Supplemental Table 4. Enriched GO terms for differentially expressed protein-coding genes that correlated with the expressed transcription factors in the SLG and PG.

		enrichment				relevant genes		
	SLG:blue		red			!	į.	
	cluster	green	cluster		contributed	contributed	contributed	
	(205	cluster	(36		genes in	genes in	genes in red	
GO term IDs	eenesl	(189 senss)	genesi	J	Nue duster	green cluste		
nolecular_function%%%D-erythro-sphingosine kinase activity%%%GO:0017050	J	L		L	L	<u> </u>	Sphk1;	
nolecular function%%%D4 dopamine receptor binding%%%G0:0031751	L	L		L	L	L	Ppp1r1b;	
nolecular function%%%denatured protein binding%%%GO:0031249		L		L	L	<u> </u>	Hspa1a;	
nolecular_function%%6deoxyhypusine monooxygenase activity%66%GO:0019135	J	L		L	L	<u> </u>	Dohh;	
rolecular_function%00/metal.chelating.activity/00/96G0:004691.1		L		L	L	L	Appe	
nolecular_function%%%oxygen sensor activity%%%GO:0019826	J	L		L	L	i	Egin2;	
nolecular_function%%%sphinganine kinase activity%%%GO:0008481	L	<u>L</u>		L	L	<u> </u>	Sphk1;	
olecular_function%MMtranscription factor binding%MMGO:0008134	1			L	Lef1;Mndal;i		Hes6;Junb;Pi	k3r2;
nolecular_function%%%acylglycerollipase activity%%%GO:0047372	1		L	1	1	Abhd6;MgII;	1	l
rolecular_function%NNAchloride.channel.inhibitor.activityKXNAGQ:0019869	1			1		Cftr:Stx7:	<u> </u>	l
olecular_function%%%growth factor activity%%%GO:0008083	L		i	1	L	Fgf9;Klk1b3;	Cxcl12;	
olecular function%%%hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds								1:Klk1b21:Klk1b22:Klk1
olecular function%%serine-type endopeptidase activity%%%GO:0004252]							1b21;Klk1b22;Klk1b24;
olecular_function%%%titin binding%%%GO:0031432						Camk2d;Capi	3;	
tolecular function WWW.CCR10 chemokine receptor binding WWW.GO:0031735			I		Ccl19:Cxcl13		J	
nolecular_function%%%CD4 receptor binding%%%GO:0042609			l		Il16;Lck;	i	1	
iolecular function%%%GTP binding%%%GO:0005525			I	T	9930111121	Acsm1;Rerg;	ind1;Tubb2b;	
olecular_function%%%GTPase activator activity%%%GO:0005096			ļ	T	Acap1;Als2cl	Stxbp5l;	Rapigap;	
olecular function%MMGTPase activityWWMGO:0003924			!	T	9930111121	Rerg;Rnd1;Tu	bb2b;	
olecular function 9000/CAM-3 receptor activity/9000GO:0030369			[T	Iteal:Iteb2:	Ţ	1	
olecular function%%%MHC class II protein complex binding%%%GO:0023026			[T		DMb2;H2-Oa;I	12-Ob;	
olecular function%%%RNA polymerase II core promoter proximal region sequence-specific			!	T	Akna:Ebf1:Et	Mafb;Nfe2I3;	Junb:Pitx1:	
olecular function%%%RNA polymerase II distal enhancer sequence-specific DNA binding%%			!		Fli1;Ikzf1;Me		1	1
olecular function%%%SH2 domain binding%%%GO:0042169			!	T	Lat2;Lax1;Ld	k;Ptpn6;Skap1		
olecular function%%%SH3 domain binding%%%GO:0017124			!	T	Cd3e:Hcls1:h	Cttnbo2:Dov	3:Fmn1:Mapt	
olecular function%%%SH3/SH2 adaptor activity%%%GO:0005070			!	T		12d1a:Sh2d2a		
iolecular_function%%%T cell receptor binding%%%GO:0042608			!		Dock2:H2-07	7:Lck:	1	1
olecular function%%%antigen binding%%%GO:0003823			T	f	Cd2;Cd40;Cd	148:lei:Lck:	7	1
iolecular_function%%%chemokine.activity%%%GO:0008009			T			Ccl5:Cxcl13:	Cxcl12:	1
olecular function%%%interleukin-2 binding%%GO:0019976			!	f	II2rb:II2rg:	·	ļ	1
olecular: function 9000 non-membrane spanning protein tyrosine kinase activity 9000 GO:000			!		Btk:Grap:Lck		1	1
olecular function%%%phosphotyrosine binding%%%GO:0001784			†	t		imsn1;Vav1;	P#3/2:	1
olecular function%%%orotein kinase binding%%%GO:0019901			İ	+		Bcl2014:Fam8		
iolecular function%%forotein tyrosine kinase binding%%%GO:1990782			i	t	Cd4;Ptpn22;		1	1
nolecular function WW/sphinepsine-1-phosphate receptor activity/9896GD 0038036			†	t	Stort-Stor4		Snhk1:	1

	enrichment							
		green	!					
	blue	cluster	red		contributed	contributed	contributed	
	cluster	(189	cluster		genes in	genes in	genes in red	
GO term IDs	(205 genes)	genesi	(36 genes)		blue cluster	green duster	cluster	
cellular_component%%%extracellular.exosome%%%GO:0070062		L	L		Arhadib;Card	Abhd6;Acpp;A	Aif11,Apoe;C1	qc;Cxcl12;Hsp
cellular component%99MHC class II protein complex6999GO:0042613			L			DMb2;H2-Oa;H	2-0b;	
cellular_component%%%T cell receptor complex%%%GO:0042101			1			Skap1;Trat1;	L	
cellular component%%%alpha-beta T cell receptor complex%%%GO:0042105		L	<u> </u>		Cd3e;Cd3g,9	tpn6;	1	
cellular_component%XXXcell-cell_junction%XXGQ:0005911		L	L		Cd2:Cd3e:Cd	Ngfc/Pak1:	L	
cellular component%90%cytoplasmic side of plasma membrane%90%GO:00098		L	i		Cd2;Msn;Ptp	n22;Ptpn7;	i	
cellular component%%%external side of plasma membrane%66G0:0009897			<u> </u>		Cd19:Ccr7:C	CdS9a:Mcam:l	Clptm1;Cxcl1	2;
cellular component%%%extrinsic component of cytoplasmic side of plasma me			<u> </u>		Btk;Grap;Kci		L	
cellular component%906immunological synapse90906GO:0001772		L	<u> </u>		Card11;Cd28	Stx7;	i	
cellular_component%%%integrin alphai_bsta2.complex%%6G0:0034687			<u> </u>		ItgaLitgb2:		İ	
cellular component%%%lintrinsic component of the cytoplasmic side of the plan			1		Rasa3;Rasal3		L	
cellular_component%%%membrane.raft%%%GO:0045121			L		Btk:Card11:0	Ngfr;Nos1;Pi4I	(2a;Slc2a4;	
cellular_component%%%uropod%%%GO:0001931		L	L		Icam2;Msn;		اـــــا	
cellular_component%90%T-tubule%66%GO:0030315			L			Camk2d;Capn3		
cellular_component%%%apisal plasma membrane%%%GO:0016324		1	L		Cyp4t18:Fan	Acy3:Ato4a:Cf	Hspa1a:	
cellular_component%%%azurophil.granule%%%GO:0042582			L		L	Nos1;Stx7;	i	
cellular component%%%extracellular space%%%GO:0005615			<u>L</u> _	l	Cd19:Cd22:	Acop:Alpl:Atp4	Apoe;C1qc;C	cl12;Fam132
cellular_component%%%neuromuscular junction%%%GO:0031594			<u> </u>		Prkcq;	Camk2d;Musk	Postn Unc13b	5
cellular_component%908BRCA2-BRAF3S complex6096GO:0002111		<u> </u>		l	L	L	Hmg20b;	
cellular_component%000blood.microparticle00006Q:0072562		<u> </u>			lgi:Msn:	Acsm1:	ApperClocity	ipala;
cellular component%%%integral component of lysosomal membrane%%%GO:		i			I	i	Ato13a2:	

				enrichment			relevant genes	
		blu	e	green	red			
		clus (20	er 5	cluster (189	cluster (36	genes in	contributed genes in green	contributed seenes in red
	GO term IDs	een	 S	genesi	genes)	 blue cluster	cluster	cluster
ological process	NNNB cell activation/NNGO-0042113 NNNB cell homeostasis/NNGO-0001782	·				 Bankt;Bink;	Cd40;icosl;Lat2;i I2c;Nckap11;Pik3;	ax1;Pik3cd;Pri
iological process	90958 cell receptor signaling pathway9095GO:0050853				!	 Cd79b;Klhl6	Lat2;LclcMef2c;	Nckap1l;Prkcb
siological process	9866T cell costimulation/666G0:0031295 9866T cell differentiation/686G0:0030217	·				 Card11;Ccl1	9;Cd28;Cd3e;Spr Llkaf1:II7c;Lck:9t	:Tnfrsf13c;
intenient process	999 NT coll migration 999 GO 0073 C79					 itgb7;Msn;f	dyo1g;S1pr1;	
piological process	NONT cell receptor VIDU recombination%WKGO.0033153 NONT cell receptor signaling pathwayMWKGO:0050852			ļ	ļ	 		or Skoot That
notogical process	%%%adaptive immune response%%%G:0002250				İ	 Btk;Cd4;Cd7	Efcab4b;	
	SSS Sertisen processing and presentation of expensus peolide anties NNNapoptotic processNNNGO:0006915	nusia.N				 H2-DMa:H2	-DMb2:H2-Da: M Bcl2l14;Fam17	i mb.
iological process	906Mcellular response to interferon-beta%6%GO:0035458				İ	 0020444124	DOMEST SEASON	Adams (Tennal)
iological process	NN Kcellular response to interferon-gamma NN KGO:0071346 NN Kchemokine-mediated signaling pathway KNN GO:0070098					 Cd19;Cd22	Ccl5;Gbp4;Gbp8 Ccl5;Cxcl13;	Gbp9;H2-Q7;
iological process	%%%defense response to protozoan%%%GO:0042832			L				
iological process inlogical process	900Md efense response900MGO:0006952 900Mestablishment of Ticell polarity900MGO:0001768				ļ	 9930111J21	IRik1;Gd83;Cxd1 Dock?	Cxcl12;
infeeiral erecess	900/Wheterntynic cellicell adhesing/900650 0034113					 Cd2;itgb2;it	Dock2; a Rnase10;	İ
iological process inlogical process	NNNhomeostasis of number of cells NNNGO:0048872 NN Nirmoune response NNNGO:0006955			 	 	 Card11;Ccri	HI7r:Pik3cd:Rass J.NgfcP2ry14:	f2; Cwtt2:
iological process	98999mmunological synapse formation99996GO:0001771					 Cd19;Docka	:,Msn;	<u> </u>
iological process iological process	%%%innate immune response/66%GO:0045087 %%%integrin-mediated signaling pathway/66%GO:0007229				 	 Btk:Cd84:Gi itgal;itgb2;i	Lon2:Mif; tgb7;Thy1;Tspan	C1qc; 32;Vav1;
intenient process	9090 Winterdouble 12 correction 9090 W.G.O.: 0072 E10			L		 Cd19;Ccr7; Coro1a:II16	ł	ļ
notogical process	WWW.puper.chemotasis/WW.CO.0030595 WWW.puper.chemotasis/WW.CO.0030595				İ	 Cor7;Cxcl13	5180: ;lkaf1;ll7r; ;Ccl5;	1
						 Cd19;Cd22	CcIS;	ļ
	988/marginal zone B cell differentiation/989GO:0002315 988/mast cell activation/989GO:0045576					 Dock10;Mfr Cd48;Lcp2;8	Ki Yhoh;	İ
biological_process	NN Vinature conventional dendritic cell differentiation NNNSQ-009702	29	-			 Cd19:Ccr7; Cd19;Ccr7;	<u> </u>	
siological process	9868natural killer cell activation/9866G0:0030101 9868natural killer cell activation/9866G0:0030101 9868negative regulation of B cell activation/9866G0:0050869				ļ	 il2rb;itgb2;]	İ
biological process	NKKnegative regulation of B cell activation/KKKGC:0050869 NKKnegative regulation of B cell receptor signaling pathway/KKKGC:0	05089			 	 Bankt;ingg: Lpxn;Ptpn6;	5d;Samsn1;Tbc1	110c;
biological process	9896Mnegative regulation of MAP kinase activity%999GO:0043407					 Ptpn6;Rgs1	4;	Apoe;
biological process	986% negative regulation of T cell apoptotic process% 660:0070233 986% negative regulation of T cell mediated cytotoxicity 6986GO:00019	15	-	ļ	 	 Cd5;Prkcq; II7r:Ptprc;	 	
biological process	Notice experience of Local receptor signaling pathwork(NSGO) in Notice experience of Local receptor signaling pathwork(NSGO) in Notice experience of antigen processing and presentation of peg	05086			ļ	 Ptnn22-Ptn	n6:Thyd:Ubash3a	,
biological process biological process	NNSnegative regulation of antigen processing and presentation of peg NNSnegative regulation of immunoglobulin secretion NNSGO:005102	otide a	-		 	 H2-Oa;H2-O Voreb3:	ib;	
biological process	90909/negative regulation of interleukin-4 production96909GO:0032713					 Vpreb3; Cd83;Lef1;		
biological process	NNNnegative regulation of interleukin-6 productionNNNGO:0932715 NNNnegative regulation of interleukin-6 secretionNNGO:1900165				 	 Nckap1l;Tris Bank1:Cd84	Pton22:	
iological process	9065/negative regulation of macrophage apoptotic process/9956O:200	00110			ļ	 Cd5;St6gal1	i .	1
biological process	9885 neartive regulation of myeloid dendritic cell activation 986460.00 9885 negative thymic Ticell selection 988460-0045060	30886			 	 Cd37;Tspan Ccr7:Cd2%1	32: d3e:Dock2:Ptpro	;Spn;
piological process	%%%neutrophii chemotaxis%%%%GU3U3U593							11;Vav1;
hinlegical process	%% Koeptistyl-tyrosine autophosphorysation 9000650:0038083 %% Kplatelet aggregation 90006G0:0070527		-		 	 Btk:Grap:Lc Ptpn6;Tspar	132:Ubash3a:	
biological process	10036 positive regulation of 8 cell differentiation 10036 GO:0045579					 ikzf1;il2rg;ir	op6d:Nckap1l; Q Mif;	
biological process biological process	NSNSpositive regulation of 8 cell differentiation/NNNG0.0045579 NSNSpositive regulation of 8 cell proliferation/NNSG0.0030890 NSNSpositive regulation of CD4-positive, alpha-beta T cell differentiatio	in%9030				 Cd83;Nckap	dl;Sash3;	
motogical_process	25/25/DOCUME LEGISLATION OF DITLESS SCHAFFASSINGSTRATES TO SECTION ASSAULT.					 Cd19:Cd22	Wot4: Capn3;	Rapigao:
biological process	%%%positive regulation of NF-kappaB transcription factor activity/6986 %%%positive regulation of T cell chemotaxis%6%GO:0010820	6000			ļ			Sphk1;
biological process	NNNsporitive regulation of T cell themotaxis/NNNGC0.0010820 NNNsporitive regulation of T cell proliferation/NNSGC0.0043102 NNNsporitive regulation of T helper 1 cell differentiation/NNSGC0.00458 NN Noporitive regulation of alleba beta T rell profiferation/NNSGC0.00458 NN Noporitive regulation of alleba receptor mediated signaling pathwa	C27				 Card11;Ccl1	9;Cc15;Cor7;Cd28	Cd3e;Cd4;Co
biological_process	NN Noosibe regulation of alpha-beta T cell proliferation NN NG C 0046*	641				 Ccl19;Ccr7; Cd28:Cd3e:	Ptprc:	
biological process	NKKpositive regulation of antigen receptor-mediated signaling pathwo NKKpositive regulation of calcium-mediated signaling NKKGO:005085	w90000				 Ptprc; Cd3e;Cd4;It		
biological process	9090% positive regulation of cell adhesion mediated by integrin90906 O:C	00336				 Nckap1l;Ptp	r Tgfb2;	!
biological process	NNNoositive regulation of cell proliferation in bone marrow/NNNGO.00	07186		ļ	 	 Lef1;Mef2c	 	
biological process	NSS occibe receision of cell-cell adhesion mediated by interin NSSG NSS occibe regulation of dendritic cell antigen processing and present NSS occibe regulation of enthrocite differentiation/NSSG 0.0045648	tation			1	 Cd19;Ccr7;	1	1
biological process	NNNpositive regulation of erythrocyte differentiation/NNNGO.0045648 NNNpositive regulation of gamma-delta T cell differentiation/NNNGO.0	8 0455				 Ets1;ingp5d Lck;Nckap1	:Nckapil;	
biological process	986% positive regulation of germinal center formation 9696 GO:0002636					 H2-DMa;Trr	frsf13c;	1
piological_process	%%% positive repulation of granulocyte differentiation %%% GD 303085; %% Kpositive regulation of humoral immune responses %% GD 3020292;	2		 	 	 Hcls1:Lef1: Ccr7;H2-DN		
iological process	986%positive regulation of immunoglobulin production%9660:000263	39				 Cd37;II4ra;9	ash3;	
biological process	NNSpositive regulation of interferon-gamma production/66%GO.0032 NNSpositive regulation of interferon-gamma secretion%8%GO.19027				 	 Cd3e;II27ra Cd2;Ptpn22		
iological process	996% positive regulation of interleukin-10 production 6996 GD 0032733.				ļ	 Cd28:Cd83:	Sash3:	ļ
notogical process niological process	%%%positive regulation of interleukin-12 production%%%GO.0032735 8%%positive regulation of interleukin-2 biosynthetic process%%%GO.0	04508	-		 	 Cd19;Ccr7;i Card11;Cd2	.040; 8;Cd3e;Prkco:	
biological process	NNNaositive regulation of interleukin-2 biosynthetic processiveNGC 0 NNNpositive regulation of interleukin-4 productionNNNGC 0032753 NNNaositive regulation of isotrone switching to leG isotronesNNNGC 00	14030			ļ	 Cd28;Cd3e;	8;Cd3e;Prkcq; Prkcq;Sash3;	Į
entopical process inlogical process	NNSpositive regulation of isotype switching to leG isotypes/999660:00 NNSpositive regulation of neutrophil chemotavis/NNSG0:0090023.	14830		<u> </u>	ł	 Cd28;Cd40; Cd19:Ccr71	Ptprc; Yckap II: Rac2: Sel	i
iological process	9090% positive regulation of phagocytosis 90906 O:0050766				ļ	 Ccr7;Cd209	b;Dock2;	Rapigap;
onoeical process iological process	NNSpositive regulation of phosphatidylinositol 3-kinase signaling/9999 NNSpositive regulation of tumor necrosis factor production NNSGO:01	⊌0:00 03276		<u> </u>	<u> </u>	 Cd19;Ccr7;I	e PrrSI;Tgfb2; Id2;Sash3;	<u> </u>
iological process	Missepathor regulation of tumor necrosis factor production MISSEQUANI MISSEQUATIVE regulation of two sine obsestmentation of \$14T protein MISSEQUATIVE MISSEQUATI	6%GO:			ļ	 Cd5;Hds1;	1	Ţ
siological_process siological process	SSSporitive repulation of viral entry into host set19996GO:0046598 SSSSporitive thymic T cell selection/SSSGO:0045059		-		ļ	 Cd4:Trim30 Dock2;H2-D	a: Ma;Ptprc;	
					ļ	 Card11;Ptps Ptprc;	n6;Ptprc;	Ţ
iningical process	%%%regulation of 8 cell receptor signaling pathway/60%GO:0050855_ %%%regulation of T cell differentiation%%%GO:0045580			 	 	 Ptprc; Card11;H2-	Da;	
iological_process	NWScepulation of defense response to virus/00/6GO 0050688 NWScepulation of mast cell chemotaxis/90/6GO 0060753				ļ	 Cd37:Gbp4	Son:Tspan32:	Ţ
notogical process	%%Kregulation of mast cell chemotaxis%%%GO:0060753 %%Kregulation of mast cell degranulation%%%GO:0043304		-	ļ	 	 Rac2; Rac2;	 	
iological process	9099/release of seguestered calcium ion into cytosol9999/GO:0051209					 Cd19;Lck;Pt	prc;	I
iological process	%%%brain renin-angiotensin system%%%GO:0002035 %%%cellular potassium ion homeostasis%%%GO:0030007					 	Klk1b26;Mif; Band:Camk2d:	
hiningical process	900/Vicellular resonate to asmotic stressW40VGO:0071470					 	Serpinb6a;Sk2	24;
iological process	900Matty acid biosynthetic process/600GO:0006633 900Mglucose homeostasis/600GO:0042593				}	 	Acsm1,Elovl7;F Ngfr,Pfkm,Rph	a2h;Mgll,Sc5c 3al;Slc2a4;Stxl
notogical process	NINNEGONAG GEVEROPMENTNINNIGO:UUU84Ub					 	Serpinb6a,Serp	inb6b;
siological process	NNN country regulation of release of sequestered calcium ion into cyto NNN contine regulation of ayon extension (NNSCO 1045773	050(96)				 -+	Tgfb2: Mapt:Nef:Pak1	Appe:
biological process	NNNpositive regulation of focal adhesion assembly 93/49G:0051894					 Thy1;	Fmn1;Vegfa;W	nt4;
biological process	NNNepositive regulation of focal adhesion assembly/NNNGC:0051894 NNNepositive regulation of neuron death/NNNGC:1901216 NNNepositive regulation of protein secretion/NNNGC:0050714				ļ <u>-</u>	 Prkcq;	Fmn1;Vegfa;W Mapt;Ngfr;Nos Myo18a;Rph3a	1; Ato13a2:
		911				 Cd5:		
biological process biological process	NN Negositive regulation of synaptic transmission, choinergic NNNGC U. NN Negolation of endocannabinoid signaling pathway NNNGC 200012	24				 	Musk;Ngfr; Abhd6:Mell:	
biological process	NNNregulation of endocannabinoid signaling pathwayNNNGO:200012 NNNresponse to hypoxiaNNNGO:0001666					 Prkcb;	Camk2d,Hmox	Egin2;
nonogical process	%%%44600H2Ei0n%%%45U3U042311	19907			-	 	Cftr;Klk1b1;No	Appe;
		~				 	1	Pitx1;Rarg;
biological process	%%Sgrowth plate cartilage chondrocyte growth%%SGO:0003430 %%Sligid transport involved in lipid storage%%SGO:0010877			ļ		 	 	Rarg; Apoe;
hiningical process	9000 (negative regulation of DNA damage reconnect signal transduction	by pS				 	ļ	Pcbp4;
biological process	%%% agative regulation of GTP binding%%%GO:1904425 %% Angative regulation of adipose tissue development%%%GO:19041	178				 	 -	Bapigap: Lmna:
protogical process	NUMBER OF PROPERTY OF THE PROPERTY OF THE STATE OF THE ST	48025				 	1	Pcbp4;8bm4
biological process	NKKnegative regulation of microvillus assemblyKKKGC:1903697 NKKnegative regulation of presynaptic membrane organization/KKKGI			ļ		 	∤	Rap1gap; Apoe;
biological process	909050 exative regulation of thyroid sland epithelial cell proliferation 90%	9660:				 -1	!	Rapieao:
biological process	900Mpeptidyl-aspartic acid autophosphorylation900MGO:1990938			ļ		 	 	Atp13a2;
biological process	NNNpeptidyl-lysine modification to peptidyl-hypusineNNNGO:000861 NNNpolyamine importNNNGO:1905122	^		<u> </u>		 	1	Dohh; Atp13a2;
piological process	996 Spositive regulation of dendritic spine maintenance 9999 GO 19029 998 Spositive regulation of lipid transport across blood brain barrier 999	152		ļ		 	 	Apoe; Apoe;
biological process	9999 positive regulation of low-density lipoprotein particle receptor cat			 		 	1	Apoe;
biological process	NNNepositive regulation of phospholipid effluxINNSGO:1902995			ļ		 	 	Apoe;
	NSVicepulation of actorylogoroms durining 0016243 NSVicepulation of plucopyloramidase activity/NSVIGO:1905123 NSVicepulation of lyssomal protein attabalic process NSVIGO:190516					 	į	Atp13a2;
biological process								Ato13a2: