

Supplementary Materials for

Neutrophilic inflammation in the respiratory mucosa predisposes to RSV infection

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Other Supplementary Material for this manuscript includes the following: (available at science.sciencemag.org/content/370/6513/eaax9301/suppl/DC1)

MDAR Reproducibility Checklist (PDF)

Materials and Methods

Flow cytometry reagents for murine studies

Target	Clone or order number	Fluorochrome	Vendor	Final concentration and dilution
Live cells	L34957	Aqua	Invitrogen	1:500
CD3	17A2	AF700	eBioscience	2 mg/ml
CD3	145-2C11	FITC	Biolegend	2.5 mg/ml
CD4	GK1.5	PE	eBioscience	0.5 mg/ml
CD8	53-6.7	eFluor780	eBioscience	0.5 mg/ml
CD11b	M1/70	AF700	eBioscience	0.5 mg/ml
CD11c	HL3	PE-CF594	BD Horizon	1 mg/ml
CD19	6D5	FITC	Biolegend	5 mg/ml
CD44	IM7	PE-Cy7	Biolegend	2 mg/ml
CD45	30-F11	BV605	Biolegend	0.25 mg/ml
CD62L	MEL-14	BV421	Biolegend	1 mg/ml
CD64	X54-5/7	APC	Biolegend	1 mg/ml
CD69	H1.2F3	BUV737	BD Horizon	1 mg/ml
CD103	2E7	PerCP-Cy5.5	Biolegend	1 mg/ml
Fc block (CD16/32)	93		Biolegend	2.5 mg/ml
Granzyme B	GB11	PECF594	BD Horizon	1:200
IFN-γ	XMG1.2	BV711	BD Horizon	1 mg/ml
Ly6C	HK1.4	BV421	Biolegend	0.125 mg/ml
Ly6C	HK1.4	eFluor450	eBioscience	0.25 mg/ml
Ly6G	1A8	FITC	Biolegend	5 mg/ml
Ly6G	1A8	APC-Cy7	Biolegend	0.5 mg/ml
Ly6G	1A8	BV785	Biolegend	1 mg/ml
MHC-II	M5/114.15.2	APC-eF780	eBiosciences	1 mg/ml
Siglec-F	E50-2440	PE	BD Pharmingen	1 mg/ml
Tetramer	RSV M ₁₈₇₋₁₉₅	Alexa647	NIH Tetramer facility	15 mg/ml

qPCR reagents for murine studies

Gene	Primer/Probe	Assay ID or	Vendor
		order number	
Ccl2	TaqMan® Gene Expression Assay	Mm00441242_m1	Thermo Fisher (ABI)
		FAM	
Cxcl2	TaqMan® Gene Expression Assay	Mm00436450_m1	Thermo Fisher (ABI)
		FAM	
Cxcl10	TaqMan® Gene Expression Assay	Mm00445235_m1	Thermo Fisher (ABI)
		FAM	
Gapdh	TaqMan® Gene Expression Assay	4351309	Thermo Fisher (ABI)
		VIC	
Il1b	TaqMan® Gene Expression Assay	Mm00434228_m1	Thermo Fisher (ABI)
		FAM	
	Fwd: 5'-	Previously	Invitrogen
	gaactcagtgtaggtagaatgtttgca-3'	reported (65)	
L gene	Rev: 5'-ttcagctatcattttctctgccaat-3'		Invitrogen
	Probe: 5'-(FAM)tttgaacctgtct		Eurofin
	gaacattcccggtt(TAM)-3'		
Tnfa	Fwd: 5'-catcttctcaaaattcgagtgacaa-	Previously	Invitrogen
	3'	reported (64)	
	Rev: 5'-tgggagtagacaaggtacaaccc-	• , ,	Invitrogen
	3'		· ·
	Probe:5'-(FAM)cacgtcgtagcaaac		Eurofin
	(TAM)-3'		

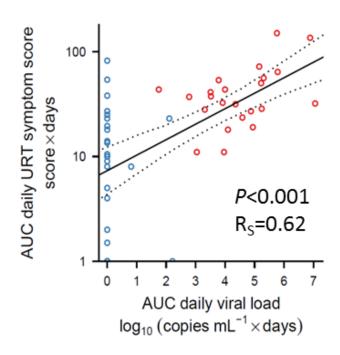


Fig. S1: Correlation between total upper respiratory tract symptom scores and viral load.

Correlation between area under the curve (AUC) of upper respiratory tract (URT) symptoms and AUC of daily viral load within the "Cold" (red, n=23) and "No Cold" (blue, n=25) groups was assessed using Spearman's test.

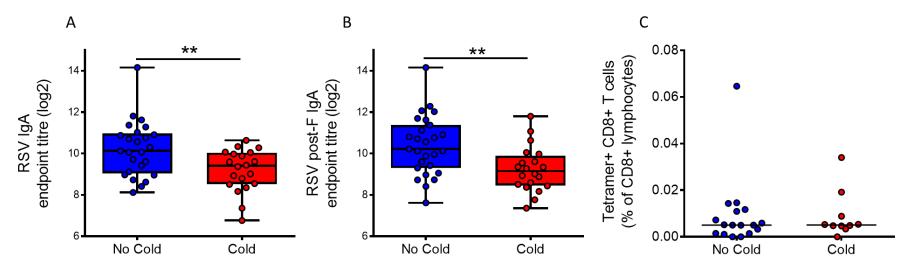


Fig. S2: Pre-inoculation nasal anti-RSV antibody levels, but not anti-RSV CD8⁺ T cell proportions, are associated with protection from infection.

Baseline levels of (**A**) total anti-RSV IgA and (**B**) post-F specific IgA in nasal lavage from "No Cold" (n=25, blue) and "Cold" (n=20, red) groups were measured by ELISA. (**C**) Frequencies of RSV-specific tetramer positive CD8⁺T cells in the lung from "No Cold" (n=17) and "Cold" (n=10) groups were quantified by flow cytometry. Data in panels A and B are represented as medians with interquartile ranges and minimum and maximum values. Data in panel C are represented as medians. Significance was tested by Mann Whitney U test. **P<0.01.

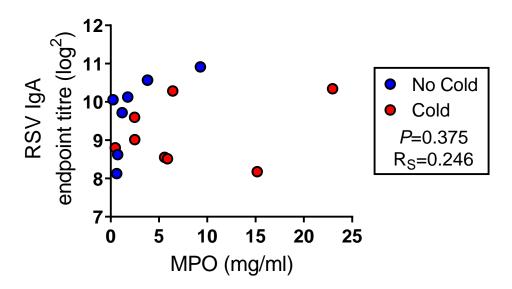


Fig. S3: Pre-inoculation nasal anti-RSV antibody levels are not associated with measures of neutrophilic inflammation.

Levels of total anti-RSV IgA and myeloperoxidase (MPO) were measured by ELISA and correlation determined in baseline samples from "No Cold" (n=7) and "Cold" (n=8) groups. Significance was tested in the combined group by Spearman's test.

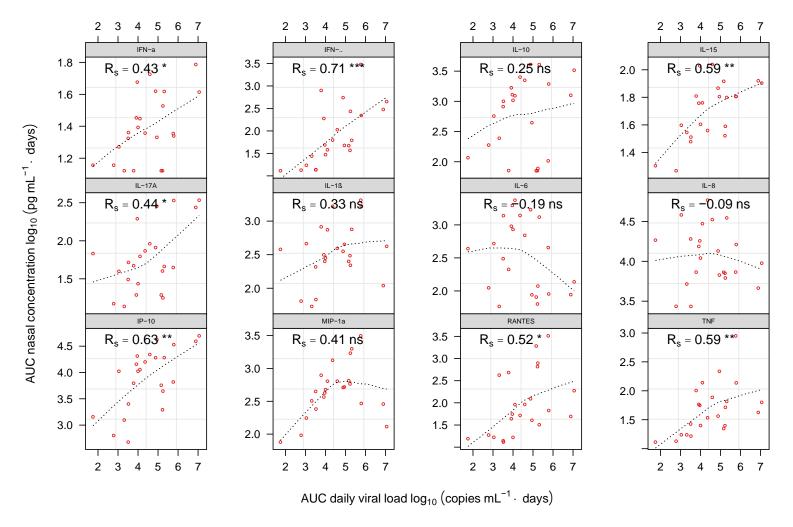


Fig. S4: Cumulative viral load correlates with the levels of several inflammatory mediators.

Within the Cold group (n=23), correlations between area under the curve (AUC) levels of daily viral load and cytokine/chemokine mediator levels for (**A**) IFN- α , (**B**) IL-17A, (**C**) CXCL10/IP-10, (**D**) IFN- γ , (**E**) IL-1 β , (**F**) CCL3/MIP-1 α , (**G**) IL-10, (**H**) IL-6, (**I**) CCL5/RANTES, (**J**) IL-15, (**K**) CXCL8/IL-8 and (**L**) TNF- α . Correlations were assessed using Spearman's test. *P<0.05, **P<0.01, ***P<0.001, ns=not significant.

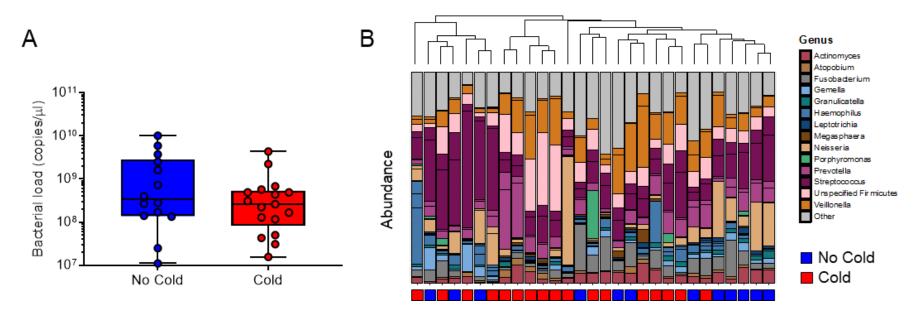
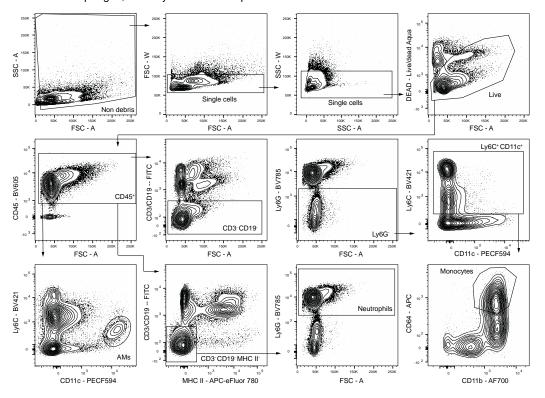


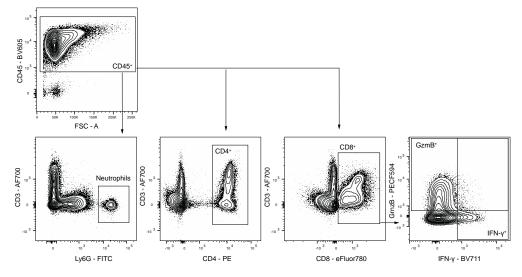
Fig. S5: The airway microbiome at point of virus exposure is not associated with susceptibility to infection.

(A) Bacterial load, measured by 16S qPCR, from baseline nasopharyngeal swabs of No Cold (n=12) and Cold (n=17) participants. (B) Baseline bacterial community ordered by Bray-Curtis hierarchical clustering where the top 20 OTUs are shown. Data in part A are represented as median and interquartiles with minimum and maximum values.

A Alveolar macrophages, monocytes and neutrophils



B T cell staining panel - Intracellular cytokine stain (gated to live cells as above)



C T cell staining panel - CD8+ tetramer stain (gated to live cells as above)

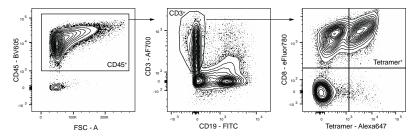


Fig. S6: Gating strategies for identifying murine lung cells.

(A) Mice were treated with mock (PBS) or 5-10 μg rCXCL1 i.n.. (A) At 12 hours or 18 hours post-RSV infection airway and lung innate immune cells were obtained by collagenase digestion and stained for the indicated cell surface molecules. After excluding debris and gating on single, live, CD45⁺ cells, the depicted gates were used to identify AMs, monocytes, and neutrophils. (B) Mice were treated with mock (PBS) or 10 μg rCXCL1 i.n. and after 12 hours infected with mock (PBS) or 7.5×10⁵ FFU RSV i.n.. After 8 days, lung cells were obtained by collagenase digestion and stained for the indicated cell surface molecules. After excluding debris and gating on single, live, CD45⁺ cells, the depicted gates were used to identify neutrophils, CD4⁺ and CD8⁺ T cells as well as GzmB⁺ and IFN-γ⁺ CD8⁺ T cells. (C) After excluding debris and gating on single, live, CD45⁺ cells, the depicted gates were used to identify RSV tetramer⁺ CD8⁺ T cells.

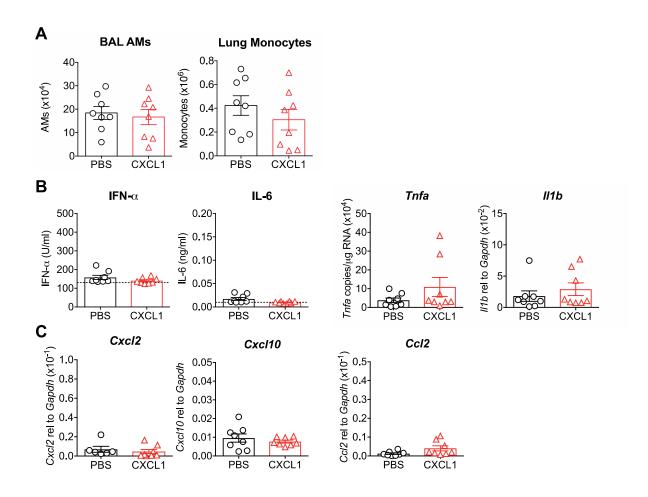


Fig. S7: Treatment with rCXCL1 alone causes no change in alveolar macrophages, monocytes or inflammatory mediators in the lung.

Mice were treated with mock (PBS) or 10 μ g rCXCL1 i.n. and after 12 hours, cells and mediators were quantified in the lung. (A) BAL AMs and lung monocytes were quantified 12 hours post CXCL1 treatment by flow cytometry. (B) IFN- α and IL-6 was quantified in BAL using ELISA and levels of *Il1b* and *Tnfa* were determined in lung tissue using qPCR. (C) *Cxcl2*, *Cxcl10*, and *Ccl2* were determined in lung tissue using qPCR. Data are presented as mean±SEM of eight individual mice per group, pooled from two independent experiments. The dotted line represents the limit of detection of the assay. Statistical significance was analyzed using unpaired, two-tailed Student's t test.

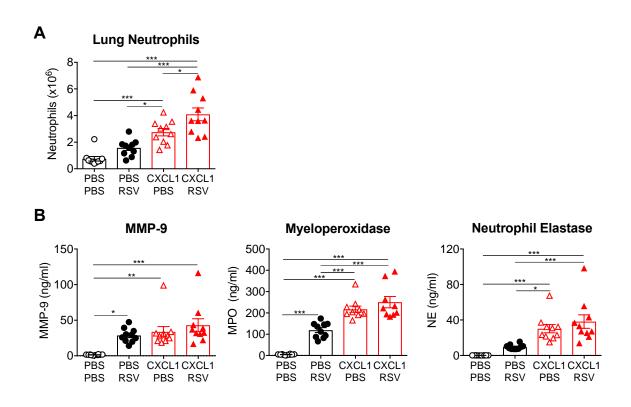


Fig. S8: RSV infection of rCXCL1 pre-treated mice enhances the early production of neutrophil markers.

Mice were treated with mock (PBS) or $5 \mu g$ rCXCL1 i.n. and after 9 hours infected with mock (PBS) or 7.5×10^5 FFU RSV i.n. for 18 hours. (**A**) The total number of lung neutrophils was quantified by flow cytometry as previously described in (65). (**B**) MMP-9, MPO and NE was quantified in BAL using ELISA. The data are presented as mean±SEM of 10 individual mice per group, pooled from two independent experiments. Statistical significance of differences was analyzed by one-way ANOVA with Tukey's post hoc test.*P<0.05, **P<0.01, ***P<0.001.

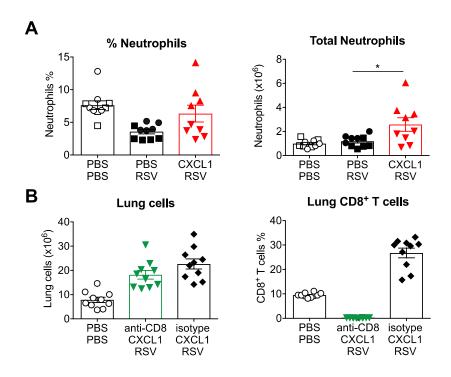


Fig. S9: Treatment with rCXCL1 pre-RSV infection does not result in an increase in neutrophil frequency on day 8 p.i. and treatment with anti-CD8 antibodies is sufficient to remove CD8⁺ T cells during RSV infection.

Mice were treated with mock (PBS) or 8 μg or 10 μg rCXCL1 i.n. and after 12 hours infected with mock (PBS) or 7.5×10⁵ FFU RSV i.n.. (**A**) The frequency and total number of lung neutrophils was quantified by flow cytometry. (**B**) To deplete CD8⁺ T cells, mice were treated with 250 μg anti-CD8 or isotype control i.p. on day -1, day 2 and day 5 p.i. and lung were analyzed on day 8 p.i.. Total number of lung cells and frequency of CD8⁺ T cells as quantified by flow cytometry. Data from (**A**) are presented as mean±SEM of 10 (PBS/PBS, PBS/RSV) or 9 (CXCL1/RSV) mice, pooled from two independent experiments - repeat 1 (10 μg CXCL1; circles) and repeat 2 (8 μg CXCL1; squares). Data from (**B**) are presented as mean±SEM of 10 mice, pooled from two independent experiments. Data in (**A** and **B**) were analyzed using one-way ANOVA with Tukey's post hoc test. **P*<0.05

Table S1

	Cold (n=23)	No Cold (n=25)	P-value
Age in years, mean	23.3 (18-50)	23.6 (18-39)	0.84
(range)			
Sex (M:F)	12:11	15:10	0.77
Ethnicity (n=)			
White	17 (74%)	19 (76%)	>0.99
Black	1 (4%)	4 (16%)	0.37
Asian	2 (9%)	0	0.22
Mixed	1 (4%)	2 (8%)	>0.99
Other	2 (9%)	0	0.22

Table S1: Demographics

Volunteer demographics were collected at study enrolment and categorized on subsequent development of a symptomatic infection following RSV inoculation (Cold, n=23) or not (No Cold, n=25). A two-tailed t-test was used to assess significance in volunteer age. Fisher's exact tests were used to assess significance in sex and ethnicity data.

Table S2: Baseline DEGs between "Cold" and "No Cold" groups (Padj<0.1, LFC>0.5)

	GeneName	baseMean	log ² FoldChange	lfcSE	stat	Pvalue	Padj
ENSG00000129455	KLK8	64.04073471	4.50463631	0.725538	6.208681	0.0000000005	0.0000078
ENSG00000140519	RHCG	327.2661994	3.899687376	0.687333	5.673651	0.0000000140	0.0001025
ENSG00000143536	CRNN	717.7315072	3.961919136	0.710893	5.573155	0.0000000250	0.0001124
ENSG00000136688	IL36G	119.3575404	3.485458598	0.629406	5.537698	0.0000000306	0.0001124
ENSG00000203785	SPRR2E	549.5597617	3.759191643	0.694542	5.412479	0.0000000622	0.0001823
ENSG00000244617	ASPRV1	201.6683348	2.541982486	0.473897	5.363995	0.0000000814	0.0001990
ENSG00000163216	SPRR2D	493.240127	3.489918519	0.673736	5.179946	0.0000002219	0.0004651
ENSG00000172137	CALB2	7.432513115	3.827424619	0.744758	5.139154	0.0000002760	0.0005060
ENSG00000102837	OLFM4	9.018542922	2.379694573	0.485505	4.901481	0.0000009512	0.0015502
ENSG00000164867	NOS3	39.06236907	2.172068356	0.455328	4.770338	0.0000018392	0.0024524
ENSG00000104327	CALB1	97.2215325	3.213472664	0.672135	4.780991	0.0000017443	0.0024524
ENSG00000145879	SPINK7	214.5721968	3.777459369	0.795095	4.750953	0.0000020246	0.0024747
ENSG00000167755	KLK6	219.7775905	3.749018528	0.793685	4.723561	0.0000023175	0.0026149
ENSG00000143369	ECM1	368.3426926	2.548748229	0.543078	4.693155	0.0000026902	0.0028186
ENSG00000088386	SLC15A1	58.06521529	1.444700757	0.309249	4.671646	0.0000029880	0.0029218
ENSG00000167754	KLK5	58.04069283	4.183165833	0.901151	4.642025	0.0000034501	0.0031629
ENSG00000244094	SPRR2F	174.9314565	3.559094351	0.769266	4.62661	0.0000037170	0.0032071
ENSG00000197948	FCHSD1	433.0477186	0.555918016	0.122298	4.545597	0.0000054780	0.0044639
ENSG00000188508	KRTDAP	56.82226766	4.12052942	0.913535	4.510532	0.0000064665	0.0049922
ENSG00000165799	RNASE7	76.05592952	2.591086011	0.578846	4.476294	0.0000075950	0.0055702
ENSG00000158825	CDA	31.30464651	3.126427907	0.70532	4.432636	0.0000093088	0.0060990
ENSG00000172005	MAL	315.8263003	2.780102998	2.780102998 0.629321 4.417623 0.00000997		0.0000099792	0.0060990
ENSG00000188100	FAM25A	52.79654449	3.385115694	0.766093	4.418675	0.0000099308	0.0060990
ENSG00000178734	LMO7DN	7.032824408	2.363797695	0.534435	4.422982	0.0000097348	0.0060990
ENSG00000256618	MTRNR2L1	31.19207611	4.405844562	1.017059	4.331946	0.0000147797	0.0078477
ENSG00000166396	SERPINB7	133.8826024	1.568727074	0.362378	4.328974	0.0000149805	0.0078477
ENSG00000105427	CNFN	357.4556348	2.628314998	0.606082	4.336567	0.0000144726	0.0078477
ENSG00000169035	KLK7	460.4004676	3.236932356	0.746379	4.336849	0.0000144540	0.0078477
ENSG00000177243	DEFB103B	12.86752713	4.068667323	0.94596	4.301099	0.0000169953	0.0083096
ENSG00000176797	DEFB103A	12.86752713	4.068667323	0.94596	4.301099	0.0000169953	0.0083096
ENSG00000196805	SPRR2B	12.46642556	4.007415528	0.94584	4.236884	0.0000226643	0.0105675
ENSG00000255823	MTRNR2L8	99.96331934	-2.063829514	0.487551	-4.23305	0.0000230542	0.0105675
ENSG00000185966	LCE3E	18.55284064	4.403689631	1.044843	4.214692	0.0000250120	0.0111174
ENSG00000269741	KLK9	38.39528424	3.634649191	0.869249	4.181368	0.0000289761	0.0125006
ENSG00000163202	LCE3D	21.85709696	3.766259743	0.907597	4.149703	0.0000332906	0.0136037
ENSG00000172382	PRSS27	235.5149533	2.146835495	0.51743	4.149036	0.0000333878	0.0136037
ENSG00000265590	AP000275.65	13.45435781	-2.313482025	0.565829	-4.08866	0.0000433880	0.0172004
ENSG00000163221	S100A12	117.0760162	2.42404596	0.595909	4.067813	0.0000474564	0.0183182
ENSG00000115602	IL1RL1	44.99164745	2.186332063	0.544735	4.01357	0.0000598072	0.0224936
ENSG00000185873	TMPRSS11B	162.1426424	2.930935532	0.738498	3.968781	0.0000722414	0.0264909
ENSG00000183307	CECR6	16.55877878	1.882385854	0.478856	3.93101	0.0000845897	0.0302625

ENSG00000169509	CRCT1	124.6713786	3.255307448	0.839868	3.875975	0.0001061984	0.0353209
ENSG00000087128	TMPRSS11E	856.279728	2.335954629	0.603236	3.872373	0.0001077807	0.0353209
ENSG00000235568	NFAM1	385.2546016	2.109095274	0.544836	3.871064	0.0001083611	0.0353209
ENSG00000143631	FLG	60.85365689	2.707724203	0.703833	3.847112	0.0001195184	0.0381108
ENSG00000059728	MXD1	3049.682399	1.568764572	0.411317	3.814	0.0001367357	0.0407370
ENSG00000204421	LY6G6C	11.23753312	2.015579995	0.530386	3.800212	0.0001445722	0.0407370
ENSG00000137558	PI15	7.292990874	2.650754443	0.696318	3.806818	0.0001407663	0.0407370
ENSG00000188373	C10orf99	11.24888949	3.740112396	0.980735	3.813582	0.0001369669	0.0407370
ENSG00000125910	S1PR4	174.6183595	2.16060284	0.569216	3.795754	0.0001471953	0.0407370
ENSG00000186474	KLK12	66.90156166	2.810027115	0.739856	3.798075	0.0001458243	0.0407370
ENSG00000101210	EEF1A2	8.860473621	1.927591183	0.50611	3.808641	0.0001397326	0.0407370
ENSG00000261272	MUC22	53.13744678	2.376412656	0.628685	3.779973	0.0001568455	0.0418293
ENSG00000154262	ABCA6	91.04472433	0.918131079	0.242831	3.780947	0.0001562332	0.0418293
ENSG00000162384	C1orf123	400.5115764	-0.274660048	0.072946	-3.76525	0.0001663849	0.0435810
ENSG00000180871	CXCR2	559.0871712	2.296300313	0.613115	3.745302	0.0001801766	0.0447868
ENSG00000196549	MME	223.9783358	2.350426949	0.628268	3.74112	0.0001832022	0.0447868
ENSG00000136943	CTSV	169.9791044	1.651903131	0.441093	3.745024	0.0001803766	0.0447868
ENSG00000204020	LIPN	40.67847121	2.99211748	0.797534	3.751711	0.0001756320	0.0447868
ENSG00000135636	DYSF	374.8411619	2.317309474	0.621536	3.728362	0.0001927284	0.0462954
ENSG00000113749	HRH2	69.49149917	2.193258848	0.588972	3.723878	0.0001961854	0.0462954
ENSG00000204021	LIPK	6.857510391	2.959242988	0.798168	3.707544	0.0002092793	0.0462954
ENSG00000068976	PYGM	17.33765035	2.050543859	0.552144	3.713782	0.0002041850	0.0462954
ENSG00000211448	DIO2	155.321791	1.510686245	0.406436	3.716914	0.0002016710	0.0462954
ENSG00000128917	DLL4	11.45535912	2.447852976	0.660082	3.708409	0.0002085653	0.0462954
ENSG00000188897	CTD-3088G3.8	323.1906061	1.78061636	0.480706	3.70417	0.0002120839	0.0462954
ENSG00000125810	CD93	601.1405142	1.759188231	0.475308	3.701152	0.0002146229	0.0462954
ENSG00000178150	ZNF114	7.989085047	2.029484872	0.549584	3.692762	0.0002218314	0.0471569
ENSG00000149564	ESAM	18.14827649	1.523369052	0.41299	3.688637	0.0002254587	0.0472433
ENSG00000203710	CR1	411.1933018	2.299624216	0.627107	3.667037	0.0002453771	0.0481389
ENSG00000163464	CXCR1	453.8760438	2.616490966	0.712521	3.672159	0.0002405100	0.0481389
ENSG00000120129	DUSP1	6115.128063	1.732263316	0.473872	3.655551	0.0002566297	0.0481389
ENSG00000152137	HSPB8	900.9324017	1.778499688	0.487281	3.649845	0.0002623991	0.0481389
ENSG00000184508	HDDC3	101.6802136	-0.391065227	0.106941	-3.65684	0.0002553462	0.0481389
ENSG00000206172	HBA1	9.437796303	3.255644841	0.885269	3.677576	0.0002354608	0.0481389
ENSG00000141096	DPEP3	8.922090167	2.600257498	0.709629	3.66425	0.0002480641	0.0481389
ENSG00000076662	ICAM3	139.9038075	2.270536264	0.620081	3.661675	0.0002505716	0.0481389
ENSG00000244482	LILRA6	189.3604241	2.418416833	0.662635	3.649695	0.0002625518	0.0481389
ENSG00000170373	CST1	131.6759055	-3.542321735	0.97027	-3.65086	0.0002613632	0.0481389
ENSG00000171476	HOPX	495.7867843	1.529493784	0.420797	3.634752	0.0002782483	0.0503870
ENSG00000254415	SIGLEC14	45.14160974	1.877309137	0.517712	3.626168	0.0002876585	0.0514558
ENSG00000081237	PTPRC	4546.785921	1.738982361	0.480872	3.616312	0.0002988305	0.0519840
ENSG00000107736	CDH23	109.6230575	0.860731249	0.238059	3.615619	0.0002996305	0.0519840
ENSG00000142347	MYO1F	1440.496128	1.976436605	0.546849	3.614228	0.0003012436	0.0519840
ENSG00000188404	SELL	592.631915	1.4423354	0.40133	3.593889	0.0003257790	0.0523150

ENSG00000163219	ARHGAP25	554.8197482	1.597820813	0.44492	3.591254	0.0003290910	0.0523150
ENSG00000132965	ALOX5AP	361.1835711	1.581896625	0.440738	3.5892	0.0003316943	0.0523150
ENSG00000132359	RAP1GAP2	213.009783	1.296496824	0.360265	3.598735	0.0003197694	0.0523150
ENSG00000185862	EVI2B	461.495179	1.699127547	0.472435	3.596531	0.0003224895	0.0523150
ENSG00000276070	CCL4L2	68.6673633	1.767519198	0.491474	3.596362	0.0003226984	0.0523150
ENSG00000239998	LILRA2	156.1708969	2.41359626	0.67145	3.594603	0.0003248862	0.0523150
ENSG00000156282	CLDN17	49.71152413	3.337239908	0.926759	3.600977	0.0003170233	0.0523150
ENSG00000163563	MNDA	868.6380366	2.092578113	0.58443	3.580547	0.0003428759	0.0523886
ENSG00000100908	EMC9	129.5613142	-0.518890144	0.14484	-3.5825	0.0003403253	0.0523886
ENSG00000124126	PREX1	1676.142545	1.370895286	0.382525	3.583807	0.0003386230	0.0523886
ENSG00000116741	RGS2	2515.481448	2.068800406	0.579639	3.569118	0.0003581852	0.0525386
ENSG00000159884	CCDC107	36.05187668	-0.506034534	0.141596	-3.57379	0.0003518523	0.0525386
ENSG00000077420	APBB1IP	243.778356	1.64456222	0.460633	3.570225	0.0003566752	0.0525386
ENSG00000185201	IFITM2	1123.511188	1.573639347	0.440251	3.574411	0.0003510174	0.0525386
ENSG00000198576	ARC	12.59565389	1.921251953	0.54003	3.557676	0.0003741507	0.0543370
ENSG00000012779	ALOX5	542.1569197	1.341197064	0.3777	3.55096	0.0003838295	0.0551962
ENSG00000147408	CSGALNACT1	47.32334612	1.736073692	0.489823	3.544287	0.0003936766	0.0552874
ENSG00000127084	FGD3	488.0688261	1.329285081	0.375463	3.540387	0.0003995406	0.0552874
ENSG00000160593	AMICA1	1529.369162	1.427087059	0.402968	3.541442	0.0003979461	0.0552874
ENSG00000184922	FMNL1	417.2457271	1.543935634	0.435267	3.547097	0.0003895014	0.0552874
ENSG00000203786	KPRP	5.488623737	3.534762474	1.000553	3.532808	0.0004111703	0.0563649
ENSG00000115008	IL1A	41.13563665	2.044716665	0.579827	3.526423	0.0004212131	0.0572070
ENSG00000085514	PILRA	213.260431	1.839828677	0.522145	3.523597	0.0004257310	0.0572901
ENSG00000015285	WAS	196.6610082	1.566856851	0.445876	3.514111	0.0004412283	0.0588358
ENSG00000204305	AGER	31.35634892	1.115269179	0.317594	3.511616	0.0004453905	0.0588557
ENSG00000081041	CXCL2	121.8368299	1.121447805	0.320025	3.504247	0.0004578998	0.0599685
ENSG00000117115	PADI2	311.0156325	1.595711216	0.455678	3.501843	0.0004620517	0.0599768
ENSG00000186806	VSIG10L	112.6784624	1.836473622	0.524908	3.498656	0.0004676100	0.0601658
ENSG00000123329	ARHGAP9	479.2259745	1.504954786	0.430779	3.493566	0.0004766144	0.0607911
ENSG00000197405	C5AR1	1048.994493	2.117769646	0.606742	3.490394	0.0004823089	0.0609871
ENSG00000111181	SLC6A12	40.50839526	1.247431148	0.357807	3.486322	0.0004897108	0.0612578
ENSG00000169715	MT1E	513.315856	-0.685757788	0.196795	-3.48464	0.0004928019	0.0612578
ENSG00000132510	KDM6B	579.8129011	1.305400127	0.375133	3.479832	0.0005017278	0.0618432
ENSG00000189051	RNF222	48.81576384	2.238886942	0.643902	3.477063	0.0005069389	0.0619648
ENSG00000130775	THEMIS2	767.653598	1.653998209	0.477286	3.465427	0.0005293899	0.0625580
ENSG00000016602	CLCA4	2436.442163	1.817346604	0.523652	3.470523	0.0005194464	0.0625580
ENSG00000151702	FLI1	244.7806654	1.307265921	0.377325	3.464563	0.0005310932	0.0625580
ENSG00000126860	EVI2A	228.3966342	1.699506437	0.489786	3.469899	0.0005206545	0.0625580
ENSG00000127507	ADGRE2	416.7557519	1.753547713	0.506288	3.463541	0.0005331160	0.0625580
ENSG00000059804	SLC2A3	905.4839017	2.010343885	0.581013	3.460064	0.0005400461	0.0628682
ENSG00000114268	PFKFB4	165.0457522	1.460312211	0.422942	3.452745	0.0005549131	0.0635896
ENSG00000155926	SLA	742.9187908	1.459286381	0.422635	3.452832	0.0005547350	0.0635896
ENSG00000159337	PLA2G4D	13.88198456	1.569829037	0.455069	3.44965	0.0005613144	0.0638245
ENSG00000171608	PIK3CD	776.2463976	1.270669369	0.368994	3.443601	0.0005740223	0.0647674

ENSG00000129353	0.0659737
	0.0650727
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	0.0659737
ENSG00000124216 SNAII 7.696103487 1.970326867 0.574818 3.427739 0.0006086298	0.0661288
ENSG00000152518 ZFP36L2 658.0270618 0.533612565 0.155805 3.424877 0.0006150775	0.0663379
ENSG00000140678 ITGAX 1565.747602 1.594065917 0.465752 3.42256 0.0006203438	0.0664175
ENSG00000082074 FYB 991.9259765 1.340812758 0.392852 3.413019 0.0006424741	0.0665579
ENSG00000197081 <i>IGF2R</i> 4115.112231 0.870500071 0.254689 3.41789 0.0006310867	0.0665579
ENSG00000106780 <i>MEGF9</i> 783.34156 1.002450648 0.293299 3.417844 0.0006311927	0.0665579
ENSG00000178372 CALML5 227.8365785 1.723079938 0.505537 3.408413 0.0006534185	0.0665579
ENSG00000033327 GAB2 587.0589028 1.009740964 0.2958 3.413589 0.0006411326	0.0665579
ENSG00000091592 <i>NLRP1</i> 904.1310348 0.92872128 0.272274 3.410982 0.0006472944	0.0665579
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ENSG00000183091 NEB 147.948048 1.165209102 0.342494 3.402126 0.0006686381	0.0676385
ENSG00000095370 SH2D3C 124.8445678 1.396717987 0.410791 3.40007 0.0006736854	0.0676823
ENSG00000105329 TGFB1 135.7183389 1.026453687 0.30292 3.388533 0.0007026760	0.0701146
ENSG00000151726 ACSL1 3497.092379 1.115803771 0.329795 3.383326 0.0007161359	0.0709749
ENSG00000213190 <i>MLLT11</i> 34.96655406 0.991937175 0.293853 3.375624 0.0007364847	0.0720184
ENSG00000128016 ZFP36 2290.304626 1.418453692 0.420154 3.376035 0.0007353859	0.0720184
ENSG00000183625 CCR3 42.86315786 2.443863244 0.726592 3.363461 0.0007697164	0.0728125
ENSG00000120738 <i>EGR1</i> 617.768747 2.058619948 0.613673 3.354587 0.0007948363	0.0728125
ENSG00000057657 PRDM1 535.5767203 1.000608405 0.298692 3.349963 0.0008082233	0.0728125
ENSG00000181016	0.0728125
ENSG00000120156 TEK 12.27850013 2.088865477 0.62069 3.365391 0.0007643512	0.0728125
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ENSG00000066336 SPII 474.2143771 1.539695642 0.4568 3.370612 0.0007500137	0.0728125
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ENSG00000161638 ITGA5 427.2568365 1.294966403 0.385826 3.356348 0.0007897905	0.0728125
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ENSG00000167916	0.0728125
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ENSG00000099308 MAST3 289.4385807 1.096338807 0.327958 3.342928 0.0008289942	0.0728125
ENSG00000175489 LRRC25 220.170772 1.705010136 0.508146 3.355353 0.0007926364	0.0728125
ENSG00000171777 RASGRP4 169.2813114 2.401692932 0.718349 3.343353 0.0008277259	0.0728125
ENSG00000105501 SIGLEC5 68.90107457 2.374748837 0.709128 3.348828 0.0008115406	0.0728125
ENSG00000177663 <i>IL17RA</i> 892.8199897 0.919762481 0.273986 3.356964 0.0007880339	0.0728125
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ENSG00000115165 CYTIP 605.0026885 1.549162056 0.465529 3.327745 0.0008755193	0.0732848
ENSG00000173559 NABPI 3508.644402 1.454169197 0.437143 3.326532 0.0008793378	0.0732848
ENSG00000175315 CST6 43.40935031 1.437118927 0.431248 3.332468 0.0008607948	0.0732848

ENSGO0000198153 SIRPM \$20,3180461 1.149654662 0.345046 3.331828 0.0008627758 0.0732248 ENSGO0000163209 SPRICE	ENSG00000133246	PRAM1	42.79085834	1.154190513	0.346598	3.330052	0.0008682973	0.0732848
ENSG0000018390								
ENSG0000018390	ENSG00000163209			1.892942748			0.0008906446	
ENSG00000115590 ILIR2 359.8218257 2.191449718 0.661145 3.31463 0.0009176438 0.0747778 ENSG00000124882 ERG		C19orf35	14.74118642	2.027840744	0.610195	3.323266	0.0008897002	0.0733931
ENSG00000113070	ENSG00000115590	IL1R2	359.8218257	2.191449718	0.661145	3.31463	0.0009176438	0.0747778
ENSG00000178726	ENSG00000124882	EREG	227.0051715	1.760952973	0.531171	3.315229	0.0009156795	0.0747778
ENSG00000197943	ENSG00000113070	HBEGF	280.9775264	1.604054578	0.484422	3.311273	0.0009287250	0.0752626
ENSG00000162572 SCNNID S2.00949878 0.77980895 0.236387 3.298826 0.0009709000 0.0768620 ENSG00000153887 MPZ 43.30825426 1.23987961 0.376097 3.296706 0.0009782593 0.0768620 ENSG00000151948 GLTIDI 194.0027529 2.453177853 0.744772 3.29586 0.0009811975 0.0768620 ENSG00000151948 GLTIDI 194.0027529 2.453177853 0.744772 3.293865 0.0009882004 0.0768620 ENSG0000014527 CARDI-I 189.6181425 0.664667081 0.201809 3.923245 0.0009903816 0.0768620 ENSG00000198342 ZNF442 55.2332415 0.633468395 0.191935 3.30043 0.0009635028 0.0768620 ENSG00000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG00000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG0000016375 FCHO1 85.17477418 1.396035122 0.426313 3.274673 0.0010578446 0.0812380 ENSG0000016375 FCHO1 85.17477418 1.396035122 0.426313 3.274673 0.0010578446 0.0812380 ENSG00000163546 SJ0008 10866.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG0000013346 SJ0008 10866.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG0000011336 HCK 871.1965188 1.616043212 0.495987 3.258239 0.0011210598 0.0843267 ENSG0000010203 FOLR3 1.09684464 2.94775516 0.906403 3.251838 0.0011411927 0.0853732 ENSG0000010203 FOLR3 1.09684464 2.94775516 0.906403 3.251838 0.001146131 0.0853732 ENSG00000159516 SPRR2G 8.90036315 2.970580876 0.902619 3.22707 0.0012506472 0.0899771 ENSG00000159516 SPRR2G 8.90036315 2.970580876 0.902619 3.22502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.90036315 2.970580876 0.902619 3.22502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.90036315 2.970580876 0.902619 3.22552 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 1.285404679 1.20525803 0.305399 3.21652 0.001257392 0.0915786 E	ENSG00000178726	THBD	569.6998692	2.072148166	0.626151	3.30934	0.0009351605	0.0753678
ENSG0000014113	ENSG00000197943	PLCG2	550.1524259	0.988242075	0.299196	3.302994	0.0009565855	0.0766732
ENSG00000141131 LYRMM 209.8049346 -0.386119827 0.117153 -3.29586 0.0009811975 0.0768620 ENSG00000151948 GLTIDI 194.0027529 2.453177853 0.744772 3.293865 0.000983004 0.0768620 ENSG0000141527 CARDI4 189.6181425 0.664607081 0.201809 3.293245 0.0009903816 0.0768620 ENSG00000163218 PGLYRP4 55.29332415 -0.6633468395 0.191935 -3.30043 0.0009653628 0.0768620 ENSG00000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG00000163715 PCHOI 85.17477418 1.396035122 0.426313 3.274673 0.0010267976 0.0912688 ENSG00000167759 KLKI3 432.5007784 2.177708944 0.667258 3.261671 0.001097881 0.0840192 ENSG00000143546 SIDOAN 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG000001336 HCK 871.1965188 1.616043212 0.495987 3.25822 0.0011187671 0.0843267 ENSG000001203 PCLR3 10.09684646 2.947475316 0.905643 3.25185 0.0011411927 0.0853732 ENSG000001203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG0000015310 SPIIKS 1396.236797 1.525317868 0.47005 3.241184 0.001193453 0.0873346 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012575197 0.0899771 ENSG0000015338 LCIPAI 147.920447 1.58966916 0.492758 3.225502 0.0012575197 0.0899771 ENSG0000015338 SLCIPAI 147.920447 1.58966916 0.492758 3.225502 0.0012575197 0.0899771 ENSG0000015338 SLCIPAI 147.920447 1.58966916 0.492758 3.22610 0.0012575197 0.0989771 ENSG0000015308 LARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0012575197 0.0915786 ENSG0000015308 LARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG0000015308 LARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG0000015300 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012575190 0.0915786 ENSG0000015300 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012575100 0.0915786 ENSG0000015479 CILOT96 14.69699214 1.595803871 0.681848 3.	ENSG00000162572	SCNN1D	52.00949878	0.779800895	0.236387	3.298826	0.0009709006	0.0768620
ENSG00000151948 GLT1D1 194.0027529 2.453177853 0.744772 3.293865 0.0009882004 0.0768620 ENSG00000141527 CARD14 189.6181425 0.664607081 0.201809 3.293245 0.0009903816 0.0768620 ENSG00000198342 ZNF442 55.29332415 -0.633468395 0.191935 -3.30043 0.0009653628 0.0768620 ENSG00000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG0000013475 FCH01 85.17477418 1.396035122 0.426313 3.274673 0.001057846 0.0812380 ENSG00000167759 KLK13 432.5007784 2.177708944 0.667258 3.263671 0.0010997881 0.0840192 ENSG00000143546 S100A8 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG00000213347 MXD3 159.4639724 1.254876515 0.385071 3.25882 0.0011187671 0.0843267 ENSG000001336 HCK 871.1965188 1.616043212 0.495987 3.258239 0.0011210598 0.0843267 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.996403 3.258188 0.0011411927 0.0853732 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.996403 3.258188 0.0011814721 0.0853732 ENSG0000013710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0877386 ENSG00000119535 CSF3R 3574.954552 2.277942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG0000015429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012575297 0.0899771 ENSG00000153307 SAMSN1 447.0759092 1.459101124 0.453116 3.220151 0.0012373831 0.0999771 ENSG00000153307 SAMSN1 447.0759092 1.459101124 0.453116 3.220151 0.001234896 0.0915786 ENSG0000015391 SAMSN1 447.0759092 1.459101124 0.453116 3.220151 0.001234896 0.0915786 ENSG0000015391 TPKG1 146.6351541 0.982323984 0.305399 3.216525 0.0012575312 0.0915786 ENSG0000015307 SAMSN1 447.0759092 1.459101124 0.453116 3.20154 0.0013435703 0.091	ENSG00000158887	MPZ	43.30825426	1.239879961	0.376097	3.296706	0.0009782593	0.0768620
ENSG0000141527 CARD14 189.6181425 0.664607081 0.201809 3.293245 0.0009903816 0.0768620 ENSG0000198342 ZNF442 55.29332415 -0.633468395 0.191935 -3.30043 0.0009653628 0.0768620 ENSG0000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG00000130475 FCHO1 85.17477418 1.396035122 0.426313 3.274673 0.0010578446 0.0812380 ENSG00000167759 KLK13 432.5007784 2.177708944 0.667258 3.263671 0.0010997881 0.0840192 ENSG0000143546 SJOAR 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG0000013347 MXD3 159.4639724 1.254876515 0.385071 3.25882 0.001141977 0.0843267 ENSG00000101336 HCK 871.1965188 1.616043212 0.495987 3.258239 0.001120598 0.0843267 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.001141927 0.0853732 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG00000153710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.001193453 0.0877386 ENSG0000015916 SPR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012576472 0.0899771 ENSG0000158429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG0000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012573937 0.0099771 ENSG0000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.001237370 0.0912786 ENSG00000158801 TRG1 146.6351541 0.982323984 0.305399 3.216525 0.001247170 0.0899771 ENSG0000015380 TRKG1 146.6351541 0.982323984 0.305399 3.216525 0.001237310 0.0915786 ENSG0000015380 TRKG1 4.66959214 1.958308711 0.453163 3.20154 0.001335703 0.0915786 ENSG0000015380 TRKG1 4.469699214 1.958308711 0.453116 3.20151 0.00135797 0.0915786 ENSG0000015388 TRKG1 4.469699214 1.958308711 0.453166 0.204646 0.0013673106 0.0915786 ENSG00000153	ENSG00000214113	LYRM4	209.8049346	-0.386119827	0.117153	-3.29586	0.0009811975	0.0768620
ENSG0000198342 ZNF442 55.29332415 -0.633468395 0.191935 -3.30043 0.009653628 0.0768620	ENSG00000151948	GLT1D1	194.0027529	2.453177853	0.744772	3.293865	0.0009882004	0.0768620
ENSG00000163218 PGLYRP4 35.40514359 1.507393971 0.45914 3.283079 0.0010267976 0.0792688 ENSG00000130475 FCHO1 85.17477418 1.396035122 0.426313 3.274673 0.0010578446 0.0812380 ENSG00000167759 KLK13 432.5007784 2.177708944 0.667258 3.263671 0.0010997881 0.0840192 ENSG00000143546 S100A8 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG000001336 HCK 871.1965188 1.616043212 0.495987 3.25822 0.0011187671 0.0843267 ENSG0000010336 HCK 871.1965188 1.616043212 0.495987 3.25823 0.0011210598 0.0843267 ENSG0000010336 HCK 871.1965188 1.616043212 0.495987 3.25823 0.001141027 0.0853732 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.001146131 0.0853732 ENSG00000133710 SPINK3 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0877386 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.902019 3.22707 0.0012596472 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.902019 3.22707 0.001257927 0.0899771 ENSG0000015536 SCF2R 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG0000015530 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015931 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015930 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015930 SAMSNI 447.0759092 1.459101124 0.453116 3.20151 0.0012812317 0.0915786 ENSG0000015936 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015936 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015936 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0915786 ENSG0000015936 SAMSNI 447.0759092 1.459101124 0.453116 3.203164 0.001367570 0.0915786 ENS	ENSG00000141527	CARD14	189.6181425	0.664607081	0.201809	3.293245	0.0009903816	0.0768620
ENSG00000130475 FCHO1 85.17477418 1.396035122 0.426313 3.274673 0.0010578446 0.0812380 ENSG00000167759 KLK13 432.5007784 2.177708944 0.667258 3.263671 0.0010997881 0.0840192 ENSG00000143546 S100A8 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG00000213347 MXD3 159.4639724 1.254876515 0.385071 3.25882 0.0011187671 0.0843267 ENSG00000101336 HCK 871.1965188 1.616043212 0.495987 3.258239 0.0011210598 0.0843267 ENSG00000204542 CCOrfl 6.023863346 3.043601347 0.935576 3.253185 0.0011411927 0.0853732 ENSG0000010203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG0000015920 FOLR3 130.9684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG00000119235 CSF3R 3574.954552 2.277942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000159516 SPRR2G 8.90054649 0.706259 3.205500 0.0012573831 0.0899771 ENSG00000159530 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012373831 0.0899771 ENSG0000016255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.001247170 0.0899771 ENSG00000158018 INPP5D 539,7586028 0.759423223 0.236774 3.207374 0.001335259 0.0915786 ENSG00000152342 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG0000015296 ZNF1/7 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000158081 INPP5D 539,7586028 0.759423223 0.236774 3.207374 0.001335259 0.0915786 ENSG00000152926 ZNF1/7 700.4702591 0.667203224 0.208406 3.20146	ENSG00000198342	ZNF442	55.29332415	-0.633468395	0.191935	-3.30043	0.0009653628	0.0768620
ENSG00000167759	ENSG00000163218	PGLYRP4	35.40514359	1.507393971	0.45914	3.283079	0.0010267976	0.0792688
ENSG00000143546 \$\$I00A8\$ 10686.37567 2.151083123 0.659681 3.260795 0.0011110021 0.0843267 ENSG00000213347 MXD3 159.4639724 1.254876515 0.385071 3.25882 0.0011187671 0.0843267 ENSG00000101336 HCK 871.1965188 1.616043212 0.495987 3.258239 0.0011210598 0.0843267 ENSG00000204542 C6orf15 6.203863346 3.043601347 0.935576 3.253185 0.0011411927 0.0853732 ENSG00000110203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG00000133710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0875346 ENSG00000119535 CSF3R 3574.954552 2.277942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.97080876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000154429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 C15orf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012373831 0.099771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.001231377 0.0912287 ENSG00000168018 INPF5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG0000018001 TRGI 146.6351541 0.982323984 0.303399 3.216525 0.0012975312 0.0915786 ENSG00000157368 RARP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000157310 CHST11 408.7728418 1.186643045 0.370603 3.201464 0.0013673106 0.0915786 ENSG00000173101 CHST11 408.7728418 1.186643045 0.370603 3.201490 0.0013651076 0.0915786 ENSG0000013471 AOC3 22.77300856 1.226591369 0.381788 3.21036 0.0013513616 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0	ENSG00000130475	FCHO1	85.17477418	1.396035122	0.426313	3.274673	0.0010578446	0.0812380
ENSG00000213347 MXD3	ENSG00000167759	KLK13	432.5007784	2.177708944	0.667258	3.263671	0.0010997881	0.0840192
ENSG00000101336	ENSG00000143546	S100A8	10686.37567	2.151083123	0.659681	3.260795	0.0011110021	0.0843267
ENSG0000010204542	ENSG00000213347	MXD3	159.4639724	1.254876515	0.385071	3.25882	0.0011187671	0.0843267
ENSG00000110203 FOLR3 10.09684646 2.947475316 0.906403 3.251838 0.0011466131 0.0853732 ENSG00000062282 DGAT2 385.1136643 1.889009237 0.582431 3.243316 0.0011814721 0.0875244 ENSG00000133710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0877386 ENSG00000119535 CSF3R 3574.954552 2.277942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000159429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 CISorf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.001247170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000188001 TPRG1 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000188001 TPRG1 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000187479 CIIorf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.20184 0.0013561901 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173160 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000101336	НСК	871.1965188	1.616043212	0.495987	3.258239	0.0011210598	0.0843267
ENSG0000062282 DGAT2 385.1136643 1.889009237 0.582431 3.24316 0.0011814721 0.0875244 ENSG00000133710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0877386 ENSG00000119535 CSF3R 3574.954552 2.277942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000159429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 C150rf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.00125748962 0.0899771 ENSG00000160255 TGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000187479 C110rf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG0000013471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000204542	C6orf15	6.203863346	3.043601347	0.935576	3.253185	0.0011411927	0.0853732
ENSG00000133710 SPINK5 1396.236797 1.523517868 0.47005 3.241184 0.0011903453 0.0877386 ENSG00000119535 CSF3R 3574.954552 2.2777942108 0.706229 3.225502 0.0012575197 0.0899771 ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000154429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 C15orf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000182018 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013615076 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.001361076 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.001361076 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.001361076 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.001355665 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013513616 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000110203	FOLR3	10.09684646	2.947475316	0.906403	3.251838	0.0011466131	0.0853732
ENSG00000119535	ENSG00000062282	DGAT2	385.1136643	1.889009237	0.582431	3.243316	0.0011814721	0.0875244
ENSG00000159516 SPRR2G 8.900936315 2.970580876 0.920519 3.22707 0.0012506472 0.0899771 ENSG00000154429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 CI5orf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000152926 ZNF117 700.4702591 <td< td=""><td>ENSG00000133710</td><td>SPINK5</td><td>1396.236797</td><td>1.523517868</td><td>0.47005</td><td>3.241184</td><td>0.0011903453</td><td>0.0877386</td></td<>	ENSG00000133710	SPINK5	1396.236797	1.523517868	0.47005	3.241184	0.0011903453	0.0877386
ENSG00000154429 CCSAP 160.9765066 0.524627084 0.162647 3.225554 0.0012572927 0.0899771 ENSG00000188549 C15orf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 <t< td=""><td>ENSG00000119535</td><td>CSF3R</td><td>3574.954552</td><td>2.277942108</td><td>0.706229</td><td>3.225502</td><td>0.0012575197</td><td>0.0899771</td></t<>	ENSG00000119535	CSF3R	3574.954552	2.277942108	0.706229	3.225502	0.0012575197	0.0899771
ENSG00000188549 C15orf52 151.2467778 0.785723445 0.243249 3.23012 0.0012373831 0.0899771 ENSG00000160255 ITGB2 1285.404679 1.207525803 0.373976 3.22889 0.0012427170 0.0899771 ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000187479 C110rf96 14.69699214	ENSG00000159516	SPRR2G	8.900936315	2.970580876	0.920519	3.22707	0.0012506472	0.0899771
ENSG00000160255	ENSG00000154429	CCSAP	160.9765066	0.524627084	0.162647	3.225554	0.0012572927	0.0899771
ENSG00000173638 SLC19A1 147.9920447 1.589686916 0.492758 3.2261 0.0012548962 0.0899771 ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.2012407 0.0013651076 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166	ENSG00000188549	C15orf52	151.2467778	0.785723445	0.243249	3.23012	0.0012373831	0.0899771
ENSG00000155307 SAMSNI 447.0759092 1.459101124 0.453116 3.220151 0.0012812317 0.0912287 ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000059377 TBXAS1 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG000000173868 PHOSPHO1 209.3184166	ENSG00000160255	ITGB2	1285.404679	1.207525803	0.373976	3.22889	0.0012427170	0.0899771
ENSG00000162747 FCGR3B 1127.66368 2.265580387 0.706557 3.206507 0.0013435703 0.0915786 ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000059377 TBXASI 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG0000017310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG000000160229 ZNF66 56.13988521 <	ENSG00000173638	SLC19A1	147.9920447	1.589686916	0.492758	3.2261	0.0012548962	0.0899771
ENSG00000168918 INPP5D 539.7586028 0.759423223 0.236774 3.207374 0.0013395295 0.0915786 ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000059377 TBXAS1 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG000000160229 ZNF66 56.13988521	ENSG00000155307	SAMSN1	447.0759092	1.459101124	0.453116	3.220151	0.0012812317	0.0912287
ENSG00000188001 TPRGI 146.6351541 0.982323984 0.305399 3.216525 0.0012975312 0.0915786 ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000187479 TBXASI 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG000000160229 ZNF66 56.13988521	ENSG00000162747	FCGR3B	1127.66368	2.265580387	0.706557	3.206507	0.0013435703	0.0915786
ENSG00000120318 ARAP3 312.6943691 0.880062277 0.274794 3.202629 0.0013617921 0.0915786 ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000059377 TBXAS1 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG000000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000168918	INPP5D	539.7586028	0.759423223	0.236774	3.207374	0.0013395295	0.0915786
ENSG00000152926 ZNF117 700.4702591 0.667203224 0.208406 3.201464 0.0013673106 0.0915786 ENSG00000059377 TBXAS1 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000188001	TPRG1	146.6351541	0.982323984	0.305399	3.216525	0.0012975312	0.0915786
ENSG00000059377 TBXASI 356.7962638 1.33421913 0.415333 3.212407 0.0013162757 0.0915786 ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000120318	ARAP3	312.6943691	0.880062277	0.274794	3.202629	0.0013617921	0.0915786
ENSG00000187479 C11orf96 14.69699214 1.958308711 0.611243 3.203816 0.0013561901 0.0915786 ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000152926	ZNF117	700.4702591	0.667203224	0.208406	3.201464	0.0013673106	0.0915786
ENSG00000171310 CHST11 408.7728418 1.186643045 0.370603 3.201929 0.0013651076 0.0915786 ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000059377	TBXAS1	356.7962638	1.33421913	0.415333	3.212407	0.0013162757	0.0915786
ENSG00000131471 AOC3 22.77300856 1.226591369 0.381778 3.212835 0.0013143161 0.0915786 ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000187479	C11orf96	14.69699214	1.958308711	0.611243	3.203816	0.0013561901	0.0915786
ENSG00000173868 PHOSPHO1 209.3184166 2.627190768 0.818348 3.21036 0.0013256865 0.0915786 ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000171310	CHST11	408.7728418	1.186643045	0.370603	3.201929	0.0013651076	0.0915786
ENSG00000160229 ZNF66 56.13988521 0.87651468 0.273497 3.204843 0.0013513616 0.0915786	ENSG00000131471	AOC3	22.77300856	1.226591369	0.381778	3.212835	0.0013143161	0.0915786
	ENSG00000173868	PHOSPHO1	209.3184166	2.627190768	0.818348	3.21036	0.0013256865	0.0915786
ENSG00000188505 NCCRP1 649.3820155 1.424720362 0.443692 3.211057 0.0013224755 0.0915786	ENSG00000160229	ZNF66	56.13988521	0.87651468	0.273497	3.204843	0.0013513616	0.0915786
	ENSG00000188505	NCCRP1	649.3820155	1.424720362	0.443692	3.211057	0.0013224755	0.0915786

ENSG00000100985	MMP9	105.0085456	1.801939784	0.560903	3.212569	0.0013155353	0.0915786
ENSG00000189056	RELN	20.41484416	1.821826465	0.570354	3.194201	0.0014021827	0.0934873
ENSG00000130592	LSP1	1872.970387	0.886506466	0.277959	3.189347	0.0014259475	0.0946416
ENSG00000106541	AGR2	41664.02551	-0.714062434	0.224157	-3.18555	0.0014447875	0.0954601
ENSG00000104894	CD37	157.4882807	1.249881462	0.393085	3.179671	0.0014744245	0.0969814
ENSG00000146112	PPP1R18	570.9228967	1.216818205	0.382862	3.178213	0.0014818607	0.0970354
ENSG00000112137	PHACTR1	270.347717	1.480915393	0.466756	3.17278	0.0015098686	0.0970487
ENSG00000112195	TREML2	177.9198685	2.368986837	0.747134	3.170764	0.0015203883	0.0970487
ENSG00000170423	KRT78	380.5887664	1.924890584	0.607367	3.169241	0.0015283781	0.0970487
ENSG00000188215	DCUN1D3	490.9316317	0.865486098	0.27282	3.172375	0.0015119764	0.0970487
ENSG00000101236	RNF24	802.5230879	0.95210711	0.300246	3.171085	0.0015187079	0.0970487
ENSG00000087589	CASS4	294.9893157	1.73106507	0.544957	3.176515	0.0014905605	0.0970487
ENSG00000147168	IL2RG	270.2098958	0.933031134	0.294288	3.170466	0.0015219465	0.0970487
ENSG00000125378	BMP4	17.60094942	-1.212353032	0.38289	-3.16632	0.0015438084	0.0976060
ENSG00000111052	LIN7A	40.68503686	1.801629323	0.569401	3.164079	0.0015557467	0.0979386
ENSG00000115935	WIPF1	622.5961766	1.143319049	0.361607	3.161768	0.0015681439	0.0982972
ENSG00000126233	SLURP1	62.95038101	1.64617095	0.521552	3.156293	0.0015978817	0.0997350

Table S3: Biological processes enriched at baseline between "Cold" and "No Cold" groups

ID	Description	GeneRatio	BgRatio	Pvalue Pvalue	P.adjust	qvalue	geneID	Count
GO:0042119	neutrophil activation	0.157895	0.028536908	1.06E- 15	2.36E- 12	2.11E- 12	PADI2/CDA/S100A12/S100A8/MNDA/FCGR3B/SELL/PTPRC/ CR1/CXCR2/CXCR1/MME/IGF2R/CALML5/ALOX5/FOLR3/ SLC2A3/ARHGAP9/OLFM4/ITGAX/UNC13D/PRAM1/ SLC44A2/C5AR1/SIGLEC5/SIGLEC14/LILRA2/SIRPA/CD93/ MMP9/PREX1/ITGB2/NFAM1	33
GO:0002283	neutrophil activation involved in immune response	0.15311	0.027961567	4.04E- 15	3.89E- 12	3.48E- 12	PADI2/CDA/S100A12/S100A8/MNDA/FCGR3B/SELL/PTPRC/ CR1/CXCR2/CXCR1/MME/IGF2R/CALML5/ALOX5/FOLR3/ SLC2A3/ARHGAP9/OLFM4/ITGAX/UNC13D/PRAM1/ SLC44A2/C5AR1/SIGLEC5/SIGLEC14/LILRA2/SIRPA/CD93/ MMP9/ITGB2/NFAM1	32
GO:0002446	neutrophil mediated immunity	0.148325	0.02870951	5.47E- 14	3.16E- 11	2.83E- 11	PADI2/CDA/S100A12/S100A8/MNDA/FCGR3B/SELL/PTPRC/ CR1/CXCR2/CXCR1/MME/IGF2R/CALML5/ALOX5/FOLR3/ SLC2A3/ARHGAP9/OLFM4/ITGAX/UNC13D/PRAM1/ SLC44A2/C5AR1/SIGLEC5/SIGLEC14/SIRPA/CD93/ MMP9/ITGB2/NFAM1	31
GO:0043312	neutrophil degranulation	0.148325	0.027904033	2.54E- 14	1.84E- 11	1.64E- 11	PADI2/CDA/S100A12/S100A8/MNDA/FCGR3B/SELL/PTPRC/ CR1/CXCR2/CXCR1/MME/IGF2R/CALML5/ALOX5/FOLR3/ SLC2A3/ARHGAP9/OLFM4/ITGAX/UNC13D/PRAM1/ SLC44A2/C5AR1/SIGLEC5/SIGLEC14/SIRPA/CD93/ MMP9/ITGB2/NFAM1	31
GO:0008544	epidermis development	0.138756	0.02617801	2.02E- 13	9.74E- 11	8.70E- 11	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/EREG/SPINK5/SPINK6/CTSV/CALML5/LIPK/LIPN/ CST6/KRT78/BMP4/KRT24/ZFP36/CNFN/KLK5/KLK7/KLK8/ KLK12/KLK13/SNA11/WAS	29
GO:0050900	leukocyte migration	0.133971	0.027098556	2.94E- 12	1.06E- 09	9.50E- 10	PIK3CD/PADI2/CSF3R/ECM1/S100A12/S100A8/SELL/IL1A/ CXCR2/CXCR1/INPP5D/CXCL2/TEK/JAML/ESAM/ITGA5/ SELPLG/ITGAX/ADGRE2/TGFB1/C5AR1/SIRPA/THBD/HCK/ MMP9/PREX1/ITGB2/IL17RA	28
GO:0043588	skin development	0.119617	0.023646511	2.89E- 11	7.61E- 09	6.80E- 09	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/ASPRV1/EREG/SPINK5/SPINK6/CTSV/LIPK/LIPN/ KRT78/KRT24/ZFP36/CNFN/KLK5/KLK8/KLK12/KLK13/SNAI1	25
GO:0009913	epidermal cell differentiation	0.114833	0.020079397	5.69E- 12	1.65E- 09	1.47E- 09	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/EREG/SPINK5/SPINK6/CTSV/LIPK/LIPN/KRT78/ BMP4/KRT24/ZFP36/CNFN/KLK5/KLK8/KLK12/KLK13	24
GO:0030216	keratinocyte differentiation	0.110048	0.017260227	1.74E- 12	7.18E- 10	6.42E- 10	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/EREG/SPINK5/SPINK6/CTSV/LIPK/LIPN/KRT78/ KRT24/ZFP36/CNFN/KLK5/KLK8/KLK12/KLK13	23
GO:0031424	keratinization	0.095694	0.013002704	3.83E- 12	1.23E- 09	1.10E- 09	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/SPINK5/SPINK6/LIPK/LIPN/KRT78/KRT24/CNFN/ KLK5/KLK8/KLK12/KLK13	20

GO:0070268	cornification	0.086124	0.006501352	1.63E- 15	2.36E- 12	2.11E- 12	FLG/LCE3D/SPRR3/SPRR2D/SPRR2B/SPRR2E/SPRR2F/ SPRR2G/SPINK5/SPINK6/LIPK/LIPN/KRT78/KRT24/ KLK5/KLK8/KLK12/KLK13	18
GO:0097530	granulocyte migration	0.062201	0.007134227	3.21E- 09	7.75E- 07	6.92E- 07	PIK3CD/CSF3R/S100A12/S100A8/IL1A/CXCR2/CXCL2/ JAML/ADGRE2/C5AR1/PREX1/ITGB2/IL17RA	13
GO:0002521	leukocyte differentiation	0.090909	0.027558829	5.55E- 06	7.65E- 04	6.83E- 04	PIK3CD/PTPRC/CR1/ZFP36L2/INPP5D/EGR1/SPINK5/AGER/ PRDM1/SP11/GAB2/BMP4/DLL4/PLCG2/EV12B/TGFB1/ MMP9/PREX1/NFAM1	19
GO:0002768	immune response- regulating cell surface receptor signaling pathway	0.08134	0.026350613	4.07E- 05	3.37E- 03	3.01E- 03	PIK3CD/THEMIS2/MNDA/PTPRC/CR1/WIPF1/INPP5D/ FYB1/GAB2/PRKCB/PLCG2/ICAM3/C5AR1/LILRA2/ HCK/NFAM1/WAS	17
GO:0002429	immune response- activating cell surface receptor signaling pathway	0.076555	0.024509522	6.00E- 05	4.34E- 03	3.88E- 03	PIK3CD/THEMIS2/MNDA/PTPRC/CR1/WIPF1/INPP5D/ FYB1/PRKCB/PLCG2/ICAM3/C5AR1/LILRA2/HCK/ NFAM1/WAS	16
GO:0042110	T cell activation	0.076555	0.02686842	1.74E- 04	1.12E- 02	9.99E- 03	PIK3CD/PTPRC/CR1/ZFP36L2/EGR1/SPINK5/AGER/ TREML2/PRDM1/APBB1IP/JAML/BMP4/DLL4/ TGFB1/PREX1/WAS	16
GO:0060326	cell chemotaxis	0.07177	0.015534204	9.89E- 07	1.51E- 04	1.35E- 04	PIK3CD/PADI2/CSF3R/S100A12/S100A8/CXCR2/ CXCR1/CXCL2/HBEGF/JAML/ADGRE2/C5AR1/ PREX1/ITGB2/IL17RA	15
GO:0030098	lymphocyte differentiation	0.07177	0.018871181	1.07E- 05	1.23E- 03	1.10E- 03	PIK3CD/PTPRC/CR1/ZFP36L2/INPP5D/EGR1/SPINK5/ PRDM1/SPI1/BMP4/DLL4/PLCG2/TGFB1/PREX1/ NFAM1	15
GO:0031349	positive regulation of defense response	0.07177	0.025947874	3.80E- 04	1.93E- 02	1.72E- 02	PGLYRP4/S100A12/S100A8/NLRC4/IL1RL1/EREG/ PLCG2/ICAM3/TGFB1/KLK5/KLK7/LILRA2/HCK/ ITGB2/IL17RA	15
GO:0040017	positive regulation of locomotion	0.07177	0.028191704	8.91E- 04	3.30E- 02	2.95E- 02	PIK3CD/PTPRC/IL1A/CXCL2/HBEGF/AGER/RELN/TEK/ ITGA5/BMP4/TGFB1/C5AR1/MMP9/PREX1/SNAI1	15
GO:0030595	leukocyte chemotaxis	0.066986	0.01167942	1.70E- 07	3.07E- 05	2.75E- 05	PIK3CD/PADI2/CSF3R/S100A12/S100A8/CXCR2/ CXCR1/CXCL2/JAML/ADGRE2/C5AR1/PREX1/ITGB2/ IL17RA	14
GO:1901342	regulation of vasculature development	0.066986	0.017662965	2.18E- 05	2.10E- 03	1.88E- 03	ECM1/IL1A/CCR3/EGR1/SPINK5/NOS3/TEK/ITGA5/ BMP4/DLL4/PRKCB/SERPINB7/C5AR1/ITGB2	14
GO:0002697	regulation of immune effector process	0.066986	0.023128704	3.76E- 04	1.93E- 02	1.72E- 02	PTPRC/CR1/SPINK5/AGER/GAB2/UNC13D/PRAM1/ ADGRE2/TGFB1/C5AR1/KLK5/KLK7/ITGB2/WAS	14
GO:0051346	negative regulation of hydrolase activity	0.066986	0.024394454	6.37E- 04	2.63E- 02	2.35E- 02	ECM1/RGS2/CR1/NLRC4/SPINK5/SPINK6/SPINK7/ NOS3/P115/CST6/A2ML1/SERPINB7/CST1/MMP9	14

GO:0052547	regulation of	0.066986	0.024509522	6.67E-	2.72E-	2.43E-	ECM1/S100A8/CR1/NLRC4/SPINK5/SPINK6/SPINK7/	14
	peptidase activity			04	02	02	P115/CST6/A2ML1/NLRP1/SERPINB7/CST1/MMP9	
GO:0030335	positive regulation	0.066986	0.025430067	9.52E-	3.37E-	3.02E-	PIK3CD/PTPRC/IL1A/CXCL2/HBEGF/RELN/TEK/ITGA5/	14
	of cell migration			04	02	02	BMP4/TGFB1/C5AR1/MMP9/PREX1/SNAI1	
GO:1903706	regulation of	0.066986	0.025775272	1.08E-	3.71E-	3.32E-	CSF3R/CR1/ZFP36L2/INPP5D/SPINK5/AGER/PRDM1/	14
	hemopoiesis			03	02	02	SPI1/BMP4/PRKCB/EVI2B/ZFP36/TGFB1/NFAM1	
GO:2000147	positive regulation	0.066986	0.026465681	1.39E-	4.30E-	3.84E-	PIK3CD/PTPRC/IL1A/CXCL2/HBEGF/RELN/TEK/ITGA5/	14
	of cell motility			03	02	02	BMP4/TGFB1/C5AR1/MMP9/PREX1/SNAI1	
GO:0051272	positive regulation	0.066986	0.027213624	1.80E-	4.97E-	4.44E-	PIK3CD/PTPRC/IL1A/CXCL2/HBEGF/RELN/TEK/ITGA5/	14
	of cellular			03	02	02	BMP4/TGFB1/C5AR1/MMP9/PREX1/SNAI1	
	component							
	movement							
GO:0097529	myeloid leukocyte	0.062201	0.010298602	2.61E-	4.45E-	3.98E-	PIK3CD/CSF3R/S100A12/S100A8/IL1A/CXCR2/CXCL2/	13
	migration			07	05	05	JAML/ADGRE2/C5AR1/PREX1/ITGB2/IL17RA	
GO:0042742	defense response to	0.062201	0.016684886	5.13E-	3.81E-	3.40E-	PGLYRP4/S100A12/S100A8/NLRC4/SPINK5/DEFB103B/	13
	bacterium			05	03	03	DEFB103A/C10orf99/RNASE7/NLRP1/C5AR1/KLK5/KLK7	
GO:0045861	negative regulation	0.062201	0.020021863	3.13E-	1.71E-	1.53E-	ECM1/CR1/NLRC4/IL1R2/SPINK5/SPINK6/SPINK7/	13
	of proteolysis			04	02	02	PI15/CST6/A2ML1/SERPINB7/CST1/MMP9	
GO:0030099	myeloid cell	0.062201	0.022438295	9.09E-	3.32E-	2.96E-	PIK3CD/CSF3R/INPP5D/SPI1/GAB2/FLI1/BMP4/	13
	differentiation			04	02	02	PRKCB/EVI2B/RASGRP4/ZFP36/TGFB1/MMP9	
GO:0002683	negative regulation	0.062201	0.023704045	1.49E-	4.31E-	3.85E-	PADI2/MNDA/PTPRC/CR1/IL1RL1/INPP5D/SPINK5/	13
	of immune system			03	02	02	PRDM1/BMP4/ZFP36/TGFB1/LILRA2/SAMSN1	
	process							
GO:0071621	granulocyte	0.057416	0.00632875	8.34E-	1.86E-	1.66E-	PIK3CD/CSF3R/S100A12/S100A8/CXCR2/CXCL2/	12
	chemotaxis			09	06	06	JAML/ADGRE2/C5AR1/PREX1/ITGB2/IL17RA	
GO:0010466	negative regulation	0.057416	0.015131465	8.45E-	5.82E-	5.20E-	ECM1/CR1/NLRC4/SPINK5/SPINK6/SPINK7/PI15/	12
	of peptidase activity			05	03	03	CST6/A2ML1/SERPINB7/CST1/MMP9	
GO:0050673	epithelial cell	0.057416	0.020769806	1.46E-	4.30E-	3.84E-	ECM1/CCR3/EREG/SLURP1/TEK/JAML/BMP4/	12
	proliferation			03	02	02	DLL4/ZFP36/TGFB1/C5AR1/KLK8	
GO:1990266	neutrophil migration	0.052632	0.005810943	3.61E-	7.45E-	6.66E-	PIK3CD/CSF3R/S100A12/S100A8/IL1A/CXCR2/	11
				08	06	06	CXCL2/JAML/C5AR1/PREX1/ITGB2	
GO:1904018	positive regulation	0.052632	0.009665727	6.07E-	7.98E-	7.13E-	ECM1/IL1A/CCR3/EGR1/NOS3/TEK/ITGA5/	11
	of vasculature			06	04	04	PRKCB/SERPINB7/C5AR1/ITGB2	
	development						1 Mi ob, obia in (b), obiati, 11 ob2	
GO:0030217	T cell differentiation	0.052632	0.01294517	9.07E-	6.11E-	5.46E-	PIK3CD/PTPRC/CR1/ZFP36L2/EGR1/SPINK5/	11
22.0030217	1 con aniorentation	0.002002	0.01271017	05	03	03	PRDM1/BMP4/DLL4/TGFB1/PREX1	11
GO:0042113	B cell activation	0.052632	0.015591738	4.54E-	2.15E-	1.92E-	PIK3CD/MNDA/PTPRC/ZFP36L2/INPP5D/	11
33.00-72113	2 con activation	0.032032	0.013371730	04	02	02	PRDM1/PRKCB/PLCG2/TGFB1/SAMSN1/NFAM1	
GO:0045765	regulation of	0.052632	0.015706806	4.83E-	2.25E-	2.01E-	ECM1/IL1A/CCR3/SPINK5/NOS3/TEK/ITGA5/	11
(ゼロ・ロログラン/アン			0.012/00000	T T.OJE-	4.4315	2.01L-	LUM 1/1LIM CUNJ/SI MNS/MOSJ/TEN/MUJ/	111

GO:0032103	positive regulation of response to external stimulus	0.052632	0.016167079	6.14E- 04	2.57E- 02	2.30E- 02	S100A12/S100A8/IL1RL1/CXCL2/AGER/TGFB1/ C5AR1/KLK5/KLK7/THBD/IL17RA	11
GO:0050678	regulation of epithelial cell proliferation	0.052632	0.017662965	1.26E- 03	4.01E- 02	3.59E- 02	ECM1/CCR3/EREG/SLURP1/TEK/JAML/BMP4/ DLL4/ZFP36/TGFB1/C5AR1	11
GO:0032496	response to lipopolysaccharide	0.052632	0.018180772	1.59E- 03	4.55E- 02	4.06E- 02	\$100A8/CXCL2/PRDM1/NOS3/PLCG2/ZFP36/ TGFB1/C5AR1/LILRA2/THBD/HCK	11
GO:0006959	humoral immune response	0.052632	0.018468443	1.80E- 03	4.97E- 02	4.44E- 02	PGLYRP4/S100A12/S100A8/CR1/SPINK5/ DEFB103B/DEFB103A/RNASE7/C5AR1/KLK5/KLK7	11
GO:0030593	neutrophil chemotaxis	0.047847	0.005178068	1.26E- 07	2.43E- 05	2.18E- 05	PIK3CD/CSF3R/S100A12/S100A8/CXCR2/ CXCL2/JAML/C5AR1/PREX1/ITGB2	10
GO:0002703	regulation of leukocyte mediated immunity	0.047847	0.009493125	3.15E- 05	2.68E- 03	2.40E- 03	PTPRC/CR1/AGER/GAB2/UNC13D/PRAM1/ ADGRE2/TGFB1/ITGB2/WAS	10
GO:0051091	positive regulation of DNA binding transcription factor activity	0.047847	0.014153386	8.11E- 04	3.17E- 02	2.83E- 02	S100A12/S100A8/NLRC4/AGER/RELN/PRKCB/ CARD14/TGFB1/ITGB2/NFAM1	10
GO:0010951	negative regulation of endopeptidase activity	0.047847	0.014383522	9.17E- 04	3.32E- 02	2.96E- 02	CR1/NLRC4/SPINK5/SPINK6/SPINK7/CST6/ A2ML1/SERPINB7/CST1/MMP9	10
GO:1902105	regulation of leukocyte differentiation	0.047847	0.014613659	1.03E- 03	3.61E- 02	3.22E- 02	CR1/ZFP36L2/INPP5D/SPINK5/AGER/PRDM1/ BMP4/EVI2B/TGFB1/NFAM1	10
GO:0050851	antigen receptor- mediated signaling pathway	0.047847	0.014786261	1.13E- 03	3.80E- 02	3.40E- 02	PIK3CD/THEMIS2/MNDA/PTPRC/INPP5D/ FYB1/PRKCB/PLCG2/NFAM1/WAS	10
GO:0019730	antimicrobial humoral response	0.043062	0.006041079	4.90E- 06	7.09E- 04	6.34E- 04	PGLYRP4/S100A12/S100A8/SPINK5/DEFB103B/ DEFB103A/RNASE7/KLK5/KLK7	9
GO:0045766	positive regulation of angiogenesis	0.043062	0.008457511	7.27E- 05	5.13E- 03	4.59E- 03	ECM1/IL1A/CCR3/NOS3/TEK/ITGA5/PRKCB/ C5AR1/ITGB2	9
GO:0018149	peptide cross-linking	0.038278	0.003394511	5.01E- 07	8.05E- 05	7.19E- 05	FLG/LCE3E/LCE3D/SPRR3/SPRR2D/SPRR2B/ SPRR2E/SPRR2F	8
GO:0051092	positive regulation of NF-kappaB transcription factor activity	0.038278	0.008054772	2.94E- 04	1.64E- 02	1.46E- 02	S100A12/S100A8/NLRC4/AGER/PRKCB/CARD14/ TGFB1/ITGB2	8
GO:0050864	regulation of B cell activation	0.038278	0.008917784	5.81E- 04	2.51E- 02	2.24E- 02	MNDA/PTPRC/ZFP36L2/INPP5D/PRDM1/ TGFB1/SAMSN1/NFAM1	8

GO:0045619	regulation of lymphocyte differentiation	0.038278	0.008975318	6.06E- 04	2.57E- 02	2.30E- 02	CR1/ZFP36L2/INPP5D/SPINK5/PRDM1/ BMP4/TGFB1/NFAM1	8
GO:0050866	negative regulation of cell activation	0.038278	0.010010931	1.23E- 03	3.99E- 02	3.57E- 02	MNDA/INPP5D/PRDM1/NOS3/BMP4/TGFB1/ THBD/SAMSN1	8
GO:0007492	endoderm development	0.033493	0.004545193	4.58E- 05	3.49E- 03	3.12E- 03	DUSP1/ARC/ITGA5/BMP4/TGFB1/MMP9/ ITGB2	7
GO:0001704	formation of primary germ layer	0.033493	0.007249295	8.30E- 04	3.20E- 02	2.86E- 02	DUSP1/ITGA5/BMP4/KDM6B/MMP9/SNAII/ ITGB2	7
GO:0050777	negative regulation of immune response	0.033493	0.0075945	1.09E- 03	3.71E- 02	3.32E- 02	PTPRC/CR1/IL1RL1/INPP5D/SPINK5/TGFB1/ SAMSN1	7
GO:0002819	regulation of adaptive immune response	0.033493	0.007767102	1.24E- 03	3.99E- 02	3.57E- 02	PTPRC/CR1/IL1RL1/AGER/TGFB1/SAMSN1/ WAS	7
GO:0001906	cell killing	0.033493	0.007997238	1.47E- 03	4.30E- 02	3.84E- 02	PGLYRP4/S100A12/PTPRC/AGER/DEFB103B/ DEFB103A/UNC13D	7
GO:0072006	nephron development	0.033493	0.007939704	1.41E- 03	4.30E- 02	3.84E- 02	EGR1/CALB1/TEK/ACTA2/BMP4/SERPINB7/ TGFB1	7
GO:0050832	defense response to fungus	0.028708	0.002301364	7.68E- 06	9.66E- 04	8.63E- 04	\$100A12/\$100A8/\$C10orf99/\$RNASE7/\$TGFB1/\$IL17RA	6
GO:0009620	response to fungus	0.028708	0.003106841	4.49E- 05	3.49E- 03	3.12E- 03	\$100A12/\$100A8/\$C10orf99/\$RNASE7/\$TGFB1/\$IL17RA	6
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	0.028708	0.003106841	4.49E- 05	3.49E- 03	3.12E- 03	PGLYRP4/S100A12/SPINK5/RNASE7/KLK5/ KLK7	6
GO:0050830	defense response to Gram-positive bacterium	0.028708	0.005235602	8.02E- 04	3.17E- 02	2.83E- 02	PGLYRP4/DEFB103B/DEFB103A/C10orf99/ RNASE7/C5AR1	6
GO:0050853	B cell receptor signaling pathway	0.028708	0.005293136	8.50E- 04	3.21E- 02	2.87E- 02	PIK3CD/MNDA/PTPRC/PRKCB/PLCG2/ NFAMI	6
GO:0007613	memory	0.028708	0.006098613	1.77E- 03	4.97E- 02	4.44E- 02	HRH2/RELN/CALB1/ARC/ITGA5/KLK8	6
GO:0072012	glomerulus vasculature development	0.023923	0.001438352	1.05E- 05	1.23E- 03	1.10E- 03	EGR1/TEK/ACTA2/BMP4/SERPINB7	5
GO:0061437	renal system vasculature development	0.023923	0.00155342	1.56E- 05	1.56E- 03	1.39E- 03	EGR1/TEK/ACTA2/BMP4/SERPINB7	5
GO:0061440	kidney vasculature development	0.023923	0.00155342	1.56E- 05	1.56E- 03	1.39E- 03	EGR1/TEK/ACTA2/BMP4/SERPINB7	5

GO:0002886	regulation of myeloid leukocyte mediated immunity	0.023923	0.0025315	1.78E- 04	1.12E- 02	9.99E- 03	GAB2/UNC13D/PRAM1/ADGRE2/ITGB2	5
GO:0043300	regulation of leukocyte degranulation	0.023923	0.0025315	1.78E- 04	1.12E- 02	9.99E- 03	GAB2/UNC13D/PRAM1/ADGRE2/ITGB2	5
GO:0045123	cellular extravasation	0.023923	0.002876704	3.27E- 04	1.74E- 02	1.56E- 02	PIK3CD/IL1A/JAML/SELPLG/ITGB2	5
GO:0031663	lipopolysaccharide- mediated signaling pathway	0.023923	0.003049307	4.30E- 04	2.14E- 02	1.91E- 02	PRDM1/NOS3/TGFB1/L1LRA2/HCK	5
GO:0045576	mast cell activation	0.023923	0.003221909	5.56E- 04	2.48E- 02	2.22E- 02	PIK3CD/\$100A12/GAB2/UNC13D/ADGRE2	5
GO:0006968	cellular defense response	0.023923	0.003452045	7.65E- 04	3.07E- 02	2.75E- 02	MNDA/CXCR2/CCR3/LSP1/C5AR1	5
GO:0032835	glomerulus development	0.023923	0.003624648	9.56E- 04	3.37E- 02	3.02E- 02	EGR1/TEK/ACTA2/BMP4/SERPINB7	5
GO:0032945	negative regulation of mononuclear cell proliferation	0.023923	0.003969852	1.44E- 03	4.30E- 02	3.84E- 02	MNDA/INPP5D/PRDM1/BMP4/TGFB1	5
GO:0050672	negative regulation of lymphocyte proliferation	0.023923	0.003969852	1.44E- 03	4.30E- 02	3.84E- 02	MNDA/INPP5D/PRDM1/BMP4/TGFB1	5
GO:1900004	negative regulation of serine-type endopeptidase activity	0.019139	0.000747943	1.33E- 05	1.43E- 03	1.28E- 03	CR1/SPINK5/SPINK6/SPINK7	4
GO:1902572	negative regulation of serine-type peptidase activity	0.019139	0.000747943	1.33E- 05	1.43E- 03	1.28E- 03	CR1/SPINK5/SPINK6/SPINK7	4
GO:0072109	glomerular mesangium development	0.019139	0.000863011	2.50E- 05	2.19E- 03	1.96E- 03	EGR1/ACTA2/BMP4/SERPINB7	4
GO:1900003	regulation of serine- type endopeptidase activity	0.019139	0.000863011	2.50E- 05	2.19E- 03	1.96E- 03	CR1/SPINK5/SPINK6/SPINK7	4
GO:1902571	regulation of serine- type peptidase activity	0.019139	0.000863011	2.50E- 05	2.19E- 03	1.96E- 03	CR1/SPINK5/SPINK6/SPINK7	4
GO:0045577	regulation of B cell differentiation	0.019139	0.001495886	2.47E- 04	1.49E- 02	1.33E- 02	ZFP36L2/INPP5D/PRDM1/NFAM1	4

GO:0001958	endochondral ossification	0.019139	0.00155342	2.87E- 04	1.63E- 02	1.45E- 02	CSGALNACT1/TEK/BMP4/PHOSPHO1	4
GO:0036075	replacement	0.019139	0.00155342	2.87E-	1.63E-	1.45E-	CSGALNACT1/TEK/BMP4/PHOSPHO1	4
GO:0036073	ossification	0.019139	0.00155542	04	02	02	CSGALNACII/IEN/BMP4/PHOSPHOI	4
GO:0061311	cell surface receptor	0.019139	0.001610954	3.32E-	1.74E-	1.56E-	BMP4/DLL4/TGFB1/SNAII	4
00.0001311	signaling pathway	0.019139	0.001010934	04	02	02	DIVIT 4/DLL4/TOT BT/SIVATT	4
	involved			04	02	02		
	in heart development							
GO:1900271	regulation of long-	0.019139	0.001726023	4.36E-	2.14E-	1.91E-	AGER/RELN/CALB1/ARC	4
00.1700271	term synaptic	0.017137	0.001720023	04	02	02	TODAY NEED TYTHE	'
	potentiation				\ <u>-</u>	02		
GO:0050869	negative regulation	0.019139	0.001783557	4.96E-	2.28E-	2.03E-	MNDA/INPP5D/PRDM1/SAMSN1	4
	of B cell activation			04	02	02		
GO:0043616	keratinocyte	0.019139	0.002243829	1.20E-	3.99E-	3.57E-	EREG/SLURP1/ZFP36/KLK8	4
	proliferation			03	02	02		
GO:0090184	positive regulation	0.019139	0.002301364	1.32E-	4.16E-	3.72E-	EGR1/BMP4/SERPINB7/TGFB1	4
	of kidney			03	02	02		
	development							
GO:0002820	negative regulation	0.019139	0.002358898	1.45E-	4.30E-	3.84E-	PTPRC/CR1/IL1RL1/SAMSN1	4
	of adaptive immune			03	02	02		
	response							
GO:0072110	glomerular	0.014354	0.000575341	1.93E-	1.19E-	1.06E-	EGR1/BMP4/SERPINB7	3
	mesangial cell			04	02	02		
	proliferation							
GO:0072672	neutrophil	0.014354	0.000632875	2.63E-	1.55E-	1.39E-	PIK3CD/IL1A/JAML	3
	extravasation			04	02	02		
GO:1901722	regulation of cell	0.014354	0.000747943	4.48E-	2.15E-	1.92E-	EGR1/BMP4/SERPINB7	3
	proliferation			04	02	02		
	involved in							
GO 0000103	kidney development	0.014254	0.000005477	7. CCF	2 40E	2.225	ECDI/DIADA/GEDDUIDA	
GO:0090192	regulation of	0.014354	0.000805477	5.66E-	2.48E-	2.22E-	EGR1/BMP4/SERPINB7	3
	glomerulus			04	02	02		
GO:1900424	development regulation of defense	0.014354	0.000805477	5.66E-	2.48E-	2.22E-	SPINK5/KLK5/KLK7	3
GO:1900424	response to	0.014554	0.000803477	04	02	02	SPHNAJ/KLKJ/KLK/	3
	bacterium			04	02	02		
GO:0030889	negative regulation	0.014354	0.000920545	8.55E-	3.21E-	2.87E-	MNDA/INPP5D/PRDM1	3
30.0030009	of B cell	0.01+334	0.000920343	04	02 02	02	MINDENTINI I JU/I KUMI	3
	proliferation			07	02	02		
GO:0097709	connective tissue	0.014354	0.001035614	1.22E-	3.99E-	3.57E-	IL1A/AGER/TGFB1	3
00.00/110/	replacement	0.01 1554	1 0.001033014	03	02	02	1	

GO:0072111	cell proliferation	0.014354	0.001150682	1.68E-	4.76E-	4.26E-	EGR1/BMP4/SERPINB7	3
	involved in kidney			03	02	02		
	development							

Table S4: Molecular functions enriched at baseline between "Cold" and "No Cold" groups

ID	Description	GeneRatio	BgRatio	Pvalue	P.adjust	qvalue	geneID	Coun
								t
GO:001717 1	serine hydrolase activity	0.0591133	0.015961738	1.06E-04	7.29E-03	6.50E-03	TMPRSS11B/TMPRSS11E/RELN/CTSV/PRSS27 /KLK5/KLK6/KLK7/KLK8/KLK12/KLK13/MMP9	12
GO:000823	serine-type peptidase activity	0.0591133	0.01567362	8.93E-05	7.29E-03	6.50E-03	TMPRSS11B/TMPRSS11E/RELN/CTSV/PRSS27/ KLK5/KLK6/KLK7/KLK8/KLK12/KLK13/MMP9	12
GO:000425 2	serine-type endopeptidase activity	0.054187192	0.014060159	1.45E-04	8.28E-03	7.38E-03	TMPRSS11B/TMPRSS11E/CTSV/PRSS27/KLK5/ KLK6/KLK7/KLK8/KLK12/KLK13/MMP9	11
GO:006113 4	peptidase regulator activity	0.054187192	0.012561945	5.33E-05	7.29E-03	6.50E-03	NLRC4/MAL/SPINK5/SPINK6/SPINK7/PI15/ CST6/A2ML1/NLRP1/SERPINB7/CST1	11
GO:003041 4	peptidase inhibitor activity	0.044334975	0.010487496	2.97E-04	1.36E-02	1.21E-02	NLRC4/SPINK5/SPINK6/SPINK7/PI15/CST6/ A2ML1/SERPINB7/CST1	9
GO:001995 5	cytokine binding	0.039408867	0.005819984	2.43E-05	5.01E-03	4.47E-03	CSF3R/IL1R2/IL1RL1/CXCR2/CXCR1/CCR3/ ZFP36/IL2RG	8
GO:000489 6	cytokine receptor activity	0.039408867	0.005243748	1.13E-05	4.66E-03	4.15E-03	CSF3R/IL1R2/IL1RL1/CXCR2/CXCR1/CCR3/ IL17RA/IL2RG	8
GO:007085	growth factor receptor binding	0.034482759	0.007606316	9.29E-04	3.15E-02	2.81E-02	ECM1/IL1A/IL36G/EREG/HBEGF/ AGR2/ITGA5	7
GO:000515 4	epidermal growth factor receptor binding	0.019704433	0.001901579	5.70E-04	2.14E-02	1.90E-02	EREG/HBEGF/AGR2/ITGA5	4
GO:001995 6	chemokine binding	0.019704433	0.001382966	1.61E-04	8.28E-03	7.38E-03	CXCR2/CXCR1/CCR3/ZFP36	4
GO:000184 8	complement binding	0.019704433	0.001210096	9.31E-05	7.29E-03	6.50E-03	CR1/C5AR1/CD93/ITGB2	4
GO:000184 6	opsonin binding	0.014778325	0.00080673	5.22E-04	2.14E-02	1.90E-02	CR1/CD93/ITGB2	3
GO:000417 5	endopeptidase activity	0.068965517	0.02702547	1.28E-03	3.52E-02	3.14E-02	CLCA4/ASPRV1/MME/TMPRSS11B/TMPRSS11E/CTSV/ PRSS27/KLK5/KLK6/KLK7/KLK8/KLK12/KLK13/MMP9	14
GO:006113 5	endopeptidase regulator activity	0.039408867	0.010314625	1.24E-03	3.52E-02	3.14E-02	NLRC4/SPINK5/SPINK6/SPINK7/CST6/A2ML1/SERPINB7/ CST1	8
GO:000486 6	endopeptidase inhibitor activity	0.039408867	0.009968883	9.95E-04	3.15E-02	2.81E-02	NLRC4/SPINK5/SPINK6/SPINK7/CST6/A2ML1/SERPINB7/ CST1	8

Mediator (log ₁₀ pg/ml)	Cold (n=23, unless otherwise stated) Median	No Cold (n=25, unless otherwise stated) Median	P-value
IFN-α	0.046	0.046	0.176
IFN-β	1.866	0.856	0.617
IFN-γ	0	0	0.314
IL-1β	1.193	0.870	0.086
IL-6	0.991	0.659	0.103
IL-8	3.170	2.923	0.356
IL-10	0.803	0.803	0.068
IL-15	0.419	0.329	0.391
IL-17A	0.609	0.144	0.039*
CXCL10 (IP-10)	1.991	1.715	0.054
LCN-2	6.704 (n=10)	5.875 (n=9)	0.017*
MIP-1α	0.903	0.732	0.192
MPO	6.758 (n=10)	5.861 (n=9)	0.010*
CCL5 (RANTES)	0.254	0.369	0.665
TNF-α	0	0	0.692

Table S5: Day 0 cytokine levels in infected and uninfected volunteers Day 0 mediator levels in the upper respiratory tract were determined in participants who subsequently developed symptomatic RSV infection (Cold, n=23) and those that did not (No Cold, n=25). Statistical analyses used two-tailed Mann Whitney U tests; *P<0.05.

Table S6: DEGs between day 3 and day 0 in the "No Cold" group (P-value<0.01, LFC>0.5)

	GeneName	baseMean	log ² Fold	lfcSE	stat	Pvalue	Padj
ENSG00000268173	AC007192.4	34.09618	Change 10.71285	1.946479	5.503707	3.72E-08	0.000546
ENSG00000163734	CXCL3	149.3781	1.440807	0.321685	4.478942	7.50E-06	0.055023
ENSG00000081041	CXCL2	174.802	1.436306	0.349674	4.107556	4.00E-05	0.195535
ENSG00000177606	JUN	1314.332	0.725754	0.189651	3.826781	0.00013	0.274872
ENSG00000163739	CXCL1	1567.606	1.058814	0.272342	3.887809	0.000101	0.274872
ENSG00000159231	CBR3	89.53077	-0.80421	0.21029	-3.82427	0.000131	0.274872
ENSG00000140519	RHCG	205.5315	2.384514	0.629577	3.787487	0.000152	0.279058
ENSG00000143536	CRNN	332.3173	2.42925	0.700976	3.465527	0.000529	0.644422
ENSG00000137331	IER3	1131.598	0.773632	0.225847	3.425471	0.000614	0.644422
ENSG00000123119	NECAB1	17.4312	1.396028	0.40761	3.424915	0.000615	0.644422
ENSG00000196993	NPIPB9	90.3268	-0.60766	0.177412	-3.42512	0.000615	0.644422
ENSG00000169203	RP11- 231C14.4	249.1964	-0.64802	0.187268	-3.46041	0.000539	0.644422
ENSG00000280893	AC009133.23	9.701738	-2.5609	0.758312	-3.3771	0.000733	0.691727
ENSG00000067082	KLF6	1426.194	0.520046	0.157306	3.305947	0.000947	0.694302
ENSG00000186474	KLK12	25.34081	1.839293	0.551663	3.334085	0.000856	0.694302
ENSG00000113070	HBEGF	259.5387	1.320102	0.402212	3.282104	0.00103	0.719647
ENSG00000091128	LAMB4	79.02638	1.205408	0.370164	3.256417	0.001128	0.719647
ENSG00000132932	ATP8A2	24.55841	0.602019	0.184236	3.267642	0.001084	0.719647
ENSG00000139318	DUSP6	775.636	0.686782	0.215349	3.189164	0.001427	0.807516
ENSG00000203852	HIST2H3A	311.1639	1.57602	0.502519	3.136242	0.001711	0.838019
ENSG00000165794	SLC39A2	27.49601	1.602373	0.51099	3.135821	0.001714	0.838019
ENSG00000154734	ADAMTS1	34.50457	1.779	0.565144	3.147873	0.001645	0.838019
ENSG00000183336	BOLA2	5.369005	-9.99524	3.22335	-3.10089	0.001929	0.913049
ENSG00000121742	GJB6	75.14953	1.351585	0.437849	3.086874	0.002023	0.923257
ENSG00000265590	AP000275.65	33.19193	-1.87079	0.607592	-3.07902	0.002077	0.923257
ENSG00000169509	CRCT1	43.10019	2.246315	0.786001	2.857904	0.004264	0.971488
ENSG00000090104	RGS1	260.8477	0.758897	0.261628	2.900676	0.003724	0.971488
ENSG00000263961	C1orf186	9.726597	1.104421	0.381009	2.898677	0.003747	0.971488
ENSG00000143878	RHOB	1806.952	0.509216	0.179492	2.83699	0.004554	0.971488
ENSG00000115602	IL1RL1	51.0304	1.606061	0.559536	2.870347	0.0041	0.971488
ENSG00000185873	TMPRSS11B	126.1337	2.320712	0.77744	2.98507	0.002835	0.971488
ENSG00000124875	CXCL6	692.2134	0.849458	0.286733	2.962539	0.003051	0.971488
ENSG00000145879	SPINK7	90.93384	2.305832	0.75561	3.051617	0.002276	0.971488
ENSG00000112394	SLC16A10	25.4085	1.106001	0.3716	2.976325	0.002917	0.971488
ENSG00000155918	RAET1L	74.83194	1.296183	0.451471	2.871022	0.004091	0.971488
ENSG00000197181	PIWIL2	16.37803	0.889869	0.298332	2.982817	0.002856	0.971488
ENSG00000104368	PLAT	1629.246	1.266039	0.433067	2.923424	0.003462	0.971488
ENSG00000111215	PRR4	92.77336	-0.82179	0.277502	-2.96137	0.003063	0.971488
ENSG00000018236	CNTN1	68.40497	0.892821	0.307411	2.904322	0.00368	0.971488
ENSG00000279777	AC004813.1	52.62626	-0.60351	0.20639	-2.92413	0.003454	0.971488
ENSG00000128965	CHAC1	76.63318	0.803606	0.281341	2.856341	0.004286	0.971488

ENSG00000185864	NPIPB4	335.7528	-0.52362	0.177264	-2.95391	0.003138	0.971488
ENSG00000171401	KRT13	3674.625	1.533781	0.527322	2.908621	0.00363	0.971488
ENSG00000175906	ARL4D	476.1744	0.578185	0.203438	2.842066	0.004482	0.971488
ENSG00000269404	SPIB	27.53031	0.814364	0.278475	2.924367	0.003452	0.971488
ENSG00000169035	KLK7	193.8601	1.85068	0.640657	2.888722	0.003868	0.971488
ENSG00000129455	KLK8	26.1473	2.13996	0.750293	2.852164	0.004342	0.971488
ENSG00000088882	CPXM1	53.04393	0.761404	0.266631	2.855645	0.004295	0.971488
ENSG00000156282	CLDN17	19.61386	2.754695	0.950417	2.898406	0.003751	0.971488
ENSG00000128342	LIF	164.0332	0.589717	0.206526	2.855406	0.004298	0.971488
ENSG00000163751	CPA3	103.1778	1.764197	0.637979	2.765291	0.005687	0.990244
ENSG00000188818	ZDHHC11	88.32456	-0.54877	0.198388	-2.76616	0.005672	0.990244
ENSG00000136943	CTSV	147.4117	0.920501	0.328398	2.803004	0.005063	0.990244
ENSG00000188070	C11orf95	136.192	0.50528	0.181364	2.785993	0.005336	0.990244
ENSG00000170426	SDR9C7	8.854919	2.309243	0.821713	2.81028	0.00495	0.990244
ENSG00000166211	SPIC	20.23969	0.594662	0.215019	2.765632	0.005681	0.990244
ENSG00000165799	RNASE7	49.36023	1.409505	0.504665	2.792952	0.005223	0.990244
ENSG00000197253	TPSB2	75.30485	1.871105	0.675495	2.769975	0.005606	0.990244
ENSG00000198156	NPIPB6	98.34868	-0.54924	0.198827	-2.76241	0.005738	0.990244
ENSG00000269711	CTD- 3214H19.16	10.41424	10.46232	3.708287	2.821336	0.004782	0.990244
ENSG00000105427	CNFN	181.4197	1.277771	0.454088	2.813927	0.004894	0.990244
ENSG00000022556	NLRP2	93.76168	1.077863	0.386322	2.790064	0.00527	0.990244
ENSG00000142619	PADI3	97.15799	0.547472	0.20942	2.614223	0.008943	1
ENSG00000143556	S100A7	630.9285	1.955151	0.744234	2.627063	0.008613	1
ENSG00000196754	S100A2	4500.136	1.346063	0.492669	2.732187	0.006292	1
ENSG00000179914	ITLN1	48.25683	-1.69569	0.651444	-2.60297	0.009242	1
ENSG00000135919	SERPINE2	144.2735	1.144279	0.440156	2.599711	0.00933	1
ENSG00000132465	JCHAIN	62.01675	0.908242	0.345234	2.630798	0.008518	1
ENSG00000118785	SPP1	24.56759	1.089926	0.412914	2.639595	0.008301	1
ENSG00000120738	EGR1	360.8778	1.082594	0.406853	2.660894	0.007793	1
ENSG00000254245	PCDHGA3	16.88847	-0.81997	0.308613	-2.65694	0.007885	1
ENSG00000253159	PCDHGA12	23.25894	-0.70802	0.257928	-2.74503	0.006051	1
ENSG00000133710	SPINK5	1205.992	0.789563	0.296293	2.664807	0.007703	1
ENSG00000120149	MSX2	27.93288	0.635925	0.244592	2.599942	0.009324	1
ENSG00000276180	HIST1H4I	123.343	0.605086	0.230213	2.62837	0.00858	1
ENSG00000170667	RASA4B	32.38069	-0.65927	0.252296	-2.61307	0.008973	1
ENSG00000164604	GPR85	21.83782	0.745677	0.286781	2.600157	0.009318	1
ENSG00000107984	DKK1	176.808	0.807979	0.297051	2.720003	0.006528	1
ENSG00000117983	MUC5B	72.21829	-1.39958	0.515548	-2.71474	0.006633	1
ENSG00000175518	UBQLNL	18.33565	-0.77311	0.288423	-2.68046	0.007352	1
ENSG00000165474	GJB2	526.7655	0.911625	0.347925	2.620178	0.008788	1
ENSG00000134901	KDELC1	36.77971	0.505743	0.196205	2.577628	0.009948	1
ENSG00000249240	AC069368.3	5.588089	-1.7672	0.665496	-2.65546	0.00792	1
ENSG00000188508	KRTDAP	20.60571	2.121478	0.781522	2.714549	0.006637	1
ENSG00000102313	ІТІН6	35.36962	-0.71756	0.263563	-2.72252	0.006479	1

ENSG00000268089	GABRQ	21.23443	1.933114	0.706636	2.73566	0.006226	1
ENSG00000198763	MT-ND2	2776.095	-0.57408	0.215711	-2.66133	0.007783	1

Table S7: DEGs between day 3 and day 0 in the "Cold" group (*P-value*<0.01, LFC>0.5)

	eName	baseMean	log ² Fold Change	lfcSE	stat	<i>P</i> value	<i>P</i> adj
ENSG00000125378 BMF	P4	22.04009	1.543324	0.297741	5.183448	2.18E-07	0.003195
ENSG00000132326 <i>PER</i>	2	1311.424	-0.66742	0.14176	-4.70814	2.50E-06	0.018336
ENSG00000140006 WDI	R89	150.7693	0.632335	0.15182	4.165032	3.11E-05	0.114173
ENSG00000184313 MRC	OH7	105.3837	-0.78921	0.204508	-3.85906	0.000114	0.271157
ENSG00000129757 CDK	KN1C	101.3036	0.671943	0.17645	3.80812	0.00014	0.271157
ENSG00000173451 THA	P2	76.44963	0.624654	0.165438	3.775758	0.00016	0.271157
ENSG00000277117	SLG	38.58432	1.309042	0.340901	3.839948	0.000123	0.271157
ENSG00000127129 EDN	12	292.3299	2.41171	0.668713	3.606497	0.00031	0.281593
ENSG00000135045 C901	rf40	111.4209	0.591656	0.163835	3.611298	0.000305	0.281593
ENSG00000153485 TME	EM251	175.3835	0.621159	0.172678	3.597203	0.000322	0.281593
ENSG00000206172	.1	21.72477	-3.39372	0.944417	-3.59346	0.000326	0.281593
ENSG00000204172	P9	156.9233	-0.68697	0.193771	-3.54528	0.000392	0.287681
ENSG00000198929 NOS	1AP	147.7733	-0.72025	0.209007	-3.44607	0.000569	0.31136
ENSG00000118508 RAB	32	180.2051	0.58683	0.17011	3.449702	0.000561	0.31136
ENSG00000196859 KRT	39	38.21066	0.952273	0.274481	3.469356	0.000522	0.31136
ENSG00000152284 TCF	7L1	33.26154	-0.7667	0.230403	-3.32767	0.000876	0.3195
ENSG00000240583 AQP	21	61.98687	-1.05708	0.322695	-3.2758	0.001054	0.3195
ENSG00000175164 ABO)	228.5686	-0.58983	0.178901	-3.29698	0.000977	0.3195
ENSG00000006327 TNF	RSF12A	480.2161	0.932948	0.2811	3.318923	0.000904	0.3195
ENSG00000172000 ZNF	556	17.04258	0.87804	0.266582	3.293689	0.000989	0.3195
ENSG00000198342 ZNF	442	63.13852	0.754397	0.227406	3.317401	0.000909	0.3195
ENSG00000225828 FAM	1229A	41.86062	-0.5085	0.156767	-3.24367	0.00118	0.320019
ENSG00000185880 TRIA	M69	1353.204	0.629862	0.194459	3.239051	0.001199	0.320019
ENSG00000132881 RSG	1	106.1672	0.534104	0.167607	3.186653	0.001439	0.338339
ENSG00000221886 ZBE	D8	178.3149	0.656915	0.206286	3.184482	0.00145	0.338339
ENSG00000163359 COL	.6A3	109.9409	-1.36855	0.436338	-3.13645	0.00171	0.349108
ENSG00000122641 INH	BA	71.23154	1.845157	0.586767	3.144618	0.001663	0.349108
ENSG00000129474 AJU	BA	371.5591	0.690348	0.222181	3.107139	0.001889	0.355797
ENSG00000188290 HES	4	312.5322	0.669324	0.224127	2.986357	0.002823	0.360848
ENSG00000179914 ITLN	V1	71.80596	1.857605	0.620404	2.994186	0.002752	0.360848
ENSG00000164404 GDF	79	21.44236	0.717419	0.240885	2.97826	0.002899	0.360848
ENSG00000036448 MYC	DM2	36.698	0.731788	0.245223	2.984168	0.002844	0.360848
ENSG00000123411	F4	100.528	-0.51143	0.171315	-2.98534	0.002833	0.360848
ENSG00000132481 TRIA	M47	188.1067	0.510921	0.172017	2.970178	0.002976	0.360848
ENSG00000187187 ZNF	546	84.94763	0.720698	0.233248	3.089832	0.002003	0.360848
ENSG00000159885 ZNF	222	88.79954	0.594934	0.200539	2.966677	0.00301	0.360848
ENSG00000261221 ZNF	865	88.98932	-0.55707	0.187852	-2.96546	0.003022	0.360848
ENSG00000132801 ZSW	YIM3	109.449	0.520946	0.174892	2.978677	0.002895	0.360848
ENSG00000177854 TME	EM187	153.3936	0.525238	0.17367	3.024343	0.002492	0.360848
ENSG00000278705 HIST	Г1Н4В	594.7796	0.677645	0.231015	2.933342	0.003353	0.369876
ENSG00000203724 C1o	rf53	43.69044	0.605087	0.208161	2.906826	0.003651	0.374903

ENSG00000232040	ZBED9	37.2166	0.83489	0.285474	2.924569	0.003449	0.374903
ENSG00000104267	CA2	209.3763	0.919822	0.315283	2.917449	0.003529	0.374903
ENSG00000122254	HS3ST2	22.89722	1.033907	0.354774	2.914269	0.003565	0.374903
ENSG00000177606	JUN	1569.743	0.662493	0.234252	2.828126	0.004682	0.384771
ENSG00000164082	GRM2	20.58784	-0.7129	0.250317	-2.84799	0.0044	0.384771
ENSG00000163536	SERPINI1	52.52468	0.54397	0.196048	2.774681	0.005526	0.384771
ENSG00000019991	HGF	57.15752	0.646882	0.228819	2.827044	0.004698	0.384771
ENSG00000090266	NDUFB2	674.9224	0.514751	0.180961	2.844548	0.004447	0.384771
ENSG00000255823	MTRNR2L8	88.69851	0.80221	0.284671	2.818019	0.004832	0.384771
ENSG00000135094	SDS	374.6442	0.833066	0.295145	2.82257	0.004764	0.384771
ENSG00000175985	PLEKHD1	84.74293	-0.67052	0.240603	-2.78682	0.005323	0.384771
ENSG00000108821	COL1A1	144.2349	-0.83705	0.296719	-2.82103	0.004787	0.384771
ENSG00000261857	MIA	203.7857	0.827884	0.292163	2.833632	0.004602	0.384771
ENSG00000142530	FAM71E1	19.35397	0.555792	0.197434	2.815074	0.004877	0.384771
ENSG00000170775	GPR37	104.9986	0.566107	0.206773	2.737821	0.006185	0.389828
ENSG00000197019	SERTAD1	621.5665	0.515149	0.188775	2.728909	0.006354	0.391678
ENSG00000078401	EDN1	78.41643	1.222486	0.448687	2.724583	0.006438	0.392048
ENSG00000040608	RTN4R	19.66314	0.599538	0.220824	2.715001	0.006628	0.392048
ENSG00000113209	PCDHB5	15.93101	0.681644	0.252213	2.702646	0.006879	0.393004
ENSG00000196345	ZKSCAN7	91.34475	0.52829	0.195666	2.699956	0.006935	0.393055
ENSG00000165917	RAPSN	21.05145	-0.63449	0.236171	-2.68658	0.007219	0.400593
ENSG00000145632	PLK2	1570.018	0.505878	0.18918	2.67406	0.007494	0.401224
ENSG00000198939	ZFP2	25.53408	0.761238	0.284628	2.674505	0.007484	0.401224
ENSG00000186480	INSIG1	1680.1	0.590828	0.220892	2.674736	0.007479	0.401224
ENSG00000198670	LPA	68.50585	-0.60768	0.227745	-2.66823	0.007625	0.40529
ENSG00000214756	METTL12	90.15136	0.507306	0.190443	2.663816	0.007726	0.407007
ENSG00000149243	KLHL35	30.62397	0.540832	0.203969	2.651538	0.008013	0.407759
ENSG00000239282	GATSL3	163.1875	0.518584	0.195348	2.65467	0.007939	0.407759
ENSG00000088538	DOCK3	53.29586	-0.54609	0.207448	-2.6324	0.008478	0.414453
ENSG00000241360	PDXP	67.81247	0.52209	0.19822	2.633894	0.008441	0.414453
ENSG00000242866	STRC	49.76977	-0.67549	0.257248	-2.62583	0.008644	0.418498
ENSG00000162772	ATF3	603.2502	0.697791	0.268797	2.595975	0.009432	0.420723
ENSG00000187094	CCK	60.47584	0.800681	0.309839	2.584187	0.009761	0.420723
ENSG00000198785	GRIN3A	14.96359	1.201367	0.460333	2.60978	0.00906	0.420723
ENSG00000187720	THSD4	175.5152	-0.56348	0.218724	-2.57622	0.009989	0.420723
ENSG00000280006	AC009060.2	90.4094	-0.81421	0.315713	-2.57896	0.00991	0.420723

Table S8: Biological Processes Enriched in "Cold" group (d0 vs d3)

ID	Description	Gene Ratio	BgRatio	Pvalue	P.adjus t	Qvalue	geneID	Count
GO:0044057	Regulation of system process	0.148	0.0295106	6.99E- 05	2.16E- 02	1.75E- 02	EDN2/NOS1AP/PER2/CCK/GDF9/ EDN1/AQP1/INHBA/HGF	9
GO:0010035	Response to inorganic substance	0.131	0.0272913	2.40E- 04	3.67E- 02	2.97E- 02	JUN/EDN1/AQP1/HGF/GPR37/ CA2/HBA1/COL1A1	8
GO:0042326	Negative regulation of phosphorylation	0.131	0.0248321	1.26E- 04	3.33E- 02	2.69E- 02	JUN/ATF3/INHBA/HGF/CDKN1C/ AJUBA/BMP4/RTN4R	8
GO:0015711	Organic anion transport	0.115	0.0190139	1.52E- 04	3.53E- 02	2.85E- 02	PER2/CCK/GRM2/EDN1/AQP1/CA2/ HBA1	7
GO:0000302	Response to reactive oxygen species	0.115	0.0122961	9.54E- 06	5.89E- 03	4.76E- 03	JUN/EDN1/AQP1/HGF/GPR37/ HBA1/COL1A1	7
GO:0042542	Response to hydrogen peroxide	0.098	0.0071377	4.70E- 06	4.35E- 03	3.52E- 03	JUN/AQP1/HGF/GPR37/HBA1/ COL1A1	6
GO:0042476	Odontogenesis	0.098	0.0068378	3.66E- 06	4.35E- 03	3.52E- 03	EDN1/AQP1/INHBA/CA2/BMP4/ COL1A1	6
GO:2001236	Regulation of extrinsic signalling pathway	0.082	0.009237	2.47E- 04	3.67E- 02	2.97E- 02	ATF3/INHBA/HGF/BMP4/ TNFRSF12A	5
GO:0044070	Regulation of anion transport	0.066	0.0050384	2.51E- 04	3.67E- 02	2.97E- 02	PER2/CCK/EDN1/CA2	4
GO:0050886	Endocrine process	0.066	0.0046785	1.89E- 04	3.67E- 02	2.97E- 02	EDN2/GDF9/EDN1/INHBA	4
GO:0060395	SMAD protein signal transduction	0.066	0.0034789	5.94E- 05	2.16E- 02	1.75E- 02	JUN/GDF9/INHBA/BMP4	4
GO:0015669	Gas transport	0.049	0.0011396	4.33E- 05	2.01E- 02	1.62E- 02	AQP1/CA2/HBA1	3

Table S9: Biological Processes Enriched in "No Cold" group (d0 vs d3)

ID	Description	Gene	BgRatio	Pvalue Pvalue	P.adjus	Qvalue	geneID	Count
		Ratio			t			
GO:0008544	Epidermis	0.116	0.017694	2.87E-	5.48E-	4.73E-	CRCT1/S100A7/SPINK5/MSX2/CTSV/	8
	development			05	03	03	DKK1/CNFN/KLK7	
GO:0043588	Skin development	0.116	0.014335	6.24E-	2.09E-	1.80E-	CRCT1/S100A7/SPINK5/MSX2/CTSV/	8
	_			06	03	03	DKK1/ATP8A2/CNFN	
GO:0042742	Defense response to	0.101	0.015055	7.86E-	8.76E-	7.57E-	S100A7/JCHAIN/CXCL6/SPINK5/MU	7
	bacterium			05	03	03	C5B/RNASE7/KLK7	
GO:0002687	Positive regulation of	0.072	0.006358	7.69E-	8.76E-	7.57E-	S100A7/CXCL6/CXCL1/CXCL3/CXC	5
	leukocyte migration			05	03	03	L2	
GO:0002688	Regulation of	0.072	0.005638	4.33E-	6.77E-	5.85E-	S100A7/CXCL6/CXCL1/CXCL3/CXC	5
	leukocyte chemotaxis			05	03	03	L2	-
GO:0002690	Positive regulation of	0.072	0.004679	1.75E-	3.90E-	3.37E-	S100A7/CXCL6/CXCL1/CXCL3/CXC	5
	leukocyte chemotaxis			05	03	03	L2	-
GO:0019730	Antimicrobial	0.058	0.003239	7.27E-	8.76E-	7.57E-	JCHAIN/SPINK5/RNASE7/KLK7	4
	humoral response			05	03	03		
GO:0019731	Antibacterial humoral	0.058	0.002879	4.56E-	6.77E-	5.85E-	JCHAIN/SPINK5/RNASE7/KLK7	4
	response			05	03	03		
GO:0071622	Regulation of	0.058	0.002219	1.60E-	3.90E-	3.37E-	S100A7/CXCL1/CXCL3/CXCL2	4
	granulocyte			05	03	03		
	chemotaxis							
GO:0001893	Maternal placenta	0.058	0.001739	5.90E-	2.09E-	1.80E-	SPP1/CTSV/GJB2/LIF	4
	development			06	03	03		
GO:0071624	Positive regulation of	0.058	0.0015	3.18E-	2.09E-	1.80E-	S100A7/CXCL1/CXCL3/CXCL2	4
	granulocyte			06	03	03		
	chemotaxis							
GO:0046697	Decidualization	0.058	0.00114	9.94E-	1.33E-	1.15E-	SPP1/CTSV/GJB2/LIF	4
				07	03	03	1	

Table S10: Molecular Functions Enriched in "No Cold" group (d0 vs d3)

ID	Description	GeneRatio	BgRatio	Pvalue	P.adjust	qvalue	geneID	Count
GO:0030545	receptor regulator activity	0.114	0.027947	7.26E- 04	1.11E- 02	9.74E- 03	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/HBEGF/DKK1/LIF	8
GO:0004175	endopeptidase activity	0.114	0.027025	5.83E- 04	9.80E- 03	8.58E- 03	TMPRSS11B/PLAT/CTSV/TPSB2/KLK7/KLK8/KLK12/ADAMTS1	8
GO:0048018	receptor ligand activity	0.114	0.026276	4.84E- 04	9.80E- 03	8.58E- 03	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/HBEGF/DKK1/LIF	8
GO:0017171	serine hydrolase activity	0.100	0.015962	1.24E- 04	3.81E- 03	3.34E- 03	TMPRSS11B/PLAT/CTSV/TPSB2/KLK7/KLK8/KLK12	7
GO:0008236	serine-type peptidase activity	0.100	0.015674	1.11E- 04	3.81E- 03	3.34E- 03	TMPRSS11B/PLAT/CTSV/TPSB2/KLK7/KLK8/KLK12	7
GO:0004252	serine-type endopeptidase activity	0.100	0.01406	5.62E- 05	3.45E- 03	3.02E- 03	TMPRSS11B/PLAT/CTSV/TPSB2/KLK7/KLK8/KLK12	7
GO:0005125	cytokine activity	0.086	0.012677	2.59E- 04	5.95E- 03	5.21E- 03	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/LIF	6
GO:0005539	glycosaminoglycan binding	0.086	0.012274	2.17E- 04	5.71E- 03	5.00E- 03	SERPINE2/JCHAIN/CXCL6/HBEGF/RNASE7/ADAMTS1	6
GO:0004867	serine-type endopeptidase inhibitor activity	0.057	0.005474	5.86E- 04	9.80E- 03	8.58E- 03	SERPINE2/SPINK5/SPINK7/ITIH6	4
GO:0042379	chemokine receptor binding	0.057	0.003457	9.98E- 05	3.81E- 03	3.34E- 03	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:0008009	chemokine activity	0.057	0.002766	4.13E- 05	3.45E- 03	3.02E- 03	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:0045236	CXCR chemokine receptor binding	0.057	0.000922	4.26E- 07	7.84E- 05	6.86E- 05	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:0042834	peptidoglycan binding	0.029	0.000807	1.41E- 03	2.00E- 02	1.75E- 02	JCHAIN/RNASE7	2

Table S11: KEGG Pathways Enriched in "No Cold" group (d0 vs d3)

ID	Description	GeneRatio	BgRatio	Pvalue	P.adjust	qvalue	geneSymbol	Count
hsa04657	IL-17 signaling pathway	0.226	0.012515	7.88E- 08	7.25E- 06	6.14E- 06	JUN/\$100A7/CXCL6/CXCL1/CXCL3/CXCL2/MUC5B	7
hsa04060	Cytokine- cytokine receptor interaction	0.194	0.039564	1.16E- 03	2.67E- 02	2.26E- 02	ILIRLI/CXCL6/CXCLI/CXCL3/CXCL2/LIF	6
hsa04668	TNF signaling pathway	0.161	0.014803	8.11E- 05	3.73E- 03	3.16E- 03	JUN/CXCL1/CXCL3/CXCL2/LIF	5
hsa05132	Salmonella infection	0.129	0.011573	4.15E- 04	1.27E- 02	1.08E- 02	JUN/CXCL1/CXCL3/CXCL2	4
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	0.097	0.009151	2.74E- 03	4.21E- 02	3.56E- 02	JUN/CXCL1/HBEGF	3
hsa05134	Legionellosis	0.097	0.007401	1.49E- 03	2.74E- 02	2.32E- 02	CXCL1/CXCL3/CXCL2	3

Table S12: Molecular Functions enriched in the WGCNA "Brown" module

ID	Description	GeneRatio	BgRatio	Pvalue	P.adjust	qvalue	geneID	Count
GO:0004175	endopeptidase activity	0.29	0.027025	4.25E-04	3.72E-03	2.80E-03	TMPRSS11B/KLK7/KLK8/KLK12	4
GO:0017171	serine hydrolase activity	0.29	0.015962	5.60E-05	6.54E-04	4.92E-04	TMPRSS11B/KLK7/KLK8/KLK12	4
GO:0008236	serine-type peptidase activity	0.29	0.015674	5.22E-05	6.54E-04	4.92E-04	TMPRSS11B/KLK7/KLK8/KLK12	4
GO:0004252	serine-type endopeptidase activity	0.29	0.01406	3.42E-05	6.54E-04	4.92E-04	TMPRSS11B/KLK7/KLK8/KLK12	4

Table S13: Molecular Functions enriched in the WGCNA "Turquoise" module

ID	Description	GeneRatio	BgRatio	Pvalue	P.adjust	qvalue	geneID	Count
GO:1901681	sulfur compound binding	0.15	0.0133687	2.27E-03	2.36E-02	1.64E-02	SERPINE2/HBEGF/ADAMTS1	3
GO:0061134	peptidase regulator activity	0.15	0.0125619	1.90E-03	2.26E-02	1.57E-02	SERPINE2/SPINK5/ITIH6	3
GO:0005539	glycosaminoglycan binding	0.15	0.0122738	1.78E-03	2.26E-02	1.57E-02	SERPINE2/HBEGF/ADAMTS1	3
GO:0030414	peptidase inhibitor activity	0.15	0.0104875	1.13E-03	1.88E-02	1.31E-02	SERPINE2/SPINK5/ITIH6	3
GO:0061135	endopeptidase regulator activity	0.15	0.0103146	1.08E-03	1.88E-02	1.31E-02	SERPINE2/SPINK5/ITIH6	3
GO:0004866	endopeptidase inhibitor activity	0.15	0.0099689	9.80E-04	1.88E-02	1.31E-02	SERPINE2/SPINK5/ITIH6	3
GO:0008201	heparin binding	0.15	0.0092198	7.81E-04	1.88E-02	1.31E-02	SERPINE2/HBEGF/ADAMTS1	3
GO:0004867	serine-type endopeptidase inhibitor activity	0.15	0.0054742	1.69E-04	1.41E-02	9.80E-03	SERPINE2/SPINK5/ITIH6	3

Table S14: Molecular Functions enriched in the WGCNA "Blue" module

ID	Description	GeneRati o	BgRatio	Pvalu e	P.adjus t	qvalu e	geneID	Coun
GO:003054 5	receptor regulator activity	0.43	0.02794 7	1.15E- 06	1.17E- 05	4.63E -06	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/LI F	6
GO:004801 8	receptor ligand activity	0.43	0.02627 6	8.00E- 07	9.76E- 06	3.87E -06	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/LI F	6
GO:000512 5	cytokine activity	0.43	0.01267 7	1.07E- 08	3.26E- 07	1.30E -07	CXCL6/CXCL1/CXCL3/CXCL2/SPP1/LI F	6
GO:000512 6	cytokine receptor binding	0.36	0.01544 3	1.51E- 06	1.32E- 05	5.23E -06	CXCL6/CXCL1/CXCL3/CXCL2/LIF	5
GO:000122 8	transcriptional activator activity, RNA polymerase II transcription regulatory region	0.29	0.02368	2.57E- 04	1.74E- 03	6.91E -04	JUN/EGR1/KLF6/SPIB	4
GO:000166 4	G-protein coupled receptor binding	0.29	0.01509 7	4.51E- 05	3.44E- 04	1.37E -04	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:004237 9	chemokine receptor binding	0.29	0.00345 7	1.26E- 07	1.92E- 06	7.62E -07	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:000800 9	chemokine activity	0.29	0.00276 6	5.05E- 08	1.03E- 06	4.08E -07	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:004523	CXCR chemokine receptor binding	0.29	0.00092	4.80E- 10	2.93E- 08	1.16E -08	CXCL6/CXCL1/CXCL3/CXCL2	4
GO:000098 2	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence	0.21	0.02304 9	3.66E- 03	1.49E- 02	5.91E -03	JUN/EGRI/KLF6	3
GO:000115 8	enhancer sequence- specific DNA binding	0.14	0.00530 1	2.43E- 03	1.23E- 02	4.90E -03	JUN/SPIB	2
GO:000098 0	RNA polymerase II distal enhancer sequence-specific DNA binding	0.14	0.00414 9	1.50E- 03	8.29E- 03	3.29E -03	JUN/SPIB	2
GO:007041 2	R-SMAD binding	0.07	0.00132 5	1.84E- 02	4.68E- 02	1.86E -02	JUN	1
GO:000196 5	G-protein alpha-subunit binding	0.07	0.00109	1.52E- 02	4.04E- 02	1.60E -02	RGS1	1
GO:007183	HMG box domain binding	0.07	0.00103	1.44E- 02	4.00E- 02	1.59E -02	JUN	1
GO:000113 4	transcription factor activity, transcription factor recruiting	0.07	0.00080	1.12E- 02	3.26E- 02	1.30E -02	LIF	1
GO:003354	MAP kinase phosphatase activity	0.07	0.00080 7	1.12E- 02	3.26E- 02	1.30E -02	DUSP6	1
GO:001701 7	MAP kinase tyrosine/serine/threonin e phosphatase activity	0.07	0.00074	1.04E- 02	3.26E- 02	1.30E -02	DUSP6	1
GO:003549 7	cAMP response element binding	0.07	0.00074 9	1.04E- 02	3.26E- 02	1.30E -02	JUN	1