

Supplementary Tables and Figures

Supplementary Table 1: Gene probes significantly associated with total IgE in the GACRS and CAMP using differential gene expression. . ■ Significant in both cohorts after adjustment for recent inhaled corticosteroid (ICS) use.

Probe IDs	Gene Symbols	Chromosome	Adjusted P-Value		Significant after ICS adjustment	
			GACRS	CAMP	GACRS	CAMP
2470364	PRSS33	16	2.79E-09	2.44E-10	■	■
1780239	OLIG2	21	1.65E-08	2.27E-12	■	■
7570484	TFF3	21	2.39E-08	6.74E-13	■	■
2030142	CLC	19	3.77E-08	4.03E-09	■	■
5360048	CCL23	17	1.49E-07	2.96E-10	■	■
2030403	OLIG1	21	1.49E-07	7.83E-07	■	■
7320324	EMR4P	19	1.49E-07	7.10E-06	■	■
940519	GPR44	11	1.97E-07	2.14E-08	■	■
6450504	FLJ43093	6	2.45E-07	2.02E-08	■	■
2940767	CEBPE	14	2.67E-07	2.62E-13	■	■
1030278	C10orf33	10	3.28E-07	3.85E-10	■	■
5720470	LOC653381	15	1.51E-06	4.92E-05	■	■
780369	SIGLEC8	19	1.55E-06	5.00E-09	■	■
510463	PIK3R6	17	2.92E-06	2.02E-08	■	■
4180338	LGALS12	11	6.06E-06	3.72E-04	■	■
5720059	GFOD1	6	8.71E-06	1.81E-03	■	■
2190671	CCR3	3	1.77E-05	9.16E-05	■	■
1240446	CAT	11	2.08E-05	-	■	
6200253	THBS4	5	2.27E-05	-	■	
1850068	C13orf27	13	2.32E-05	-	■	
5870474	RHOBTB3	5	2.72E-05	2.83E-03	■	
830519	IL5RA	3	3.51E-05	2.01E-02	■	■
4490324	SMPD3	16	5.63E-05	2.24E-06	■	■
7550022	STXBP5	6	6.70E-05	-	■	
6660315	INPP1	2	1.53E-04	6.42E-05	■	■
4480497	SIGLEC10	19	1.57E-04	-	■	
130187	PAPSS1	4	1.79E-04	-	■	
2510356	EMR1	19	2.46E-04	5.50E-03	■	■
2710400	DSC2	18	2.49E-04	-	■	
1050253	ACOT11	1	2.56E-04	2.14E-04	■	■
4610338	CAMK1	3	3.04E-04	6.83E-05	■	■
4290368	PSTPIP2	18	3.22E-04	1.87E-03	■	■
1300546	VSTM1	19	4.64E-04	1.87E-06	■	■
4200047	RNF14	5	4.65E-04	3.10E-05	■	■

1740022	SPNS3	17	6.16E-04	6.60E-09	■	■
4810181	ZBTB42	14	7.51E-04	2.69E-08	■	■
520053	OXER1	2	9.28E-04	2.64E-03	■	
1430541	LOC647308	14	9.38E-04	-	■	
2230678	ACACB	12	1.01E-03	-	■	
5050093	KBTBD11	8	1.01E-03	-	■	
5570711	IDO1	8	1.07E-03	2.44E-10	■	■
60576	LOC642639	9	1.18E-03	1.70E-03	■	■
1660703	MGC72080	7	2.31E-03	-	■	
5390661	VLDLR	9	2.31E-03	-	■	
1230286	LTC4S	5	2.54E-03	6.86E-06	■	■
7610131	EPAS1	2	3.24E-03	2.36E-02	■	
1230487	SRGAP3	3	3.32E-03	-	■	■
2680202	HYAL3	3	3.40E-03	-	■	
5820373	ALDH6A1	14	4.07E-03	-	■	
6560239	CYP4F12	19	4.23E-03	2.00E-05	■	■
7320441	C7orf68	7	4.55E-03	-	■	
2640735	BHLHB2	3	5.76E-03	-	■	
1300242	ZNF440	19	6.61E-03	-	■	
4640398	C6orf97	6	7.94E-03	-	■	
1240201	BACE2	21	8.20E-03	2.31E-02	■	
4050768	CHST13	3	8.20E-03	-	■	
5290148	GPT2	16	8.81E-03	-	■	
150309	SLC24A3	20	1.17E-02	-	■	
6380040	COL9A2	1	1.19E-02	1.35E-03	■	■
2640731	HTR3A	11	1.19E-02	-	■	
290189	FAM124B	2	1.32E-02	1.16E-02	■	■
2480068	CD63	12	1.47E-02	-	■	
4150017	PAQR7	1	1.53E-02	-	■	
6650196	E2F5	8	1.54E-02	-	■	
4120224	GPR18	13	1.54E-02	-	■	
2570661	TRERF1	6	1.73E-02	-	■	
5260142	C20orf79	20	1.79E-02	-	■	
3440689	ACYP1	14	2.20E-02	-	■	
7560180	SUSD1	9	2.24E-02	-	■	
2760500	CD38	4	2.34E-02	-	■	
2350278	PNOC	8	2.58E-02	-	■	
3420300	EEF2K	16	2.66E-02	1.21E-04	■	■
5220612	ECHDC3	10	2.76E-02	-	■	
1500608	HSD3B7	16	3.15E-02	1.29E-02	■	
4640768	VPREB3	22	3.62E-02	-	■	
780725	ADAM8	10	3.80E-02	-	■	
2070520	CDCA7	2	3.80E-02	-	■	
7380670	MYB	6	4.04E-02	3.10E-05		■

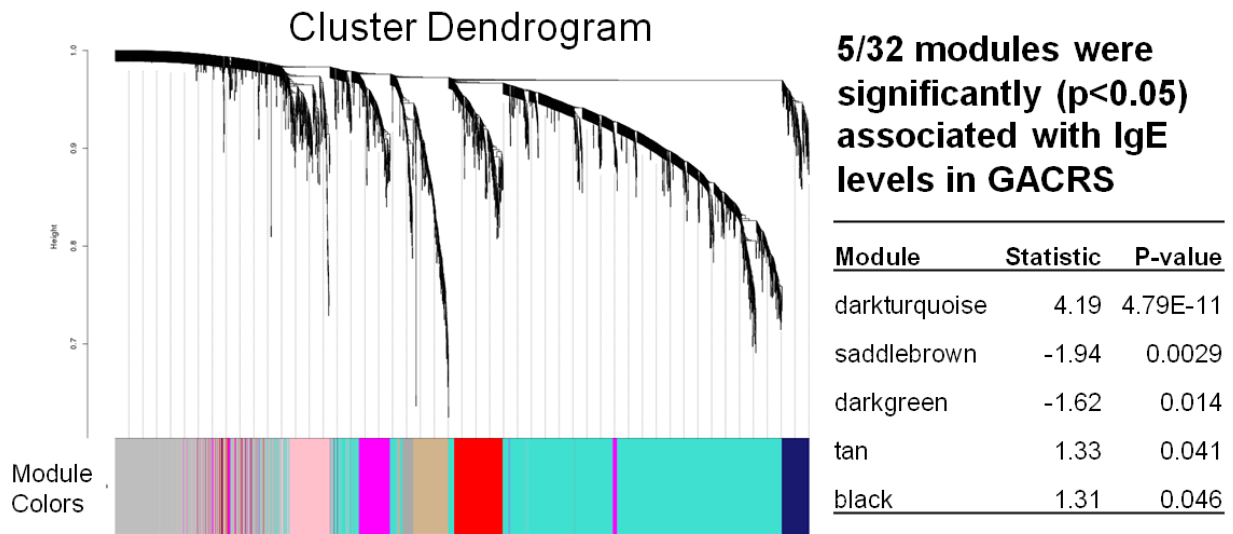
3440674	ASB2	14	4.24E-02	-	
7380273	GPR114	16	4.39E-02	1.75E-02	■
6380102	ATP8B3	19	4.70E-02	-	
3130543	RNASE3	14	-	4.15E-04	■
870138	ADORA3	1	-	8.04E-04	■
2640068	RNASE2	14	-	1.01E-03	■
1690446	PNPLA6	19	-	1.32E-03	■
5260070	HES4	1	-	1.39E-03	■
1400601	C20orf100	20	-	1.58E-03	■
2810253	ACSF2	17	-	1.70E-03	■
6280440	BIK	22	-	7.57E-03	■
1010736	TOX2	20	-	1.03E-02	■
1240025	C17orf38	17	-	1.29E-02	
10253	PPIL5	14	-	1.60E-02	
580475	OLFM2	19	-	1.70E-02	■
160437	BRI3BP	12	-	2.26E-02	
430446	KRT81	12	-	2.36E-02	
2360273	SLC16A14	2	-	2.49E-02	
5360735	FAM54B	1	-	2.70E-02	
4120750	OBFC1	10	-	3.09E-02	
2260747	HRK	12	-	3.09E-02	
6520215	ANXA1	9	-	3.09E-02	
4070424	C16orf93	16	-	3.61E-02	■
3130196	KCTD15	19	-	4.84E-02	
6020224	FBP1	9	-	4.87E-02	

Supplementary Table 2; Biological processes (raw p<0.01, fold enrichment>5, genes>1) enriched among the 42 replicated genes from the IgE-associated modules. *Of the 42 genes that were in the GACRS IgE-associated module and in the CAMP IgE-associated module; 39 could be mapped in GO.*

GO biological process	# Genes in GO Group	# Genes in this study	# Expected Genes	Fold Enrichment	Raw P-value
positive regulation of gliogenesis (GO:0014015)	51	3	0.09	31.74	0.0001
regulation of T cell tolerance induction (GO:0002664)	12	2	0.02	89.92	0.0003
regulation of tolerance induction (GO:0002643)	18	2	0.03	59.95	0.0006
regulation of gliogenesis (GO:0014013)	101	3	0.19	16.03	0.0009
positive regulation of neurogenesis (GO:0050769)	416	5	0.77	6.48	0.0010
regulation of lymphocyte mediated immunity (GO:0002706)	126	3	0.23	12.85	0.0017
leukotriene metabolic process (GO:0006691)	32	2	0.06	33.72	0.0018
positive regulation of nervous system development (GO:0051962)	477	5	0.88	5.66	0.0019
regulation of lymphocyte activation (GO:0051249)	478	5	0.89	5.64	0.0019
positive regulation of glial cell differentiation (GO:0045687)	33	2	0.06	32.7	0.0019
positive regulation of cell development (GO:0010720)	483	5	0.9	5.59	0.0020
monocarboxylic acid metabolic process (GO:0032787)	484	5	0.9	5.57	0.0020
positive regulation of dendritic spine development (GO:0060999)	40	2	0.07	26.98	0.0027
lymphocyte chemotaxis (GO:0048247)	43	2	0.08	25.09	0.0031
regulation of T cell activation (GO:0050863)	329	4	0.61	6.56	0.0033
regulation of leukocyte mediated immunity (GO:0002703)	167	3	0.31	9.69	0.0038
regulation of leukocyte cell-cell adhesion (GO:1903037)	344	4	0.64	6.27	0.0038
regulation of immune effector process (GO:0002697)	363	4	0.67	5.95	0.0046
lymphocyte migration (GO:0072676)	56	2	0.1	19.27	0.0052
regulation of glial cell differentiation (GO:0045685)	59	2	0.11	18.29	0.0057
oligodendrocyte differentiation (GO:0048709)	65	2	0.12	16.6	0.0068
regulation of lymphocyte proliferation (GO:0050670)	210	3	0.39	7.71	0.0071
regulation of mononuclear cell proliferation (GO:0032944)	211	3	0.39	7.67	0.0072
regulation of dendritic spine development (GO:0060998)	67	2	0.12	16.11	0.0072
positive regulation of dendrite development (GO:1900006)	69	2	0.13	15.64	0.0077

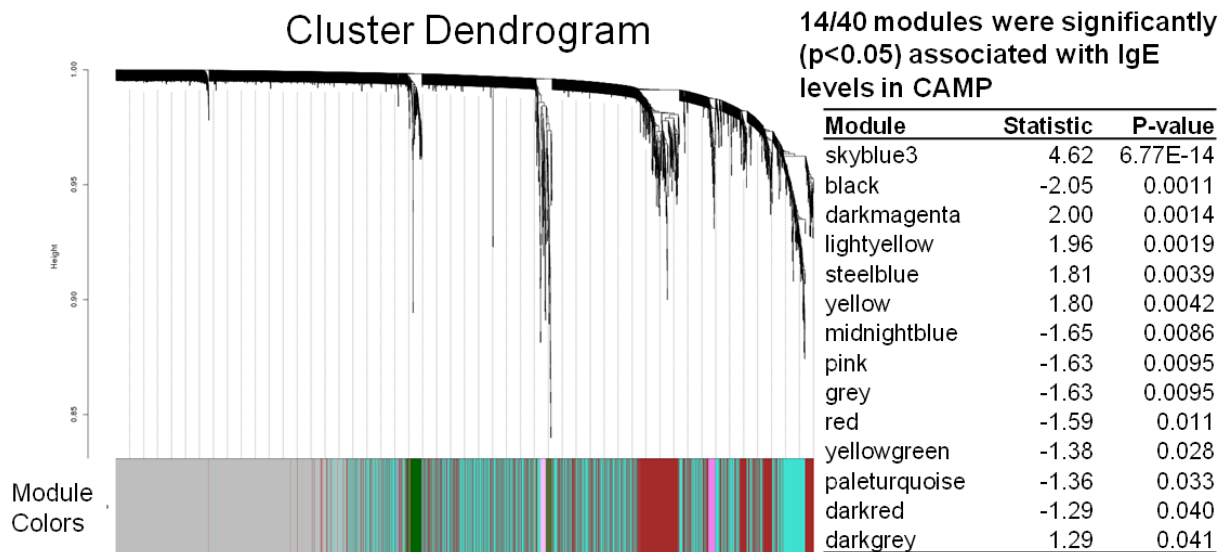
organic hydroxy compound metabolic process (GO:1901615)	421	4	0.78	5.13	0.0077
neuron fate commitment (GO:0048663)	70	2	0.13	15.42	0.0079
regulation of cell-cell adhesion (GO:0022407)	425	4	0.79	5.08	0.0079
regulation of leukocyte proliferation (GO:0070663)	219	3	0.41	7.39	0.0080
positive regulation of T cell differentiation (GO:0045582)	73	2	0.14	14.78	0.0085
chemokine-mediated signaling pathway (GO:0070098)	74	2	0.14	14.58	0.0087
cell fate commitment (GO:0045165)	227	3	0.42	7.13	0.0088

Supplementary Figure 1A: Cluster dendrogram detailing module assignment and the relationship between the resulting modules and serum total IgE in GACRS



The dark turquoise module, referred to as the GACRS module, was selected as the module of interest given its high level of significance.

Supplementary Figure 1B: Cluster dendrogram detailing module assignment and the relationship between the resulting modules and serum total IgE levels in CAMP



The sky blue 3 module, referred to as the CAMP module, was selected as the module of interest given its high level of significance.

Supplementary Table 3: Biological processes enriched (raw $p < 0.01$, fold enrichment > 5 , genes > 1) among the 103 genes comprising the significant module in the GACRS Data. Of the 103 genes in the GACRS module; 100 could be mapped in GO

GO biological process	# Genes in GO Group	# Genes in this study	# Expected Genes	Fold Enrichment	Raw P-value
positive regulation of leukocyte activation (GO:0002696)	369	9	1.75	5.13	7.71E-05
positive regulation of cell activation (GO:0050867)	379	9	1.8	5	9.41E-05
positive regulation of gliogenesis (GO:0014015)	51	4	0.24	16.5	0.000134
regulation of gliogenesis (GO:0014013)	101	5	0.48	10.42	0.000149
regulation of glial cell differentiation (GO:0045685)	59	4	0.28	14.27	0.000227
oligodendrocyte differentiation (GO:0048709)	65	4	0.31	12.95	0.000322
regulation of forebrain neuron differentiation (GO:2000977)	4	2	0.02	100.1	0.000328
neuron fate commitment (GO:0048663)	70	4	0.33	12.02	0.000421
regulation of oligodendrocyte differentiation (GO:0048713)	31	3	0.15	20.36	0.000552
regulation of lymphocyte proliferation (GO:0050670)	210	6	1	6.01	0.000569
regulation of mononuclear cell proliferation (GO:0032944)	211	6	1	5.98	0.000583
positive regulation of glial cell differentiation (GO:0045687)	33	3	0.16	19.13	0.000655
regulation of leukocyte proliferation (GO:0070663)	219	6	1.04	5.76	0.000705
glial cell differentiation (GO:0010001)	148	5	0.7	7.11	0.000806
regulation of leukocyte mediated immunity (GO:0002703)	167	5	0.79	6.3	0.00136
positive regulation of astrocyte differentiation (GO:0048711)	10	2	0.05	42.08	0.00142
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	172	5	0.82	6.12	0.00154
ventral spinal cord development (GO:0021517)	46	3	0.22	13.72	0.00162
regulation of T cell tolerance induction (GO:0002664)	12	2	0.06	35.07	0.00194
gliogenesis (GO:0042063)	193	5	0.92	5.45	0.00251
production of molecular mediator involved in inflammatory response (GO:0002532)	15	2	0.07	28.06	0.00288
regulation of lymphocyte mediated immunity (GO:0002706)	126	4	0.6	6.68	0.00339
granulocyte differentiation (GO:0030851)	17	2	0.08	24.76	0.00359
negative regulation of hemopoiesis (GO:1903707)	128	4	0.61	6.58	0.00359
amine metabolic process (GO:0009308)	64	3	0.3	9.86	0.00395

regulation of tolerance induction (GO:0002643)	18	2	0.09	23.38	0.00398
negative regulation of wound healing (GO:0061045)	65	3	0.31	9.71	0.00412
somatic stem cell population maintenance (GO:0035019)	66	3	0.31	9.56	0.00429
regulation of wound healing (GO:0061041)	135	4	0.64	6.23	0.00431
protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)	139	4	0.66	6.06	0.00476
aromatic amino acid family catabolic process (GO:0009074)	20	2	0.1	21.04	0.00481
positive regulation of dendrite development (GO:1900006)	69	3	0.33	9.15	0.00484
cell maturation (GO:0048469)	144	4	0.68	5.84	0.00538
positive regulation of myeloid leukocyte mediated immunity (GO:0002888)	23	2	0.11	18.3	0.00619
negative regulation of response to wounding (GO:1903035)	76	3	0.36	8.31	0.00626
positive regulation of vasculature development (GO:1904018)	151	4	0.72	5.57	0.00632
diencephalon development (GO:0021536)	78	3	0.37	8.09	0.00671
negative regulation of myeloid cell differentiation (GO:0045638)	79	3	0.38	7.99	0.00694
regulation of astrocyte differentiation (GO:0048710)	25	2	0.12	16.83	0.0072
regulation of response to wounding (GO:1903034)	158	4	0.75	5.33	0.00737
regulation of T cell proliferation (GO:0042129)	158	4	0.75	5.33	0.00737
regulation of glial cell proliferation (GO:0060251)	27	2	0.13	15.59	0.00827
regulation of transforming growth factor beta production (GO:0071634)	27	2	0.13	15.59	0.00827
positive regulation of lymphocyte differentiation (GO:0045621)	85	3	0.4	7.43	0.00843
regulation of blood coagulation (GO:0030193)	86	3	0.41	7.34	0.00869
regulation of hemostasis (GO:1900046)	86	3	0.41	7.34	0.00869
aromatic amino acid family metabolic process (GO:0009072)	28	2	0.13	15.03	0.00884
positive regulation of acute inflammatory response (GO:0002675)	28	2	0.13	15.03	0.00884
regulation of hematopoietic progenitor cell differentiation (GO:1901532)	87	3	0.41	7.26	0.00896
positive regulation of neutrophil chemotaxis (GO:0090023)	29	2	0.14	14.51	0.00942
B cell receptor signaling pathway (GO:0050853)	90	3	0.43	7.01	0.0098
embryonic placenta development (GO:0001892)	90	3	0.43	7.01	0.0098

Supplementary Table 4: Biological processes enriched (raw $p < 0.01$, fold enrichment > 5 , genes > 1) among the 38 genes comprising the significant module in the CAMP Data. Of the 38 genes in the module that were replicated in CAMP; 36 could be mapped in GO

GO biological process	# Genes in GO Group	# Genes in this study	# Expected Genes	Fold Enrichment	Raw P-value
oligodendrocyte differentiation (GO:0048709)	65	3	0.11	26.98	0.0002
regulation of T cell tolerance induction (GO:0002664)	12	2	0.02	97.42	0.0003
regulation of tolerance induction (GO:0002643)	18	2	0.03	64.94	0.0005
inflammatory response (GO:0006954)	465	5	0.8	6.28	0.0011
regulation of lymphocyte mediated immunity (GO:0002706)	126	3	0.22	13.92	0.0014
leukotriene metabolic process (GO:0006691)	32	2	0.05	36.53	0.0015
positive regulation of glial cell differentiation (GO:0045687)	33	2	0.06	35.42	0.0016
glial cell differentiation (GO:0010001)	148	3	0.25	11.85	0.0022
regulation of receptor activity (GO:0010469)	546	5	0.93	5.35	0.0023
regulation of cell activation (GO:0050865)	577	5	0.99	5.06	0.0029
regulation of leukocyte mediated immunity (GO:0002703)	167	3	0.29	10.5	0.0030
positive regulation of gliogenesis (GO:0014015)	51	2	0.09	22.92	0.0037
gliogenesis (GO:0042063)	193	3	0.33	9.09	0.0045
regulation of glial cell differentiation (GO:0045685)	59	2	0.1	19.81	0.0049
regulation of lymphocyte proliferation (GO:0050670)	210	3	0.36	8.35	0.0057
regulation of mononuclear cell proliferation (GO:0032944)	211	3	0.36	8.31	0.0058
regulation of cell-cell adhesion (GO:0022407)	425	4	0.73	5.5	0.0060
multicellular organismal response to stress (GO:0033555)	66	2	0.11	17.71	0.0060
regulation of leukocyte proliferation (GO:0070663)	219	3	0.37	8.01	0.0064
neuron fate commitment (GO:0048663)	70	2	0.12	16.7	0.0067
positive regulation of endothelial cell proliferation (GO:0001938)	73	2	0.12	16.01	0.0073
regulation of heart contraction (GO:0008016)	231	3	0.4	7.59	0.0074
regulation of angiogenesis (GO:0045765)	232	3	0.4	7.56	0.0074
chemokine-mediated signaling pathway (GO:0070098)	74	2	0.13	15.8	0.0075
regulation of vasculature development (GO:1901342)	256	3	0.44	6.85	0.0097

Supplementary Table 5: Replicated genes between the significant GACRS and CAMP modules R from WGCNA

Gene Symbol	Gene Name
ABTB2	Ankyrin Repeat And BTB (POZ) Domain Containing 2
ACOT11	acyl-CoA thioesterase 11
ADORA3	Adenosine A3 Receptor
ATP8B3	ATPase, Aminophospholipid Transporter, Class I, Type 8B, Member 3
PYROXD2	Pyridine Nucleotide-Disulphide Oxidoreductase Domain 2 (previously c10orf33)
CACNG6	Calcium Channel, Voltage-Dependent, Gamma Subunit 6
CAMK1	calcium/calmodulin-dependent protein kinase I
CCL23	chemokine (C-C motif) ligand 23
CCR3	chemokine (C-C motif) receptor 3
CD9	CD9 Molecule
CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon
CLC	Charcot-Leyden crystal protein
CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12
EMR1	Adhesion G Protein-Coupled Receptor E1 (alias ADGRE1)
EMR4P	Adhesion G Protein-Coupled Receptor E4, Pseudogene
FLJ43093	Unknown
GFOD1	Glucose-Fructose Oxidoreductase Domain Containing 1
GPR44	G protein-coupled receptor 44
IDO1	indoleamine 2,3-dioxygenase 1
IL5RA	Interleukin 5 Receptor, Alpha
INPP1	inositol polyphosphate-1-phosphatase
LGALS12	Galectin 12
LOC642639	Unknown
LOC653381	Sorbitol Dehydrogenase (alias: SORD2)
LTC4S	leukotriene C4 synthase
OLIG1	oligodendrocyte transcription factor 1
OLIG2	oligodendrocyte lineage transcription factor 2
PIK3R6	phosphoinositide-3-kinase, regulatory subunit 6
PRSS33	protease, serine, 33
RNASE2	Ribonuclease A Family Member 2
RNF14	ring finger protein 14
SIGLEC8	sialic acid binding Ig-like lectin 8
SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane
SPNS3	spinster homolog 3 (Drosophila)
TFF3	trefoil factor 3 (intestinal)
THBS4	Thrombospondin 4
VSTM1	V-set and transmembrane domain containing 1
ZBTB42	zinc finger and BTB domain containing 42

Supplementary Table 6: Gene sets overlapping the gene set of 31 Common genes

Gene Set Description	# genes overlap	p-value	FDR (q-value)	Genes
Neutrophils versus Monocytes (GSE22886)	5	1.35×10^{-7}	6.55×10^{-4}	<i>GPR44, CCR3, IL5RA, CLC, SIGLEC8</i>
Bone Marrow derived macrophages with MLL4 knockout: control versus LPS stimulated (GSE30971)	4	6.57×10^{-6}	1.07×10^{-2}	<i>EMR1, CCL23, OLIG2, OLIG1</i>
Eosinophils versus Th1 cells (GSE3982)	4	6.57×10^{-6}	1.07×10^{-2}	<i>SMPD3, CCL23, IDO1, CEBPE</i>