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Pertussis Toxin Exacerbates and Prolongs Airway Inflammatory Responses during *Bordetella pertussis* Infection

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Throughout infection, pathogenic bacteria induce dramatic changes in host transcriptional repertoires. An understanding of how bacterial factors influence host reprogramming will provide insight into disease pathogenesis. In the human respiratory pathogen *Bordetella pertussis*, the causative agent of whooping cough, pertussis toxin (PT) is a key virulence factor that promotes colonization, suppresses innate immune responses during early infection, and causes systemic disease symptoms. To determine the full extent of PT-associated gene regulation in the airways through the peak of infection, we measured global transcriptional profiles in the lungs of BALB/c mice infected with wild-type (WT) or PT-deficient (Δ PT) *B. pertussis*. Δ PT bacteria were inoculated at a dose equivalent to the WT dose and at a high dose (Δ PT^{high}) to distinguish effects caused by higher bacterial loads achieved in WT infection from effects associated with PT. The results demonstrated that PT was associated with a significant upregulation of immune and inflammatory response genes as well as several other genes implicated in airway pathology. In contrast to the early, transient responses observed for Δ PT^{high} infection, WT infection induced a prolonged expression of inflammatory genes and increased the extent and duration of lung histopathology. In addition, the administration of purified PT to Δ PT^{high}-infected mice 1 day after bacterial inoculation exacerbated and prolonged inflammatory responses and airway pathology. These data indicate that PT not only is associated with exacerbated host airway responses during peak *B. pertussis* infection but also may inhibit host mechanisms of attenuating and resolving inflammation in the airways, suggesting possible links between PT and pertussis disease symptoms.

Bacterial toxins disrupt a broad range of eukaryotic cell functions, causing changes in host physiology that often underlie severe disease pathology. For the human respiratory pathogen *Bordetella pertussis*, multiple toxins act in concert to facilitate the adhesion, survival, and proliferation of bacteria within the airways (48). Among these toxins, pertussis toxin (PT) has emerged as a key virulence factor for its ability to promote bacterial colonization (17), modulate host immune responses (14), cause systemic effects (53, 56), and, possibly, boost transmission (52). Previous studies using infant mice associated PT with lethal *B. pertussis* infection (31, 85), and in humans, *B. pertussis* strains that lack functional PT display reduced pathogenicity (10). Despite its well-established role as a virulence factor, mechanistic links between PT and pertussis disease symptoms have not been well defined.

Pertussis can be fatal in infants (62), and it hampers patients of all ages with a range of symptoms, the most severe of which include pneumonia, pulmonary hypertension, encephalopathy, and the hallmark paroxysmal cough (whooping cough) that can last for weeks or even months after bacterial clearance (48). The incidence of pertussis is highest in developing nations, accounting for 90 to 95% of the estimated 16 million worldwide cases and 195,000 deaths in 2008 (87). In developed countries, reemergent pertussis has sparked significant public health concerns in recent years, where the efficacy of widespread vaccination programs seems to be waning (33). Interestingly, the characterization of resurgent pertussis in some countries highlights *B. pertussis* strains with increased promoter activity at the *ptx* locus (52), suggesting that higher levels of PT contribute to increased virulence in these strains.

At the molecular level, PT modifies inhibitory G proteins, effectively uncoupling signaling through cognate receptors. PT is a secreted exotoxin of the AB₅ configuration, comprised of one active subunit (S1) and a pentameric binding oligomer (77). After

interactions with glycosylated molecules on the surface of mammalian cells (49, 86), PT undergoes endocytosis and retrograde trafficking to the endoplasmic reticulum (ER), where the active subunit dissociates and enters the cytoplasm (66). S1 catalyzes the ADP-ribosylation of the G_i α and G_o α subunits (37, 54, 81), preventing the G-protein activation required for subsequent adenyl cyclase inhibition and other downstream effects. ADP-ribosylation activity accounts for many of the reported effects of PT, but the B oligomer can also affect signaling through binding properties (3, 36, 60).

A comparison of wild-type (WT) and PT-deficient (Δ PT) strains in mouse models of *B. pertussis* infection indicates that PT heightens virulence through the modulation of host immune responses. PT confers a colonization advantage to WT bacteria such that within 24 to 48 h postinoculation, mice infected with WT *B. pertussis* have a 10- to 50-fold-higher bacterial load in their lungs than mice inoculated with equal numbers of the Δ PT strain (17). This difference arises primarily from the PT-mediated inhibition of resident airway macrophages, as clodronate liposome depletion of macrophages prior to infection restores colonization by the Δ PT strain to WT levels (18). In addition, PT interferes with the chemotaxis of multiple cell types *in vitro* and *in vivo* (4, 22, 76). In

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the case of neutrophils, PT reduces early influx into the mouse respiratory tract by suppressing the expressions of genes for the neutrophil-attracting chemokines keratinocyte-derived chemokine (KC) and lipopolysaccharide-induced CXC chemokine (LIX) and macrophage inflammatory protein 2 (MIP-2) (4). The inhibitory functions of PT extend to adaptive immunity, where it was shown to suppress the serum antibody response to *B. pertussis* (16), decrease the expression and cell surface levels of antigen-presenting molecules (47, 73), suppress the induction of regulatory T cells (20), and decrease the antibody-mediated clearance of bacteria (41).

In addition to the immunosuppressive functions described above, several lines of evidence implicate PT in heightened inflammatory responses. When used as an adjuvant, PT promotes experimental autoimmune diseases (2, 57, 92), and recent studies showed that PT induces the development of Th17 cells (5, 19, 35), now recognized as major contributors to autoimmune pathogenesis (84). Previous studies reported increased gamma interferon (IFN- γ) and tumor necrosis factor alpha (TNF- α) secretion by lymphocytes, splenocytes, and macrophages in response to PT (64, 82, 91). In addition, at the peak of *B. pertussis* infection, PT enhances neutrophil influx into the airways through the upregulation of interleukin-17 (IL-17) and the neutrophil-attracting chemokines (5).

Because G proteins play an integral role in diverse cellular processes, we hypothesized that PT would induce multiple effects on the host respiratory tract during *B. pertussis* infection, including the upregulation of inflammatory responses. Our results present the first global, *in vivo* evaluation of host transcriptional responses affected by PT in the context of pertussis infection. The results reveal that PT activity is associated with an extensive upregulation of inflammatory genes at the peak of infection and highlight several genes that may contribute to pertussis-evoked airway pathology and disease. In addition, our results reveal the novel finding that PT increases the extent and duration of inflammatory responses and pathology in lungs of *B. pertussis*-infected mice.

MATERIALS AND METHODS

Bacterial strains. The WT, Δ PT, and PT* *B. pertussis* strains used in this study are streptomycin- and nalidixic acid-resistant derivatives of Tohama I (17). The Δ PT strain does not produce PT due to an in-frame deletion spanning all 5 PT genes (17). The PT* strain produces enzymatically inactive toxin, as it carries two amino acid substitutions in the S1 subunit (R9K and E129G) that abrogate ADP-ribosylation activity (65). All *B. pertussis* strains were grown on Bordet-Gengou (BG) agar plates supplemented with 10% defibrinated sheep blood and 200 μ g/ml streptomycin.

Mouse infections. Six- to eight-week old female BALB/c mice (Charles River Laboratories) were anesthetized with inhaled isoflurane and intranasally (i.n.) inoculated with 50 μ l of either sterile phosphate-buffered saline (PBS) or a suspension of *B. pertussis* in PBS. Inocula contained approximately 1×10^6 CFU of WT, Δ PT, or PT* bacteria for the normal dose or 1.5×10^7 to 4×10^7 CFU (WT^{high}, Δ PT^{high}, and PT*^{high}) for high-dose experiments. In selected experiments, mice received intranasal treatment with 50 μ l PBS or 50 μ l purified PT (100 ng) at 24 h postinoculation. At the indicated times postinoculation, mice were euthanized by carbon dioxide inhalation followed by thoracotomy. Unless otherwise stated, the lungs were intracardially perfused with 5 ml of sterile PBS. For analyses of bacterial counts, the trachea and right lung (cranial, medial, caudal, and postcaval lobes) were dissected, immersed in 2 ml of sterile PBS, and homogenized. Serial dilutions of homogenates were

plated onto BG blood agar plates with 200 μ g/ml streptomycin, and CFU were determined by counting colonies after 4 to 5 days of growth at 37°C. Lung tissue for other purposes was collected as described below. Animal procedures were performed according to a protocol approved by the University of Maryland Baltimore (UMB) Institutional Animal Care and Use Committee.

RNA isolation and processing. After the perfusion of the lungs, the left lobe was removed and immediately frozen in a dry-ice–ethanol bath. RNA was extracted by using RNA Stat60 (TelTest, Inc.). Each frozen lung sample was homogenized immediately after the addition of Stat60 (1 ml per 75 to 100 mg tissue) by using an Omni TH mixer (Omni, Inc.). Homogenates were incubated for 4 min at room temperature to allow nucleoprotein complexes to dissociate and were combined with 200 μ l chloroform. After gentle mixing (1 min), rest at room temperature (1 min), and centrifugation, 400 μ l of the aqueous phase was mixed with 500 μ l isopropanol and stored at -20°C for 1 to 2 h. After precipitation and centrifugation, pellets were washed with 80% ethanol, dried briefly in a DNA Speedvac instrument (Savant), and resuspended in 50 μ l H₂O. The concentration of each sample was determined by using a NanoDrop spectrophotometer (ND-1000; Thermo Scientific). Twenty-five micrograms of RNA was combined with 10 μ l RDD buffer (Qiagen), 2.5 μ l DNase (Qiagen), and distilled water (dH₂O) up to a final volume of 100 μ l and incubated at 25°C for 10 min. DNase samples were subsequently purified by using the RNeasy minikit (Qiagen), and final concentrations were determined by using the NanoDrop ND-1000 spectrophotometer. For quantitative real-time PCR (qPCR), cDNA was generated from 1 μ g of RNA by using a reverse transcription system (Promega) with random primers. For microarray hybridization, RNA quality was determined by using an Agilent 2100 Bioanalyzer. cRNA was prepared from 150 ng of RNA by using the Illumina TotalPre RNA amplification kit. The transcription reaction mixture to generate cRNA was incubated for 14 h at 37°C.

Microarray processing and statistical analysis. Individual cRNA samples were hybridized onto Illumina MouseRef8_v2.0 bead array chips containing 25,697 probes ($n = 3$ per group for samples from infected mice, and $n = 2$ for PBS-treated mice). Sample probe profiles were extracted and normalized by the median method implemented in the beadarray R package (25). Differential expression analysis was performed on normalized data by using the limma R package (75) to compare gene expression profiles among different time points and infection strains. All lists were filtered to include only probes with a false discovery rate (FDR) of ≤ 0.05 and a fold change (FC) of ≥ 1.5 . The FDR represents the expected proportion of false-positive results in a set of significant hypotheses (9). Functions and pathways relevant to significant probes were assigned by using Ingenuity Pathway Analysis (IPA) (Ingenuity Systems) functional and pathway annotations, with *P* values calculated by using Fisher's exact test.

Quantitative real-time PCR. qPCR was carried out by using the 7500 Fast real-time PCR system (Applied Biosystems) and Fast SYBR green master mix (catalog number ABI4385617). Each reaction mixture contained the following: 12.5 μ l SYBR green mix, 6 μ l H₂O, 0.75 μ l each forward and reverse primers (0.3 μ M final concentration), and 5 μ l cDNA (~ 300 ng). Primer sequences were obtained from the Universal ProbeLibrary for mouse (Roche Applied Science), from qPrimerDepot (NCBI), or were designed to flank an intron and yield a cDNA-based product with a length of between 60 and 130 bp. Primer sequences can be found in Table S1 in the supplemental material. Relative gene expression changes were calculated by using the $\Delta\Delta C_T$ method, and the mouse housekeeping gene hypoxanthine phosphoribosyltransferase (HPRT) was used for expression normalization.

Bronchoalveolar lavage fluid and neutrophil counts. A 20-gauge blunt-ended needle was inserted into a small incision toward the top of the trachea in euthanized mice and tied in place with surgical thread. Bronchoalveolar lavage (BAL) was performed by flushing the lungs twice with 0.7 ml of sterile PBS (1.4 ml PBS total). In lungs used for the collec-

tion of BAL fluid cells as well as the isolation of RNA, equivalent proportions of lung tissue and BAL fluid cells were combined prior to the freezing of samples for RNA extraction (one-sixth of the total lung tissue with one-sixth of the isolated BAL fluid cells). Aliquots of BAL fluid were used for cell counting on a hemocytometer and for cytospin centrifugation. Cytospin slides were stained with modified Wright's stain, and 200 to 800 cells from multiple microscope fields were counted and identified.

Pathology. After euthanasia by carbon dioxide inhalation, the lungs and trachea were exposed via dissection. The right bronchiole was tied off by using suture string, a piece of the caudal lobe was collected for RNA isolation, and the rest of the right lobes were dissected for bacterial load determinations. Subsequently, 0.35 ml of 4% paraformaldehyde (PFA) was intratracheally perfused into the left lobe. The trachea was tied shut to allow the fixation of the lung in an inflated state. The inflated left lobe was dissected from the thoracic cavity and fixed in 4% PFA for 60 h at 4°C. Paraffin-embedded sections of lung tissue were prepared at the UMB Histology Core and stained with hematoxylin and eosin. Histopathological evaluations were conducted by a pathologist at the University of Maryland Baltimore with experience evaluating rodent lungs who was blinding to experimental conditions. Sections were given a score of between 0 and 5 in the following categories: peribronchiolar inflammation, perivascular inflammation, epithelial cell damage, edema, hemorrhage, and numbers of eosinophils, neutrophils, macrophages, and lymphocytes. Reported pathology scores reflect the sum of these values for each mouse.

Cytokine ELISA. Tissue for protein analysis was collected immediately after euthanasia, without lung perfusion. The cranial, medial, and caudal lobes of the right lung were collected into 2 ml of ice-cold PBS, and the left lobe was collected into PBS–2% bovine serum albumin (BSA)–0.5% Triton X-100. After homogenization, serial dilutions of samples from the right lung were plated onto BG agar with streptomycin to determine CFU per lung. Left lobe homogenates were centrifuged twice ($17,000 \times g$ at 4°C for 5 min) to remove cells and debris. Supernatants were collected into a separate tube, aliquoted, and stored at -80°C . An enzyme-linked immunosorbent assay (ELISA) was performed at the UMB Cytokine Core Laboratory.

Statistical analysis. Statistical analysis was performed on log-transformed data by using GraphPad Prism for Macintosh 4.0c (GraphPad Software, San Diego, CA). Student's two-tailed, unpaired *t* test was used for comparing 2 groups. For comparisons of 3 or more groups, data were analyzed by using one-way analysis of variance (ANOVA) followed by Bonferroni's multiple-comparison posttest for pairwise comparisons.

Microarray data accession number. Raw and normalized data sets were deposited into the NCBI Gene Expression Omnibus database under accession number [GSE33995](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE33995).

RESULTS

Microarray analysis of lung transcriptional responses to WT and Δ PT-deficient *B. pertussis*. To further understand the effects of PT on host airway responses during *B. pertussis* infection, we carried out genome-wide expression arrays for mice infected with either WT or PT-deficient *B. pertussis* bacteria. Groups of BALB/c mice were intranasally inoculated with PBS, 1.3×10^6 CFU of the WT, or 1.3×10^6 CFU of the Δ PT strain (WT with PT genes deleted) (Fig. 1A). Because PT increases bacterial loads of WT *B. pertussis* by at least 10-fold over those of the Δ PT strain within 1 to 2 days postinoculation (dpi) (17), differential host responses to these infections might arise either directly from the activity of PT or from differences in bacterial loads. Thus, a fourth group of mice was inoculated with a high dose (3.1×10^7 CFU) of the Δ PT strain (Δ PT^{high}) (Fig. 1A) to achieve bacterial loads equivalent to those of the WT through the peak of infection. Infected mice were euthanized at 6 h and at 1, 2, 4, and 7 dpi ($n = 5$ per time point). PBS-treated mice were euthanized at 6 h and at 2 dpi ($n = 3$ per time point). Whole lung tissue was isolated from each mouse,

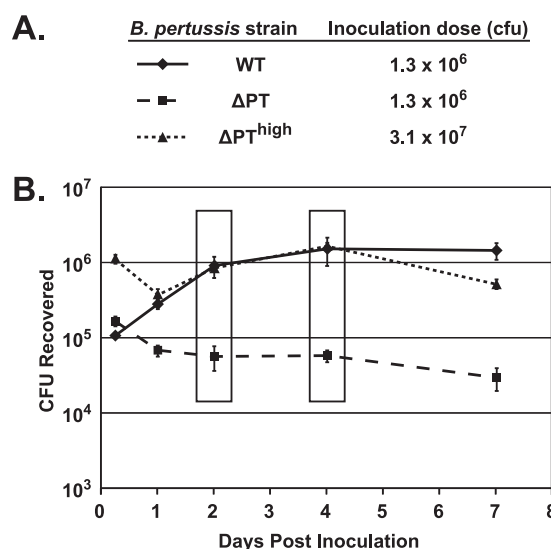


FIG 1 Infection strategy and respiratory tract colonization of mice for genome-wide expression analysis. (A) BALB/c mice (female, 7 weeks of age) were intranasally inoculated with either PBS or the indicated strain and dose of *B. pertussis*: WT and Δ PT. A high dose ($24\times$) of the Δ PT strain (Δ PT^{high}) was used to control for differences in bacterial loads between the WT and low-dose Δ PT infections. (B) Bacterial loads recovered from the lungs of mice at 6 h or 1, 2, 4, or 7 days postinoculation. Graphed values represent mean CFU in three mice $\pm$ standard errors of the means. Lungs of PBS-treated control mice were harvested at 6 h and 2 dpi ($n = 5$). RNA was isolated from lungs of all mice, and individual samples at 2 and 4 dpi were processed further for microarray analysis (boxes).

RNA was extracted from the left lobe of each lung, and bacterial counts per animal were determined from homogenates of the trachea plus right lung lobes. Bacterial loads were equivalent in the lungs of WT- and Δ PT^{high}-infected mice at 1, 2, and 4 dpi (Fig. 1B), with peak numbers being reached by day 4. As observed previously (15, 17), there were significantly fewer Δ PT strain cells in mouse airways after inoculation with the lower dose, demonstrating the important role of PT in promoting bacterial infection in this model.

Previously, we found that PT inhibited early (1 dpi) neutrophil recruitment to the lungs of *B. pertussis*-infected mice, but by 4 dpi, PT activity was associated with increased neutrophil influx and the expression of neutrophil-recruiting chemokines (4, 5). We reasoned that PT may be associated with additional proinflammatory responses at the peak of infection and that the transition to this proinflammatory stage might result from changes both prior to and at day 4. Thus, global gene expression patterns in individual mouse lung samples at 2 and 4 dpi were assessed by microarray analysis, using the Illumina MouseRef8_v2.0 platform to screen for over 24,000 mouse transcripts. Microarray data were analyzed via multiple comparisons at each time point, with most efforts being focused on the discovery of PT-associated changes in host gene expression levels. Infected mice were compared to mock-infected mice, WT- and Δ PT^{high}-infected mice were compared to Δ PT-infected mice, and WT-infected mice were compared to Δ PT^{high}-infected mice. All resulting lists were filtered to include only those genes with statistically significant differential expression levels (false discovery rate [FDR] of ≤ 0.05 and fold change [FC] of ≥ 1.5).

Summary of comparisons. The total number of genes regu-

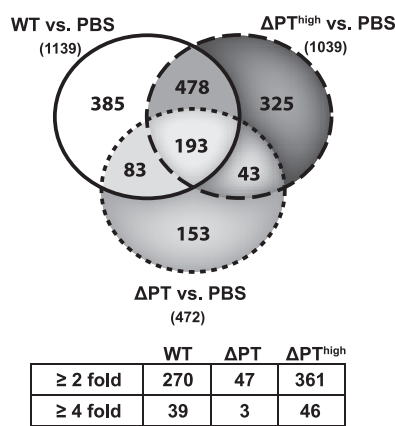


FIG 2 Global gene expression level changes in mouse lung during infection with WT or PT-deficient *B. pertussis*. cDNA generated from lung samples harvested at 2 and 4 dpi was hybridized onto Illumina Mouse Ref8_v2.0 chips carrying probes for >24,000 mouse genes. The diagram shows numbers of unique and common differentially regulated probes between WT-infected (solid circle), ΔPT-infected (dashed circle), and ΔPT^{high}-infected (dotted circle) mice compared to PBS-treated mice. The total number of genes regulated during each infection at either time point is shown in parentheses below each label. The table shows the number of genes regulated at least 2- and 4-fold for each comparison. Data reflect probes with an FDR of ≤0.05 and a fold change of ≥1.5.

lated in the lung during each *B. pertussis* infection was determined by comparisons to values for mice inoculated with PBS (Fig. 2). WT-infected mice displayed 1,139 differentially expressed genes (including 270 genes with changes of more than 2-fold and 39 with changes of more than 4-fold). Infection with the ΔPT strain induced the fewest changes, with differences detected by only 472 probes (47 genes with changes of more than 2-fold and 3 with changes of more than 4-fold). A total of 1,039 differences were observed for ΔPT^{high}-infected mice (361 genes with changes of more than 2-fold and 46 with changes of more than 4-fold). To validate the array data, qPCR measurements were performed for selected genes from the RNA samples used in the microarray analysis to assess relative transcript abundances and expression changes over time. Results from the qPCR analysis were consistent with those of the microarray analysis, although for some genes, qPCR detected fold changes of a greater magnitude than those reported by array data (see Table S2 in the supplemental material).

Analyses revealed 193 genes that were differentially expressed (relative to values for PBS-treated mice) in all three infections (Fig. 2; see also Table S3 in the supplemental material). Ingenuity

Pathway Analysis (IPA) software was used to identify enriched functions among this group of genes. Highly significant functional categories included “cell death” ($P = 6.55 \times 10^{-6}$), “cell cycle” (3.06×10^{-5}), and “connective tissue development and function” ($P = 1.77 \times 10^{-4}$), indicating that many of these genes function in cell turnover and the structural integrity of lung tissue. Transcripts involved in pro- as well as antiapoptotic responses were affected, including Bcl-binding component 3, CD40, TRAF2, and the transcription regulators SMAD6, IKBA, and FOSB. Several genes involved in cell growth (Wnt2, insulin-like growth factor-binding protein 3, microtubule-associated protein tau, and platelet-derived growth factor receptor B) as well as the maintenance and development of blood vessels (angiopoietin 1, cadherin 5, cysteine-rich protein 1, and gap junction membrane channel protein alpha 5) were downregulated. Furthermore, some changes suggested a trend toward a loss of connective tissue, as transcripts encoding components of the extracellular matrix were downregulated, including collagen types IIIa1 and IVa5, spondin, elastin, gelsolin, perlecan, keratins 10 and 23, as well as a lysyl oxidase enzyme required for the integrity of matrix proteins (45). In addition, cathepsin K, a protease that degrades elastin and collagen, was upregulated. These common changes represent PT-independent effects of *B. pertussis* on host gene expression and suggest a dynamic interplay between cell death and renewal amid infection-induced tissue damage.

The assessment of responses over time revealed a distinct course of gene expression changes for each infection (Table 1). Compared to PBS-treated mice, WT-infected lungs showed moderate changes at 2 dpi (309 genes) and more extensive regulation at 4 dpi (971 genes), with the majority of genes being upregulated. ΔPT-infected lungs displayed moderate changes at both time points, with the regulation of 376 genes at 2 dpi declining to 179 genes at 4 dpi. In contrast, ΔPT^{high}-infected lungs had the highest number of differentially regulated genes at 2 dpi (872 genes), the majority of which were upregulated. This number declined to 379 genes by 4 dpi. Remarkably, a direct comparison of samples from ΔPT^{high}- and ΔPT-infected mice revealed zero significant differences in gene expression levels at 4 dpi (Table 1), despite robust differences at 2 dpi and the disparity in bacterial loads at 4 dpi (Fig. 1B). These data indicate that the high dose of *B. pertussis* elicited a broad, early host response but that, in the absence of PT, these gene expression changes were short lived despite the continued presence of high bacterial loads.

PT-associated transcriptional responses. The 385 genes regulated uniquely in WT infection but not in ΔPT infections (Fig. 2)

TABLE 1 Summary of microarray data comparisons^a

Infection comparison	No. of genes					
	Day 2			Day 4		
	Upregulated	Downregulated	Total	Upregulated	Downregulated	Total
WT vs PBS	118	191	309	753	218	971
ΔPT vs PBS	121	255	376	108	71	179
ΔPT ^{high} vs PBS	662	210	872	223	156	379
WT vs ΔPT	11	0	11	539	43	582
ΔPT ^{high} vs ΔPT	792	102	894	0	0	0
WT vs ΔPT ^{high}	38	700	738	315	21	336

^a Genes with an FDR of ≤0.05 and an FC of ≥1.5.

represent changes potentially associated with PT. However, some of these genes did not show significant differences in direct comparisons of WT- to Δ PT- or Δ PT^{high}-infected mice (see Table S4 in the supplemental material). To exclude potential false-positive results and to enrich for true PT-associated genes, we filtered the 385 WT infection-specific genes to include only genes that also displayed significant FC values of ≥ 1.5 in direct comparisons of WT to Δ PT and WT to Δ PT^{high} infections at both time points. In addition, genes that were regulated in common with the other infections (versus PBS) but for which the WT FC was ≥ 1.5 times that of the Δ PT or Δ PT^{high} FC were also included in this list. The filtered list contains 91 genes whose regulation was specifically linked with PT production during *B. pertussis* infection (89 upregulated and 2 downregulated) (Table 2). The list reveals numerous genes not previously reported to have an association with PT, including a large cohort of inflammatory response genes and several genes with links to airway pathology, indicating an important role for PT in pertussis disease pathogenesis.

(i) Immune and inflammatory responses. An analysis of the 91 PT-associated genes using IPA showed that immune and inflammatory responses represented the most significantly enriched functions identified at 4 dpi (Fig. 3A; see also Table S5 in the supplemental material). In addition, immune and inflammatory cell signaling pathways dominated the list of top IPA canonical pathways enriched in PT-associated genes (see Table S6 in the supplemental material). Several of the most robustly induced changes involved cytokine and chemokine genes (Table 2), suggesting a major effect of PT on cell recruitment and activation. Transcripts for the neutrophil-attracting chemokines CXCL1 (KC), CXCL2 (MIP-2), and CXCL5 (LIX) displayed some of the greatest fold changes, consistent with our previous report that the expression levels of these chemokines and the influx of neutrophils greatly increase during WT *B. pertussis* infection. PT was also associated with an upregulated expression of the CXCR2 gene (IL-8 receptor), which encodes the primary CXCL1, CXCL2, and CXCL5 receptors (71) and the CSF3 (granulocyte colony-stimulating factor [G-CSF]) receptor, which is involved in neutrophil maturation and mobilization (26). Two members of the IL-6 family of cytokines, IL-6 and oncostatin M (OSM), were upregulated in association with PT as well as the OSM receptor. *In vitro*, PT stimulates IL-6 secretion from dendritic cells, which contributes to the differentiation of cocultured naive CD4⁺ T cells into Th17 cells (19). The function of OSM during *B. pertussis* infection has not been described, although it was reported to carry profibrotic activities in some pulmonary disorders and matrix-destructive properties in others (55, 68, 70). The expression levels of two IL-1 family cytokines, IL-1 β and IL-33, also increased in the presence of PT. IL-1 β is associated with disease in multiple inflammatory disorders (8). IL-1 β is essential for recovery from *B. pertussis* infection in a mouse model, and PT contributes to IL-1 β production by bone marrow-derived macrophages incubated with *B. pertussis* (90). The discovery of IL-33 induction represents a novel finding in the context of PT-associated responses, and it may be interesting in light of its contribution to inflammation and airway pathology in asthma (12). Furthermore, recent studies found that IL-33 production by lung-resident innate lymphoid cells (ILCs) and the IL-33-mediated induction of amphiregulin by ILCs play a crucial role in airway tissue repair after influenza virus infection (51). Our finding that PT increases both IL-33 and amphiregulin expression levels suggests that the upregulation of repair mechanisms may be

another important aspect of PT-associated responses in *B. pertussis* infection. Finally, the presence of PT correlated with gamma interferon (IFN- γ) induction as well as the upregulation of interferon-inducible genes (Table 2), including members of a GTPase family recently ascribed an antibacterial function (39). Another IFN- γ -induced host defense involves the limiting of the availability of tryptophan by the induction of enzymes involved in tryptophan metabolism, and the gene for one such enzyme, indoleamine 2,3-dioxygenase, was among the PT-associated genes.

Additional PT-linked proinflammatory responses to *B. pertussis* infection included increased expression levels of transcripts involved in lipopolysaccharide (LPS) signaling, including the LPS receptor CD14, LPS-binding protein (LBP), and a lysophosphatidic acid receptor recently shown to modulate LPS-induced inflammatory responses (93). PT was also correlated with increased expression levels of genes encoding inflammation-associated adhesion molecules, including P-selectin, vascular cell adhesion molecule, and C-lectin type 4e, a sensor for damaged cells expressed on macrophages (89). The increased expression levels of adhesion molecules likely contribute to inflammatory cell recruitment to the lungs.

Amid the numerous proinflammatory responses described above, genes involved in the control of immune responses were also induced in association with PT (Table 2). Homologs of antichymotrypsin (SERPINA3N, -A3F, and -A3G) and two inter-alpha trypsin inhibitors (ITIH1 and ITIH4) were upregulated. SERPINA3N inhibits granzyme B activity (74), mitigating the activity of cytotoxic T lymphocytes and natural killer cells that secrete granzyme B to induce apoptosis. ITIH1 was reported previously to possess anti-inflammatory activity through the inhibition of complement proteins (30). Lipocalin-2, a molecule involved in antimicrobial defense (28), protects against airway inflammation in a mouse model of allergic asthma (23). In addition, the tumor necrosis factor receptor superfamily 9 protein (Tnfrsf9) was shown previously to push the balance between Th17 cells and Tregs in favor of Treg generation (40). Finally, zinc finger protein 36 was reported previously to bind and destabilize cytokine mRNAs to reduce inflammatory responses (13). Therefore, the upregulation of proinflammatory genes associated with PT is potentially balanced by the induction of anti-inflammatory gene expression, which presumably prevents the lethality of this infection.

(ii) Genes implicated in pathology. An analysis of PT-associated transcripts at 4 dpi revealed a significant enrichment of genes that mediate some aspects of airway and pulmonary pathology (Fig. 3B). Specifically, the IPA “airway hyperresponsiveness” (AHR) annotation category ($P < 2.3 \times 10^{-5}$) included the differential regulation of genes for the cytokines IFN- γ and IL-6, the chemokine CCL2, receptors in the leukotriene and TNF receptor families, and the transcription factor SOCS3. CCL2 can activate mast cells, and the administration of CCL2 to mouse airways was shown previously to induce prolonged AHR (88). The leukotriene B4 receptor and IL-1 β are linked to the increased synthesis of eicosanoids, such as leukotrienes and prostaglandins, known to induce smooth muscle contraction. In addition, one of the most highly induced PT-associated genes (slc26a4) encodes an anion transporter, pendrin, shown to mediate AHR and inflammation in asthma (58). The gene encoding tissue inhibitor of metalloprotease 1 (TIMP-1) was a highly upregulated PT-associated gene (Table 2). Increased TIMP-1 expression levels have been associ-

TABLE 2 PT-associated gene expression level changes^a

ID	Gene	WT vs PBS		WT vs ΔPT		WT vs ΔPT ^{high}	
		FDR	FC	FDR	FC	FDR	FC
Cytokines and chemokines							
14825	Chemokine (C-X-C motif) ligand 1	0.000	18.2	0.000	18.2	0.000	8.0
16176	Interleukin-1 beta	0.000	11.1	0.000	11.0	0.000	6.0
20311	Chemokine (C-X-C motif) ligand 5	0.000	4.6	0.000	5.4	0.001	4.2
20310	Chemokine (C-X-C motif) ligand 2	0.000	3.2	0.000	2.9	0.000	2.5
77125	Interleukin-33	0.000	3.1	0.000	2.7	0.001	2.7
18413	Oncostatin M	0.000	2.9	0.000	3.1	0.000	2.5
20296	Chemokine (C-C motif) ligand 2	0.000	2.4	0.000	2.5	0.000	2.5
16193	Interleukin-6	0.000	2.3	0.000	2.3	0.001	2.2
15978	Gamma interferon	0.000	1.8	0.004	1.7	0.002	1.7
Other secreted proteins							
16819	Lipocalin 2	0.000	14.0	0.001	8.2	0.008	2.4
76905	Leucine-rich alpha-2-glycoprotein 1	0.000	5.1	0.000	4.5	0.005	2.5
15458	Hemopexin	0.000	3.4	0.000	2.9	0.000	2.2
20201	S100 calcium-binding protein A8 (calgranulin B)	0.000	3.0	0.001	3.6	0.001	2.4
20202	S100 calcium-binding protein A9 (calgranulin B)	0.000	2.6	0.001	3.2	0.000	2.3
11839	Amphiregulin	0.000	2.4	0.009	1.8	0.001	2.3
21923	Tenascin C	0.000	2.0	0.000	1.9	0.001	1.7
16803	Lipopolysaccharide-binding protein	0.000	2.0	0.008	2.2	0.035	1.7
245195	Resistin-like gamma	0.000	1.9	0.001	2.1	0.008	1.5
246316	Leucine-rich repeat LGI family, member 2	0.000	1.6	0.005	1.5	0.005	1.5
71690	Endothelial cell-specific molecule 1	0.000	−1.7	0.000	−2.0	0.041	−2.1
Immune receptors/adhesion molecules							
12475	CD14 antigen	0.000	6.2	0.000	6.5	0.001	3.4
12986	Colony-stimulating factor 3 receptor (granulocyte)	0.000	4.8	0.000	3.3	0.000	3.2
12765	Interleukin-8 receptor, beta	0.000	3.2	0.000	2.9	0.000	2.7
20344	Selectin, platelet	0.000	2.2	0.008	1.8	0.003	1.8
213233	TAP-binding protein-like	0.000	2.1	0.001	1.7	0.002	1.8
14128	Fc receptor, IgE, low affinity II, alpha polypeptide	0.000	1.9	0.004	1.8	0.031	1.6
20343	Selectin, lymphocyte	0.000	1.8	0.003	2.0	0.027	1.6
18414	Oncostatin M receptor	0.000	1.8	0.003	1.8	0.005	1.6
56619	C-type lectin domain family 4, member e	0.001	1.7	0.004	1.7	0.003	1.7
58218	Triggering receptor expressed on myeloid cells 3	0.000	1.6	0.001	1.8	0.002	1.6
Transmembrane proteins							
23985	Solute carrier family 26, member 4	0.000	9.4	0.000	9.3	0.000	5.4
235712	MAS-related GPR, member A2B	0.000	2.5	0.000	2.3	0.001	2.4
21942	Tumor necrosis factor receptor superfamily, member 9	0.000	2.4	0.000	2.2	0.001	1.9
76574	Major facilitator superfamily domain containing 2a	0.000	2.3	0.005	2.2	0.011	1.8
22329	Vascular cell adhesion molecule 1	0.000	1.8	0.000	1.9	0.005	1.8
50930	Tumor necrosis factor superfamily, member 14	0.000	1.8	0.001	1.6	0.004	1.6
11541	Adenosine A2b receptor	0.000	1.8	0.001	1.8	0.015	1.6
20351	Semaphorin 4A	0.000	1.8	0.003	1.7	0.014	1.5
68279	Mucolipin 2 (TRPML1)	0.000	1.7	0.002	1.7	0.005	1.6
14745	Lysophosphatidic acid receptor 1	0.000	1.7	0.004	1.5	0.002	1.6
16995	Leukotriene B4 receptor 1	0.001	1.7	0.005	1.8	0.010	1.5
16404	Integrin alpha 7	0.001	1.5	0.000	1.8	0.004	1.6
68713	Interferon-induced transmembrane protein 1	0.001	1.5	0.004	1.5	0.005	1.5
Enzymes							
15930	Indoleamine 2,3-dioxygenase 1	0.000	3.7	0.000	3.6	0.000	3.1
51797	CTP synthase	0.000	3.1	0.000	2.6	0.001	2.3
626578	Guanylate-binding protein 10	0.000	3.0	0.000	2.8	0.001	2.2
229900	Guanylate-binding protein 7	0.000	2.8	0.000	2.8	0.004	2.3
22375	Tryptophanyl-tRNA synthetase	0.000	2.6	0.000	2.1	0.004	1.8
21816	Transglutaminase 1, K polypeptide	0.000	2.2	0.012	1.8	0.000	2.0
69581	<i>ras</i> homolog gene family, member U	0.000	1.9	0.001	1.8	0.007	1.6

(Continued on following page)

TABLE 2 (Continued)

ID	Gene	WT vs PBS		WT vs Δ PT		WT vs Δ PT ^{high}	
		FDR	FC	FDR	FC	FDR	FC
71780	Myoinositol 1-phosphate synthase A1	0.000	1.9	0.001	1.9	0.019	1.6
18113	Nicotinamide N-methyltransferase	0.000	1.9	0.000	1.8	0.001	1.8
20656	Superoxide dismutase 2, mitochondrial	0.000	1.9	0.001	1.7	0.001	1.7
56045	SAM domain and HD domain, 1	0.000	1.8	0.002	1.6	0.003	1.6
71893	NADPH oxidase organizer 1	0.000	1.8	0.000	2.1	0.039	1.6
14528	GTP cyclohydrolase 1	0.000	1.8	0.000	2.1	0.011	1.6
66725	Leucine-rich repeat kinase 2	0.001	1.8	0.028	1.5	0.016	1.6
223920	Sterol O-acyltransferase 2	0.000	1.8	0.004	1.6	0.002	1.6
70025	Acyl-CoA thioesterase 7	0.001	1.8	0.040	1.6	0.044	1.6
19734	Regulator of G-protein signaling 16	0.000	1.7	0.003	1.8	0.002	1.9
56454	Aldehyde dehydrogenase 18 family, member A1	0.000	1.7	0.001	1.6	0.005	1.5
80914	Uridine-cytidine kinase 2	0.001	1.5	0.000	1.8	0.003	1.7
235674	Acetyl coenzyme A acyltransferase 1B	0.004	−1.6	0.003	−2.0	0.014	−1.5
Peptidases							
21929	Tumor necrosis factor, alpha-induced protein 3	0.000	2.0	0.000	2.2	0.015	1.6
240913	ADAMTS4	0.000	1.9	0.000	2.1	0.000	2.0
19186	Proteasome (prosome, macropain) 28 subunit, alpha	0.000	1.8	0.002	1.7	0.011	1.5
17392	Matrix metalloproteinase 3	0.000	1.7	0.005	1.5	0.007	1.5
Protease inhibitors							
21857	Tissue inhibitor of metalloproteinase 1	0.000	10.4	0.000	12.1	0.000	5.0
20716	Serine peptidase inhibitor, clade A, member 3N	0.000	6.8	0.000	7.8	0.000	4.6
16427	Inter-alpha-trypsin inhibitor, heavy chain 4	0.000	5.7	0.000	4.8	0.003	3.5
20715	Serine peptidase inhibitor, clade A, member 3G	0.000	3.7	0.000	2.7	0.008	2.1
238393	Serine peptidase inhibitor, clade A, member 3F	0.000	2.9	0.000	2.5	0.002	2.3
16424	Inter-alpha-trypsin inhibitor, heavy chain 1	0.000	2.3	0.000	2.6	0.000	2.2
433016	Predicted gene 5483	0.000	2.0	0.001	2.4	0.001	2.1
Nuclear proteins							
12702	Suppressor of cytokine signaling 3	0.000	3.4	0.000	3.7	0.000	2.5
16477	Jun-B oncogene	0.000	2.6	0.000	2.4	0.001	1.7
18030	Nuclear factor, interleukin-3 regulated	0.000	2.4	0.000	2.5	0.000	2.4
16362	Interferon regulatory factor 1	0.000	2.4	0.000	2.2	0.000	2.1
80859	Nuclear factor of kappa light polypeptide gene	0.000	2.2	0.000	2.4	0.009	1.6
20846	Signal transducer and activator of transcription 1	0.000	2.2	0.000	2.5	0.005	1.8
22695	Zinc finger protein 36	0.000	2.1	0.004	1.8	0.045	1.5
23882	Growth arrest and DNA-damage-inducible 45 gamma	0.001	2.0	0.005	2.0	0.007	1.9
Structural proteins							
27375	Tight-junction protein 3	0.000	2.3	0.002	1.8	0.010	1.6
78785	CAP-GLY domain-containing protein family, member 4	0.000	1.9	0.000	1.7	0.005	1.5
73710	Tubulin, beta 2B	0.000	1.7	0.011	1.5	0.002	1.5
16906	Lamin B1	0.000	1.7	0.000	2.1	0.008	1.5
Other							
24108	Ubiquitin D	0.000	1.8	0.045	1.6	0.015	1.6
78388	Major vault protein	0.000	1.9	0.001	1.6	0.002	1.6
71982	Sorting nexin 10	0.000	2.2	0.000	2.3	0.007	1.6
56722	LPS-induced TNF- α factor	0.000	1.7	0.001	1.8	0.002	1.8
547253	Poly(ADP-ribose) polymerase family, member 14	0.004	1.7	0.002	2.1	0.036	1.7

^a ID, NCBI Entrez Gene Identifier; FDR, false discovery rate; FC, fold change (values at 4 dpi); SAM, S-adenosylmethionine; HD, histidine and aspartic acid; CoA, coenzyme A; LGI, leucine-rich glioma-inactivated; TAP, transporter associated with antigen processing; GPR, G protein-coupled receptor; ADAMTS, a disintegrin and metalloprotease with thrombospondin motifs; CAP-GLY, cytoskeleton-associated protein, glycine-rich.

ated with reduced pulmonary function (72) and pneumonia (21) but may play a protective role against airway inflammation and hyperresponsiveness (69).

Another symptom of severe pertussis includes pulmonary hypertension (48). PT-specific changes revealed an upregulation of

resistin-like gamma (retnlg in mice and RETNLB in humans), which codes for a secreted protein linked to scleroderma-associated pulmonary hypertension in humans (6). RETNLB induces the proliferation of primary human pulmonary smooth muscle and endothelial cells (6) and may contribute to airway remodeling

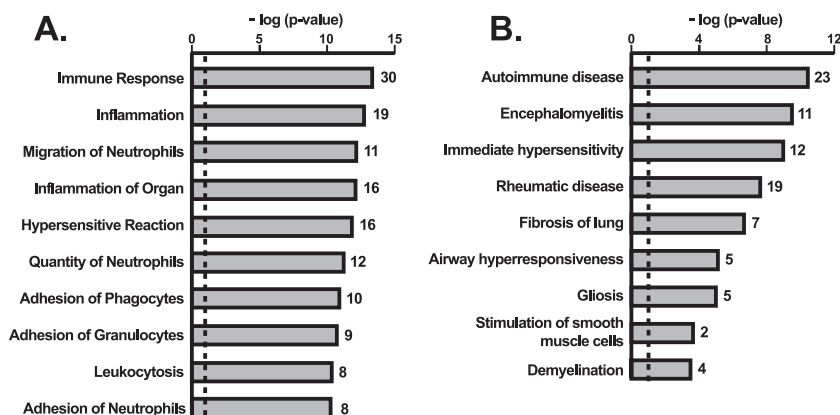


FIG 3 PT-dependent regulation of immune response-related functions. Genes regulated specifically in the presence of pertussis toxin (Table 2) were analyzed by using Ingenuity Pathway Analysis. Graphs show the 10 most significantly enriched overall (A) and pathology-related (B) functional annotations. Numbers to the right of each bar indicate the total number of differentially regulated genes related to a given function. The dashed line indicates a significance threshold of a P value of 0.05.

in asthma (27). Pulmonary hypertension can also be associated with compromised connective tissue (32). The “connective tissue disorders” IPA function revealed PT-associated genes that promote connective tissue autoimmune disorders ($P < 3.8 \times 10^{-4}$). Upregulated genes in this category include transcripts for the proteases MMP3 and ADAMST4, known to degrade extracellular matrix components, and for proteins associated with arthritis, including CXCL1, CXCL5, and TIMP1.

Finally, it is possible that an altered signaling of nerves innervating the trachea and bronchi contributes to prolonged cough in pertussis. Interestingly, multiple functions related to neurological disease showed significant enrichment among PT-associated genes, including transcripts involved in encephalomyelitis ($P = 2.97 \times 10^{-10}$), gliosis ($P = 4.44 \times 10^{-5}$) (CCL2, IDO1, IL-6, interferon regulatory factor 1 [IRF1], SELL, SEMA4A, STAT1, TIMP1, TNFSF14, and VCAM1), and axon damage ($P = 4.33 \times 10^{-4}$). In the central nervous system CCL2, IL-6, and IFN- γ can promote demyelination, and IRF1 contributes to pathogenesis in the experimental autoimmune encephalomyelitis (EAE) model of multiple sclerosis (MS) (67). The enrichment of PT-associated genes for these functions is consistent with the frequent usage of PT as an adjuvant to promote EAE (11, 92), the mouse model of MS.

Overall, these data highlight the major stimulatory effect of PT on immune and inflammatory responses during peak infection, indicating the potentially important role that PT may play in pertussis disease pathogenesis.

PT-associated changes in gene expression depend on ADP-ribosylation activity. Previous studies indicated a sufficiency of the PT B oligomer, which lacks the enzymatic activity of the A (S1) subunit, in mediating some effects of PT in other models (3, 36, 60, 78). Therefore, we asked whether the enzymatic activity of PT was required for the altered expression of the PT-associated genes with the highest fold changes. Mice were infected with either WT *B. pertussis* (7.5×10^5 CFU) or a strain producing an inactive form of PT (PT*) with changes to the active site that disrupt the toxin’s ability to ADP-ribosylate substrate G proteins. PT* bacteria were inoculated at regular (7.5×10^5 CFU) and high (1.5×10^7 CFU) doses to control for bacterial loads during infection, as discussed above. At 4 dpi, mean bacterial counts in the lungs were 1.8×10^6

CFU in WT-infected mice, 2.4×10^5 CFU in PT*-infected mice, and 2.5×10^6 CFU in PT*^{high}-infected mice (data not shown). In all cases, expression level changes in WT-infected lungs were significantly higher than those induced by infection with the PT* strain at regular or high doses (Fig. 4). In addition, there were no significant differences among these genes between responses to infection with the PT* strain (from this experiment) and responses to infection with the Δ PT strain (from other experiments [data not shown]). These results indicate that the binding of PT is not sufficient to drive some of the highest changes in gene expression levels reported in this array and that a fully active toxin is required.

PT-dependent and -independent time course of inflammatory gene expression. Despite the presence of equal bacterial loads

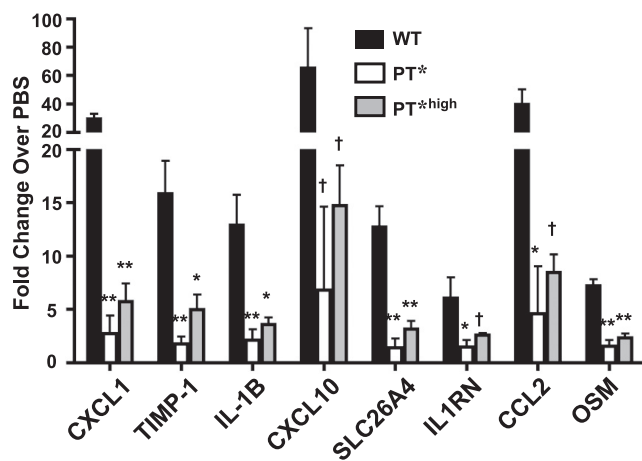


FIG 4 PT-associated upregulation of inflammatory genes requires ADP-ribosylation activity. BALB/c mice ($n = 3$ to 4 per group) were intranasally inoculated with PBS, WT *B. pertussis* (7.5×10^5 CFU), or a *B. pertussis* strain that produces enzymatically inactive PT (PT*) (7.5×10^5 CFU). Another group of mice was inoculated with a higher dose (1.5×10^7 CFU) of PT* (PT*^{high}). Transcript abundances in the lung at 4 dpi were assayed by using qPCR and normalized to levels in PBS-treated mice. Error bars indicate standard deviations. **, $P < 0.001$; *, $P < 0.01$; †, $P < 0.05$ (significantly different from WT values).

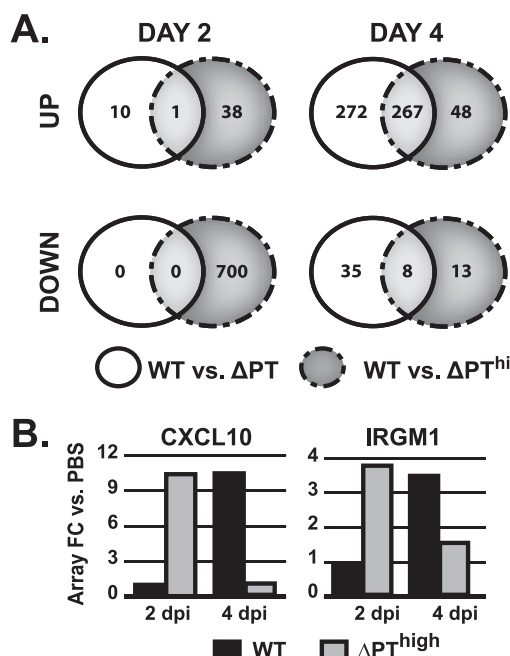


FIG 5 Time course of PT-associated gene regulation during *B. pertussis* infection. (A) Diagram showing genes differentially regulated in the mouse lung at 2 and 4 dpi. In a comparison of *X* versus *Y*, “UP” indicates genes expressed at higher levels in *X* than in *Y*, and “DOWN” refers to genes expressed at lower levels in *X* than in *Y*. Numbers indicate genes differentially expressed in the WT-versus- Δ PT comparison, the WT-versus- Δ PT^{high} comparison, or both comparisons (light gray), for probes with an FDR of <0.05 and a fold change of >1.5. (B) Examples of the reciprocal regulation patterns seen at 2 dpi in Δ PT^{high} infection versus PBS treatment and at 4 dpi in WT infection versus PBS treatment.

in WT- and Δ PT^{high}-infected mice between 1 and 4 dpi (Fig. 1B), a marked difference in the timing of transcriptional responses between these two infections was apparent (Table 1 and Fig. 5A). As mentioned above, robust changes in lung gene expression levels did not occur until 4 dpi in WT-infected mice. Indeed, a direct comparison of WT- and Δ PT-infected mice revealed only 11 dif-

ferences at 2 dpi but 582 differences at 4 dpi (Table 1; see also Table S4 in the supplemental material). In contrast, Δ PT^{high}-infected mice showed an upregulation of a large number of genes at 2 dpi, many of which returned to near-background expression levels at 4 dpi. Three hundred twenty-seven of the genes with altered expression levels at 4 dpi in WT infection displayed near-equivalent regulation at 2 dpi in Δ PT^{high}-infected mice (in comparison to PBS-treated mice). These genes are listed in Table S7 in the supplemental material, and examples of the reciprocal regulation pattern are shown in Fig. 5B.

Two possibilities might explain these results. On the one hand, PT may have inhibited responses in WT infection that are elicited in the Δ PT^{high} infection at 2 dpi. Alternatively, responses in Δ PT^{high} infection at 2 dpi arose from higher bacterial loads (10^6 CFU) present from the outset in Δ PT^{high}-infected mice (Fig. 1B). Bacterial loads in WT-infected mice did not reach 10^6 CFU until 2 dpi, so if changes require a 2-day lag time, high-bacterial-load-induced gene regulation would not be detected until 4 dpi, as observed in our experiment. To distinguish between these possibilities, we compared lung transcriptional responses in mice inoculated with equally high doses of WT and PT-deficient strains (4×10^7 CFU for WT^{high} versus Δ PT^{high} infection). We reasoned that if high bacterial loads cause temporal differences in changes in gene expression levels, there should be no differences, or possibly greater responses in WT^{high}-infected mice, at 2 dpi. In contrast, if PT production inhibits responses at 2 dpi, WT^{high}-infected mice would display lower fold changes in gene expression levels than those observed for Δ PT^{high}-infected mice.

A comparison of gene expression changes at 2 dpi between WT^{high} and Δ PT^{high} infections revealed distinct patterns for different genes (Fig. 6A). Two out of nine genes (IL-6 and OSM) were expressed at higher levels in WT^{high}-infected mice, indicating that PT likely contributes to the increased expression levels of these genes, consistent with data from a previous report in the case of IL-6 (19). Six out of nine genes showed no significant difference in expression levels between WT^{high}- and Δ PT^{high}-infected mice, consistent with a correlation with early bacterial loads. The remaining gene (IFN- γ) was expressed at significantly lower levels in WT^{high}-infected mice, indicating that PT may inhibit its expres-

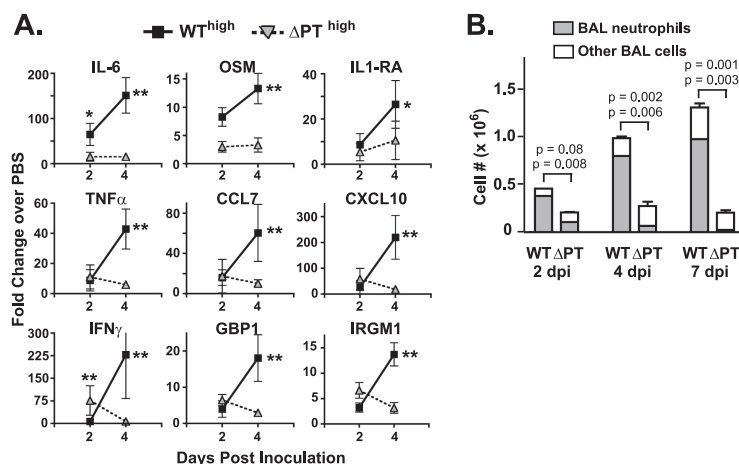


FIG 6 Comparison of responses in WT^{high} and Δ PT^{high} infections. Mice were inoculated with a high dose of either the WT or Δ PT *B. pertussis* strain ($n = 4$ per group). (A) Gene expression levels were measured in whole lung tissue at 2, 4, and 7 dpi. *, $P < 0.05$; **, $P < 0.001$. (B) Total cells and neutrophils from BAL fluid collected at 2, 4, and 7 dpi. Significant differences reflect total cell numbers (top) and neutrophil counts (bottom).

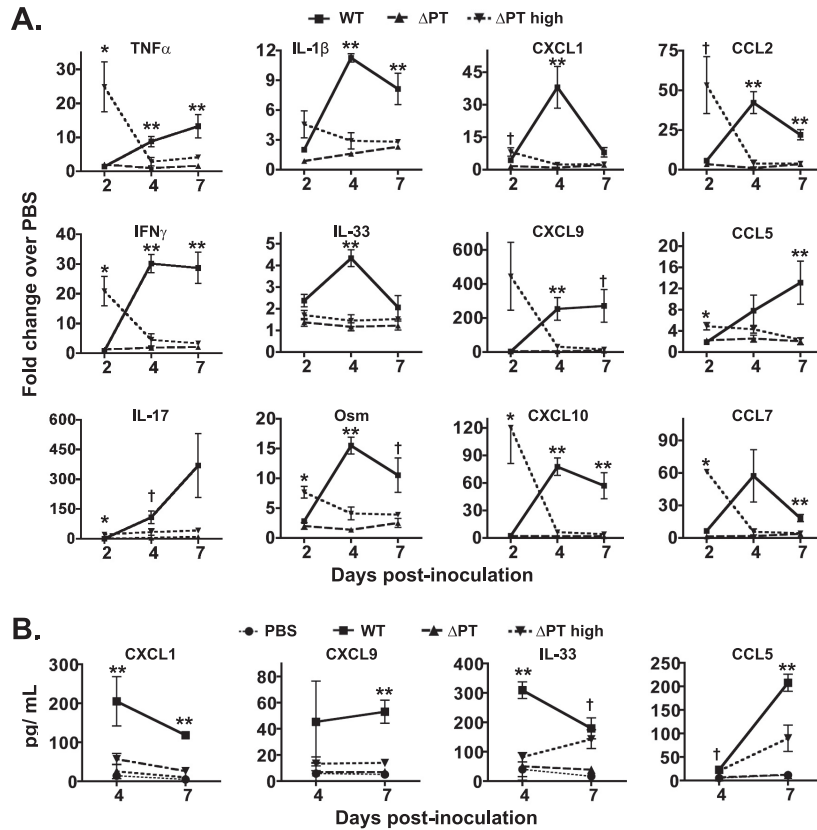


FIG 7 Increased and sustained cytokine and chemokine expression levels associated with PT in the lungs of *B. pertussis*-infected mice. (A) WT- or ΔPT-infected lungs were screened for cytokine and chemokine gene expression by qPCR at 2, 4, and 7 dpi (RNA samples from infection shown in Fig. 1). Changes in gene expression levels were normalized to values for PBS-treated mice. (B) In a separate experiment using a similar inoculation strategy as that described in the legend of Fig. 1, cytokine and chemokine levels were detected by ELISAs of mouse lung tissue harvested at 4 and 7 dpi. Significantly different ($P < 0.05$) values were detected for ΔPT^{high} versus WT and ΔPT infections (*), WT versus ΔPT and ΔPT^{high} infections (**), and either WT or ΔPT^{high} infection versus ΔPT infection (†).

sion at this early time point. By 4 dpi, all nine genes were expressed at significantly higher levels in WT^{high}-infected mice (Fig. 6A), consistent with either induction associated with PT activity or the higher bacterial loads in WT^{high}-infected mice at 2 dpi. Therefore, a combination of effects likely contributed to the difference in the timing of transcriptional responses between WT and ΔPT^{high} infections in the original experiment. The time course of bacterial loads likely influenced the timing of the changes in expression levels for most of the 327 genes, with inhibition by PT delaying the expression of a smaller subset until 4 dpi in WT infection. Such bacterial-load-driven patterns of increased gene expression levels in response to WT infection may be ascribed as indirectly associated with the presence of PT, in light of the function of PT to promote increased bacterial numbers during *B. pertussis* infection in this model (17).

Immune and inflammatory cells recruited to the lung during infection may contribute to the observed changes in gene expression levels and may explain some of the differences between WT- and ΔPT-infected mice. As such, we assessed total cell and neutrophil numbers in the airways (BAL fluid) of WT^{high}- and ΔPT^{high}-infected mice (Fig. 6B). At 2 dpi, WT^{high}-infected mice had ~2-fold more total cells and neutrophils than did ΔPT^{high}-infected mice. Thus, at this early time point, it is unlikely that such a modest difference in numbers of recruited cells contributed greatly to the overall differences in lung gene expression levels. At

4 and 7 dpi, more pronounced differences were observed. WT^{high} infection induced an influx of higher total cell numbers as well as >10-fold more neutrophils than did ΔPT^{high} infection. In this experiment, neutrophil numbers in ΔPT^{high}-infected mouse lungs at 2 dpi were 4- to 5-fold higher than the numbers that we previously reported for WT-infected mice at this time point but were not significantly different at 4 dpi. Our analysis of PT-associated genes (Table 1) did not identify an enrichment of neutrophil-specific genes, so neutrophil recruitment is unlikely to have been a major contributor to the PT-associated differential gene expression at 4 dpi.

Sustained expression of inflammatory genes in the presence of PT. Since we previously observed that certain cytokine gene expression levels peaked at 7 dpi in WT-infected mice (5), we hypothesized that the effects of PT on WT *B. pertussis* infection would sustain inflammatory gene expression beyond 4 dpi, versus the early and transient upregulation induced by ΔPT^{high} infection. Samples from WT-, ΔPT-, and ΔPT^{high}-infected mice at 2, 4, and 7 dpi were assayed by qPCR for the expression of several cytokines and chemokines to determine if the WT infection-induced gene upregulation observed at 4 dpi was maintained through 7 dpi. At 2 and 4 dpi, qPCR measurements confirmed the patterns of gene expression observed in the array data (Fig. 7A). In addition, the results showed that at 7 dpi in WT infection, transcripts for genes encoding TNF- α , IFN- γ , IL-1 β , IL-17, CXCL9, CXCL10, CCL2,

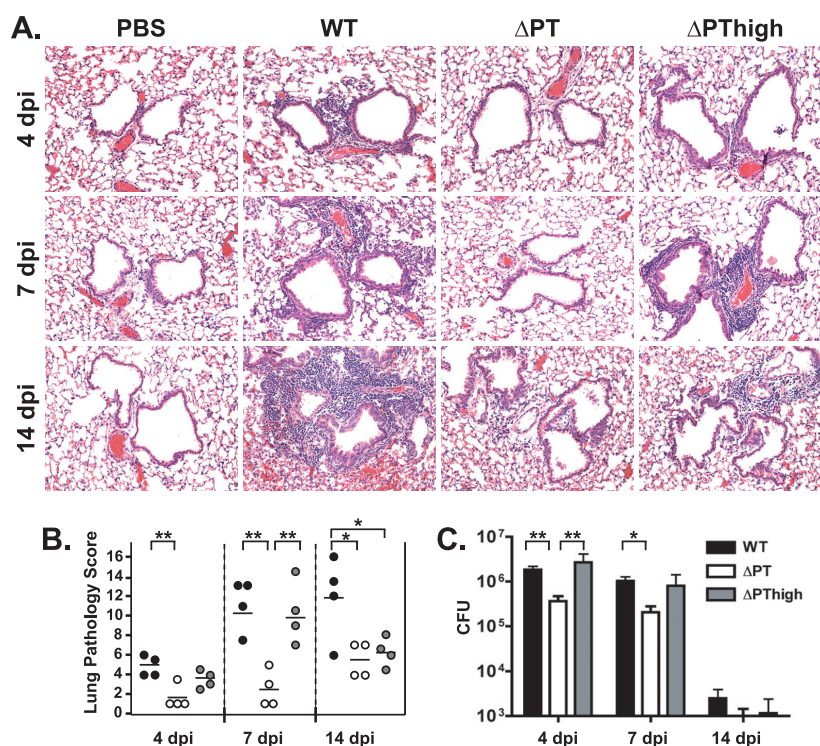


FIG 8 PT promotes sustained inflammation in the lungs of *B. pertussis*-infected mice. (A) Fixed lung tissue sections (5 µm) from mice inoculated with PBS or the WT, ΔPT, or ΔPT^{high} *B. pertussis* strain (4 mice per group) were stained with hematoxylin and eosin. Representative pictures from each strain at each time point are shown. Magnification, ×20. (B) Pathology scores of lung sections were assigned by a pathologist blinded to the experimental treatment. (C) Mean bacterial numbers recovered from lungs for each group. Legend colors apply to panels B and C. **, $P < 0.01$; *, $P < 0.05$.

CCL5, and CCL7 were maintained at levels significantly above the levels in ΔPT- and ΔPT^{high}-infected mice (Fig. 7A). In WT-infected mice, genes encoding TNF-α, IL-17, CXCL9, and CCL5 displayed higher expression levels at 7 dpi than at 4 dpi. Of note, several of these genes displayed the reciprocal regulation pattern discussed above (upregulation in ΔPT^{high}-infected mice at 2 dpi and upregulation to similar levels in WT-infected mice at 4 dpi). The observation that ΔPT^{high}-induced expression subsides by 4 dpi yet the WT-induced expression levels remain high at 7 dpi further supports the idea that, in WT infection, PT prolongs inflammatory responses elicited by sufficient bacterial loads in the airways.

To further validate some of these findings, we assayed lung homogenates from infected mice for levels of CXCL1, IL-33, CXCL9, and CCL5 by ELISAs (Fig. 7B). At 4 dpi, levels of CXCL1 and IL-33 were significantly higher in samples from WT *B. pertussis* infection than from the other infections. By 7 dpi, levels of CXCL1, CXCL9, and CCL5 were significantly higher in WT-infected mice, while IL-33 levels declined to those observed for samples from ΔPT^{high}-infected mice. Together, these results further validate the array data and demonstrate that PT plays a role in prolonged inflammatory gene expression in the airways of *B. pertussis*-infected mice.

Prolonged inflammatory pathology in the lungs of WT-infected mice. We next investigated whether the PT-associated expression of inflammatory genes at 4 and 7 dpi correlated with extended inflammatory pathology in the lungs of WT-infected mice. Lung tissue from mice infected with the WT, ΔPT, or ΔPT^{high} strain was isolated at 4, 7, and 14 dpi, and lung sections

were evaluated for pathology. Representative views of lung sections from each infection are shown in Fig. 8A. Scores were assigned by a pathologist who was blinded to experimental treatment to measure changes in the following categories: bronchiolar inflammation, vessel inflammation, epithelial cell damage, hemorrhage, and numbers of eosinophils, neutrophils, macrophages, and leukocytes (Fig. 8B). At 4 dpi, lungs from all three infections showed only mild changes compared to lungs from mock-infected mice, including slight perivascular inflammation in WT and ΔPT^{high} infections, reflecting an influx of neutrophils and lymphocytes (Fig. 8A). By 7 dpi, moderate perivascular and mild peribronchiolar inflammation were apparent in both WT- and ΔPT^{high}-infected mice, with a slight indication of hemorrhage in all of the WT-infected mice and half of the latter. In addition, macrophage influx increased at this time point, possibly reflecting a recruitment of monocytes by the upregulated chemokines CCL2 and CCL7 (monocyte chemoattractant proteins 1 and 3, respectively) (Fig. 7A). At 14 dpi, WT-infected lungs showed increased inflammation compared to that at 7 dpi (Fig. 8A and B), despite significant bacterial clearance from the lungs by this time point (Fig. 8C). Slight epithelial cell damage was noted, as were hemorrhage and an influx of neutrophils, lymphocytes, and macrophages. In contrast, the level of inflammation in ΔPT^{high}-infected mice declined by 14 dpi to levels observed for ΔPT-infected mice (Fig. 8A and B). These results show that an important effect of PT is to enhance and prolong airway inflammatory pathology during *B. pertussis* infection. Although an upregulation of inflammatory genes occurs by 4 dpi in WT infection, significant inflammatory

pathology in the lung becomes apparent only by 7 dpi and increases further at 14 dpi.

PT administration prolongs inflammatory pathology in ΔPT^{high} -infected mice. We reasoned that if PT enhances airway inflammation and pathology during *B. pertussis* infection, the airway administration of purified PT to ΔPT^{high} -infected mice should delay the resolution of inflammation and result in more intense, longer-lived inflammatory responses. Therefore, we inoculated mice with a high dose of the ΔPT strain, administered purified PT 24 h later (100 ng i.n.), and tested the effects of this treatment on subsequent airway inflammatory responses during infection. Control ΔPT^{high} -infected mice were treated with PBS at 24 h postinoculation, and other control mice were treated with PT without bacterial infection. PT administration at 24 h postinoculation did not significantly increase bacterial numbers in these mice (Fig. 9A), similarly to previously reported findings (17). Lung transcriptional responses were assayed at 3 and 7 dpi and showed that PT administration significantly increased the expression levels of TNF- α , CCL2, and CXCL10 in ΔPT^{high} -infected mice (Fig. 9B). In addition, histopathology analysis revealed exacerbated airway pathology at 7 and 14 dpi in ΔPT^{high} -infected mice treated with PT (Fig. 9C). PT treatment without bacterial infection did not significantly increase levels of inflammatory gene expression or pathology (data not shown). These data support the hypothesis that PT enhances and prolongs inflammatory gene expression and pathology during *B. pertussis* infection independently of bacterial loads. The data also demonstrate the long-lived effect of a single dose of PT in this model, as we observed previously (17, 18).

DISCUSSION

In this study, we used microarray technology to measure global lung gene expression changes associated with PT during *B. pertussis* infection in a mouse model, to assess the role of this toxin in modulating host airway responses, and to identify possible links between PT and *B. pertussis*-induced respiratory pathology. We compared infections by wild-type (PT-producing) and PT-deficient strains, and to control for the different bacterial loads achieved by these strains at the peak of infection, we also made comparisons to mice infected with a higher dose of the PT-deficient strain, which equalizes the bacterial loads (between the WT and ΔPT strains) at the peak of infection. By this approach, the differential expression of genes between WT infection and infection with either dose of the ΔPT strain identified potential PT-associated genes. By eliminating genes whose expression was apparently dependent on the timing of high bacterial loads rather than on PT, we identified a list of 91 genes whose altered expression levels can confidently be associated with PT production during *B. pertussis* infection. Data from this analysis and subsequent experiments demonstrated several important effects of PT during this bacterial infection: (i) PT plays an important role in altering airway gene expression in response to this infection, primarily through the upregulation of genes toward the peak of infection; (ii) immune and inflammatory responses dominated the most significant functional categories regulated by PT, with several cytokines and chemokines being among the most highly upregulated genes at the peak of *B. pertussis* infection; (iii) several other highly induced genes associated with PT are linked with pathology in the airways and other tissues; (iv) PT was associated with increased and sustained inflammatory gene expression levels and

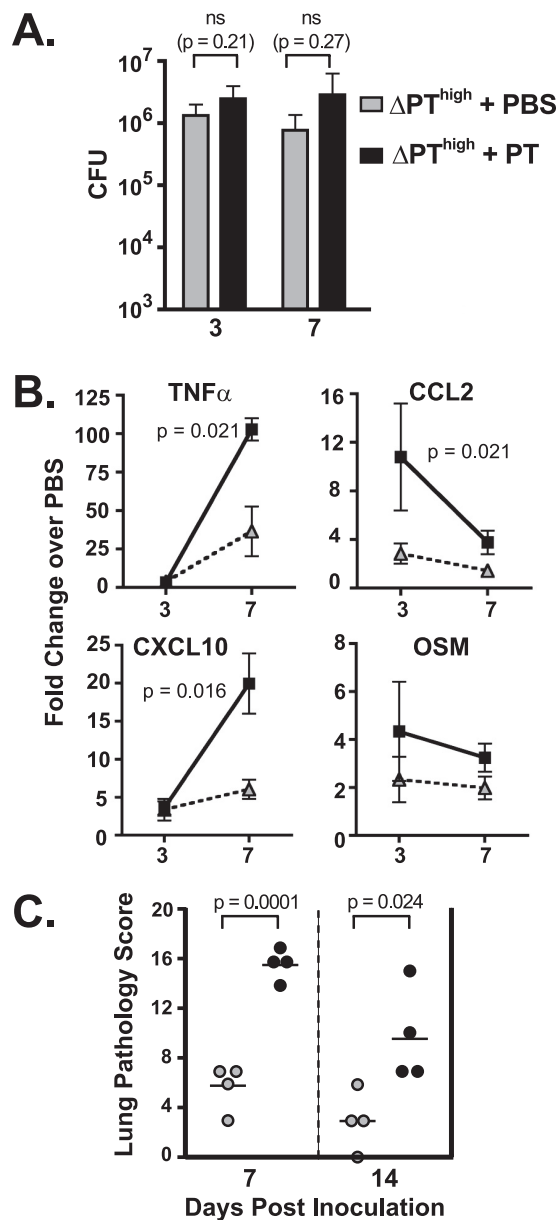


FIG 9 PT treatment exacerbates inflammation in ΔPT^{high} -infected mice. Mice were inoculated with a high dose of the ΔPT strain and treated with either PBS or 100 ng PT at 24 h postinoculation ($n = 4$ per group). PT treatment did not significantly increase lung bacterial loads (A) but was associated with elevated cytokine and chemokine transcript levels (B) and heightened lung pathology (C).

airway pathology through the peak of *B. pertussis* infection; and (v) PT administration heightened and prolonged inflammatory pathology associated with infection by a PT-deficient *B. pertussis* strain. Together, these data indicate that PT plays an important role in exacerbating pertussis airway disease pathology through the modulation of gene expression, in addition to other direct effects on host responses.

Our results comparing WT-infected to mock-infected mice are similar to those of a previously reported microarray analysis of wild-type *B. pertussis*-infected mouse lungs (using C3H mice and a higher dose of bacteria), in which a total of 1,841 genes (out of

22,000 tested) were differentially regulated (FDR < 0.05) at 1, 3, or 5 dpi (7). In that study, the response peaked at day 3 but was still high at day 5, and the majority of upregulated genes were involved in immune and inflammatory responses. In comparison, the total number of genes (out of ~24,000 tested) regulated in the WT infection in our study without regard to fold change equaled 3,737 (FDR ≤ 0.05). The higher number of regulated genes in our study may be related to the age or strain of mice or a greater sensitivity of our assay system.

Previously, we found that the expression of certain inflammatory cytokine and chemokine genes was upregulated in *B. pertussis* WT-infected mouse lungs at 4 dpi but not in Δ PT-infected mice (5), implicating PT in this response. The broadly important role of PT in upregulating multiple inflammatory responses to *B. pertussis* at the peak of infection was a major finding in the present study, in which a comparison of WT-infected to Δ PT- and Δ PT^{high}-infected mice identified immune and inflammatory responses as the most significantly upregulated functions. As well as previously identified upregulated cytokines and chemokines, such as KC (CXCL-1), IL-6, IFN- γ , and TNF- α , our study also revealed the PT-associated upregulation of cytokines such as IL-33 and oncostatin M, which were not previously reported in association with *B. pertussis* infection. These cytokines play roles in tissue damage and repair in the airways (50, 61) and may be involved in similar activities during *B. pertussis* infection.

The upregulation of cytokine and chemokine expression in the lungs raises the possibility that the presence of recruited immune and inflammatory cells contributes to the overall gene expression profile and differences between WT- and Δ PT-infected mice. Neutrophil numbers in the airways were not dramatically different between WT- and Δ PT^{high}-infected mice, and likewise, there was no enrichment of neutrophil-specific genes among the PT-associated genes. However, differences in other recruited cells may contribute to PT-associated gene expression. Future investigations could broadly address this question by assaying genome-wide expression profiles specifically in BAL fluid cell populations isolated from WT- or Δ PT-infected mice. It is likely that the majority of PT-associated responses occur in resident cells of the lung tissue exposed to the bacteria. The identification of which cells are responsible for specific gene expression differences would be a complex task, but we aim to investigate the specific cellular expression of at least a small number of genes that may contribute significantly to pertussis pathology.

For several cytokines and chemokines, we showed that the PT-associated upregulation of gene expression was sustained through 7 dpi and that differential gene expression correlated with protein production in lung tissue. These sustained effects of PT were reflected in the histopathology of infected lung tissue, with the highest levels being observed for WT-infected mice at 14 dpi. At 7 dpi, lung pathology was greater for WT-infected than for Δ PT-infected mice, consistent with data from a previous report (38), but Δ PT^{high}-infected mice had a level of pathology similar to that of WT-infected mice, presumably reflecting the earlier and more transient inflammatory responses observed for the Δ PT^{high} infection. The treatment of Δ PT^{high}-infected mice with purified PT increased inflammatory gene expression levels and prolonged airway pathology without significantly increasing bacterial loads. Since a similar treatment of uninfected mice with PT did not elicit inflammatory responses, this demonstrates that PT contributes

significantly to the overall pathology in pertussis airway disease through an exacerbation of host responses to infection.

In addition to the multitude of upregulated inflammatory genes and pathways associated with PT contributing to airway pathology, other genes potentially associated with airway pathology were also highly upregulated by PT. One such gene encodes the membrane transporter SLC26A4 (pendrin), which participates in anion exchange at the apical surface of epithelial cells and negatively affects the volume of airway surface liquid (ASL) (58). ASL provides hydration around cilia, allowing proper ciliary beating, and thus plays an essential role in airway clearance. Pendrin overexpression increased inflammation and mucus production in asthma and chronic obstructive pulmonary disease (COPD) models (59) and potentiated allergen-induced airway hyperresponsiveness (AHR) in asthma (58), suggesting that it could play a role in AHR and cough in pertussis. In the kidney, pendrin can affect epithelial sodium channel (ENaC) activity and modulate the ENaC response to hormones that regulate blood pressure (83), and therefore, it is tempting to speculate that the altered pendrin regulation of ENaC in pertussis infection contributes to the pulmonary hypertension observed in lethal pertussis infections of infants (62). In addition, some serine proteases affect ENaC activation and ASL volume control, suggesting that specific serine protease inhibitors, including members of the SERPIN family, could participate in the regulation of ENaC activity (29). Two SERPIN protease inhibitors were among the other pathology-related genes identified as being PT upregulated in our study.

The inclusion of the Δ PT^{high} infection in this analysis revealed interesting differences from WT infection in the time course of responses despite equivalent bacterial loads at 2 and 4 dpi. At 2 dpi, responses peaked in the Δ PT^{high} infection, while responses to WT infection were still relatively modest. However, at 4 dpi, there was a broad response to WT infection, while most responses to Δ PT^{high} infection had returned to background levels. Numerous genes showed this reciprocal regulation pattern (see Table S7 in the supplemental material). To determine whether this was related to PT activity or to the higher dose and earlier bacterial loads of the Δ PT^{high} infection, we compared WT^{high} and Δ PT^{high} infections at these time points. The data indicated that the majority of the higher-level responses to Δ PT^{high} infection (than the responses to WT infection at the regular dose) were due to the earlier high bacterial loads achieved after the high initial dose. However, PT also appeared to inhibit the expression of a small number of genes at 2 dpi, and we cannot rule out the possibility that the PT inhibition of gene expression is more substantial at this time point. Although these data demonstrate that PT is not absolutely necessary for many of these responses, in a natural infection, the initial inoculum is likely to be relatively small and would require significant growth of the bacteria in the airways, which would require PT activity. In addition, the transient nature of the responses to Δ PT^{high} infection versus the greater and more prolonged responses to WT infection indicates that PT plays a role in sustaining many of the bacterial-load-induced responses. The mechanisms by which PT achieves these effects is not clear, but our data demonstrate that its ADP-ribosylation activity is required. One possibility is that PT activity inhibits host mechanisms to attenuate and resolve inflammation that occur after the initiation of infection. A candidate target for PT in this effect might be the sphingosine-1-phosphate (S1P) signaling pathway, since S1P receptors are PT-sensitive G-protein-coupled receptors

(GPCRs) (42). S1P signaling has been shown to attenuate acute lung injury induced by the intratracheal administration of LPS to mice (63) and can alleviate experimental allergic airway inflammation in mice (46). Recently, signaling specifically through S1P receptor 1 (S1P₁) was shown to suppress the pulmonary cytokine storm after influenza virus infection in mice, and endothelial cells were found to be the target of this activity (79). S1P signaling is known to enhance pulmonary endothelial barrier function (24). Therefore, the PT inhibition of S1P₁ signaling on the pulmonary endothelium may cause vascular leakage into the airways and promote increased levels of cytokine and chemokine production, characteristics of peak pertussis infection in the mouse model. In addition, several endogenous lipid mediators of the resolution of inflammation (resolvins and lipoxins) act through PT-sensitive GPCRs (43, 80), and therefore, PT may mediate sustained inflammatory responses by the inhibition of these mechanisms as well.

It is likely that not all of the effects of PT on host responses and pathology would be identified by changes in gene expression, since PT may act more directly on GPCR signaling pathways to induce pathology. Several PT-sensitive GPCRs are involved in inflammatory processes, such as chemokine, leukotriene, and prostaglandin receptors. In addition, a recent report outlined one possible mechanism by which PT might exacerbate cough responses, by inhibiting the desensitization of bradykinin receptors (34). Bradykinin, a peptide implicated in airway inflammatory diseases (1), signals through the activation of bradykinin B2 receptors, GPCRs that couple with both G_q and G_i (44). Preliminary data indicate that PT (but not PT*) inhibits B2 receptor desensitization in guinea pig vagal sensory neurons regulating bradykinin-evoked cough (34), which may correlate with the paroxysmal nature (inability to stop coughing) of pertussis cough episodes.

Currently, no effective treatment for pertussis exists. With an increasing rate of pertussis infection despite widespread vaccination, there is clearly a need for a further understanding of the molecular mechanisms of pertussis pathogenesis. By demonstrating the robust, PT-associated exacerbation of airway inflammation and pathology, this study emphasizes the importance of PT as a critical virulence factor of *B. pertussis*. Further work in this direction may reveal novel targets for therapeutic intervention in pertussis patients, which may alleviate the severe and prolonged cough and reduce the rate of transmission of this disease.

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C.E.C. and N.H.C. conceived of and designed the experiments. Y.S. normalized and carried out statistical analysis of microarray data. C.E.C. performed the experiments. C.E.C. and N.H.C. analyzed the data. C.E.C. and N.H.C. wrote the paper.

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Supplemental Table 1. qPCR Primers

Gene	Forward	Reverse
Ccl2	5' - AGGTCCCTGTCATGCTTCTG - 3'	5' - GGGATCATCTTGCTGGTGAA - 3'
Ccl5	5' - TGCAGAGGACTCTGAGACAGC - 3'	5' - GAGTGGTGTCCGAGCCATA - 3'
Ccl7	5' - TTCTGTGCCTGCTGCTCATA - 3'	5' - TTGACATAGCAGCATGTGGAT - 3'
Cxcl10	5' - GCTGCCGTCATTTTCTGC - 3'	5' - TCTCACTGGCCCGTCATC - 3'
Cxcl9	5' - CTTTTCCTCTTGGGCATCAT - 3'	5' - GCATCGTGCATTCTTATCA - 3'
Gbp1	5' - CAGACTCCTGGAAAGGGACTC - 3'	5' - CTTGGATTCAAAGTATTTTCTCAGC - 3'
HPRT	5' - GCTGACCTGCTGGATTACATTAA - 3'	5' - TGATCATTACAGTAGCTCTTCAGTCTGA - 3'
IFNg	5' - CTGCCACGGCACAGTCATTG - 3'	5' - TGCATCCTTTTTTCGCCTTGC - 3'
IL-17	5' - ACCTCAACCGTTCCACGTCA - 3'	5' - CAGGGTCTTCATTGCGGTG - 3'
IL-1b	5' - TGTGAAATGCCACCTTTTGA - 3'	5' - GGTCAAAGGTTTGAAGCAG - 3'
IL-1rn	5' - TGTGCCAAGTCTGGAGATGA - 3'	5' - TTCTTTGTTCTTGCTCAGATCAGT - 3'
IL-33	5' - ATCACGGCAGAATCATCGAG - 3'	5' - GCGGTGCTGCTGAACTTT - 3'
IL-6	5' - TGTCTATACCACTTCACAAGTCGGAG - 3'	5' - GCACAACTCTTTTCTCATTTCCAC - 3'
Irgm1	5' - AAGGCCACTAACATCGAATCA - 3'	5' - TGCCTTATCTCACTTAATACTCCTCA - 3'
KC	5' - GCTTGAAGGTGTTGCCCTCA - 3'	5' - GTGGCTATGACTTCGGTTTGG - 3'
Osm	5' - TGCTCCAACTCTTCCTCTCAG - 3'	5' - CAGGTTTTGGAGGCGGATA - 3'
Retnla	5' - CCTCCACTGTAACGAAGACTC - 3'	5' - CACACCCAGTAGCAGTCATCC - 3'
Saa3	5' - GTTGACAGCCAAAGATGGGT - 3'	5' - CCCGAGCATGGAAGTATTTG - 3'
Slc26a4	5' - AGGAATGGCTCCTCAGTGAC - 3'	5' - CTGCCAGCAGGGCATAAG - 3'
Timp1	5' - GCAAAGAGCTTTCTCAAAGACC - 3'	5' - AGGGATAGATAAACAGGGAAACACT - 3'
TNFA	5' - GACCCTCACACTCAGATCATCTTCT - 3'	5' - CCACTTGGTGGTTTGCTAGGA - 3'

Supplemental Table 2. qPCR Validation of Array Data

Gene	DAY 2 FOLD CHANGE						DAY 4 FOLD CHANGE					
	WT vs PBS		Δ PT vs PBS		Δ PT ^{high} vs PBS		WT vs PBS		Δ PT vs PBS		Δ PT ^{high} vs PBS	
	A	qPCR	A	qPCR	A	qPCR	A	qPCR	A	qPCR	A	qPCR
SAA3	3.3	8.1 (5.8)	1.7	3.2 (0.7)	29.3	123.8 (75.6)	39.7	118.1 (58.0)	ns	1.5 (1.3)	6.6	16.9 (7.2)
KC	4.4	4.4 (1.6)	1.5	1.7 (0.3)	7.4	8.2 (3.4)	18.2	38.0 (16.7)	ns	0.9 (0.4)	2.3	2.4 (1.2)
IL-1B	2.1	2.0 (0.3)	ns	0.9 (0.3)	5.3	4.6 (2.4)	11.1	11.3 (0.4)	ns	1.6 (0.2)	ns	3.2 (1.5)
TIMP1	ns	1.3 (0.4)	ns	1.1 (0.3)	6.0	6.4 (2.9)	10.4	18.3 (11.7)	ns	1.0 (0.3)	2.0	3.9 (1.0)
CXCL10	ns	2.3 (1.5)	ns	2.1 (0.7)	10.5	120.3 (68.6)	10.3	77.8 (16.5)	ns	2.0 (1.4)	ns	6.3 (4.5)
SLC26A4	2.6	5.6 (3.2)	1.6	2.8 (1.7)	3.2	6.7 (2.1)	9.4	15.2 (4.9)	ns	1.7 (0.8)	3.9	4.9 (3.5)
CCL7	1.4	6.5 (3.1)	ns	1.5 (0.9)	6.7	61.2 (2.5)	9.1	57.3 (41.8)	ns	1.8 (1.3)	ns	5.6 (4.8)
RETNLA	ns	3.5 (2.4)	ns	5.9 (5.4)	7.4	21.4 (11.7)	6.4	15.1 (5.0)	ns	0.9 (0.5)	4.3	41.0 (17.8)

A = fold change detected by microarray; ns = no significant change; qPCR values give mean fold change (SD in parenthesis)

Supplemental Table 3. Genes regulated in infected versus uninfected mice

Entrez ID	Gene*	WT vs. PBS				ΔPT vs. PBS				ΔPT ^{high} vs. PBS			
		2 dpi		4 dpi		2 dpi		4 dpi		2 dpi		4 dpi	
		FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC
GENES REGULATED AT BOTH TIME POINTS IN ALL STRAINS													
18626	period homolog 1 (Drosophila)	0.00	3.7	0.00	3.7	0.00	3.4	0.00	5.0	0.02	2.4	0.00	3.8
18626	period homolog 1 (Drosophila)	0.00	3.2	0.00	2.6	0.00	3.0	0.00	3.8	0.01	2.0	0.00	3.4
18627	period homolog 2 (Drosophila)	0.00	2.5	0.00	1.9	0.00	2.4	0.00	2.9	0.00	2.2	0.00	2.8
18627	period homolog 2 (Drosophila)	0.00	2.3	0.00	1.9	0.00	2.4	0.00	3.0	0.00	2.2	0.00	2.7
547343	H2-D1 histocompatibility 2, D region locus 1	0.00	2.3	0.00	2.4	0.00	2.3	0.04	2.2	0.00	3.8	0.00	3.4
18830	phospholipid transfer protein	0.00	2.2	0.00	2.1	0.00	1.8	0.00	2.5	0.00	2.4	0.00	2.5
229599	predicted gene 129	0.00	2.1	0.00	1.7	0.00	2.2	0.00	2.2	0.02	1.6	0.00	2.2
16371	Iroquois related homeobox 1 (Drosophila)	0.00	2.0	0.00	2.1	0.00	1.6	0.04	1.7	0.02	1.7	0.04	1.6
14282	FBJ osteosarcoma oncogene B	0.00	1.9	0.00	1.6	0.00	1.7	0.00	1.9	0.02	1.6	0.00	1.8
16905	lamin A	0.00	1.9	0.00	1.9	0.00	1.6	0.03	1.5	0.00	2.0	0.01	1.5
224742	ATP-binding cassette, sub-family F (GCN20), member 1	0.00	1.8	0.00	1.9	0.00	1.6	0.01	1.7	0.02	1.8	0.00	1.6
16905	lamin A	0.00	1.8	0.00	2.2	0.00	1.6	0.02	1.6	0.01	2.0	0.02	1.5
53376	ubiquitin specific peptidase 2	0.00	1.8	0.00	1.6	0.00	2.2	0.00	2.5	0.01	1.6	0.00	2.0
66058	transmembrane protein 176A	0.00	1.8	0.00	2.9	0.00	1.7	0.01	1.9	0.01	2.4	0.00	2.1
74178	serine/threonine kinase 40	0.00	1.7	0.00	1.8	0.00	1.7	0.01	1.6	0.01	1.8	0.01	1.5
66158	CAAX box 1 homolog A (human)	0.00	1.6	0.00	1.8	0.01	1.5	0.03	1.8	0.01	2.1	0.03	1.6
13688	eukaryotic translation initiation factor 4E binding protein 2	0.00	1.5	0.00	1.6	0.00	1.5	0.00	1.8	0.05	1.7	0.00	1.8
56316	gamma-glutamyl carboxylase	0.00	-1.6	0.00	-1.6	0.00	-1.6	0.01	-1.6	0.01	-1.6	0.00	-1.7
69183	C1q and tumor necrosis factor related protein 2	0.01	-1.6	0.00	-1.8	0.00	-1.7	0.05	-1.6	0.01	-1.9	0.01	-1.7
67017	RIKEN cDNA 2010011I20 gene	0.00	-1.6	0.00	-1.7	0.00	-1.6	0.02	-1.6	0.01	-1.6	0.01	-1.6
94179	keratin 23	0.00	-1.7	0.00	-1.7	0.00	-1.7	0.03	-1.7	0.00	-1.8	0.00	-1.8
29820	tumor necrosis factor receptor superfamily, member 19	0.00	-1.7	0.00	-1.9	0.00	-2.0	0.02	-1.6	0.00	-2.1	0.01	-1.7
192159	pre-mRNA processing factor 8	0.00	-1.9	0.00	-1.6	0.00	-1.6	0.02	-1.7	0.00	-1.9	0.01	-1.6
22413	wingless-related MMTV integration site 2	0.00	-1.9	0.00	-2.5	0.00	-2.2	0.00	-2.0	0.00	-2.1	0.00	-2.2
15360	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0.00	-2.2	0.00	-2.9	0.00	-2.1	0.01	-1.9	0.00	-3.4	0.00	-2.4
16182	interleukin 18 receptor 1	0.00	-2.3	0.00	-1.6	0.00	-2.5	0.00	-2.4	0.02	-1.8	0.00	-1.9
11865	aryl hydrocarbon receptor nuclear translocator-like	0.00	-2.3	0.00	-2.1	0.00	-2.5	0.00	-2.3	0.00	-2.2	0.00	-2.2
13191	dynactin 1	0.00	-4.0	0.00	-3.4	0.00	-4.2	0.00	-3.1	0.00	-3.8	0.00	-3.5
100689	spondin 2, extracellular matrix protein	0.00	-4.5	0.00	-2.1	0.00	-5.2	0.00	-4.4	0.00	-3.1	0.00	-5.0
GENES REGULATED IN AT LEAST ONE TIME POINT IN ALL STRAINS													
225341	LIM and senescent cell antigen like domains 2	0.00	1.6	0.00	1.7			0.00	2.1	0.03	2.1	0.00	1.9
13855	epsin 2	0.00	1.7	0.00	1.6			0.01	1.9	0.01	1.6	0.00	1.8
15019	histocompatibility 2, Q region locus 1	0.01	1.6	0.00	2.3			0.03	1.8	0.01	2.2	0.00	2.6

18035	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.00	1.6	0.00	2.5		0.05	1.5	0.03	1.9	0.03	1.6
18596	platelet derived growth factor receptor, beta polypeptide	0.01	-1.5	0.00	-1.9		0.02	-1.6	0.01	-1.7	0.01	-1.6
74116	peptidase inhibitor 16	0.00	-1.9	0.00	-1.8		0.01	-1.8	0.01	-1.9	0.01	-1.6
20210	serum amyloid A 3	0.00	3.3	0.00	39.7	0.02	1.7		0.00	29.3	0.00	6.6
16819	lipocalin 2	0.00	3.8	0.00	14.0	0.00	2.2		0.00	9.4	0.00	5.8
68891	CD177 antigen	0.01	1.7	0.00	7.9	0.00	1.8		0.00	7.1	0.00	12.4
14962	complement factor B	0.00	1.8	0.00	4.9	0.00	1.6		0.00	5.8	0.00	3.3
19695	regenerating islet-derived 3 gamma	0.00	1.8	0.00	4.7	0.00	2.8		0.00	4.8	0.01	4.2
231507	placenta-specific 8	0.01	1.5	0.00	4.2	0.00	1.6		0.00	4.2	0.01	2.3
20308	chemokine (C-C motif) ligand 9	0.01	1.6	0.00	2.6	0.00	1.6		0.00	4.1	0.02	1.9
17219	minichromosome maintenance deficient 6	0.00	1.8	0.00	3.4	0.00	1.7		0.00	3.8	0.00	1.7
19039	lectin, galactoside-binding, soluble, 3 binding protein	0.01	1.6	0.00	2.7	0.00	1.6		0.01	3.7	0.00	2.8
13038	cathepsin K	0.04	1.5	0.00	1.9	0.01	1.6		0.00	3.4	0.05	1.9
224742	ATP-binding cassette, sub-family F (GCN20), member 1	0.01	1.6	0.00	1.6	0.00	1.5		0.02	1.7	0.00	1.6
83671	synaptotagmin-like 2	0.00	-1.7	0.00	-1.8	0.00	-1.7		0.01	-1.6	0.02	-1.5
14613	gap junction membrane channel protein alpha 5	0.00	-1.8	0.00	-1.6	0.00	-1.7		0.03	-1.6	0.04	-1.5
12069	brain expressed X-linked 2	0.00	-1.7	0.00	-2.2	0.02	-1.6		0.02	-1.7	0.01	-1.5
22030	TNF receptor-associated factor 2	0.00	-1.7	0.01	-1.6	0.00	-1.9		0.02	-1.7	0.01	-1.7
14199	four and a half LIM domains 1	0.00	-1.8	0.00	-1.7	0.00	-1.5		0.01	-1.7	0.01	-1.5
70784	RAS-like, family 12	0.00	-1.7	0.00	-1.5	0.00	-1.7		0.01	-1.7	0.00	-1.7
13617	endothelin receptor type A	0.00	-1.7	0.00	-1.6	0.00	-2.0		0.03	-1.7	0.00	-1.7
69551	RIKEN cDNA 2310022B05 gene	0.00	-1.6	0.00	-1.9	0.00	-1.5		0.01	-1.7	0.01	-1.5
74013	raftlin family member 2	0.01	-1.6	0.00	-1.7	0.00	-1.8		0.01	-1.8	0.00	-1.7
11514	adenylate cyclase 8	0.00	-1.7	0.00	-1.8	0.00	-1.9		0.01	-1.8	0.00	-1.8
12069	brain expressed X-linked 2	0.00	-1.8	0.00	-2.2	0.01	-1.5		0.01	-1.9	0.00	-1.8
71145	scavenger receptor class A, member 5 (putative)	0.00	-1.6	0.00	-2.2	0.00	-1.7		0.00	-1.9	0.01	-1.8
26897	acyl-CoA thioesterase 1	0.00	-1.8	0.00	-1.7	0.00	-1.7		0.01	-2.0	0.01	-1.6
18979	paraoxonase 1	0.01	-1.5	0.00	-1.6	0.01	-1.6		0.01	-2.3	0.00	-1.9
227753	gelsolin	0.00	-2.2	0.00	-2.2	0.00	-2.9		0.00	-3.3	0.00	-2.0
16600	Kruppel-like factor 4 (gut)	0.00	2.3	0.03	1.6	0.00	1.9	0.00	2.4		0.03	1.7
75750	solute carrier family 10 (sodium/bile acid cotransporter) member 6	0.00	1.9	0.00	2.1	0.00	1.6	0.02	2.2		0.02	1.6
53608	mitogen-activated protein kinase kinase kinase 6	0.00	1.9	0.00	1.5	0.01	1.6	0.02	2.0		0.01	2.1
67876	coenzyme Q10 homolog B (S. cerevisiae)	0.00	1.8	0.00	1.7	0.01	1.5	0.00	2.0		0.01	1.6
108116	solute carrier organic anion transporter family, member 3a1	0.01	-1.5	0.00	-1.5	0.00	-1.5	0.02	-1.6		0.01	-1.5
21939	CD40 antigen	0.00	-2.0	0.00	-1.5	0.00	-1.8	0.01	-1.6		0.00	-1.7
13717	elastin	0.00	-2.3	0.00	-1.9	0.00	-2.4	0.01	-2.2		0.00	-1.9
16905	lamin A	0.00	1.6	0.00	2.0	0.00	1.6	0.05	1.6	0.01	2.0	
67629	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.00	1.5	0.00	1.6	0.00	1.6	0.01	1.5	0.01	1.8	
54636	WD repeat domain 45	0.00	-1.6	0.00	-1.6	0.00	-1.7	0.01	-1.6	0.01	-1.7	
70439	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.00	-2.2	0.01	-1.8	0.00	-1.9	0.04	-1.9	0.00	-2.1	
319168	histone cluster 1, H2ah	0.03	1.6	0.00	2.9	0.00	1.9		0.00	4.5		
23985	solute carrier family 26, member 4	0.00	2.6	0.00	9.4	0.01	1.6		0.01	3.9		
52033	PDZ binding kinase	0.02	1.5	0.00	3.0	0.00	1.6		0.00	3.8		
319167	histone cluster 1, H2ag	0.00	1.6	0.00	2.0	0.00	1.6		0.00	2.9		

66822	F-box protein 25	0.01	-1.5	0.00	-1.8	0.00	-1.5		0.02	-1.5		
23792	a disintegrin and metallopeptidase domain 23; similar to ADAM23	0.00	-1.7	0.00	-1.5	0.00	-1.9		0.02	-1.5		
209837	solute carrier family 38, member 5	0.01	-1.5	0.00	-1.6	0.00	-1.5		0.03	-1.6		
241556	tetraspanin 18	0.00	-1.6	0.00	-1.6	0.00	-1.9		0.04	-1.6		
12562	cadherin 5	0.00	-1.6	0.00	-1.6	0.00	-1.6		0.01	-1.6		
245867	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	0.01	-1.5	0.00	-1.7	0.00	-1.7		0.03	-1.6		
14199	four and a half LIM domains 1	0.00	-1.6	0.00	-1.7	0.00	-1.6		0.01	-1.7		
57740	serine/threonine kinase 32C	0.00	-1.7	0.00	-1.6	0.00	-1.5		0.00	-1.8		
219134	shisa homolog 2 (Xenopus laevis)	0.02	-1.5	0.00	-1.9	0.00	-1.5		0.01	-1.8		
218100	zinc finger protein 322A	0.00	-1.6	0.00	-1.5	0.00	-1.6				0.02	-1.6
16007	cysteine rich protein 61	0.00	2.1	0.00	2.4			0.01	2.0		0.01	2.7
17130	MAD homolog 6 (Drosophila)	0.00	1.7	0.00	1.6			0.01	1.9		0.00	1.7
227731	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	0.00	1.8	0.00	2.1			0.02	1.6	0.02	1.7	
17183	matrilin 4	0.00	1.7	0.00	1.8			0.03	1.6	0.04	1.7	
170770	BCL2 binding component 3	0.02	-1.5	0.00	-1.7			0.01	-1.6	0.01	-1.5	
11737	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	0.00	-1.6	0.00	-1.8			0.03	-1.5	0.01	-1.7	
14238	forkhead box F2			0.00	-2.2	0.00	-1.7	0.05	-1.5	0.02	-1.7	0.00 -1.8
76500	inositol hexaphosphate kinase 2			0.00	1.6	0.00	1.6	0.01	1.7	0.03	1.6	0.01 1.7
21785	trefoil factor 2 (spasmolytic protein 1)			0.00	3.1	0.05	1.7			0.00	3.1	0.00 4.3
21946	peptidoglycan recognition protein 1			0.00	3.3	0.02	1.6			0.00	3.1	0.00 4.0
18703	polymeric immunoglobulin receptor			0.00	3.6	0.00	1.8			0.00	2.9	0.00 3.0
228801	cDNA sequence U46068			0.00	2.3	0.04	1.7			0.00	2.7	0.00 2.5
76933	interferon, alpha-inducible protein 27 like 2A			0.00	1.8	0.01	1.8			0.00	2.7	0.02 2.1
57321	telomeric repeat binding factor 2, interacting protein			0.00	1.5	0.00	1.5			0.02	1.5	0.01 1.5
16661	keratin 10			0.00	-1.6	0.00	-1.5			0.00	-1.7	0.00 -1.5
16009	insulin-like growth factor binding protein 3			0.00	-2.0	0.01	-1.6			0.00	-2.5	0.00 -1.7
17762	microtubule-associated protein tau			0.00	-1.6	0.00	-1.5			0.01	-1.7	0.00 -1.7
74013	raftlin family member 2			0.00	-1.8	0.00	-1.7			0.00	-1.9	0.00 -1.7
110956	DNA segment, Chr 17, human D6S56E 5			0.00	3.3	0.00	1.7			0.00	4.1	
319165	histone cluster 1, H2ad			0.00	2.7	0.00	1.8			0.00	4.1	
319169	histone cluster 1, H2ak			0.00	2.7	0.00	1.7			0.00	4.0	
233406	protein regulator of cytokinesis 1			0.00	2.7	0.00	2.0			0.00	4.0	
319170	histone cluster 1, H2an			0.00	2.5	0.00	1.9			0.00	3.9	
18140	ubiquitin-like, containing PHD and RING finger domains, 1			0.00	2.9	0.00	1.7			0.00	3.8	
319173	histone cluster 1, H2af			0.00	2.6	0.00	2.0			0.00	3.8	
319171	histone cluster 1, H2ao			0.00	2.5	0.00	1.7			0.00	3.5	
21973	topoisomerase (DNA) II alpha			0.00	2.3	0.00	1.5			0.00	3.0	
20878	aurora kinase A			0.00	2.0	0.00	1.6			0.00	2.8	
71819	kinesin family member 23			0.00	2.0	0.01	1.5			0.00	2.6	
12830	collagen, type IV, alpha 5			0.00	-1.6	0.01	-1.5			0.03	-1.5	
14623	gap junction protein, beta 6			0.00	-1.6	0.01	-1.5			0.02	-1.6	
18647	PFTAIRE protein kinase 1			0.00	-1.7	0.00	-1.6			0.01	-1.6	
69225	carbohydrate kinase domain containing			0.00	-1.6	0.00	-1.6			0.01	-1.6	
76477	procollagen C-endopeptidase enhancer 2			0.00	-1.7	0.00	-1.8			0.00	-1.9	
56198	hairly/enhancer-of-split related with YRPW motif-like			0.00	-1.5	0.00	-1.5					0.00 -1.6

74521	protein phosphatase 4, regulatory subunit 4			0.00	-1.6	0.00	-1.5				0.01	-1.6	
67866	WAP four-disulfide core domain 1			0.00	-1.5	0.00	-1.6				0.01	-1.5	1
30953	schwannomin interacting protein 1			0.00	-1.5	0.00	-1.6				0.01	-1.6	
15481	similar to heat shock protein 8; heat shock protein 8			0.00	2.2			0.02	1.8	0.04	1.8	0.02	1.7
667977	predicted gene 8909			0.00	2.2			0.05	1.7	0.04	2.4	0.00	2.7
20818	signal recognition particle receptor, B subunit			0.00	2.1			0.01	1.6	0.05	1.9		
20973	synaptogyrin 2			0.00	2.0			0.02	1.6	0.01	1.9	0.01	1.7
16010	insulin-like growth factor binding protein 4			0.00	1.9			0.04	1.5	0.04	1.8		
56264	carboxypeptidase X 1 (M14 family)			0.00	1.7			0.04	1.5	0.01	2.3	0.01	1.7
56744	platelet factor 4			0.00	1.6			0.02	1.6	0.00	2.1		
67245	pellino 1			0.00	1.5			0.03	1.6	0.03	1.6		
19303	paxillin			0.00	1.5			0.01	1.5	0.01	1.7		
11666	ATP-binding cassette, sub-family D (ALD), member 1			0.00	1.5			0.05	1.5	0.01	1.7		
13641	ephrin B1			0.00	-1.5			0.04	-1.6	0.01	-1.7		
225642	gastrin releasing peptide	0.02	1.7			0.00	1.7	0.00	2.1	0.01	1.6	0.00	1.8
18029	nuclear factor I/C	0.00	1.7			0.00	1.8	0.03	1.6	0.02	1.6	0.01	1.6
14786	growth factor receptor bound protein 7	0.00	-1.6			0.00	-1.7	0.02	-1.5	0.03	-1.5	0.01	-1.5
58187	claudin 10	0.00	-1.9			0.00	-1.8	0.02	-1.7	0.00	-2.0	0.00	-1.9
57349	pro-platelet basic protein	0.02	1.8			0.00	1.9	0.01	2.3	0.00	2.2		
13087	cytochrome P450, family 2, subfamily a, polypeptide 5	0.00	1.7			0.01	1.7	0.04	1.9	0.04	-1.7		
213742	inactive X specific transcripts	0.00	-2.2			0.00	-1.9	0.01	-1.8	0.00	-2.2		
18628	period homolog 3 (Drosophila)	0.00	1.7			0.00	1.8	0.01	2.0			0.00	2.0
229599	predicted gene 129	0.00	1.7			0.00	1.7	0.01	1.8			0.01	1.7
14605	TSC22 domain family, member 3	0.01	1.6			0.01	1.5	0.03	1.8			0.02	1.7
26457	solute carrier family 27 (fatty acid transporter), member 1	0.01	1.5			0.00	2.0	0.01	1.7			0.01	1.5
114249	nephronectin	0.01	1.5			0.00	1.7	0.01	1.6			0.00	1.7
241128	family with sequence similarity 124, member B	0.00	-1.6			0.00	-1.6	0.02	-1.5			0.01	-1.5
68895	RAS-like, family 11, member A	0.00	-1.7			0.00	-2.0	0.03	-1.6			0.00	-1.8
27357	glycogenin	0.00	-1.5			0.00	-1.9	0.03	-1.6			0.00	-1.8
12753	circadian locomotor output cycles kaput	0.01	-1.5			0.00	-1.8	0.02	-1.6			0.00	-1.7
27357	glycogenin	0.00	-1.5			0.00	-2.1	0.01	-1.7			0.01	-1.7
16949	lysyl oxidase-like 1	0.00	-1.8			0.00	-1.9	0.02	-1.7			0.01	-1.7
16948	lysyl oxidase	0.00	-1.9			0.00	-2.5	0.04	-1.9			0.01	-1.6
52666	DNA segment, Chr 10, ERATO Doi 610, expressed	0.00	-1.7			0.00	-1.5			0.01	-1.5	0.01	-1.5
15530	perlecan (heparan sulfate proteoglycan 2)	0.00	-1.6			0.00	-1.6			0.02	-1.5	0.01	-1.5
11468	actin, gamma 2, smooth muscle, enteric	0.01	-1.6			0.00	-1.5			0.00	-2.1	0.01	-1.7
58187	claudin 10	0.00	-1.8			0.00	-2.1			0.00	-2.0	0.00	-2.1
69202	parathymosin	0.00	1.6			0.00	1.7			0.03	1.6		
66175	musculoskeletal, embryonic nuclear protein 1	0.00	-1.7			0.00	-1.7			0.03	-1.5		
242700	interleukin 28 receptor alpha	0.00	-1.6			0.00	-1.5			0.02	-1.5		
101543	WT1-interacting protein	0.00	-1.6			0.00	-1.6			0.01	-1.5		
103135	pancreas protein 2; ubiquitin specific peptidase 52	0.00	-1.7			0.00	-1.6			0.01	-1.6		
108089	ring finger protein 144A	0.01	-1.5			0.00	-1.6			0.01	-1.6		
328949	mutated in colorectal cancers	0.00	-1.5			0.00	-1.6			0.02	-1.6		
66836	transmembrane protein 223	0.00	-1.5			0.00	-1.8			0.01	-1.6		
20384	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	0.00	-1.8			0.00	-1.7			0.02	-1.6		
11600	angiopoietin 1	0.01	-1.5			0.00	-1.9			0.01	-1.8		

20384	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	0.00	-2.1	0.00	-2.2		0.01	-1.9		
16527	potassium channel, subfamily K, member 3	0.01	1.6	0.00	1.8				0.03	1.5
16478	Jun proto-oncogene related gene d	0.01	1.5	0.00	1.7				0.01	1.5
75560	E1A binding protein p400	0.00	-1.5	0.00	-1.5				0.01	-1.6
53412	protein phosphatase 1, regulatory (inhibitor) subunit 3C	0.01	-1.5	0.01	-1.6				0.01	-1.6
78908	immunoglobulin superfamily, member 3	0.00	-1.7	0.00	-1.6				0.01	-1.5
432731	zinc finger protein 187	0.00	-1.6	0.00	-1.6				0.01	-1.5
20315	chemokine (C-X-C motif) ligand 12	0.00	-1.6	0.00	-1.6				0.01	-1.6
66446	exosome component 7	0.00	-1.7	0.00	-1.6				0.01	-1.5
20652	sterol O-acyltransferase 1	0.00	-1.8	0.00	-1.6				0.00	-1.8
72748	haloacid dehalogenase-like hydrolase domain containing 3	0.01	-1.7	0.01	-1.7				0.00	-2.2
218952	fermitin family homolog 2 (Drosophila)	0.00	-1.6	0.00	-1.7				0.00	-1.6
69590	glutathione peroxidase 8 (putative)	0.00	-1.6	0.00	-1.8				0.01	-1.6
57875	angiopoietin-like 4	0.01	-1.7	0.00	-1.9				0.01	-1.6
12825	collagen, type III, alpha 1	0.00	-1.6			0.02	-1.5	0.01	-1.5	-1.6
13087	cytochrome P450, family 2, subfamily a, polypeptide 5	0.01	1.6			0.01	1.9	0.03	-1.8	
14605	TSC22 domain family, member 3	0.00	1.6			0.00	2.0		0.00	1.7
268709	family with sequence similarity 107, member A	0.00	1.6			0.03	1.8		0.01	1.7
380916	leucine-rich repeats and calponin homology (CH) domain containing 1	0.01	1.5			0.04	1.6		0.01	1.6
80987	NCK interacting protein with SH3 domain			0.00	1.8	0.02	1.6		0.00	1.6
21937	tumor necrosis factor receptor superfamily, member 1a			0.00	2.0	0.04	1.5		0.02	1.6
240725	sulfatase 1			0.00	-1.6	0.01	-1.6		0.01	-1.5
66922	related RAS viral (r-ras) oncogene homolog 2			0.00	-1.6	0.02	-1.5		0.01	-1.5
15139	hemolytic complement			0.00	-1.8	0.01	-1.9		0.01	-1.7
15139	hemolytic complement			0.00	-1.8	0.01	-1.9		0.01	-1.7

*Duplicate entries indicate results from multiple probes for the same gene

Supplemental Table 4. WT vs. ΔPT gene regulation at 2 and 4 dpi

		WT vs. ΔPT		WT vs. ΔPT ^{high}	
Entrez ID	Gene*	FDR	FC	FDR	FC
Regulated at 2 dpi in WT vs. ΔPT and WT vs. ΔPT ^{high}					
16176	interleukin 1 beta	0.00	2.3	0.01	-2.5
76574	major facilitator superfamily domain containing 2A	0.00	2.0	0.00	2.2
Regulated at 2 dpi in WT vs. ΔPT but not WT vs. ΔPT ^{high}					
14825	chemokine (C-X-C motif) ligand 1	0.00	3.0		
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.00	2.2		
77125	interleukin 33	0.00	2.0		
76905	leucine-rich alpha-2-glycoprotein 1	0.00	2.0		
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.01	2.0		
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.02	1.9		
54325	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0.02	1.7		
246133	potassium voltage-gated channel, Isk-related subfamily, gene 2	0.01	1.7		
16598	Kruppel-like factor 2 (lung)	0.01	1.6		
Regulated at 2 dpi in WT vs. ΔPT ^{high} but not WT vs. ΔPT					
11537	complement factor D (adipsin)			0.01	3.2
13087	Cyp2a5 cytochrome P450, family 2, subfamily a, polypeptide 5			0.00	3.0
12350	carbonic anhydrase 3			0.01	2.9
13087	Cyp2a5 cytochrome P450, family 2, subfamily a, polypeptide 5			0.00	2.9
13087	Cyp2a5 cytochrome P450, family 2, subfamily a, polypeptide 5			0.00	2.8
11450	adiponectin, C1Q and collagen domain containing			0.02	2.5
79235	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)			0.00	2.0
17189	myoglobin			0.05	2.0
76722	creatine kise, mitochondrial 2			0.02	2.0
14262	flavin containing monooxygese 3			0.00	1.9
11464	Actc1 actin, alpha, cardiac muscle 1			0.02	1.9
241041	predicted gene 4956			0.00	1.8
16009	Igfbp3 insulin-like growth factor binding protein 3			0.00	1.8
13106	cytochrome P450, family 2, subfamily e, polypeptide 1			0.03	1.8
76722	creatine kise, mitochondrial 2			0.04	1.8
53419	corin			0.02	1.7
14262	flavin containing monooxygese 3			0.00	1.7
14311	cell death-inducing DFFA-like effector c			0.00	1.7
17888	myosin, heavy polypeptide 6, cardiac muscle, alpha			0.05	1.7
13087	cytochrome P450, family 2, subfamily a, polypeptide 4			0.00	1.7
14077	Fabp3 fatty acid binding protein 3, muscle and heart			0.03	1.6
108075	latent transforming growth factor beta binding protein 4			0.00	1.6
68404	neuritin 1			0.00	1.6
64082	Popdc2 popeye domain containing 2			0.01	1.6
234564	expressed sequence AU018778			0.00	1.6
18626	period homolog 1 (Drosophila)			0.02	1.6
76477	procollagen C-endopeptidase enhancer 2			0.00	1.6
18979	paraoxose 1			0.02	1.5
18295	osteoglycin			0.02	1.5
16600	Kruppel-like factor 4 (gut)			0.02	1.5
72393	Fas apoptotic inhibitory molecule 2			0.01	1.5
15360	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2			0.02	1.5
22004	tropomyosin 2, beta			0.01	1.5
227753	gelsolin			0.01	1.5
11733	ankyrin 1, erythroid			0.03	1.5
14859	glutathione S-transferase, alpha 3			0.01	1.5
16008	insulin-like growth factor binding protein 2			0.01	1.5
107769	transmembrane 6 superfamily member 1			0.05	-1.5
74145	coagulation factor XIII, A1 subunit			0.03	-1.5
19361	RAD51 homolog (S. cerevisiae)			0.01	-1.5
14466	glucosidase, beta, acid			0.02	-1.5
72935	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41			0.05	-1.5
78816	Gem-interacting protein			0.02	-1.5
12145	chemochine (C-X-C motif) receptor 5			0.01	-1.5
11491	a disintegrin and metallopeptidase domain 17			0.01	-1.5
12575	cyclin-dependent kise inhibitor 1A (P21)			0.02	-1.5
75608	chromatin modifying protein 4B			0.02	-1.5
76846	ribosomal protein S9			0.01	-1.5
12545	cell division cycle 7 (S. cerevisiae)			0.02	-1.5
14118	fibrillin 1			0.04	-1.5

26886	centromere protein H	0.01	-1.5
19942		0.00	-1.5
54519	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0.03	-1.5
232984	UDP-Glcc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	0.02	-1.5
404710	IQ motif containing GTPase activating protein 3	0.02	-1.5
11637	similar to adenylate kinase 2; adenylate kinase 2	0.03	-1.5
16796	LIM and SH3 protein 1	0.03	-1.5
12477	cytotoxic T-lymphocyte-associated protein 4	0.01	-1.5
26914	H2A histone family, member Y	0.03	-1.5
63986	ia Maturation Factor-Gamma (Gmfg) From Mus Musculus At 1.50 A Resolution; predicted gene 9835; glia maturatio	0.01	-1.5
66141	interferon induced transmembrane protein 3	0.02	-1.5
69769	tumor necrosis factor, alpha-induced protein 8-like 2	0.01	-1.5
20305	chemokine (C-C motif) ligand 6	0.00	-1.5
54519	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0.01	-1.5
214901	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	0.02	-1.5
76438	raftlin lipid raft linker 1	0.02	-1.5
56459	SUMO1 activating enzyme subunit 1	0.01	-1.5
16918	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	0.02	-1.5
22629	rosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, eta polypeptide	0.02	-1.5
23845	C-type lectin domain family 5, member a	0.02	-1.5
73710	tubulin, beta 2B	0.02	-1.5
26388	interferon activated gene 202B	0.04	-1.5
116810	forkhead box N4	0.00	-1.5
26425	nucleotide binding protein 1	0.03	-1.5
73723	SH3 domain binding glutamic acid-rich protein-like 3	0.04	-1.5
279572	toll-like receptor 13	0.01	-1.5
67963	Niemann Pick type C2	0.02	-1.5
26416	mitogen-activated protein kase 14	0.01	-1.5
20684	nuclear antigen Sp100	0.01	-1.5
26382	FYVE, RhoGEF and PH domain containing 2	0.01	-1.5
19650	retinoblastoma-like 1 (p107)	0.02	-1.5
13496	AT rich interactive domain 3A (BRIGHT-like)	0.01	-1.5
19261	sigl-regulatory protein alpha	0.00	-1.5
69769	tumor necrosis factor, alpha-induced protein 8-like 2	0.00	-1.5
56628	C-type lectin domain family 7, member a	0.03	-1.5
72536	GTPase-activating protein; T-cell activation Rho GTPase-activating protein; T-cell activation GTPase activating prot	0.02	-1.5
68713	interferon induced transmembrane protein 1	0.00	-1.5
67877	N-acetyltransferase 5; predicted gene 7984; N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	0.01	-1.5
70110	interferon-induced protein 35	0.03	-1.5
67951	tubulin, beta 6	0.01	-1.5
245847	amidohydrolase domain containing 2	0.02	-1.5
110355	adrenergic receptor kase, beta 1	0.01	-1.5
545384	cDNA sequence BC094916	0.04	-1.5
27370	ribosomal protein S26	0.01	-1.5
12257	translocator protein	0.01	-1.5
58218	triggering receptor expressed on myeloid cells 3	0.01	-1.5
229323	G protein-coupled receptor 171	0.04	-1.5
70218	kinesin family member 18B	0.00	-1.5
70454	centromere protein L	0.01	-1.5
110454	lymphocyte antigen 6 complex, locus A	0.02	-1.5
56212	ras homolog gene family, member G	0.01	-1.5
83768	dipeptidylpeptidase 7	0.01	-1.5
50934	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	0.01	-1.6
23969	protein kase C and casein kase substrate in neurons 1	0.01	-1.6
228608	spermine oxidase	0.02	-1.6
226162	deleted in primary ciliary dyskinesia	0.01	-1.6
16571	kinesin family member 4	0.02	-1.6
21899	toll-like receptor 6	0.02	-1.6
26410	mitogen-activated protein kase kase kase 8	0.03	-1.6
18102	Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23) (NDPK-A) (nm23-M1); non-meta	0.02	-1.6
14793	cell division cycle associated 3	0.00	-1.6
574428	zinc finger, MYND-type containing 15	0.03	-1.6
208628	kinetochore associated 1	0.02	-1.6
622339	glyceraldehyde-3-phosphate dehydrogese pseudogene	0.04	-1.6
70466	cytoskeleton associated protein 2-like	0.01	-1.6
69928	apoptosis-inducing, TAF9-like domain 1	0.01	-1.6
70385	coiled-coil domain containing 99	0.02	-1.6
20750	secreted phosphoprotein 1	0.02	-1.6
76293	microfibrillar-associated protein 4	0.02	-1.6
51944	D segment, Chr 2, ERATO Doi 750, expressed	0.04	-1.6
20230	special AT-rich sequence binding protein 1	0.01	-1.6
16407	integrin alpha E, epithelial-associated	0.02	-1.6

26442	proteasome (prosome, macropain) subunit, alpha type 5	0.05	-1.6
70454	centromere protein L	0.03	-1.6
66061	Tctex1 domain containing 2	0.00	-1.6
63986	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.04	-1.6
320484	RAS protein activator like 3	0.00	-1.6
23997	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	0.01	-1.6
27050	ribosomal protein S3	0.01	-1.6
14235	forkhead box M1	0.01	-1.6
16619	kallikrein 1-related peptidase b27	0.01	-1.6
22172	thymidylate synthase, pseudogene	0.02	-1.6
14457	growth arrest specific 7	0.02	-1.6
50498	Epstein-Barr virus induced gene 3	0.02	-1.6
245195	resistin like gamma	0.02	-1.6
50931	interleukin 27 receptor, alpha	0.00	-1.6
15374	hematological and neurological expressed sequence 1	0.04	-1.6
215632	pleckstrin and Sec7 domain containing 4	0.04	-1.6
23834	cell division cycle 6 homolog (S. cerevisiae)	0.01	-1.6
67629	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.01	-1.6
57913	leucine-rich and death domain containing	0.03	-1.6
22271	uridine phosphorylase 1	0.04	-1.6
75495	MORN repeat containing 5	0.00	-1.6
14235	forkhead box M1	0.04	-1.6
54683	peroxiredoxin 5	0.01	-1.6
13654	early growth response 2	0.03	-1.6
16421	integrin beta 7	0.01	-1.6
56417	adenosine deaminase, R-specific	0.02	-1.6
22637	zeta-chain (TCR) associated protein kise	0.01	-1.6
381413	G protein-coupled receptor 176	0.01	-1.6
16970	lymphoid-restricted membrane protein	0.00	-1.6
27643	ubiquitin-like 4	0.01	-1.6
243910	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	0.02	-1.6
12984	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	0.01	-1.6
18413	oncostatin M	0.01	-1.6
108670	epithelial stromal interaction 1 (breast)	0.01	-1.6
22388	WD repeat domain 1	0.03	-1.6
56619	C-type lectin domain family 4, member e	0.01	-1.6
67397	endoplasmic reticulum protein 29	0.03	-1.6
14841	germ cell-specific gene 2	0.01	-1.6
13032	cathepsin C	0.01	-1.6
94181	N-acetylneuraminic acid synthase (sialic acid synthase)	0.00	-1.6
22146	tubulin, alpha 1C	0.00	-1.6
21897	toll-like receptor 1	0.01	-1.6
60406	sin3 associated polypeptide	0.01	-1.6
14026	similar to Ena-VASP-like; Ena-vasodilator stimulated phosphoprotein	0.02	-1.6
66422	dCTP pyrophosphatase 1	0.00	-1.6
674706	similar to zinc finger protein 341	0.01	-1.6
217203	transmembrane protein 106A	0.01	-1.6
22154	tubulin, beta 5	0.01	-1.6
219144	ADP-ribosylation factor-like 11	0.01	-1.6
108912	cell division cycle associated 2	0.00	-1.6
50778	regulator of G-protein sigling 1	0.03	-1.6
213391	Ras association (RalGDS/AF-6) domain family member 4	0.01	-1.6
17392	matrix metalloproteinase 3	0.03	-1.6
19264	protein tyrosine phosphatase, receptor type, C	0.01	-1.6
22256	uracil D glycosylase	0.01	-1.6
217653	expressed sequence C79407	0.00	-1.6
15270	H2A histone family, member X	0.01	-1.6
216859	centaurin, beta 1	0.00	-1.6
17079	CD180 antigen	0.03	-1.6
630499	predicted gene 7035	0.01	-1.6
13732	epithelial membrane protein 3	0.00	-1.6
74157	FtsJ methyltransferase domain containing 2	0.01	-1.6
11821	adenine phosphoribosyl transferase	0.01	-1.6
11881	arylsulfatase B	0.01	-1.6
13555	E2F transcription factor 1	0.02	-1.6
17216	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0.01	-1.6
21934	tumor necrosis factor receptor superfamily, member 11a	0.03	-1.6
20821	tripartite motif-containing 21	0.01	-1.6
18726	paired-Ig-like receptor A3	0.01	-1.6
20198	S100 calcium binding protein A4	0.00	-1.6
16852	lectin, galactose binding, soluble 1	0.01	-1.6
11867	actin related protein 2/3 complex, subunit 1B	0.01	-1.6

15978	interferon gamma	0.02	-1.6
17159	mannosidase 2, alpha B1	0.02	-1.6
114564	; predicted gene 2635; component of Sp100-rs; predicted gene 2666; predicted gene 7582; predicted gene 7592; p	0.01	-1.6
12842	collagen, type I, alpha 1	0.03	-1.6
67052	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0.01	-1.6
56743	linker for activation of T cells family, member 2	0.00	-1.6
621823	proteasome (prosome, macropain) 28 subunit, beta	0.00	-1.6
232983	chemokine (C-X-C motif) ligand 17	0.02	-1.6
20375	SFFV proviral integration 1	0.02	-1.6
12316	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.00	-1.6
12257	translocator protein	0.01	-1.6
214854	neuralized homolog 3 homolog (Drosophila)	0.03	-1.6
18718	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.01	-1.6
232983	chemokine (C-X-C motif) ligand 17	0.01	-1.6
75612	glucosamine (N-acetyl)-6-sulfatase	0.00	-1.6
214359	transmembrane protein 51	0.02	-1.6
12489	CD33 antigen	0.01	-1.6
547343	histocompatibility 2, D region locus 1	0.01	-1.6
15016	histocompatibility 2, Q region locus 5	0.01	-1.6
17833	mucin 5, subtypes A and C, tracheobronchial/gastric	0.01	-1.6
230738	zinc finger CCCH type containing 12A	0.03	-1.6
70719	histocompatibility (minor) HA-1	0.00	-1.6
14667	GM2 ganglioside activator protein	0.01	-1.6
171285	hepatitis A virus cellular receptor 2	0.00	-1.6
29870	G two S phase expressed protein 1	0.01	-1.6
27052	acyloxyacyl hydrolase	0.01	-1.6
93692	glutaredoxin	0.04	-1.6
17312	C-type lectin domain family 10, member A	0.00	-1.6
110006	glucuronidase, beta	0.00	-1.6
72075	opioid growth factor receptor	0.03	-1.6
72119	TPX2, microtubule-associated protein homolog (Xenopus laevis)	0.00	-1.7
74015	FCH domain only 1	0.00	-1.7
13806	o enolase 1, alpha non-neuron; hypothetical protein LOC100044223; predicted gene 5506; predicted gene 5855; hy	0.02	-1.7
243771	poly (ADP-ribose) polymerase family, member 12	0.01	-1.7
80901	chemokine (C-X-C motif) receptor 6	0.00	-1.7
66102	chemokine (C-X-C motif) ligand 16	0.03	-1.7
74107	centrosomal protein 55	0.00	-1.7
106795	transcription factor 19	0.01	-1.7
21356	TAP binding protein	0.04	-1.7
320832	signal-regulatory protein beta 1; similar to SIRP beta 1 cell surface protein	0.00	-1.7
71893	DPH oxidase organizer 1	0.01	-1.7
21812	transforming growth factor, beta receptor I	0.01	-1.7
56264	carboxypeptidase X 1 (M14 family)	0.03	-1.7
102545	CKLF-like MARVEL transmembrane domain containing 7	0.00	-1.7
12982	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0.01	-1.7
17857	myxovirus (influenza virus) resistance 1	0.00	-1.7
21815	TGFB-induced factor homeobox 1	0.00	-1.7
68662	secretoglobulin, family 3A, member 1	0.03	-1.7
27007	killer cell lectin-like receptor subfamily K, member 1	0.01	-1.7
11630	absent in melanoma 1	0.01	-1.7
218454	lipoma HMGIC fusion partner-like 2	0.00	-1.7
12458	chemokine (C-C motif) receptor 6	0.00	-1.7
17969	neutrophil cytosolic factor 1	0.00	-1.7
19106	eukaryotic translation initiation factor 2-alpha kinase 2	0.02	-1.7
12226	3-cell translocation gene 1, anti-proliferative; similar to myocardial vascular inhibition factor	0.01	-1.7
268857	NLR family, CARD domain containing 3	0.01	-1.7
18636	complement factor properdin	0.01	-1.7
11867	actin related protein 2/3 complex, subunit 1B	0.00	-1.7
12505	CD44 antigen	0.00	-1.7
140795	purinergic receptor P2Y, G-protein coupled, 14	0.03	-1.7
22375	tryptophanyl-tRNA synthetase	0.03	-1.7
15458	hemopexin	0.03	-1.7
56744	platelet factor 4	0.02	-1.7
109225	membrane-spanning 4-domains, subfamily A, member 7	0.00	-1.7
15040	histocompatibility 2, T region locus 23; similar to RT1 class Ib, locus H2-Q-like, grc region	0.05	-1.7
16362	interferon regulatory factor 1	0.04	-1.7
17219	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	0.01	-1.7
71279	solute carrier family 29 (nucleoside transporters), member 3	0.00	-1.7
68195	ribonuclease T2B; ribonuclease T2A	0.02	-1.7
20133	ribonucleotide reductase M1	0.00	-1.7
54683	peroxiredoxin 5	0.02	-1.7
51788	H2A histone family, member Z; predicted gene 6722; predicted gene 8203	0.00	-1.7

56644	C-type lectin domain family 7, member a	0.01	-1.7
19260	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0.00	-1.7
56150	MAD2 mitotic arrest deficient-like 1 (yeast)	0.00	-1.7
16551	kinesin family member 11	0.00	-1.7
66442	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.00	-1.7
18037	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	0.01	-1.7
213391	Ras association (RalGDS/AF-6) domain family member 4	0.01	-1.7
12825	collagen, type III, alpha 1	0.00	-1.7
27060	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	0.01	-1.7
69810	C-type lectin domain family 4, member b1	0.00	-1.7
18724	receptor A11; paired-Ig-like receptor A5; paired-Ig-like receptor A6; paired-Ig-like receptor A4; paired-Ig-like receptor A3	0.00	-1.7
270152	adhesion molecule, interacts with CXADR antigen 1	0.00	-1.7
75909	transmembrane protein 49	0.00	-1.7
21939	CD40 antigen	0.01	-1.7
12511	CD6 antigen	0.00	-1.7
17874	myeloid differentiation primary response gene 88	0.02	-1.7
23900	hematopoietic cell sigl transducer	0.01	-1.7
107435	histone aminotransferase 1	0.01	-1.7
68949	RIKEN cD 1500012F01 gene	0.00	-1.7
12047	B-cell leukemia/lymphoma 2 related protein A1d	0.00	-1.7
18817	polo-like kinase 1 (Drosophila)	0.00	-1.7
623474	RAD54 homolog B (S. cerevisiae)	0.01	-1.7
14159	feline sarcoma oncogene	0.00	-1.7
12765	chemokine (C-X-C motif) receptor 2	0.04	-1.7
67893	transmembrane protein 86A	0.00	-1.7
20867	stress-induced phosphoprotein 1	0.01	-1.7
106869	tumor necrosis factor, alpha-induced protein 8	0.03	-1.7
12500	CD3 antigen, delta polypeptide	0.01	-1.7
66442	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.00	-1.7
213391	Ras association (RalGDS/AF-6) domain family member 4	0.00	-1.7
230098	RIKEN cD E130306D19 gene	0.00	-1.7
15000	histocompatibility 2, class II, locus Mb2	0.01	-1.7
11432	acid phosphatase 2, lysosomal	0.02	-1.7
12226	3-cell translocation gene 1, anti-proliferative; similar to myocardial vascular inhibition factor	0.01	-1.7
56722	LPS-induced TN factor	0.01	-1.7
12945	deleted in malignant brain tumors 1	0.00	-1.7
19186	proteasome (prosome, macropain) 28 subunit, alpha	0.01	-1.7
58203	Z-D binding protein 1	0.00	-1.7
64099	parvin, gamma	0.00	-1.7
16977	leucine rich repeat containing 23	0.00	-1.7
74131	SAM and SH3 domain containing 3	0.01	-1.7
15361	high mobility group AT-hook 1	0.01	-1.7
268396	SH3 and PX domains 2B	0.01	-1.8
16319	inner centromere protein	0.00	-1.8
17748	metallothionein 1	0.00	-1.8
78816	Gem-interacting protein	0.00	-1.8
13078	cytochrome P450, family 1, subfamily b, polypeptide 1	0.01	-1.8
18987	POU domain, class 2, transcription factor 2	0.00	-1.8
22171	thymidylate synthase	0.00	-1.8
80859	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	0.04	-1.8
12266	complement component 3	0.00	-1.8
16854	lectin, galactose binding, soluble 3	0.00	-1.8
66566	RIKEN cD 2310079N02 gene	0.01	-1.8
18753	protein kinase C, delta	0.02	-1.8
16391	interferon regulatory factor 9	0.04	-1.8
107272	phosphoserine aminotransferase 1	0.01	-1.8
67133	glycoprotein 2 (zymogen granule membrane)	0.00	-1.8
67855	aspartic peptidase, retroviral-like 1	0.01	-1.8
19366	RAD54 like (S. cerevisiae)	0.00	-1.8
677289	lymphocyte specific 1	0.00	-1.8
17386	matrix metalloproteinase 13	0.00	-1.8
13123	cytochrome P450, family 7, subfamily b, polypeptide 1	0.05	-1.8
20539	protein 5; similar to Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5; solute carrier family 7	0.00	-1.8
67742	SAM domain, SH3 domain and nuclear localization signals, 1	0.01	-1.8
19171	proteasome (prosome, macropain) subunit, beta type 10	0.01	-1.8
15978	interferon gamma	0.01	-1.8
22040	three prime repair exonuclease 1	0.00	-1.8
30955	phosphoinositide-3-kinase, catalytic, gamma polypeptide	0.00	-1.8
209086	sterile alpha motif domain containing 9-like	0.03	-1.8
171285	hepatitis A virus cellular receptor 2	0.01	-1.8
231712	TRAF type zinc finger domain containing 1	0.00	-1.8
171504	apolipoprotein B48 receptor	0.00	-1.8

19277	protein tyrosine phosphatase, receptor type, O	0.01	-1.8
14972	histocompatibility 2, K1, K region; similar to H-2K(d) antigen	0.00	-1.8
19186	proteasome (prosome, macropain) 28 subunit, alpha	0.00	-1.8
67865	regulator of G-protein siglling 10	0.00	-1.8
14156	flap structure specific endonuclease 1	0.00	-1.8
21939	CD40 antigen	0.04	-1.8
16178	interleukin 1 receptor, type II	0.01	-1.8
18707	phosphatidylinositol 3-kise catalytic delta polypeptide	0.01	-1.8
229900	guanylate binding protein 6	0.03	-1.8
108101	fermitin family homolog 3 (Drosophila)	0.01	-1.8
71934	carbonic anhydrase 13	0.00	-1.8
16149	associated)	0.01	-1.8
59027	nicotimide phosphoribosyltransferase	0.01	-1.8
13163	Fas death domain-associated protein	0.01	-1.8
18301	FXYP domain-containing ion transport regulator 5	0.00	-1.8
21391	thromboxane A synthase 1, platelet	0.00	-1.8
106582	nurim (nuclear envelope membrane protein)	0.00	-1.8
72925	membrane-associated ring finger (C3HC4) 1	0.00	-1.8
667977	predicted gene 8909	0.04	-1.8
18301	FXYP domain-containing ion transport regulator 5	0.00	-1.8
27371	SH2 domain protein 2A	0.01	-1.8
15018	ility 2, Q region locus 2; similar to MHC class Ib antigen; histocompatibility 2, Q region locus 7; histocompatibility 2,	0.01	-1.8
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.01	-1.8
246177	myosin IG	0.00	-1.8
213233	TAP binding protein-like	0.01	-1.8
18950	similar to purine nucleoside phosphorylase; purine-nucleoside phosphorylase 1	0.03	-1.8
13030	cathepsin B	0.00	-1.8
83408	similar to immunity-associated nucleotide 4; GTPase, IMAP family member 3	0.00	-1.8
12363	caspase 4, apoptosis-related cysteine peptidase; hypothetical protein LOC100044206	0.01	-1.8
13449	docking protein 2	0.00	-1.8
18826	lymphocyte cytosolic protein 1	0.01	-1.8
269582	claspin homolog (Xenopus laevis)	0.00	-1.8
26570	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	0.00	-1.8
56644	C-type lectin domain family 7, member a	0.01	-1.8
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.01	-1.8
319167	stone cluster 1, H2ah; histone cluster 1, H2ai; similar to histone 2a; histone cluster 1, H2an; histone cluster 1, H2ac	0.00	-1.9
18854	promyelocytic leukemia	0.02	-1.9
14960	histocompatibility 2, class II antigen A, alpha	0.00	-1.9
14130	Fc receptor, IgG, low affinity IIb	0.02	-1.9
19141	legumain	0.01	-1.9
14991	histocompatibility 2, M region locus 3	0.02	-1.9
69169	Fas apoptotic inhibitory molecule 3	0.03	-1.9
74153	ubiquitin-like modifier activating enzyme 7	0.01	-1.9
14824	granulin	0.01	-1.9
171207	Rho GTPase activating protein 4	0.00	-1.9
102595	pleckstrin homology domain containing, family O member 2	0.01	-1.9
246707	elastin microfibril interfacier 2	0.00	-1.9
15374	hematological and neurological expressed sequence 1	0.00	-1.9
327957	RIKEN cD A430084P05 gene	0.01	-1.9
231712	TRAF type zinc finger domain containing 1	0.02	-1.9
16912	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctiol peptidase 2)	0.00	-1.9
67177	chromatin licensing and D replication factor 1	0.00	-1.9
68743	anillin, actin binding protein	0.00	-1.9
19171	proteasome (prosome, macropain) subunit, beta type 10	0.01	-1.9
12229	Bruton agammaglobulinemia tyrosine kise	0.00	-1.9
239743	kelch-like 6 (Drosophila)	0.00	-1.9
102545	CKLF-like MARVEL transmembrane domain containing 7	0.01	-1.9
14728	leukocyte immunoglobulin-like receptor, subfamily B, member 4	0.00	-1.9
12046	B-cell leukemia/lymphoma 2 related protein A1c	0.00	-1.9
14190	fibrinogen-like protein 2	0.00	-1.9
68298	non-SMC condensin I complex, subunit D2	0.00	-1.9
20351	cytoplasmic domain, (semaphorin) 4A	0.01	-1.9
12501	CD3 antigen, epsilon polypeptide	0.00	-1.9
433016	predicted gene 5483	0.00	-1.9
110033	kinesin family member 22	0.00	-1.9
17381	matrix metallopeptidase 12	0.00	-1.9
239743	kelch-like 6 (Drosophila)	0.00	-1.9
52673	DNA segment, Chr 13, ERATO Doi 608, expressed	0.01	-1.9
12702	suppressor of cytokine siglling 3	0.01	-1.9
219132	dicted gene 6904; predicted gene 4902; DNA segment, Chr 14, ERATO Doi 668, expressed; PHD finger protein 11	0.00	-1.9
234779	phospholipase C, gamma 2	0.00	-1.9
71607	sorting nexin 20	0.00	-1.9

67895	pyrophosphatase (inorganic) 1	0.01	-1.9
16792	lysosomal-associated protein transmembrane 5	0.00	-1.9
16906	lamin B1	0.01	-1.9
319176	histone cluster 2, H2ac	0.00	-1.9
11799	baculoviral IAP repeat-containing 5	0.00	-1.9
12978	colony stimulating factor 1 receptor	0.01	-1.9
12524	CD86 antigen	0.02	-1.9
225594	il protein LOC100044195; predicted gene 4841; similar to immunity-related GTPase family, cinema 1	0.00	-1.9
667370	RIKEN cDNA I830012O16 gene	0.02	-1.9
16197	interleukin 7 receptor	0.00	-1.9
12363	caspase 4, apoptosis-related cysteine peptidase; hypothetical protein LOC100044206	0.03	-1.9
27226	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.00	-1.9
16881	ligase I, D, ATP-dependent	0.00	-1.9
30935	torsin family 3, member A	0.00	-1.9
71819	kinesin family member 23	0.00	-1.9
15368	heme oxygenase (decycling) 1	0.00	-1.9
65972	interferon gamma inducible protein 30	0.00	-1.9
16149	associated)	0.01	-1.9
17313	matrix Gla protein	0.00	-1.9
16498	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0.00	-1.9
18727	paired-Ig-like receptor A4	0.00	-1.9
20847	sigl transducer and activator of transcription 2	0.02	-1.9
73804	kinesin family member 2C	0.00	-1.9
235712	MAS-related GPR, member A2B	0.02	-1.9
108670	epithelial stromal interaction 1 (breast)	0.00	-2.0
15170	protein tyrosine phosphatase, non-receptor type 6	0.00	-2.0
19156	prosaposin	0.00	-2.0
23962	2'-5' oligoadenylate synthetase-like 2	0.02	-2.0
70785	DENN/MADD domain containing 1C	0.00	-2.0
70218	kinesin family member 18B	0.00	-2.0
18301	FXRD domain-containing ion transport regulator 5	0.01	-2.0
14793	cell division cycle associated 3	0.00	-2.0
110168	G protein-coupled receptor 18	0.01	-2.0
17002	lactotransferrin	0.03	-2.0
269582	claspin homolog (Xenopus laevis)	0.00	-2.0
12523	CD84 antigen	0.00	-2.0
14528	GTP cyclohydrolase 1	0.01	-2.0
27261	docking protein 3	0.00	-2.0
230787	cD sequence BC013712	0.00	-2.0
12332	capping protein (actin filament), gelsolin-like	0.00	-2.0
107995	cell division cycle 20 homolog (S. cerevisiae)	0.00	-2.0
22041	transferrin	0.00	-2.0
19200	proline-serine-threonine phosphatase-interacting protein 1	0.00	-2.0
21355	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.01	-2.0
268697	cyclin B1	0.00	-2.0
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.01	-2.0
13717	elastin	0.00	-2.0
384009	GLI pathogenesis-related 2	0.00	-2.0
13014	cystatin B	0.00	-2.0
60530	fidgetin-like 1	0.00	-2.0
74191	purinergic receptor P2Y, G-protein coupled 13	0.00	-2.0
100340	sphingomyelin phosphodiesterase, acid-like 3B	0.01	-2.0
74096	hydrogen voltage-gated channel 1	0.00	-2.0
16822	lymphocyte cytosolic protein 2	0.00	-2.0
12526	CD8 antigen, beta chain 1	0.00	-2.0
13057	cytochrome b-245, alpha polypeptide	0.01	-2.0
93695	glycoprotein (transmembrane) nmb	0.00	-2.0
12774	chemokine (C-C motif) receptor 5	0.00	-2.0
54445	unc-93 homolog B1 (C. elegans)	0.00	-2.0
21810	transforming growth factor, beta induced	0.00	-2.0
321019	G protein-coupled receptor 183	0.00	-2.0
71982	sorting nexin 10	0.03	-2.0
12362	caspase 1; hypothetical protein LOC100044207	0.01	-2.0
56193	pleckstrin	0.00	-2.0
170743	toll-like receptor 7	0.00	-2.0
11898	argininosuccinate synthetase 1	0.00	-2.0
56045	SAM domain and HD domain, 1	0.02	-2.0
12721	coronin, actin binding protein 1A	0.00	-2.0
27056	interferon regulatory factor 5	0.00	-2.0
108995	TBC1 domain family, member 10c	0.00	-2.0
70024	minichromosome maintenance deficient 10 (S. cerevisiae)	0.00	-2.1
15040	histocompatibility 2, T region locus 23; similar to RT1 class Ib, locus H2-Q-like, grc region	0.00	-2.1

105855	NCK associated protein 1 like	0.00	-2.1
20343	selectin, lymphocyte	0.01	-2.1
16948	lysyl oxidase	0.03	-2.1
20556	schlafen 2	0.00	-2.1
12511	CD6 antigen	0.00	-2.1
12475	CD14 antigen	0.03	-2.1
16362	interferon regulatory factor 1	0.02	-2.1
20345	selectin, platelet (p-selectin) ligand	0.00	-2.1
54141	sperm associated antigen 5	0.00	-2.1
17218	minichromosome maintenance deficient 5, cell division cycle 46 (<i>S. cerevisiae</i>)	0.00	-2.1
20296	chemokine (C-C motif) ligand 2	0.01	-2.1
11799	baculoviral IAP repeat-containing 5	0.00	-2.1
18703	polymeric immunoglobulin receptor	0.00	-2.1
13537	dual specificity phosphatase 2	0.01	-2.1
625360	similar to 2-cell-stage, variable group, member 3	0.00	-2.1
16362	interferon regulatory factor 1	0.01	-2.1
547253	poly (ADP-ribose) polymerase family, member 14	0.02	-2.1
107995	cell division cycle 20 homolog (<i>S. cerevisiae</i>)	0.00	-2.1
11816	apolipoprotein E	0.00	-2.1
20491	src-like adaptor	0.00	-2.1
17387	matrix metalloproteinase 14 (membrane-inserted)	0.00	-2.1
13034	cathepsin E	0.00	-2.1
15959	interferon-induced protein with tetratricopeptide repeats 3	0.00	-2.1
18751	protein kise C, beta	0.00	-2.1
20878	aurora kise A	0.00	-2.1
24110	ubiquitin specific peptidase 18	0.00	-2.1
14961	histocompatibility 2, class II antigen A, beta 1	0.00	-2.1
17219	minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>)	0.00	-2.1
24055	SH3-domain binding protein 2	0.00	-2.2
11690	arachidate 5-lipoxygenase activating protein	0.00	-2.2
12502	CD3 antigen, gamma polypeptide	0.00	-2.2
12986	colony stimulating factor 3 receptor (granulocyte)	0.00	-2.2
15900	interferon regulatory factor 8	0.01	-2.2
15212	hexosaminidase B	0.00	-2.2
622408	predicted gene 6320	0.00	-2.2
233571	pyrimidinergic receptor P2Y, G-protein coupled, 6	0.00	-2.2
67844	RAB32, member RAS oncogene family	0.00	-2.2
20202	S100 calcium binding protein A9 (calgranulin B)	0.00	-2.2
13040	cathepsin S	0.00	-2.2
268697	cyclin B1	0.00	-2.2
14969	histocompatibility 2, class II antigen E beta	0.01	-2.2
78416	ribonuclease, Rse A family, 6	0.00	-2.2
27060	T-cell, immune regulator 1, ATPase, H ⁺ transporting, lysosomal V0 protein A3	0.00	-2.2
12615	centromere protein A	0.00	-2.2
80861	DEXH (Asp-Glu-X-His) box polypeptide 58	0.01	-2.2
22040	three prime repair exonuclease 1	0.00	-2.2
15109	histidine ammonia lyase	0.00	-2.2
216869	arrestin, beta 2	0.00	-2.2
226652	Rho GTPase activating protein 30	0.00	-2.2
12524	CD86 antigen	0.00	-2.2
19419	RAS guanyl releasing protein 1	0.00	-2.2
21928	tumor necrosis factor, alpha-induced protein 2	0.01	-2.2
13038	cathepsin K	0.00	-2.2
16913	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	0.00	-2.2
12774	chemokine (C-C motif) receptor 5	0.00	-2.2
237256	zinc finger CCCH type containing 12D	0.00	-2.2
21810	transforming growth factor, beta induced	0.00	-2.2
14191	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0.00	-2.2
21838	thymus cell antigen 1, theta	0.00	-2.2
16612	kallikrein 1	0.00	-2.2
14998	histocompatibility 2, class II, locus DMA	0.00	-2.2
17085	lymphocyte antigen 9	0.00	-2.2
228801	cD sequence U46068	0.00	-2.3
107995	cell division cycle 20 homolog (<i>S. cerevisiae</i>)	0.00	-2.3
64138	cathepsin Z	0.00	-2.3
14289	formyl peptide receptor 2	0.00	-2.3
21928	tumor necrosis factor, alpha-induced protein 2	0.00	-2.3
12534	cyclin-dependent kise 1	0.00	-2.3
76933	interferon, alpha-inducible protein 27 like 2A	0.00	-2.3
228801	cDNA sequence U46068	0.00	-2.3
12870	ceruloplasmin	0.00	-2.3
64138	cathepsin Z	0.00	-2.3

78317	coiled-coil domain containing 88B	0.00	-2.3
74481	basic leucine zipper transcription factor, ATF-like 2	0.01	-2.3
19039	lectin, galactoside-binding, soluble, 3 binding protein	0.00	-2.3
54445	unc-93 homolog B1 (C. elegans)	0.00	-2.3
14968	histocompatibility 2, class II antigen E alpha	0.00	-2.3
21785	trefoil factor 2 (spasmodic protein 1)	0.00	-2.3
74558	predicted gene 1966; predicted gene 8995; GTPase, very large interferon inducible 1	0.01	-2.3
74568	mixed lineage kise domain-like	0.00	-2.3
16994	lymphotoxin B	0.00	-2.3
16323	inhibin beta-A	0.00	-2.3
19354	RAS-related C3 botulinum substrate 2	0.00	-2.4
22177	TYRO protein tyrosine kise binding protein	0.00	-2.4
279572	toll-like receptor 13	0.00	-2.4
16963	chemokine (C motif) ligand 1	0.00	-2.4
80885	niacin receptor 1	0.00	-2.4
17916	myosin IF	0.00	-2.4
73149	C-type lectin domain family 4, member a3	0.00	-2.4
12259	complement component 1, q subcomponent, alpha polypeptide	0.00	-2.4
11799	baculoviral IAP repeat-containing 5	0.00	-2.4
72042	coactosin-like 1 (Dictyostelium)	0.00	-2.4
16818	lymphocyte protein tyrosine kise	0.00	-2.4
56743	linker for activation of T cells family, member 2	0.00	-2.4
21877	thymidine kise 1	0.00	-2.4
14129	Fc receptor, IgG, high affinity I	0.01	-2.4
16362	interferon regulatory factor 1	0.00	-2.4
14999	histocompatibility 2, class II, locus Mb1	0.00	-2.4
22376	Wiskott-Aldrich syndrome homolog (human)	0.00	-2.4
212032	hexokise 3	0.00	-2.4
21946	peptidoglycan recognition protein 1	0.00	-2.4
17357	MARCKS-like 1	0.00	-2.4
219132	dicted gene 6904; predicted gene 4902; DNA segment, Chr 14, ERATO Doi 668, expressed; PHD finger protein 11	0.00	-2.4
15170	protein tyrosine phosphatase, non-receptor type 6	0.00	-2.4
54483	Mediterranean fever	0.00	-2.5
16819	lipocalin 2	0.00	-2.5
65221	solute carrier family 15, member 3	0.00	-2.5
21354	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.00	-2.5
12508	CD53 antigen	0.00	-2.5
12721	coronin, actin binding protein 1A	0.00	-2.5
20716	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0.02	-2.5
21973	topoisomerase (D) II alpha	0.00	-2.5
229900	guanylate binding protein 6	0.01	-2.5
20201	S100 calcium binding protein A8 (calgranulin A)	0.00	-2.5
108907	nucleolar and spindle associated protein 1	0.00	-2.5
52033	PDZ binding kise	0.00	-2.5
68891	CD177 antigen	0.00	-2.5
14961	histocompatibility 2, class II antigen A, beta 1	0.00	-2.5
13733	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0.00	-2.5
22169	cytidine monophosphate (UMP-CMP) kise 2, mitochondrial	0.00	-2.5
641240	histocompatibility 2, class II antigen A, beta 1; response to metastatic cancers 2	0.00	-2.5
107321	leupaxin	0.00	-2.5
11857	Rho, GDP dissociation inhibitor (GDI) beta	0.00	-2.5
16643	killer cell lectin-like receptor, subfamily D, member 1	0.00	-2.5
17858	myxovirus (influenza virus) resistance 2	0.01	-2.5
15958	interferon-induced protein with tetratricopeptide repeats 2	0.01	-2.5
231655	2'-5' oligoadenylate synthetase-like 1	0.00	-2.6
18140	ubiquitin-like, containing PHD and RING finger domains, 1	0.00	-2.6
14131	Fc receptor, IgG, low affinity III	0.00	-2.6
14204	interleukin 4 induced 1	0.00	-2.6
23962	2'-5' oligoadenylate synthetase-like 2	0.01	-2.6
20846	sigl transducer and activator of transcription 1	0.00	-2.6
24110	ubiquitin specific peptidase 18; similar to ubiquitin specific protease UBP43	0.01	-2.6
12774	chemokine (C-C motif) receptor 5	0.00	-2.6
20315	chemokine (C-X-C motif) ligand 12	0.01	-2.6
12721	coronin, actin binding protein 1A	0.00	-2.6
20308	chemokine (C-C motif) ligand 9	0.00	-2.6
21926	tumor necrosis factor	0.00	-2.6
83433	triggering receptor expressed on myeloid cells 2	0.00	-2.6
319165	stone cluster 1, H2ah; histone cluster 1, H2ai; similar to histone 2a; histone cluster 1, H2an; histone cluster 1, H2ac	0.00	-2.6
16154	interleukin 10 receptor, alpha	0.00	-2.6
435565	Interferon inducible GTPase 1B	0.00	-2.6
319173	histone cluster 1, H2af	0.00	-2.7
20846	sigl transducer and activator of transcription 1	0.01	-2.7

13041	cathepsin W	0.00	-2.7
20293	chemokine (C-C motif) ligand 12	0.00	-2.7
13051	chemokine (C-X3-C) receptor 1	0.00	-2.7
20555	schlafen 1	0.00	-2.7
15958	interferon-induced protein with tetratricopeptide repeats 2	0.01	-2.7
19695	regenerating islet-derived 3 gamma	0.00	-2.7
56620	C-type lectin domain family 4, member n	0.00	-2.7
14744	G-protein coupled receptor 65	0.00	-2.7
269799	C-type lectin domain family 4, member a1	0.00	-2.7
20311	chemokine (C-X-C motif) ligand 5	0.00	-2.7
246728	2'-5' oligoadenylate synthetase 2	0.00	-2.7
22324	vav 1 oncogene	0.00	-2.7
100034251	predicted gene 11428	0.00	-2.8
80910	G protein-coupled receptor 84	0.00	-2.8
14017	ecotropic viral integration site 2a	0.00	-2.8
69550	bone marrow stromal cell antigen 2	0.00	-2.8
23880	FYN binding protein	0.00	-2.8
17972	neutrophil cytosolic factor 4	0.00	-2.8
104759	phospholipase D family, member 4	0.00	-2.8
626578	guanylate-binding protein 10; RIKEN cDNA 5830443L24 gene	0.02	-2.8
21928	tumor necrosis factor, alpha-induced protein 2	0.00	-2.8
15163	hematopoietic cell specific Lyn substrate 1	0.00	-2.8
219131	PHD finger protein 11	0.00	-2.8
16988	leukocyte specific transcript 1	0.00	-2.8
231507	placenta-specific 8	0.00	-2.8
24088	toll-like receptor 2	0.00	-2.8
14130	Fc receptor, IgG, low affinity IIb	0.00	-2.8
110956	D segment, Chr 17, human D6S56E 5	0.00	-2.8
18405	orosomucoid 1	0.00	-2.8
319169	histone cluster 1, H2ak	0.00	-2.8
14961	histocompatibility 2, class II antigen A, beta 1	0.00	-2.9
12265	class II transactivator	0.00	-2.9
24110	ubiquitin specific peptidase 18; similar to ubiquitin specific protease UBP43	0.00	-2.9
319168	histone cluster 1, H2ah	0.00	-2.9
12986	colony stimulating factor 3 receptor (granulocyte)	0.00	-2.9
20715	serine (or cysteine) peptidase inhibitor, clade A, member 3G	0.02	-2.9
102084	NLR family, CARD domain containing 5	0.00	-2.9
233406	protein regulator of cytokinesis 1	0.00	-2.9
72054	cytochrome P450, family 4, subfamily f, polypeptide 18	0.00	-3.0
12721	coronin, actin binding protein 1A	0.00	-3.0
21822	T-cell specific GTPase	0.01	-3.0
14469	guanylate binding protein 2	0.00	-3.0
72310	tural killer cell group 7 sequence	0.00	-3.0
26388	interferon activated gene 202B	0.00	-3.0
319170	histone cluster 1, H2an	0.00	-3.0
319171	stone cluster 1, H2ah; histone cluster 1, H2ai; similar to histone 2a; histone cluster 1, H2an; histone cluster 1, H2ac	0.00	-3.0
72054	cytochrome P450, family 4, subfamily f, polypeptide 18	0.00	-3.1
219131	PHD finger protein 11	0.00	-3.1
74748	SLAM family member 8	0.00	-3.1
68774	membrane-spanning 4-domains, subfamily A, member 6D	0.00	-3.1
20303	chemokine (C-C motif) ligand 4	0.00	-3.1
227659	solute carrier family 2 (facilitated glucose transporter), member 6	0.00	-3.1
382045	G protein-coupled receptor 114	0.00	-3.1
16181	interleukin 1 receptor antagonist	0.00	-3.1
56644	C-type lectin domain family 7, member a	0.00	-3.1
12642	cholesterol 25-hydroxylase	0.00	-3.1
23960	2'-5' oligoadenylate synthetase 1G	0.00	-3.1
14962	complement factor B	0.00	-3.2
54123	interferon regulatory factor 7	0.00	-3.2
98365	SLAM family member 9	0.00	-3.2
218630	cyclin O	0.00	-3.3
12515	CD69 antigen	0.00	-3.3
12514	CD68 antigen	0.00	-3.3
15959	interferon-induced protein with tetratricopeptide repeats 3	0.00	-3.3
13733	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0.00	-3.3
246256	Fc receptor, IgG, low affinity IV	0.00	-3.3
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.00	-3.3
55932	guanylate binding protein 3	0.00	-3.3
12260	complement component 1, q subcomponent, beta polypeptide	0.00	-3.4
80910	G protein-coupled receptor 84	0.00	-3.4
23833	CD52 antigen	0.00	-3.4
12262	complement component 1, q subcomponent, C chain	0.00	-3.4

17474	C-type lectin domain family 4, member d	0.00	-3.4
20304	chemokine (C-C motif) ligand 5	0.00	-3.5
231655	2'-5' oligoadenylate synthetase-like 1	0.00	-3.5
15944	immunity-related GTPase family M member 1	0.00	-3.5
17084	lymphocyte antigen 86	0.00	-3.5
54396	immunity-related GTPase family M member 2	0.00	-3.6
55932	guanylate binding protein 3	0.00	-3.7
15930	indoleamine 2,3-dioxygenase 1	0.03	-3.7
60533	CD274 antigen	0.00	-3.8
11629	allograft inflammatory factor 1	0.00	-3.8
14468	guanylate binding protein 1	0.00	-3.8
11810	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	0.00	-3.9
15953	interferon gamma inducible protein 47	0.00	-4.0
20302	chemokine (C-C motif) ligand 3	0.00	-4.0
11629	allograft inflammatory factor 1	0.00	-4.1
23960	2'-5' oligoadenylate synthetase 1G	0.00	-4.2
68891	CD177 antigen	0.00	-4.2
229898	guanylate binding protein 5	0.00	-4.4
18406	orosomucoid 2	0.00	-4.5
55985	chemokine (C-X-C motif) ligand 13	0.00	-4.7
20306	chemokine (C-C motif) ligand 7	0.00	-4.7
10038882	ISG15 ubiquitin-like modifier	0.00	-4.8
109225	membrane-spanning 4-domains, subfamily A, member 7	0.00	-4.8
20293	chemokine (C-C motif) ligand 12	0.00	-4.8
68774	membrane-spanning 4-domains, subfamily A, member 6D	0.00	-4.9
433470	expressed sequence AA467197	0.00	-4.9
21857	tissue inhibitor of metalloproteinase 1	0.00	-4.9
20307	chemokine (C-C motif) ligand 8	0.00	-4.9
21857	tissue inhibitor of metalloproteinase 1	0.00	-5.0
215900	family with sequence similarity 26, member F	0.00	-5.7
57262	resistin like alpha	0.00	-5.7
16145	interferon gamma induced GTPase	0.00	-6.0
20303	chemokine (C-C motif) ligand 4	0.00	-7.7
58185	radical S-adenosyl methionine domain containing 2	0.00	-8.1
20210	serum amyloid A 3	0.00	-8.9
15945	chemokine (C-X-C motif) ligand 10	0.00	-10.9
17329	chemokine (C-X-C motif) ligand 9	0.00	-22.6

Regulated at 4 dpi in WT vs. ΔPT and WT vs. ΔPT^{high}

20210	serum amyloid A 3	0.00	45.8	0.00	6.1
14825	chemokine (C-X-C motif) ligand 1	0.00	18.2	0.00	8.0
17329	chemokine (C-X-C motif) ligand 9	0.00	14.9	0.00	6.2
21857	tissue inhibitor of metalloproteinase 1	0.00	12.1	0.00	5.0
21857	tissue inhibitor of metalloproteinase 1	0.00	11.9	0.00	4.9
16176	interleukin 1 beta	0.00	11.0	0.00	6.0
15945	chemokine (C-X-C motif) ligand 10	0.00	10.2	0.00	6.7
23985	solute carrier family 26, member 4	0.00	9.3	0.00	5.4
20306	Ccl7 chemokine (C-C motif) ligand 7	0.00	8.5	0.00	6.5
16819	lipocalin 2	0.00	8.2	0.01	2.4
20716	Serpina3n serine (or cysteine) peptidase inhibitor, clade A, member 3N	0.00	7.8	0.00	4.6
55985	chemokine (C-X-C motif) ligand 13	0.00	7.0	0.04	2.8
12475	CD14 antigen	0.00	6.5	0.00	3.4
20303	chemokine (C-C motif) ligand 4	0.00	5.7	0.01	2.7
229898	guanylate binding protein 5	0.00	5.6	0.00	3.1
16145	interferon gamma induced GTPase	0.00	5.4	0.00	3.5
20311	Cxcl5 chemokine (C-X-C motif) ligand 5	0.00	5.4	0.00	4.2
12642	cholesterol 25-hydroxylase	0.00	5.1	0.01	2.8
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.00	4.8	0.00	3.5
14204	interleukin 4 induced 1	0.00	4.8	0.01	2.3
215900	family with sequence similarity 26, member F	0.00	4.7	0.00	3.8
68774	membrane-spanning 4-domains, subfamily A, member 6D	0.00	4.5	0.01	2.8
76905	leucine-rich alpha-2-glycoprotein 1	0.00	4.5	0.00	2.5
60533	CD274 antigen	0.00	4.2	0.00	3.3
21928	tumor necrosis factor, alpha-induced protein 2	0.00	4.1	0.00	2.9
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.00	4.0	0.00	3.0
17474	C-type lectin domain family 4, member d	0.00	3.9	0.00	2.7
14468	guanylate binding protein 1	0.00	3.9	0.00	3.1
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.00	3.8	0.00	2.9
319168	histone cluster 1, H2ah	0.00	3.8	0.04	2.1
110956	D segment, Chr 17, human D6S56E 5	0.00	3.7	0.00	2.2
546546	serine (or cysteine) peptidase inhibitor, clade A, member 3H	0.00	3.7	0.00	3.0
12702	suppressor of cytokine signaling 3	0.00	3.7	0.00	2.5

20293	chemokine (C-C motif) ligand 12	0.00	3.7	0.00	2.4
15944	immunity-related GTPase family M member 1	0.00	3.7	0.02	2.1
58185	radical S-adenosyl methionine domain containing 2	0.00	3.6	0.04	2.0
20201	S100 calcium binding protein A8 (calgranulin A)	0.00	3.6	0.00	2.4
15930	indoleamine 2,3-dioxygenase 1	0.00	3.6	0.00	3.1
21928	tumor necrosis factor, alpha-induced protein 2	0.00	3.6	0.00	2.4
71893	NADPH oxidase organizer 1	0.00	3.5	0.02	2.0
319170	histone cluster 1, H2an	0.00	3.4	0.01	2.1
54396	immunity-related GTPase family M member 2	0.00	3.4	0.00	2.6
233406	protein regulator of cytokinesis 1	0.00	3.4	0.00	2.2
319173	histone cluster 1, H2af	0.00	3.4	0.01	2.0
12986	colony stimulating factor 3 receptor (granulocyte)	0.00	3.3	0.00	3.2
18140	ubiquitin-like, containing PHD and RING finger domains, 1	0.00	3.3	0.01	1.9
14469	guanylate binding protein 2	0.00	3.3	0.00	2.3
20202	S100 calcium binding protein A9 (calgranulin B)	0.00	3.2	0.00	2.3
12870	ceruloplasmin	0.00	3.2	0.02	1.8
319171	histone cluster 1, H2ap	0.00	3.1	0.01	2.1
18413	oncostatin M	0.00	3.1	0.00	2.5
100034251	predicted gene 11428	0.00	3.1	0.02	1.9
52033	PDZ binding kise	0.00	3.1	0.00	2.1
55932	guanylate binding protein 3	0.00	3.1	0.01	2.1
218630	cyclin O	0.00	3.0	0.02	1.5
15953	interferon gamma inducible protein 47	0.00	3.0	0.00	2.5
20310	chemokine (C-X-C motif) ligand 2	0.00	2.9	0.00	2.5
72054	CYP4F18	0.00	2.9	0.01	2.1
15458	hemopexin	0.00	2.9	0.00	2.2
68774	membrane-spanning 4-domains, subfamily A, member 6D	0.00	2.9	0.03	2.0
12765	chemokine (C-X-C motif) receptor 2	0.00	2.9	0.00	2.7
20302	chemokine (C-C motif) ligand 3	0.00	2.9	0.00	2.3
16181	interleukin 1 receptor antagonist	0.00	2.9	0.00	2.3
55932	guanylate binding protein 3	0.00	2.8	0.01	2.2
626578	guanylate binding protein 10	0.00	2.8	0.00	2.2
12986	colony stimulating factor 3 receptor (granulocyte)	0.00	2.8	0.00	2.1
13123	cytochrome P450, family 7, subfamily b, polypeptide 1	0.00	2.8	0.00	2.1
229900	guanylate binding protein 7	0.00	2.8	0.00	2.3
12265	class II transactivator	0.00	2.8	0.01	2.0
74558	GTPase, very large interferon inducible 1	0.00	2.8	0.00	2.0
11799	baculoviral IAP repeat-containing 5	0.00	2.7	0.01	1.7
20715	serine (or cysteine) peptidase inhibitor, clade A, member 3G	0.00	2.7	0.01	2.1
77125	interleukin 33	0.00	2.7	0.00	2.7
12774	chemokine (C-C motif) receptor 5	0.00	2.7	0.02	1.9
231507	placenta-specific 8	0.00	2.7	0.03	1.9
433470	expressed sequence AA467197	0.00	2.7	0.02	1.7
74748	SLAM family member 8	0.00	2.6	0.02	2.0
74481	basic leucine zipper transcription factor, ATF-like 2	0.00	2.6	0.00	2.4
107995	cell division cycle 20 homolog (S. cerevisiae)	0.00	2.6	0.00	2.2
15439	haptoglobin	0.00	2.6	0.01	2.0
21928	Tnfrsf25 tumor necrosis factor, alpha-induced protein 2	0.00	2.6	0.00	2.1
21822	T-cell specific GTPase	0.00	2.6	0.01	2.0
16424	inter-alpha trypsin inhibitor, heavy chain 1	0.00	2.6	0.00	2.2
434341	NLR family, CARD domain containing 5	0.00	2.6	0.03	1.7
80885	niacin receptor 1	0.00	2.6	0.02	1.9
51797	cytidine 5'-triphosphate synthase	0.00	2.6	0.00	2.3
21810	transforming growth factor, beta induced	0.00	2.6	0.00	2.1
24088	toll-like receptor 2	0.00	2.6	0.03	1.7
238393	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0.00	2.5	0.00	2.3
20296	chemokine (C-C motif) ligand 2	0.00	2.5	0.00	2.5
17219	minichromosome maintenance deficient 6 (S. cerevisiae)	0.00	2.5	0.00	2.0
21810	transforming growth factor, beta induced	0.00	2.5	0.01	1.7
20846	sigl transducer and activator of transcription 1	0.00	2.5	0.02	1.9
20846	sigl transducer and activator of transcription 1	0.00	2.5	0.01	1.8
108907	nucleolar and spindle associated protein 1	0.00	2.5	0.00	1.7
18030	Nfil3 nuclear factor, interleukin 3, regulated	0.00	2.5	0.00	2.4
51797	cytidine 5'-triphosphate synthase	0.00	2.5	0.00	2.3
51797	cytidine 5'-triphosphate synthase	0.00	2.5	0.00	2.2
72054	CYP4F18	0.00	2.5	0.00	1.7
20315	chemokine (C-X-C motif) ligand 12	0.00	2.4	0.00	2.2
12051	B-cell leukemia/lymphoma 3	0.00	2.4	0.00	2.0
11629	allograft inflammatory factor 1	0.00	2.4	0.01	1.8
16477	Jun-B oncogene	0.00	2.4	0.00	1.7
21877	thymidine kise 1	0.00	2.4	0.02	1.6
433016	predicted gene 5483	0.00	2.4	0.00	2.1

233079	free fatty acid receptor 2	0.00	2.4	0.00	1.8
65221	solute carrier family 15, member 3	0.00	2.4	0.01	1.8
80859	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	0.00	2.4	0.01	1.6
12534	cyclin-dependent kinase 1	0.00	2.4	0.01	1.7
14728	leukocyte immunoglobulin-like receptor, subfamily B, member 4	0.00	2.4	0.03	1.7
16362	interferon regulatory factor 1	0.00	2.4	0.00	1.9
17218	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0.00	2.3	0.00	2.0
107995	cell division cycle 20 homolog (S. cerevisiae)	0.00	2.3	0.00	1.7
16193	interleukin 6	0.00	2.3	0.00	2.2
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.00	2.3	0.02	1.9
246707	elastin microfibril interfacer 2	0.00	2.3	0.03	1.6
235712	MAS-related GPR, member A2B	0.00	2.3	0.00	2.4
21973	topoisomerase (D) II alpha	0.00	2.3	0.02	1.6
71982	sorting nexin 10	0.00	2.3	0.01	1.6
17392	matrix metalloproteinase 3	0.00	2.2	0.00	2.2
21942	tumor necrosis factor receptor superfamily, member 9	0.00	2.2	0.00	1.9
11847	argase type II	0.00	2.2	0.01	1.8
231655	2'-5' oligoadenylate synthetase-like 1	0.00	2.2	0.05	1.7
212032	hexokinase 3	0.00	2.2	0.00	1.7
21929	tumor necrosis factor, alpha-induced protein 3	0.00	2.2	0.01	1.6
20555	schlafen 1	0.00	2.2	0.03	1.7
16362	interferon regulatory factor 1	0.00	2.2	0.00	2.1
21926	tumor necrosis factor	0.00	2.2	0.00	1.9
15439	haptoglobin	0.00	2.2	0.01	2.0
16948	lysyl oxidase	0.00	2.2	0.00	1.8
107995	cell division cycle 20 homolog (S. cerevisiae)	0.00	2.2	0.02	1.7
16362	interferon regulatory factor 1	0.00	2.2	0.00	2.2
14191	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0.00	2.2	0.01	1.8
76574	major facilitator superfamily domain containing 2A	0.00	2.2	0.01	1.8
16803	lipopolysaccharide binding protein	0.01	2.2	0.03	1.7
100689	spondin 2, extracellular matrix protein	0.00	2.1	0.00	2.4
245195	resistin like gamma	0.00	2.1	0.01	1.5
225594	GTPase family, cinema 1	0.00	2.1	0.00	2.1
23882	growth arrest and D-damage-inducible 45 gamma	0.00	2.1	0.00	2.0
16906	lamin B1	0.00	2.1	0.01	1.5
547253	poly (ADP-ribose) polymerase family, member 14	0.00	2.1	0.04	1.7
70024	minichromosome maintenance deficient 10 (S. cerevisiae)	0.00	2.1	0.02	1.6
240913	a disintegrin-like and metalloproteinase with thrombospondin type 1 motif, 4	0.00	2.1	0.00	2.0
230738	zinc finger CCCH type containing 12A	0.00	2.1	0.00	1.7
14528	GTP cyclohydrolase 1	0.00	2.1	0.01	1.6
22375	tryptophanyl-tRNA synthetase; similar to tryptophanyl-tRNA synthetase	0.00	2.1	0.00	1.8
20293	chemokine (C-C motif) ligand 12	0.00	2.1	0.01	1.8
71893	DPH oxidase organizer 1	0.00	2.1	0.04	1.6
22041	transferrin	0.00	2.1	0.01	1.8
67895	pyrophosphatase (inorganic) 1	0.00	2.1	0.00	1.7
12363	caspase 4, apoptosis-related cysteine peptidase; hypothetical protein LOC100044206	0.00	2.1	0.04	1.5
384009	GLI pathogenesis-related 2	0.00	2.1	0.01	1.6
22375	tryptophanyl-tRNA synthetase; similar to tryptophanyl-tRNA synthetase	0.00	2.1	0.01	1.6
74568	mixed lineage kinase domain-like	0.00	2.1	0.00	1.9
20211	serum amyloid A 4	0.00	2.0	0.00	2.0
80910	G protein-coupled receptor 84	0.00	2.0	0.00	1.7
57875	angiopoietin-like 4	0.00	2.0	0.00	2.1
12363	caspase 4, apoptosis-related cysteine peptidase; hypothetical protein LOC100044206	0.00	2.0	0.00	1.8
20303	chemokine (C-C motif) ligand 4	0.00	2.0	0.04	1.6
319176	histone cluster 2, H2ac	0.00	2.0	0.01	1.6
110033	kinesin family member 22	0.00	2.0	0.03	1.5
23882	growth arrest and D-damage-inducible 45 gamma	0.01	2.0	0.01	1.9
14187	aldo-keto reductase family 1, member B8	0.00	2.0	0.02	1.6
22256	uracil D glycosylase	0.00	2.0	0.00	1.5
67951	tubulin, beta 6	0.00	2.0	0.00	2.0
19171	proteasome (prosome, macropain) subunit, beta type 10	0.00	2.0	0.01	1.7
268697	cyclin B1	0.00	2.0	0.02	1.5
229900	guanylate binding protein 6	0.00	2.0	0.01	1.7
17219	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	0.00	2.0	0.01	1.7
20343	selectin, lymphocyte	0.00	2.0	0.03	1.6
229323	G protein-coupled receptor 171	0.00	2.0	0.01	1.6
435565	Interferon inducible GTPase 1B	0.01	2.0	0.01	1.8
72310	tural killer cell group 7 sequence	0.00	2.0	0.03	1.6
71819	kinesin family member 23	0.00	1.9	0.02	1.5
16362	interferon regulatory factor 1	0.00	1.9	0.00	1.9
17874	myeloid differentiation primary response gene 88	0.00	1.9	0.00	1.8
16323	inhibin beta-A	0.00	1.9	0.04	1.6

12981	colony stimulating factor 2 (granulocyte-macrophage)	0.00	1.9	0.00	1.8
26570	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	0.00	1.9	0.01	1.6
17357	MARCKS-like 1	0.00	1.9	0.00	1.9
14156	flap structure specific endonuclease 1	0.00	1.9	0.01	1.5
22329	vascular cell adhesion molecule 1	0.00	1.9	0.00	1.8
21355	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.00	1.9	0.03	1.6
20249	stearoyl-Coenzyme A desaturase 1	0.00	1.9	0.00	1.9
26415	mitogen-activated protein kinase 13	0.00	1.9	0.00	1.7
71780	myo-inositol 1-phosphate synthase A1	0.00	1.9	0.02	1.6
22324	vav 1 oncogene	0.00	1.9	0.01	1.6
76561	sorting nexin 7	0.00	1.9	0.00	2.1
21923	tenascin C	0.00	1.9	0.00	1.7
13078	cytochrome P450, family 1, subfamily b, polypeptide 1	0.00	1.9	0.03	1.6
19734	regulator of G-protein signaling 16	0.00	1.8	0.00	1.9
216161	strawberry notch homolog 2 (Drosophila)	0.00	1.8	0.00	1.8
66107	RIKEN cD 1100001G20 gene	0.00	1.8	0.00	1.6
21816	transglutaminase 1, K polypeptide	0.01	1.8	0.00	2.0
80914	uridine-cytidine kinase 2	0.00	1.8	0.00	1.7
27375	tight junction protein 3	0.00	1.8	0.01	1.6
11541	adenosine A2b receptor	0.00	1.8	0.02	1.6
56193	pleckstrin	0.00	1.8	0.02	1.5
21923	tenascin C	0.00	1.8	0.01	1.5
56722	LPS-induced TN factor	0.00	1.8	0.00	1.8
54483	Mediterranean fever	0.00	1.8	0.00	1.8
12615	centromere protein A	0.00	1.8	0.01	1.7
22695	zinc finger protein 36	0.00	1.8	0.04	1.5
67742	SAM domain, SH3 domain and nuclear localization signals, 1	0.01	1.8	0.05	1.6
621823	proteasome (prosome, macropain) 28 subunit, beta	0.00	1.8	0.00	1.9
18113	nicotinamide N-methyltransferase	0.00	1.8	0.00	1.8
16404	integrin alpha 7	0.00	1.8	0.00	1.6
58218	triggering receptor expressed on myeloid cells 3	0.00	1.8	0.00	1.6
18414	oncostatin M receptor	0.00	1.8	0.00	1.6
16178	interleukin 1 receptor, type II	0.01	1.8	0.00	1.7
240354	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.00	1.8	0.00	1.6
11839	amphiregulin	0.01	1.8	0.00	2.3
20344	selectin, platelet	0.01	1.8	0.00	1.8
69581	ras homolog gene family, member U	0.00	1.8	0.01	1.6
15368	heme oxygenase (decycling) 1	0.00	1.8	0.01	1.6
16995	leukotriene B4 receptor 1	0.00	1.8	0.01	1.5
11799	baculoviral IAP repeat-containing 5	0.01	1.8	0.03	1.6
14128	Fc receptor, IgE, low affinity II, alpha polypeptide	0.00	1.8	0.03	1.6
269582	claspin homolog (Xenopus laevis)	0.00	1.8	0.01	1.5
17216	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0.00	1.7	0.00	1.6
56619	C-type lectin domain family 4, member e	0.00	1.7	0.00	1.6
213233	TAP binding protein-like	0.00	1.7	0.00	1.8
78785	CAP-GLY domain containing linker protein family, member 4	0.00	1.7	0.00	1.5
69550	bone marrow stromal cell antigen 2	0.00	1.7	0.02	1.5
15978	interferon gamma	0.00	1.7	0.00	1.7
20656	superoxide dismutase 2, mitochondrial	0.00	1.7	0.00	1.7
404710	IQ motif containing GTPase activating protein 3	0.00	1.7	0.00	1.6
15978	interferon gamma	0.00	1.7	0.00	1.5
20351	cytoplasmic domain, (semaphorin) 4A	0.00	1.7	0.01	1.5
56619	C-type lectin domain family 4, member e	0.00	1.7	0.00	1.7
11799	baculoviral IAP repeat-containing 5	0.00	1.7	0.01	1.6
14058	coagulation factor X	0.00	1.7	0.00	1.5
19224	prostaglandin-endoperoxide synthase 1	0.01	1.7	0.01	1.5
16912	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	0.00	1.7	0.02	1.5
19186	proteasome (prosome, macropain) 28 subunit, alpha	0.00	1.7	0.01	1.5
68279	mucolipin 2	0.00	1.7	0.00	1.6
18035	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.00	1.7	0.01	1.6
20539	Slc7a5 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0.00	1.7	0.00	1.5
22271	uridine phosphorylase 1	0.00	1.6	0.00	1.8
50930	tumor necrosis factor (ligand) superfamily, member 14	0.00	1.6	0.00	1.6
223920	sterol O-acyltransferase 2	0.00	1.6	0.00	1.6
19224	prostaglandin-endoperoxide synthase 1	0.00	1.6	0.00	1.7
24108	ubiquitin D	0.04	1.6	0.01	1.6
56045	SAM domain and HD domain, 1	0.00	1.6	0.00	1.6
12575	cyclin-dependent kinase inhibitor 1A (P21)	0.00	1.6	0.00	1.6
19698	avian reticuloendotheliosis viral (v-rel) oncogene related B	0.00	1.6	0.01	1.6
11535	adrenomedullin	0.02	1.6	0.00	1.8
70025	acyl-CoA thioesterase 7	0.04	1.6	0.04	1.6
20309	chemokine (C-X-C motif) ligand 15	0.03	1.6	0.02	1.5

320982	ADP-ribosylation factor-like 4C	0.00	1.6	0.01	1.5
78388	major vault protein	0.00	1.6	0.00	1.6
16420	integrin beta 6	0.00	1.6	0.00	1.7
57444	interferon-stimulated protein	0.00	1.6	0.02	1.5
14120	fructose biphosphatase 2	0.00	1.6	0.00	1.7
56454	aldehyde dehydrogese 18 family, member A1	0.00	1.6	0.00	1.5
16420	integrin beta 6	0.01	1.5	0.00	1.7
66725	leucine-rich repeat kise 2	0.03	1.5	0.02	1.6
215615	arginyl aminopeptidase (aminopeptidase B)	0.00	1.5	0.00	1.6
68713	interferon induced transmembrane protein 1	0.00	1.5	0.00	1.5
73710	tubulin, beta 2a, pseudogene 2; tubulin, beta 2B	0.01	1.5	0.00	1.5
17392	matrix metalloproteinase 3	0.00	1.5	0.01	1.5
66953	cell division cycle associated 7	0.00	1.5	0.00	1.5
20848	similar to Stat3B; signal transducer and activator of transcription 3	0.00	1.5	0.00	1.7
14745	lysophosphatidic acid receptor 1	0.00	1.5	0.00	1.6
19246	protein tyrosine phosphatase, non-receptor type 1	0.05	1.5	0.01	1.6
20810	spermidine synthase	0.00	1.5	0.00	1.6
246316	leucine-rich repeat LGI family, member 2	0.00	1.5	0.00	1.5
13849	epoxide hydrolase 1, microsomal	0.00	-1.5	0.00	-1.5
319317	small nucleolar RNA host gene 11 (non-protein coding)	0.02	-1.5	0.03	-1.5
66873	RIKEN cD 1200009O22 gene	0.00	-1.5	0.02	-1.6
18627	period homolog 2 (Drosophila)	0.01	-1.6	0.03	-1.5
64929	sciellin	0.00	-1.7	0.00	-1.6
225642	gastrin releasing peptide	0.00	-1.9	0.01	-1.5
235674	acetyl-Coenzyme A acyltransferase 1B	0.00	-2.0	0.01	-1.5
71690	endothelial cell-specific molecule 1	0.00	-2.0	0.04	-2.1

Regulated at 4 dpi in WT vs. ΔPT but not in WT vs. ΔPT^{high}

57262	resistin like alpha	0.00	10.2
18405	orosomucoid 1	0.00	5.7
18406	orosomucoid 2	0.00	4.9
319169	histone cluster 1, H2ak	0.00	4.0
319165	histone cluster 1, H2ad	0.00	3.7
18703	polymeric immunoglobulin receptor	0.00	3.4
20307	chemokine (C-C motif) ligand 8	0.00	3.2
246256	Fc receptor, IgG, low affinity IV	0.00	3.1
14962	complement factor B	0.00	3.0
100038882	ISG15 ubiquitin-like modifier	0.00	2.8
26464	vanin 3	0.00	2.7
14131	Fc receptor, IgG, low affinity III	0.00	2.5
26388	interferon activated gene 202B	0.00	2.5
26464	vanin 3	0.00	2.5
21354	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.00	2.5
20308	chemokine (C-C motif) ligand 9	0.01	2.4
14130	Fc receptor, IgG, low affinity IIb	0.00	2.4
23960	2'-5' oligoadenylate synthetase 1G	0.00	2.3
56620	C-type lectin domain family 4, member n	0.00	2.3
17972	neutrophil cytosolic factor 4	0.00	2.3
11629	allograft inflammatory factor 1	0.00	2.2
14961	histocompatibility 2, class II antigen A, beta 1	0.02	2.2
12774	chemokine (C-C motif) receptor 5	0.00	2.2
15439	haptoglobin	0.00	2.2
14289	formyl peptide receptor 2	0.01	2.2
227659	solute carrier family 2 (facilitated glucose transporter), member 6	0.00	2.1
20750	secreted phosphoprotein 1	0.03	2.1
232983	chemokine (C-X-C motif) ligand 17	0.00	2.1
22177	TYRO protein tyrosine kise binding protein	0.00	2.1
319167	histone cluster 1, H2ag	0.00	2.1
74191	purinergic receptor P2Y, G-protein coupled 13	0.00	2.1
54123	interferon regulatory factor 7	0.00	2.1
64406	trans-acting transcription factor 5	0.00	2.1
56644	C-type lectin domain family 7, member a	0.03	2.1
73804	kinesin family member 2C	0.00	2.0
268697	cyclin B1	0.00	2.0
23833	CD52 antigen	0.01	2.0
19171	proteasome (prosome, macropain) subunit, beta type 10	0.00	2.0
232983	chemokine (C-X-C motif) ligand 17	0.02	2.0
12260	complement component 1, q subcomponent, beta polypeptide	0.00	2.0
11810	apolipoprotein B mR editing enzyme, catalytic polypeptide 1	0.01	2.0
15163	hematopoietic cell specific Lyn substrate 1	0.00	2.0
74137	NUAK family, SNF1-like kise, 2	0.00	2.0
246728	2'-5' oligoadenylate synthetase 2	0.00	2.0

14961	histocompatibility 2, class II antigen A, beta 1	0.00	2.0
15170	protein tyrosine phosphatase, non-receptor type 6	0.00	2.0
14999	histocompatibility 2, class II, locus Mb1	0.01	1.9
12738	claudin 2	0.01	1.9
12262	complement component 1, q subcomponent, C chain	0.00	1.9
26415	mitogen-activated protein kinase 13	0.00	1.9
100340	sphingomyelin phosphodiesterase, acid-like 3B	0.00	1.9
279572	toll-like receptor 13	0.01	1.9
67177	chromatin licensing and D replication factor 1	0.00	1.9
51788	H2A histone family, member Z	0.00	1.9
17084	lymphocyte antigen 86	0.02	1.9
68743	anillin, actin binding protein	0.00	1.9
56644	C-type lectin domain family 7, member a	0.00	1.9
20878	aurora kinase A	0.01	1.9
12721	coronin, actin binding protein 1A	0.01	1.9
382045	G protein-coupled receptor 114	0.00	1.9
12515	CD69 antigen	0.01	1.9
18727	paired-Ig-like receptor A4	0.02	1.9
13051	chemokine (C-X3-C) receptor 1	0.00	1.9
23962	2'-5' oligoadenylate synthetase-like 2	0.00	1.9
81910	ribosome binding protein 1	0.00	1.9
66102	chemokine (C-X-C motif) ligand 16	0.00	1.9
17829	mucin 1, transmembrane	0.03	1.9
20345	selectin, platelet (p-selectin) ligand	0.01	1.9
320832	signal-regulatory protein beta 1; similar to SIRP beta 1 cell surface protein	0.01	1.9
14793	cell division cycle associated 3	0.00	1.8
12266	complement component 3	0.00	1.8
22375	tryptophanyl-tRNA synthetase	0.00	1.8
73149	C-type lectin domain family 4, member a3	0.01	1.8
56150	MAD2 mitotic arrest deficient-like 1 (yeast)	0.00	1.8
106795	transcription factor 19	0.01	1.8
18636	complement factor properdin	0.00	1.8
16453	Janus kinase 3	0.00	1.8
22146	tubulin, alpha 1C	0.00	1.8
13537	dual specificity phosphatase 2	0.00	1.8
12984	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	0.00	1.8
12575	cyclin-dependent kinase inhibitor 1A (P21)	0.00	1.8
12654	chitinase 3-like 1	0.01	1.8
12774	chemokine (C-C motif) receptor 5	0.00	1.8
16988	leukocyte specific transcript 1	0.00	1.8
19354	RAS-related C3 botulinum substrate 2	0.01	1.8
14281	FBJ osteosarcoma oncogene	0.01	1.8
15270	H2A histone family, member X	0.00	1.8
71934	carbonic anhydrase 13	0.00	1.8
22171	thymidylate synthase	0.00	1.8
14776	glutathione peroxidase 2	0.01	1.8
17829	mucin 1, transmembrane	0.00	1.8
269582	claspin homolog (Xenopus laevis)	0.00	1.8
23880	FYN binding protein	0.01	1.8
16154	interleukin 10 receptor, alpha	0.00	1.8
16994	lymphotoxin B	0.02	1.8
14998	histocompatibility 2, class II, locus DMA	0.01	1.8
108096	solute carrier organic anion transporter family, member 1a5	0.00	1.8
12721	coronin, actin binding protein 1A	0.03	1.8
26425	nucleotide binding protein 1	0.00	1.8
19186	proteasome (prosome, macropain) 28 subunit, alpha	0.00	1.8
14017	ecotropic viral integration site 2a	0.02	1.8
22169	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0.00	1.8
64292	prostaglandin H synthase	0.00	1.7
626834	kallikrein related-peptidase 13	0.00	1.7
68195	ribonuclease T2B; ribonuclease T2A	0.00	1.7
230787	cD sequence BC013712	0.02	1.7
19106	Eif2ak2 eukaryotic translation initiation factor 2-alpha kinase 2	0.00	1.7
12122	BH3 interacting domain death agonist	0.00	1.7
16913	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	0.00	1.7
17392	matrix metalloproteinase 3	0.00	1.7
20847	sigl transducer and activator of transcription 2	0.00	1.7
78317	coiled-coil domain containing 88B	0.00	1.7
27375	tight junction protein 3	0.00	1.7
20304	chemokine (C-C motif) ligand 5	0.02	1.7
24110	ubiquitin specific peptidase 18; similar to ubiquitin specific protease UBP43	0.00	1.7
18037	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	0.00	1.7

268396	SH3 and PX domains 2B	0.00	1.7
13710	E74-like factor 3	0.00	1.7
13032	cathepsin C	0.00	1.7
54325	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0.01	1.7
54141	sperm associated antigen 5	0.00	1.7
16612	kallikrein 1	0.00	1.7
23960	2'-5' oligoadenylate synthetase 1G	0.00	1.7
19039	lectin, galactoside-binding, soluble, 3 binding protein	0.01	1.7
57783	TNFAIP3 interacting protein 1	0.00	1.7
12721	coronin, actin binding protein 1A	0.01	1.7
15900	interferon regulatory factor 8	0.00	1.7
14130	Fc receptor, IgG, low affinity IIb	0.01	1.7
13653	early growth response 1	0.01	1.7
17829	mucin 1, transmembrane	0.01	1.7
623474	RAD54 homolog B (S. cerevisiae)	0.00	1.7
71566	RIKEN cD 9030425E11 gene	0.01	1.7
109225	membrane-spanning 4-domains, subfamily A, member 7	0.02	1.7
13449	docking protein 2	0.00	1.7
75909	transmembrane protein 49	0.01	1.7
237256	zinc finger CCCH type containing 12D	0.00	1.7
216643	gamma-aminobutyric acid (GABA) A receptor, pi	0.00	1.7
70218	kinesin family member 18B	0.00	1.7
233571	pyrimidinergic receptor P2Y, G-protein coupled, 6	0.00	1.7
60530	fidgetin-like 1	0.00	1.7
18817	polo-like kinase 1 (Drosophila)	0.00	1.7
18173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.01	1.7
231655	2'-5' oligoadenylate synthetase-like 1	0.00	1.7
641240	hypothetical LOC641240	0.02	1.7
22172	thymidylate synthase, pseudogene	0.00	1.7
22321	valyl-tR synthetase	0.00	1.7
219131	PHD finger protein 11	0.02	1.7
214523	transmembrane protease, serine 4	0.01	1.6
108912	cell division cycle associated 2	0.00	1.6
21356	TAP binding protein	0.02	1.6
140474	mucin 4	0.00	1.6
16822	lymphocyte cytosolic protein 2	0.01	1.6
80910	G protein-coupled receptor 84	0.00	1.6
14129	Fc receptor, IgG, high affinity I	0.00	1.6
71607	sorting nexin 20	0.00	1.6
243910	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	0.00	1.6
269799	C-type lectin domain family 4, member a1	0.04	1.6
19419	RAS guanyl releasing protein 1	0.01	1.6
58210	secreted and transmembrane 1B	0.00	1.6
15959	interferon-induced protein with tetratricopeptide repeats 3	0.00	1.6
16881	ligase I, D, ATP-dependent	0.00	1.6
404236	MAS-related GPR, member A7	0.00	1.6
21899	toll-like receptor 6	0.00	1.6
17829	mucin 1, transmembrane	0.01	1.6
11542	adenosine A3 receptor	0.00	1.6
29870	G two S phase expressed protein 1	0.00	1.6
72042	coactosin-like 1 (Dictyostelium)	0.02	1.6
22321	valyl-tR synthetase	0.00	1.6
27226	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.01	1.6
12362	caspase 1	0.01	1.6
18826	lymphocyte cytosolic protein 1	0.03	1.6
13052	coxsackie virus and adenovirus receptor	0.01	1.6
57783	TNFAIP3 interacting protein 1	0.00	1.6
13057	cytochrome b-245, alpha polypeptide	0.02	1.6
52673	DNA segment, Chr 13, ERATO Doi 608, expressed	0.00	1.6
213002	interferon induced transmembrane protein 6	0.02	1.6
18726	paired-Ig-like receptor A3	0.00	1.6
67844	RAB32, member RAS oncogene family	0.01	1.6
27056	interferon regulatory factor 5	0.04	1.6
17858	myxovirus (influenza virus) resistance 2	0.00	1.6
24110	ubiquitin specific peptidase 18	0.00	1.6
104886	RAB15, member RAS oncogene family	0.00	1.6
219132	PHD finger protein 11	0.01	1.6
14068	coagulation factor VII	0.01	1.6
15170	protein tyrosine phosphatase, non-receptor type 6	0.00	1.6
18301	FXD domain-containing ion transport regulator 5	0.01	1.6
219131	PHD finger protein 11	0.01	1.6
76507	amiloride binding protein 1 (amine oxidase, copper-containing)	0.01	1.6

226652	Rho GTPase activating protein 30	0.04	1.6
228608	spermine oxidase	0.00	1.6
11720	methionine adenosyltransferase I, alpha	0.00	1.6
11867	actin related protein 2/3 complex, subunit 1B	0.00	1.6
99887	transmembrane protein 56	0.00	1.6
13555	E2F transcription factor 1	0.00	1.6
330890	piwi-like homolog 4 (Drosophila)	0.03	1.6
13733	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0.04	1.6
56743	linker for activation of T cells family, member 2	0.01	1.6
15186	histidine decarboxylase	0.00	1.6
107094	ribosomal R processing 12 homolog (S. cerevisiae)	0.00	1.6
70025	acyl-CoA thioesterase 7	0.02	1.6
20848	sigl transducer and activator of transcription 3	0.00	1.6
18301	FXD domain-containing ion transport regulator 5	0.01	1.6
13733	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0.02	1.6
13038	cathepsin K	0.04	1.6
18707	phosphatidylinositol 3-kinase catalytic delta polypeptide	0.00	1.6
12575	cyclin-dependent kinase inhibitor 1A (P21)	0.01	1.6
98238	leucine rich repeat containing 59	0.00	1.6
231830	MICAL-like 2	0.00	1.6
23912	ras homolog gene family, member f	0.00	1.6
108115	solute carrier organic anion transporter family, member 4a1	0.00	1.6
64138	cathepsin Z	0.00	1.6
14744	G-protein coupled receptor 65	0.01	1.6
22375	tryptophanyl-tRNA synthetase; similar to tryptophanyl-tRNA synthetase	0.01	1.6
81840	sortilin-related VPS10 domain containing receptor 2	0.00	1.6
622408	predicted gene 6320	0.01	1.6
22040	three prime repair exonuclease 1	0.00	1.6
16182	interleukin 18 receptor 1	0.01	1.6
17916	myosin IF	0.01	1.6
18724	paired-Ig-like receptor A11	0.03	1.6
12759	clusterin	0.01	1.6
24099	tumor necrosis factor (ligand) superfamily, member 13b	0.00	1.5
22154	tubulin, beta 5	0.00	1.5
12522	CD83 antigen	0.03	1.5
230738	zinc finger CCCH type containing 12A	0.01	1.5
21985	tumor protein D52	0.01	1.5
80861	DEXH (Asp-Glu-X-His) box polypeptide 58	0.00	1.5
13041	cathepsin W	0.02	1.5
27261	docking protein 3	0.01	1.5
327957	RIKEN cD A430084P05 gene	0.01	1.5
17395	matrix metalloproteinase 9	0.01	1.5
80914	uridine-cytidine kinase 2	0.00	1.5
72155	centromere protein N	0.00	1.5
106582	nurim (nuclear envelope membrane protein)	0.01	1.5
18971	polymerase (D directed), delta 1, catalytic subunit	0.00	1.5
26941	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	0.00	1.5
68195	ribonuclease T2B; ribonuclease T2A	0.00	1.5
14950	histocompatibility 13	0.01	1.5
14356	fractured callus expressed transcript 1	0.00	1.5
16918	myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	0.00	1.5
16498	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0.00	1.5
17387	matrix metalloproteinase 14 (membrane-inserted)	0.00	1.5
15958	interferon-induced protein with tetratricopeptide repeats 2	0.03	1.5
24055	SH3-domain binding protein 2	0.01	1.5
11867	actin related protein 2/3 complex, subunit 1B	0.00	1.5
15958	interferon-induced protein with tetratricopeptide repeats 2	0.01	1.5
14609	gap junction protein, alpha 1	0.01	1.5
14159	feline sarcoma oncogene	0.00	1.5
72027	solute carrier family 39 (zinc transporter), member 4	0.00	1.5
20556	schlafen 2	0.02	1.5
214854	neuralized homolog 3 homolog (Drosophila)	0.01	1.5
233066	expressed sequence A1428936	0.01	1.5
14629	glutamate-cysteine ligase, catalytic subunit	0.01	1.5
107272	phosphoserine aminotransferase 1	0.00	1.5
76261	RIKEN cD 0610040J01 gene	0.00	1.5
106344	replication factor C (activator 1) 4	0.00	1.5
66058	transmembrane protein 176A	0.00	1.5
50783	LSM4 homolog, U6 small nuclear R associated (S. cerevisiae)	0.00	1.5
231440	prostate androgen-regulated mucin-like protein 1	0.01	1.5
72112	protein phosphatase 1, regulatory (inhibitor) subunit 14D	0.01	1.5
24110	ubiquitin specific peptidase 18	0.01	1.5

105855	NCK associated protein 1 like	0.02	1.5
53314	basic leucine zipper transcription factor, ATF-like	0.01	1.5
674706	similar to zinc finger protein 341	0.00	1.5
20848	signal transducer and activator of transcription 3	0.00	1.5
16186	interleukin 2 receptor, gamma chain	0.02	1.5
17153	myelin and lymphocyte protein, T-cell differentiation protein	0.03	1.5
234779	phospholipase C, gamma 2	0.01	1.5
20969	syndecan 1	0.01	1.5
626152	similar to Epiplakin	0.00	1.5
12721	coronin, actin binding protein 1A	0.01	1.5
16149	CD74 antigen (invariant polypeptide of MHC, class II antigen-associated)	0.05	1.5
12554	cadherin 13	0.00	-1.5
53376	ubiquitin specific peptidase 2	0.00	-1.5
108075	latent transforming growth factor beta binding protein 4	0.00	-1.5
81877	tenascin XB	0.00	-1.5
233335	synemin, intermediate filament protein	0.02	-1.5
17022	lumican	0.03	-1.5
17196	myelin basic protein	0.02	-1.6
18627	period homolog 2 (Drosophila)	0.01	-1.6
50490	NADPH oxidase 4	0.01	-1.6
12069	brain expressed X-linked 2	0.00	-1.6
15360	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0.01	-1.6
53315	sulfotransferase family 1D, member 1	0.01	-1.6
53374	carbohydrate (chondroitin 6/keratan) sulfotransferase 3	0.02	-1.6
234564	expressed sequence AU018778	0.01	-1.6
16009	insulin-like growth factor binding protein 3	0.01	-1.6
22364	pre-B lymphocyte gene 3	0.00	-1.6
14311	cell death-inducing DFFA-like effector c	0.02	-1.6
57349	pro-platelet basic protein	0.02	-1.6
13118	cytochrome P450, family 4, subfamily a, polypeptide 12B	0.00	-1.7
12069	brain expressed X-linked 2	0.00	-1.7
241041	predicted gene 4956	0.01	-1.7
14262	flavin containing monooxygenase 3	0.00	-1.7
18295	osteoglycin	0.00	-1.7
14262	flavin containing monooxygenase 3	0.00	-1.7
21835	thyroid hormone responsive SPOT14 homolog (Rattus)	0.03	-1.8
15129	hemoglobin, beta adult major chain	0.05	-1.8
71145	scavenger receptor class A, member 5 (putative)	0.00	-1.9
217258	ATP-binding cassette, sub-family A (ABC1), member 8a	0.00	-2.0
11450	adiponectin, C1Q and collagen domain containing	0.01	-2.1
13106	cytochrome P450, family 2, subfamily e, polypeptide 1	0.01	-2.2
13087	cytochrome P450, family 2, subfamily a, polypeptide 5	0.04	-2.2
13087	cytochrome P450, family 2, subfamily a, polypeptide 5	0.03	-2.4
12350	carbonic anhydrase 3	0.05	-2.4

Regulated at 4 dpi in WT vs. $\Delta P T^{high}$ but not in WT vs. $\Delta P T$

20568	secretory leukocyte peptidase inhibitor	0.00	3.0
15116	hyaluron synthase1	0.01	2.2
17025	aminolevulinatase, delta-, dehydratase	0.01	2.1
74145	coagulation factor XIII, A1 subunit	0.00	1.8
12825	collagen, type III, alpha 1	0.00	1.8
72748	haloacid dehalogenase-like hydrolase domain containing 3	0.01	1.7
215418	cysteine-serine-rich nuclear protein 1	0.04	1.7
11910	activating transcription factor 3	0.01	1.7
12508	CD53 antigen	0.01	1.6
73712	dermokine	0.00	1.6
20867	stress-induced phosphoprotein 1	0.00	1.6
20315	chemokine (C-X-C motif) ligand 12	0.02	1.6
73712	dermokine	0.00	1.6
68981	small nuclear ribonucleoprotein polypeptide A'	0.00	1.6
59027	nicotinamide phosphoribosyltransferase	0.00	1.6
21817	transglutaminase 2, C polypeptide	0.00	1.6
110196	farnesyl diphosphate synthetase	0.01	1.6
69104	membrane-associated ring finger (C3HC4) 5	0.00	1.6
13197	growth arrest and D-damage-inducible 45 alpha	0.00	1.6
328162	tR methyltransferase 61 homolog A (S. cerevisiae)	0.00	1.6
103742	RIKEN cD 1810046J19 gene	0.00	1.6
12608	CCAAT/enhancer binding protein (C/EBP), beta	0.00	1.6
14190	fibrinogen-like protein 2	0.00	1.6
14950	histocompatibility 13	0.01	1.5
13200	dolichyl-di-phosphooligosaccharide-protein glycotransferase	0.00	1.5
12457	repression 4-like (S. cerevisiae)	0.01	1.5

17153	myelin and lymphocyte protein, T-cell differentiation protein	0.02	1.5
20377	secreted frizzled-related protein 1	0.00	1.5
13681	eukaryotic translation initiation factor 4A1	0.00	1.5
27279	tumor necrosis factor receptor superfamily, member 12a	0.02	1.5
20818	sigl recognition particle receptor, B subunit	0.00	1.5
67134	NOP56 ribonucleoprotein homolog (yeast)	0.01	1.5
13167	diazepam binding inhibitor	0.00	1.5
320713	similar to mKIAA1915 protein; myb-like, SWIRM and MPN domains 1	0.00	1.5
227731	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	0.01	1.5
19650	retinoblastoma-like 1 (p107)	0.00	1.5
70025	acyl-CoA thioesterase 7	0.02	1.5
68298	non-SMC condensin I complex, subunit D2	0.00	1.5
14056	enhancer of zeste homolog 2 (Drosophila)	0.00	1.5
11692	growth factor, erv1 (S. cerevisiae)-like (augments liver regeneration)	0.01	1.5
15894	intercellular adhesion molecule 1	0.00	1.5
68713	interferon induced transmembrane protein 1	0.01	1.5
235047	zinc finger protein 809	0.02	1.5
217995	HEAT repeat containing 1	0.01	1.5
66143	eukaryotic translation elongation factor 1 epsilon 1	0.01	1.5
622339	glyceraldehyde-3-phosphate dehydrogenase pseudogene	0.01	1.5
108148	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2	0.02	1.5
93692	glutaredoxin	0.01	1.5
235493	cD sequence BC031353	0.01	-1.5
56464	cathepsin F	0.00	-1.5
18628	period homolog 3 (Drosophila)	0.01	-1.5
114249	nephronectin	0.01	-1.5
66182	ADP-ribosylation factor 4-like	0.00	-1.5
16008	insulin-like growth factor binding protein 2	0.01	-1.6
52897	RNA binding protein, fox-1 homolog (C. elegans) 3	0.01	-1.6
12937	protocadherin alpha 6	0.02	-1.6
11812	apolipoprotein C-I	0.01	-1.6
17207	mcf.2 transforming sequence-like	0.00	-1.7
53877	eosinophil-associated, ribonuclease A family, member 4	0.02	-1.8
11815	apolipoprotein D	0.01	-1.8
67133	glycoprotein 2 (zymogen granule membrane)	0.02	-2.3

*Duplicate entries indicate results from multiple probes for the same gene

Supplemental Table 5. Functions Enriched in PT-Associated Genes

IPA Functional Annotation	p-value	# Molecules
immune response	4.27E-14	30
inflammation	1.78E-13	19
migration of neutrophils	1.46E-12	11
inflammation of organ	1.72E-12	16
hypersensitive reaction	2.14E-12	16
quantity of neutrophils	3.35E-12	12
adhesion of phagocytes	1.11E-11	10
adhesion of granulocytes	1.72E-11	9
leukocytosis	3.47E-11	8
adhesion of neutrophils	4.02E-11	8
autoimmune disease	4.24E-11	23
synthesis of nitric oxide	6.86E-11	9
quantity of phagocytes	7.34E-11	14
quantity of myeloid cells	9.66E-11	14
function of leukocytes	9.71E-11	17
inflammatory response	1.81E-10	18
accumulation of phagocytes	2.07E-10	9
accumulation of leukocytes	3.07E-10	11
atherosclerosis	3.29E-10	13
quantity of granulocytes	3.92E-10	13
cell movement of leukocytes	4.80E-10	18
leukocyte migration	5.57E-10	19
dermatitis	5.59E-10	13
cytosis	6.14E-10	11
migration of phagocytes	1.12E-09	12
digestive organ tumor	1.13E-09	22
accumulation of myeloid cells	1.41E-09	9
immediate hypersensitivity	1.60E-09	12
homing of cells	2.02E-09	15
necrosis	2.64E-09	12
infiltration of leukocytes	3.36E-09	12
encephalomyelitis	3.76E-09	10
mobilization of cells	3.98E-09	7
cell movement of neutrophils	3.98E-09	12
cell movement of granulocytes	4.69E-09	13
activation of cells	8.40E-09	18
psoriasis	8.76E-09	16
delayed hypersensitive reaction	9.88E-09	8
chemotaxis of cells	1.02E-08	14
cell death of liver	1.07E-08	10
function of phagocytes	1.31E-08	12
activation of blood cells	1.36E-08	16
cell rolling of mononuclear leukocytes	1.39E-08	5
chemotaxis of leukocytes	1.50E-08	12
inflammatory response of cells	1.81E-08	6
accumulation of granulocytes	1.82E-08	7
cell movement of myeloid cells	1.93E-08	14
activation of leukocytes	2.00E-08	15
encephalopathy	2.11E-08	20
rheumatic disease	2.16E-08	19
quantity of leukocytes	2.21E-08	19
cell movement of phagocytes	2.25E-08	14
recruitment of mononuclear leukocytes	2.59E-08	7
atopic dermatitis	2.73E-08	10
proliferation of immune cells	2.94E-08	15

adhesion of immune cells	3.31E-08	11
fibrosis	3.54E-08	12
fibrosis of organ	3.56E-08	10
infiltration by mononuclear leukocytes	3.61E-08	8
cell movement of mononuclear leukocytes	4.05E-08	12
mobilization of blood cells	4.43E-08	6
infection of mammalia	5.42E-08	12
size of lesion	5.42E-08	9
experimental autoimmune encephalomyelitis	5.91E-08	9
apoptosis of leukocytes	6.14E-08	12
carcinoma	6.44E-08	29
quantity of monocytes	6.72E-08	7
binding of myeloid cells	6.99E-08	6
fibrosis of liver	6.99E-08	6
activation of myeloid cells	7.32E-08	10
erythropoiesis	7.64E-08	9
binding of phagocytes	8.37E-08	7
necrosis of liver	8.37E-08	7
quantity of bone marrow cells	8.82E-08	8
Sjogren's syndrome	8.98E-08	8
Lymphocyte migration	9.26E-08	10
developmental process of red blood cells	1.08E-07	8
proliferation of lymphocytes	1.09E-07	14
cell rolling of leukocytes	1.18E-07	6
infiltration by lymphocytes	1.45E-07	7
NK cell migration	1.57E-07	5
function of myeloid cells	1.63E-07	10
inflammation of liver	1.65E-07	7
apoptosis of myeloid cells	1.69E-07	8
myelopoiesis	1.76E-07	10
myelopoiesis	1.76E-07	10
migration of cells	1.89E-07	22
chemotaxis of myeloid cells	2.04E-07	10
cell movement of T lymphocytes	2.04E-07	8
recruitment of lymphocytes	2.08E-07	6
apoptosis of phagocytes	2.14E-07	8
sensitization of macrophages	2.20E-07	3
binding of leukocytes	2.35E-07	8
function of macrophages	2.35E-07	8
recruitment of granulocytes	2.46E-07	8
transmigration of phagocytes	2.49E-07	6
function of antigen presenting cells	2.54E-07	9
fibrosis of lung	2.55E-07	7
inflammation of lung	2.57E-07	8
production of nitric oxide	2.57E-07	8
cell movement	2.59E-07	23
cell death	2.70E-07	31
arthritis	2.89E-07	17
size of atherosclerotic lesion	2.95E-07	6
function of lymphocytes	3.30E-07	10
chemotaxis of phagocytes	3.37E-07	10
development of Th17 cells	3.54E-07	4
neutrophilia	3.74E-07	5
developmental process of Th2 cells	4.44E-07	6
recruitment of phagocytes	4.52E-07	8
apoptosis of microglia	4.61E-07	4
cell rolling of lymphocytes	4.61E-07	4
generation of Th17 cells	4.61E-07	4

cancer	5.18E-07	32
recruitment of leukocytes	5.57E-07	9
damage of kidney	5.60E-07	6
response of mononuclear leukocytes	5.78E-07	8
infiltration of myeloid cells	6.01E-07	8
damage of organ	6.07E-07	10
proliferation of T lymphocytes	6.49E-07	12
tumorigenesis	6.56E-07	34
generation of antigen presenting cells	7.47E-07	4
apoptosis of liver cells	7.67E-07	7
accumulation of neutrophils	7.79E-07	5
acne	8.07E-07	6
colorectal cancer	9.00E-07	14
apoptosis of tumor cell lines	9.42E-07	17
development of helper T lymphocytes	9.72E-07	5
activation of granulocytes	9.93E-07	7
chemotaxis of neutrophils	1.03E-06	8
gastrointestinal tract cancer	1.04E-06	15
binding of leukemia cell lines	1.08E-06	5
arthritis of ankle joint	1.10E-06	3
cell rolling of phagocytes	1.15E-06	4
synthesis of reactive oxygen species	1.15E-06	10
influx of leukocytes	1.20E-06	6
plaque psoriasis	1.38E-06	6
trafficking of T lymphocytes	1.40E-06	4
binding of granulocytes	1.47E-06	5
cell death of fibrosarcoma cell lines	1.47E-06	5
inhibition of cells	1.47E-06	6
differentiation of blood cells	1.54E-06	14
urological disorder	1.56E-06	15
accumulation of mononuclear leukocytes	1.57E-06	6
rheumatoid arthritis	1.64E-06	14
binding of interferon-gamma activated sequence	1.69E-06	4
quantity of antigen presenting cells	1.70E-06	8
arrest in growth of tumor cell lines	1.78E-06	6
antiviral response	1.89E-06	6
vascular lesion	1.96E-06	7
generation of phagocytes	2.02E-06	4
developmental process of helper T lymphocytes	2.04E-06	7
quantity of cytokine	2.08E-06	9
differentiation of leukocytes	2.09E-06	13
infection of lung	2.40E-06	4
quantity of protein in blood	2.41E-06	12
apoptosis of lymphocytes	2.69E-06	9
cell death of immune cells	2.80E-06	13
cell death of organ	2.98E-06	15
apoptosis of trophoblast cells	3.05E-06	3
bleeding of skin	3.05E-06	3
injury of organ	3.27E-06	8
antimicrobial response	3.50E-06	7
infiltration of granulocytes	3.50E-06	7
differentiation of Th1 cells	3.62E-06	5
cell rolling of granulocytes	3.85E-06	4
development of erythroid progenitor cells	3.85E-06	4
accumulation of antigen presenting cells	3.93E-06	5
quantity of interleukin	3.94E-06	7
hematopoiesis	4.14E-06	15
activation of phagocytes	4.31E-06	9

infarction	4.31E-06	8
adhesion of lymphoma cell lines	4.45E-06	4
proliferation of synovial cells	4.45E-06	4
generation of leukocytes	4.61E-06	7
glucose metabolism disorder	4.78E-06	14
apoptosis of organ	4.81E-06	12
systemic lupus erythematosus	5.10E-06	6
necrosis of tumor cell lines	5.12E-06	4
transmigration of neutrophils	5.12E-06	4
function of T lymphocytes	5.14E-06	8
apoptosis	5.31E-06	25
differentiation of Th2 cells	5.36E-06	5
morphology of leukocytes	5.81E-06	9
antiviral response of cells	5.86E-06	4
lymphadenopathy	5.86E-06	4
differentiation of cells	6.15E-06	21
infiltration by neutrophils	6.22E-06	6
activation of neutrophils	6.22E-06	6
splenomegaly	6.22E-06	5
erythropoiesis of erythroid progenitor cells	6.50E-06	3
recruitment of natural killer cells	6.50E-06	3
adhesion of mononuclear leukocytes	6.53E-06	6
morphology of mononuclear leukocytes	6.85E-06	7
proliferation of hepatic stellate cells	7.58E-06	4
diabetes mellitus	8.12E-06	12
formation of osteoclasts	8.25E-06	5
production of reactive oxygen species	8.29E-06	8
binding of neutrophils	8.56E-06	4
glomerulonephritis	8.65E-06	6
quantity of cells	8.88E-06	21
catabolism of L-tryptophan	8.91E-06	3
formation of granulation tissue	8.91E-06	3
genital tumor	9.06E-06	13
infection by bacteria	9.59E-06	10
activation of hepatic stellate cells	9.64E-06	4
emigration of leukocytes	9.64E-06	5
differentiation of antigen presenting cells	1.03E-05	6
response of lymphocytes	1.03E-05	6
cell movement of tumor cell lines	1.13E-05	11
morphology of myeloid cells	1.13E-05	6
survival of organism	1.16E-05	11
inborn error of metabolism	1.24E-05	9
hepatitis	1.28E-05	7
growth of tumor	1.29E-05	8
binding of cells	1.30E-05	10
immune response of T lymphocytes	1.30E-05	5
replication of HIV-1	1.30E-05	5
differentiation of helper T lymphocytes	1.34E-05	6
activation-induced cell death of lymphocytes	1.35E-05	4
differentiation of osteoclasts	1.46E-05	6
recruitment of neutrophils	1.46E-05	6
apoptosis of muscle cells	1.47E-05	7
activation of natural killer cells	1.47E-05	5
accumulation of peripheral blood monocytes	1.48E-05	2
binding of LPS/IL1 response element	1.48E-05	2
cytostasis of rhabdomyosarcoma cell lines	1.48E-05	2
depletion of L-tryptophan	1.48E-05	2
inflammation of endothelial cells	1.48E-05	2

inflammatory response of endothelial cells	1.48E-05	2
activation of lymphocytes	1.50E-05	9
quantity of mononuclear leukocytes	1.51E-05	13
differentiation of myeloid cells	1.51E-05	7
healing	1.51E-05	7
of bone-marrow-derived monocyte/macrophage	1.54E-05	3
hyperplasia	1.55E-05	10
apoptosis of macrophages	1.56E-05	5
proliferation of connective tissue cells	1.63E-05	9
induction of RNA	1.66E-05	4
recruitment of eosinophils	1.66E-05	4
accumulation of lymphocytes	1.76E-05	5
delay in initiation of interphase	1.83E-05	4
maturation of dendritic cells	1.86E-05	5
quantity of T lymphocytes	1.91E-05	11
inding of interferon-stimulated response elemer	1.95E-05	3
cell rolling of T lymphocytes	1.95E-05	3
proliferation of effector T lymphocytes	1.95E-05	3
injury of liver	1.97E-05	5
quantity of metal	1.98E-05	10
apoptosis of fibrosarcoma cell lines	2.02E-05	4
localization of cells	2.02E-05	4
growth of cells	2.19E-05	19
airway hyperresponsiveness	2.21E-05	5
proliferation of lymphatic system cells	2.34E-05	6
binding of tumor cell lines	2.43E-05	6
arrest in growth of leukemia cell lines	2.43E-05	3
secretion of nitric oxide	2.43E-05	3
cell movement of eosinophils	2.46E-05	5
quantity of Ca2+	2.56E-05	9
cell-mediated response	2.62E-05	7
adhesion of lymphocytes	2.88E-05	5
cell movement of leukemia cell lines	2.88E-05	5
gliosis	2.88E-05	5
aggregation of leukocytes	2.91E-05	4
formation of neointima	2.91E-05	4
quantity of helper T lymphocytes	2.92E-05	6
generation of dendritic cells	2.98E-05	3
abnormal morphology of leukocytes	3.04E-05	7
morphology of organ	3.06E-05	17
binding of DNA	3.14E-05	10
production of superoxide	3.20E-05	5
prostate cancer	3.45E-05	9
extravasation of cells	3.45E-05	4
cell rolling of neutrophils	3.61E-05	3
binding of mononuclear leukocytes	3.71E-05	5
class switching	3.75E-05	4
migration of tumor cell lines	3.85E-05	9
T cell response	3.90E-05	5
cell movement of epithelial cells	4.09E-05	5
inhibition of leukocytes	4.40E-05	4
migration of keratinocytes	4.40E-05	4
recruitment of T lymphocytes	4.40E-05	4
apoptosis of cytotrophoblastic cells	4.43E-05	2
arrest in growth of fibrosarcoma cell lines	4.43E-05	2
binding of IRF1/IRF2 binding site	4.43E-05	2
carotid atherosclerosis	4.43E-05	2
cell rolling of peripheral blood leukocytes	4.43E-05	2

cytostasis of melanoma cell lines	4.43E-05	2
engagement of leukocytes	4.43E-05	2
proliferation of colony-forming erythroid cells	4.43E-05	2
trafficking of B lymphocytes	4.43E-05	2
proliferation of cells	4.47E-05	23
metastasis	4.51E-05	10
differentiation of epithelial cells	4.64E-05	7
differentiation of keratinocytes	4.72E-05	5
myocardial infarction	4.94E-05	5
apoptosis of T lymphocytes	5.00E-05	7
ankylosing spondylitis	5.12E-05	3
delay in interphase of tumor cell lines	5.12E-05	3
generation of regulatory T lymphocytes	5.12E-05	3
recruitment of inflammatory leukocytes	5.12E-05	3
apoptosis of neutrophils	5.12E-05	4
injury of cells	5.12E-05	4
neuropathy	5.37E-05	9
differentiation of phagocytes	5.57E-05	6
quantity of lymphocytes	5.70E-05	12
development of blood vessel	5.92E-05	11
amyloidosis	5.93E-05	4
binding of C/EBP binding site	6.01E-05	3
osteoclastogenesis of macrophages	6.01E-05	3
quantity of Th17 cells	6.01E-05	3
growth of tumor cells	6.31E-05	6
differentiation of erythroid progenitor cells	6.37E-05	4
development of bone marrow	6.75E-05	5
cellular homeostasis	6.98E-05	16
organismal death	6.98E-05	17
apoptosis of hepatocytes	7.04E-05	5
osteoarthritis	7.04E-05	6
neuromuscular disease	7.25E-05	13
binding of endothelial cells	7.32E-05	4
septic shock	7.35E-05	6
lymphomagenesis	7.49E-05	8
differentiation of connective tissue cells	7.73E-05	9
behavior	8.10E-05	12
quantity of immunoglobulin	8.28E-05	8
adhesion of HCAEC cells	8.85E-05	2
adhesion of acute myeloid leukemia blast cells	8.85E-05	2
apoptosis of insulinoma cells	8.85E-05	2
cell death of carcinoma	8.85E-05	2
distribution of embryonic cells	8.85E-05	2
hyperplasia of synovial cells	8.85E-05	2
inactivation of lymphocytes	8.85E-05	2
invasion of blood-derived mast cells	8.85E-05	2
metastasis of colon cancer cell lines	8.85E-05	2
infection of antigen presenting cells	9.26E-05	3
differentiation of leukemia cell lines	9.40E-05	5
accumulation of T lymphocytes	9.51E-05	4
progressive motor neuropathy	9.91E-05	8
movement disorder	1.01E-04	13
adhesion of eosinophils	1.06E-04	3
localization of blood cells	1.06E-04	3
binding of protein binding site	1.06E-04	7
infiltration by T lymphocytes	1.08E-04	4
concentration of lipid	1.14E-04	4
development of myeloid cells	1.14E-04	4

gliosis of brain	1.20E-04	3
progressive supranuclear palsy	1.20E-04	3
proliferation of bone marrow cells	1.21E-04	4
proliferation of lymphoma cell lines	1.21E-04	4
ovarian cancer	1.25E-04	8
apoptosis of lymphoblastoid cell lines	1.35E-04	3
inflammatory response of antigen presenting cell	1.35E-04	3
lupus nephritis	1.35E-04	3
mobilization of hematopoietic progenitor cells	1.35E-04	3
quantity of IgG	1.37E-04	7
recruitment of macrophages	1.44E-04	4
accumulation of natural killer cells	1.47E-04	2
development of erythroid precursor cells	1.47E-04	2
experimentally-induced arthritis of ankle joint	1.47E-04	2
formation of amyloid-beta plaques	1.47E-04	2
hantavirus pulmonary syndrome	1.47E-04	2
morphology of melanoma cell lines	1.47E-04	2
necrosis of cervical cancer cell lines	1.47E-04	2
quantity of IL-3 in blood	1.47E-04	2
quantity of colony-forming unit blood cells	1.47E-04	2
release of neutrophils	1.47E-04	2
replication of Murine cytomegalovirus	1.47E-04	2
activation of T lymphocytes	1.49E-04	7
infection of phagocytes	1.51E-04	3
rectum cancer	1.51E-04	3
Parkinson's disease	1.52E-04	6
differentiation of dendritic cells	1.61E-04	4
proliferation of splenocytes	1.61E-04	4
apoptosis of cardiomyocytes	1.64E-04	5
cell movement of monocytes	1.64E-04	5
aggregation of phagocytes	1.69E-04	3
generation of nitric oxide	1.69E-04	3
growth of liver cells	1.69E-04	3
proliferation of memory T lymphocytes	1.69E-04	3
liver tumor	1.70E-04	8
quantity of IgE	1.70E-04	5
proliferation of fibroblasts	1.78E-04	6
adhesion of T lymphocytes	1.80E-04	4
apoptosis of leukemia cell lines	1.82E-04	7
development of osteoclasts	1.88E-04	3
tumorigenesis of liver	1.88E-04	3
cytolysis of lymphocytes	1.90E-04	5
migration of monocytes	1.90E-04	4
endotoxin shock response	2.00E-04	5
morphology of lymphatic system cells	2.00E-04	4
generation of reactive oxygen species	2.02E-04	5
chronic B-cell leukemia	2.10E-04	4
growth of leukemia cell lines	2.10E-04	4
abnormal morphology of monocytes	2.20E-04	2
activation of hypothalamus-pituitary-adrenal axis	2.20E-04	2
adhesion of natural killer cells	2.20E-04	2
adhesion of postcapillary venule	2.20E-04	2
cell rolling of leukemia cell lines	2.20E-04	2
generation of nitrite	2.20E-04	2
healing of skin	2.20E-04	2
necrosis of endothelial cell lines	2.20E-04	2
permeability of tight junctions	2.20E-04	2
quantity of 5,6,7,8-tetrahydrobiopterin	2.20E-04	2

quantity of endocrine cell lines	2.20E-04	2
quantity of enzyme	2.21E-04	4
endothelial cell development	2.22E-04	6
clearance of virus	2.30E-04	3
proliferation of myeloma cell lines	2.30E-04	3
inflammation of intestine	2.32E-04	4
urination disorder	2.32E-04	6
differentiation of T lymphocytes	2.48E-04	7
endocrine gland tumor	2.48E-04	7
atherogenesis	2.53E-04	3
transmigration of monocytes	2.53E-04	3
growth of leukocyte cell lines	2.56E-04	4
binding of lymphocytes	2.69E-04	4
homing of T lymphocytes	2.69E-04	4
G0/G1 phase transition of tumor cell lines	2.77E-04	3
activation-induced cell death of T lymphocytes	2.77E-04	3
cytostasis	2.87E-04	6
proliferation of liver cells	2.87E-04	5
tumorigenesis of tumor cell lines	2.96E-04	5
cell movement of helper T lymphocytes	3.04E-04	3
influx of neutrophils	3.04E-04	4
inhibition of T lymphocytes	3.04E-04	3
carcinoma in situ	3.05E-04	5
accumulation of TREG cells	3.07E-04	2
apoptosis of cholangiocarcinoma cell lines	3.07E-04	2
localization of T lymphocytes	3.07E-04	2
osteoclastogenesis of osteoclast precursor cells	3.07E-04	2
proliferation of cytotoxic T cells	3.07E-04	2
replication of poxviridae	3.07E-04	2
stimulation of hepatoma cell lines	3.07E-04	2
stimulation of smooth muscle cells	3.07E-04	2
survival of hepatic stellate cells	3.07E-04	2
activation of neuroglia	3.09E-04	4
collagen-induced arthritis	3.09E-04	4
angiogenesis	3.21E-04	10
quantity of dendritic cells	3.23E-04	4
cell death of lymphoma cell lines	3.24E-04	5
abnormal morphology of myeloid progenitor cells	3.31E-04	3
acute myocardial infarction	3.31E-04	3
hematopoiesis of bone marrow	3.31E-04	3
cell damage	3.35E-04	6
differentiation of macrophages	3.53E-04	4
survival of T lymphocytes	3.53E-04	4
edema of skin	3.60E-04	3
function of cytotoxic T cells	3.60E-04	3
mobilization of leukocytes	3.60E-04	3
fragmentation of DNA	3.64E-04	5
experimentally-induced diabetes	3.69E-04	4
quantity of macrophages	3.75E-04	5
interaction of leukocytes	3.86E-04	4
adhesion of monocytes	3.91E-04	3
cell movement of bone marrow cells	3.91E-04	3
apoptosis of lymphatic system cells	4.02E-04	4
quantity of eosinophils	4.02E-04	4
cell death of hair cells	4.09E-04	2
fibrogenesis of liver	4.09E-04	2
generation of naive T lymphocytes	4.09E-04	2
induction of nitric oxide	4.09E-04	2

inhibition of antigen presenting cells	4.09E-04	2
inhibition of connective tissue cells	4.09E-04	2
osteoclastogenesis of macrophage cancer cell line	4.09E-04	2
regulation of antigen presenting cells	4.09E-04	2
NK cell proliferation	4.23E-04	3
Th2 immune response	4.23E-04	3
quantity of IFNG in blood	4.23E-04	3
quantity of mast cells	4.23E-04	3
Alzheimer's disease	4.32E-04	8
homing of mononuclear leukocytes	4.44E-04	5
hematological neoplasia	4.47E-04	10
cell death of cervical cancer cell lines	4.52E-04	6
proliferation of hematopoietic progenitor cells	4.56E-04	5
peroxidation of lipid	4.57E-04	3
quantity of GPT in blood	4.57E-04	3
proliferation of muscle cells	4.71E-04	6
incidence of tumor	4.81E-04	6
growth of tumor cell lines	4.82E-04	10
choroidal neovascularization	4.93E-04	3
infection by Herpesviridae	4.93E-04	3
abnormal morphology of cervical lymph node	5.24E-04	2
accumulation of dendritic cells	5.24E-04	2
cardioprotection	5.24E-04	2
formation of granulocyte-macrophage progenitor cells	5.24E-04	2
damage of axons	5.24E-04	2
infiltration by mast cells	5.24E-04	2
ischemic acute renal failure	5.24E-04	2
necrosis of leukemia cell lines	5.24E-04	2
size of phagocytes	5.24E-04	2
tolerization	5.24E-04	2
volume of organ	5.24E-04	2
abnormal morphology of B-cell follicle	5.30E-04	3
binding of synthetic promoter	5.30E-04	3
quantity of natural killer T lymphocytes	5.30E-04	4
suppression of cells	5.30E-04	3
apoptosis of hepatoma cell lines	5.35E-04	4
developmental process of T lymphocytes	5.39E-04	8
development of blood cells	5.44E-04	10
generation of lymphocytes	5.56E-04	5
hematopoiesis of blood cells	5.56E-04	4

Supplemental Table 6. Canonical pathways enriched in PT-associated genes

IPA Canonical Pathway	-log (p-val)	Percent*
Role of JAK family kinases in IL-6-type Cytokine Signaling	5.6	15.4
Atherosclerosis Signaling	5.6	5.2
Acute Phase Response Signaling	4.6	3.7
IL-15 Production	3.9	12.0
Hepatic Fibrosis / Hepatic Stellate Cell Activation	3.9	3.7
Interferon Signaling	3.8	10.3
IL-17A Signaling in Fibroblasts	3.6	8.3
Role of PKR in Interferon Induction and Antiviral Response	3.3	7.0
Type I Diabetes Mellitus Signaling	3.3	3.6
Role of IL-17A in Psoriasis	3.3	27.3
iNOS Signaling	3.2	6.7
IL-12 Signaling and Production in Macrophages	3.0	3.3
T Helper Cell Differentiation	2.8	4.4
Glucocorticoid Receptor Signaling	2.8	1.9
Prolactin Signaling	2.6	4.0
Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F	2.6	10.0
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	2.5	9.1
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	2.5	2.3
IL-22 Signaling	2.4	8.3
Role of Hypercytokinemia/hyperchemokine in the Pathogenesis of Influenza	2.3	6.7
Role of JAK2 in Hormone-like Cytokine Signaling	2.2	5.7
IL-9 Signaling	2.1	5.7
Oncostatin M Signaling	2.1	5.9
Role of Cytokines in Mediating Communication between Immune Cells	2.1	5.1
Graft-versus-Host Disease Signaling	2.1	4.7
LXR/RXR Activation	2.1	2.5
Neuroprotective Role of THOP1 in Alzheimer's Disease	2.1	5.3
Retinoic acid Mediated Apoptosis Signaling	2.0	4.2
Activation of IRF by Cytosolic Pattern Recognition Receptors	1.8	3.8
Lymphotoxin α Receptor Signaling	1.8	3.6
Role of JAK1 and JAK3 in α Cytokine Signaling	1.7	3.2
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	1.7	1.3
Communication between Innate and Adaptive Immune Cells	1.7	2.4
JAK/Stat Signaling	1.7	3.2
Growth Hormone Signaling	1.6	2.9
IL-10 Signaling	1.6	2.9
IL-17 Signaling	1.6	2.8
Crosstalk between Dendritic Cells and Natural Killer Cells	1.5	2.7
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	1.5	2.4
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	1.5	9.1
HMGB1 Signaling	1.4	2.2
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	1.4	1.4
Folate Biosynthesis	1.3	6.3
Colorectal Cancer Metastasis Signaling	1.3	1.3
Granzyme B Signaling	1.3	6.3
Protein Ubiquitination Pathway	1.3	1.2

*Percentage of PT-associated molecules out of total molecules involved in pathway

Supplemental Table 7. Reciprocally regulated genes at 2 and 4 dpi

ID	Gene Name	Δ PT ^{high} 2 dpi vs. PBS		WT 4 dpi vs. PBS	
		FDR	FC	FDR	FC
17329	chemokine (C-X-C motif) ligand 9	0.003	29.8	0.000	21.6
55985	chemokine (C-X-C motif) ligand 13	0.004	10.9	0.000	10.9
15945	chemokine (C-X-C motif) ligand 10	0.011	10.5	0.000	10.3
16145	interferon gamma induced GTPase	0.020	7.4	0.000	7.5
57262	resistin like alpha	0.000	7.4	0.000	6.4
68774	membrane-spanning 4-domains, subfamily A, member 6I	0.008	6.7	0.000	5.6
20306	chemokine (C-C motif) ligand 7	0.015	6.7	0.000	9.1
215900	family with sequence similarity 26, member F	0.015	6.0	0.000	5.6
229898	guanylate binding protein 5	0.019	5.7	0.000	5.9
18406	orosomucoid 2	0.001	5.3	0.000	5.2
17474	C-type lectin domain family 4, member d	0.001	5.1	0.000	4.0
100034251	predicted gene 11428	0.000	4.6	0.000	3.8
12642	cholesterol 25-hydroxylase	0.011	4.5	0.000	5.0
546546	serine peptidase inhibitor, clade A, member 3H	0.016	4.4	0.000	6.3
11629	allograft inflammatory factor 1	0.008	4.3	0.000	3.1
55932	guanylate binding protein 3	0.021	4.1	0.000	4.3
15953	interferon gamma inducible protein 47	0.020	4.0	0.000	3.5
14131	Fc receptor, IgG, low affinity III	0.005	3.9	0.000	3.3
54396	immunity-related GTPase family M member 2	0.014	3.9	0.000	3.9
55932	guanylate binding protein 3	0.015	3.9	0.000	3.6
15944	immunity-related GTPase family M member 1	0.014	3.8	0.000	3.5
68774	membrane-spanning 4-domains, subfamily A, member 6I	0.005	3.8	0.000	2.8
14468	guanylate binding protein 1	0.033	3.8	0.000	4.3
56620	C-type lectin domain family 4, member n	0.001	3.7	0.000	2.6
24088	toll-like receptor 2	0.013	3.7	0.000	3.2
74748	SLAM family member 8	0.028	3.5	0.000	2.9
14204	interleukin 4 induced 1	0.015	3.4	0.000	4.7
60533	CD274 antigen	0.025	3.4	0.000	3.9
20302	chemokine (C-C motif) ligand 3	0.004	3.4	0.000	3.1
21822	T-cell specific GTPase 2	0.034	3.4	0.000	2.8
20846	signal transducer and activator of transcription 1	0.025	3.3	0.000	3.0
14130	Fc receptor, IgG, low affinity IIb	0.011	3.3	0.000	2.6
16181	interleukin 1 receptor antagonist	0.014	3.3	0.000	3.0
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.011	3.3	0.000	4.4
102084	expressed sequence AI451557	0.025	3.2	0.000	2.7
14728	macrophage immunoglobulin-like receptor, subfamily B, member 1	0.002	3.2	0.000	2.8
16427	inter alpha-trypsin inhibitor, heavy chain 4	0.003	3.2	0.000	4.2
435565	interferon inducible GTPase 1	0.020	3.1	0.000	2.8
22177	TYRO protein tyrosine kinase binding protein	0.001	3.1	0.000	2.5
12265	class II transactivator	0.025	3.0	0.000	3.1
21928	tumor necrosis factor, alpha-induced protein 2	0.014	3.0	0.000	3.7
18173	family 11 (proton-coupled divalent metal ion transporter)	0.012	2.9	0.000	2.1
14469	guanylate binding protein 2	0.046	2.9	0.000	3.0
12515	CD69 antigen	0.050	2.9	0.000	2.0
16323	inhibin beta-A	0.012	2.9	0.000	2.4
65221	solute carrier family 15, member 3	0.015	2.9	0.000	2.7
20293	(C-C motif) ligand 12; similar to monocyte chemoattractant protein 1	0.018	2.9	0.000	2.1
17972	neutrophil cytosolic factor 4	0.008	2.9	0.000	2.3
227659	solute carrier family 2 (facilitated glucose transporter), member 1	0.014	2.9	0.000	2.0
21810	transforming growth factor, beta induced	0.009	2.8	0.000	2.6
12534	cell division cycle 2 homolog A (S. pombe)	0.006	2.8	0.000	2.5
246256	Fc receptor, IgG, low affinity IV	0.015	2.8	0.000	2.4
20303	chemokine (C-C motif) ligand 4	0.015	2.8	0.000	2.0
73149	C-type lectin domain family 4, member a3	0.010	2.8	0.000	2.2
20315	chemokine (C-X-C motif) ligand 12	0.042	2.8	0.000	2.8
74481	basic leucine zipper transcription factor, ATF-like 2	0.023	2.8	0.000	2.8
21877	predicted gene 6091; thymidine kinase 1	0.001	2.7	0.000	2.0
108907	nucleolar and spindle associated protein 1	0.002	2.7	0.000	2.0
12774	chemokine (C-C motif) receptor 5	0.027	2.7	0.000	2.4
72054	cytochrome P450, family 4, subfamily f, polypeptide 18	0.006	2.7	0.000	2.3
17357	MARCKS-like 1; predicted gene 9106	0.021	2.7	0.000	2.1
74558	GTPase, very large interferon inducible 1	0.022	2.7	0.000	2.9
72054	cytochrome P450, family 4, subfamily f, polypeptide 18	0.006	2.7	0.000	2.2
72310	natural killer cell group 7 sequence	0.022	2.7	0.000	2.2
23880	FYN binding protein	0.016	2.7	0.000	2.1
218630	cyclin O	0.013	2.7	0.001	2.3
21810	transforming growth factor, beta induced	0.009	2.7	0.000	2.4
12870	ceruloplasmin	0.004	2.6	0.000	3.1

ID	Gene Name	Δ PT ^{high} 2 dpi vs. PBS		WT 4 dpi vs. PBS	
21926	tumor necrosis factor	0.016	2.6	0.000	2.3
14999	histocompatibility 2, class II, locus Mb1	0.030	2.6	0.000	2.5
11799	baculoviral IAP repeat-containing 5	0.009	2.6	0.000	1.9
269799	C-type lectin domain family 4, member a1	0.048	2.6	0.000	1.9
268697	cyclin B1	0.001	2.6	0.000	1.9
17218	chromosome maintenance deficient 5, cell division cycl	0.011	2.6	0.000	2.3
11799	baculoviral IAP repeat-containing 5	0.003	2.5	0.000	2.1
14289	formyl peptide receptor 2	0.006	2.5	0.000	2.2
22040	three prime repair exonuclease 1	0.009	2.5	0.000	1.8
16362	interferon regulatory factor 1	0.032	2.5	0.000	2.8
16154	interleukin 10 receptor, alpha	0.012	2.5	0.000	1.9
21354	transporter 1, ATP-binding cassette, sub-family B (MDR/TA	0.036	2.5	0.000	2.3
13123	cytochrome P450, family 7, subfamily b, polypeptide 1	0.029	2.5	0.000	3.2
20555	schlafen 1	0.019	2.4	0.000	2.1
70218	kinesin family member 18B	0.002	2.4	0.000	1.9
219132	PHD finger protein 11	0.037	2.4	0.000	1.9
100340	sphingomyelin phosphodiesterase, acid-like 3B	0.022	2.4	0.000	2.4
20847	signal transducer and activator of transcription 2	0.029	2.4	0.000	2.1
246728	2'-5' oligoadenylate synthetase 2	0.033	2.4	0.000	2.0
23833	CD52 antigen	0.011	2.4	0.000	1.8
14191	oncogene homolog 1, feline sarcoma viral (Fgr) oncogene hom	0.006	2.4	0.000	2.5
56193	pleckstrin	0.009	2.4	0.000	2.1
268697	cyclin B1	0.003	2.4	0.000	1.9
21928	tumor necrosis factor, alpha-induced protein 2	0.034	2.4	0.000	3.2
54483	Mediterranean fever	0.014	2.3	0.000	2.1
16988	leukocyte specific transcript 1	0.001	2.3	0.000	1.6
68298	non-SMC condensin I complex, subunit D2	0.007	2.3	0.000	1.7
14156	flap structure specific endonuclease 1	0.008	2.3	0.000	2.2
107995	cell division cycle 20 homolog (S. cerevisiae)	0.002	2.3	0.000	2.1
16612	kallikrein 1	0.015	2.3	0.000	1.9
246707	elastin microfibril interfacer 2	0.010	2.3	0.000	2.4
74568	mixed lineage kinase domain-like	0.044	2.3	0.000	2.2
56644	C-type lectin domain family 7, member a	0.014	2.3	0.000	2.1
18727	paired-Ig-like receptor A4	0.010	2.3	0.000	2.1
107995	cell division cycle 20 homolog (S. cerevisiae)	0.002	2.3	0.000	2.0
13537	dual specificity phosphatase 2	0.029	2.3	0.000	1.9
16852	lectin, galactose binding, soluble 1	0.003	2.3	0.000	1.8
667370	RIKEN cDNA I830012O16 gene	0.038	2.3	0.001	1.7
104759	phospholipase D family, member 4	0.024	2.3	0.001	1.7
110033	kinesin family member 22	0.009	2.3	0.001	1.7
22324	vav 1 oncogene	0.012	2.3	0.000	1.7
212032	hexokinase 3	0.013	2.3	0.000	1.7
15900	interferon regulatory factor 8	0.037	2.2	0.000	2.0
12984	interleukin 2 receptor, beta 2, low-affinity (granulocyte-i	0.004	2.2	0.000	1.9
230738	zinc finger CCCH type containing 12A	0.016	2.2	0.000	2.6
21928	tumor necrosis factor, alpha-induced protein 2	0.018	2.2	0.000	2.4
69550	bone marrow stromal cell antigen 2	0.002	2.2	0.001	1.6
14017	ecotropic viral integration site 2a	0.029	2.2	0.003	1.6
12721	coronin, actin binding protein 1A	0.029	2.2	0.001	2.0
230787	cDNA sequence BC013712	0.005	2.2	0.001	1.9
12982	interleukin 2 receptor, alpha, low-affinity (granulocyte-r	0.008	2.2	0.000	1.8
269582	claspin homolog (Xenopus laevis)	0.008	2.2	0.001	1.6
27226	proteinase A2, group VII (platelet-activating factor acetylhydrola	0.002	2.2	0.008	1.5
12774	chemokine (C-C motif) receptor 5	0.038	2.2	0.001	2.0
107995	cell division cycle 20 homolog (S. cerevisiae)	0.005	2.2	0.000	2.0
65972	interferon gamma inducible protein 30	0.017	2.2	0.000	1.7
20539	transporter family 7 (cationic amino acid transporter, y+ system),	0.008	2.2	0.000	2.3
15270	H2A histone family, member X	0.002	2.2	0.000	1.8
71893	NADPH oxidase organizer 1	0.009	2.2	0.000	3.1
12986	colony stimulating factor 3 receptor (granulocyte)	0.012	2.2	0.000	2.4
269582	claspin homolog (Xenopus laevis)	0.009	2.2	0.000	1.7
26464	vanin 3	0.015	2.1	0.000	3.0
229323	G protein-coupled receptor 171	0.015	2.1	0.000	2.0
17219	minichromosome maintenance deficient 6	0.012	2.1	0.000	2.0
12362	caspase 1; hypothetical protein LOC100044207	0.025	2.1	0.000	1.9
327957	RIKEN cDNA A430084P05 gene	0.031	2.1	0.001	1.6
67742	SH3 domain, SH3 domain and nuclear localization signals	0.029	2.1	0.000	2.3

ID	Gene Name	Δ PT ^{high} 2 dpi vs. PBS		WT 4 dpi vs. PBS	
12774	chemokine (C-C motif) receptor 5	0.020	2.1	0.001	1.9
70024	minichromosome maintenance deficient 10 (S. cerevisiae)	0.015	2.1	0.000	1.8
19366	RAD54 like (S. cerevisiae)	0.002	2.1	0.001	1.5
171285	hepatitis A virus cellular receptor 2	0.021	2.1	0.000	1.8
14130	Fc receptor, IgG, low affinity IIb	0.022	2.1	0.000	1.7
18636	complement factor properdin	0.010	2.1	0.000	1.7
20556	schlafen 2	0.002	2.1	0.001	1.5
60530	fidgetin-like 1	0.013	2.1	0.003	1.5
80885	niacin receptor 1	0.032	2.1	0.000	2.3
27056	interferon regulatory factor 5	0.024	2.1	0.000	1.7
16994	lymphotoxin B	0.033	2.1	0.002	1.7
21391	thromboxane A synthase 1, platelet	0.005	2.1	0.001	1.5
56644	C-type lectin domain family 7, member a	0.014	2.1	0.000	2.2
16453	Janus kinase 3	0.044	2.1	0.000	2.1
106795	transcription factor 19	0.004	2.1	0.000	1.7
19200	proline-serine-threonine phosphatase-interacting protein	0.002	2.1	0.000	1.6
12051	B-cell leukemia/lymphoma 3	0.032	2.1	0.000	2.6
11847	arginase type II	0.005	2.1	0.000	2.0
73804	kinesin family member 2C	0.010	2.1	0.000	1.7
623474	RIKEN cDNA E130016E03 gene	0.007	2.1	0.000	1.7
404710	IQ motif containing GTPase activating protein 3	0.006	2.1	0.000	1.6
18173	family 11 (proton-coupled divalent metal ion transporter	0.035	2.1	0.001	1.8
230073	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0.041	2.1	0.001	1.7
18301	FXYD domain-containing ion transport regulator 5	0.004	2.1	0.000	1.6
14793	cell division cycle associated 3	0.004	2.0	0.001	1.5
12508	CD53 antigen	0.002	2.0	0.001	1.5
14235	forkhead box M1; RIKEN cDNA 4933413G19 gene	0.004	2.0	0.000	1.6
16905	lamin A	0.012	2.0	0.000	1.9
71934	carbonic anhydrase 13	0.011	2.0	0.000	1.7
12721	coronin, actin binding protein 1A	0.022	2.0	0.001	1.7
72042	coactosin-like 1 (Dictyostelium)	0.009	2.0	0.000	1.6
20375	SFFV proviral integration 1	0.028	2.0	0.005	1.6
11857	Rho, GDP dissociation inhibitor (GDI) beta	0.017	2.0	0.000	1.5
71607	sorting nexin 20	0.021	2.0	0.000	1.7
81840	sortilin-related VPS10 domain containing receptor 2	0.005	2.0	0.000	2.0
622408	predicted gene 6320	0.010	2.0	0.007	1.5
52673	DNA segment, Chr 13, ERATO Doi 608, expressed	0.033	2.0	0.000	1.6
20211	serum amyloid A 4	0.048	2.0	0.000	2.4
74191	purinergic receptor P2Y, G-protein coupled 13	0.016	2.0	0.000	1.9
243910	core of kappa light polypeptide gene enhancer in B-cells in	0.013	2.0	0.000	1.7
16362	interferon regulatory factor 1	0.045	2.0	0.000	2.3
225594	similar to immunity-related GTPase family, cinema 1	0.022	2.0	0.000	2.2
11867	actin related protein 2/3 complex, subunit 1B	0.010	2.0	0.000	1.9
26570	family 7 (cationic amino acid transporter, y+ system),	0.009	2.0	0.000	1.9
15368	heme oxygenase (decycling) 1	0.004	2.0	0.000	1.7
14190	fibrinogen-like protein 2	0.011	2.0	0.000	1.6
219132	PHD finger protein 11	0.038	2.0	0.006	1.5
320832	regulatory protein beta 1; similar to SIRP beta 1 cell surfac	0.005	1.9	0.000	2.3
22375	tryptophanyl-tRNA synthetase	0.037	1.9	0.000	2.0
20345	selectin, platelet (p-selectin) ligand	0.013	1.9	0.000	1.8
18724	paired-Ig-like receptor A11	0.008	1.9	0.002	1.7
15000	histocompatibility 2, class II, locus Mb2	0.019	1.9	0.012	1.7
67844	RAB32, member RAS oncogene family	0.014	1.9	0.001	1.6
22041	transferrin	0.033	1.9	0.000	2.5
22172	thymidylate synthase, pseudogene	0.008	1.9	0.000	1.7
237256	zinc finger CCH type containing 12D	0.007	1.9	0.000	1.6
66442	NUDC80 kinetochore complex component, homolog (S. α	0.012	1.9	0.000	1.5
12363	caspase 4, apoptosis-related cysteine peptidase	0.030	1.9	0.000	2.2
67895	pyrophosphatase (inorganic) 1	0.049	1.9	0.000	2.0
16822	lymphocyte cytosolic protein 2	0.011	1.9	0.000	1.6
234779	phospholipase C, gamma 2	0.032	1.9	0.001	1.6
20810	spermidine synthase	0.028	1.9	0.000	2.0
16186	predicted gene 614; interleukin 2 receptor, gamma chain	0.016	1.9	0.000	1.9
78816	Gem-interacting protein	0.014	1.9	0.004	1.6
20810	spermidine synthase	0.019	1.9	0.000	2.0
22171	thymidylate synthase	0.004	1.9	0.001	1.6
108912	cell division cycle associated 2	0.005	1.9	0.001	1.5
107272	phosphoserine aminotransferase 1	0.033	1.9	0.000	1.8
15170	protein tyrosine phosphatase, non-receptor type 6	0.032	1.9	0.000	1.6

ID	Gene Name	Δ PT ^{high} 2 dpi vs. PBS		WT 4 dpi vs. PBS	
20540	ier family 7 (cationic amino acid transporter, y+ system),	0.015	1.9	0.001	1.5
14086	omolog 1, actin bundling protein (Strongylocentrotus pur	0.022	1.9	0.000	1.7
18037	r of kappa light polypeptide gene enhancer in B-cells inh	0.022	1.9	0.000	1.7
66107	RIKEN cDNA 1100001G20 gene	0.018	1.9	0.000	1.9
20867	stress-induced phosphoprotein 1	0.030	1.9	0.000	1.8
56150	MAD2 mitotic arrest deficient-like 1 (yeast)	0.009	1.9	0.002	1.6
16178	interleukin 1 receptor, type II	0.047	1.9	0.000	2.0
26410	mitogen-activated protein kinase kinase 8	0.020	1.9	0.000	1.9
18826	lymphocyte cytosolic protein 1	0.020	1.9	0.002	1.6
11799	baculoviral IAP repeat-containing 5	0.018	1.8	0.001	1.6
216161	strawberry notch homolog 2 (Drosophila)	0.030	1.8	0.000	2.0
75909	transmembrane protein 49	0.014	1.8	0.000	2.0
232983	chemokine (C-X-C motif) ligand 17	0.012	1.8	0.000	2.0
228608	spermine oxidase	0.022	1.8	0.000	2.0
13449	docking protein 2	0.004	1.8	0.000	1.7
18301	FXFD domain-containing ion transport regulator 5	0.004	1.8	0.000	1.6
12721	coronin, actin binding protein 1A	0.024	1.8	0.000	1.6
26425	nucleotide binding protein 1	0.033	1.8	0.000	1.9
674706	similar to zinc finger protein 341	0.016	1.8	0.000	1.9
105348	golgi membrane protein 1	0.013	1.8	0.000	1.7
20750	secreted phosphoprotein 1	0.013	1.8	0.000	1.9
208228	Mps One Binder kinase activator-like 2A (yeast)	0.028	1.8	0.000	1.6
12489	CD33 antigen	0.024	1.8	0.002	1.5
57913	leucine-rich and death domain containing	0.027	1.8	0.000	1.7
12266	complement component 3	0.013	1.8	0.000	1.6
16571	kinesin family member 4	0.008	1.8	0.002	1.5
67855	aspartic peptidase, retroviral-like 1	0.045	1.8	0.000	1.7
20821	tripartite motif-containing 21	0.034	1.8	0.001	1.6
26415	mitogen-activated protein kinase 13	0.006	1.8	0.000	2.1
240354	sa associated lymphoid tissue lymphoma translocation c	0.013	1.8	0.000	1.8
20973	synaptogyrin 2	0.027	1.8	0.002	1.7
27060	une regulator 1, ATPase, H+ transporting, lysosomal V0	0.029	1.8	0.001	1.5
12047	B-cell leukemia/lymphoma 2 related protein A1d	0.023	1.8	0.001	1.5
233079	free fatty acid receptor 2	0.024	1.7	0.000	2.4
67951	tubulin, beta 6	0.019	1.7	0.000	1.8
320982	ADP-ribosylation factor-like 4C	0.036	1.7	0.000	1.7
17215	minichromosome maintenance deficient 3 (S. cerevisiae	0.009	1.7	0.000	1.7
15894	intercellular adhesion molecule 1	0.038	1.7	0.000	2.0
19143	suppression of tumorigenicity 14 (colon carcinoma)	0.042	1.7	0.000	1.9
17216	chromosome maintenance deficient 2 mitotin (S. cerevis	0.023	1.7	0.000	1.7
224823	cDNA sequence BC011248	0.015	1.7	0.000	1.6
14381	glucose-6-phosphate dehydrogenase X-linked	0.025	1.7	0.000	1.7
13132	disabled homolog 2 (Drosophila)	0.012	1.7	0.000	1.7
22256	uracil DNA glycosylase	0.019	1.7	0.001	1.6
14950	histocompatibility 13	0.020	1.7	0.000	1.9
212377	RIKEN cDNA F730047E07 gene	0.045	1.7	0.000	1.7
17470	CD200 antigen; similar to MRC OX-2 antigen homolog	0.009	1.7	0.000	1.6
54683	peroxiredoxin 5	0.016	1.7	0.000	1.6
18746	pyruvate kinase, muscle	0.019	1.7	0.001	1.6
75608	chromatin modifying protein 4B	0.030	1.7	0.000	1.6
12654	chitinase 3-like 1	0.023	1.7	0.000	2.0
11867	actin related protein 2/3 complex, subunit 1B	0.022	1.7	0.000	1.6
18643	profilin 1	0.020	1.7	0.001	1.5
19224	prostaglandin-endoperoxide synthase 1	0.023	1.7	0.000	1.8
20973	synaptogyrin 2	0.038	1.6	0.000	1.7
621823	proteasome (prosome, macropain) 28 subunit, beta	0.019	1.6	0.000	1.6
637082	RAF-interacting protein with forkhead-associated domai	0.011	1.6	0.001	1.6
18103	static cells 2, protein (NM23B) expressed in; predicted c	0.021	1.6	0.000	1.7
19224	prostaglandin-endoperoxide synthase 1	0.019	1.6	0.000	1.7
27407	ATP-binding cassette, sub-family F (GCN20), member 2	0.019	1.6	0.000	1.6
18174	family 11 (proton-coupled divalent metal ion transporter	0.039	1.6	0.000	1.7
16828	lactate dehydrogenase A	0.016	1.6	0.000	1.7
22321	valyl-tRNA synthetase	0.042	1.6	0.000	1.6
19698	vian reticuloendotheliosis viral (v-rel) oncogene related	0.023	1.6	0.000	1.8
20295	chemokine (C-C motif) ligand 17	0.029	1.6	0.001	1.6
17217	hromosome maintenance deficient 4 homolog (S. cerev	0.049	1.6	0.000	1.6
14187	aldo-keto reductase family 1, member B8	0.022	1.6	0.000	2.1
56619	C-type lectin domain family 4, member e	0.021	1.6	0.000	1.8
19224	prostaglandin-endoperoxide synthase 1	0.038	1.6	0.000	1.9
77056	transmembrane and coiled-coil domains 4	0.021	1.6	0.000	1.5

ID	Gene Name	$\Delta P T^{high}$ 2 dpi vs. PBS		WT 4 dpi vs. PBS	
217847	peptidase inhibitor, clade A (alpha-1 antiproteinase, anti	0.025	1.6	0.001	1.7
72027	solute carrier family 39 (zinc transporter), member 4	0.046	1.5	0.000	1.8
214523	transmembrane protease, serine 4	0.025	1.5	0.000	1.7
24047	chemokine (C-C motif) ligand 19	0.030	1.5	0.000	1.6
236082	dehydrogenase/reductase (SDR family) X chromosome	0.034	1.5	0.000	1.6
98238	leucine rich repeat containing 59	0.045	1.5	0.000	1.8
276770	eukaryotic translation initiation factor 5A	0.046	1.5	0.000	1.7
14058	coagulation factor X	0.026	1.5	0.000	1.6
76167	small nuclear ribonucleoprotein 35 (U11/U12)	0.035	1.5	0.000	1.6
12336	calpain, small subunit 1	0.042	1.5	0.000	1.6
208624	linked glycosylation 3 homolog (yeast, alpha-1,3-mannos	0.046	1.5	0.001	1.5
73385	family with sequence similarity 177, member A	0.044	1.5	0.000	2.0
26415	mitogen-activated protein kinase 13	0.036	1.5	0.000	1.9
66570	centromere protein M	0.021	1.5	0.001	1.6
20388	surfactant associated protein B	0.029	1.5	0.003	1.5
14793	cell division cycle associated 3	0.021	1.5	0.006	1.5
71755	dihydrodiol dehydrogenase (dimeric)	0.015	-1.5	0.001	-1.5
73316	calreticulin 3	0.036	-1.5	0.000	-1.5
66873	TLR4 interactor with leucine-rich repeats	0.014	-1.5	0.000	-1.8
69660	transmembrane BAX inhibitor motif containing 1	0.020	-1.5	0.000	-1.5
67120	tetratricopeptide repeat domain 14	0.030	-1.5	0.003	-1.5
234267	glycoprotein m6a	0.015	-1.5	0.000	-1.6
225583	RIKEN cDNA A730017C20 gene	0.021	-1.5	0.000	-1.5
19024	re phosphatase, receptor-type, F interacting protein, bin	0.012	-1.5	0.000	-1.6
68659	RIKEN cDNA 1110032E23 gene	0.012	-1.5	0.002	-1.5
18984	P450 (cytochrome) oxidoreductase	0.015	-1.5	0.001	-1.6
20742	spectrin beta 2	0.013	-1.6	0.000	-1.5
76560	protease, serine, 8 (prostasin)	0.031	-1.6	0.000	-1.7
81600	chitinase, acidic	0.012	-1.6	0.000	-2.1
11670	aldehyde dehydrogenase family 3, subfamily A1	0.038	-1.6	0.001	-1.6
56338	thioredoxin interacting protein	0.013	-1.6	0.001	-1.7
13143	death-associated protein kinase 2	0.014	-1.6	0.000	-1.6
66350	phospholipase A2, group X1IA	0.024	-1.6	0.001	-1.5
77045	B-cell CLL/lymphoma 7A	0.011	-1.6	0.000	-1.5
117158	secretoglobins, family 3A, member 2	0.012	-1.6	0.001	-1.5
13849	epoxide hydrolase 1, microsomal	0.008	-1.7	0.000	-1.6
19049	protein phosphatase 1, regulatory (inhibitor) subunit 1B	0.028	-1.7	0.000	-1.6
66959	dual specificity phosphatase 26 (putative)	0.016	-1.7	0.001	-1.6
18984	P450 (cytochrome) oxidoreductase	0.010	-1.7	0.001	-1.5
269016	SH3 domain containing ring finger 2	0.011	-1.7	0.002	-1.5
13009	cysteine and glycine-rich protein 3	0.027	-1.7	0.008	-1.7
27273	pyruvate dehydrogenase kinase, isoenzyme 4	0.015	-1.7	0.002	-1.5
77583	notum pectinacetylesterase homolog (Drosophila)	0.005	-1.8	0.000	-1.6
13009	cysteine and glycine-rich protein 3	0.010	-1.8	0.012	-1.7
15464	histidine rich calcium binding protein	0.007	-1.9	0.025	-1.6
59006	myozenin 2	0.029	-1.9	0.004	-1.8
83679	phosphodiesterase 4D interacting protein (myomegalin)	0.016	-1.9	0.023	-1.5
20517	solute carrier family 22 (organic cation transporter), membe	0.007	-2.0	0.003	-1.6
52609	chromobox homolog 7	0.003	-2.0	0.001	-1.7
20517	solute carrier family 22 (organic cation transporter), membe	0.004	-2.1	0.013	-1.6
17189	myoglobin	0.019	-2.4	0.006	-1.9
66402	sarcolipin	0.013	-2.5	0.006	-2.0
17189	myoglobin	0.015	-2.5	0.047	-1.8