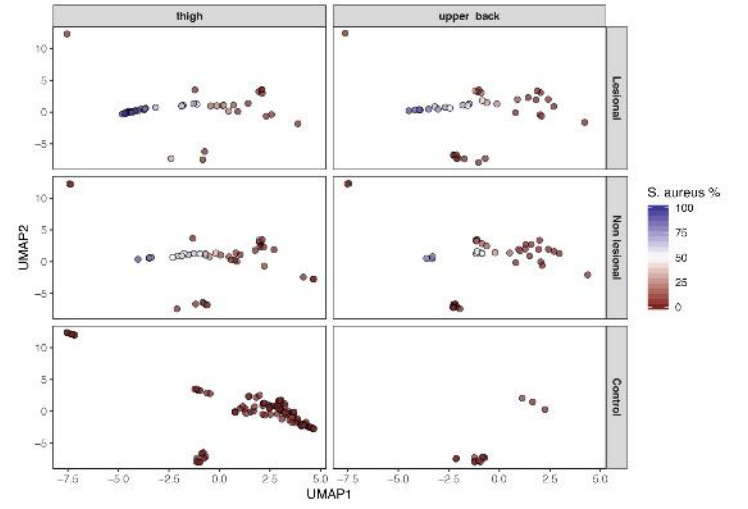
a.


UMAP2
UMAP1
lesional
LES
NON_LES
clinical_group_loc
thigh AD
thigh CTRL
upper_back AD
upper_back CTRL

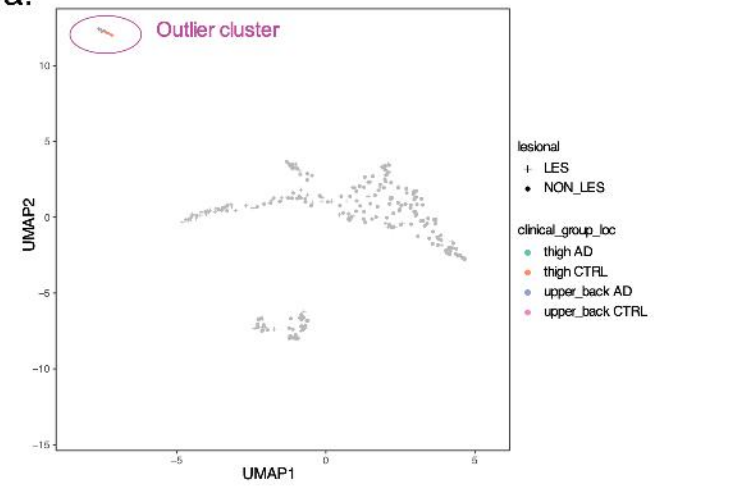
b.


Lesional
Non lesional
Control
UMAP2
UMAP1
lesional
LES
NON_LES
anatomical_location
thigh
upper_back
clinical_group_loc
thigh AD
thigh CTRL
upper_back AD
upper_back CTRL

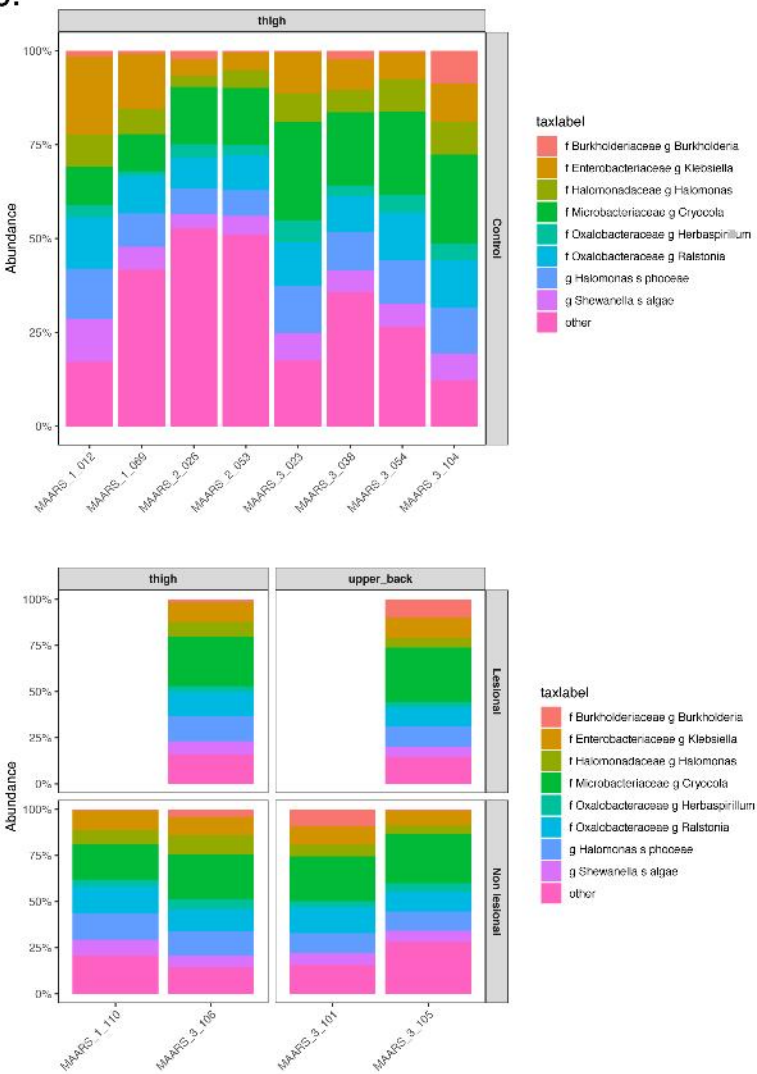
c.


thigh
upper_back
Lesional
Non lesional
Control
UMAP2
UMAP1
S. aureus %
100
75
50
25
0

a.


Outlier cluster
UMAP2
UMAP1
lesional
LES
NON_LES
clinical_group_loc
thigh AD
thigh CTRL
upper_back AD
upper_back CTRL

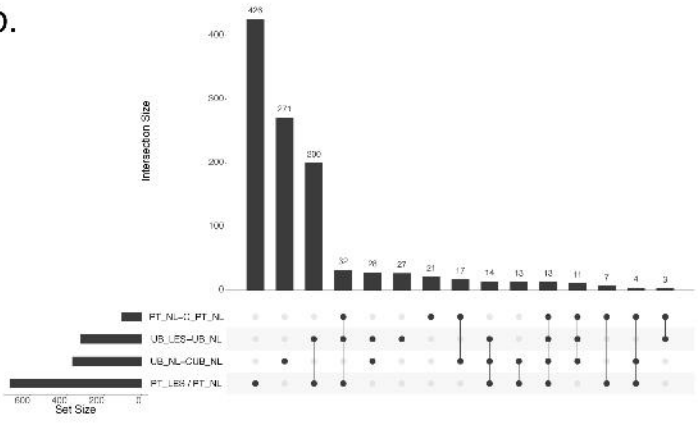
b.


thigh
upper_back
Control
Lesional
Non lesional
Abundance
taxlabel
f Burkholderiaceae g Burkholderia
f Enterobacteriaceae g Klebsiella
f Halomonadaceae g Halomonas
f Microbacteriaceae g Cryocola
f Oxalobacteraceae g Herbaspirillum
f Oxalobacteraceae g Ralstonia
g Halomonas s phocaeae
g Shewanella s algae
other
MAARS_1_012
MAARS_1_069
MAARS_2_025
MAARS_2_053
MAARS_3_023
MAARS_3_038
MAARS_3_054
MAARS_3_104
MAARS_1_110
MAARS_3_106
MAARS_3_101
MAARS_3_105

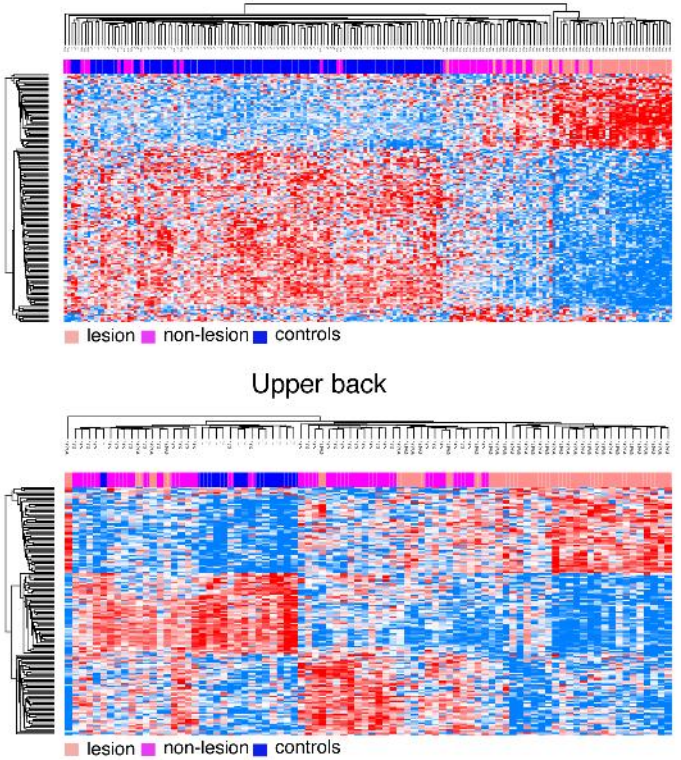
a.

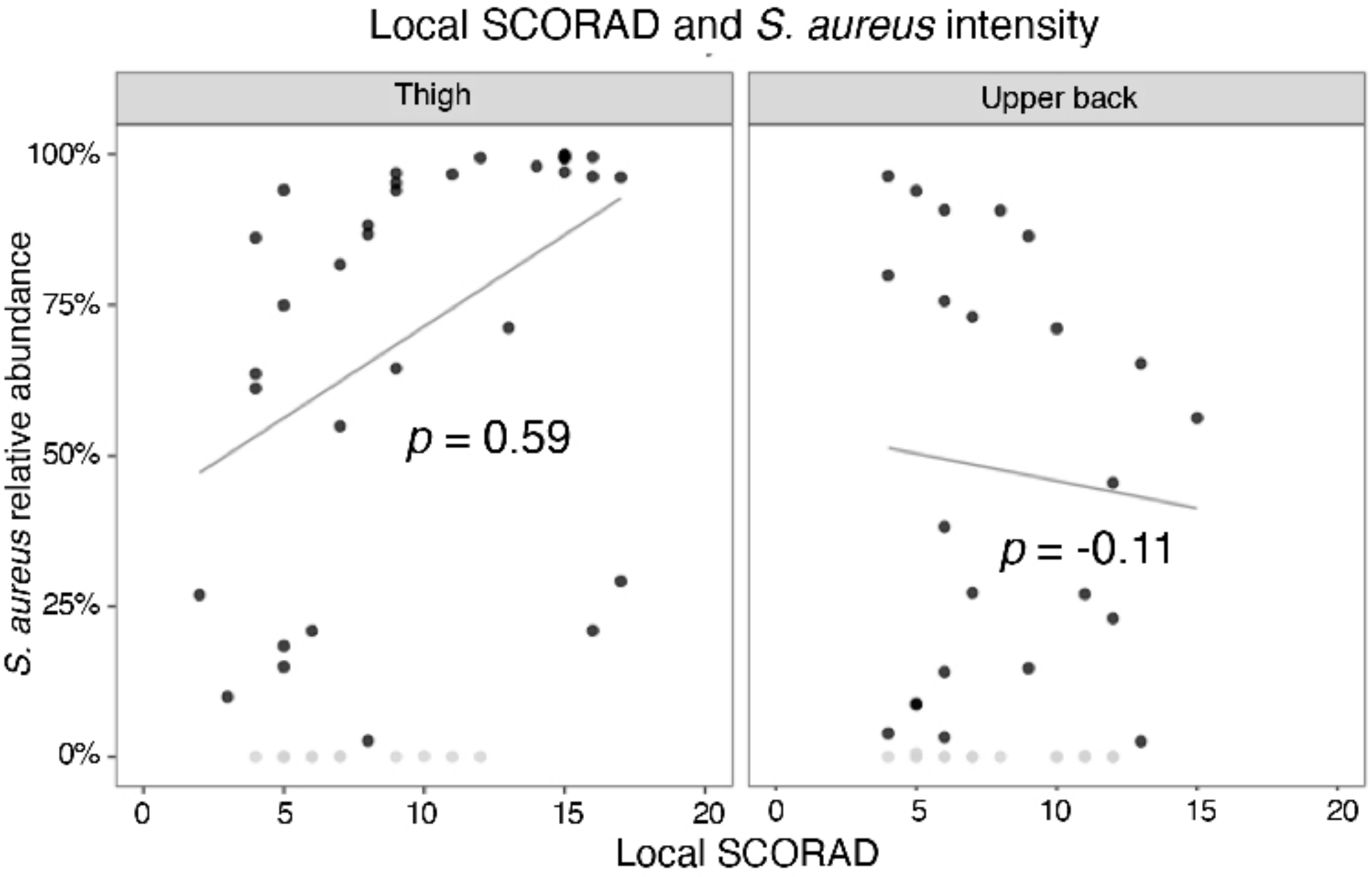
Experimental groups	All DEGs	Upregulated	Downregulated
PT_LES / PT_NL	709	491	218
PT_NL / CPT	108	54	54
UB_LES / UB_NL	328	218	110
UB_NL / CUB	371	68	303

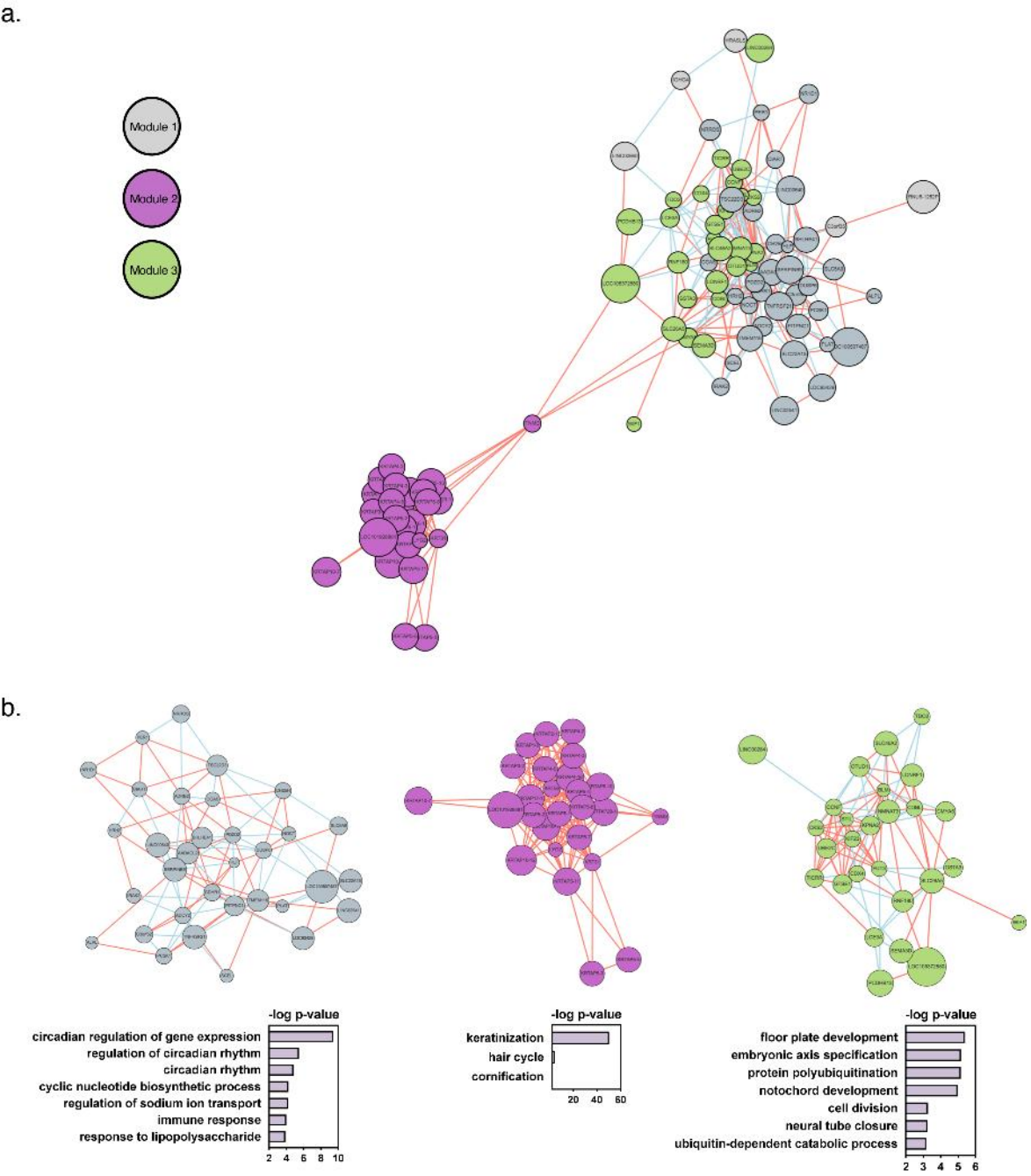
b.

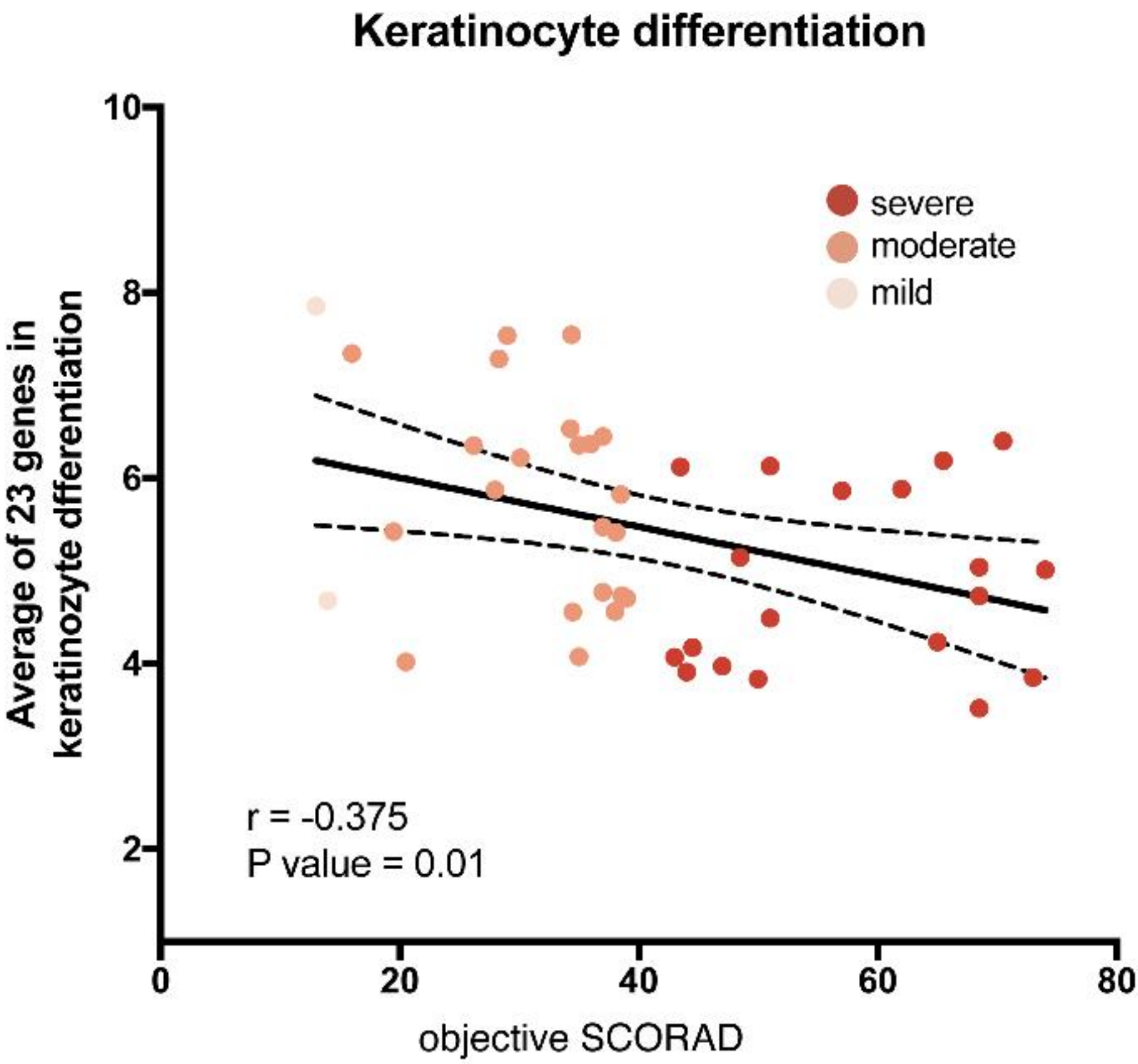


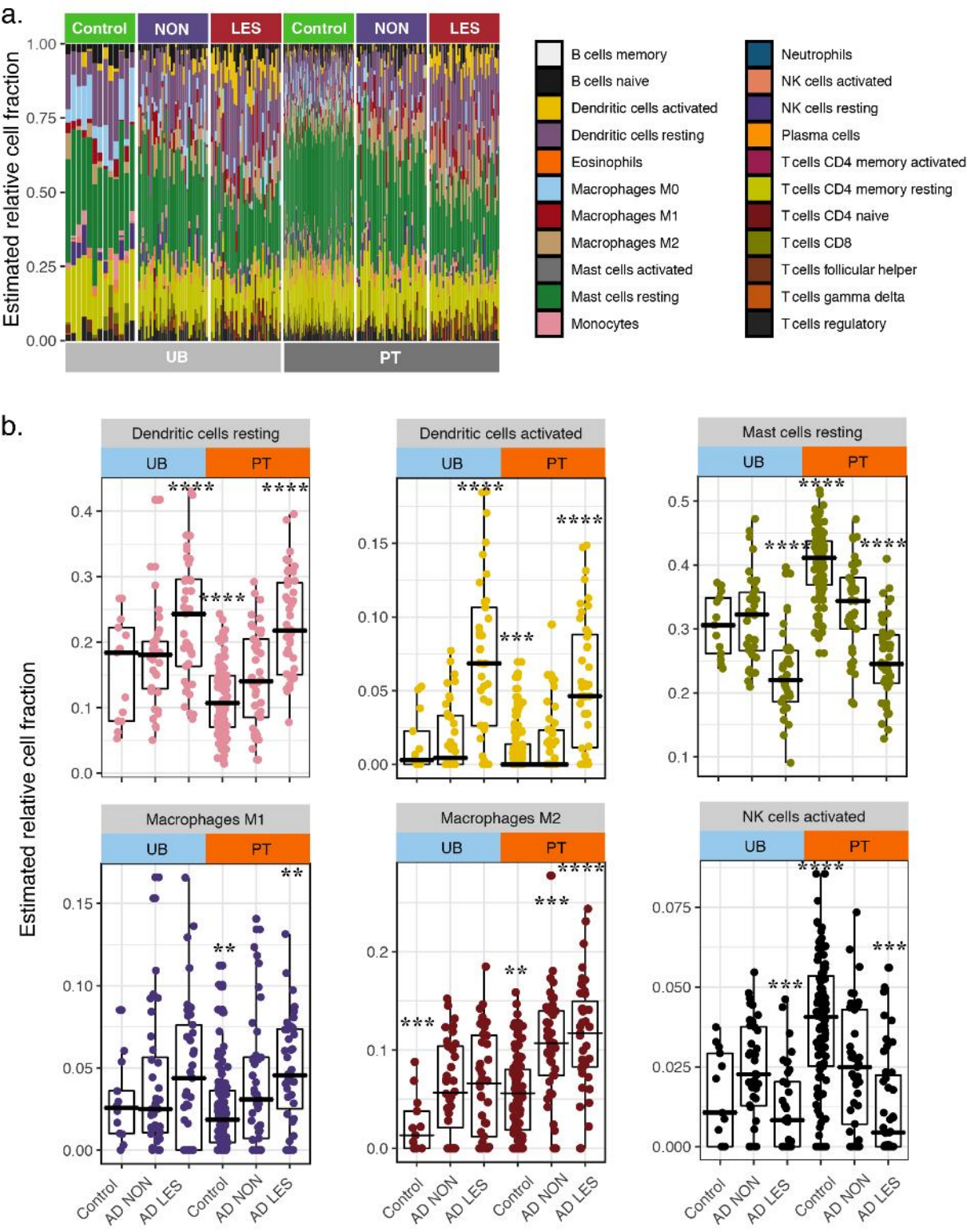
c.




Local SCORAD and S. aureus intensity
Thigh
Upper back
100%
75%
50%
25%
0%
S. aureus relative abundance
p = 0.59
p = -0.11
0
5
10
15
20
Local SCORAD


a.
Module 1
Module 2
Module 3
b.
-log p-value
circadian regulation of gene expression
regulation of circadian rhythm
circadian rhythm
cyclic nucleotide biosynthetic process
regulation of sodium ion transport
immune response
response to lipopolysaccharide
2 4 6 8 10
-log p-value
keratinization
hair cycle
cornification
20 40 60
-log p-value
floor plate development
embryonic axis specification
protein polyubiquitination
notochord development
cell division
neural tube closure
ubiquitin-dependent catabolic process
2 3 4 5 6


Keratinocyte differentiation
Average of 23 genes in keratinozyte dfferentiation
10
8
6
4
2
0
20
40
60
80
objective SCORAD
severe
moderate
mild
r = -0.375
P value = 0.01


a.
Control
NON
LES
Control
NON
LES
Estimated relative cell fraction
1.00
0.75
0.50
0.25
0.00
UB
PT
B cells memory
B cells naive
Dendritic cells activated
Dendritic cells resting
Eosinophils
Macrophages M0
Macrophages M1
Macrophages M2
Mast cells activated
Mast cells resting
Monocytes
Neutrophils
NK cells activated
NK cells resting
Plasma cells
T cells CD4 memory activated
T cells CD4 memory resting
T cells CD4 naive
T cells CD8
T cells follicular helper
T cells gamma delta
T cells regulatory
b.
Estimated relative cell fraction
Dendritic cells resting
Dendritic cells activated
Mast cells resting
Macrophages M1
Macrophages M2
NK cells activated
UB
PT
Control
AD NON
AD LES

Supporting information to:

Noora Ottman, Mauricio Barrientos-Somarribas, Nanna Fyhrquist, et al.

Microbial and transcriptional differences elucidate atopic dermatitis heterogeneity across skin sites

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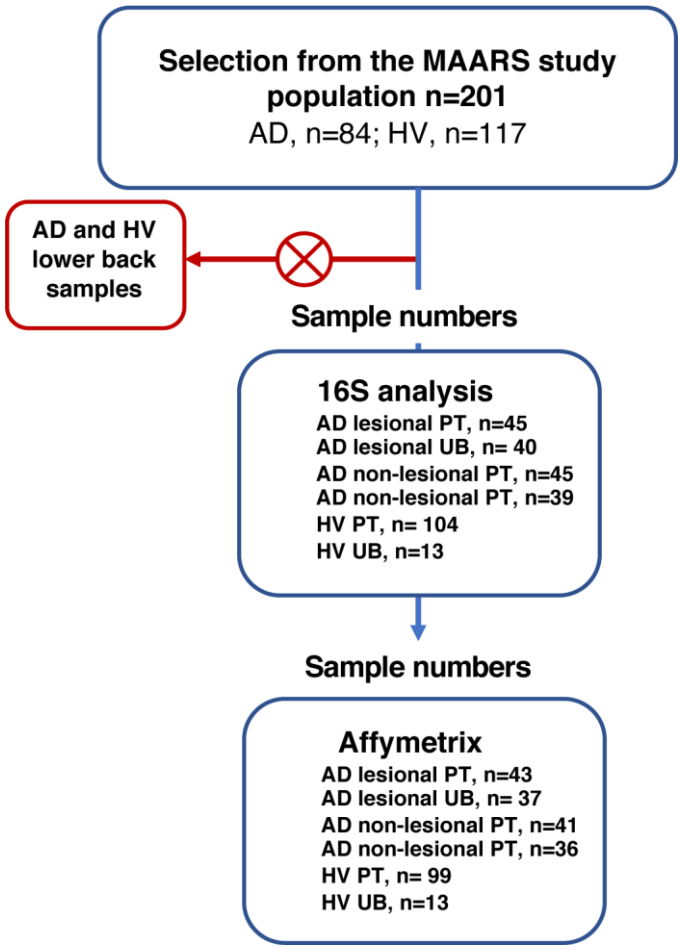


Figure E1. Patient and control numbers and sample numbers per anatomical location and study method.

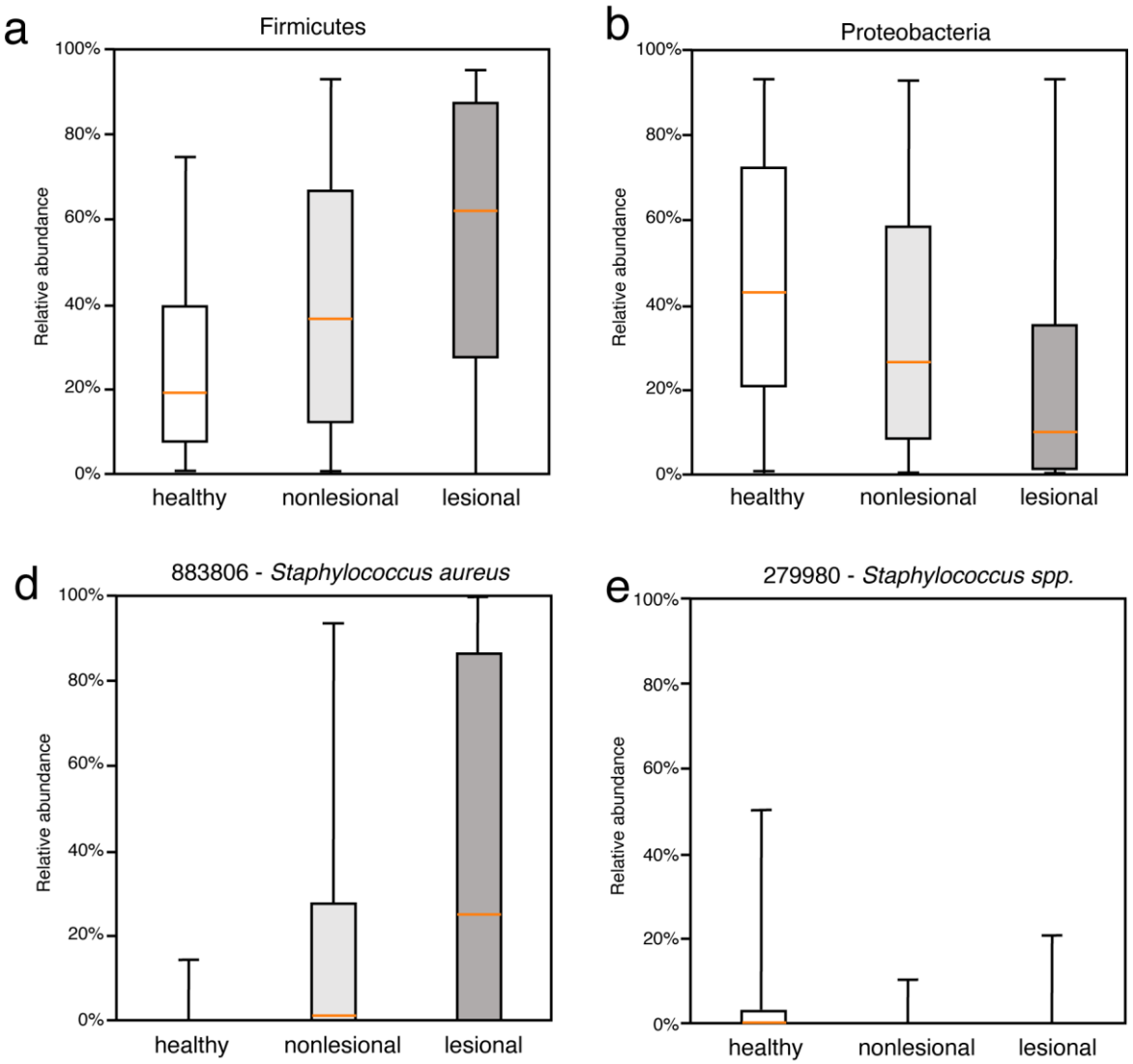


Figure E2. ANCOM abundance barplots of differentially abundant phyla and OUT between clinical groups. a) The Firmicutes phyla shows an increasing trend from healthy to nonlesional to lesional. b) Proteobacteria show the inverse trend to Firmicutes, gradually decreasing from healthy to nonlesional to lesional. c) OTU 883806 assigned to *S. aureus* phyla shows an increasing trend from healthy to nonlesional to lesional, in agreement with previous reports. d) OTU 279980 assigned up to genus level to *Staphlococcus* is present in low levels in the healthy and depleted in the AD samples.

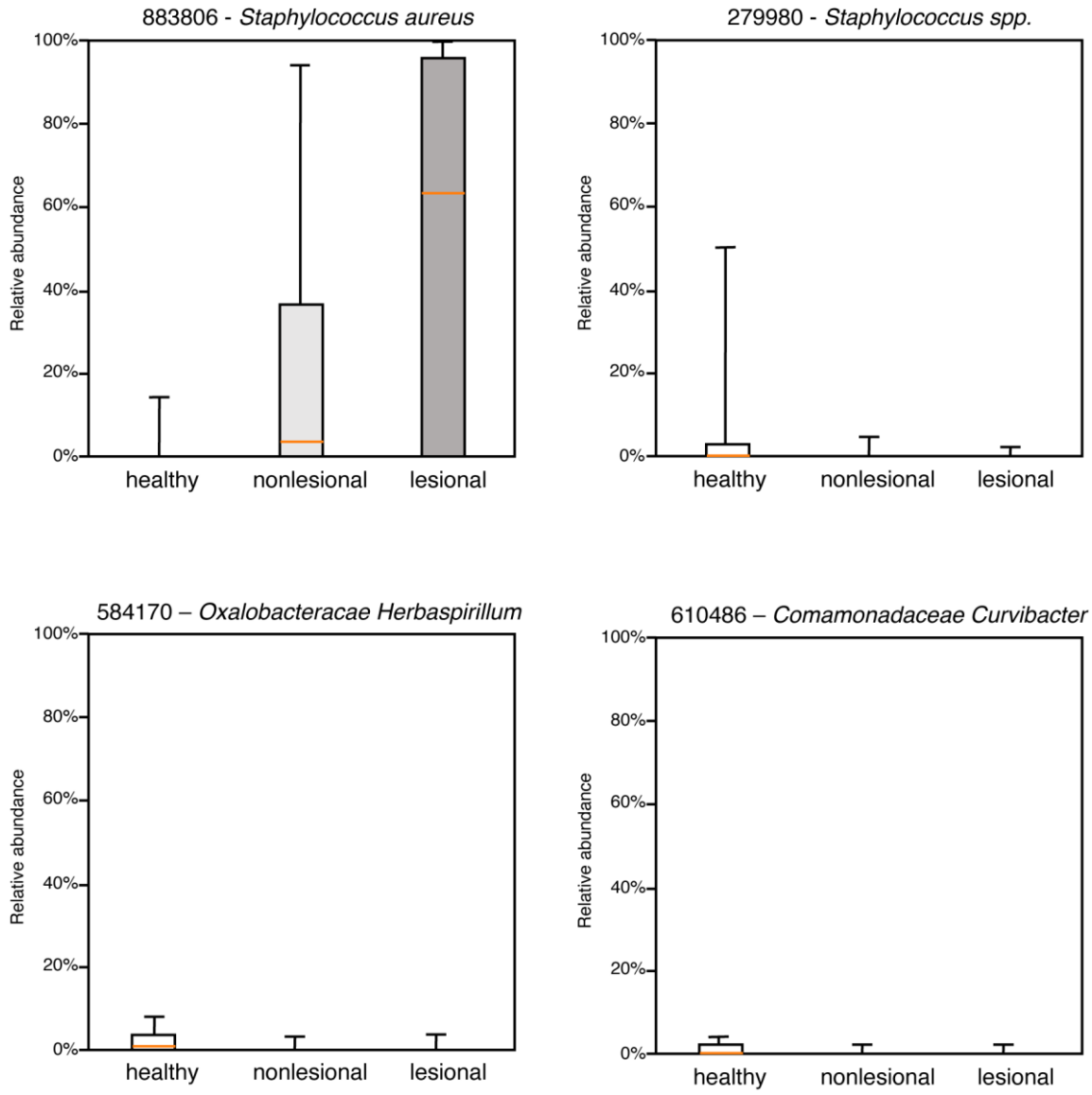


Figure E3. ANCOM-based barplots of differentially abundant OTUs between clinical groups in each skin site. a) Thigh - OTUs 883806 (*S. aureus*) and 279980 (*Staphylococcus spp.*) showed the same trends as in the general population tests. b) Upper back – OTUs 584170 (*Herbaspirillum spp*). and 610486 (*Curvibacter spp*) were found increased in healthy controls with respect to both lesional and nonlesional samples in upper back. No changes in *Staphylococcus* species were found in upper back.

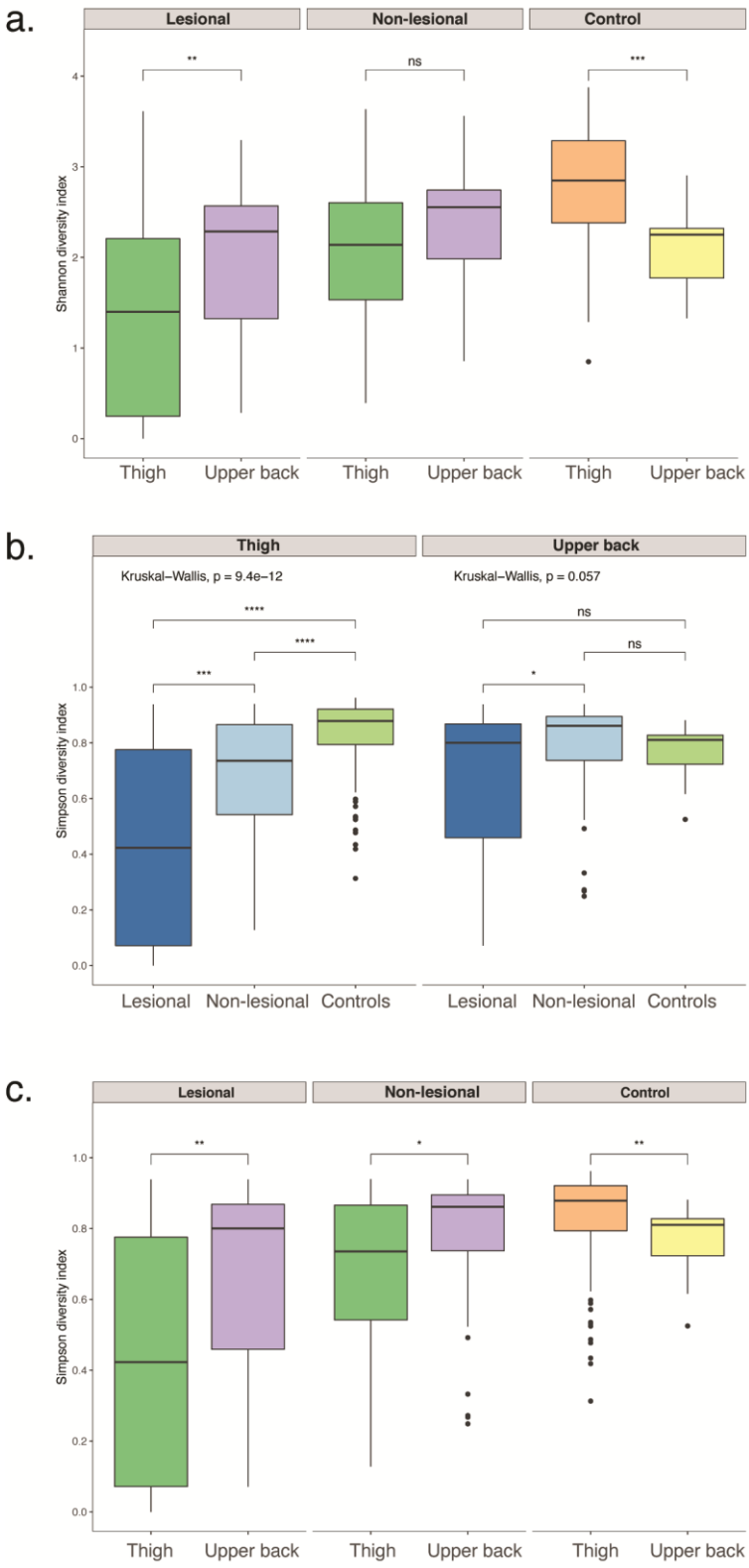


Figure E4. Alpha diversity of the samples. a) Healthy upper back samples are of lower diversity than thigh samples as reported previously. However, the trend reverses with the increase of *S. aureus* in thigh lesions while nonlesional diversity is similar between sites. b and c) The Simpson diversity index shows the same patterns as the Shannon diversity index, intra-skinsite (b) and inter-skin site (c).

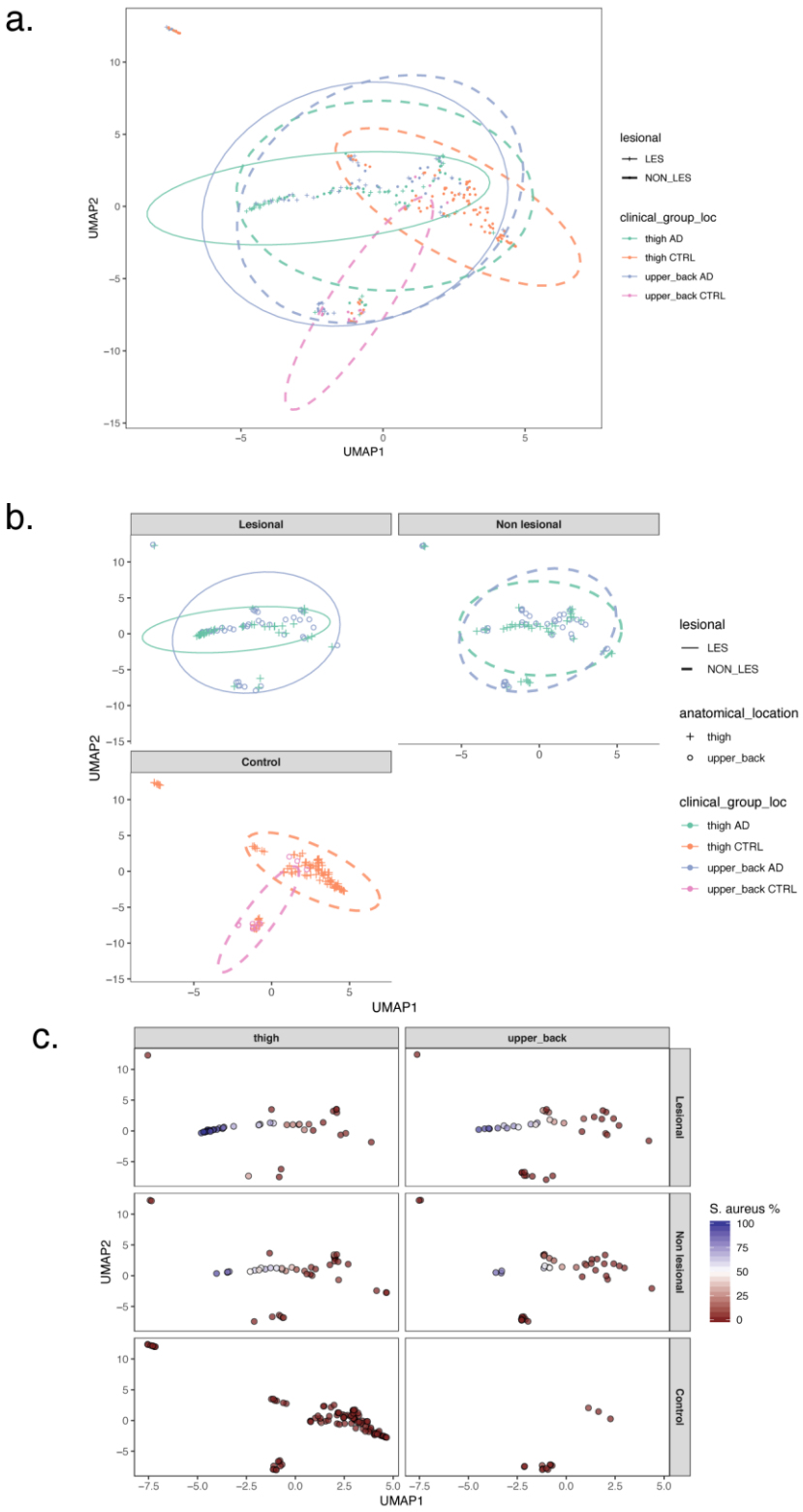


Figure E5. Alternative visualizations of the UMAP Bray-Curtis ordination of the samples in figure 2B. a) Standard plot of the ordination with all the samples in the same axis. b) Samples separated by clinical status, highlighting differences between skin sites. Nonlesional samples are mostly overlapping, while controls show two dissimilar populations. Lesional thigh and upper back samples are also similar, but *S .aureus* high samples differentiate the variance of the group. c) Samples separated by clinical group and skin site, and coloured by *S. aureus* relative abundance. High *S. aureus* samples tend to cluster together, and these mostly coincide with thigh lesional samples.

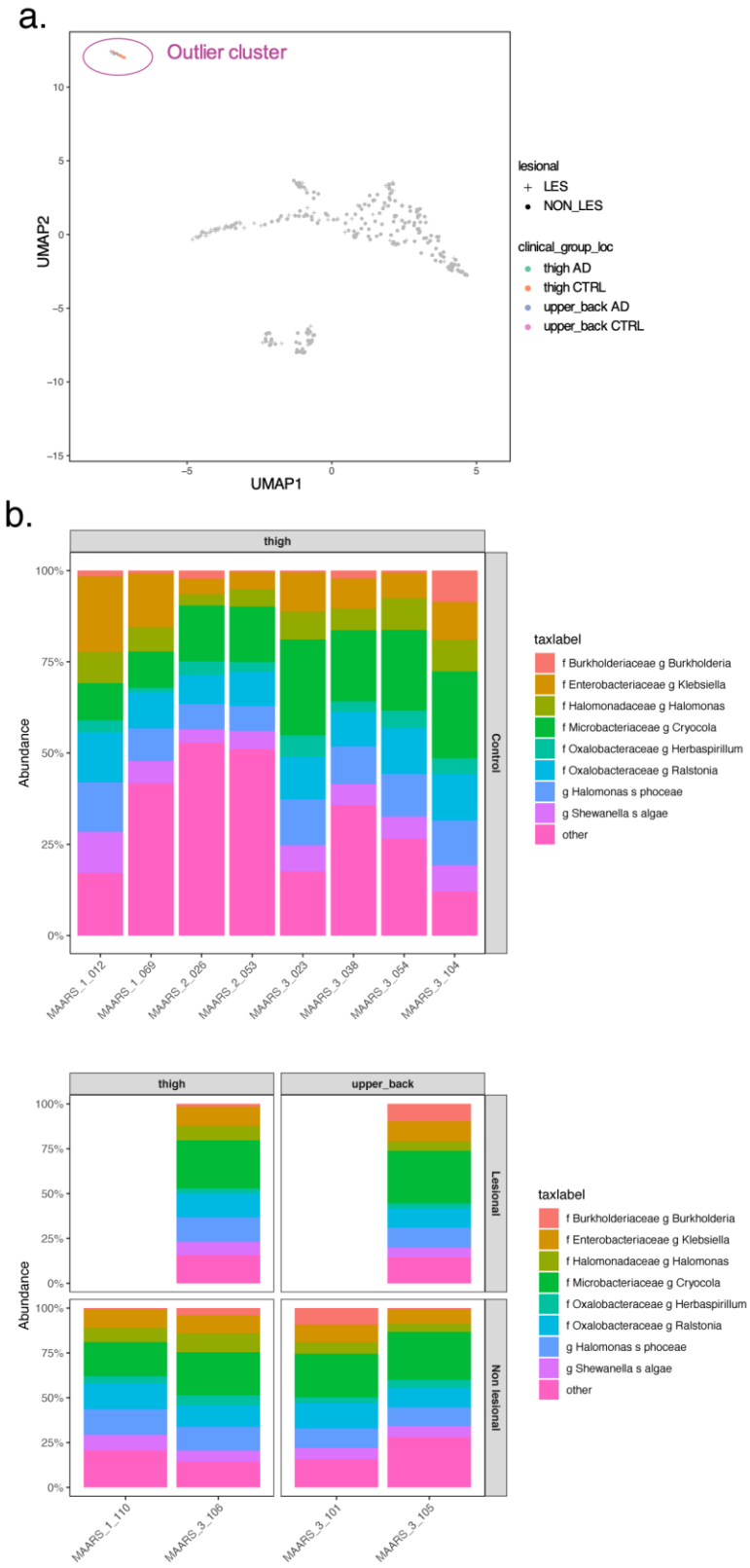


Figure E6. Barplots describing an outlier sample population according to the Bray-Curtis UMAP ordination. a) UMAP ordination highlighting the outlier population. b) Barplot highlighting the most prevalent OTUs in the outlier population. Lesional and non lesional samples from AD were found in the cluster, form both skin sites, as well as thigh control samples. However, no upper back healthy controls formed part of the group.

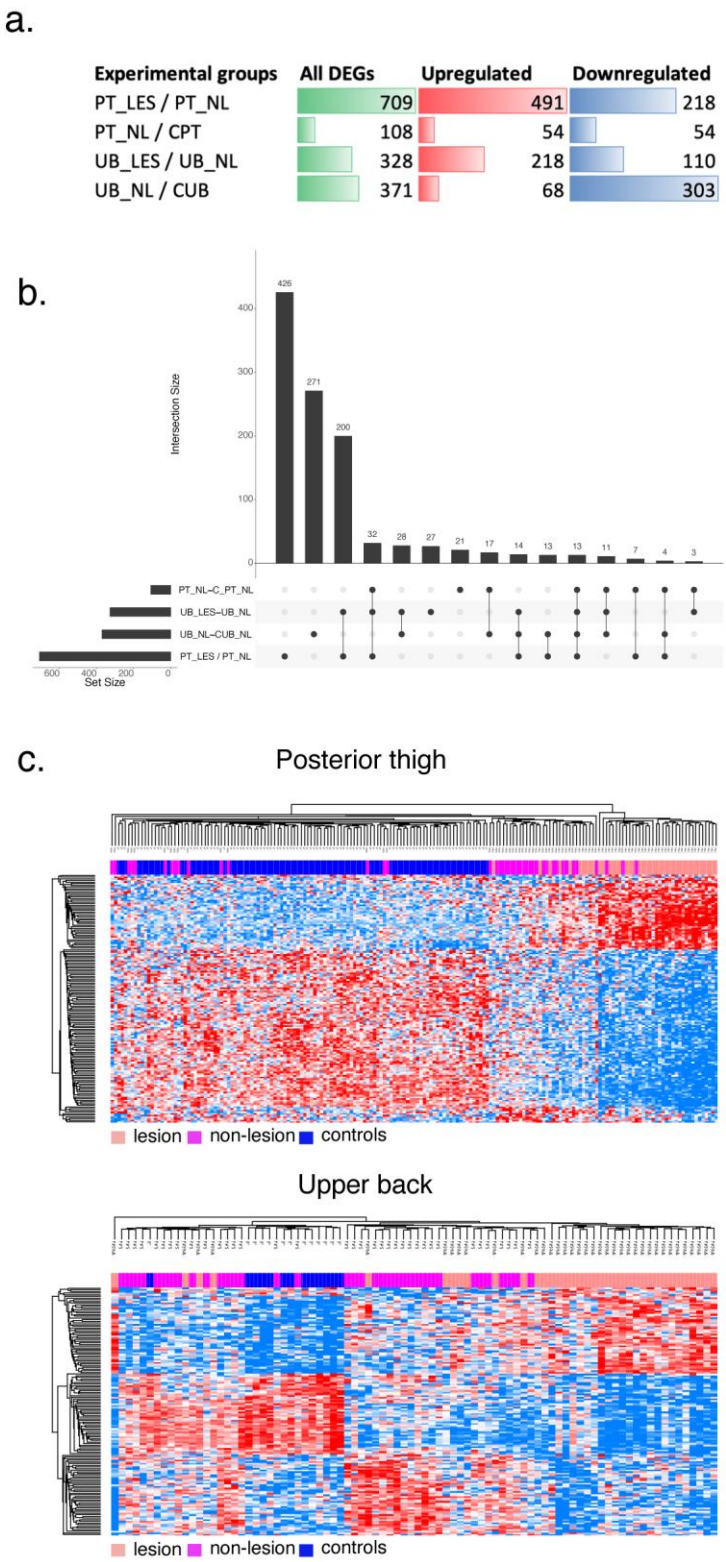


Figure E7. Summary of the results differential gene expression between conditions. Legend: PT = posterior thigh, UB = upper back, LES = lesional, NL = non lesional, C* = controls. a) Number of DEGs per comparison, and number of up- and downregulated genes. b) UpSet plot highlighting overlaps in the DEGs between conditions. c) Heatmaps showing clustering of samples based on all DEG genes found in thigh and upper back respectively.

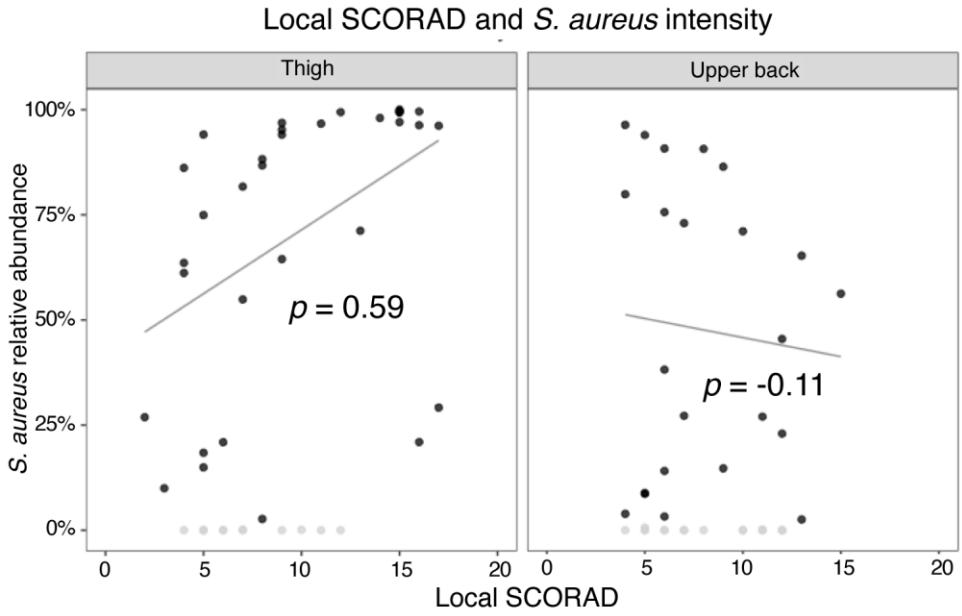


Figure E8. Association between *S. aureus* relative abundance and a SCORAD-based severity score (i.e local SCORAD) measured at the site of the lesions.

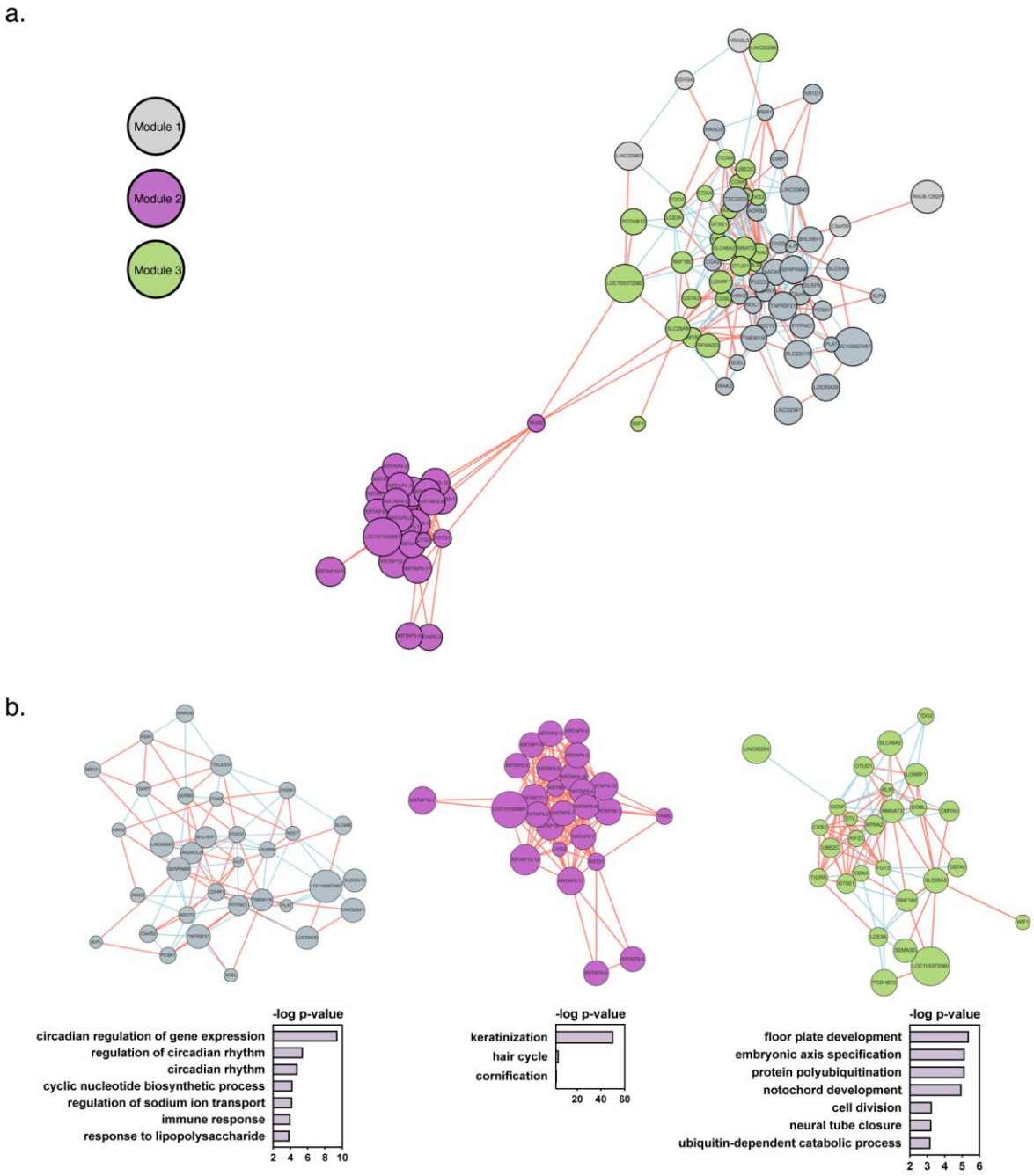


Figure E9. Analysis of the gene co-expression network of DEG genes between *S. aureus* high and *S. aureus* absent. (a) Module analysis revealed three distinct modules of genes. (b) The gray and purple modules were strongly enriched for circadian regulation of gene expression and keratinization respectively.

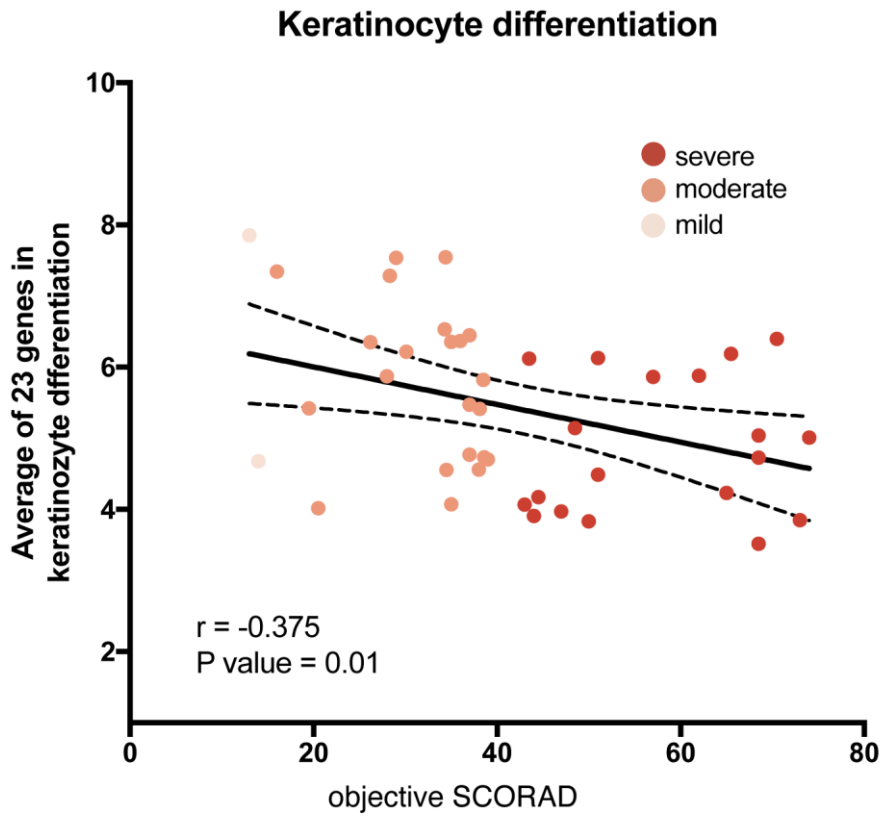


Figure E10. Correlation of average expression of 23 genes involved in keratinocyte differentiation with disease severity SCORAD values.

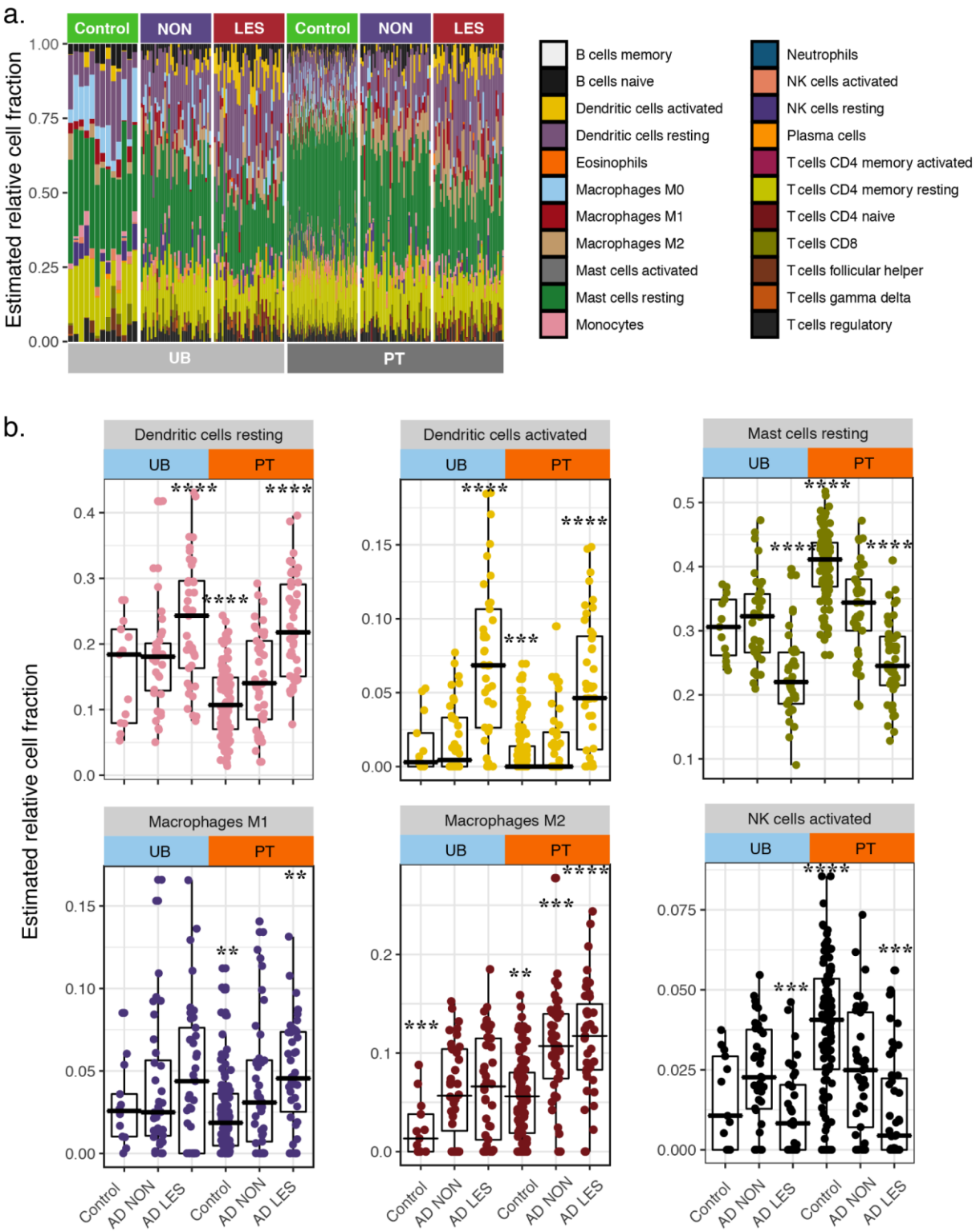


Figure E11. Supplemental Figure 1. Side specific leukocyte composition determined by the CIBERSORT algorithm. Estimated cell fractions from transcriptome wide gene expression signatures, partitioned according to the investigated skin site as well as affection (A). Significantly changed cell populations between the different skin site and groups (B). **p<0.01, ***p<0.001, ***p<0.0001.

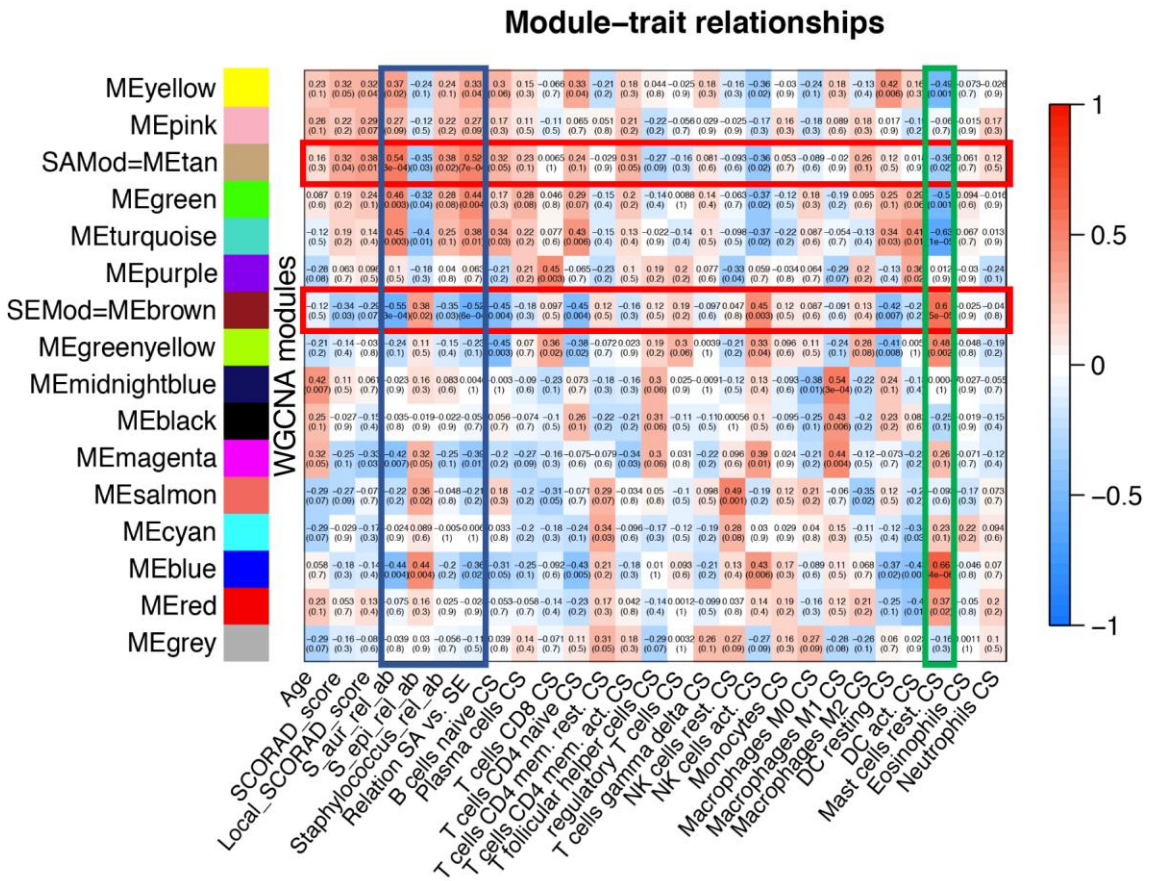


Figure E12. Module trait relationships in lesional thigh skin. Weighted gene co-expression analysis (WGCNA) was used to determine gene co-expression modules associated with the clinical features (age and SCORAD), selected skin microbes (*Staphylococcus aureus*, *Staphylococcus epidermidis* and their relation) and estimated cell sub-types in the lesional thigh skin. The leukocyte deconvolution algorithm Cibersort (CS) was applied on transcriptomics data to estimate the relative cell fractions within the affected skin sites. WGCNA-modules are indicated as color-code bar on the left. Correlation coefficient between the module eigengenes and clinical, microbial and cell features are indicated in red-blue color code on the right. Major module-trait associations between tan and brown WGCNA-modules (indicated as red rectangles), microbes (indicated as blue rectangles) and mast cells (indicated as green rectangles) are highlighted.

Table E1. Thigh_LES / Thigh_NON-LES

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
3.618	8.12956	10.03275305	4.2E-20	7.318E-18	35.01265871	70.1	ENSG00000206073
3.447	3.83615	13.01969251	7E-30	2.75E-26	57.11270048	100.5	ENSG00000170465
3.409	6.68447	12.22807581	3.2E-27	5.274E-24	51.10350472	90.34	ENSG00000124102
3.264	4.2732	14.03195713	2.5E-33	7.987E-29	64.88748639	106.4	ENSG00000163221
3.206	8.30859	13.74678675	2.4E-32	3.75E-28	62.68950632	101.4	ENSG00000186832
3.096	3.72667	11.90228448	3.8E-26	5.221E-23	48.65532722	78.69	ENSG00000184330
3.09	7.46787	12.07703037	1E-26	1.52E-23	49.96642226	80.32	ENSG00000163220
3.036	4.78988	12.74219306	6E-29	1.46E-25	54.99753534	85.69	ENSG00000134827
3.009	3.9568	9.519514366	1.6E-18	1.856E-16	31.42618312	53.52	ENSG00000171711
2.977	4.9424	10.60851161	6.3E-22	1.995E-19	39.12716448	63.12	ENSG00000244094
2.886	6.12545	13.6038489	7.3E-32	7.665E-28	61.58979398	89.86	ENSG00000185962
2.576	6.31863	11.81041184	7.7E-26	8.237E-23	47.96801637	64.68	ENSG00000205420
2.512	3.32708	9.449374797	2.7E-18	2.944E-16	30.94260819	44.15	ENSG00000196611
2.502	7.88756	10.43276797	2.3E-21	6.198E-19	37.86184111	51.64	ENSG00000143546
2.449	5.41135	8.943290608	8.9E-17	6.646E-15	27.5043823	39.31	ENSG00000012223
2.412	9.35758	11.61355373	3.5E-25	2.946E-22	46.50019709	59	ENSG00000057149
2.338	5.92833	8.567122733	1.1E-15	6.452E-14	25.01111886	34.94	ENSG00000181333
2.171	5.69324	12.57713819	2.2E-28	4.862E-25	53.74364986	60.05	ENSG00000198074
2.123	4.61294	11.4977675	8.3E-25	6.088E-22	45.64014123	51.13	ENSG00000188293
2.122	7.66326	8.58443104	1E-15	5.818E-14	25.1245973	31.81	ENSG00000167755
2.113	5.38777	9.088834062	3.3E-17	2.72E-15	28.48369627	34.83	ENSG00000262406
2.058	7.38119	9.436163882	2.9E-18	3.175E-16	30.85171105	36.09	ENSG00000185966
2.057	5.6736	7.093472782	1.4E-11	3.017E-10	15.84810743	22.35	ENSG00000196805
1.985	4.06774	9.90627831	1E-19	1.62E-17	34.12131664	37.67	ENSG00000136694
1.954	9.86212	9.225983752	1.3E-17	1.169E-15	29.41365193	33.01	ENSG00000185479
1.912	3.23286	8.997637562	6.2E-17	4.829E-15	27.86913916	31	ENSG00000200972
1.9	5.76848	10.5820101	7.7E-22	2.333E-19	38.93585478	40.11	ENSG00000137558
1.826	6.5029	10.34136654	4.5E-21	1.105E-18	37.20694607	37.15	ENSG00000169469
-1.824	6.39769	-8.857094002	1.6E-16	1.128E-14	26.92816448	-28.8	ENSG00000168671
1.821	6.10436	9.571293512	1.1E-18	1.356E-16	31.78422237	32.68	ENSG00000007908
1.752	4.44352	9.442390792	2.8E-18	3.058E-16	30.89454769	30.76	ENSG00000182585
-1.719	5.01741	-9.807601343	2.1E-19	3E-17	33.42922634	-32.1	ENSG00000226005
-1.709	6.23047	-10.36185177	3.9E-21	9.819E-19	37.35353008	-34.89	ENSG00000236543
-1.706	8.35267	-9.996296342	5.5E-20	9.31E-18	34.75524067	-32.86	ENSG00000125571
1.668	6.06162	13.14185775	2.7E-30	1.214E-26	58.04643968	49.32	ENSG00000172382
1.613	5.38595	9.102872783	3E-17	2.482E-15	28.57857346	26.65	ENSG00000172752
1.597	9.08783	12.86426109	2.3E-29	6.694E-26	55.92692299	45.71	ENSG00000186831
-1.592	5.92028	-10.65932463	4.4E-22	1.43E-19	39.49446436	-34	ENSG00000174808
1.584	5.78275	11.7519293	1.2E-25	1.121E-22	47.53124681	39.48	ENSG00000137648
1.571	7.17238	5.796703953	2E-08	2.393E-07	8.751782383	12.08	ENSG00000075673
1.565	3.90207	11.10724234	1.6E-23	7.587E-21	42.75868566	35.69	ENSG00000153802
1.562	9.59258	12.79669352	3.9E-29	1.036E-25	55.41227506	44.38	ENSG00000165474
1.472	5.9401	4.511832401	9.9E-06	6.723E-05	2.819511954	7.366	ENSG00000169245

1.472	5.71527	9.707390709	4.3E-19	5.666E-17	32.72946298	27.03	ENSG00000275385
1.455	9.5919	7.509577375	1.1E-12	2.977E-11	18.32848585	17.42	ENSG00000163202
1.418	7.37578	8.21885352	1.1E-14	4.95E-13	22.75454492	19.76	ENSG00000188373
1.408	5.15737	8.515733442	1.6E-15	8.738E-14	24.67492279	20.83	ENSG00000101670
1.405	6.3953	8.478940355	2.1E-15	1.085E-13	24.4348907	20.63	ENSG00000206384
1.386	5.40433	8.041339066	3.6E-14	1.428E-12	21.62473066	18.63	ENSG00000140519
1.373	7.08427	11.89805897	4E-26	5.221E-23	48.62368476	34.88	ENSG00000159337
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1.354	8.61231	11.16415329	1E-23	5.369E-21	43.17664749	31.14	ENSG00000121742
1.352	5.51888	7.955838993	6.3E-14	2.327E-12	21.0856646	17.85	ENSG00000175592
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1.257	9.02441	10.7606784	2.1E-22	7.216E-20	40.22898521	27.26	ENSG00000041982
1.248	6.30544	8.481359988	2E-15	1.075E-13	24.45065862	18.33	ENSG00000088882
1.247	6.22696	9.315833662	6.8E-18	6.682E-16	30.02652864	21.41	ENSG00000136688
1.236	4.80267	12.99184993	8.7E-30	3.036E-26	56.90010343	35.91	ENSG00000115919
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1.151	5.48176	3.893790412	0.00013	0.0006787	0.411563651	4.485	ENSG00000138755
1.151	5.45563	10.8947531	7.6E-23	3.004E-20	41.20439913	25.46	ENSG00000172243
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1.143	3.79755	9.692798293	4.8E-19	6.208E-17	32.62782906	20.93	ENSG00000163600
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1.098	5.77228	8.783775257	2.6E-16	1.767E-14	26.4402919	17.1	ENSG00000184557
1.097	5.43916	9.963263899	6.9E-20	1.138E-17	34.52233946	21.03	ENSG00000188404
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0.874	7.44888	9.025602733	5.1E-17	4.076E-15	28.05726319	14.23	ENSG00000101955
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0.872	4.75768	8.880923064	1.4E-16	9.762E-15	27.08717511	13.84	ENSG00000163823
0.872	3.35009	5.093604477	7E-07	5.98E-06	5.35766659	5.369	ENSG00000177257
-0.871	4.04024	-9.280185511	8.7E-18	8.334E-16	29.78302853	-14.87	ENSG00000170615
0.87	8.20262	8.3145001	6.1E-15	2.838E-13	23.36909948	12.37	ENSG00000090382
-0.865	7.14834	-5.470670667	1.1E-07	1.109E-06	7.13520465	-6.02	ENSG00000139292
0.861	7.17278	6.688016403	1.5E-10	2.641E-09	13.52164666	8.462	ENSG00000006327
0.861	4.75161	9.115384941	2.7E-17	2.313E-15	28.66319453	14.26	ENSG00000134061
0.86	4.90682	10.14592716	1.9E-20	3.72E-18	35.81422948	16.97	ENSG00000113532

0.86	7.62208	11.4721999	1E-24	6.904E-22	45.45056557	20.64	ENSG00000184060
0.86	2.676	7.327457254	3.3E-12	8.232E-11	17.2317251	9.874	ENSG00000171889
0.859	7.12275	11.04723694	2.4E-23	1.135E-20	42.31875337	19.41	ENSG00000062716
0.858	3.72288	9.364892711	4.8E-18	4.927E-16	30.3623572	14.85	ENSG00000065675
0.858	4.92731	9.235868673	1.2E-17	1.095E-15	29.48093859	14.52	ENSG00000150637
0.857	6.06076	10.44544721	2.1E-21	5.697E-19	37.95286282	17.72	ENSG00000113356
0.856	5.0228	8.00763829	4.5E-14	1.748E-12	21.41184978	11.42	ENSG00000090889
-0.853	8.29082	-3.153432616	0.00181	0.0072218	-2.055605325	-2.338	ENSG00000268751
0.852	6.64675	10.93439316	5.7E-23	2.387E-20	41.49358521	18.94	ENSG00000103187
0.851	5.24136	6.531456984	3.7E-10	5.996E-09	12.64854403	8.034	ENSG00000204936
0.851	4.98428	9.962245788	7E-20	1.14E-17	34.51516623	16.3	ENSG00000173559
0.851	7.00459	9.196740946	1.6E-17	1.412E-15	29.21479997	14.3	ENSG00000081237
0.85	7.86664	9.88665584	1.2E-19	1.837E-17	33.98345418	16.08	ENSG00000159399
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0.849	5.34341	10.14556698	1.9E-20	3.72E-18	35.81167261	16.74	ENSG00000111206
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0.846	6.22207	9.794345001	2.3E-19	3.239E-17	33.33647829	15.77	ENSG00000176928
0.846	6.92615	8.829472691	1.9E-16	1.323E-14	26.74412296	13.29	ENSG00000088325
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0.836	5.68441	7.212391582	6.6E-12	1.56E-10	16.5476654	9.344	ENSG00000274641
0.834	4.1787	8.314487986	6.1E-15	2.838E-13	23.3690214	11.86	ENSG00000119508
0.833	6.8914	8.564962132	1.2E-15	6.522E-14	24.99696195	12.44	ENSG00000068489
0.832	8.57984	5.506120304	9.1E-08	9.414E-07	7.307461774	5.856	ENSG00000126709
-0.832	6.72308	-9.37358093	4.5E-18	4.667E-16	30.42191818	-14.43	ENSG00000162706
0.83	5.98858	8.708008751	4.4E-16	2.758E-14	25.93834958	12.74	ENSG00000109805
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0.828	7.52913	9.006781888	5.8E-17	4.592E-15	27.93062165	13.45	ENSG00000163874
0.826	8.87457	10.39708575	3E-21	7.716E-19	37.60591254	16.95	ENSG00000092295
0.824	7.26772	8.311251985	6.3E-15	2.891E-13	23.34816406	11.7	ENSG00000148773
0.823	7.11934	10.29863663	6.1E-21	1.43E-18	36.9015522	16.64	ENSG00000153048
0.823	4.00316	9.455934771	2.6E-18	2.831E-16	30.98776573	14.48	ENSG00000175426
0.822	4.24648	7.594967832	6.3E-13	1.829E-11	18.84852605	10.03	ENSG00000116824
0.822	6.29453	8.315012382	6.1E-15	2.838E-13	23.37240176	11.68	ENSG00000157456
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0.819	3.75385	6.279462293	1.5E-09	2.187E-08	11.27401844	7.229	ENSG00000187116
0.819	7.91582	7.538079138	8.9E-13	2.531E-11	18.50165896	9.864	ENSG00000127954
0.819	6.14556	8.725442568	3.9E-16	2.496E-14	26.05364455	12.61	ENSG00000137812
-0.818	6.56884	-3.908164334	0.00012	0.0006462	0.464049185	-3.207	ENSG00000167676
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0.817	4.41412	8.523651807	1.5E-15	8.36E-14	24.72665463	12.1	ENSG00000211964
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0.811	6.52126	8.592415379	9.6E-16	5.545E-14	25.17698641	12.18	ENSG00000173083
0.81	3.58522	6.404260607	7.5E-10	1.158E-08	11.94992215	7.394	ENSG00000123496
-0.81	6.22827	-8.138606008	1.9E-14	8.012E-13	22.24204626	-11.11	ENSG00000253047
0.808	6.25329	9.062167504	4E-17	3.227E-15	28.30367642	13.26	ENSG00000176890
0.808	4.73167	7.923968925	7.8E-14	2.795E-12	20.88559469	10.59	ENSG00000073737
0.806	4.25945	11.05914535	2.2E-23	1.054E-20	42.40599801	18.25	ENSG00000123342
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0.804	5.30312	8.593682254	9.6E-16	5.518E-14	25.18530138	12.07	ENSG00000129810
0.803	3.96127	6.762675319	9.7E-11	1.789E-09	13.94304102	8.046	ENSG00000145649
0.802	4.7346	8.879602037	1.4E-16	9.828E-15	27.07835421	12.72	ENSG00000140030
0.802	5.45206	2.805608225	0.00542	0.018891	-3.049734319	1.818	ENSG00000211892
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0.799	6.10257	7.835462589	1.4E-13	4.636E-12	20.33248123	10.28	ENSG00000101447
0.798	6.67859	7.506247188	1.1E-12	3.032E-11	18.30827879	9.543	ENSG00000140968
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0.795	5.23771	7.53615954	9E-13	2.559E-11	18.48998289	9.574	ENSG00000117091
0.795	5.25674	7.834746497	1.4E-13	4.65E-12	20.32802118	10.22	ENSG00000138778
0.793	6.94733	4.717732312	4E-06	2.918E-05	3.688604495	4.282	ENSG00000204869
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0.792	6.67175	6.199894843	2.3E-09	3.268E-08	10.84810339	6.835	ENSG00000138642
0.792	6.38356	8.226481067	1.1E-14	4.737E-13	22.80340673	11.06	ENSG00000121966
0.792	7.41446	8.982844888	6.8E-17	5.266E-15	27.76974597	12.8	ENSG00000204291
0.791	5.35477	8.169973115	1.6E-14	6.634E-13	22.4420301	10.92	ENSG00000170312
0.791	6.43733	9.932749151	8.6E-20	1.373E-17	34.307478	15.08	ENSG00000011422
0.791	7.48749	5.023524839	9.7E-07	8.082E-06	5.03854869	4.754	ENSG00000268104
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0.788	2.60779	4.813007093	2.6E-06	1.965E-05	4.101699273	4.402	ENSG00000213886
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0.78	6.2229	8.001074434	4.7E-14	1.813E-12	21.37044796	10.39	ENSG00000187498
0.779	5.73556	6.391456823	8.1E-10	1.236E-08	11.88013885	7.086	ENSG00000162692
0.779	5.61794	4.840918067	2.3E-06	1.75E-05	4.224011639	4.394	ENSG00000161905
0.778	5.03543	7.743103868	2.5E-13	7.847E-12	19.75926629	9.811	ENSG00000169607
0.776	4.02946	9.527759294	1.5E-18	1.783E-16	31.48313534	13.82	ENSG00000120217
0.774	5.32525	8.444512523	2.6E-15	1.333E-13	24.21080248	11.29	ENSG00000117399
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0.772	7.01897	8.363670464	4.4E-15	2.129E-13	23.68657894	11.08	ENSG00000123975
0.771	4.5298	4.816825566	2.5E-06	1.937E-05	4.118398184	4.316	ENSG00000273727
0.77	6.50256	7.613520076	5.6E-13	1.641E-11	18.96199342	9.432	ENSG00000111331
0.769	6.19335	8.639429457	7E-16	4.181E-14	25.48599582	11.65	ENSG00000090339
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0.766	6.08801	9.993498084	5.6E-20	9.448E-18	34.73549853	14.76	ENSG00000122861
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0.765	7.60201	6.56269464	3.1E-10	5.094E-09	12.82159654	7.28	ENSG00000277734
0.765	5.19868	8.356744622	4.6E-15	2.222E-13	23.64179772	10.96	ENSG00000251442
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0.764	5.04369	9.06787228	3.8E-17	3.11E-15	28.34216603	12.54	ENSG00000113749
0.763	2.90018	7.052281318	1.7E-11	3.786E-10	15.60757618	8.208	ENSG00000127318
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0.762	5.13637	7.576999302	7E-13	2.028E-11	18.73879193	9.262	ENSG00000090659
0.759	5.40642	6.803248858	7.6E-11	1.436E-09	14.17339282	7.68	ENSG00000163519
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0.758	4.55396	8.766373189	3E-16	1.951E-14	26.32480494	11.77	ENSG00000065328
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0.751	6.09437	6.145204749	3.2E-09	4.314E-08	10.5576499	6.382	ENSG00000151012
0.751	2.89029	7.759790629	2.2E-13	7.139E-12	19.86252748	9.5	ENSG00000236481
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0.747	5.71385	7.757789134	2.2E-13	7.215E-12	19.85013471	9.453	ENSG00000164687
0.747	4.78771	7.207537449	6.8E-12	1.599E-10	16.51896179	8.344	ENSG00000176920
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0.745	5.32564	9.293670469	7.9E-18	7.727E-16	29.87508728	12.75	ENSG00000196754
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0.744	6.20983	7.972910899	5.7E-14	2.125E-12	21.19303085	9.852	ENSG00000158714
0.743	5.14456	8.226854276	1.1E-14	4.736E-13	22.80579815	10.38	ENSG00000169679
0.743	6.16761	11.37661426	2.1E-24	1.364E-21	44.74294557	17.59	ENSG00000166451

0.742	4.42743	10.11088078	2.4E-20	4.54E-18	35.56561544	14.56	ENSG00000128578
0.742	5.40679	8.40352579	3.4E-15	1.679E-13	23.94467501	10.73	ENSG00000156970
0.741	6.10494	8.619067173	8.1E-16	4.74E-14	25.35205024	11.19	ENSG00000105011
0.741	5.46054	6.973876196	2.8E-11	5.796E-10	15.15231207	7.825	ENSG00000153283
0.739	5.09025	7.239704924	5.6E-12	1.345E-10	16.70940909	8.319	ENSG00000113263
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0.734	6.19338	9.154808873	2.1E-17	1.804E-15	28.93019563	12.24	ENSG00000165480
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0.732	4.42502	9.335907559	5.9E-18	5.938E-16	30.16384157	12.61	ENSG00000164430
0.731	4.74417	7.864805523	1.1E-13	3.922E-12	20.51544781	9.466	ENSG00000081985
0.729	3.99853	5.301140839	2.5E-07	2.389E-06	6.323537417	4.808	ENSG00000229035
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0.728	4.85433	7.674995237	3.8E-13	1.153E-11	19.33919777	9.045	ENSG00000169684
0.727	3.97776	6.910252913	4.1E-11	8.14E-10	14.78538233	7.56	ENSG00000178562
0.724	8.44682	9.526521605	1.6E-18	1.792E-16	31.4745845	12.9	ENSG00000171056
0.724	4.42404	8.342546557	5.1E-15	2.412E-13	23.55006008	10.35	ENSG00000203710
0.723	6.848	7.958687839	6.2E-14	2.297E-12	21.10357176	9.546	ENSG00000158869
0.72	5.55224	9.567913497	1.2E-18	1.384E-16	31.7608235	12.92	ENSG00000157193
-0.718	5.58821	-6.863721624	5.3E-11	1.039E-09	14.51846047	-7.378	ENSG00000203392
0.718	4.52673	8.004884118	4.6E-14	1.773E-12	21.3944753	9.578	ENSG00000117090
-0.716	3.85621	-8.92378721	1E-16	7.505E-15	27.37375501	-11.45	ENSG00000250320
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0.715	3.05117	8.297136756	6.9E-15	3.127E-13	23.25723881	10.13	ENSG00000277089
-0.715	5.83802	-8.195335732	1.3E-14	5.681E-13	22.60405261	-9.92	ENSG00000153930
0.715	7.18142	8.878897529	1.4E-16	9.853E-15	27.07365026	11.33	ENSG00000102879
0.713	5.07122	5.836012516	1.7E-08	1.983E-07	8.951513129	5.548	ENSG00000183347
0.712	3.16688	5.056448584	8.3E-07	7.028E-06	5.188025229	4.33	ENSG00000211787
0.712	5.97074	6.353709095	1E-09	1.499E-08	11.67498705	6.407	ENSG00000248485
-0.711	8.0695	-11.84724707	5.9E-26	7.099E-23	48.24341538	-17.95	ENSG00000188177
0.711	8.96645	9.156389784	2.1E-17	1.795E-15	28.94091421	11.86	ENSG00000102265
0.71	6.02489	8.458425984	2.4E-15	1.225E-13	24.30130418	10.38	ENSG00000276043
0.709	6.67721	5.646841688	4.5E-08	4.865E-07	7.999768432	5.214	ENSG00000158481
-0.709	5.11563	-6.593764357	2.6E-10	4.335E-09	12.9942922	-6.799	ENSG00000256199
0.709	3.69131	7.792456963	1.8E-13	5.916E-12	20.06506214	9.032	ENSG00000163599
0.708	4.08987	7.112202352	1.2E-11	2.72E-10	15.95778117	7.73	ENSG00000110848
-0.707	5.15295	-5.088778037	7.1E-07	6.101E-06	5.335573871	-4.348	ENSG00000206077
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-0.703	4.86494	-9.579380226	1.1E-18	1.3E-16	31.84021954	-12.63	ENSG00000251141
0.702	6.32363	8.837568901	1.8E-16	1.266E-14	26.79803757	11.05	ENSG00000154217
0.702	6.3465	2.616572626	0.00943	0.0303643	-3.544357153	1.422	ENSG00000211893
0.701	5.02039	8.240654992	9.9E-15	4.375E-13	22.8942725	9.81	ENSG00000160593
-0.699	6.41532	-7.172565994	8.5E-12	1.951E-10	16.31253916	-7.743	ENSG00000176971
0.698	6.91291	9.16638496	1.9E-17	1.703E-15	29.00870239	11.68	ENSG00000101224
-0.698	6.79321	-10.44871592	2E-21	5.611E-19	37.97633501	-14.45	ENSG00000167748
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0.697	5.91744	7.408019845	2E-12	5.222E-11	17.71478595	8.155	ENSG00000078237
0.696	6.07784	9.548522805	1.3E-18	1.557E-16	31.62665993	12.45	ENSG00000187840
0.696	8.32213	5.47836531	1.1E-07	1.071E-06	7.172520639	4.857	ENSG00000084110
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0.694	4.93862	8.351425533	4.8E-15	2.288E-13	23.60741946	9.932	ENSG00000035499
0.694	5.06605	6.132041025	3.4E-09	4.607E-08	10.48802006	5.874	ENSG00000133106
0.694	5.16857	7.847364403	1.3E-13	4.332E-12	20.40664523	8.944	ENSG00000134242
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0.693	6.4972	7.62777594	5.1E-13	1.514E-11	19.04929966	8.514	ENSG00000143476
0.692	4.36538	10.61272644	6.1E-22	1.955E-19	39.15760682	14.68	ENSG00000205755
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0.691	5.37957	8.727661088	3.9E-16	2.474E-14	26.06832496	10.65	ENSG00000154096
0.69	5.92523	9.606730541	8.8E-19	1.098E-16	32.02976758	12.45	ENSG00000113368
0.689	9.62517	6.016632713	6.4E-09	8.186E-08	9.882280606	5.651	ENSG00000108821
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0.688	6.15806	6.876549489	5E-11	9.731E-10	14.59192452	7.087	ENSG00000163638
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0.683	8.00663	5.722498003	3E-08	3.391E-07	8.377533013	5.139	ENSG00000199347
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0.679	6.01565	7.55266791	8.2E-13	2.325E-11	18.5904566	8.202	ENSG00000163563
0.678	5.90551	6.728942527	1.2E-10	2.126E-09	13.75224587	6.734	ENSG00000167286
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0.672	5.84621	9.171632529	1.9E-17	1.647E-15	29.04430631	11.24	ENSG00000102575
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0.661	4.68561	5.182132053	4.5E-07	4.043E-06	5.765889434	4.191	ENSG00000147138
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0.648	4.8799	6.693984825	1.4E-10	2.564E-09	13.55521543	6.373	ENSG00000072571
0.647	4.34176	6.944419803	3.3E-11	6.796E-10	14.98215003	6.78	ENSG00000185306
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0.642	5.71482	7.671406544	3.9E-13	1.173E-11	19.31712686	7.971	ENSG00000130508
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0.641	4.62705	7.250732165	5.3E-12	1.268E-10	16.77482213	7.232	ENSG00000184661
0.641	6.48268	7.39611205	2.2E-12	5.588E-11	17.64317426	7.48	ENSG00000167759
0.641	4.8191	3.288907049	0.00115	0.0048361	-1.639408962	1.883	ENSG00000176136
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0.637	5.06906	7.87103652	1.1E-13	3.785E-12	20.55435342	8.262	ENSG00000104998
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-0.637	7.47947	-8.971809287	7.4E-17	5.611E-15	27.69565042	-10.28	ENSG00000165312
-0.637	6.23074	-7.221657762	6.3E-12	1.483E-10	16.60249329	-7.131	ENSG00000103528
0.636	5.69913	7.303189265	3.8E-12	9.424E-11	17.08687352	7.262	ENSG00000100526
0.636	5.1746	7.088593001	1.4E-11	3.096E-10	15.81956444	6.901	ENSG00000106952
0.636	6.05917	5.867789602	1.4E-08	1.7E-07	9.113721124	4.992	ENSG00000089127
0.636	4.51959	6.973605154	2.8E-11	5.802E-10	15.15074413	6.709	ENSG00000111796
0.635	3.49849	4.909568097	1.7E-06	1.312E-05	4.527330902	3.668	ENSG00000108702
-0.634	3.83322	-6.97879229	2.7E-11	5.638E-10	15.18075799	-6.702	ENSG00000224020
-0.634	6.76935	-4.220894384	3.4E-05	0.0002062	1.64782024	-2.832	ENSG00000198523
0.634	6.28835	8.635684228	7.2E-16	4.271E-14	25.46134663	9.601	ENSG00000123609
-0.634	7.66613	-10.40961779	2.7E-21	7.099E-19	37.6957596	-13.03	ENSG00000090006
0.633	5.28603	7.972314851	5.7E-14	2.13E-12	21.18927999	8.389	ENSG00000110934
0.633	6.26686	9.929860084	8.8E-20	1.395E-17	34.28714985	12.06	ENSG00000100368
-0.633	5.7299	-8.303685759	6.6E-15	3.034E-13	23.29941438	-8.973	ENSG00000226237
0.632	5.21179	8.616477538	8.2E-16	4.806E-14	25.33502738	9.537	ENSG00000114013
-0.632	8.79751	-7.816510083	1.5E-13	5.151E-12	20.21452125	-8.098	ENSG00000178597
0.632	5.71508	7.659726954	4.2E-13	1.258E-11	19.24533967	7.823	ENSG00000143110
0.632	4.88301	8.238400734	1E-14	4.427E-13	22.87981506	8.845	ENSG00000026751
-0.631	5.04325	-5.193954492	4.3E-07	3.839E-06	5.820833554	-4.019	ENSG00000268416
-0.63	8.39669	-7.145999883	9.9E-12	2.256E-10	16.1561679	-6.935	ENSG00000153246
0.63	4.89025	9.550245983	1.3E-18	1.544E-16	31.63857753	11.27	ENSG00000071539
0.63	6.45844	6.73306516	1.1E-10	2.081E-09	13.77552863	6.262	ENSG00000154589
0.63	4.0856	8.300733709	6.7E-15	3.077E-13	23.28040087	8.927	ENSG00000155307
0.629	6.38634	7.944698239	6.8E-14	2.483E-12	21.01567275	8.281	ENSG00000123338
-0.629	5.02668	-7.58678587	6.6E-13	1.92E-11	18.79853873	-7.661	ENSG00000235703
0.629	4.1434	4.201559256	3.7E-05	0.0002215	1.572333337	2.786	ENSG00000278030
0.628	5.50471	9.577830245	1.1E-18	1.3E-16	31.8294849	11.29	ENSG00000123473
0.628	4.56697	8.216047662	1.2E-14	5.031E-13	22.73657714	8.755	ENSG00000148459
0.628	7.68428	5.959558877	8.6E-09	1.083E-07	9.585875933	5.067	ENSG00000158786
0.628	5.94279	6.207907416	2.2E-09	3.142E-08	10.89081501	5.434	ENSG00000163606
-0.626	6.30462	-8.228869003	1.1E-14	4.681E-13	22.81870904	-8.75	ENSG00000224660
-0.626	3.93823	-8.238006004	1E-14	4.433E-13	22.87728374	-8.764	ENSG00000231154
0.626	4.50784	7.570181991	7.3E-13	2.109E-11	18.69720063	7.598	ENSG00000117650
-0.626	5.28721	-7.814731037	1.6E-13	5.205E-12	20.20345731	-8.014	ENSG00000255648
-0.625	6.42632	-6.038192199	5.7E-09	7.332E-08	9.994792738	-5.151	ENSG00000254860
-0.624	6.30276	-8.228891777	1.1E-14	4.681E-13	22.818855	-8.723	ENSG00000136457
0.624	5.93131	3.134279502	0.00193	0.0076214	-2.113145709	1.694	ENSG00000125740
0.624	3.99499	7.723543624	2.8E-13	8.758E-12	19.63839499	7.834	ENSG00000174371
0.624	6.58916	7.748484111	2.4E-13	7.6E-12	19.79254567	7.877	ENSG00000169403

0.623	4.94253	7.838644633	1.3E-13	4.555E-12	20.35230297	8.023	ENSG00000093009
-0.623	4.65103	-3.065021454	0.00242	0.0092669	-2.318508389	-1.631	ENSG00000187288
0.623	7.26607	8.23652032	1E-14	4.47E-13	22.86775694	8.718	ENSG00000197506
-0.623	5.30222	-6.726337487	1.2E-10	2.156E-09	13.73753883	-6.183	ENSG00000144891
0.623	5.4562	8.189982578	1.4E-14	5.868E-13	22.56983157	8.633	ENSG00000139618
0.621	5.4938	7.700740348	3.2E-13	9.919E-12	19.49771823	7.756	ENSG00000123485
-0.621	5.0838	-6.612861067	2.3E-10	3.912E-09	13.10072058	-5.982	ENSG00000228798
-0.62	6.93573	-6.511093426	4.1E-10	6.647E-09	12.53604524	-5.821	ENSG00000101333
0.62	4.56917	6.696159767	1.4E-10	2.535E-09	13.5674533	6.102	ENSG00000051341
0.62	2.19767	6.539298043	3.5E-10	5.758E-09	12.69192796	5.858	ENSG00000254651
0.619	5.02402	7.856306762	1.2E-13	4.118E-12	20.46241216	8	ENSG00000134690
0.619	5.68884	6.702351047	1.4E-10	2.452E-09	13.60230516	6.104	ENSG00000117724
0.618	3.85538	7.844126361	1.3E-13	4.406E-12	20.38646129	7.971	ENSG00000197249
-0.618	8.26237	-8.645406881	6.7E-16	4.054E-14	25.52534796	-9.378	ENSG00000124374
0.618	7.74277	9.854041209	1.5E-19	2.233E-17	33.75457074	11.63	ENSG00000060558
0.618	4.7128	3.256480325	0.00129	0.0053263	-1.740491256	1.787	ENSG00000274428
0.618	4.54851	7.769794646	2.1E-13	6.762E-12	19.92449888	7.838	ENSG00000120280
0.617	7.80907	7.937547018	7.1E-14	2.584E-12	20.97077562	8.113	ENSG00000011600
0.617	6.73257	11.14377361	1.2E-23	5.863E-21	43.02689697	14.14	ENSG00000132334
-0.617	6.30708	-4.25533821	3E-05	0.0001813	1.783035256	-2.793	ENSG00000118729
0.616	5.80152	5.585922685	6.1E-08	6.456E-07	7.6984046	4.445	ENSG00000148346
0.616	5.32746	3.710556282	0.00026	0.0012716	-0.242449625	2.212	ENSG00000239951
0.615	7.91868	11.8252317	6.9E-26	8.085E-23	48.07878957	15.48	ENSG00000112033
-0.615	7.27207	-11.17812758	9.2E-24	5.09E-21	43.27938187	-14.17	ENSG00000100307
-0.615	4.44012	-3.160388449	0.00177	0.0070797	-2.034628374	-1.692	ENSG00000174697
-0.615	7.44009	-7.193668709	7.4E-12	1.729E-10	16.43702193	-6.841	ENSG00000095637
0.614	4.70949	8.42345211	3E-15	1.502E-13	24.07396803	8.923	ENSG00000153976
0.613	4.2243	6.93335513	3.5E-11	7.191E-10	14.918357	6.41	ENSG00000148848
-0.613	4.67276	-6.532347095	3.6E-10	5.969E-09	12.6534671	-5.789	ENSG00000260625
0.613	7.97272	9.108010317	2.9E-17	2.408E-15	28.61331223	10.14	ENSG00000075618
0.613	4.937	6.947396491	3.3E-11	6.69E-10	14.99932367	6.427	ENSG00000121807
0.613	3.75367	6.732774413	1.1E-10	2.084E-09	13.7738863	6.091	ENSG00000105835
0.613	7.38002	6.8755241	5E-11	9.772E-10	14.58604879	6.312	ENSG00000137804
0.613	6.50786	3.376713428	0.00085	0.003703	-1.361099526	1.881	ENSG00000146070
0.612	5.76176	9.036237449	4.7E-17	3.798E-15	28.12888032	9.99	ENSG00000168404
-0.612	6.74661	-9.311324473	7E-18	6.853E-16	29.9957034	-10.49	ENSG00000164292
0.611	6.93485	5.322222565	2.3E-07	2.177E-06	6.423371986	4.059	ENSG00000087116
0.611	8.70586	7.461531243	1.4E-12	3.912E-11	18.03749364	7.232	ENSG00000171954
0.61	3.89228	10.12779187	2.1E-20	4.117E-18	35.68553665	12.01	ENSG00000165490
0.61	4.04238	7.801759835	1.7E-13	5.623E-12	20.12283466	7.785	ENSG00000101916
-0.609	10.664	-7.209661124	6.7E-12	1.582E-10	16.53151802	-6.808	ENSG00000198854
0.609	8.91008	8.428953866	2.9E-15	1.457E-13	24.10969613	8.859	ENSG00000162511
0.609	7.70711	6.751176984	1E-10	1.895E-09	13.87793204	6.081	ENSG00000173918
-0.609	6.57221	-9.999700196	5.3E-20	9.134E-18	34.77925848	-11.73	ENSG00000110318
-0.609	5.30917	-3.185236022	0.00163	0.0065878	-1.959346926	-1.697	ENSG00000164434

-0.609	6.06264	-7.709118295	3.1E-13	9.538E-12	19.5493736	-7.617	ENSG00000125355
-0.609	9.7004	-5.809278264	1.9E-08	2.255E-07	8.815562482	-4.697	ENSG00000197084
0.608	5.60658	7.14798751	9.8E-12	2.231E-10	16.16785418	6.696	ENSG00000114948
0.608	6.32872	4.511650672	9.9E-06	6.726E-05	2.818759333	3.042	ENSG00000158488
-0.608	6.64617	-3.186881934	0.00162	0.0065544	-1.954341083	-1.696	ENSG00000157150
0.607	5.29709	8.338609667	5.2E-15	2.46E-13	23.5246381	8.672	ENSG00000133216
-0.607	5.02427	-7.041286059	1.9E-11	4.01E-10	15.54352775	-6.515	ENSG00000261390
0.607	10.1704	7.223952939	6.2E-12	1.464E-10	16.61608088	6.801	ENSG00000275379
0.607	5.01735	10.03666972	4.1E-20	7.154E-18	35.04033719	11.76	ENSG00000146242
0.606	3.15312	5.553714713	7.2E-08	7.515E-07	7.540095561	4.332	ENSG00000237702
-0.606	8.77052	-9.614271204	8.3E-19	1.045E-16	32.08207008	-10.96	ENSG00000266028
0.606	6.84761	6.941416771	3.4E-11	6.9E-10	14.96482939	6.35	ENSG00000082074
0.606	4.63464	9.361939323	4.9E-18	5.014E-16	30.34211655	10.48	ENSG00000151651
0.606	9.34661	11.17171715	9.7E-24	5.248E-21	43.23224938	13.94	ENSG00000216285
-0.606	4.39388	-5.517025467	8.7E-08	8.932E-07	7.360626787	-4.277	ENSG00000034971
0.605	4.69282	8.731271341	3.8E-16	2.424E-14	26.09221892	9.338	ENSG00000105639
0.605	5.01655	6.971913418	2.8E-11	5.856E-10	15.14095862	6.387	ENSG00000136250
-0.605	8.82221	-11.21783104	6.8E-24	4.065E-21	43.57149242	-14.01	ENSG00000126351
-0.605	5.09756	-6.821524585	6.8E-11	1.304E-09	14.27745823	-6.146	ENSG00000134716
0.604	4.55183	2.731328719	0.00676	0.0228337	-3.247963683	1.311	ENSG00000240382
0.604	5.33844	8.469473282	2.2E-15	1.15E-13	24.37322059	8.857	ENSG00000132357
-0.604	7.05751	-10.25529608	8.4E-21	1.89E-18	36.59230192	-12.13	ENSG00000121671
-0.603	6.53732	-6.742001321	1.1E-10	1.986E-09	13.82602967	-6.012	ENSG00000171346
-0.603	6.70653	-2.853371598	0.00469	0.0167034	-2.919634019	-1.404	ENSG00000234638
0.603	2.27944	6.647553845	1.9E-10	3.268E-09	13.29461587	5.862	ENSG00000223872
-0.602	3.4114	-5.730531663	2.9E-08	3.265E-07	8.417872402	-4.542	ENSG00000237735
-0.602	4.36237	-6.79940903	7.8E-11	1.467E-09	14.15155231	-6.088	ENSG00000231646
0.601	5.23986	8.970548999	7.4E-17	5.646E-15	27.68719148	9.699	ENSG00000122952
0.601	6.8446	10.24462668	9.1E-21	1.999E-18	36.51625112	12.04	ENSG00000160703
0.601	4.92075	2.958378207	0.00339	0.0125321	-2.626399378	1.483	ENSG00000132465
0.6	7.08567	6.262347617	1.7E-09	2.385E-08	11.18207333	5.269	ENSG00000221963
0.6	7.10155	8.478759888	2.1E-15	1.085E-13	24.43371475	8.812	ENSG00000110218
-0.6	5.39863	-7.88276679	1E-13	3.535E-12	20.62764559	-7.792	ENSG00000130518
0.599	7.98676	9.321347379	6.5E-18	6.511E-16	30.06423056	10.29	ENSG00000100504
0.598	5.20377	9.738100266	3.5E-19	4.612E-17	32.94357065	11.05	ENSG00000171310
-0.598	7.95222	-3.14658052	0.00185	0.0073641	-2.076227758	-1.635	ENSG00000175084
0.598	9.52142	5.638671797	4.7E-08	5.058E-07	7.959205958	4.383	ENSG00000274267
-0.597	6.30932	-5.954468585	8.9E-09	1.108E-07	9.559542577	-4.809	ENSG00000242086
-0.597	5.43626	-6.635462529	2E-10	3.48E-09	13.22695834	-5.789	ENSG00000042832
0.596	5.93286	4.490890697	1.1E-05	7.301E-05	2.732951841	2.96	ENSG00000157601
-0.595	6.96782	-5.720682406	3E-08	3.419E-07	8.368422348	-4.475	ENSG00000275395
-0.595	7.20222	-9.785842377	2.5E-19	3.427E-17	33.27701834	-11.07	ENSG00000214944
0.595	6.60685	6.771461929	9.2E-11	1.708E-09	13.99284609	5.968	ENSG00000170379
-0.594	4.94019	-6.95501495	3.1E-11	6.424E-10	15.04329994	-6.242	ENSG00000233382
0.594	4.58955	7.412653442	1.9E-12	5.104E-11	17.74267143	6.956	ENSG00000089685

0.594	3.21446	7.4104124	2E-12	5.171E-11	17.72918322	6.951	ENSG00000151790
0.594	8.77007	9.287214558	8.3E-18	8.029E-16	29.83100628	10.14	ENSG00000116649
0.593	5.38921	6.216798342	2.1E-09	3.006E-08	10.93825575	5.145	ENSG00000100078
0.593	6.11124	7.733352162	2.6E-13	8.281E-12	19.69898305	7.461	ENSG00000134516
-0.592	7.22762	-8.086183912	2.7E-14	1.089E-12	21.90881103	-8.031	ENSG00000179859
0.591	6.21628	6.731965474	1.2E-10	2.091E-09	13.76931714	5.871	ENSG00000137819
-0.59	7.76251	-8.730462497	3.8E-16	2.432E-14	26.08686525	-9.093	ENSG00000102349
0.59	5.96389	8.199915731	1.3E-14	5.536E-13	22.63334121	8.187	ENSG00000130775
-0.589	9.35327	-8.456550942	2.4E-15	1.237E-13	24.289103	-8.618	ENSG00000107485
0.589	6.5391	8.420306521	3E-15	1.528E-13	24.05354651	8.554	ENSG00000110876
-0.589	6.88542	-10.24520666	9E-21	1.999E-18	36.52038436	-11.81	ENSG00000197776
-0.589	5.91253	-9.409759304	3.5E-18	3.756E-16	30.67021281	-10.27	ENSG00000227051
-0.588	5.55662	-4.47850744	1.1E-05	7.659E-05	2.681927766	-2.907	ENSG00000155428
-0.588	5.22315	-7.896027299	9.3E-14	3.269E-12	20.71057699	-7.663	ENSG00000255145
-0.588	4.51439	-8.614081396	8.3E-16	4.865E-14	25.31927886	-8.862	ENSG00000156042
0.587	7.4261	9.641322175	6.9E-19	8.659E-17	32.26984883	10.66	ENSG00000176619
0.586	5.24265	6.050876646	5.3E-09	6.883E-08	10.06112815	4.852	ENSG00000137462
0.586	5.97812	10.3360818	4.7E-21	1.139E-18	37.16914889	11.91	ENSG00000129235
0.585	6.53785	6.584851382	2.7E-10	4.535E-09	12.94469262	5.595	ENSG00000138496
-0.585	5.04699	-5.934331003	9.9E-09	1.224E-07	9.455530751	-4.68	ENSG00000113205
-0.585	10.5654	-8.981726997	6.9E-17	5.294E-15	27.76223812	-9.448	ENSG00000100234
-0.584	6.29592	-8.369052469	4.3E-15	2.061E-13	23.7213922	-8.395	ENSG00000128573
0.584	7.14595	6.313902009	1.2E-09	1.838E-08	11.45958768	5.199	ENSG00000282988
-0.583	6.42629	-9.67652857	5.4E-19	6.911E-17	32.51459289	-10.66	ENSG00000162591
0.583	3.88197	8.876760496	1.4E-16	9.975E-15	27.05938264	9.242	ENSG00000163376
0.583	2.79471	6.254363928	1.7E-09	2.488E-08	11.13924471	5.106	ENSG00000162892
0.583	3.58291	4.568145127	7.8E-06	5.382E-05	3.053962562	2.978	ENSG00000211697
0.583	5.52841	8.529711158	1.5E-15	8.084E-14	24.76625883	8.643	ENSG00000149781
0.582	6.2982	6.64584307	1.9E-10	3.298E-09	13.28503795	5.661	ENSG00000087303
-0.582	6.29595	-7.771279889	2.1E-13	6.719E-12	19.93370355	-7.386	ENSG00000084444
-0.582	7.71183	-5.813458031	1.9E-08	2.212E-07	8.836786515	-4.499	ENSG00000165072
0.582	6.10232	8.767599837	3E-16	1.939E-14	26.33294155	9.036	ENSG00000155380
0.582	7.91883	5.388113932	1.7E-07	1.62E-06	6.737427595	3.946	ENSG00000260314
0.581	5.62481	9.453815007	2.6E-18	2.864E-16	30.97317212	10.21	ENSG00000092929
0.58	7.17757	7.037897196	1.9E-11	4.075E-10	15.52380066	6.22	ENSG00000108679
0.58	8.03946	7.958458816	6.2E-14	2.297E-12	21.10213204	7.66	ENSG00000100170

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127 **Table E2.** Thigh_NON-LES / Thigh_CTRL

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
2.659	10.3237	15.08972281	6E-37	1.904E-32	72.10031806	96.3	ENSG00000159516
2.65	8.12956	8.286860873	7.3E-15	5.647E-12	23.17309541	37.46	ENSG00000206073
2.584	10.1618	13.66042584	4.7E-32	7.381E-28	61.29809256	80.95	ENSG00000143556
2.569	5.6736	9.989322016	5.7E-20	1.393E-16	34.49999249	49.43	ENSG00000196805
2.241	9.5919	13.04337582	5.8E-30	6.1E-26	56.66518178	65.52	ENSG00000163202
-2.003	6.24598	-4.969104638	1.3E-06	6.58E-05	5.042299947	-11.82	ENSG00000188984

-1.993	6.59981	-4.880003843	1.9E-06	9.185E-05	4.650699315	-11.4	ENSG00000162877
1.96	7.38119	10.13045667	2.1E-20	5.452E-17	35.48126937	38.57	ENSG00000185966
-1.923	5.74934	-11.48185117	9.4E-25	7.381E-21	45.12317225	-46.2	ENSG00000156076
1.882	7.46787	8.292641874	7.1E-15	5.572E-12	23.20971784	26.63	ENSG00000163220
-1.871	6.06906	-4.518189183	9.7E-06	0.000344	3.12099437	-9.385	ENSG00000184210
-1.681	6.07306	-5.017499163	1E-06	5.486E-05	5.257413993	-10.09	ENSG00000214491
1.642	7.37578	10.73493032	2.5E-22	8.73E-19	39.74299514	35.48	ENSG00000188373
-1.603	6.18375	-4.485100651	1.1E-05	0.0003859	2.986034828	-7.939	ENSG00000147160
-1.482	5.90733	-4.455728808	1.3E-05	0.0004256	2.866938476	-7.26	ENSG00000119915
1.479	7.61311	11.37274365	2.1E-24	1.21E-20	44.33037036	35.01	ENSG00000181374
-1.474	6.09368	-6.884882437	4.7E-11	1.389E-08	14.75067526	-15.22	ENSG00000263639
-1.423	6.39769	-7.790347089	1.8E-13	9.924E-11	20.08232549	-18.12	ENSG00000168671
-1.352	6.5234	-4.452987392	1.3E-05	0.0004297	2.85585649	-6.615	ENSG00000069482
1.342	7.88756	6.308062085	1.3E-09	2.159E-07	11.58528063	11.93	ENSG00000143546
1.269	5.92833	5.242650099	3.4E-07	2.232E-05	6.280270863	8.21	ENSG00000181333
-1.263	6.7444	-4.249859738	3E-05	0.0008438	2.050943398	-5.708	ENSG00000105668
-1.262	7.88138	-3.335150206	0.00098	0.0130563	-1.161885623	-3.796	ENSG00000151365
1.206	5.71527	8.968698248	7.5E-17	1.246E-13	27.58557208	19.45	ENSG00000275385
-1.188	5.92028	-8.970888626	7.4E-17	1.246E-13	27.60003497	-19.17	ENSG00000174808
1.154	5.39774	11.05337695	2.3E-23	1.054E-19	42.02282957	26.12	ENSG00000103534
1.149	6.0454	7.424242329	1.8E-12	7.622E-10	17.8766008	13.49	ENSG00000064886
1.139	3.9568	4.061747817	6.5E-05	0.001545	1.334468169	4.764	ENSG00000171711
1.12	9.35758	6.079473559	4.5E-09	6.338E-07	10.38548377	9.344	ENSG00000057149
1.11	5.38777	5.384188669	1.7E-07	1.273E-05	6.941548252	7.52	ENSG00000262406
1.08	5.69324	7.055513654	1.7E-11	5.446E-09	15.72295474	11.63	ENSG00000198074
1.067	6.3953	7.259177573	5E-12	1.831E-09	16.90380642	12.05	ENSG00000206384
-1.065	8.18504	-8.778252738	2.8E-16	3.47E-13	26.33487164	-16.58	ENSG00000189182
1.063	5.18866	6.81798341	7E-11	1.965E-08	14.3738251	10.8	ENSG00000119125
1.041	3.92811	4.884643885	1.9E-06	9.031E-05	4.670949225	5.967	ENSG00000149968
-0.996	4.37353	-8.455624856	2.4E-15	2.368E-12	24.2479657	-14.56	ENSG00000186207
0.988	5.9401	3.413076611	0.00075	0.0105856	-0.915307979	3.087	ENSG00000169245
0.987	9.72256	7.572570466	7.2E-13	3.294E-10	18.7624155	11.98	ENSG00000168703
-0.984	3.74659	-5.814437811	1.9E-08	2.034E-06	9.035360513	-7.608	ENSG00000227012
-0.982	5.70414	-3.88241119	0.00013	0.002702	0.677829881	-3.809	ENSG00000185640
0.967	6.5029	6.177866489	2.6E-09	4.027E-07	10.89798016	8.298	ENSG00000169469
0.959	3.72667	4.155316213	4.5E-05	0.0011285	1.687334936	4.17	ENSG00000184330
-0.94	5.30917	-5.545402144	7.5E-08	6.584E-06	7.711544301	-6.696	ENSG00000164434
-0.918	6.23047	-6.27522828	1.5E-09	2.486E-07	11.41097785	-8.088	ENSG00000236543
0.9	5.61794	6.311074633	1.3E-09	2.135E-07	11.60130583	8.01	ENSG00000161905
-0.885	6.31976	-8.382310554	3.9E-15	3.522E-12	23.77956614	-12.76	ENSG00000178776
0.881	6.12545	4.684215902	4.6E-06	0.000187	3.810750135	4.701	ENSG00000185962
-0.876	6.93126	-7.170199916	8.6E-12	2.97E-09	16.3852313	-9.693	ENSG00000166923
-0.873	4.98293	-10.34192074	4.5E-21	1.28E-17	36.96164385	-17.76	ENSG00000180720
0.856	5.41135	3.526168542	0.0005	0.0077372	-0.548276999	2.826	ENSG00000012223
-0.841	5.12246	-4.125023766	5.1E-05	0.0012518	1.572330959	-3.613	ENSG00000087128

-0.819	7.41165	-3.304962195	0.00109	0.0141579	-1.256012021	-2.426	ENSG00000179593
-0.818	5.37135	-6.496731201	4.5E-10	9.187E-08	12.59937925	-7.647	ENSG00000254153
0.816	5.68078	7.153817074	9.5E-12	3.142E-09	16.2902002	8.991	ENSG00000165949
0.806	4.91541	7.364312456	2.6E-12	1.009E-09	17.52180956	9.334	ENSG00000169313
0.789	6.50619	8.687117698	5.1E-16	5.739E-13	25.74122239	12.06	ENSG00000128203
-0.786	5.12392	-3.454555867	0.00065	0.0094478	-0.781948553	-2.508	ENSG00000226510
0.785	6.68447	3.173899282	0.00169	0.0198858	-1.655571202	2.175	ENSG00000124102
0.784	5.48176	2.991175448	0.00306	0.0310239	-2.187724467	1.972	ENSG00000138755
0.784	5.45206	3.09168311	0.00222	0.0243882	-1.898620563	2.081	ENSG00000211892
-0.777	5.52205	-4.89234866	1.8E-06	8.755E-05	4.704609001	-4.465	ENSG00000134824
-0.777	5.34046	-4.216078698	3.5E-05	0.0009304	1.920212575	-3.464	ENSG00000170509
-0.774	5.2912	-3.909454482	0.00012	0.002487	0.775179163	-3.038	ENSG00000124939
-0.772	8.35267	-5.099294056	6.8E-07	3.961E-05	5.624829505	-4.761	ENSG00000125571
0.767	5.69025	8.272630252	8.1E-15	6.053E-12	23.08300527	10.81	ENSG00000197353
0.748	7.10188	5.730324138	2.9E-08	2.913E-06	8.61633432	5.641	ENSG00000105664
-0.746	4.32985	-2.81638071	0.00525	0.0456548	-2.66931194	-1.701	ENSG00000226281
0.743	5.10309	6.875845425	5E-11	1.452E-08	14.69962413	7.656	ENSG00000110079
0.742	6.48246	4.715660001	4E-06	0.0001673	3.943726067	4.002	ENSG00000131386
-0.736	7.59242	-3.278813456	0.00119	0.0151336	-1.336911706	-2.152	ENSG00000064763
-0.731	6.33164	-5.653753446	4.3E-08	4.15E-06	8.238927583	-5.387	ENSG00000106809
-0.727	7.23936	-5.449057852	1.2E-07	9.86E-06	7.249248421	-5.025	ENSG00000117594
-0.714	5.37125	-4.903398134	1.7E-06	8.454E-05	4.752956615	-4.12	ENSG00000164694
0.714	8.16106	7.947374699	6.7E-14	4.217E-11	21.04786452	9.406	ENSG00000106819
0.713	4.94288	7.073311808	1.5E-11	5.048E-09	15.82527576	7.714	ENSG00000198829
-0.712	5.31244	-3.113073555	0.00207	0.023117	-1.835952006	-1.911	ENSG00000173930
0.702	6.22696	5.910330189	1.1E-08	1.326E-06	9.518668414	5.58	ENSG00000136688
-0.699	6.8946	-11.36257411	2.3E-24	1.21E-20	44.25658768	-16.52	ENSG00000145284
-0.698	5.29421	-5.854340171	1.5E-08	1.722E-06	9.235751593	-5.46	ENSG00000169213
0.696	6.2293	7.373317544	2.5E-12	9.661E-10	17.575005	8.073	ENSG00000023445
0.694	4.82504	5.112222188	6.4E-07	3.787E-05	5.683340163	4.302	ENSG00000186481
0.691	7.68428	7.389862725	2.2E-12	9.061E-10	17.67284858	8.051	ENSG00000158786
-0.677	6.42313	-3.567237344	0.00043	0.0069247	-0.412318193	-2.278	ENSG00000103089
-0.675	5.01741	-4.342850463	2.1E-05	0.000617	2.415440625	-3.164	ENSG00000226005
-0.674	5.24207	-7.052187538	1.7E-11	5.5E-09	15.70385178	-7.247	ENSG00000168490
-0.672	5.615	-7.187465589	7.7E-12	2.705E-09	16.48553568	-7.473	ENSG00000188624
0.665	6.58916	9.315939804	6.8E-18	1.34E-14	29.89968103	11.42	ENSG00000169403
0.66	9.85667	8.57631288	1.1E-15	1.128E-12	25.02380365	9.878	ENSG00000125780
-0.652	6.53732	-8.218406888	1.2E-14	8.248E-12	22.74052282	-9.092	ENSG00000171346
-0.644	5.12021	-4.326848336	2.2E-05	0.0006527	2.352235028	-3	ENSG00000115008
-0.639	5.07122	-5.893942043	1.2E-08	1.435E-06	9.435650643	-5.054	ENSG00000183347
0.635	6.17115	6.669580822	1.7E-10	4.049E-08	13.54679142	6.212	ENSG00000173369
-0.633	5.16118	-2.992877903	0.00304	0.0309071	-2.182901246	-1.593	ENSG00000178445
0.632	6.30158	7.445018669	1.6E-12	6.793E-10	18.00001997	7.458	ENSG00000187474
0.627	4.13672	6.088850441	4.3E-09	6.104E-07	10.43406529	5.248	ENSG00000225107
-0.625	7.06446	-8.817988359	2.1E-16	2.76E-13	26.59470263	-9.802	ENSG00000092969

-0.622	7.59825	-3.069760231	0.00238	0.0256808	-1.962434572	-1.631	ENSG00000094796
0.62	7.68282	8.615492175	8.3E-16	8.974E-13	25.27692146	9.352	ENSG00000029153
-0.615	3.97307	-7.453302142	1.5E-12	6.542E-10	18.04928698	-7.275	ENSG00000164651
0.613	5.17779	5.466717343	1.1E-07	9.188E-06	7.333513115	4.263	ENSG00000248991
-0.608	5.3067	-5.416590733	1.4E-07	1.123E-05	7.094883245	-4.164	ENSG00000166415
-0.608	4.41902	-2.989757901	0.00307	0.0310931	-2.191738571	-1.526	ENSG00000100341
0.607	5.9452	5.0984198	6.8E-07	3.97E-05	5.62087707	3.745	ENSG00000177575
-0.604	6.46089	-5.91154694	1.1E-08	1.322E-06	9.524839005	-4.801	ENSG00000189433
0.594	5.45563	6.335798656	1.1E-09	1.906E-07	11.73303165	5.318	ENSG00000172243
0.588	4.6535	8.868750694	1.5E-16	2.038E-13	26.92750452	9.308	ENSG00000171119
-0.586	5.20231	-10.81961884	1.3E-22	5.247E-19	40.3471239	-12.82	ENSG00000007402
-0.582	6.91074	-5.946219418	9.3E-09	1.149E-06	9.70107388	-4.678	ENSG00000223863

Table E3. Upper_back_LES / Upper_back_NON-LES

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
2.585	3.72667	9.230941579	1.2E-17	4.843E-14	29.36073485	43.72	ENSG00000184330
2.528	6.68447	8.420091535	3E-15	3.427E-12	24.04032144	36.69	ENSG00000124102
2.507	3.32708	8.760488581	3.1E-16	5.436E-13	26.24335703	38.88	ENSG00000196611
2.409	7.46787	8.743720939	3.5E-16	5.481E-13	26.1337671	37.23	ENSG00000163220
2.36	8.12956	6.079548581	4.5E-09	3.123E-07	10.37758303	19.7	ENSG00000206073
2.217	4.2732	8.851319057	1.7E-16	3.771E-13	26.83887473	34.97	ENSG00000163221
2.167	3.83615	7.601879615	6E-13	2.457E-10	18.94760589	26.49	ENSG00000170465
2.159	4.61294	10.85670148	1E-22	1.594E-18	40.67021895	47.48	ENSG00000188293
2.156	5.6736	6.906320929	4.2E-11	7.157E-09	14.87253139	22.38	ENSG00000196805
2.128	6.12545	9.316228238	6.8E-18	3.565E-14	29.9343032	36.53	ENSG00000185962
2.1	4.9424	6.950243414	3.2E-11	5.803E-09	15.12231102	22.04	ENSG00000244094
2.042	8.30859	8.132017063	2E-14	1.519E-11	22.2132238	27.96	ENSG00000186832
2.036	7.38119	8.667583049	5.8E-16	8.332E-13	25.63751555	31.01	ENSG00000185966
2.026	5.69324	10.90460351	7.1E-23	1.594E-18	41.01388191	44.88	ENSG00000198074
1.981	3.9568	5.82088989	1.8E-08	9.179E-07	9.05686157	15.34	ENSG00000171711
1.979	4.78988	7.714771155	2.9E-13	1.387E-10	19.63201104	24.8	ENSG00000134827
1.87	5.92833	6.362647162	9.5E-10	9.413E-08	11.8711112	16.87	ENSG00000181333
1.809	5.38777	7.225213437	6.1E-12	1.574E-09	16.70965329	20.28	ENSG00000262406
1.796	7.37578	9.6715694	5.6E-19	3.508E-15	32.34994606	32.79	ENSG00000188373
1.74	5.41135	5.902456462	1.2E-08	6.543E-07	9.468719175	13.8	ENSG00000012223
1.724	6.31863	7.343492233	3E-12	8.868E-10	17.40467592	19.87	ENSG00000205420
1.642	9.5919	7.872465152	1.1E-13	6.088E-11	20.59816215	21.29	ENSG00000163202
1.566	6.10436	7.646543873	4.5E-13	1.958E-10	19.21764914	19.33	ENSG00000007908
-1.555	6.39769	-7.012776731	2.2E-11	4.35E-09	15.47974336	-16.57	ENSG00000168671
1.548	7.88756	5.993338269	7.2E-09	4.435E-07	9.9326509	12.6	ENSG00000143546
-1.409	6.24598	-2.879027406	0.00434	0.0227511	-2.531843519	-3.329	ENSG00000188984
1.394	9.35758	6.233491021	1.9E-09	1.632E-07	11.18363081	12.14	ENSG00000057149
1.374	4.06774	6.369257135	9.1E-10	9.128E-08	11.9065664	12.42	ENSG00000136694
1.358	5.51888	7.422083167	1.8E-12	6.098E-10	17.87044186	15.94	ENSG00000175592
1.325	5.9401	3.772864592	0.0002	0.0019497	0.262518129	4.897	ENSG00000169245

-1.319	8.18504	-8.954663877	8.3E-17	2.4E-13	27.52021688	-21.22	ENSG00000189182
1.285	6.5029	6.759697401	9.8E-11	1.496E-08	14.04643958	12.86	ENSG00000169469
-1.275	7.96606	-4.186956331	3.9E-05	0.0005016	1.783873808	-5.615	ENSG00000124935
-1.267	4.32985	-3.941067912	0.00011	0.0011349	0.863718474	-5.04	ENSG00000226281
1.264	6.06162	9.2471703	1.1E-17	4.843E-14	29.46968411	21.43	ENSG00000172382
-1.203	7.88138	-2.617797258	0.00939	0.0417419	-3.21662548	-2.438	ENSG00000151365
1.201	6.22696	8.329966695	5.5E-15	5.809E-12	23.46492156	17.12	ENSG00000136688
1.198	3.23286	5.234054695	3.5E-07	1.03E-05	6.224368556	7.727	ENSG00000200972
-1.177	6.07306	-2.894371228	0.00414	0.021929	-2.489726178	-2.805	ENSG00000214491
1.16	5.78275	7.992320812	5E-14	3.289E-11	21.34019079	15.43	ENSG00000137648
1.121	5.85516	8.283517659	7.5E-15	6.63E-12	23.16970161	15.83	ENSG00000148798
-1.117	6.09368	-4.296674711	2.5E-05	0.0003473	2.210009756	-5.141	ENSG00000263639
1.106	4.01297	8.486352974	2E-15	2.375E-12	24.4655126	16.27	ENSG00000090104
1.104	5.77228	8.20381302	1.3E-14	1.031E-11	22.66526058	15.34	ENSG00000184557
-1.102	6.23047	-6.20551024	2.3E-09	1.834E-07	11.03603295	-9.525	ENSG00000236543
1.097	4.44352	5.492052969	9.8E-08	3.665E-06	7.440870634	7.69	ENSG00000182585
-1.096	8.35267	-5.968800146	8.2E-09	4.962E-07	9.806869505	-8.866	ENSG00000125571
-1.089	5.90733	-2.695514961	0.00751	0.0351114	-3.019297189	-2.313	ENSG00000119915
-1.064	5.92028	-6.616412623	2.3E-10	2.975E-08	13.25086733	-10.26	ENSG00000174808
1.057	3.6294	6.044236416	5.5E-09	3.618E-07	10.19476992	8.733	ENSG00000134028
-1.046	7.23936	-6.461360707	5.4E-10	6.112E-08	12.40331621	-9.692	ENSG00000117594
-1.045	5.34046	-4.669661539	4.9E-06	8.977E-05	3.728632013	-5.543	ENSG00000170509
-1.034	5.01741	-5.477888306	1.1E-07	3.877E-06	7.372892296	-7.211	ENSG00000226005
-1.028	5.07315	-4.567754149	7.8E-06	0.0001296	3.303123483	-5.254	ENSG00000253745
1.024	5.48176	3.218135154	0.00146	0.0096188	-1.552678733	2.904	ENSG00000138755
1.022	5.97654	6.218216205	2.1E-09	1.739E-07	11.10299699	8.867	ENSG00000102962
-1.018	6.5234	-2.761802715	0.00618	0.0301744	-2.846695934	-2.249	ENSG00000069482
-1.008	9.03191	-2.691147059	0.0076	0.0354565	-3.030531809	-2.135	ENSG00000159763
-1	5.24207	-8.622393936	7.9E-16	1.08E-12	25.34405488	-15.1	ENSG00000168490
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-0.981	8.29082	-3.370783264	0.00087	0.0062842	-1.079250303	-3.003	ENSG00000268751
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0.967	4.00151	7.014264803	2.2E-11	4.35E-09	15.48827482	10.31	ENSG00000227471
0.965	6.41278	6.352322226	1E-09	9.806E-08	11.81578184	8.683	ENSG00000111335
0.959	5.76848	4.96332502	1.3E-06	2.964E-05	4.998244944	5.65	ENSG00000137558
0.959	7.95533	5.05159491	8.5E-07	2.112E-05	5.392238588	5.821	ENSG00000170345
0.959	9.08783	7.175275938	8.3E-12	2.048E-09	16.41839243	10.62	ENSG00000186831
0.95	5.83048	6.534265462	3.6E-10	4.47E-08	12.80008099	8.975	ENSG00000106366
-0.949	5.29421	-6.555354651	3.2E-10	4.01E-08	12.91543446	-9.01	ENSG00000169213
0.946	8.63872	5.414697671	1.4E-07	4.976E-06	7.071301521	6.471	ENSG00000108691
0.935	4.42722	6.045275178	5.4E-09	3.606E-07	10.20013645	7.725	ENSG00000158485
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0.922	4.6504	9.775450963	2.7E-19	2.094E-15	33.06369102	17.13	ENSG00000253161
0.911	7.06628	10.09549148	2.7E-20	2.808E-16	35.2827009	17.84	ENSG00000139629

0.909	8.07917	7.97786533	5.5E-14	3.502E-11	21.25034979	12.06	ENSG00000197641
-0.898	6.48822	-7.053251674	1.7E-11	3.668E-09	15.71222087	-9.665	ENSG00000156284
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-0.885	6.35435	-3.875882625	0.00014	0.0014056	0.627979818	-3.423	ENSG00000141469
0.882	8.55801	7.843622826	1.3E-13	6.832E-11	20.42058366	11.37	ENSG00000227300
0.882	8.57984	5.421445333	1.4E-07	4.848E-06	7.103375611	6.045	ENSG00000126709
0.881	9.59258	6.703350634	1.4E-10	1.953E-08	13.73218449	8.693	ENSG00000165474
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0.878	5.71527	5.379706446	1.7E-07	5.718E-06	6.905478357	5.94	ENSG00000275385
0.869	6.3953	4.873740281	2E-06	4.112E-05	4.604181906	4.963	ENSG00000206384
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0.865	5.71604	6.432100698	6.4E-10	7.084E-08	12.24495849	7.949	ENSG00000100985
0.864	6.21568	7.358451841	2.7E-12	8.325E-10	17.49309206	9.991	ENSG00000103044
0.862	4.46042	6.464531033	5.4E-10	6.07E-08	12.42050474	7.995	ENSG00000272666
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0.85	5.09426	7.828645443	1.4E-13	7.159E-11	20.32852216	10.92	ENSG00000135114
0.847	4.41917	5.348903473	2E-07	6.485E-06	6.760203277	5.67	ENSG00000257764
0.842	6.02164	5.837882541	1.6E-08	8.591E-07	9.142307929	6.551	ENSG00000184613
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0.809	7.99928	7.00680131	2.3E-11	4.453E-09	15.44549695	8.603	ENSG00000163207
0.806	10.1618	3.510534995	0.00053	0.0042325	-0.62833418	2.64	ENSG00000143556
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0.795	5.97717	6.188146168	2.5E-09	1.975E-07	10.94468003	6.838	ENSG00000189057
0.794	5.15737	4.459231727	1.2E-05	0.0001939	2.858697315	3.893	ENSG00000101670
0.793	6.81	7.348194715	2.9E-12	8.698E-10	17.43245683	9.151	ENSG00000025708
0.792	10.5357	8.807230814	2.3E-16	4.75E-13	26.54942411	12.39	ENSG00000105427
0.791	6.84914	7.861924167	1.2E-13	6.398E-11	20.53321798	10.23	ENSG00000088826
0.789	6.09437	6.00110994	6.9E-09	4.318E-07	9.972567933	6.442	ENSG00000151012
0.787	3.49849	5.656102377	4.3E-08	1.842E-06	8.23805316	5.802	ENSG00000108702
-0.784	5.92552	-5.0585657	8.2E-07	2.061E-05	5.423592647	-4.769	ENSG00000115425
0.78	3.92811	3.015266635	0.00283	0.0162213	-2.150590881	1.988	ENSG00000149968
0.78	7.68282	8.930422967	9.8E-17	2.564E-13	27.36004272	12.49	ENSG00000029153
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0.758	6.60186	5.823092408	1.8E-08	9.132E-07	9.067926186	5.876	ENSG00000183760
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0.754	5.38595	3.950601102	0.0001	0.0011011	0.898484778	3.009	ENSG00000172752
0.753	5.21855	4.915624235	1.6E-06	3.533E-05	4.787688788	4.361	ENSG00000073756
0.753	3.86045	5.098317152	6.8E-07	1.758E-05	5.603058818	4.641	ENSG00000102837
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0.711	7.13189	4.887836812	1.8E-06	3.915E-05	4.665799493	4.082	ENSG00000276410
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0.7	4.34176	6.980841402	2.7E-11	5.097E-09	15.2969397	7.403	ENSG00000185306
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0.699	6.49276	8.202703471	1.3E-14	1.031E-11	22.65825767	9.715	ENSG00000198805
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0.694	5.38921	6.750235732	1E-10	1.565E-08	13.9935448	6.926	ENSG00000100078
0.693	4.7128	3.390666112	0.00081	0.005949	-1.016112251	2.142	ENSG00000274428
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0.661	4.94684	6.054068209	5.2E-09	3.467E-07	10.24559092	5.475	ENSG00000154839
0.661	5.06034	4.903238658	1.7E-06	3.687E-05	4.733289619	3.81	ENSG00000226145
0.658	6.67175	4.786384433	2.9E-06	5.749E-05	4.225609027	3.643	ENSG00000138642
0.658	5.44758	8.034203897	3.8E-14	2.618E-11	21.60102614	8.832	ENSG00000137563
0.658	5.00475	5.314262782	2.4E-07	7.489E-06	6.597614901	4.356	ENSG00000126787
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0.655	6.19099	4.687454862	4.6E-06	8.395E-05	3.80373186	3.496	ENSG00000174502
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0.654	6.0454	3.480215606	0.00059	0.0046114	-0.727570686	2.11	ENSG00000064886
0.653	4.78771	5.85207143	1.5E-08	8.06E-07	9.213799396	5.106	ENSG00000176920
0.653	6.06243	6.927831629	3.7E-11	6.442E-09	14.9947269	6.814	ENSG00000280693
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0.652	5.41671	5.583934568	6.2E-08	2.519E-06	7.885129249	4.701	ENSG00000112984
0.651	4.75768	6.154611846	3E-09	2.276E-07	10.76878179	5.547	ENSG00000163823
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0.646	4.08987	6.029482619	5.9E-09	3.835E-07	10.11862117	5.318	ENSG00000110848
0.645	8.65091	5.750481271	2.6E-08	1.219E-06	8.704824019	4.895	ENSG00000185664
0.645	6.30544	4.072976777	6.2E-05	0.0007326	1.351305717	2.712	ENSG00000088882
0.644	7.68428	5.675276738	3.9E-08	1.695E-06	8.33240647	4.777	ENSG00000158786
0.644	7.26772	6.031614402	5.9E-09	3.81E-07	10.12961545	5.297	ENSG00000148773
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-0.642	5.43088	-4.127031301	5E-05	0.0006133	1.555157281	-2.761	ENSG00000183378
0.642	2.93682	5.040960914	8.9E-07	2.2E-05	5.344475149	3.885	ENSG00000169429
0.641	4.54575	5.771196454	2.3E-08	1.121E-06	8.808061474	4.893	ENSG00000094804
0.641	4.92731	6.409525924	7.3E-10	7.678E-08	12.1231294	5.856	ENSG00000150637
-0.641	7.26544	-6.951903579	3.2E-11	5.802E-09	15.13177281	-6.727	ENSG00000153993
0.64	6.10257	5.831059243	1.7E-08	8.828E-07	9.107974904	4.974	ENSG00000101447
-0.638	8.50418	-5.176763522	4.7E-07	1.289E-05	5.960535578	-4.04	ENSG00000131969
-0.638	5.26241	-2.939296598	0.0036	0.0196582	-2.365209896	-1.559	ENSG00000223392
0.637	9.08052	5.896600005	1.2E-08	6.703E-07	9.43900472	5.046	ENSG00000122862
-0.637	6.50943	-6.403889491	7.5E-10	7.838E-08	12.09275867	-5.814	ENSG00000109819
0.637	8.33514	8.207544839	1.2E-14	1.031E-11	22.68881784	8.856	ENSG00000182481
-0.636	4.85493	-5.168373374	4.9E-07	1.337E-05	5.922092886	-4.017	ENSG00000127324
0.636	6.07987	6.182940579	2.6E-09	2.017E-07	10.91732948	5.464	ENSG00000166851
0.636	5.93286	4.447439039	1.3E-05	0.0002023	2.810948498	3.104	ENSG00000157601
-0.636	8.44775	-5.111370349	6.4E-07	1.67E-05	5.662237229	-3.938	ENSG00000166869
0.635	5.68441	5.092372902	7E-07	1.802E-05	5.576150187	3.911	ENSG00000274641
-0.635	5.81775	-6.357567525	9.8E-10	9.594E-08	11.84388238	-5.725	ENSG00000165238
0.634	4.74417	6.332148419	1.1E-09	1.06E-07	11.70785945	5.672	ENSG00000081985
0.633	5.24136	4.512740943	9.9E-06	0.0001587	3.076702428	3.17	ENSG00000204936
0.633	5.9424	4.738196592	3.6E-06	6.99E-05	4.019201921	3.445	ENSG00000151006
-0.633	3.94792	-3.838908385	0.00016	0.0015832	0.495808518	-2.407	ENSG00000178449
0.632	5.60658	6.903042385	4.2E-11	7.257E-09	14.85392936	6.561	ENSG00000114948
-0.631	6.48937	-6.091988085	4.2E-09	2.981E-07	10.44216946	-5.281	ENSG00000228065
-0.63	3.32775	-3.855804923	0.00015	0.0015022	0.556069313	-2.413	ENSG00000259517
0.629	5.68078	4.544749242	8.6E-06	0.0001411	3.20815948	3.186	ENSG00000165949
0.629	7.23398	7.079025199	1.5E-11	3.185E-09	15.86071585	6.807	ENSG00000146072
0.628	6.34077	6.947482737	3.3E-11	5.865E-09	15.10658041	6.584	ENSG00000184731
0.628	5.75813	6.819340938	6.9E-11	1.115E-08	14.3810313	6.377	ENSG00000138180
-0.628	6.42313	-2.723205604	0.00692	0.0329853	-2.947675451	-1.355	ENSG00000103089
0.627	6.25625	6.368555042	9.2E-10	9.135E-08	11.9027992	5.664	ENSG00000101057
0.626	7.58922	5.659583079	4.2E-08	1.814E-06	8.255162855	4.623	ENSG00000143119

-0.626	3.96668	-3.889803458	0.00013	0.0013454	0.678032467	-2.434	ENSG00000231346
0.626	6.11937	6.008094767	6.7E-09	4.212E-07	10.00847625	5.116	ENSG00000115956
0.625	5.65204	6.796770944	7.9E-11	1.253E-08	14.25418221	6.319	ENSG00000171848
-0.624	3.89058	-3.735182295	0.00023	0.0021967	0.13102367	-2.267	ENSG00000268100
0.623	4.87838	5.15284227	5.2E-07	1.417E-05	5.851063045	3.911	ENSG00000183813
-0.623	6.55727	-2.950397921	0.00348	0.0191177	-2.334165915	-1.531	ENSG00000228639
0.622	4.12223	6.011638112	6.5E-09	4.161E-07	10.02670405	5.093	ENSG00000158859
-0.621	6.91074	-5.224345609	3.7E-07	1.069E-05	6.179493938	-3.995	ENSG00000223863
0.62	7.26861	5.585047451	6.1E-08	2.508E-06	7.890545106	4.47	ENSG00000145386
0.619	4.9875	6.14905122	3.1E-09	2.333E-07	10.73968182	5.268	ENSG00000134057
0.618	8.87457	7.230198622	6E-12	1.54E-09	16.73880091	6.942	ENSG00000092295
-0.617	6.83796	-3.19617913	0.00157	0.0101883	-1.619119581	-1.73	ENSG00000131941
0.617	6.30158	5.982852266	7.6E-09	4.637E-07	9.878853232	5.006	ENSG00000187474
0.616	6.8914	5.887019763	1.3E-08	6.948E-07	9.39044415	4.867	ENSG00000068489
0.616	4.70101	4.225138131	3.4E-05	0.0004416	1.931090075	2.756	ENSG00000248329
0.616	7.83721	7.525990449	9.6E-13	3.707E-10	18.49100403	7.396	ENSG00000077238
0.615	7.92183	7.844862884	1.3E-13	6.832E-11	20.42821061	7.93	ENSG00000059728
0.615	4.91472	4.805464288	2.7E-06	5.35E-05	4.307812968	3.428	ENSG00000170542
0.614	4.70338	5.570968441	6.6E-08	2.647E-06	7.822090821	4.412	ENSG00000080986
0.614	6.91291	7.482722827	1.3E-12	4.583E-10	18.23194515	7.304	ENSG00000101224
-0.614	5.50791	-3.21088929	0.0015	0.0098034	-1.574651542	-1.733	ENSG00000254682
0.613	5.08059	6.820396494	6.9E-11	1.114E-08	14.38697076	6.234	ENSG00000105173
-0.61	6.30276	-7.463918791	1.4E-12	5.024E-10	18.11964835	-7.225	ENSG00000136457
0.609	4.24648	5.228953498	3.6E-07	1.051E-05	6.200782953	3.923	ENSG00000116824
-0.609	7.55855	-3.229410733	0.00141	0.0093225	-1.518395535	-1.736	ENSG00000203837
-0.607	5.63636	-4.554767508	8.2E-06	0.0001362	3.249465133	-3.087	ENSG00000280916
0.606	9.79201	8.77815847	2.8E-16	5.425E-13	26.35896081	9.436	ENSG00000168461
-0.606	7.14834	-3.558104662	0.00045	0.0037232	-0.471071245	-2.028	ENSG00000139292
-0.604	6.93573	-5.890361867	1.2E-08	6.88E-07	9.407377976	-4.774	ENSG00000101333
-0.604	3.11989	-3.433203797	0.0007	0.0052739	-0.879900481	-1.905	ENSG00000124003
-0.603	3.33735	-2.885580296	0.00425	0.0224095	-2.513882028	-1.43	ENSG00000174827
0.603	6.19335	6.286967302	1.4E-09	1.279E-07	11.46704939	5.326	ENSG00000090339
0.601	4.80267	5.868292749	1.4E-08	7.511E-07	9.295691147	4.719	ENSG00000115919
0.601	3.72288	6.091197962	4.2E-09	2.987E-07	10.43806423	5.029	ENSG00000065675
0.599	5.34341	6.652029231	1.8E-10	2.464E-08	13.44752848	5.833	ENSG00000111206
0.599	5.91506	7.482394853	1.3E-12	4.583E-10	18.22998499	7.125	ENSG00000085831
-0.598	6.36592	-5.381074535	1.7E-07	5.685E-06	6.911945858	-4.049	ENSG00000112379
0.598	4.42502	7.085197355	1.4E-11	3.112E-09	15.89632965	6.484	ENSG00000164430
-0.597	8.5381	-3.983183976	8.9E-05	0.0009919	1.017867246	-2.417	ENSG00000175315
0.597	3.75385	4.248226732	3.1E-05	0.0004089	2.020671404	2.695	ENSG00000187116
0.596	4.42743	7.542082246	8.7E-13	3.395E-10	18.58758744	7.187	ENSG00000128578
-0.595	6.22827	-5.552105521	7.2E-08	2.877E-06	7.730585762	-4.247	ENSG00000253047
-0.595	5.63663	-5.637901719	4.7E-08	1.987E-06	8.14871771	-4.359	ENSG00000154263
0.595	8.9664	7.584061427	6.7E-13	2.712E-10	18.84014619	7.238	ENSG00000165272
0.593	5.4599	5.219992793	3.8E-07	1.086E-05	6.159397138	3.809	ENSG00000168078

0.593	6.59634	6.920474107	3.8E-11	6.655E-09	14.95290254	6.176	ENSG00000167600
0.592	6.14556	5.864304107	1.4E-08	7.638E-07	9.275539092	4.646	ENSG00000137812
0.591	4.5298	3.430640521	0.00071	0.0053128	-0.888152118	1.864	ENSG00000273727
0.591	8.32213	4.322002443	2.2E-05	0.0003167	2.309726085	2.749	ENSG00000084110
0.591	8.61928	5.261354942	3.1E-07	9.224E-06	6.350903488	3.848	ENSG00000103257
0.59	4.52673	6.109688328	3.8E-09	2.76E-07	10.53423674	4.967	ENSG00000117090
0.589	7.72544	4.409558113	1.5E-05	0.0002318	2.658295047	2.832	ENSG00000124610
0.588	3.66268	6.654705411	1.8E-10	2.443E-08	13.46233476	5.731	ENSG00000258689
-0.588	5.15018	-3.206540321	0.00152	0.0099036	-1.587817781	-1.657	ENSG00000140284
0.588	8.20262	5.217305965	3.8E-07	1.097E-05	6.146998815	3.772	ENSG00000090382
-0.588	4.52291	-2.917950655	0.00385	0.0207051	-2.424595782	-1.419	ENSG00000279301
-0.587	4.76059	-3.102825238	0.00214	0.0129811	-1.896938462	-1.567	ENSG00000091513
0.587	6.20354	4.890093004	1.8E-06	3.883E-05	4.675675131	3.37	ENSG00000132514
-0.586	9.20233	-5.803877762	2E-08	9.739E-07	8.971505495	-4.517	ENSG00000165953
-0.586	6.30907	-5.272532551	2.9E-07	8.859E-06	6.402861968	-3.828	ENSG00000164128
0.586	5.14772	6.429650983	6.5E-10	7.133E-08	12.23172346	5.381	ENSG00000258232
-0.586	4.94641	-8.952784177	8.4E-17	2.4E-13	27.50778883	-9.415	ENSG00000097096
-0.585	5.32734	-8.036339839	3.8E-14	2.618E-11	21.61434925	-7.855	ENSG00000151623
-0.585	5.87461	-3.792575609	0.00019	0.0018343	0.331768316	-2.18	ENSG00000165548
0.585	5.0228	5.080789529	7.4E-07	1.884E-05	5.52378694	3.585	ENSG00000090889
0.584	6.64675	6.964679541	2.9E-11	5.452E-09	15.20463725	6.15	ENSG00000103187
-0.584	5.7782	-2.584645065	0.01032	0.0447534	-3.299140393	-1.159	ENSG00000253125
-0.583	5.44892	-5.294204258	2.6E-07	8.134E-06	6.503850909	-3.836	ENSG00000174514
0.583	6.67859	5.093916243	6.9E-07	1.79E-05	5.583134199	3.589	ENSG00000140968
0.583	4.68947	3.268062159	0.00124	0.0083684	-1.400042254	1.694	ENSG00000169248
-0.582	5.04325	-4.451782724	1.3E-05	0.0001992	2.828523678	-2.849	ENSG00000268416
0.582	6.48072	5.147732942	5.4E-07	1.445E-05	5.827733568	3.65	ENSG00000147168
-0.582	3.60808	-4.670042473	4.9E-06	8.967E-05	3.730237314	-3.088	ENSG00000100024

Table E4. Upper_back_NON-LES / Upper_back_CTRL

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
-3.12	4.94002	-5.93838979	9.7E-09	1.847E-06	9.6749633	-25.01	ENSG00000184227
-2.442	6.59981	-3.45985741	0.00064	0.0125426	-0.692408509	-7.807	ENSG00000162877
-2.406	6.06906	-3.360608711	0.0009	0.0164478	-1.007801287	-7.328	ENSG00000184210
-2.38	6.24598	-3.41577874	0.00074	0.0141629	-0.833510364	-7.447	ENSG00000188984
-2.367	6.07306	-4.087798131	5.9E-05	0.0019896	1.492444579	-10.01	ENSG00000214491
2.341	10.3237	7.685923796	3.5E-13	5.87E-10	19.40070527	29.15	ENSG00000159516
-2.282	5.90733	-3.968712192	9.5E-05	0.0029062	1.053427626	-9.184	ENSG00000119915
-2.178	6.18375	-3.525823719	0.0005	0.0105454	-0.478185287	-7.185	ENSG00000147160
-2.098	3.36446	-5.66341199	4.1E-08	5.764E-06	8.308087419	-15.5	ENSG00000250411
2.081	9.5919	7.004799543	2.3E-11	1.553E-08	15.41146759	22.13	ENSG00000163202
-2.019	5.26709	-3.959833556	9.8E-05	0.0029951	1.021151281	-8.095	ENSG00000204195
-1.964	4.04687	-4.560301532	8E-06	0.0003987	3.344111392	-10.01	ENSG00000250266
-1.952	4.19424	-5.602919117	5.6E-08	7.374E-06	8.014001776	-14.16	ENSG00000132915
-1.916	5.42736	-5.01836117	9.9E-07	7.45E-05	5.30035634	-11.5	ENSG00000249365

-1.899	7.88138	-2.903571839	0.00402	0.0471881	-2.351142156	-4.55	ENSG00000151365
-1.847	5.07315	-5.762005714	2.5E-08	3.908E-06	8.792555707	-14.06	ENSG00000253745
-1.835	6.5234	-3.496467852	0.00056	0.0114335	-0.573968819	-5.97	ENSG00000069482
-1.831	4.35216	-5.826677916	1.7E-08	3.011E-06	9.113775613	-14.2	ENSG00000173124
-1.773	4.61631	-4.308685704	2.4E-05	0.0009588	2.336501232	-8.2	ENSG00000146453
-1.76	3.33735	-5.915060334	1.1E-08	2.067E-06	9.557109913	-14.01	ENSG00000174827
-1.759	4.41902	-5.009093691	1E-06	7.71E-05	5.259259286	-10.53	ENSG00000100341
-1.755	5.30917	-5.992217752	7.2E-09	1.483E-06	9.948199222	-14.29	ENSG00000164434
-1.726	7.41165	-4.029134771	7.4E-05	0.0023949	1.274761784	-7.124	ENSG00000179593
-1.712	4.05076	-4.925092627	1.5E-06	0.0001061	4.889571238	-9.953	ENSG00000259283
-1.709	4.8191	-5.723696905	3E-08	4.564E-06	8.603559615	-12.86	ENSG00000176136
-1.7	6.52985	-5.378978775	1.7E-07	1.935E-05	6.946624559	-11.49	ENSG00000185499
-1.696	2.98437	-8.431419021	2.8E-15	1.113E-11	24.01717165	-24.67	ENSG00000157330
-1.695	4.06002	-7.797300721	1.7E-13	3.06E-10	20.07462976	-21.63	ENSG00000225611
1.694	7.38119	5.066888004	7.9E-07	6.23E-05	5.516553881	10.34	ENSG00000185966
-1.67	5.16118	-4.567984775	7.8E-06	0.0003886	3.375639275	-8.531	ENSG00000178445
-1.648	5.57868	-5.100582302	6.7E-07	5.456E-05	5.667656411	-10.17	ENSG00000103740
-1.644	5.58043	-5.769946163	2.4E-08	3.768E-06	8.831849262	-12.54	ENSG00000176194
-1.632	5.31244	-4.128351661	5E-05	0.0017633	1.644527069	-7.021	ENSG00000173930
-1.63	5.74217	-4.922689938	1.6E-06	0.0001065	4.879071994	-9.469	ENSG00000130208
-1.614	4.32985	-3.525641349	0.0005	0.0105454	-0.478782561	-5.325	ENSG00000226281
1.595	7.37578	6.030636155	5.9E-09	1.264E-06	10.14432906	13.12	ENSG00000188373
-1.579	5.50791	-5.803081338	2E-08	3.354E-06	8.996260713	-12.16	ENSG00000254682
-1.56	5.18037	-5.07926192	7.5E-07	5.948E-05	5.571951107	-9.559	ENSG00000116882
-1.557	6.42313	-4.745790118	3.5E-06	0.0002061	4.117633438	-8.494	ENSG00000103089
-1.555	7.59242	-4.007477631	8.1E-05	0.0025626	1.195092918	-6.36	ENSG00000064763
-1.549	4.89682	-4.874004601	2E-06	0.000128	4.667230508	-8.846	ENSG00000101049
-1.545	7.65361	-4.994628923	1.1E-06	8.132E-05	5.195237762	-9.201	ENSG00000095321
-1.519	5.70414	-3.473911205	0.00061	0.0121223	-0.647075943	-4.89	ENSG00000185640
-1.519	3.28162	-7.246694288	5.4E-12	4.997E-09	16.80130842	-17.11	ENSG00000256612
-1.5	4.642	-5.588072387	6E-08	7.845E-06	7.942195134	-10.83	ENSG00000166391
-1.49	3.48891	-9.587150962	1E-18	1.595E-14	31.60778705	-26.81	ENSG00000152463
-1.479	5.7782	-4.600841979	6.7E-06	0.0003464	3.510970124	-7.652	ENSG00000253125
-1.475	3.46154	-5.451133882	1.2E-07	1.429E-05	7.28684204	-10.21	ENSG00000047936
-1.472	5.12246	-4.175137351	4.1E-05	0.001516	1.821598202	-6.452	ENSG00000087128
-1.465	4.13752	-7.982266702	5.3E-14	1.203E-10	21.20643923	-19.44	ENSG00000138769
-1.443	5.71038	-6.372755706	9E-10	2.595E-07	11.93094872	-13.05	ENSG00000165140
-1.437	8.18822	-5.844322125	1.6E-08	2.79E-06	9.201880952	-11.2	ENSG00000186480
1.428	9.72256	6.336955664	1.1E-09	3.113E-07	11.74067696	12.79	ENSG00000168703
-1.427	7.42109	-4.319674081	2.3E-05	0.0009285	2.379487188	-6.631	ENSG00000057252
-1.406	3.11989	-5.61534495	5.2E-08	7.037E-06	8.074212211	-10.23	ENSG00000124003
1.4	7.61311	6.229698533	2E-09	5.054E-07	11.17521493	12.18	ENSG00000181374
-1.383	5.90725	-7.658203343	4.2E-13	6.463E-10	19.23387883	-17.11	ENSG00000166816
-1.374	5.51919	-5.591604197	5.9E-08	7.749E-06	7.959263553	-9.927	ENSG00000267475
-1.368	5.34243	-7.448093403	1.6E-12	1.827E-09	17.98140248	-16.15	ENSG00000214456

-1.349	5.01909	-8.043148377	3.6E-14	1.033E-10	21.5823383	-18.13	ENSG00000143028
-1.331	6.28375	-8.004654763	4.6E-14	1.162E-10	21.34447787	-17.75	ENSG00000105552
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-0.728	9.47444	-7.347369544	2.9E-12	2.961E-09	17.38866214	-8.397	ENSG00000104823
0.728	5.18387	3.81628385	0.00017	0.0045804	0.508152548	2.742	ENSG00000181143
-0.728	6.57367	-5.240996729	3.4E-07	3.244E-05	6.305977576	-4.705	ENSG00000162836
-0.726	8.79337	-7.596596049	6.2E-13	8.889E-10	18.86442492	-8.861	ENSG00000131473
-0.724	3.10211	-2.955578192	0.00342	0.0423216	-2.207435564	-1.785	ENSG00000225489
-0.723	3.06299	-5.956831683	8.8E-09	1.715E-06	9.768370194	-5.827	ENSG00000280634
0.721	9.77076	5.155521985	5.2E-07	4.382E-05	5.915759426	4.535	ENSG00000107165
-0.721	7.15628	-5.278586531	2.8E-07	2.827E-05	6.47920127	-4.717	ENSG00000076555
-0.72	7.4757	-5.450689825	1.2E-07	1.429E-05	7.284737444	-4.978	ENSG00000101417
-0.719	3.14684	-5.137383955	5.6E-07	4.743E-05	5.833613798	-4.493	ENSG00000091138
0.718	5.69025	4.476592233	1.2E-05	0.0005357	3.003513722	3.542	ENSG00000197353
0.716	4.94288	4.107067517	5.4E-05	0.0018824	1.564545311	3.053	ENSG00000198829
-0.715	5.79068	-4.793447955	2.8E-06	0.0001727	4.320509693	-3.965	ENSG00000215218
-0.714	2.99248	-4.013577353	7.9E-05	0.0025214	1.217493631	-2.929	ENSG00000197408
-0.714	4.69039	-5.417885773	1.4E-07	1.647E-05	7.129633892	-4.887	ENSG00000158406
0.713	8.66494	5.586762878	6.1E-08	7.845E-06	7.935868694	5.142	ENSG00000147697
-0.712	7.07716	-7.871720466	1.1E-13	2.141E-10	20.52813565	-9.231	ENSG00000278535
-0.711	5.81263	-6.611656634	2.3E-10	8.949E-08	13.21992869	-6.848	ENSG00000178537

-0.709	4.45555	-3.375854527	0.00085	0.0157838	-0.959895367	-2.177	ENSG00000186115
-0.706	6.1495	-4.05900693	6.6E-05	0.0021798	1.385265936	-2.95	ENSG00000183098
0.705	6.22696	3.435532324	0.00069	0.0134739	-0.770479245	2.228	ENSG00000136688
-0.704	5.22212	-6.124461502	3.5E-09	8.209E-07	10.62718283	-5.952	ENSG00000167701
0.703	7.21863	4.532387295	9.1E-06	0.0004375	3.229942337	3.547	ENSG00000169900
-0.702	5.33006	-6.0524792	5.2E-09	1.146E-06	10.25625159	-5.814	ENSG00000171617
-0.701	6.59341	-5.543330066	7.6E-08	9.478E-06	7.726685872	-4.991	ENSG00000253692
0.701	6.50265	4.601017495	6.7E-06	0.0003464	3.511695217	3.625	ENSG00000106258
-0.701	6.60005	-3.747497383	0.00022	0.0056052	0.268278331	-2.56	ENSG00000149485
-0.7	6.01088	-4.06271318	6.5E-05	0.0021552	1.399025872	-2.933	ENSG00000135218
-0.7	8.39669	-5.176386281	4.7E-07	4.06E-05	6.010538642	-4.43	ENSG00000153246
-0.699	3.02273	-4.749626516	3.5E-06	0.0002051	4.133902637	-3.816	ENSG00000269289
-0.698	5.0372	-3.320179222	0.00103	0.0182398	-1.133883409	-2.082	ENSG00000135480
-0.695	6.74131	-8.290174779	7.2E-15	2.517E-11	23.12407826	-9.834	ENSG00000083123
-0.694	4.49564	-4.534674251	9E-06	0.000435	3.239273772	-3.502	ENSG00000118557
-0.693	6.87	-3.204260051	0.00153	0.0241195	-1.487645407	-1.951	ENSG00000150471
-0.692	2.03349	-3.145127289	0.00186	0.02786	-1.663660593	-1.889	ENSG00000211972
-0.689	6.47218	-7.99918638	4.8E-14	1.162E-10	21.31074076	-9.171	ENSG00000160211
-0.684	3.49579	-5.32877288	2.2E-07	2.325E-05	6.711999549	-4.553	ENSG00000162949
-0.684	4.09015	-6.625113309	2.1E-10	8.543E-08	13.29351502	-6.609	ENSG00000144834
-0.68	4.31762	-3.079012441	0.00231	0.0324561	-1.856879472	-1.794	ENSG00000173432
-0.68	8.03009	-6.91388674	4E-11	2.197E-08	14.89713277	-7.075	ENSG00000157045
-0.68	5.80184	-4.643411825	5.6E-06	0.0002966	3.687512802	-3.571	ENSG00000107317
-0.678	5.8106	-4.858025889	2.1E-06	0.0001353	4.59807952	-3.852	ENSG00000111058
-0.678	4.36565	-6.711305073	1.3E-10	5.62E-08	13.76728225	-6.704	ENSG00000269416
-0.676	3.65778	-6.538766074	3.5E-10	1.269E-07	12.82313755	-6.388	ENSG00000242136
-0.674	5.60306	-3.43127753	0.0007	0.0136268	-0.784083593	-2.125	ENSG00000124664
-0.674	6.11275	-3.654587214	0.00031	0.0072456	-0.04954696	-2.359	ENSG00000158825
0.673	5.91506	5.908342147	1.1E-08	2.116E-06	9.523235746	5.35	ENSG00000085831
-0.672	6.1069	-4.334025506	2.1E-05	0.000882	2.435770305	-3.141	ENSG00000141448
-0.67	6.11491	-3.169118383	0.00172	0.0262782	-1.592612024	-1.852	ENSG00000113070
-0.67	7.60276	-5.94869537	9.1E-09	1.759E-06	9.727133826	-5.384	ENSG00000131373
-0.668	6.01473	-7.227581943	6.1E-12	5.453E-09	16.69038792	-7.498	ENSG00000166016
-0.668	6.53258	-4.895382535	1.8E-06	0.0001177	4.760038762	-3.841	ENSG00000181019
-0.665	3.76267	-8.827734885	2E-16	1.033E-12	26.56558045	-10.45	ENSG00000259370
-0.665	6.0298	-3.882093647	0.00013	0.0037842	0.741261017	-2.578	ENSG00000171208
-0.665	6.23524	-2.979624175	0.00317	0.0401899	-2.140188282	-1.662	ENSG00000163975
-0.664	6.70933	-6.273603141	1.6E-09	4.063E-07	11.40584412	-5.845	ENSG00000072042
0.662	4.34176	4.636358715	5.7E-06	0.000304	3.658168652	3.471	ENSG00000185306
-0.66	6.65956	-3.560717584	0.00044	0.0095653	-0.363393228	-2.213	ENSG00000233836
-0.659	7.45285	-7.019061488	2.1E-11	1.457E-08	15.49255659	-7.038	ENSG00000142197
-0.659	6.0002	-5.016083777	1E-06	7.513E-05	5.290251432	-3.95	ENSG00000128944
-0.658	4.38247	-6.331794003	1.1E-09	3.147E-07	11.71330648	-5.889	ENSG00000204950
-0.658	7.22031	-4.782967252	3E-06	0.0001794	4.275750302	-3.636	ENSG00000170271
-0.658	5.81775	-4.620295498	6.2E-06	0.0003227	3.591477569	-3.426	ENSG00000165238

0.657	5.32678	3.627665798	0.00035	0.0078862	-0.140305851	2.271	ENSG00000248554
-0.655	4.84697	-5.172255172	4.8E-07	4.108E-05	5.991748149	-4.139	ENSG00000164211
-0.65	4.04568	-3.855548644	0.00015	0.004085	0.646810628	-2.491	ENSG00000197372
0.65	8.95058	3.505643225	0.00054	0.0111613	-0.544108704	2.124	ENSG00000187223
-0.648	8.5381	-3.037225435	0.00264	0.0355464	-1.977043612	-1.671	ENSG00000175315
-0.647	5.81914	-4.965919771	1.3E-06	9.102E-05	5.068615728	-3.816	ENSG00000251615
-0.647	7.11222	-5.645551044	4.5E-08	6.21E-06	8.221004928	-4.753	ENSG00000198736
0.647	5.43262	5.080268222	7.4E-07	5.934E-05	5.576461045	3.964	ENSG00000261040
-0.646	7.86766	-6.857126799	5.6E-11	2.789E-08	14.57828749	-6.625	ENSG00000169241
-0.645	6.14698	-5.738495244	2.8E-08	4.309E-06	8.676453736	-4.872	ENSG00000093217
0.644	6.01449	4.220385533	3.4E-05	0.0013084	1.994490819	2.877	ENSG00000259341
-0.644	4.4987	-3.555548937	0.00045	0.0097061	-0.380461013	-2.153	ENSG00000168269
0.643	6.58916	5.206406019	4E-07	3.652E-05	6.147444172	4.11	ENSG00000169403
-0.639	7.94215	-8.761388477	3.1E-16	1.389E-12	26.13473854	-9.916	ENSG00000100075
-0.636	8.89637	-6.391386169	8.1E-10	2.45E-07	12.03026781	-5.787	ENSG00000169738
-0.636	7.57845	-5.792616657	2.1E-08	3.456E-06	8.944259878	-4.887	ENSG00000153904
-0.636	7.67203	-5.037794813	9.1E-07	6.926E-05	5.386735441	-3.842	ENSG00000062282
-0.635	3.79362	-7.554454379	8.1E-13	1.027E-09	18.61275368	-7.683	ENSG00000203797
-0.635	3.09524	-6.610540143	2.3E-10	8.949E-08	13.21382793	-6.116	ENSG00000253844
-0.634	4.4216	-5.299296839	2.6E-07	2.599E-05	6.575058715	-4.178	ENSG00000116761
0.633	8.70375	3.04076006	0.00261	0.0353428	-1.966938172	1.635	ENSG00000118520
-0.633	4.07028	-5.156214496	5.2E-07	4.379E-05	5.91890035	-3.978	ENSG00000143627
-0.631	6.4751	-5.135824998	5.7E-07	4.754E-05	5.826564243	-3.942	ENSG00000102359
-0.63	6.90365	-6.974357346	2.8E-11	1.683E-08	15.2387468	-6.656	ENSG00000023330
-0.63	5.02262	-4.964619773	1.3E-06	9.128E-05	5.062896126	-3.713	ENSG00000079385
0.629	7.23491	4.53807187	8.9E-06	0.0004321	3.253144356	3.176	ENSG00000174944
-0.628	5.33732	-5.23448643	3.5E-07	3.298E-05	6.276076291	-4.051	ENSG00000182379
-0.628	5.12738	-4.879052127	1.9E-06	0.0001253	4.689113369	-3.59	ENSG00000175928
-0.627	6.04958	-4.299170583	2.5E-05	0.0009865	2.299354367	-2.891	ENSG00000111863
-0.626	5.76233	-5.81850864	1.8E-08	3.127E-06	9.073050637	-4.845	ENSG00000138758
-0.625	4.62251	-4.940394715	1.4E-06	0.0001007	4.956536237	-3.651	ENSG00000170231
-0.624	8.52312	-6.856478386	5.6E-11	2.789E-08	14.57465525	-6.401	ENSG00000111684
-0.623	5.95832	-4.841224357	2.3E-06	0.000145	4.525568787	-3.515	ENSG00000171612
-0.622	7.63751	-6.389586988	8.2E-10	2.451E-07	12.0206674	-5.653	ENSG00000116906
0.621	5.10309	3.322056524	0.00103	0.0181532	-1.128059725	1.854	ENSG00000110079
-0.616	4.73167	-3.941487975	0.00011	0.0031549	0.954661	-2.451	ENSG00000073737
-0.616	6.5491	-5.272216871	2.9E-07	2.897E-05	6.449779126	-4.021	ENSG00000135929
-0.615	4.80272	-5.349119522	2E-07	2.175E-05	6.806876004	-4.121	ENSG00000124615
-0.615	5.94278	-5.013412829	1E-06	7.59E-05	5.278405039	-3.682	ENSG00000075643
0.614	6.94779	3.951030979	0.0001	0.0030798	0.989214074	2.452	ENSG00000142973
-0.613	7.1875	-6.970765791	2.8E-11	1.687E-08	15.21840208	-6.471	ENSG00000114054
0.613	7.9037	7.061444289	1.7E-11	1.156E-08	15.73417121	6.613	ENSG00000116191
-0.612	6.90746	-4.632124905	5.8E-06	0.0003093	3.640571986	-3.205	ENSG00000213096
-0.611	6.79187	-3.940659029	0.00011	0.0031591	0.951663038	-2.431	ENSG00000089723
-0.61	4.07515	-5.335666866	2.1E-07	2.27E-05	6.744114322	-4.067	ENSG00000163406

-0.609	5.22512	-4.507557188	1E-05	0.0004757	3.128883895	-3.044	ENSG00000224307
0.609	7.73985	4.114746831	5.3E-05	0.0018429	1.593361311	2.605	ENSG00000170423
-0.608	2.44137	-6.776474136	8.9E-11	4.191E-08	14.12826867	-6.106	ENSG00000236846
0.607	3.39459	4.065432942	6.4E-05	0.0021422	1.409130309	2.546	ENSG00000165606
-0.607	6.45122	-6.413350962	7.1E-10	2.208E-07	12.14762588	-5.556	ENSG00000147155
0.607	8.44615	3.95231331	0.0001	0.0030672	0.993862698	2.426	ENSG00000124882
-0.606	7.22913	-6.562510104	3.1E-10	1.137E-07	12.95205652	-5.766	ENSG00000157617
-0.606	7.57883	-5.75719688	2.5E-08	3.987E-06	8.768778952	-4.604	ENSG00000163931
-0.605	8.14771	-3.481949221	0.00059	0.0118712	-0.621073423	-1.955	ENSG00000125398
-0.604	8.26073	-5.16479731	4.9E-07	4.213E-05	5.957856185	-3.81	ENSG00000011198
0.603	6.52126	4.168305957	4.2E-05	0.0015518	1.795635515	2.637	ENSG00000173083
-0.601	6.87831	-7.10483722	1.3E-11	9.325E-09	15.9825295	-6.549	ENSG00000072274
0.6	8.43197	3.809825143	0.00018	0.0046672	0.48546491	2.255	ENSG00000124212
-0.6	6.55514	-2.910000439	0.00394	0.046629	-2.333507066	-1.443	ENSG00000167772
0.6	5.44758	5.139138847	5.6E-07	4.716E-05	5.841551417	3.749	ENSG00000137563
-0.6	2.76423	-5.071764429	7.7E-07	6.117E-05	5.538372311	-3.664	ENSG00000149054
0.599	7.68225	6.015606536	6.4E-09	1.352E-06	10.06749122	4.912	ENSG00000148344
-0.599	4.09849	-3.78821986	0.00019	0.0049872	0.409819243	-2.229	ENSG00000144057
-0.599	9.62517	-3.408535237	0.00076	0.0144743	-0.856540788	-1.867	ENSG00000108821
0.598	7.53722	4.661508767	5.1E-06	0.0002788	3.762974694	3.165	ENSG00000168389
0.597	9.23938	4.466232051	1.2E-05	0.0005561	2.961730889	2.935	ENSG00000178372
0.597	5.17779	3.077623627	0.00232	0.0324937	-1.86089759	1.572	ENSG00000248991
-0.595	6.00956	-4.982996646	1.2E-06	8.517E-05	5.14386199	-3.527	ENSG00000010319
0.594	8.18827	3.620661436	0.00036	0.0080627	-0.163820736	2.049	ENSG00000188393
0.593	7.62411	4.254614096	3E-05	0.0011574	2.12634468	2.684	ENSG00000173239
-0.592	5.65481	-3.369913385	0.00087	0.0160322	-0.978587291	-1.813	ENSG00000135917
-0.592	9.88628	-6.501485832	4.3E-10	1.455E-07	12.62138101	-5.543	ENSG00000101856
-0.591	5.93115	-5.214579754	3.9E-07	3.535E-05	6.184829971	-3.79	ENSG00000001561
-0.59	4.47705	-3.902634154	0.00012	0.0035507	0.814738934	-2.309	ENSG00000115616
-0.59	4.68689	-5.168583822	4.9E-07	4.159E-05	5.975058954	-3.727	ENSG00000239035
-0.59	2.80639	-5.801385043	2E-08	3.366E-06	8.98782672	-4.545	ENSG00000092377
0.59	5.77004	3.169563133	0.00172	0.026265	-1.591290225	1.631	ENSG00000226904
0.59	9.14221	5.19375968	4.3E-07	3.828E-05	6.089693309	3.755	ENSG00000261150
-0.589	5.59974	-6.593613266	2.6E-10	9.743E-08	13.12142286	-5.652	ENSG00000197982
-0.589	4.48959	-3.581286527	0.00041	0.0090442	-0.295249974	-1.993	ENSG00000255501
-0.589	5.12847	-6.19991781	2.3E-09	5.861E-07	11.01944286	-5.079	ENSG00000160932
0.588	9.01987	4.825937002	2.4E-06	0.0001534	4.459772347	3.301	ENSG00000179477
-0.587	7.15383	-4.686405058	4.6E-06	0.0002574	3.867188896	-3.134	ENSG00000119681
-0.586	6.0221	-5.988409858	7.4E-09	1.504E-06	9.928809976	-4.767	ENSG00000104219
-0.584	5.78151	-3.155933148	0.0018	0.0271705	-1.631721035	-1.602	ENSG00000077274
-0.582	4.8845	-3.291139673	0.00114	0.0195024	-1.223585732	-1.713	ENSG00000151364
-0.582	6.89777	-4.797607996	2.8E-06	0.0001701	4.338298186	-3.234	ENSG00000205155

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logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
-2.801	7.05034	-3.880446988	0.00027	0.0412546	0.341291733	-9.981	ENSG00000221852
-2.546	4.66177	-3.742490762	0.00043	0.0478352	-0.049587373	-8.581	ENSG00000198271
-2.484	5.12212	-4.156628348	0.00011	0.0301706	1.146373607	-9.833	ENSG00000241233
-2.425	5.23096	-4.069594618	0.00015	0.0338143	0.88958398	-9.294	ENSG00000205867
2.42	6.22207	3.767612333	0.00039	0.0458578	0.020997698	8.241	ENSG00000211892
-2.356	5.41965	-4.346963124	5.8E-05	0.0242805	1.717093413	-9.986	ENSG00000212657
-2.226	4.58017	-4.482996046	3.6E-05	0.0231291	2.132140664	-9.887	ENSG00000196224
-2.124	5.04685	-4.641841401	2.1E-05	0.0210235	2.62368571	-9.946	ENSG00000241598
-2.12	4.94852	-3.779958042	0.00038	0.0457272	0.055784195	-7.255	ENSG00000244537
-1.939	3.45943	-3.836860042	0.00031	0.0431998	0.216942383	-6.792	ENSG00000196156
-1.803	5.69756	-4.445746769	4.1E-05	0.023824	2.017928121	-7.907	ENSG00000186860
1.779	8.14831	3.712007511	0.00047	0.049614	-0.134873647	5.92	ENSG00000185962
-1.766	4.31821	-4.971797571	6.4E-06	0.0133418	3.665701884	-9.168	ENSG00000204571
-1.677	7.0097	-4.45111435	4E-05	0.023824	2.034360395	-7.369	ENSG00000094796
-1.514	3.40512	-4.171796616	0.0001	0.0301706	1.191403577	-6.026	ENSG00000212725
-1.388	3.5339	-4.283601509	7.2E-05	0.0242805	1.525760656	-5.755	ENSG00000226005
-1.253	7.40331	-3.987913391	0.00019	0.0372975	0.651121765	-4.657	ENSG00000119457
1.168	5.66237	3.809394997	0.00034	0.0444578	0.138987403	4.046	ENSG00000138135
-1.14	7.84924	-4.600788795	2.4E-05	0.0210235	2.495971451	-5.268	ENSG00000179094
1.117	5.55873	5.843317873	2.6E-07	0.0074281	6.518117498	7.351	ENSG00000170542
-1.114	4.32564	-4.319621624	6.3E-05	0.0242805	1.634370764	-4.675	ENSG00000185940
-1.103	4.82985	-4.044160699	0.00016	0.0345287	0.81506353	-4.186	ENSG00000170442
1.101	7.61902	3.819080412	0.00033	0.044217	0.166442211	3.828	ENSG00000104368
-1.093	6.27275	-4.427832471	4.4E-05	0.023824	1.963148539	-4.764	ENSG00000174156
-1.083	5.44831	-4.120730594	0.00012	0.0311444	1.04012836	-4.231	ENSG00000205869
-1.044	4.93486	-3.997185137	0.00019	0.0367921	0.678063188	-3.894	ENSG00000242516
-1.037	3.93464	-3.798111797	0.00036	0.0457252	0.10705268	-3.574	ENSG00000156076
-1.033	8.18929	-4.062617932	0.00015	0.0338143	0.869118711	-3.95	ENSG00000126368
-1.004	3.35795	-3.818817106	0.00033	0.044217	0.165695314	-3.492	ENSG00000204572
-0.993	3.24123	-5.614142436	6.1E-07	0.0074281	5.757343455	-6.17	ENSG00000170615
0.983	5.59355	3.733617839	0.00044	0.0478352	-0.074453458	3.301	ENSG00000140534
-0.982	4.95585	-4.037811012	0.00016	0.0350219	0.796496686	-3.719	ENSG00000212900
-0.98	4.66518	-4.787919457	1.2E-05	0.0156673	3.081734284	-4.806	ENSG00000249731
-0.952	6.28716	-4.539811307	3E-05	0.0212791	2.307132878	-4.311	ENSG00000159208
0.933	4.68673	3.946358672	0.00022	0.0379842	0.530780612	3.41	ENSG00000175426
-0.931	2.64979	-3.915951484	0.00024	0.0389782	0.443149136	-3.366	ENSG00000233725
-0.927	4.20591	-4.814291512	1.1E-05	0.0156673	3.165000592	-4.583	ENSG00000000005
-0.916	4.94181	-4.300108696	6.8E-05	0.0242805	1.575481503	-3.82	ENSG00000256199
-0.908	7.3873	-3.856031847	0.0003	0.0426013	0.271542393	-3.203	ENSG00000244411
-0.905	3.51809	-4.117950481	0.00013	0.0311444	1.031919354	-3.531	ENSG00000212658
-0.898	6.05277	-4.106177697	0.00013	0.0313189	0.997188003	-3.491	ENSG00000232324
-0.881	3.0753	-3.794274832	0.00036	0.0457272	0.096205079	-3.034	ENSG00000185674
-0.863	5.99254	-5.204918542	2.8E-06	0.0097104	4.416486935	-4.796	ENSG00000169252

-0.796	5.12792	-3.776083623	0.00038	0.0457272	0.044860308	-2.719	ENSG00000230943
-0.795	4.91573	-4.024588131	0.00017	0.0360952	0.757880684	-2.994	ENSG00000203392
-0.793	6.83466	-3.983194928	0.0002	0.0372975	0.637423704	-2.94	ENSG00000241241
-0.79	6.64036	-4.312423665	6.5E-05	0.0242805	1.612633185	-3.31	ENSG00000153993
0.777	5.32221	4.849008434	1E-05	0.0150111	3.274870241	3.884	ENSG00000174004
0.757	5.67259	3.75463777	0.00041	0.0470151	-0.015491053	2.565	ENSG00000113749
0.756	3.948	3.78056542	0.00038	0.0457272	0.057497264	2.587	ENSG00000151790
-0.755	3.31436	-4.121023993	0.00012	0.0311444	1.040994856	-2.949	ENSG00000272804
-0.752	8.26541	-3.943225539	0.00022	0.0379842	0.521734347	-2.747	ENSG00000197953
-0.749	5.64608	-4.663992106	1.9E-05	0.0210235	2.692785484	-3.534	ENSG00000258479
-0.735	5.37127	-4.051017709	0.00016	0.0341922	0.835130696	-2.798	ENSG00000255864
-0.728	4.90354	-4.356717724	5.6E-05	0.0242805	1.746664187	-3.097	ENSG00000252026
0.72	6.84201	3.886550018	0.00027	0.041034	0.358764543	2.572	ENSG00000151014
-0.709	4.21085	-4.13206986	0.00012	0.0310869	1.073639174	-2.783	ENSG00000268460
-0.706	6.00971	-4.923401546	7.7E-06	0.0133418	3.51125345	-3.612	ENSG00000187372
0.702	5.05037	3.997670882	0.00019	0.0367921	0.679475549	2.617	ENSG00000175063
-0.701	3.54491	-4.796757782	1.2E-05	0.0156673	3.109621252	-3.447	ENSG00000222001
-0.697	2.76714	-3.734684985	0.00044	0.0478352	-0.071464605	-2.342	ENSG00000274414
0.684	5.9129	4.327517892	6.2E-05	0.0242805	1.658236498	2.881	ENSG00000162551
-0.681	4.7368	-3.935421915	0.00023	0.038344	0.499219736	-2.479	ENSG00000251432
0.68	7.93822	3.845564015	0.00031	0.0430962	0.241712063	2.39	ENSG00000146072
-0.677	3.55727	-3.777287494	0.00038	0.0457272	0.048253931	-2.313	ENSG00000131264
-0.676	7.8897	-4.290935758	7E-05	0.0242805	1.547840892	-2.81	ENSG00000154359
-0.676	4.52183	-3.732564544	0.00044	0.0478352	-0.077403034	-2.269	ENSG00000228798
0.674	6.12095	3.709374398	0.00047	0.049614	-0.14222172	2.242	ENSG00000137807
-0.671	9.61854	-3.791227267	0.00036	0.0457272	0.087593612	-2.309	ENSG00000136155
-0.67	4.73849	-3.786481254	0.00037	0.0457272	0.074190625	-2.301	ENSG00000164309
-0.67	9.52525	-3.924071902	0.00024	0.0388471	0.466515982	-2.429	ENSG00000148600
0.659	7.81369	3.785365856	0.00037	0.0457272	0.071042055	2.259	ENSG00000123975
0.655	5.17465	3.776743845	0.00038	0.0457272	0.046721348	2.238	ENSG00000164430
-0.65	5.93214	-3.923392305	0.00024	0.0388471	0.464559413	-2.357	ENSG00000189169
-0.65	6.42839	-3.92783861	0.00023	0.0386883	0.477363689	-2.358	ENSG00000123095
0.647	6.76047	4.132127692	0.00012	0.0310869	1.073810203	2.538	ENSG00000139318
-0.646	6.01432	-4.49096607	3.5E-05	0.0231081	2.15663167	-2.875	ENSG00000198590
0.645	6.87932	3.90713344	0.00025	0.0391367	0.417804447	2.323	ENSG00000154217
-0.641	6.87603	-3.839593375	0.00031	0.0431648	0.224717528	-2.246	ENSG00000106078
-0.639	7.1512	-3.970053822	0.0002	0.0372975	0.599319183	-2.358	ENSG00000133401
-0.639	5.21412	-4.136320026	0.00012	0.0310869	1.086211485	-2.51	ENSG00000163393
0.638	6.8047	4.555587201	2.8E-05	0.0210235	2.355888088	2.905	ENSG00000134070
-0.635	8.21341	-4.43698823	4.2E-05	0.023824	1.991133484	-2.776	ENSG00000108924
-0.624	6.30626	-3.719557054	0.00046	0.0494664	-0.113788893	-2.085	ENSG00000198270
-0.624	4.00395	-3.887831887	0.00027	0.041034	0.362436405	-2.228	ENSG00000127252
-0.618	7.02043	-3.762394734	0.0004	0.0462	0.006315483	-2.1	ENSG00000165312
0.61	9.24011	3.998395573	0.00019	0.0367921	0.68158284	2.276	ENSG00000182481
0.61	5.08669	4.066385837	0.00015	0.0338143	0.880169178	2.335	ENSG00000197299

-0.61	6.45551	-5.204989663	2.8E-06	0.0097104	4.416717593	-3.387	ENSG00000164197
-0.609	4.22056	-4.366390857	5.4E-05	0.0242805	1.776017806	-2.598	ENSG00000117834
-0.608	7.62082	-4.01148722	0.00018	0.0364662	0.719685785	-2.281	ENSG00000114529
0.608	4.54606	4.117151779	0.00013	0.0311444	1.029561494	2.371	ENSG00000171124
-0.606	5.89207	-3.911586698	0.00025	0.0389782	0.430600073	-2.186	ENSG00000157514
0.602	5.9892	3.877051164	0.00028	0.0413164	0.331576077	2.143	ENSG00000123473
-0.6	6.12856	-5.439334363	1.2E-06	0.0074281	5.181444396	-3.556	ENSG00000163864
-0.595	6.34444	-3.966369432	0.00021	0.0372975	0.588647723	-2.191	ENSG00000078295
0.593	5.44304	4.339015696	5.9E-05	0.0242805	1.693023458	2.507	ENSG00000075218
0.591	5.73764	3.9657612	0.00021	0.0372975	0.586886547	2.179	ENSG00000162063
-0.584	5.3727	-4.103400996	0.00013	0.0313705	0.989003641	-2.267	ENSG00000239521

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136 **Table E6.**

137 Thigh_LES / Upper_back_LES

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
-3.247	6.06906	-6.270210699	1.6E-09	6.184E-07	11.38186247	-28.57	ENSG00000184210
-3.211	6.59981	-6.287649634	1.4E-09	5.754E-07	11.47344378	-28.39	ENSG00000162877
-2.995	6.18375	-6.702379193	1.4E-10	7.855E-08	13.7039287	-29.54	ENSG00000147160
-2.882	6.24598	-5.718612738	3.1E-08	6.737E-06	8.581850957	-21.65	ENSG00000188984
-2.689	5.26709	-7.290006395	4.1E-12	5.218E-09	17.02759034	-30.61	ENSG00000204195
-2.657	7.88138	-5.615410891	5.2E-08	1.001E-05	8.079502113	-19.34	ENSG00000151365
-2.6	6.07306	-6.206790277	2.3E-09	8.081E-07	11.05034921	-22.48	ENSG00000214491
-2.331	5.90733	-5.603275338	5.6E-08	1.041E-05	8.020890728	-16.91	ENSG00000119915
-2.156	5.31244	-7.536707314	9E-13	1.497E-09	18.4760598	-25.96	ENSG00000173930
2.038	7.10188	12.48183849	4.5E-28	1.421E-23	52.02340811	55.74	ENSG00000105664
-1.952	6.5234	-5.140731606	5.6E-07	6.099E-05	5.861013788	-12.21	ENSG00000069482
-1.865	5.70414	-5.894940476	1.2E-08	3.201E-06	9.456131151	-14.76	ENSG00000185640
-1.834	5.16118	-6.935691976	3.5E-11	3.054E-08	15.00146952	-19.17	ENSG00000178445
-1.73	5.12246	-6.783708321	8.5E-11	5.278E-08	14.15283095	-17.41	ENSG00000087128
-1.704	4.04687	-5.468224478	1.1E-07	1.746E-05	7.375241077	-11.85	ENSG00000250266
-1.681	6.42313	-7.081140465	1.5E-11	1.409E-08	15.8252639	-18.21	ENSG00000103089
1.673	3.9568	4.771949886	3.1E-06	0.0002244	4.246264513	9.209	ENSG00000171711
-1.646	5.74217	-6.870650675	5.1E-11	3.592E-08	14.63675451	-16.94	ENSG00000130208
-1.615	4.61631	-5.425486799	1.4E-07	2.091E-05	7.173469332	-11.08	ENSG00000146453
-1.605	4.94002	-4.222569047	3.4E-05	0.0013541	2.027418608	-7.173	ENSG00000184227
-1.598	9.12902	-4.592906584	7E-06	0.0004024	3.498086479	-8.243	ENSG00000184148
-1.585	7.41165	-5.11634492	6.2E-07	6.693E-05	5.751234136	-9.836	ENSG00000179593
-1.577	7.59242	-5.620600944	5.1E-08	9.881E-06	8.10459833	-11.5	ENSG00000064763
-1.414	4.05076	-5.623098619	5E-08	9.87E-06	8.116682037	-10.32	ENSG00000259283
-1.389	5.42736	-5.028368393	9.5E-07	9.451E-05	5.358690906	-8.364	ENSG00000249365
1.345	7.16405	4.870807742	2E-06	0.0001627	4.669496646	7.672	ENSG00000116690
-1.343	4.41902	-5.285479537	2.7E-07	3.565E-05	6.521174164	-8.811	ENSG00000100341
-1.336	7.23936	-8.012241886	4.4E-14	1.542E-10	21.34986789	-17.85	ENSG00000117594
1.306	6.76519	7.495646637	1.2E-12	1.836E-09	18.23290147	15.59	ENSG00000138615
-1.299	6.09368	-4.853836002	2.1E-06	0.0001715	4.59632971	-7.366	ENSG00000263639

-1.296	5.7782	-5.57300927	6.5E-08	1.154E-05	7.875138578	-9.315	ENSG00000253125
1.27	6.43035	7.170992315	8.5E-12	9.608E-09	16.33973462	14.06	ENSG00000188257
-1.265	5.57868	-5.412286755	1.5E-07	2.212E-05	7.111399455	-8.644	ENSG00000103740
-1.244	3.36446	-4.642513892	5.6E-06	0.0003411	3.702994832	-6.536	ENSG00000250411
-1.233	6.79635	-7.818136932	1.5E-13	4.019E-10	20.16425757	-15.8	ENSG00000105852
-1.216	4.89682	-5.289376785	2.7E-07	3.526E-05	6.539149627	-7.991	ENSG00000101049
1.199	4.78988	4.537289339	8.9E-06	0.0004867	3.270549802	6.057	ENSG00000134827
-1.19	3.33735	-5.527120106	8.2E-08	1.372E-05	7.655311413	-8.429	ENSG00000174827
-1.184	4.19424	-4.698560039	4.3E-06	0.0002848	3.936708309	-6.349	ENSG00000132915
-1.171	7.65361	-5.230113349	3.6E-07	4.385E-05	6.266940434	-7.543	ENSG00000095321
-1.166	7.42109	-4.876538065	1.9E-06	0.0001601	4.694247948	-6.661	ENSG00000057252
-1.164	4.8191	-5.386761616	1.7E-07	2.397E-05	6.991709468	-7.888	ENSG00000176136
-1.161	4.95603	-6.873633819	5E-11	3.592E-08	14.65343212	-11.96	ENSG00000086696
-1.15	4.642	-5.922227618	1.1E-08	2.864E-06	9.593203559	-9.172	ENSG00000166391
-1.142	4.37664	-7.075195497	1.5E-11	1.409E-08	15.79137311	-12.35	ENSG00000170439
-1.094	5.07315	-4.719747118	3.9E-06	0.0002692	4.025666254	-5.914	ENSG00000253745
-1.092	5.15018	-5.781974717	2.2E-08	5.209E-06	8.893714021	-8.361	ENSG00000140284
-1.074	4.32985	-3.241896306	0.00135	0.0190215	-1.339023521	-3.081	ENSG00000226281
1.072	3.83615	3.650190302	0.00032	0.0069335	-0.033416759	3.747	ENSG00000170465
-1.067	4.35216	-4.695530789	4.4E-06	0.0002881	3.924016608	-5.716	ENSG00000173124
-1.056	5.18037	-4.754371952	3.4E-06	0.0002414	4.171759425	-5.779	ENSG00000116882
-1.053	4.3196	-5.748036503	2.6E-08	5.945E-06	8.726349109	-7.98	ENSG00000118849
-1.034	5.3304	-6.027191078	6E-09	1.785E-06	10.12484019	-8.501	ENSG00000005187
-1.034	6.49885	-7.575100476	7.1E-13	1.316E-09	18.70415824	-12.56	ENSG00000145244
-1.018	8.5381	-6.59051821	2.6E-10	1.286E-07	13.09256278	-9.751	ENSG00000175315
-0.99	5.58043	-4.80447995	2.7E-06	0.0002028	4.384743853	-5.516	ENSG00000176194
-0.99	6.87	-6.326901654	1.2E-09	4.747E-07	11.68024234	-8.847	ENSG00000150471
-0.98	3.86045	-6.448032471	5.9E-10	2.537E-07	12.32416935	-9.049	ENSG00000102837
-0.974	5.52205	-4.90596467	1.7E-06	0.0001442	4.821727122	-5.626	ENSG00000134824
-0.968	7.55855	-4.987968061	1.1E-06	0.0001092	5.180273093	-5.752	ENSG00000203837
-0.96	6.39769	-4.204000991	3.7E-05	0.0014358	1.956467717	-4.258	ENSG00000168671
0.948	4.9424	3.045915262	0.00257	0.0295794	-1.915387883	2.455	ENSG00000244094
0.94	5.37125	5.1609751	5E-07	5.686E-05	5.952459915	5.919	ENSG00000164694
0.93	4.44352	4.518111552	9.7E-06	0.000521	3.19263207	4.663	ENSG00000182585
0.922	6.91938	7.744349444	2.4E-13	5.929E-10	19.71804465	11.62	ENSG00000187955
-0.908	4.45555	-5.972421261	8.1E-09	2.228E-06	9.846570584	-7.348	ENSG00000186115
0.9	4.06774	4.050355746	6.8E-05	0.0022878	1.379772526	3.748	ENSG00000136694
0.897	9.02441	6.92677122	3.7E-11	3.054E-08	14.95131164	9.364	ENSG00000041982
0.886	6.12545	3.766750207	0.00021	0.00507	0.364783116	3.265	ENSG00000185962
-0.881	4.48959	-7.411128703	2E-12	2.827E-09	17.73498287	-10.31	ENSG00000255501
-0.878	6.46089	-6.876209382	5E-11	3.592E-08	14.667835	-9.048	ENSG00000189433
-0.873	5.30917	-4.121715439	5.1E-05	0.0018668	1.645298978	-3.747	ENSG00000164434
0.871	4.2732	3.37636194	0.00085	0.0139762	-0.924546959	2.673	ENSG00000163221
0.869	6.4559	4.481509317	1.1E-05	0.0005971	3.044693289	4.3	ENSG00000123610
-0.859	7.72355	-8.321662109	5.8E-15	2.301E-11	23.27386867	-12.23	ENSG00000163898

-0.857	5.57695	-6.455312057	5.6E-10	2.503E-07	12.36314169	-7.93	ENSG00000186912
0.848	5.74727	6.871077875	5.1E-11	3.592E-08	14.63914253	8.727	ENSG00000163710
-0.847	8.79419	-5.272929613	2.9E-07	3.7E-05	6.463360768	-5.533	ENSG00000169710
-0.846	6.52985	-3.701723238	0.00026	0.006033	0.141257023	-3.028	ENSG00000185499
-0.841	6.06235	-5.199181405	4.2E-07	4.877E-05	6.125831794	-5.361	ENSG00000008394
-0.833	5.92552	-5.219954752	3.8E-07	4.52E-05	6.220524412	-5.35	ENSG00000115425
0.831	7.68024	7.145800217	9.9E-12	1.044E-08	16.19506699	9.145	ENSG00000262655
0.831	8.89594	8.810561604	2.2E-16	1.742E-12	26.39347934	13.01	ENSG00000038427
-0.83	3.52267	-6.675019385	1.6E-10	8.88E-08	13.55374408	-8.13	ENSG00000205678
-0.828	5.87461	-5.209832844	4E-07	4.694E-05	6.174347448	-5.297	ENSG00000165548
-0.818	6.50786	-4.065128322	6.4E-05	0.0022074	1.434409341	-3.427	ENSG00000146070
0.818	5.40433	4.276855022	2.7E-05	0.0011549	2.236395013	3.734	ENSG00000140519
0.812	3.62383	4.996907892	1.1E-06	0.0001055	5.219653058	4.838	ENSG00000199664
-0.796	6.57021	-6.378002886	8.7E-10	3.712E-07	11.95084017	-7.214	ENSG00000174156
0.793	7.38119	3.2764751	0.0012	0.0176826	-1.233907649	2.315	ENSG00000185966
-0.785	7.17457	-5.693607978	3.5E-08	7.413E-06	8.459496948	-5.852	ENSG00000101474
-0.782	3.11989	-4.315759952	2.3E-05	0.0010225	2.387570209	-3.625	ENSG00000124003
0.779	5.18866	3.995947108	8.5E-05	0.0026934	1.180038712	3.172	ENSG00000119125
0.777	4.00557	7.611211307	5.7E-13	1.115E-09	18.91934231	9.514	ENSG00000007933
0.777	10.6199	7.914527892	8.3E-14	2.604E-10	20.75090777	10.16	ENSG00000139329
-0.776	5.51919	-4.369845912	1.8E-05	0.0008646	2.599679505	-3.679	ENSG00000267475
-0.776	8.50418	-6.111429769	3.8E-09	1.223E-06	10.55647119	-6.533	ENSG00000131969
0.772	6.02164	5.198911728	4.2E-07	4.877E-05	6.124604485	4.924	ENSG00000184613
-0.771	5.63467	-3.554691553	0.00045	0.0088881	-0.351310225	-2.578	ENSG00000167588
-0.77	7.41579	-5.527216289	8.2E-08	1.372E-05	7.655770698	-5.457	ENSG00000109084
0.764	7.37578	3.994770577	8.5E-05	0.0027006	1.175745765	3.109	ENSG00000188373
0.763	5.34371	8.436292203	2.7E-15	1.231E-11	23.99682458	11.11	ENSG00000108950
0.76	6.41899	6.098548634	4.1E-09	1.299E-06	10.49018566	6.374	ENSG00000112214
-0.758	3.54895	-6.908273092	4.1E-11	3.237E-08	14.84744077	-7.869	ENSG00000166342
-0.757	3.46154	-3.865981655	0.00014	0.0038895	0.71253619	-2.913	ENSG00000047936
-0.746	4.36907	-7.295187225	4E-12	5.218E-09	17.05769733	-8.5	ENSG00000187775
0.743	8.78409	6.093739408	4.2E-09	1.32E-06	10.46546387	6.225	ENSG00000197614
-0.741	8.67498	-5.77676957	2.3E-08	5.291E-06	8.867996737	-5.666	ENSG00000054598
-0.738	4.40259	-5.911491788	1.1E-08	2.981E-06	9.539217653	-5.872	ENSG00000183798
-0.738	3.56072	-3.103937716	0.00213	0.0261861	-1.748200307	-1.971	ENSG00000270550
-0.732	6.35435	-3.110174301	0.00209	0.0257845	-1.730056631	-1.961	ENSG00000141469
-0.731	5.34046	-3.173133622	0.0017	0.0223027	-1.54501448	-2.025	ENSG00000170509
0.726	5.71385	6.796407958	7.9E-11	4.998E-08	14.22325856	7.334	ENSG00000164687
-0.726	5.71038	-4.430425359	1.4E-05	0.0007077	2.83992497	-3.519	ENSG00000165140
-0.725	8.24435	-4.183889475	4E-05	0.001534	1.879923514	-3.19	ENSG00000133048
-0.724	6.04958	-6.858431698	5.5E-11	3.696E-08	14.56849349	-7.426	ENSG00000111863
0.722	4.17284	5.390007936	1.6E-07	2.37E-05	7.006907206	4.899	ENSG00000214787
0.721	4.36984	3.557419113	0.00045	0.0088227	-0.342335863	2.415	ENSG00000236438
-0.712	6.21117	-5.880907298	1.3E-08	3.392E-06	9.385821675	-5.608	ENSG00000234614
-0.709	4.76059	-3.63861044	0.00033	0.007167	-0.07236597	-2.465	ENSG00000091513

-0.708	8.08021	-5.838990165	1.6E-08	4.099E-06	9.176553712	-5.51	ENSG00000136943
0.707	6.01612	4.731526624	3.7E-06	0.0002606	4.075268394	3.837	ENSG00000155659
0.707	5.08498	5.39620196	1.6E-07	2.33E-05	7.035924594	4.805	ENSG00000106483
-0.707	4.92075	-3.139034365	0.0019	0.0240858	-1.645658782	-1.923	ENSG00000132465
-0.706	3.42119	-3.440658686	0.00068	0.0118256	-0.720945217	-2.234	ENSG00000211664
0.705	3.69731	7.565559719	7.5E-13	1.319E-09	18.64740923	8.551	ENSG00000164588
-0.703	7.69331	-4.699380928	4.3E-06	0.0002848	3.940148774	-3.773	ENSG00000103569
-0.699	3.73114	-2.804469729	0.00544	0.0489837	-2.579572123	-1.584	ENSG00000241566
-0.699	8.16773	-6.603358309	2.4E-10	1.227E-07	13.16237914	-6.717	ENSG00000157368
-0.692	6.74722	-6.16703353	2.8E-09	9.721E-07	10.84377238	-5.919	ENSG00000115255
0.691	6.1595	7.670671203	3.9E-13	8.77E-10	19.27501458	8.573	ENSG00000127241
0.69	7.34889	4.853807225	2.1E-06	0.0001715	4.596205825	3.912	ENSG00000142871
-0.685	5.90725	-5.24520108	3.3E-07	4.105E-05	6.336010655	-4.437	ENSG00000166816
0.685	4.70101	4.562699048	7.9E-06	0.0004482	3.374214972	3.494	ENSG00000248329
-0.682	6.65956	-5.084660052	7.3E-07	7.632E-05	5.609227275	-4.186	ENSG00000233836
0.68	5.71527	4.041210398	7.1E-05	0.0023631	1.346035114	2.819	ENSG00000275385
0.673	3.90207	4.308981098	2.4E-05	0.0010491	2.361144846	3.114	ENSG00000153802
0.671	5.69324	3.505038542	0.00054	0.010039	-0.513596742	2.191	ENSG00000198074
0.67	7.75578	6.160151186	2.9E-09	9.985E-07	10.80810924	5.72	ENSG00000165124
-0.667	3.94333	-4.941268514	1.4E-06	0.0001283	4.975493619	-3.901	ENSG00000253632
-0.665	5.29155	-7.616343194	5.5E-13	1.115E-09	18.94997368	-8.158	ENSG00000164309
-0.663	7.70729	-4.033551271	7.3E-05	0.0024111	1.317831614	-2.741	ENSG00000178033
0.657	8.56624	5.597404153	5.7E-08	1.066E-05	7.992569461	4.754	ENSG00000118523
-0.655	5.68182	-6.927143528	3.7E-11	3.054E-08	14.95340412	-6.83	ENSG00000133135
-0.645	4.91333	-5.605897161	5.5E-08	1.038E-05	8.033545169	-4.681	ENSG00000101440
-0.644	5.33943	-4.974223129	1.2E-06	0.0001146	5.119838354	-3.805	ENSG00000136546
0.642	4.2798	4.83491593	2.3E-06	0.0001838	4.515010526	3.614	ENSG00000277741
0.641	6.57753	5.182420658	4.5E-07	5.224E-05	6.049649507	4.067	ENSG00000140285
-0.641	5.50791	-3.254323705	0.00129	0.0185396	-1.301363068	-1.85	ENSG00000254682
0.639	5.9452	4.288830403	2.6E-05	0.0011135	2.282803437	2.931	ENSG00000177575
0.638	6.3953	3.472015073	0.00061	0.0109307	-0.620389822	2.051	ENSG00000206384
-0.637	8.00663	-4.808567277	2.6E-06	0.0002014	4.402198325	-3.552	ENSG00000199347
-0.633	5.04325	-4.699610511	4.3E-06	0.0002848	3.941111078	-3.398	ENSG00000268416
-0.63	5.80429	-4.351337287	2E-05	0.0009174	2.526840216	-2.966	ENSG00000168306
0.63	7.25697	5.470330946	1.1E-07	1.736E-05	7.38521793	4.386	ENSG00000017427
-0.63	5.23653	-5.484262627	1E-07	1.649E-05	7.451277678	-4.403	ENSG00000133488
-0.628	3.32775	-3.736464255	0.00023	0.0054833	0.260245999	-2.285	ENSG00000259517
-0.628	6.1081	-3.837017236	0.00016	0.0041808	0.610204403	-2.385	ENSG00000053438
0.627	5.10309	4.643047389	5.6E-06	0.0003411	3.705208495	3.296	ENSG00000110079
0.627	9.37874	4.816864621	2.5E-06	0.0001958	4.437668801	3.507	ENSG00000133800
0.62	4.59255	8.537330507	1.4E-15	7.324E-12	24.63845438	9.204	ENSG00000118473
0.619	6.2229	5.729313171	2.9E-08	6.462E-06	8.63433501	4.665	ENSG00000187498
-0.618	6.42486	-5.371120316	1.8E-07	2.545E-05	6.918584916	-4.17	ENSG00000237440
0.617	3.35009	3.250667564	0.00131	0.0187272	-1.312456474	1.779	ENSG00000177257
0.617	7.91883	5.152151809	5.3E-07	5.854E-05	5.912567017	3.874	ENSG00000260314

-0.611	8.18822	-3.435940544	0.00069	0.0119514	-0.736004095	-1.93	ENSG00000186480
-0.61	6.1069	-5.437150094	1.3E-07	1.991E-05	7.228411253	-4.203	ENSG00000141448
0.609	9.22687	5.641588775	4.6E-08	9.106E-06	8.206264927	4.469	ENSG00000166147
0.604	2.27944	6.005487601	6.7E-09	1.969E-06	10.01434694	4.934	ENSG00000223872
-0.604	6.1814	-3.93460156	0.00011	0.0031837	0.957678045	-2.394	ENSG00000236882
-0.604	7.64952	-4.141211056	4.7E-05	0.0017518	1.718541622	-2.61	ENSG00000012660
-0.602	6.61178	-5.309704702	2.4E-07	3.296E-05	6.63307874	-3.981	ENSG00000122756
-0.602	5.30892	-3.055629488	0.00249	0.0289847	-1.887600361	-1.566	ENSG00000211890
-0.599	6.48822	-4.565482135	7.8E-06	0.0004435	3.38559883	-3.057	ENSG00000156284
-0.598	8.18504	-3.938824788	0.00011	0.0031373	0.972889298	-2.375	ENSG00000189182
0.596	7.08427	4.657386662	5.2E-06	0.0003245	3.764786696	3.149	ENSG00000159337
-0.595	5.95005	-5.774227019	2.3E-08	5.291E-06	8.855441008	-4.545	ENSG00000159387
-0.592	6.60005	-4.378754589	1.8E-05	0.0008362	2.634832885	-2.815	ENSG00000149485
-0.592	3.18932	-5.773103279	2.3E-08	5.291E-06	8.849893039	-4.518	ENSG00000170477
0.588	6.22696	3.962279403	9.7E-05	0.0029764	1.057629017	2.361	ENSG00000136688
0.588	6.15393	6.349939704	1E-09	4.285E-07	11.80204491	5.288	ENSG00000152377
-0.588	5.24207	-4.921432637	1.6E-06	0.0001373	4.888987352	-3.412	ENSG00000168490
-0.588	8.39702	-4.918209112	1.6E-06	0.0001389	4.874956054	-3.408	ENSG00000184992
0.585	5.76848	2.940320487	0.00359	0.0372306	-2.212144272	1.431	ENSG00000137558
-0.585	5.96254	-9.149542031	2.2E-17	2.271E-13	28.60913311	-9.741	ENSG00000135903
-0.584	5.18387	-4.236441128	3.2E-05	0.0012979	2.080601379	-2.627	ENSG00000181143
-0.584	7.72422	-4.595402338	6.9E-06	0.0004023	3.508351432	-3.016	ENSG00000162040
-0.584	4.17954	-4.191436141	3.9E-05	0.0014962	1.908608889	-2.576	ENSG00000109158
-0.583	4.52291	-2.812866622	0.0053	0.0483	-2.557332608	-1.328	ENSG00000279301
0.583	6.73899	6.230010161	2E-09	7.361E-07	11.17144345	5.077	ENSG00000162745
-0.583	8.79751	-6.502451584	4.3E-10	2.001E-07	12.61625595	-5.461	ENSG00000178597
-0.583	8.02328	-5.396347255	1.6E-07	2.33E-05	7.036605575	-3.963	ENSG00000088386

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logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID
-3.86	6.24598	-7.609397052	5.7E-13	2.201E-10	18.99105269	-47.26	ENSG00000188984
-3.749	6.59981	-7.295127922	4E-12	1.216E-09	17.11862758	-42.73	ENSG00000162877
-3.656	6.06906	-7.013929481	2.2E-11	5.046E-09	15.48619054	-38.97	ENSG00000184210
-3.627	6.18375	-8.063809899	3.2E-14	2.687E-11	21.78249137	-48.97	ENSG00000147160
-3.324	6.07306	-7.885083815	1E-13	6.048E-11	20.67316848	-43.22	ENSG00000214491
-3.096	5.26709	-8.337333428	5.3E-15	9.712E-12	23.50752828	-44.2	ENSG00000204195
-2.988	7.88138	-6.274924536	1.5E-09	1.849E-07	11.40491485	-26.33	ENSG00000151365
-2.985	5.90733	-7.128203818	1.1E-11	2.765E-09	16.14455213	-32.7	ENSG00000119915
-2.933	6.5234	-7.676980417	3.7E-13	1.616E-10	19.40007558	-36.45	ENSG00000069482
-2.555	4.32985	-7.664271491	4.1E-13	1.682E-10	19.32299164	-31.66	ENSG00000226281
-2.432	5.70414	-7.638388878	4.8E-13	1.904E-10	19.16624493	-29.97	ENSG00000185640
-2.389	5.31244	-8.300567954	6.7E-15	1.007E-11	23.27378933	-33.87	ENSG00000173930
-2.372	7.41165	-7.606506771	5.8E-13	2.204E-10	18.97360958	-29.02	ENSG00000179593
-2.298	4.61631	-7.672629895	3.8E-13	1.617E-10	19.37367947	-28.53	ENSG00000146453
-2.29	5.16118	-8.60663985	8.8E-16	1.973E-12	25.23671109	-34.48	ENSG00000178445

-2.253	4.04687	-7.183202843	7.9E-12	2.154E-09	16.46388722	-25.01	ENSG00000250266
-2.224	7.59242	-7.872406261	1.1E-13	6.316E-11	20.59503369	-28.83	ENSG00000064763
-2.094	4.05076	-8.271951295	8.1E-15	1.064E-11	23.09225312	-29.51	ENSG00000259283
-2.035	5.42736	-7.321744596	3.4E-12	1.043E-09	17.27528259	-23.34	ENSG00000249365
-1.997	5.74217	-8.27963182	7.7E-15	1.056E-11	23.14094208	-28.18	ENSG00000130208
-1.98	4.19424	-7.807480157	1.6E-13	8.899E-11	20.1960455	-25.32	ENSG00000132915
-1.97	4.94002	-5.149090618	5.3E-07	2.644E-05	5.838404279	-12.36	ENSG00000184227
-1.969	5.12246	-7.673344392	3.8E-13	1.617E-10	19.37801394	-24.45	ENSG00000087128
-1.966	4.41902	-7.687618262	3.5E-13	1.532E-10	19.46465723	-24.49	ENSG00000100341
-1.911	7.66326	-6.927901311	3.7E-11	7.702E-09	14.99520611	-19.95	ENSG00000167755
-1.91	6.42313	-7.995791031	4.9E-14	3.675E-11	21.35860838	-25.42	ENSG00000103089
-1.906	7.42109	-7.922606862	7.8E-14	4.864E-11	20.90486495	-24.98	ENSG00000057252
-1.903	3.36446	-7.05598179	1.7E-11	4.042E-09	15.7276513	-20.5	ENSG00000250411
-1.84	6.40136	-2.862274902	0.00457	0.034854	-2.569358947	-4.308	ENSG00000204897
-1.834	5.07315	-7.85778583	1.2E-13	6.728E-11	20.50501662	-23.71	ENSG00000253745
-1.825	5.18037	-8.162531699	1.7E-14	1.845E-11	22.40136146	-25.15	ENSG00000116882
-1.806	4.8191	-8.307283815	6.4E-15	1.007E-11	23.31644324	-25.63	ENSG00000176136
-1.799	9.12902	-5.136712	5.7E-07	2.754E-05	5.781973966	-11.24	ENSG00000184148
-1.798	4.89682	-7.768325806	2.1E-13	1.034E-10	19.95638248	-22.79	ENSG00000101049
1.785	7.10188	10.86271588	9.7E-23	1.525E-18	40.6992248	39.3	ENSG00000105664
-1.761	6.50786	-8.698169244	4.7E-16	1.36E-12	25.8310518	-26.99	ENSG00000146070
-1.692	5.7782	-7.226441494	6.1E-12	1.763E-09	16.71605358	-18.97	ENSG00000253125
-1.672	5.57868	-7.107816937	1.2E-11	3.077E-09	16.02658788	-18.23	ENSG00000103740
-1.648	5.58043	-7.943452964	6.9E-14	4.505E-11	21.03386339	-21.69	ENSG00000176194
1.64	6.76519	9.346883867	5.5E-18	2.467E-14	30.13314939	28.3	ENSG00000138615
-1.613	7.65361	-7.157992417	9.2E-12	2.417E-09	16.31731276	-17.79	ENSG00000095321
-1.594	4.642	-8.158043834	1.7E-14	1.845E-11	22.37313501	-21.95	ENSG00000166391
-1.578	7.17238	-5.215394401	3.9E-07	2.006E-05	6.14251365	-10.12	ENSG00000075673
-1.569	3.33735	-7.243711114	5.5E-12	1.602E-09	16.81704169	-17.67	ENSG00000174827
-1.564	6.65935	-2.784210008	0.00578	0.0415	-2.779140373	-3.5	ENSG00000139648
-1.531	4.95603	-9.005663641	5.8E-17	2.296E-13	27.85125507	-24.86	ENSG00000086696
-1.497	5.15018	-7.87576629	1.1E-13	6.298E-11	20.61573513	-19.43	ENSG00000140284
-1.473	5.51919	-8.236392334	1E-14	1.29E-11	22.86716333	-20.61	ENSG00000267475
-1.461	6.52985	-6.351428688	1E-09	1.319E-07	11.81264217	-13.14	ENSG00000185499
-1.435	5.4815	-2.771946659	0.00599	0.0426193	-2.811601053	-3.189	ENSG00000205186
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-0.675	7.11222	-8.095650592	2.6E-14	2.31E-11	21.98162602	-9.179	ENSG00000198736
-0.674	6.08333	-5.535564804	7.9E-08	5.309E-06	7.654171725	-4.79	ENSG00000260186
0.674	6.35949	3.433488531	0.0007	0.0084145	-0.871492012	2.128	ENSG00000186049
-0.674	6.73604	-6.320928889	1.2E-09	1.494E-07	11.64966993	-6.011	ENSG00000175066
-0.673	5.96254	-10.46516939	1.8E-21	1.907E-17	37.86866077	-13.96	ENSG00000135903
-0.67	6.35435	-2.828567584	0.00506	0.0375882	-2.660605854	-1.538	ENSG00000141469
-0.667	2.42235	-3.717329757	0.00025	0.0038022	0.076211925	-2.405	ENSG00000258271
0.666	5.18866	3.394601517	0.0008	0.009319	-0.9960293	2.063	ENSG00000119125
0.662	5.08975	4.237964047	3.2E-05	0.0007352	1.987026881	2.975	ENSG00000241489
0.662	5.01741	3.382214167	0.00084	0.0096021	-1.035429484	2.036	ENSG00000226005
-0.662	6.0002	-6.920135794	3.8E-11	7.94E-09	14.95108499	-6.891	ENSG00000128944
0.657	8.78409	5.357351478	1.9E-07	1.107E-05	6.804006352	4.415	ENSG00000197614
0.657	7.97659	6.295320969	1.4E-09	1.67E-07	11.5132708	5.82	ENSG00000269981
-0.656	3.02273	-6.130247144	3.4E-09	3.547E-07	10.64362788	-5.557	ENSG00000269289
0.656	10.5188	5.143860167	5.5E-07	2.694E-05	5.814546955	4.111	ENSG00000159455
-0.655	8.78658	-10.07624798	3.1E-20	1.936E-16	35.13765839	-12.79	ENSG00000066583
0.653	4.33417	5.458344053	1.2E-07	7.297E-06	7.283123101	4.526	ENSG00000182938
-0.652	7.80287	-7.655341859	4.3E-13	1.756E-10	19.26887679	-8.062	ENSG00000128311
-0.648	4.0241	-4.754252821	3.4E-06	0.000119	4.093058698	-3.547	ENSG00000171403
-0.645	7.17086	-6.142274892	3.2E-09	3.354E-07	10.70642525	-5.482	ENSG00000160606
0.644	3.4114	5.488492395	1E-07	6.462E-06	7.427504401	4.508	ENSG00000237735
-0.644	5.22512	-6.542042596	3.4E-10	5.222E-08	12.84373379	-6.093	ENSG00000224307
-0.642	7.4757	-6.67839594	1.6E-10	2.698E-08	13.59436009	-6.293	ENSG00000101417
-0.642	4.31785	-3.934665469	0.00011	0.0019554	0.847144946	-2.545	ENSG00000224525
0.637	4.48693	6.797217314	7.9E-11	1.489E-08	14.25713708	6.438	ENSG00000228630
0.635	8.75557	4.602894456	6.7E-06	0.0002078	3.454524724	3.288	ENSG00000235942
0.635	9.5919	2.935160401	0.00365	0.029714	-2.368605548	1.548	ENSG00000163202
-0.635	3.08267	-4.919867634	1.6E-06	6.381E-05	4.81129814	-3.682	ENSG00000183850
-0.634	4.70131	-7.532084219	9.3E-13	3.181E-10	18.52586598	-7.631	ENSG00000167232
-0.634	3.75065	-6.372904362	9E-10	1.178E-07	11.92773078	-5.734	ENSG00000236924
0.633	5.58821	5.421362871	1.4E-07	8.415E-06	7.106867664	4.34	ENSG00000203392

0.633	11.2895	6.441972257	6.1E-10	8.517E-08	12.29973651	5.834	ENSG00000172867
-0.633	5.34657	-6.510638304	4.1E-10	6.097E-08	12.67238172	-5.938	ENSG00000163644
-0.63	4.87742	-4.018548506	7.8E-05	0.0015122	1.155011491	-2.59	ENSG00000163273
0.629	6.02164	4.208869186	3.6E-05	0.0008061	1.874497254	2.796	ENSG00000184613
-0.627	5.95539	-6.324977493	1.2E-09	1.472E-07	11.6712709	-5.6	ENSG00000091972
0.625	6.31625	4.34156411	2.1E-05	0.0005172	2.393128171	2.928	ENSG00000254979
-0.623	6.90522	-5.200168448	4.2E-07	2.136E-05	6.072403015	-3.976	ENSG00000167508
-0.623	6.1069	-5.513111209	8.8E-08	5.837E-06	7.545863609	-4.392	ENSG00000141448
-0.621	6.38084	-4.216539399	3.5E-05	0.0007851	1.904098247	-2.771	ENSG00000152926
-0.621	5.24469	-6.899689633	4.3E-11	8.902E-09	14.83507494	-6.434	ENSG00000122877
-0.62	5.34273	-2.996159836	0.00301	0.0256694	-2.1969787	-1.563	ENSG00000211904
-0.619	5.18352	-11.45828916	1.1E-24	3.527E-20	45.00396685	-14.82	ENSG00000217236
-0.618	8.02328	-5.684914371	3.7E-08	2.798E-06	8.383209012	-4.595	ENSG00000088386
-0.618	3.18932	-5.986722866	7.5E-09	7.002E-07	9.901268031	-5.02	ENSG00000170477
0.618	8.89594	6.505182229	4.2E-10	6.26E-08	12.64267049	5.788	ENSG00000038427
-0.616	3.33907	-6.196821631	2.4E-09	2.673E-07	10.99234066	-5.314	ENSG00000165186
-0.615	4.8253	-3.672599047	0.00029	0.0043491	-0.077618597	-2.171	ENSG00000244437
-0.613	4.77577	-4.890422285	1.8E-06	7.124E-05	4.68212183	-3.521	ENSG00000211891
0.611	6.52987	6.531880851	3.6E-10	5.48E-08	12.78822486	5.771	ENSG00000224271
-0.611	9.66728	-4.297689448	2.5E-05	0.0006017	2.220116202	-2.813	ENSG00000178363
-0.61	7.03126	-5.444366798	1.2E-07	7.703E-06	7.21639621	-4.211	ENSG00000168209
0.61	6.43035	3.418862447	0.00073	0.0087447	-0.918483808	1.91	ENSG00000188257
-0.608	3.94792	-3.560637624	0.00044	0.0059384	-0.455334886	-2.04	ENSG00000178449
-0.608	7.60276	-7.419878555	1.9E-12	5.932E-10	17.85597756	-7.135	ENSG00000131373
0.606	8.95058	4.490376023	1.1E-05	0.0003064	2.991090374	3.008	ENSG00000187223
0.606	3.20559	5.54137436	7.7E-08	5.199E-06	7.682250519	4.312	ENSG00000252544
-0.604	5.02262	-6.533023428	3.6E-10	5.471E-08	12.79446322	-5.699	ENSG00000079385
-0.601	4.97484	-7.768893219	2.1E-13	1.034E-10	19.95985046	-7.62	ENSG00000008735
-0.597	6.57021	-4.749178612	3.5E-06	0.0001215	4.071373763	-3.259	ENSG00000174156
0.595	5.37125	3.248628786	0.00132	0.0136535	-1.451964841	1.715	ENSG00000164694
0.595	5.08498	4.513183833	9.9E-06	0.0002819	3.084247885	2.978	ENSG00000106483
0.593	6.39688	4.090939288	5.8E-05	0.0011861	1.4252634	2.511	ENSG00000256248
-0.592	5.87761	-6.846029917	5.9E-11	1.182E-08	14.53171007	-6.052	ENSG00000110042
-0.59	4.42515	-3.235277234	0.00138	0.0141463	-1.492752205	-1.689	ENSG00000211899
-0.59	6.91287	-3.398272896	0.00079	0.0092377	-0.98432666	-1.83	ENSG00000199839
-0.586	8.08021	-4.802764579	2.7E-06	9.989E-05	4.301344215	-3.262	ENSG00000136943
-0.585	5.68182	-6.148297405	3.1E-09	3.267E-07	10.73790278	-4.975	ENSG00000133135
-0.585	5.04325	-4.309872186	2.4E-05	0.0005792	2.268005599	-2.706	ENSG00000268416
-0.584	6.83654	-7.585881255	6.6E-13	2.404E-10	18.84925061	-7.116	ENSG00000160216
-0.584	5.32746	-3.152612821	0.00182	0.0174583	-1.741844856	-1.6	ENSG00000239951
-0.583	7.86435	-3.605184666	0.00038	0.0052526	-0.306307436	-1.995	ENSG00000172724
-0.58	6.17049	-7.246727898	5.4E-12	1.588E-09	16.83469892	-6.538	ENSG00000065923

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141 Thigh_CTRL / Upper_back_CTRL

logFC	AveExpr	t-statistic	P.Value	adj.P.Val	B-statistic	score	ID

-4.342	5.26709	-9.604108024	9E-19	1.092E-16	32.00322354	-78.36	ENSG00000204195
-4.31	4.94002	-9.25426085	1E-17	1.102E-15	29.59409776	-73.2	ENSG00000184227
-4.237	6.24598	-6.859930072	5.5E-11	2.185E-09	14.46254988	-43.49	ENSG00000188984
-4.202	6.18375	-7.673129622	3.8E-13	2.206E-11	19.30028067	-52.17	ENSG00000147160
-4.199	6.59981	-6.709691675	1.3E-10	4.9E-09	13.60827244	-41.49	ENSG00000162877
-4.191	6.06906	-6.602904438	2.4E-10	8.586E-09	13.00900585	-40.29	ENSG00000184210
-4.011	6.07306	-7.812838694	1.6E-13	9.52E-12	20.16548694	-51.34	ENSG00000214491
-3.785	5.90733	-7.423488517	1.8E-12	9.384E-11	17.77831972	-44.43	ENSG00000119915
-3.626	7.88138	-6.25244418	1.8E-09	5.243E-08	11.09016988	-31.75	ENSG00000151365
-3.571	4.04687	-9.352438704	5.3E-18	5.848E-16	30.26594118	-61.7	ENSG00000250266
-3.517	3.36446	-10.70811246	3E-22	6.386E-20	39.85216577	-75.68	ENSG00000250411
-3.504	4.61631	-9.605599318	8.9E-19	1.085E-16	32.01358088	-63.25	ENSG00000146453
-3.449	4.05076	-11.18995923	8.4E-24	2.481E-21	43.37685445	-79.59	ENSG00000259283
-3.423	4.32985	-8.433776365	2.8E-15	2.127E-13	24.12059509	-49.83	ENSG00000226281
-3.417	6.5234	-7.343270534	3E-12	1.499E-10	17.29599731	-39.38	ENSG00000069482
-3.393	4.19424	-10.98848887	3.8E-23	9.65E-21	41.89671547	-76.08	ENSG00000132915
-3.389	5.42736	-10.01427254	4.8E-20	6.941E-18	34.87835787	-65.48	ENSG00000249365
-3.327	5.16118	-10.26837193	7.6E-21	1.266E-18	36.68472805	-66.93	ENSG00000178445
-3.31	5.31244	-9.442630694	2.8E-18	3.229E-16	30.88608252	-58.09	ENSG00000173930
-3.279	7.41165	-8.635455593	7.2E-16	6.117E-14	25.44138305	-49.65	ENSG00000179593
-3.198	5.07315	-11.25431611	5.2E-24	1.591E-21	43.85149459	-74.47	ENSG00000253745
-3.159	5.74217	-10.76063511	2.1E-22	4.45E-20	40.23375642	-68.52	ENSG00000130208
-3.148	3.33735	-11.93513196	3E-26	1.6E-23	48.92167554	-80.36	ENSG00000174827
-3.122	4.8191	-11.79284892	8.9E-26	4.048E-23	47.85513859	-78.21	ENSG00000176136
-3.118	4.41902	-10.01321245	4.8E-20	6.959E-18	34.87086075	-60.22	ENSG00000100341
-3.043	7.59242	-8.846471609	1.7E-16	1.546E-14	26.84100328	-47.96	ENSG00000064763
-2.97	5.70414	-7.658483304	4.2E-13	2.406E-11	19.21012852	-36.75	ENSG00000185640
-2.968	5.58043	-11.75163814	1.2E-25	5.382E-23	47.54687186	-73.96	ENSG00000176194
-2.962	5.57868	-10.34054172	4.5E-21	7.647E-19	37.20107468	-60.26	ENSG00000103740
-2.91	7.17238	-7.89903319	9.1E-14	5.639E-12	20.70395939	-37.94	ENSG00000075673
-2.885	4.89682	-10.23828218	9.5E-21	1.551E-18	36.4698701	-57.77	ENSG00000101049
-2.869	5.18037	-10.53591526	1.1E-21	2.003E-19	38.6058817	-60.14	ENSG00000116882
-2.809	7.42109	-9.588718359	1E-18	1.204E-16	31.8963817	-50.56	ENSG00000057252
-2.797	5.7782	-9.811733393	2.1E-19	2.717E-17	33.45209168	-52.26	ENSG00000253125
-2.79	6.42313	-9.592436238	9.7E-19	1.182E-16	31.92218576	-50.26	ENSG00000103089
-2.77	4.35216	-9.945715527	7.9E-20	1.082E-17	34.39419936	-52.92	ENSG00000173124
-2.761	6.52985	-9.858325559	1.5E-19	1.956E-17	33.77908673	-52.01	ENSG00000185499
-2.693	6.50786	-10.9210636	6.3E-23	1.52E-20	41.40337097	-59.79	ENSG00000146070
-2.668	7.65361	-9.725939379	3.8E-19	4.885E-17	32.85173595	-49.15	ENSG00000095321
-2.623	4.642	-11.02477243	2.9E-23	7.737E-21	42.16262268	-59.12	ENSG00000166391
-2.6	5.12246	-8.319882296	5.9E-15	4.291E-13	23.3822794	-36.99	ENSG00000087128
-2.582	4.06002	-13.39848206	3.6E-31	8.823E-28	60.05379815	-78.6	ENSG00000225611
-2.566	6.3465	-7.03855486	1.9E-11	8.231E-10	15.4948371	-27.52	ENSG00000211893
-2.539	5.51919	-11.66010498	2.4E-25	9.573E-23	46.86325102	-62.5	ENSG00000267475
-2.539	5.15018	-10.96819952	4.4E-23	1.105E-20	41.7481519	-56.76	ENSG00000140284

-2.524	3.46154	-10.52172863	1.2E-21	2.21E-19	38.50353901	-52.81	ENSG00000047936
-2.509	2.97431	-10.44316197	2.1E-21	3.713E-19	37.93769983	-51.86	ENSG00000203857
-2.422	5.71038	-12.06984958	1.1E-26	6.243E-24	49.93456344	-62.91	ENSG00000165140
-2.409	5.50791	-9.987414374	5.8E-20	8.196E-18	34.68851567	-46.34	ENSG00000254682
-2.384	6.40136	-3.04570675	0.00257	0.0138496	-2.43092684	-6.175	ENSG00000204897
-2.363	4.37664	-11.9489722	2.7E-26	1.465E-23	49.02560014	-60.43	ENSG00000170439
-2.358	2.98437	-13.22287405	1.4E-30	2.824E-27	58.70515461	-70.37	ENSG00000157330
-2.352	3.11989	-10.59793974	6.8E-22	1.308E-19	39.05393034	-49.78	ENSG00000124003
-2.345	5.90725	-14.64744455	2E-35	2.087E-31	69.70649543	-81.37	ENSG00000166816
-2.305	7.66326	-6.863691431	5.3E-11	2.14E-09	14.48410277	-23.68	ENSG00000167755
-2.289	8.12956	-4.671614564	4.9E-06	6.467E-05	3.442424078	-12.16	ENSG00000206073
-2.261	5.92552	-11.55820813	5.3E-25	1.973E-22	46.10401135	-54.88	ENSG00000115425
-2.259	7.88756	-6.930710327	3.6E-11	1.502E-09	14.86946366	-23.59	ENSG00000143546
-2.243	4.95603	-10.83262269	1.2E-22	2.703E-20	40.7578392	-49.16	ENSG00000086696
-2.216	5.63467	-8.33817136	5.2E-15	3.83E-13	23.50046197	-31.65	ENSG00000167588
-2.192	3.96668	-10.79479614	1.6E-22	3.553E-20	40.48230136	-47.79	ENSG00000231346
-2.186	4.13752	-13.43456314	2.7E-31	7.209E-28	60.3312279	-66.79	ENSG00000138769
-2.168	8.18822	-9.948455711	7.7E-20	1.065E-17	34.41352401	-41.43	ENSG00000186480
-2.164	5.45206	-5.569028422	6.6E-08	1.41E-06	7.571859433	-15.53	ENSG00000211892
-2.143	3.48891	-15.55197457	1.6E-38	4.928E-34	76.73192832	-81.01	ENSG00000152463
-2.143	3.28162	-11.53347017	6.3E-25	2.297E-22	45.9199778	-51.85	ENSG00000256612
-2.129	5.34243	-13.07979558	4.4E-30	6.265E-27	57.60844974	-62.52	ENSG00000214456
-2.111	5.19191	-2.606020137	0.00971	0.0407956	-3.628342129	-4.249	ENSG00000213416
-2.082	5.3304	-9.902778297	1.1E-19	1.453E-17	34.0916873	-39.49	ENSG00000005187
-2.036	6.65935	-2.976775348	0.0032	0.0165777	-2.630151253	-5.078	ENSG00000139648
-2.032	7.64952	-11.37656998	2.1E-24	6.666E-22	44.75547578	-48.13	ENSG00000012660
-2.025	7.55855	-8.512601148	1.6E-15	1.322E-13	24.63480195	-29.94	ENSG00000203837
-2.02	4.76059	-8.456689041	2.4E-15	1.853E-13	24.26979441	-29.53	ENSG00000091513
-2.016	7.17457	-11.93235232	3.1E-26	1.608E-23	48.90080734	-51.43	ENSG00000101474
-2.007	8.79419	-10.19996959	1.3E-20	2.007E-18	36.19666066	-39.95	ENSG00000169710
-2.006	8.24435	-9.449008822	2.7E-18	3.115E-16	30.9300424	-35.25	ENSG00000133048
-2.001	7.60378	-12.25360766	2.6E-27	1.647E-24	51.32069961	-53.19	ENSG00000166250
-1.999	7.91557	-11.38119123	2E-24	6.504E-22	44.78970567	-47.37	ENSG00000167315
-1.999	6.0454	-8.427497181	2.9E-15	2.207E-13	24.07974604	-29.05	ENSG00000064886
-1.993	6.03922	-5.344429823	2.1E-07	3.912E-06	6.484051463	-13.33	ENSG00000211677
-1.944	6.28375	-13.18733808	1.9E-30	3.312E-27	58.43258526	-57.79	ENSG00000105552
-1.933	5.4815	-3.066281631	0.00241	0.013157	-2.370641866	-5.062	ENSG00000205186
-1.91	7.46787	-5.492520605	9.8E-08	2.008E-06	7.197371779	-13.39	ENSG00000163220
-1.906	3.94333	-11.51353529	7.4E-25	2.554E-22	45.77175981	-45.99	ENSG00000253632
-1.894	5.01909	-12.74269978	6E-29	5.907E-26	55.03299641	-53.46	ENSG00000143028
-1.892	5.87461	-9.718603117	4E-19	5.125E-17	32.80050698	-34.81	ENSG00000165548
-1.872	6.43647	-2.914823256	0.00388	0.0194307	-2.805581405	-4.512	ENSG00000159450
-1.871	5.80429	-10.53938261	1.1E-21	1.976E-19	38.63090312	-39.26	ENSG00000168306
-1.868	7.16171	-13.66376464	4.6E-32	2.397E-28	62.09600444	-58.55	ENSG00000141179
-1.868	3.32775	-9.062898486	3.9E-17	3.813E-15	28.29447514	-30.65	ENSG00000259517

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0.845	6.19635	5.844033749	1.6E-08	3.895E-07	8.9507787	6.591	ENSG00000187170
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0.845	5.34453	4.735519158	3.7E-06	5.031E-05	3.716854804	4.591	ENSG00000221305
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0.843	10.664	7.341847202	3E-12	1.51E-10	17.28746948	9.717	ENSG00000198854
-0.843	4.07515	-8.321356998	5.8E-15	4.26E-13	23.39180344	-12	ENSG00000163406
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0.84	9.53085	8.584141194	1E-15	8.408E-14	25.10373146	12.6	ENSG00000166396
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-0.835	8.14771	-5.419131916	1.4E-07	2.793E-06	6.841958831	-5.719	ENSG00000125398
0.835	5.51324	5.590411286	6E-08	1.282E-06	7.677242511	6.031	ENSG00000252026
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0.833	6.97804	6.687947886	1.5E-10	5.493E-09	13.48571112	8.181	ENSG00000172824
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0.821	4.39914	4.159179411	4.4E-05	0.0004389	1.356633729	3.575	ENSG00000231604
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0.818	4.33417	5.619258469	5.1E-08	1.123E-06	7.819907609	5.964	ENSG00000182938
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-0.715	4.91135	-6.954503758	3.1E-11	1.318E-09	15.0068826	-7.51	ENSG00000175832
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-0.713	4.08527	-7.091816266	1.4E-11	6.125E-10	15.80605655	-7.747	ENSG00000180596
-0.713	4.0007	-8.289755895	7.2E-15	5.162E-13	23.18792144	-10.08	ENSG00000186326
-0.712	5.27422	-9.228019844	1.3E-17	1.318E-15	29.41510291	-12.04	ENSG00000257303
0.711	5.44589	3.558164183	0.00045	0.0032107	-0.818845153	2.381	ENSG00000230030

-0.71	5.33732	-6.681765729	1.5E-10	5.68E-09	13.45091489	-6.971	ENSG00000182379
0.71	7.97659	5.589923279	6E-08	1.284E-06	7.674833934	5.131	ENSG00000269981
0.71	6.25933	5.210357832	4E-07	7.059E-06	5.851596191	4.545	ENSG00000267519
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-0.707	5.0137	-6.498059023	4.4E-10	1.487E-08	12.42718038	-6.614	ENSG00000135919
-0.707	4.8253	-3.468750178	0.00062	0.0042073	-1.116539035	-2.269	ENSG00000244437
-0.706	7.06451	-8.484975977	2E-15	1.558E-13	24.45429438	-10.38	ENSG00000119711
-0.705	8.11698	-10.83510913	1.2E-22	2.684E-20	40.77596283	-15.47	ENSG00000117500
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0.704	3.84795	4.013512386	7.9E-05	0.0007338	0.801938548	2.887	ENSG00000227718
0.703	5.47392	6.9209028	3.8E-11	1.583E-09	14.81291241	7.329	ENSG00000263894
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-0.703	5.78275	-3.837524053	0.00016	0.0013261	0.154984741	-2.673	ENSG00000137648
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0.702	5.56457	4.579402073	7.4E-06	9.319E-05	3.051939367	3.601	ENSG00000196557
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0.698	7.11999	7.92498041	7.7E-14	4.831E-12	20.8667443	9.151	ENSG00000171680
0.697	5.22693	4.84045212	2.3E-06	3.301E-05	4.174193013	3.931	ENSG00000174501
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0.691	4.26705	6.556527885	3.2E-10	1.087E-08	12.75083929	6.56	ENSG00000251323
0.69	4.82562	5.282661542	2.8E-07	5.148E-06	6.191084246	4.526	ENSG00000260658
0.69	5.37125	3.092746766	0.00221	0.012285	-2.292545675	1.833	ENSG00000164694
0.69	7.28454	4.932451392	1.5E-06	2.27E-05	4.581961132	4.018	ENSG00000168079
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0.684	9.37874	4.286484695	2.6E-05	0.0002779	1.855445614	3.134	ENSG00000133800
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0.681	8.70375	3.690927465	0.00027	0.0021234	-0.364249654	2.425	ENSG00000118520
0.681	6.97765	6.551798439	3.3E-10	1.115E-08	12.72458331	6.46	ENSG00000163545
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0.676	6.14724	4.351074981	2E-05	0.0002201	2.113475763	3.178	ENSG00000180332
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0.664	3.62383	3.336557656	0.00098	0.0062014	-1.544044895	2	ENSG00000199664
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0.624	8.7663	6.704682302	1.4E-10	5.021E-09	13.5800122	6.157	ENSG00000112394
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