

Supplementary Table S6: Biological processes for genes within the Turquoise module

Category	Term	StressGO	Stress Response	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP	GO:0006954	GO:0006954	inflammatory respon:	28	1.70316302	0.20878634	REG3B, UCN,	1205	344	18082	1.22140307	1	1	0.99966876
GOTERM_BP	GO:0045087	GO:0045087	innate immune respo	20	1.21654501	0.95616434	C1QB, FGB, A	1205	400	18082	0.75029046	1	1	0.99966876
GOTERM_BP	GO:0001666	GO:0001666	response to hypoxia	14	0.85158151	0.51647718	RYR2, POSTN	1205	192	18082	1.09417358	1	1	0.99966876
GOTERM_BP	GO:0006974	GO:0006974	cellular response to C	13	0.79075426	0.99985903	UVRAG, PLK3	1205	420	18082	0.46446552	1	1	0.99985903
GOTERM_BP	GO:0006979	GO:0006979	response to oxidative	10	0.60827251	0.52957285	UCN, NQO1,	1205	133	18082	1.12825633	1	1	0.99966876
GOTERM_BP	GO:0006281	GO:0006281	DNA repair	7	0.42579075	0.99998337	DDB1, UVRAG	1205	318	18082	0.33031655	1	1	0.99998337
GOTERM_BP	GO:0007596	GO:0007596	blood coagulation	7	0.42579075	0.49066364	FGB, SHH, AC	1205	84	18082	1.25048409	1	1	0.99966876
GOTERM_BP	GO:0042742	GO:0042742	defense response to I	7	0.42579075	0.989476	ADAMTS4, GI	1205	191	18082	0.54995112	1	1	0.99966876
GOTERM_BP	GO:0051607	GO:0051607	defense response to v	7	0.42579075	0.96985789	OAS1H, CD8E	1205	167	18082	0.62898601	1	1	0.99966876
GOTERM_BP	GO:0071456	GO:0071456	cellular response to h	6	0.3649635	0.82392224	OPRD1, GNG	1205	103	18082	0.8741248	1	1	0.99966876
GOTERM_BP	GO:0009267	GO:0009267	cellular response to s	5	0.30413625	0.57261716	CTSL, LRRK2,	1205	60	18082	1.25048409	1	1	0.99966876
GOTERM_BP	GO:0009408	GO:0009408	response to heat	5	0.30413625	0.53143549	CRNN, CCKAF	1205	57	18082	1.31629905	1	1	0.99966876
GOTERM_BP	GO:0048265	GO:0048265	response to pain	5	0.30413625	0.04718072	RET, UCN, TA	1205	21	18082	3.5728117	1	1	0.99966876
GOTERM_BP	GO:0050729	GO:0050729	positive regulation of	5	0.30413625	0.61168295	TNFSF18, TNI	1205	63	18082	1.19093723	1	1	0.99966876
GOTERM_BP	GO:0006952	GO:0006952	defense response	4	0.243309	0.98562032	IRGM1, ACOI	1205	116	18082	0.51744169	1	1	0.99966876
GOTERM_BP	GO:0030168	GO:0030168	platelet activation	4	0.243309	0.48608576	FGB, ENTPD2	1205	39	18082	1.53905735	1	1	0.99966876
GOTERM_BP	GO:0034976	GO:0034976	response to endoplas	4	0.243309	0.8892522	SRPX, BCL2L1	1205	76	18082	0.78977943	1	1	0.99966876
GOTERM_BP	GO:0042060	GO:0042060	wound healing	4	0.243309	0.95432494	PDGFRA, CCA	1205	94	18082	0.63854507	1	1	0.99966876
GOTERM_BP	GO:0050728	GO:0050728	negative regulation o	4	0.243309	0.93505691	GHSR, ACOD:	1205	87	18082	0.68992226	1	1	0.99966876
GOTERM_BP	GO:0070527	GO:0070527	platelet aggregation	4	0.243309	0.46869643	FGB, PDGFRA	1205	38	18082	1.57955886	1	1	0.99966876
GOTERM_BP	GO:0002230	GO:0002230	positive regulation of	3	0.18248175	0.99788119	PKD4, IL27, P	1205	122	18082	0.36899531	1	1	0.99966876
GOTERM_BP	GO:0002526	GO:0002526	acute inflammatory r	3	0.18248175	0.31422359	KL, TNFSF4, C	1205	17	18082	2.64808396	1	1	0.99966876
GOTERM_BP	GO:0002931	GO:0002931	response to ischemia	3	0.18248175	0.70167818	UCHL1, EEF2,	1205	36	18082	1.25048409	1	1	0.99966876
GOTERM_BP	GO:0006953	GO:0006953	acute-phase response	3	0.18248175	0.68676064	REG3B, REG3	1205	35	18082	1.28621221	1	1	0.99966876
GOTERM_BP	GO:0009409	GO:0009409	response to cold	3	0.18248175	0.75552601	ZFP516, UCP:	1205	40	18082	1.12543568	1	1	0.99966876
GOTERM_BP	GO:0034341	GO:0034341	response to interfero	3	0.18248175	0.52426809	CD86, CYP27I	1205	26	18082	1.73143951	1	1	0.99966876
GOTERM_BP	GO:0034599	GO:0034599	cellular response to o	3	0.18248175	0.92878892	LRRK2, PENK,	1205	63	18082	0.71456234	1	1	0.99966876
GOTERM_BP	GO:0035902	GO:0035902	response to immobili	3	0.18248175	0.54487186	GPI1, UCN, A	1205	27	18082	1.66731213	1	1	0.99966876
GOTERM_BP	GO:0042594	GO:0042594	response to starvatio	3	0.18248175	0.72973901	UCN, CCKAR,	1205	38	18082	1.18466914	1	1	0.99966876
GOTERM_BP	GO:0042730	GO:0042730	fibrinolysis	3	0.18248175	0.26362141	FGB, TMPRSS	1205	15	18082	3.00116183	1	1	0.99966876
GOTERM_BP	GO:0042771	GO:0042771	intrinsic apoptotic sig	3	0.18248175	0.62091297	DDIT4, TRP7E	1205	31	18082	1.45217508	1	1	0.99966876
GOTERM_BP	GO:0043508	GO:0043508	negative regulation o	3	0.18248175	0.23826949	DUSP10, TRP	1205	14	18082	3.21553053	1	1	0.99966876
GOTERM_BP	GO:0046329	GO:0046329	negative regulation o	3	0.18248175	0.48121555	PER1, DUSP1	1205	24	18082	1.87572614	1	1	0.99966876
GOTERM_BP	GO:0046330	GO:0046330	positive regulation of	3	0.18248175	0.95211169	SERPINF2, W	1205	70	18082	0.64310611	1	1	0.99966876
GOTERM_BP	GO:0048266	GO:0048266	behavioral response t	3	0.18248175	0.41235658	P2RX2, TACR	1205	21	18082	2.14368702	1	1	0.99966876
GOTERM_BP	GO:0050829	GO:0050829	defense response to t	3	0.18248175	0.89500229	REG3B, IL22R	1205	56	18082	0.80388263	1	1	0.99966876
GOTERM_BP	GO:0071346	GO:0071346	cellular response to ir	3	0.18248175	0.94632119	ADAMTS13, I	1205	68	18082	0.66202099	1	1	0.99966876

Supplementary Table S6: Parent ontology analysis for turquoise module to identify Top biological processes categories described in Figure 3B.

GO Class ID	Definitions	Counts	Fractions
			<u>74</u>
GO:0006950	stress response	GO:0001666 GO:0001666 G	18.50%
			<u>36</u>
GO:0019538	protein metabolism	GO:0000165 GO:0000187 G	9.00%
			<u>23</u>
GO:0009605	response to external sti	GO:0001964 GO:0002230 G	5.75%
			<u>22</u>
GO:0006915	apoptosis	GO:0006915 GO:0006915 G	5.50%
			<u>22</u>
GO:0009719	response to endogenou	GO:0001975 GO:0007179 G	5.50%
			<u>13</u>
GO:0007155	cell adhesion	GO:0001953 GO:0007155 G	3.25%
			<u>11</u>
GO:0006629	lipid metabolism	GO:0006629 GO:0006631 G	2.75%
			<u>9</u>
GO:0009628	response to abiotic stim	GO:0001666 GO:0007602 G	2.25%
			<u>9</u>
GO:0009056	catabolism	GO:0002084 GO:0006032 G	2.25%
			<u>8</u>
GO:0042981	regulation of apoptosis	GO:0042981 GO:0043065 G	2.00%
			<u>7</u>
GO:0000165	MAPKKK cascade	GO:0000165 GO:0000187 G	1.75%
			<u>6</u>
GO:0009607	response to biotic stimu	GO:0002230 GO:0032496 G	1.50%
			<u>6</u>
GO:0043408	regulation of MAPKKK (GO:0000187 GO:0043410 G	1.50%
			<u>6</u>
GO:0006955	immunology, immune re	GO:0002250 GO:0006955 G	1.50%
			<u>3</u>
GO:0051249	regulation of lymphocyt	GO:0042102 GO:0042130 G	0.75%
			<u>3</u>

GO:0042110	T cell activation	GO:0042102 GO:0042130 G	<u>3</u>	0.75%
GO:0046879	hormone secretion	GO:0030073 GO:0032024 G	<u>3</u>	0.75%
GO:0000910	cytokinesis	GO:0000910 GO:0032465 G	<u>3</u>	0.75%
GO:0046328	regulation of JNK cascade	GO:0043508 GO:0046329 G	<u>3</u>	0.75%
GO:0051403	stress-activated MAPK	GO:0043508 GO:0046329 G	<u>3</u>	0.75%
GO:0046649	lymphocyte activation	GO:0042102 GO:0042130 G	<u>3</u>	0.75%
GO:0005975	carbohydrate metabolism	GO:0005975 GO:0006096 G	<u>3</u>	0.75%
GO:0001816	cytokine production	GO:0001816 GO:0001819 G	<u>3</u>	0.75%
GO:0007254	JNK cascade	GO:0043508 GO:0046329 G	<u>2</u>	0.75%
GO:0046651	lymphocyte proliferation	GO:0042102 GO:0042130	<u>2</u>	0.50%
GO:0042742	defense response to bacteria	GO:0042742 GO:0050829	<u>2</u>	0.50%
GO:0050670	regulation of lymphocyte	GO:0042102 GO:0042130	<u>2</u>	0.50%
GO:0006897	endocytosis	GO:0006897 GO:0006898	<u>1</u>	0.50%
GO:0046425	regulation of JAK-STAT	GO:0046426	<u>1</u>	0.25%
GO:0007259	JAK-STAT cascade	GO:0046426	<u>1</u>	0.25%
GO:0016064	humoral defense mechanism	GO:0006958	<u>1</u>	0.25%
GO:0006959	humoral immune response	GO:0006958	<u>1</u>	0.25%

GO:0019724	B cell mediated immunity	GO:0006958	<u>1</u>	0.25%
GO:0006956	complement activation	GO:0006958	<u>1</u>	0.25%
GO:0016032	viral life cycle	GO:1902188	<u>1</u>	0.25%
GO:0043122	regulation of I-kappaB kinase	GO:0043123	<u>1</u>	0.25%
GO:0006958	complement activation	GO:0006958	<u>1</u>	0.25%
GO:0042445	hormone metabolism	GO:0032455	<u>1</u>	0.25%
GO:0014065	phosphoinositide 3-kinase	GO:0014068	<u>1</u>	0.25%
GO:0017144	drug metabolism	GO:0017144	<u>1</u>	0.25%
GO:0007249	I-kappaB kinase/NF-kappaB	GO:0043123	<u>1</u>	0.25%
Total		400		100.00%

Supplementary Table S6: Biological processes for genes within the Grey module

Category	Term	Stress&protein_metabolisr	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP	GO:0006355	#N/A	regulation of	41	12.9337539	0.05970447	TENM1, DDX1	249	2279	18082	1.30643152	1	1
GOTERM_BP	GO:0030836	#N/A	positive regu	3	0.94637224	0.00632955	VIL1, CFL2, PI	249	9	18082	24.206158	0.99970472	1
GOTERM_BP	GO:0006810	#N/A	transport	31	9.77917981	0.16819611	CHRNA2, TUSC	249	1822	18082	1.23555032	1	1
GOTERM_BP	GO:0007275	#N/A	multicellular	21	6.62460568	0.07508633	HACD1, FLT1,	249	1029	18082	1.48200967	1	1
GOTERM_BP	GO:0045944	#N/A	positive regu	20	6.30914827	0.09178846	DDX5, HDAC3	249	995	18082	1.45966782	1	1
GOTERM_BP	GO:0032259	#N/A	methylation	8	2.52365931	0.00885532	COMT/D1, PRK	249	169	18082	3.43756089	0.99998864	1
GOTERM_BP	GO:0001122	#N/A	negative regu	16	5.04731861	0.07821654	DDX5, HDAC3	249	729	18082	1.5938211	1	1
GOTERM_BP	GO:0030154	#N/A	cell differenti	16	5.04731861	0.11803287	FLT1, TXNRD2	249	780	18082	1.48960972	1	1
GOTERM_BP	GO:0007614	#N/A	short-term m	3	0.94637224	0.01322775	MDK, RCAN2	249	13	18082	16.7581094	0.99999996	1
GOTERM_BP	GO:0032981	#N/A	mitochondria	3	0.94637224	0.02480758	NDUFAF8, NDU	249	18	18082	12.103079	1	1
GOTERM_BP	GO:0007165	#N/A	signal transdu	15	4.7318612	0.82402187	TENM1, CHRI1	249	1255	18082	0.86794989	1	1
GOTERM_BP	GO:0045892	#N/A	negative regu	12	3.78548896	0.17166047	MECP2, PURH	249	579	18082	1.50504609	1	1
GOTERM_BP	GO:0016310	#N/A	phosphorylat	11	3.47003155	0.33003532	RPS6KA3, PD	249	612	18082	1.30523401	1	1
GOTERM_BP	GO:0035556	#N/A	intracellular s	10	3.15457413	0.09892448	PREX2, ADCY	249	400	18082	1.81546185	1	1
GOTERM_BP	GO:0006629	#N/A	lipid metabo	9	2.83911672	0.2953743	FADS3, FDP5,	249	459	18082	1.42389165	1	1
GOTERM_BP	GO:0006351	#N/A	transcription,	37	11.6719243	0.02565234	TENM1, DDX1	249	1885	18082	1.42540241	1	1
GOTERM_BP	GO:0001701	#N/A	in utero emb	8	2.52365931	0.11825795	DDX5, HHEX,	249	299	18082	1.9429692	1	1
GOTERM_BP	GO:0006357	#N/A	regulation of	8	2.52365931	0.30107884	DDX5, HHEX,	249	397	18082	1.46334456	1	1
GOTERM_BP	GO:0010628	#N/A	positive regu	8	2.52365931	0.3082929	KDM4C, STAF	249	399	18082	1.4560095	1	1
GOTERM_BP	GO:0006468	GO:0006468	protein phos	8	2.52365931	0.67957331	RPS6KA3, TE	249	576	18082	1.00858992	1	1
GOTERM_BP	GO:0006508	GO:0006508	proteolysis	8	2.52365931	0.69011645	CPA3, C1RA,	249	582	18082	0.99819208	1	1
GOTERM_BP	GO:0016569	#N/A	covalent chrc	7	2.20820189	0.16071566	KDM4C, HDA	249	266	18082	1.91101247	1	1
GOTERM_BP	GO:0006281	GO:0006281	DNA repair	7	2.20820189	0.27164502	RDM1, ANKLI	249	318	18082	1.59851987	1	1
GOTERM_BP	GO:0016567	GO:0016567	protein ubiq	7	2.20820189	0.3774083	RFPWD3, FBXO	249	362	18082	1.40422463	1	1
GOTERM_BP	GO:0006412	GO:0006412	translation	7	2.20820189	0.47372848	MRP515, RPL	249	401	18082	1.26765416	1	1
GOTERM_BP	GO:0007283	#N/A	spermatogen	7	2.20820189	0.4887967	ADCY10, ZFP	249	407	18082	1.24896638	1	1
GOTERM_BP	GO:0006974	GO:0006974	cellular resp	7	2.20820189	0.51679291	FANCM, RFW	249	420	18082	1.2103079	1	1
GOTERM_BP	GO:0006631	#N/A	fatty acid me	6	1.89274448	0.06397654	FADS3, FADS	249	156	18082	2.79301823	1	1
GOTERM_BP	GO:0042127	#N/A	regulation of	6	1.89274448	0.20207019	PURA, HHEX,	249	227	18082	1.91943103	1	1
GOTERM_BP	GO:0006397	#N/A	mRNA proce	6	1.89274448	0.45380254	RBM4, DDX5,	249	322	18082	1.35313927	1	1
GOTERM_BP	GO:0006954	GO:0006954	inflammatory	6	1.89274448	0.50975641	TLR1, TUSC2,	249	344	18082	1.26660129	1	1
GOTERM_BP	GO:0008284	#N/A	positive regu	6	1.89274448	0.86868963	MECP2, PURH	249	542	18082	0.80389455	1	1
GOTERM_BP	GO:0007186	#N/A	G-protein co	6	1.89274448	0.99999996	PREX2, PROK	249	1706	18082	0.25539909	1	1
GOTERM_BP	GO:0001666	GO:0001666	response to l	5	1.57728707	0.26948304	MECP2, VCAI	249	193	18082	1.89110609	1	1
GOTERM_BP	GO:0030335	#N/A	positive regu	5	1.57728707	0.30603453	VIL1, FLT1, SE	249	202	18082	1.78863236	1	1
GOTERM_BP	GO:0005975	#N/A	carbohydrate	5	1.57728707	0.31317276	UGDH, PPP1F	249	206	18082	1.76258432	1	1
GOTERM_BP	GO:0006886	#N/A	intracellular f	5	1.57728707	0.39753714	TBC1D5, TON	249	232	18082	1.56505332	1	1
GOTERM_BP	GO:0008380	#N/A	RNA splicing	5	1.57728707	0.42176226	RBM4, DDX5,	249	241	18082	1.50660734	1	1
GOTERM_BP	GO:0010629	#N/A	negative regu	5	1.57728707	0.49377386	BCL11A, SERP	249	265	18082	1.37015989	1	1
GOTERM_BP	GO:0008152	#N/A	metabolic pri	5	1.57728707	0.88233252	GCDH, UGDH	249	463	18082	0.78421678	1	1
GOTERM_BP	GO:0044583	#N/A	positive regu	15	4.7318612	0.02810481	DDX5, PRMT2	249	576	18082	1.89110609	1	1
GOTERM_BP	GO:0060021	#N/A	palate devel	4	1.26182965	0.11153071	ZFP950, FRA3	249	85	18082	3.41733995	1	1
GOTERM_BP	GO:0008203	#N/A	cholesterol r	4	1.26182965	0.12340192	FDP5, STAR, I	249	89	18082	3.26375164	1	1
GOTERM_BP	GO:0007010	#N/A	cytoskeleton	4	1.26182965	0.1715229	VIL1, ARC, QF	249	104	18082	2.79301823	1	1
GOTERM_BP	GO:0016337	#N/A	single organi	4	1.26182965	0.18515969	VCAM1, ITGA	249	108	18082	2.68957311	1	1
GOTERM_BP	GO:0009887	#N/A	organ morph	4	1.26182965	0.18861298	HHEX, TGFB3	249	109	18082	2.66489813	1	1
GOTERM_BP	GO:0030324	#N/A	lung develop	4	1.26182965	0.24122075	SP1, NFIB, MI	249	124	18082	2.34253142	1	1
GOTERM_BP	GO:0048511	#N/A	rhythmic pro	4	1.26182965	0.25680667	DDX5, SP1, SI	249	128	18082	2.26932731	1	1
GOTERM_BP	GO:0042384	#N/A	cilium assem	4	1.26182965	0.26049779	CBY1, RFX3, C	249	129	18082	2.25173563	1	1
GOTERM_BP	GO:0043524	#N/A	negative regu	4	1.26182965	0.37636584	MECP2, STAR	249	160	18082	1.81546185	1	1
GOTERM_BP	GO:0060271	#N/A	cilium morph	4	1.26182965	0.41332268	CBY1, RFX3, C	249	170	18082	1.70866997	1	1
GOTERM_BP	GO:0007268	#N/A	chemical syn:	4	1.26182965	0.42064408	MECP2, KCNI	249	172	18082	1.68880172	1	1
GOTERM_BP	GO:0007568	#N/A	aging	4	1.26182965	0.42760983	VCAM1, TGFB	249	173	18082	1.67903986	1	1
GOTERM_BP	GO:0006897	#N/A	endocytosis	4	1.26182965	0.45316788	ARC, SYP, VLI	249	181	18082	1.60482815	1	1
GOTERM_BP	GO:0016477	#N/A	cell migrator	4	1.26182965	0.4883934	ARC, FLT1, IT	249	191	18082	1.52080574	1	1
GOTERM_BP	GO:0051260	#N/A	protein hom	4	1.26182965	0.50875689	CUTA, TNFSF	249	197	18082	1.47448678	1	1
GOTERM_BP	GO:0016192	#N/A	vesicle-medi	4	1.26182965	0.56150516	TRAPP1, AP	249	213	18082	1.36372721	1	1
GOTERM_BP	GO:0016055	#N/A	Wnt signalin	4	1.26182965	0.56150516	HHEX, TNK1, I	249	213	18082	1.36372721	1	1
GOTERM_BP	GO:0007166	#N/A	cell surface r	4	1.26182965	0.58053803	ADGRG4, PRC	249	219	18082	1.32636482	1	1
GOTERM_BP	GO:0008283	#N/A	cell proliferat	4	1.26182965	0.58363278	PURA, PDXX	249	220	18082	1.32033589	1	1
GOTERM_BP	GO:0007264	#N/A	small GTPase	4	1.26182965	0.63114799	DOCK11, RAP	249	236	18082	1.23082159	1	1
GOTERM_BP	GO:0001525	#N/A	angiogenesis	4	1.26182965	0.63962978	FLT1, EGF, SE	249	239	18082	1.21537195	1	1
GOTERM_BP	GO:0006955	#N/A	immune resp	4	1.26182965	0.72387479	TLR1, MCPT2	249	272	18082	1.06791873	1	1
GOTERM_BP	GO:0010468	#N/A	regulation of	4	1.26182965	0.79743974	MECP2, RBM	249	308	18082	0.94309706	1	1
GOTERM_BP	GO:0043065	#N/A	positive regu	4	1.26182965	0.84126143	ADCY10, PRN	249	335	18082	0.86708626	1	1
GOTERM_BP	GO:0007399	#N/A	nervous syste	4	1.26182965	0.89316456	TLL7, PURA,	249	377	18082	0.77048779	1	1
GOTERM_BP	GO:0002376	#N/A	immune syste	4	1.26182965	0.89919207	TLR1, CR2, C1	249	383	18082	0.75841748	1	1
GOTERM_BP	GO:0008285	#N/A	negative regu	4	1.26182965	0.90016649	TGFB3, NFIB,	249	384	18082	0.75644244	1	1
GOTERM_BP	GO:0045087	GO:0045087	innate immu	4	1.26182965	0.91464693	TLR1, CR2, C1	249	400	18082	0.72618474	1	1
GOTERM_BP	GO:0015031	#N/A	protein trans	15	4.7318612	0.03432242	RANBP3, NUF	249	592	18082	1.83999512	1	1
GOTERM_BP	GO:0043406	GO:0043406	positive regu	4	1.26182965	0.03788517	TENM1, FLT1	249	54	18082	5.37914621	1	1
GOTERM_BP	GO:0048168	#N/A	regulation of	3	0.94637224	0.04569899	ARC, STAR, S'	249	25	18082	8.71421687	1	1
GOTERM_BP	GO:0002009	#N/A	morphogene	3	0.94637224	0.04569899	HHEX, FRAS1	249	25	18082	8.71421687	1	1
GOTERM_BP	GO:0055114	#N/A	oxidation-rec	16	5.04731861	0.0465016	SDR42E1, GC	249	676	18082	1.71878045	1	1
GOTERM_BP	GO:0016571	GO:0016571	histone meth	3	0.94637224	0.05252771	MECP2, PRM	249	27	18082	8.06871932	1	1
GOTERM_BP	GO:0018279	GO:0018279	protein N-lin	3	0.94637224	0.06717096	TUSC3, MAG	249	31	18082	7.02759425	1	1
GOTERM_BP	GO:0006406	#											

GOTERM_BP.GO:0001756	#N/A	somitogenesi	3	0.94637224	0.17905733	LFNG, TTN, LI	249	56	18082	3.89027539	1	1	1
GOTERM_BP.GO:0030178	#N/A	negative regu	3	0.94637224	0.17905733	CBY1, NLK, LF	249	56	18082	3.89027539	1	1	1
GOTERM_BP.GO:0010212	#N/A	response to i	3	0.94637224	0.18399069	VCAM1, STAF	249	57	18082	3.82202494	1	1	1
GOTERM_BP.GO:0043588	#N/A	skin developr	3	0.94637224	0.18894362	FRAS1, PTCH	249	58	18082	3.75612796	1	1	1
GOTERM_BP.GO:0006694	#N/A	steroid biosy	3	0.94637224	0.20892238	SDR42E1, FDI	249	62	18082	3.51379712	1	1	1
GOTERM_BP.GO:0072659	#N/A	protein locali	3	0.94637224	0.20892238	DENND4C, TN	249	62	18082	3.51379712	1	1	1
GOTERM_BP.GO:0030326	#N/A	embryonic lir	3	0.94637224	0.21395199	FRAS1, MEGF	249	63	18082	3.45802257	1	1	1
GOTERM_BP.GO:0018108	GO:0018108	peptidyl-tyro	3	0.94637224	0.22404401	TEC, FLT1, EG	249	65	18082	3.35162187	1	1	1
GOTERM_BP.GO:0010033	#N/A	response to c	3	0.94637224	0.22404401	MAPT, GLRX2	249	65	18082	3.35162187	1	1	1
GOTERM_BP.GO:0022008	#N/A	neurogenesis	3	0.94637224	0.22404401	NUP133, BCL	249	65	18082	3.35162187	1	1	1
GOTERM_BP.GO:0071300	#N/A	cellular respc	3	0.94637224	0.22404401	ZFP105, PHC	249	65	18082	3.35162187	1	1	1
GOTERM_BP.GO:0045454	#N/A	cell redox ho	3	0.94637224	0.22404401	TXNRD3, GLR	249	65	18082	3.35162187	1	1	1
GOTERM_BP.GO:0007612	#N/A	learning	3	0.94637224	0.22910394	MCP2, ARC	249	66	18082	3.30083972	1	1	1
GOTERM_BP.GO:0043433	#N/A	negative regu	3	0.94637224	0.2443253	HDAC3, PRM	249	69	18082	3.15732495	1	1	1
GOTERM_BP.GO:0007584	#N/A	response to r	3	0.94637224	0.26467611	VCAM1, STAF	249	73	18082	2.98432085	1	1	1
GOTERM_BP.GO:0006633	#N/A	fatty acid bio	3	0.94637224	0.26976681	FADS3, FADS	249	74	18082	2.94399219	1	1	1
GOTERM_BP.GO:0008104	#N/A	protein locali	3	0.94637224	0.29519065	MCP2, CUT	249	79	18082	2.75766357	1	1	1
GOTERM_BP.GO:0009790	#N/A	embryo deve	3	0.94637224	0.29519065	MCP2, TGFE	249	79	18082	2.75766357	1	1	1
GOTERM_BP.GO:0030183	#N/A	B cell differer	3	0.94637224	0.30532997	CR2, HHEX, B	249	81	18082	2.68957311	1	1	1
GOTERM_BP.GO:0008033	#N/A	tRNA process	3	0.94637224	0.32552137	TRMO, TRMT	249	85	18082	2.56300496	1	1	1
GOTERM_BP.GO:0030900	#N/A	forebrain dev	3	0.94637224	0.33054674	HHEX, NFIB, I	249	86	18082	2.53320258	1	1	1
GOTERM_BP.GO:0032869	#N/A	cellular respc	3	0.94637224	0.34056568	STAR, SP1, DI	249	88	18082	2.47562979	1	1	1
GOTERM_BP.GO:0051028	#N/A	mRNA transp	3	0.94637224	0.34056568	NUP133, ZC3	249	88	18082	2.47562979	1	1	1
GOTERM_BP.GO:0060070	#N/A	canonical Wr	3	0.94637224	0.34555795	EGF, KLF4, LR	249	89	18082	2.44781373	1	1	1
GOTERM_BP.GO:0001889	#N/A	liver develop	3	0.94637224	0.37523291	HHEX, SP1, H	249	95	18082	2.29321497	1	1	1
GOTERM_BP.GO:0006469	GO:0006469	negative regu	3	0.94637224	0.37523291	PPP1R1A, SO	249	95	18082	2.29321497	1	1	1
GOTERM_BP.GO:0001503	#N/A	ossification	3	0.94637224	0.38012711	SP1, MGP, TN	249	96	18082	2.26932731	1	1	1
GOTERM_BP.GO:0098792	GO:0098792	xenophagy	3	0.94637224	0.41390929	CPA3, RFWD	249	103	18082	2.11510118	1	1	1
GOTERM_BP.GO:0071456	GO:0071456	cellular respc	3	0.94637224	0.41390929	SUV39H1, VL	249	103	18082	2.11510118	1	1	1
GOTERM_BP.GO:0043410	GO:0043410	positive regu	3	0.94637224	0.41866196	FLT1, LEPR, N	249	104	18082	2.09476367	1	1	1
GOTERM_BP.GO:0007623	#N/A	circadian rhy	3	0.94637224	0.43747392	DDX5, PROKF	249	108	18082	2.01717983	1	1	1
GOTERM_BP.GO:0006869	#N/A	lipid transpor	3	0.94637224	0.45136488	STAR, SPNS3,	249	111	18082	1.96266146	1	1	1
GOTERM_BP.GO:0009952	#N/A	anterior/post	3	0.94637224	0.45595206	HHEX, ARC, L	249	112	18082	1.94513769	1	1	1
GOTERM_BP.GO:0045766	#N/A	positive regu	3	0.94637224	0.49621612	FLT1, SERPIN	249	121	18082	1.80045803	1	1	1
GOTERM_BP.GO:0002230	GO:0002230	positive regu	3	0.94637224	0.50057253	CPA3, RFWD	249	122	18082	1.78570018	1	1	1
GOTERM_BP.GO:0007219	#N/A	Notch signali	3	0.94637224	0.51349619	HHEX, RCAN2	249	125	18082	1.74284337	1	1	1
GOTERM_BP.GO:0050821	#N/A	protein stabil	3	0.94637224	0.5261984	CRTAP, DN LZ	249	128	18082	1.70199548	1	1	1
GOTERM_BP.GO:0006979	GO:0006979	response to c	3	0.94637224	0.54686878	GPX3, MTF1,	249	133	18082	1.63801069	1	1	1
GOTERM_BP.GO:0006366	#N/A	transcription	3	0.94637224	0.56690121	ZFP219, BCL1	249	138	18082	1.57866248	1	1	1
GOTERM_BP.GO:0046777	GO:0046777	protein auto	3	0.94637224	0.71841135	FLT1, TN IK, N	249	183	18082	1.19046679	1	1	1
GOTERM_BP.GO:0098609	#N/A	cell-cell adhe	3	0.94637224	0.73484904	UBFD1, ERC1	249	189	18082	1.15267419	1	1	1
GOTERM_BP.GO:0032496	#N/A	response to l	3	0.94637224	0.75549364	RPS6KA3, VC	249	197	18082	1.10586509	1	1	1
GOTERM_BP.GO:0007507	#N/A	heart develop	3	0.94637224	0.87592162	VCAM1, ITGA	249	261	18082	0.8346951	1	1	1
GOTERM_BP.GO:0042493	#N/A	response to c	3	0.94637224	0.94856982	STAR, MDK, C	249	339	18082	0.64264136	1	1	1
GOTERM_BP.GO:0055085	#N/A	transmembr	3	0.94637224	0.96158159	SLC13A4, SP	249	364	18082	0.59850391	1	1	1
GOTERM_BP.GO:0007155	#N/A	cell adhesio	3	0.94637224	0.99107502	VCAM1, ITGA	249	485	18082	0.44918644	1	1	1
GOTERM_BP.GO:0006915	#N/A	apoptotic prc	3	0.94637224	0.99691554	VIL1, PURA, M	249	570	18082	0.38220249	1	1	1

Supplementary Table S6: Parent ontology analysis for Grey module to identify Top biological processes categories described in Figure 3B.

GO Class ID	Definitions	Counts	Fractions
			<u>18</u>
GO:0006950	stress respons	GO:0001666 C	15.93%
			<u>11</u>
GO:0019538	protein metabo	GO:0006412 C	9.73%
			<u>6</u>
GO:0006915	apoptosis	GO:0006915 C	5.31%
			<u>5</u>
GO:0007155	cell adhesion	GO:0007155 C	4.42%
			<u>5</u>
GO:0006629	lipid metabolis	GO:0006629 C	4.42%
			<u>4</u>
GO:0009605	response to ex	GO:0002230 C	3.54%
			<u>3</u>
GO:0009628	response to ab	GO:0001666 C	2.65%
			<u>3</u>
GO:0009607	response to bi	GO:0002230 C	2.65%
			<u>2</u>
GO:0046649	lymphocyte ac	GO:0030183 C	1.77%
			<u>2</u>
GO:0030098	lymphocyte dif	GO:0030183 C	1.77%
			<u>2</u>
GO:0000165	MAPKKK casc	GO:0043406 C	1.77%
			<u>2</u>
GO:0043408	regulation of M	GO:0043406 C	1.77%
			<u>2</u>
GO:0009719	response to en	GO:0032869 C	1.77%
			<u>2</u>
GO:0006955	immunology, ir	GO:0006955 C	1.77%
			<u>2</u>
GO:0042981	regulation of a	GO:0043065 C	1.77%
			<u>1</u>
GO:0006897	endocytosis	GO:0006897	0.88%
			<u>1</u>
GO:0005975	carbohydrate r	GO:0005975	0.88%
			<u>1</u>
GO:0042110	T cell activati	GO:0030217	0.88%
			<u>1</u>
GO:0042113	B cell activatio	GO:0030183	0.88%
Total		113	100.00%

Supplementary Table S6: Biological processes for genes within the Midnightblue module

Category	Term	Protein meta ontology	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR	
GOTERM_BP	GO:0031175	#N/A	neuron proje	5	2.94117647	0.01850231	ATP8A2, SRF,	132	139	18082	4.92751254	0.99999991	1	1
GOTERM_BP	GO:0006888	#N/A	ER to Golgi ve	4	2.35294118	0.01905674	SEC24B, SEC2	132	78	18082	7.02486403	0.99999994	1	1
GOTERM_BP	GO:0006886	#N/A	intracellular f	6	3.52941177	0.02697338	TOM1L2, SEC	132	232	18082	3.5427116	1	1	1
GOTERM_BP	GO:0006468	GO:0006468	protein phosj	6	3.52941177	0.40555239	TRIO, NEK5, /	132	576	18082	1.42692551	1	1	1
GOTERM_BP	GO:0010976	#N/A	positive regu	4	2.35294118	0.07890274	ATP8A2, ITGA	132	138	18082	3.97057532	1	1	1
GOTERM_BP	GO:0032088	#N/A	negative regu	3	1.76470588	0.08280032	DAB2IP, FOXF	132	66	18082	6.22658402	1	1	1
GOTERM_BP	GO:0006954	GO:0006954	inflammatory	4	2.35294118	0.45584453	PTGER1, AXL,	132	344	18082	1.59284708	1	1	1
GOTERM_BP	GO:0007059	#N/A	chromosome	3	1.76470588	0.13611299	USP44, HJURI	132	89	18082	4.6174668	1	1	1
GOTERM_BP	GO:0007417	#N/A	central nervo	3	1.76470588	0.13611299	ARSA, EIF2B2	132	89	18082	4.6174668	1	1	1
GOTERM_BP	GO:0006810	#N/A	transport	18	10.5882353	0.16701725	GRIA2, ATP8A	132	1822	18082	1.35330805	1	1	1
GOTERM_BP	GO:0016567	GO:0016567	protein ubiq	4	2.35294118	0.48935604	RNF135, RNF	132	362	18082	1.51364474	1	1	1
GOTERM_BP	GO:0001501	#N/A	skeletal syste	3	1.76470588	0.18177634	HOXA10, GJA	132	107	18082	3.84069669	1	1	1
GOTERM_BP	GO:0016042	#N/A	lipid cataboli	3	1.76470588	0.18698846	DAGLA, PLA2	132	109	18082	3.77022519	1	1	1
GOTERM_BP	GO:0001764	#N/A	neuron migr	3	1.76470588	0.22663808	ITGA3, AXL, S	132	124	18082	3.31414956	1	1	1
GOTERM_BP	GO:0008360	#N/A	regulation of	3	1.76470588	0.26682822	GM14137, PA	132	139	18082	2.95650752	1	1	1
GOTERM_BP	GO:0007155	#N/A	cell adhesion	6	3.52941177	0.27551671	CYFIP2, LAME	132	485	18082	1.69465792	1	1	1
GOTERM_BP	GO:0007411	#N/A	axon guidanc	3	1.76470588	0.29366038	EFNA4, RUNX	132	149	18082	2.7580842	1	1	1
GOTERM_BP	GO:0007165	#N/A	signal transd	12	7.05882353	0.30052562	TOM1L2, ADC	132	1255	18082	1.30981528	1	1	1
GOTERM_BP	GO:0043966	GO:0043966	histone H3 ac	3	1.76470588	0.04555666	TAF6L, WDR5	132	47	18082	8.74371373	1	1	1
GOTERM_BP	GO:0006357	#N/A	regulation of	5	2.94117647	0.32461097	BRD3, ZHX2,	132	397	18082	1.72524998	1	1	1
GOTERM_BP	GO:0001933	GO:0001933	negative regu	3	1.76470588	0.12394513	CTDSP1, DAB	132	84	18082	4.89231602	1	1	1
GOTERM_BP	GO:0032496	#N/A	response to li	3	1.76470588	0.4188499	UGT2B1, CNF	132	197	18082	2.08606368	1	1	1
GOTERM_BP	GO:0005975	#N/A	carbohydrate	3	1.76470588	0.44117219	GK5, GALE, G	132	206	18082	1.99492498	1	1	1
GOTERM_BP	GO:0000209	GO:0000209	protein polyu	3	1.76470588	0.17142212	UBOX5, TMEI	132	103	18082	3.98984996	1	1	1
GOTERM_BP	GO:0016310	#N/A	phosphorylat	6	3.52941177	0.45699152	GK5, TRIO, NI	132	612	18082	1.34298871	1	1	1
GOTERM_BP	GO:0006511	GO:0006511	ubiquitin-def	3	1.76470588	0.30703456	USP35, USP4	132	154	18082	2.66853601	1	1	1
GOTERM_BP	GO:0001525	#N/A	angiogenesis	3	1.76470588	0.51877192	GJA5, DAB2IF	132	239	18082	1.71947509	1	1	1
GOTERM_BP	GO:0002376	#N/A	immune syst	4	2.35294118	0.52716254	RNF135, CRA	132	383	18082	1.43065116	1	1	1
GOTERM_BP	GO:0055114	#N/A	oxidation-rec	6	3.52941177	0.54497033	DUS2, ACAD8	132	676	18082	1.21584185	1	1	1
GOTERM_BP	GO:0007507	#N/A	heart develop	3	1.76470588	0.56642045	ITGA3, SRF, T	132	261	18082	1.57453849	1	1	1
GOTERM_BP	GO:0007283	#N/A	spermatogen	4	2.35294118	0.56843941	HOXA10, DA2	132	407	18082	1.34628844	1	1	1
GOTERM_BP	GO:0016569	#N/A	covalent chrc	3	1.76470588	0.57677064	BRD3, WDR5,	132	266	18082	1.5449419	1	1	1
GOTERM_BP	GO:0045893	#N/A	positive regu	5	2.94117647	0.60390992	PCID2, SRF, T	132	576	18082	1.18910459	1	1	1
GOTERM_BP	GO:0006811	#N/A	ion transport	5	2.94117647	0.61482719	GRIA2, CRACI	132	584	18082	1.17281548	1	1	1
GOTERM_BP	GO:0007275	#N/A	multicellular	8	4.70588235	0.62227195	HOXA10, FAR	132	1029	18082	1.06499396	1	1	1
GOTERM_BP	GO:0015031	#N/A	protein trans	5	2.94117647	0.62555966	TOM1L2, IPO	132	592	18082	1.15696663	1	1	1
GOTERM_BP	GO:0006629	#N/A	lipid metabol	4	2.35294118	0.64997807	DAGLA, PLA2	132	459	18082	1.19376774	1	1	1
GOTERM_BP	GO:0043066	#N/A	negative regu	4	2.35294118	0.78195166	PCID2, AXL, R	132	566	18082	0.9680908	1	1	1
GOTERM_BP	GO:0045087	GO:0045087	innate immu	3	1.76470588	0.78954992	RNF135, AXL,	132	400	18082	1.02738636	1	1	1
GOTERM_BP	GO:0006412	GO:0006412	translation	3	1.76470588	0.79070894	EIF2B2, EIF3L	132	401	18082	1.0248243	1	1	1
GOTERM_BP	GO:0030154	#N/A	cell differenti	5	2.94117647	0.82197042	DAZAP1, ADC	132	780	18082	0.878108	1	1	1
GOTERM_BP	GO:0007049	#N/A	cell cycle	4	2.35294118	0.82640652	USP44, DAB2	132	614	18082	0.89240944	1	1	1

GOTERM_BP GO:0008152	#N/A	metabolic pr	3	1.76470588	0.85243734	ACAD8, ARSA	132	463	18082	0.88759081	1	1	1
GOTERM_BP GO:0007186	#N/A	G-protein cou	10	5.88235294	0.88030585	OLFR1408, AI	132	1706	18082	0.80295925	1	1	1
GOTERM_BP GO:0006915	#N/A	apoptotic prc	3	1.76470588	0.92148725	CYFIP2, DAB2	132	570	18082	0.72097289	1	1	1
GOTERM_BP GO:0045892	#N/A	negative regu	3	1.76470588	0.92564766	ZHX2, DAB2IF	132	579	18082	0.70976605	1	1	1
GOTERM_BP GO:0007608	#N/A	sensory perce	4	2.35294118	0.99080627	OLFR1408, O	132	1143	18082	0.47938705	1	1	1

Supplementary Table S6: Parent ontology analysis for Midnightblue module to identify Top biological processes categories described in Figure 3B.

GO Class ID	Definitions	Counts	Fractions
			<u>7</u>
GO:0019538	protein metabo	GO:0000209 C	15.91%
			<u>4</u>
GO:0006950	stress respons	GO:0006954 C	9.09%
			<u>4</u>
GO:0006915	apoptosis	GO:0006915 C	9.09%
			<u>2</u>
GO:0009605	response to ex	GO:0007411 C	4.55%
			<u>2</u>
GO:0009056	catabolism	GO:0006511 C	4.55%
			<u>2</u>
GO:0006629	lipid metabolis	GO:0006629 C	4.55%
			<u>1</u>
GO:0007155	cell adhesion	GO:0007155	2.27%
			<u>1</u>
GO:0006955	immunology, ir	GO:0045087	2.27%
			<u>1</u>
GO:0005975	carbohydrate m	GO:0005975	2.27%
			<u>1</u>
GO:0042981	regulation of a	GO:0043066	2.27%
			<u>1</u>
GO:0009607	response to bio	GO:0032496	2.27%
Total		44	100.00%

Supplementary Table S6: Biological processes for genes within the White module

Category	Term	Stress and Apoptosis	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP	GO:0006915	GO:0006915 apoptotic prc	11	9.09090909	0.00249651	PLSCR1, NCF1	111	570	18082	3.1437016	0.84350463	0.46310317	0.46310317
GOTERM_BP	GO:0006954	GO:0006954 inflammatory	7	5.78512397	0.0186539	NCF1, SGMS1	111	344	18082	3.31484391	0.99999914	1	1
GOTERM_BP	GO:0045087	GO:0045087 innate immu	7	5.78512397	0.03545812	LGALS3, LCN2	111	400	18082	2.85076577	1	1	1
GOTERM_BP	GO:0043066	GO:0043066 negative regu	6	4.95867769	0.261847	STAT5B, LGAL	111	566	18082	1.72686467	1	1	1
GOTERM_BP	GO:0043065	GO:0043065 positive regu	4	3.30578512	0.33369523	PLSCR1, DUS1	111	335	18082	1.94508538	1	1	1
GOTERM_BP	GO:0050830	GO:0050830 defense resp	3	2.47933884	0.10996483	ADAM17, NC	111	93	18082	5.25486777	1	1	1
GOTERM_BP	GO:0051607	GO:0051607 defense resp	3	2.47933884	0.27013134	PLSCR1, IFNL	111	167	18082	2.92636349	1	1	1

Supplementary Table S6: Parent ontology analysis for White module to identify Top biological processes categories described in Figure 3B.

GO Class ID	Definitions	Counts	Fractions
			<u>8</u>
GO:0006950	stress respons	GO:0006954 C	13.33%
			<u>6</u>
GO:0006915	apoptosis	GO:0006915 C	10.00%
			<u>6</u>
GO:0019538	protein metabo	GO:0001934 C	10.00%
			<u>5</u>
GO:0009607	response to bic	GO:0009617 C	8.33%
			<u>5</u>
GO:0009605	response to ex	GO:0009617 C	8.33%
			<u>2</u>
GO:0006955	immunology, ir	GO:0006955 C	3.33%
			<u>2</u>
GO:0042981	regulation of a	GO:0043065 C	3.33%
			<u>1</u>
GO:0042742	defense respo	GO:0050830	1.67%
			<u>1</u>
GO:0005975	carbohydrate r	GO:0005975	1.67%
			<u>1</u>
GO:0000165	MAPKKK casc	GO:0070374	1.67%
			<u>1</u>
GO:0043408	regulation of M	GO:0070374	1.67%
			<u>1</u>
GO:0043122	regulation of I-	GO:0043123	1.67%
			<u>1</u>
GO:0007155	cell adhesion	GO:0007155	1.67%
			<u>1</u>
GO:0009719	response to en	GO:0043434	1.67%
			<u>1</u>
GO:0007249	I-kappaB kinas	GO:0043123	1.67%
			<u>1</u>
GO:0009056	catabolism	GO:0006511	1.67%
Total		60	100.00%

Supplementary Table S6: Biological processes for genes within the Purple module

Category	Term	Stress&Endo	Stress&Endo	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP	GO:0006468	GO:0006468	protein phos	28	5.15653775	0.00304347	ROCK2, BUB1	479	576	18082	1.83504407	0.99730507	0.73842192	0.73766105
GOTERM_BP	GO:0006974	GO:0006974	cellular resp	27	4.97237569	5.64E-05	INO80C, ATF1	479	420	18082	2.42675216	0.10368844	0.02189282	0.02187027
GOTERM_BP	GO:0006281	GO:0006281	DNA repair	17	3.13075506	0.01075035	INO80C, ZRA1	479	318	18082	2.01805386	1	1	0.99948454
GOTERM_BP	GO:0018105	GO:0018105	peptidyl-seri	10	1.84162063	0.00887602	CSNK1G3, CA	479	133	18082	2.83830662	0.99999997	1	0.99948454
GOTERM_BP	GO:0032869	GO:0032869	cellular resp	7	1.28913444	0.02909291	C2CD5, GCLC	479	88	18082	3.00279939	1	1	0.99948454
GOTERM_BP	GO:0071560	GO:0071560	cellular resp	6	1.10497238	0.0223843	ACTR3, USP9	479	61	18082	3.71306342	1	1	0.99948454
GOTERM_BP	GO:0032147	GO:0032147	activation of	5	0.92081031	0.01075715	TOM1L1, TPX	479	33	18082	5.71961789	1	1	0.99948454
GOTERM_BP	GO:2001275	GO:2001275	positive regu	3	0.55248619	0.04486677	OSBPL8, C2C1	479	13	18082	8.71141802	1	1	0.99948454

GOTERM_BP_DIRECT

Supplementary Table S6: Parent ontology analysis for Purple module to identify Top biological processes categories described in Figure 3B.

GO Class ID	Definitions	Counts	Fractions
			<u>4</u>
GO:0006950	stress respons	GO:0006281 C	13.79%
			<u>3</u>
GO:0009719	response to en	GO:0032869 C	10.34%
			<u>3</u>
GO:0019538	protein metabo	GO:0006468 C	10.34%
			<u>2</u>
GO:0006915	apoptosis	GO:0006915 C	6.90%
			<u>1</u>
GO:0030098	lymphocyte dif	GO:0030217	3.45%
			<u>1</u>
GO:0042110	T cell activati	GO:0030217	3.45%
			<u>1</u>
GO:0000910	cytokinesis	GO:0032467	3.45%
			<u>1</u>
GO:0016032	viral life cycle	GO:0039694	3.45%
			<u>1</u>
GO:0007155	cell adhesion	GO:0030217	3.45%
			<u>1</u>
GO:0046649	lymphocyte ac	GO:0030217	3.45%
			<u>1</u>
GO:0006629	lipid metabolis	GO:0008654	3.45%
Total		29	100.00%

Counted Terms

17 unique terms from your data set are found belonging to at least one of the 12 "immune_class" classes