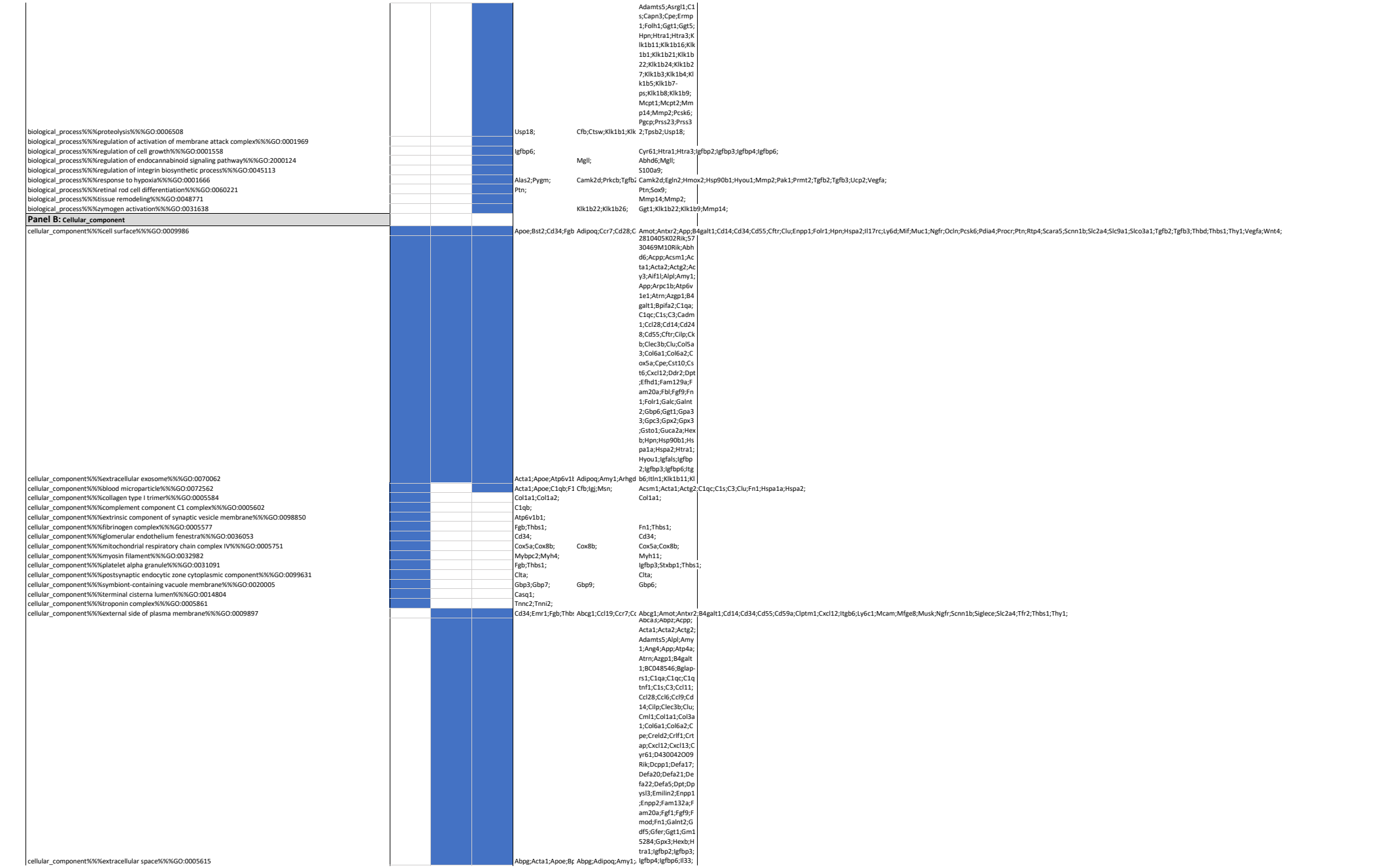
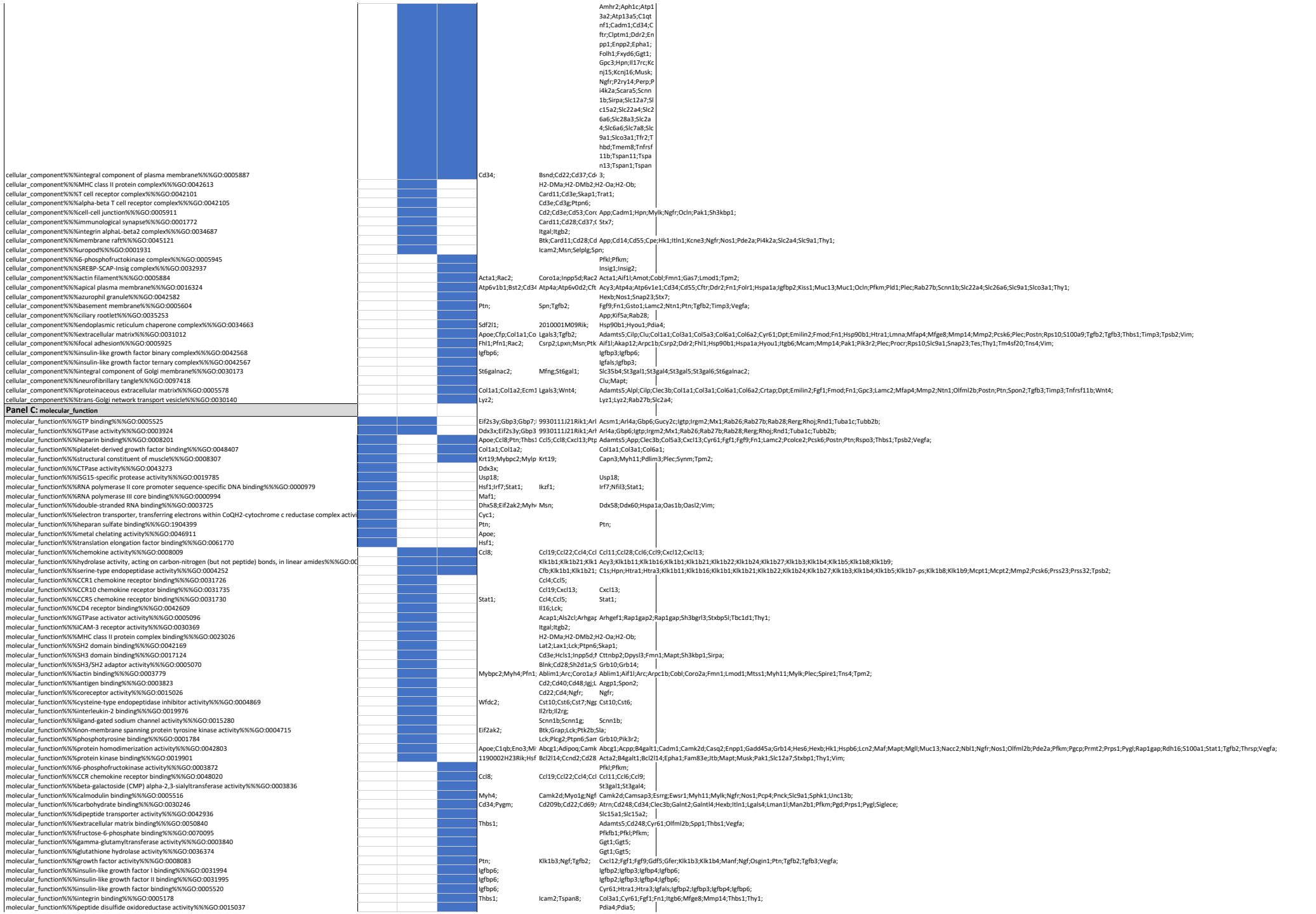
Supplemental Table 2. Enriched GO terms associated with sex-wise differentially expressed (DE) genes

Enriched GO Terms	DE between PG female_vs_ male	DE between SLG female_vs_ male	DE between SMG female_vs_ male	IDs of the DE in PG associated with the enriched GO terms	IDs of the DE in SLG associated with the enriched GO terms	IDs of the DE in SMG associated with the enriched GO terms
Panel A: biological_process						
biological_process%%%cellular response to interferon-beta%%%GO:0035458				Gbp3;Ifit3;Igtp;Irgm	9930111J21Rik1;Ifi4	Gbp6;Ifi205;Ifit1;Ifit3;Igtp;Irgm2;Stat1;
biological_process%%%cellular response to interferon-gamma%%%GO:0071346				Ccl8;Gbp3;Gbp7;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;Gbp6;Irf8;Slc26a6;
biological_process%%%innate immune response%%%GO:0045087				Bpifb1;Bst2;C1qa;C1	Btk;Cd84;Cfb;Grap;I	C1qa;C1qc;C1s;C3;Cd14;Cd55;Ddx58;Ifit1;Ifit2;Ifit3;Ifitm1;Irf7;Lcn2;Mif;Mx1;Oasl2;Ppp1r14b;S100a8;S100a9;Spon2;
biological_process%%%negative regulation of fibroblast growth factor receptor signaling pathway%%%GO:0040037				Shisa2;Thbs1;	Ngfr;Wnt4;	Ngfr;Thbs1;Wnt4;
biological_process%%%defense response to virus%%%GO:0051607				Bst2;Dhx58;Eif2ak2;	Cd40;Gm14446;Ptpr	Ddx58;Ddx60;Ifit1;Ifit2;Ifit3;Ifitm1;Il33;Isg15;Mx1;Oas1b;Oasl2;Spon2;
biological_process%%%negative regulation of peptidase activity%%%GO:0010466				Ecm1;Expi;Wfdc2;	Cst7;Ngf;Ngp;Serpin	App;BC048546;Gpc3;Ngf;Pi16;Serpinb11;Serpinb1a;Serpinb6a;Timp3;Wfdc12;
biological_process%%%protein heterotrimerization%%%GO:0070208				Col1a1;Col1a2;	Adipoq;	C1qtnf1;Col1a1;Col6a1;Col6a2;
biological_process%%%adhesion of symbiont to host%%%GO:0044406				Gbp3;Gbp7;	Gbp9;	Gbp6;
biological_process%%%blood coagulation, fibrin clot formation%%%GO:0072378				F13a1;Fgb;		
biological_process%%%defense response to Gram-positive bacterium%%%GO:0050830				Gbp3;Gbp7;Lyz2;	Gbp9;Il27ra;	Gbp6;Lyz1;Lyz2;Pld1;
biological_process%%%glycerol biosynthetic process from pyruvate%%%GO:0046327				Pck1;		
biological_process%%%hyaloid vascular plexus regression%%%GO:1990384				Ninj1;		
biological_process%%%mitochondrial electron transport, cytochrome c to oxygen%%%GO:0006123				Cox5a;Cox8b;	Cox8b;	Cox5a;Cox8b;
biological_process%%%negative regulation of angiogenesis%%%GO:0016525				1190002H23Rik;Ptn	Cxcr3;Ngfr;Ngp;	Amot;Cd59a;Ngfr;Ptn;Stat1;Thbs1;
biological_process%%%negative regulation of blood coagulation%%%GO:0030195				Apoe;Cd34;	Tspan8;	Cd34;Thbd;
biological_process%%%negative regulation of blood vessel endothelial cell migration%%%GO:0043537				1190002H23Rik;Apoe;Thbs1;		Thbs1;
biological_process%%%negative regulation of cGMP-mediated signaling%%%GO:0010754				Thbs1;		Thbs1;
biological_process%%%negative regulation of cellular response to heat%%%GO:1900035				Cd34;		Cd34;
biological_process%%%negative regulation of dendritic cell antigen processing and presentation%%%GO:0002605				Thbs1;		Thbs1;
biological_process%%%negative regulation of double-strand break repair via nonhomologous end joining%%%GO:2001033				Hsf1;		
biological_process%%%negative regulation of endothelial cell proliferation%%%GO:0001937				1190002H23Rik;Apc	Cxcr3;	Stat1;Thbs1;
biological_process%%%negative regulation of exit from mitosis%%%GO:0001100				1190002H23Rik;		
biological_process%%%negative regulation of glial cell proliferation%%%GO:0060253				Idh2;Ptn;		Ptn;
biological_process%%%negative regulation of macrophage fusion%%%GO:0034240				Stat1;		Stat1;
biological_process%%%negative regulation of matrix metallopeptidase secretion%%%GO:1904465				Idh2;		
biological_process%%%negative regulation of presynaptic membrane organization%%%GO:1901630				Apoe;		
biological_process%%%negative regulation of viral genome replication%%%GO:0045071				Bst2;Eif2ak2;Isg15;R	Ccl5;	Isg15;
biological_process%%%phosphocreatine biosynthetic process%%%GO:0046314				Ckm;		
biological_process%%%positive regulation of endothelial cell apoptotic process%%%GO:2000353				1190002H23Rik;Thb	Cd40;	Cd248;Thbs1;
biological_process%%%positive regulation of lipid transport across blood brain barrier%%%GO:1903002				Apoe;		
biological_process%%%positive regulation of transcription from RNA polymerase II promoter in response to heat stress%%				Hsf1;		
biological_process%%%positive regulation of transforming growth factor beta production%%%GO:0071636				Cd34;Thbs1;		Cd34;Thbs1;
biological_process%%%regulation of MyD88-independent toll-like receptor signaling pathway%%%GO:0034127				Irf7;		Irf7;
biological_process%%%response to interferon-alpha%%%GO:0035455				Bst2;Eif2ak2;	Tgtp1;	
biological_process%%%response to interferon-beta%%%GO:0035456				Bst2;Stat1;Xaf1;	Ikbke;	Stat1;Xaf1;
biological_process%%%response to stilbenoid%%%GO:0035634				Ifit3;Ly6d;Usp18;	Ly6d;	Ifit3;Ly6d;Usp18;
biological_process%%%response to type I interferon%%%GO:0034340				Isg15;Stat1;	Ikbke;	Isg15;Stat1;
biological_process%%%sarcomere organization%%%GO:0045214				Casq1;Krt19;Mybpc	Krt19;	Capn3;Casq2;
biological_process%%%skin morphogenesis%%%GO:0043589				Col1a1;Col1a2;		Col1a1;
biological_process%%%transcription factor TFIIIB complex assembly%%%GO:0070217				Maf1;		
biological_process%%%inflammatory response%%%GO:0006954				Ccl8;Ecm1;Thbs1;	Ccl19;Ccl22;Ccl4;Ccl	Atrn;C3;Ccl11;Ccl6;Ccl9;Cd14;Cxcl13;Ggt5;Itgb6;Mif;Ngfr;Odam;S100a8;S100a9;Sphk1;Thbs1;Tnfrsf11b;Tpsb2;
biological_process%%%positive regulation of angiogenesis%%%GO:0045766				Cd34;Ecm1;Thbs1;	Ccl5;Cxcr3;Ets1;Itgb	C3;Ccl11;Cd34;Epha1;Fgf1;Hipk2;Hspb6;Lrg1;Sphk1;Thbs1;Vegfa;
biological_process%%%renal vesicle induction%%%GO:0072034					Wnt4;	Sox9;Wnt4;
biological_process%%%B cell activation%%%GO:0042113					Bank1;Blnk;Cd40;Icosl;Lat2;Lax1;Pik3cd;Prkcb;	
biological_process%%%B cell homeostasis%%%GO:0001782					Dock10;Mef2c;Ncka	Spns2;
biological_process%%%B cell receptor signaling pathway%%%GO:0050853					Cd79b;Klhl6;Lat2;Lck;Mef2c;Nckap1l;Plcg2;Prkcb;Ptpn6;Ptprc;	
biological_process%%%T cell costimulation%%%GO:0031295					Card11;Ccl19;Cd28;Cd3e;Spn;Tnfrsf13c;	
biological_process%%%T cell migration%%%GO:0072678					Itgb7;Msn;Myo1g;S1pr1;	
biological_process%%%T cell receptor V(D)J recombination%%%GO:0033153					Lef1;Tcf7;	
biological_process%%%T cell receptor signaling pathway%%%GO:0050852					Cd28;Cd3e;Lcp2;Pde	Rbck1;Thy1;
biological_process%%%adaptive immune response%%%GO:0002250				Emr1;Fgb;Unc93b1;	Btk;Cd4;Cd79b;Cd7;	Efcab4b;
biological_process%%%androgen biosynthetic process%%%GO:0006702					Wnt4;	Wnt4;
biological_process%%%antigen processing and presentation of exogenous peptide antigen via MHC class II%%%GO:00198				Unc93b1;	H2-DMa;H2-DMb2;I	Ifi30;
biological_process%%%brown fat cell differentiation%%%GO:0050873					Adig;Adipoq;Fabp4;I	Adig;Arl4a;Lrg1;Plac8;Slc2a4;
biological_process%%%cellular potassium ion homeostasis%%%GO:0030007					Atp1a2;Bsnd;Camk2	Camk2d;
biological_process%%%cellular response to drug%%%GO:0035690					Adipoq;Ccl4;Cd69;M	Mcpt1;Mylk;Pde2a;
biological_process%%%cellular response to interleukin-1%%%GO:0071347				Ccl8;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;Fn1;
biological_process%%%cellular response to tumor necrosis factor%%%GO:0071356				Ccl8;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;Slc2a4;Zfp36l1;
biological_process%%%chemokine-mediated signaling pathway%%%GO:0070098				Ccl8;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;Cxcl12;Cxcl13;
biological_process%%%defense response to protozoan%%%GO:0042832				Gbp3;Gbp7;	Cd37;Cd40;Gbp9;Il4	Gbp6;Irf8;Irgm2;
biological_process%%%defense response%%%GO:0006952				Hsf1;Igtp;Irgm1;	9930111J21Rik1;Cdl	Cxcl12;Cxcl13;Defa17;Defa20;Defa21;Defa22;Defa5;Gm15284;Igtp;
biological_process%%%establishment of T cell polarity%%%GO:0001768					Ccl19;Ccr7;Dock2;	
biological_process%%%female sex determination%%%GO:0030237					Wnt4;	Wnt4;
biological_process%%%heterotypic cell-cell adhesion%%%GO:0034113					Cd2;Itgb2;Itgb7;Ptpr	Perp;Rnase10;
biological_process%%%immune response%%%GO:0006955				Ccl8;Oasl2;	Blnk;Ccl19;Ccl22;Ccl	Ccl11;Ccl28;Ccl6;Ccl9;Cxcl12;Cxcl13;Enpp1;Enpp2;Irf8;Nfil3;Ngfr;Oas1b;Oasl2;P2ry14;Tnfrsf11b;
biological_process%%%immunological synapse formation%%%GO:0001771					Ccl19;Dock2;Dock8;Msn;	
biological_process%%%integrin-mediated signaling pathway%%%GO:0007229					Itgal;Itgb2;Itgb7;Ptk	Col3a1;Itgb6;Thy1;
biological_process%%%interleukin-12 secretion%%%GO:0072610					Ccl19;Ccr7;	
biological_process%%%leukocyte chemotaxis%%%GO:0030595					Ccl4;Coro1a;Il16;S1p	S100a9;
biological_process%%%lymph node development%%%GO:0048535					Ccr7;Cxcl13;Ikzf1;Il7	Cd248;Cxcl13;Spns2;
biological_process%%%lymphocyte chemotaxis%%%GO:0048247				Ccl8;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;
biological_process%%%marginal zone B cell differentiation%%%GO:0002315					Dock10;Mfng;Ptk2b;	
biological_process%%%mast cell activation%%%GO:0045576					Cd48;Lcp2;Rhoh;	
biological_process%%%mature conventional dendritic cell differentiation%%%GO:0097029					Ccl19;Ccr7;	
biological_process%%%metanephric mesenchymal cell differentiation%%%GO:0072162					Wnt4;	Wnt4;
biological_process%%%metanephric tubule formation%%%GO:0072174					Wnt4;	Wnt4;
biological_process%%%monocyte chemotaxis%%%GO:0002548				Ccl8;	Ccl19;Ccl22;Ccl4;Ccl	Ccl11;Ccl6;Ccl9;
biological_process%%%myeloid dendritic cell chemotaxis%%%GO:0002408					Ccl19;Ccr7;	
biological_process%%%negative regulation of B cell activation%%%GO:0050869					Bank1;Inpp5d;Samsn1;Tbc1d10c;	
biological_process%%%negative regulation of B cell receptor signaling pathway%%%GO:0050859					Lpxn;Ptpn6;	
biological_process%%%negative regulation of MAP kinase activity%%%GO:0043407				Apoe;	Adipoq;Ptpn6;Rgs14	Dusp1;
biological_process%%%negative regulation of T cell apoptotic process%%%GO:0070233					Ccl5;Dock8;Prkcq;	
biological_process%%%negative regulation of T cell mediated cytotoxicity%%%GO:0001915					Il7r;Ptprc;	
biological_process%%%negative regulation of T cell receptor signaling pathway%%%GO:0050860					Lgals3;Ptpn22;Ptpn6	Thy1;
biological_process%%%negative regulation of antigen processing and presentation of peptide antigen via MHC class II%%%					H2-Oa;H2-Ob;	
biological_process%%%negative regulation of interleukin-4 production%%%GO:0032713					Cd83;Lef1;	
biological_process%%%negative regulation of interleukin-6 secretion%%%GO:1900165					Bank1;Cd84;Ptpn22;	
biological_process%%%negative regulation of macrophage apoptotic process%%%GO:2000110					Ccl5;St6gal1;	
biological_process%%%negative regulation of male gonad development%%%GO:2000019					Wnt4;	Wnt4;

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3a2;Atp13a5;C1qt
nf1;Cadm1;Cd34;C
ftr;Clptm1;Ddr2;En
pp1;Enpp2;Epha1;
Folh1;Fxyd6;Ggt1;
Gpc3;Hpn;Il17rc;Kc
nj15;Kcnj16;Musk;
Ngfr;P2ry14;Perp;P
i4k2a;Scara5;Scnn
1b;Sirpa;Slc12a7;Sl
c15a2;Slc22a4;Slc2
6a6;Slc28a3;Slc2a
4;Slc6a6;Slc7a8;Slc
9a1;Slco3a1;Tfr2;T
hbd;Tmem8;Tnfrsf
11b;Tspan11;Tspa
n13;Tspan1;Tspan
cellular_component%%%integral component of plasma membrane%%%GO:0005887
Cd34;
Bsnd;Cd22;Cd37;Cd
3;
cellular_component%%%MHC class II protein complex%%%GO:0042613
H2-DMa;H2-DMb2;H2-Oa;H2-Ob;
cellular_component%%%T cell receptor complex%%%GO:0042101
Card11;Cd3e;Skap1;Trat1;
cellular_component%%%alpha-beta T cell receptor complex%%%GO:0042105
Cd3e;Cd3g;Ptpn6;
cellular_component%%%cell-cell junction%%%GO:0005911
Cd2;Cd3e;Cd53;Cor
App;Cadm1;Hpn;Mylk;Ngfr;Ocln;Pak1;Sh3kbp1;
cellular_component%%%immunological synapse%%%GO:0001772
Card11;Cd28;Cd37;(
Stx7;
cellular_component%%%integrin alphaL-beta2 complex%%%GO:0034687
Itgal;Itgb2;
cellular_component%%%membrane raft%%%GO:0045121
Btk;Card11;Cd28;Cd
App;Cd14;Cd55;Cpe;Hk1;Itln1;Kcne3;Ngfr;Nos1;Pde2a;Pi4k2a;Slc2a4;Slc9a1;Thy1;
cellular_component%%%uropod%%%GO:0001931
Icam2;Msn;Selplg;Spn;
cellular_component%%%6-phosphofructokinase complex%%%GO:0005945
Pfkl;Pfkm;
cellular_component%%%SREBP-SCAP-Insig complex%%%GO:0032937
Insig1;Insig2;
cellular_component%%%actin filament%%%GO:0005884
Acta1;Rac2;
Coro1a;Inpp5d;Rac2
Acta1;Aif1l;Amot;Cobl;Fmn1;Gas7;Lmod1;Tpm2;
cellular_component%%%apical plasma membrane%%%GO:0016324
Atp6v1b1;Bst2;Cd34
Atp4a;Atp6v0d2;Cft
Acy3;Atp4a;Atp6v1e1;Cd34;Cd55;Cftr;Ddr2;Fn1;Folr1;Hspa1a;Igfbp2;Kiss1;Muc13;Muc1;Ocln;Pfkm;Pld1;Plec;Rab27b;Scnn1b;Slc22a4;Slc26a6;Slc9a1;Slco3a1;Thy1;
cellular_component%%%azurophil granule%%%GO:0042582
Hexb;Nos1;Snap23;Stx7;
cellular_component%%%basement membrane%%%GO:0005604
Ptn;
Spn;Tgfb2;
Fgf9;Fn1;Gsto1;Lamc2;Ntn1;Ptn;Tgfb2;Timp3;Vegfa;
cellular_component%%%ciliary rootlet%%%GO:0035253
App;Kif5a;Rab28;
cellular_component%%%endoplasmic reticulum chaperone complex%%%GO:0034663
Sdf2l1;
2010001M09Rik;
Hsp90b1;Hyou1;Pdia4;
cellular_component%%%extracellular matrix%%%GO:0031012
Apoe;Cfp;Col1a1;Co
Lgals3;Tgfb2;
Adamts5;Cilp;Clu;Col1a1;Col3a1;Col5a3;Col6a1;Col6a2;Cyr61;Dpt;Emilin2;Fmod;Fn1;Hsp90b1;Htra1;Lmna;Mfap4;Mfge8;Mmp14;Mmp2;Pcsk6;Plec;Postn;Rps10;S100a9;Tgfb2;Tgfb3;Thbs1;Timp3;Tpsb2;Vim;
cellular_component%%%focal adhesion%%%GO:0005925
Fhl1;Pfn1;Rac2;
Csrp2;Lpxn;Msn;Ptk
Aif1l;Akap12;Arpc1b;Csrp2;Ddr2;Fhl1;Hsp90b1;Hspa1a;Hyou1;Itgb6;Mcam;Mmp14;Pak1;Pik3r2;Plec;Procr;Rps10;Slc9a1;Snap23;Tes;Thy1;Tm4sf20;Tns4;Vim;
cellular_component%%%insulin-like growth factor binary complex%%%GO:0042568
Igfbp6;
Igfbp3;Igfbp6;
cellular_component%%%insulin-like growth factor ternary complex%%%GO:0042567
Igfals;Igfbp3;
cellular_component%%%integral component of Golgi membrane%%%GO:0030173
St6galnac2;
Mfng;St6gal1;
Slc35b4;St3gal1;St3gal4;St3gal5;St3gal6;St6galnac2;
cellular_component%%%neurofibrillary tangle%%%GO:0097418
Clu;Mapt;
cellular_component%%%proteinaceous extracellular matrix%%%GO:0005578
Col1a1;Col1a2;Ecm1
Lgals3;Wnt4;
Adamts5;Alpl;Cilp;Clec3b;Col1a1;Col3a1;Col6a1;Col6a2;Crtap;Dpt;Emilin2;Fgf1;Fmod;Fn1;Gpc3;Lamc2;Mfap4;Mmp2;Ntn1;Olfml2b;Postn;Ptn;Spon2;Tgfb3;Timp3;Tnfrsf11b;Wnt4;
cellular_component%%%trans-Golgi network transport vesicle%%%GO:0030140
Lyz2;
Lyz1;Lyz2;Rab27b;Slc2a4;
Panel C: molecular_function
molecular_function%%%GTP binding%%%GO:0005525
Eif2s3y;Gbp3;Gbp7;
9930111J21Rik1;Arl
Acsm1;Arl4a;Gbp6;Gucy2c;Igtp;Irgm2;Mx1;Rab26;Rab27b;Rab28;Rerg;Rhoj;Rnd1;Tuba1c;Tubb2b;
molecular_function%%%GTPase activity%%%GO:0003924
Ddx3x;Eif2s3y;Gbp3
9930111J21Rik1;Arl
Arl4a;Gbp6;Igtp;Irgm2;Mx1;Rab26;Rab27b;Rab28;Rerg;Rhoj;Rnd1;Tuba1c;Tubb2b;
molecular_function%%%heparin binding%%%GO:0008201
Apoe;Ccl8;Ptn;Thbs1
Ccl5;Ccl8;Cxcl13;Ptp
Adamts5;App;Clec3b;Col5a3;Cxcl13;Cyr61;Fgf1;Fgf9;Fn1;Lamc2;Pcolce2;Pcsk6;Postn;Ptn;Rspo3;Thbs1;Tpsb2;Vegfa;
molecular_function%%%platelet-derived growth factor binding%%%GO:0048407
Col1a1;Col1a2;
Col1a1;Col3a1;Col6a1;
molecular_function%%%structural constituent of muscle%%%GO:0008307
Krt19;Mybpc2;Mylp
Krt19;
Capn3;Myh11;Pdlim3;Plec;Synm;Tpm2;
molecular_function%%%CTPase activity%%%GO:0043273
Ddx3x;
molecular_function%%%ISG15-specific protease activity%%%GO:0019785
Usp18;
Usp18;
molecular_function%%%RNA polymerase II core promoter sequence-specific DNA binding%%%GO:0000979
Hsf1;Irf7;Stat1;
Ikzf1;
Irf7;Nfil3;Stat1;
molecular_function%%%RNA polymerase III core binding%%%GO:0000994
Maf1;
molecular_function%%%double-stranded RNA binding%%%GO:0003725
Dhx58;Eif2ak2;Myh
Msn;
Ddx58;Ddx60;Hspa1a;Oas1b;Oasl2;Vim;
molecular_function%%%electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activi
Cyc1;
molecular_function%%%heparan sulfate binding%%%GO:1904399
Ptn;
Ptn;
molecular_function%%%metal chelating activity%%%GO:0046911
Apoe;
molecular_function%%%translation elongation factor binding%%%GO:0061770
Hsf1;
molecular_function%%%chemokine activity%%%GO:0008009
Ccl8;
Ccl19;Ccl22;Ccl4;Ccl
Ccl11;Ccl28;Ccl6;Ccl9;Cxcl12;Cxcl13;
molecular_function%%%hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides%%%GO:00
Klk1b1;Klk1b21;Klk1
Acy3;Klk1b11;Klk1b16;Klk1b1;Klk1b21;Klk1b22;Klk1b24;Klk1b27;Klk1b3;Klk1b4;Klk1b5;Klk1b8;Klk1b9;
molecular_function%%%serine-type endopeptidase activity%%%GO:0004252
Cfb;Klk1b1;Klk1b21;
C1s;Hpn;Htra1;Htra3;Klk1b11;Klk1b16;Klk1b1;Klk1b21;Klk1b22;Klk1b24;Klk1b27;Klk1b3;Klk1b4;Klk1b5;Klk1b7-ps;Klk1b8;Klk1b9;Mcpt1;Mcpt2;Mmp2;Pcsk6;Prss23;Prss32;Tpsb2;
molecular_function%%%CCR1 chemokine receptor binding%%%GO:0031726
Ccl4;Ccl5;
molecular_function%%%CCR10 chemokine receptor binding%%%GO:0031735
Ccl19;Cxcl13;
Cxcl13;
molecular_function%%%CCR5 chemokine receptor binding%%%GO:0031730
Stat1;
Ccl4;Ccl5;
Stat1;
molecular_function%%%CD4 receptor binding%%%GO:0042609
Il16;Lck;
molecular_function%%%GTPase activator activity%%%GO:0005096
Acap1;Als2cl;Arhgap
Arhgef1;Rap1gap2;Rap1gap;Sh3bgrl3;Stxbp5l;Tbc1d1;Thy1;
molecular_function%%%ICAM-3 receptor activity%%%GO:0030369
Itgal;Itgb2;
molecular_function%%%MHC class II protein complex binding%%%GO:0023026
H2-DMa;H2-DMb2;H2-Oa;H2-Ob;
molecular_function%%%SH2 domain binding%%%GO:0042169
Lat2;Lax1;Lck;Ptpn6;Skap1;
molecular_function%%%SH3 domain binding%%%GO:0017124
Cd3e;Hcls1;Inpp5d;
Cttnbp2;Dpysl3;Fmn1;Mapt;Sh3kbp1;Sirpa;
molecular_function%%%SH3/SH2 adaptor activity%%%GO:0005070
Blnk;Cd28;Sh2d1a;S
Grb10;Grb14;
molecular_function%%%actin binding%%%GO:0003779
Mybpc2;Myh4;Pfn1;
Ablim1;Arc;Coro1a;
Ablim1;Aif1l;Arc;Arpc1b;Cobl;Coro2a;Fmn1;Lmod1;Mtss1;Myh11;Mylk;Plec;Spire1;Tns4;Tpm2;
molecular_function%%%antigen binding%%%GO:0003823
Cd2;Cd40;Cd48;Jgj;
Azgp1;Spon2;
molecular_function%%%coreceptor activity%%%GO:0015026
Cd22;Cd4;Ngfr;
Ngfr;
molecular_function%%%cysteine-type endopeptidase inhibitor activity%%%GO:0004869
Wfdc2;
Cst10;Cst6;Cst7;Ngg
Cst10;Cst6;
molecular_function%%%interleukin-2 binding%%%GO:0019976
Il2rb;Il2rg;
molecular_function%%%ligand-gated sodium channel activity%%%GO:0015280
Scnn1b;Scnn1g;
Scnn1b;
molecular_function%%%non-membrane spanning protein tyrosine kinase activity%%%GO:0004715
Eif2ak2;
Btk;Grap;Lck;Ptk2b;Sla;
molecular_function%%%phosphotyrosine binding%%%GO:0001784
Lck;Plcg2;Ptpn6;Sam
Grb10;Pik3r2;
molecular_function%%%protein homodimerization activity%%%GO:0042803
Apoe;C1qb;Eno3;Mi
Abcg1;Adipoq;Camk
Abcg1;Acpp;B4galt1;Cadm1;Camk2d;Casq2;Enpp1;Gadd45a;Grb14;Hes6;Hexb;Hk1;Hspb6;Lcn2;Maf;Mapt;Mgll;Muc13;Nacc2;Nbl1;Ngfr;Nos1;Olfml2b;Pde2a;Pfkm;Pgcp;Prmt2;Prps1;Pygl;Rap1gap;Rdh16;S100a1;Stat1;Tgfb2;Thrsp;Vegfa;
molecular_function%%%protein kinase binding%%%GO:0019901
1190002H23Rik;Hsf
Bcl2l14;Ccnd2;Cd28
Acta2;B4galt1;Bcl2l14;Epha1;Fam83e;Itb;Mapt;Musk;Pak1;Slc12a7;Stxbp1;Thy1;Vim;
molecular_function%%%6-phosphofructokinase activity%%%GO:0003872
Pfkl;Pfkm;
molecular_function%%%CCR chemokine receptor binding%%%GO:0048020
Ccl8;
Ccl19;Ccl22;Ccl4;Ccl
Ccl11;Ccl6;Ccl9;
molecular_function%%%beta-galactoside (CMP) alpha-2,3-sialyltransferase activity%%%GO:0003836
St3gal1;St3gal4;
molecular_function%%%calmodulin binding%%%GO:0005516
Myh4;
Camk2d;Myo1g;Ngf
Camk2d;Camsap3;Esrrg;Ewsr1;Myh11;Mylk;Ngfr;Nos1;Pcp4;Pnck;Slc9a1;Sphk1;Unc13b;
molecular_function%%%carbohydrate binding%%%GO:0030246
Cd34;Pygm;
Cd209b;Cd22;Cd69;
Atrn;Cd248;Cd34;Clec3b;Galnt2;Galntl4;Hexb;Itln1;Lgals4;Lman1l;Man2b1;Pfkm;Pgd;Prps1;Pygl;Siglece;
molecular_function%%%dipeptide transporter activity%%%GO:0042936
Slc15a1;Slc15a2;
molecular_function%%%extracellular matrix binding%%%GO:0050840
Thbs1;
Adamts5;Cd248;Cyr61;Olfml2b;Spp1;Thbs1;Vegfa;
molecular_function%%%fructose-6-phosphate binding%%%GO:0070095
Pfkfb1;Pfkl;Pfkm;
molecular_function%%%gamma-glutamyltransferase activity%%%GO:0003840
Ggt1;Ggt5;
molecular_function%%%glutathione hydrolase activity%%%GO:0036374
Ggt1;Ggt5;
molecular_function%%%growth factor activity%%%GO:0008083
Ptn;
Klk1b3;Ngf;Tgfb2;
Cxcl12;Fgf1;Fgf9;Gdf5;Gfer;Klk1b3;Klk1b4;Manf;Ngf;Osgin1;Ptn;Tgfb2;Tgfb3;Vegfa;
molecular_function%%%insulin-like growth factor I binding%%%GO:0031994
Igfbp6;
Igfbp2;Igfbp3;Igfbp4;Igfbp6;
molecular_function%%%insulin-like growth factor II binding%%%GO:0031995
Igfbp6;
Igfbp2;Igfbp3;Igfbp4;Igfbp6;
molecular_function%%%insulin-like growth factor binding%%%GO:0005520
Igfbp6;
Cyr61;Htra1;Htra3;Igfals;Igfbp2;Igfbp3;Igfbp4;Igfbp6;
molecular_function%%%integrin binding%%%GO:0005178
Thbs1;
Icam2;Tspan8;
Col3a1;Cyr61;Fgf1;Fn1;Itgb6;Mfge8;Mmp14;Thbs1;Thy1;
molecular_function%%%peptide disulfide oxidoreductase activity%%%GO:0015037
Pdia4;Pdia5;

molecular_function%%%phosphodiesterase I activity%%%GO:0004528						Enpp1;Enpp2;
molecular_function%%%receptor agonist activity%%%GO:0048018					Cxcl13;	Ccl11;Cxcl13;Mapt;Vegfa;
molecular_function%%%retinoic acid receptor activity%%%GO:0003708						Esrrg;Rarg;
molecular_function%%%type III transforming growth factor beta receptor binding%%%GO:0034714					Tgfb2;	Tgfb2;Tgfb3;