

## Supplementary table 1

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue
GO:0002052	positive regul 2/29		23/18723	0.000574358	0.128113766	0.090943995
GO:0019730	antimicrobial 3/29		122/18723	0.000871494	0.128113766	0.090943995
GO:1902692	regulation of 2/29		33/18723	0.001187209	0.128113766	0.090943995
GO:0060428	lung epitheliu 2/29		37/18723	0.001491766	0.128113766	0.090943995
GO:0002920	regulation of 2/29		45/18723	0.002200544	0.128113766	0.090943995
GO:2000179	positive regul 2/29		54/18723	0.003153471	0.128113766	0.090943995
GO:0042220	response to c 2/29		55/18723	0.003269337	0.128113766	0.090943995
GO:0051898	negative regu 2/29		55/18723	0.003269337	0.128113766	0.090943995
GO:0007405	neuroblast pr 2/29		58/18723	0.00362876	0.128113766	0.090943995
GO:0034329	cell junction ε 4/29		420/18723	0.003802407	0.128113766	0.090943995
GO:0006500	N-terminal pr 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0021769	orbitofrontal 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0030997	regulation of 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0044467	glial cell-deriv 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0051586	positive regul 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0051944	positive regul 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0060160	negative regu 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0060535	trachea cartil 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0072061	inner medulla 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:1900166	regulation of 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:1900168	positive regul 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:1903964	monounsatur 1/29		3/18723	0.004639745	0.128113766	0.090943995
GO:0070830	bicellular tigh 2/29		70/18723	0.005241004	0.128113766	0.090943995
GO:0009410	response to x 4/29		462/18723	0.005330036	0.128113766	0.090943995
GO:0045824	negative regu 2/29		71/18723	0.005387761	0.128113766	0.090943995
GO:0120192	tight junction 2/29		74/18723	0.005839294	0.128113766	0.090943995
GO:0022009	central nervo 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0033602	negative regu 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0060486	club cell diffe 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0072236	metanephric 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0090116	C-5 methylati 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0090325	regulation of 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0110024	positive regul 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:2000545	negative regu 1/29		4/18723	0.006181703	0.128113766	0.090943995
GO:0043297	apical junctio 2/29		78/18723	0.006467405	0.128113766	0.090943995
GO:0061844	antimicrobial 2/29		79/18723	0.00662905	0.128113766	0.090943995
GO:0120193	tight junction 2/29		80/18723	0.006792529	0.128113766	0.090943995
GO:0002088	lens developr 2/29		84/18723	0.007464688	0.128113766	0.090943995
GO:0006116	NADH oxidati 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:0021869	forebrain ven 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:0021873	forebrain neu 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:0042321	negative regu 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:0051582	positive regul 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:0060510	type II pneur 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:1904848	negative regu 1/29		5/18723	0.007721354	0.128113766	0.090943995
GO:2000177	regulation of 2/29		87/18723	0.0079878	0.128113766	0.090943995
GO:0051781	positive regul 2/29		89/18723	0.008345502	0.128113766	0.090943995

GO:0007195	adenylate cyc 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0007270	neuron-neurc 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0021853	cerebral cortε 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0032776	DNA methyla 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0032911	negative regul 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0033634	positive regul 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0051891	positive regul 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0060482	lobar bronchi 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0070072	vacuolar prot 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0071896	protein locali: 1/29	6/18723	0.009258702	0.128113766	0.090943995
GO:0043473	pigmentation 2/29	98/18723	0.010042592	0.128113766	0.090943995
GO:0010720	positive regul 3/29	298/18723	0.010740663	0.128113766	0.090943995
GO:0003310	pancreatic A c 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0006498	N-terminal pr 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0009637	response to b 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0021894	cerebral cortε 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0060534	trachea cartil. 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0060710	chorio-allantc 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0110021	cardiac muscl 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0110022	regulation of 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:1990384	hyaloid vascu 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:2000210	positive regul 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:2000394	positive regul 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:2001027	negative regul 1/29	7/18723	0.01079375	0.128113766	0.090943995
GO:0001666	response to h 3/29	307/18723	0.011638323	0.128113766	0.090943995
GO:0032526	response to r 2/29	107/18723	0.011879789	0.128113766	0.090943995
GO:0002832	negative regul 2/29	108/18723	0.012092399	0.128113766	0.090943995
GO:0003162	atrioventricul 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0032364	oxygen home 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0035754	B cell chemot 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0043045	DNA methyla 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0048149	behavioral re. 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0051584	regulation of 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0051823	regulation of 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0051890	regulation of 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0051940	regulation of 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0060158	phospholipas 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0061909	autophagosoι 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0070070	proton-transp 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:1901388	regulation of 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:1901538	changes to DI 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:1904936	interneuron r 1/29	8/18723	0.012326502	0.128113766	0.090943995
GO:0018958	phenol-conta 2/29	110/18723	0.012522641	0.128113766	0.090943995
GO:0006959	humoral imm 3/29	317/18723	0.01268542	0.128113766	0.090943995
GO:0044344	cellular respo 2/29	113/18723	0.013180479	0.128113766	0.090943995
GO:0036293	response to d 3/29	322/18723	0.013228727	0.128113766	0.090943995
GO:0043010	camera-type 3/29	322/18723	0.013228727	0.128113766	0.090943995
GO:0043279	response to a 2/29	115/18723	0.013627292	0.128113766	0.090943995
GO:0002831	regulation of 3/29	327/18723	0.013785277	0.128113766	0.090943995
GO:0033559	unsaturated f 2/29	116/18723	0.01385316	0.128113766	0.090943995

GO:0021826	substrate-ind 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0021830	interneuron r 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0021843	substrate-ind 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0031987	locomotion ir 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0032906	transforming 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0032909	regulation of 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0046602	regulation of 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0048733	sebaceous glc 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0051967	negative regu 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0060124	positive regul 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0060430	lung saccule c 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0060536	cartilage mor 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0097267	omega-hydro 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:1902774	late endosom 1/29	9/18723	0.013856961	0.128113766	0.090943995
GO:0071774	response to fi 2/29	120/18723	0.014772912	0.128113766	0.090943995
GO:0001915	negative regu 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0010968	regulation of 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0030388	fructose 1,6-t 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0035768	endothelial c 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0036363	transforming 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0042756	drinking beha 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0048755	branching mc 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0060439	trachea morp 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0060947	cardiac vascu 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0061140	lung secretor 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0072070	loop of Henle 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:2000288	positive regul 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:2000544	regulation of 1/29	10/18723	0.015385129	0.128113766	0.090943995
GO:0070482	response to c 3/29	347/18723	0.016144848	0.128113766	0.090943995
GO:0035270	endocrine sys 2/29	127/18723	0.016444365	0.128113766	0.090943995
GO:0002759	regulation of 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0014854	response to ii 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0021892	cerebral cort 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0030432	peristalsis 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0033483	gas homeost 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0033625	positive regul 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0033632	regulation of 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0034776	response to h 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0035766	cell chemota 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0060159	regulation of 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0060433	bronchus dev 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0072205	metanephric 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:1904847	regulation of 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:2000392	regulation of 1/29	11/18723	0.016911011	0.128113766	0.090943995
GO:0001976	nervous syste 1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0031223	auditory beh 1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0032536	regulation of 1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0032908	regulation of 1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0051583	dopamine up 1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0051934	catecholamin 1/29	12/18723	0.01843461	0.128113766	0.090943995

GO:0060123	regulation of	1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0060134	prepulse inhib	1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0060394	negative regu	1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0071635	negative regu	1/29	12/18723	0.01843461	0.128113766	0.090943995
GO:0001701	in utero embri	3/29	367/18723	0.018719682	0.128113766	0.090943995
GO:0045471	response to e	2/29	137/18723	0.01896573	0.128113766	0.090943995
GO:0001654	eye developn	3/29	371/18723	0.019260657	0.128113766	0.090943995
GO:0150063	visual system	3/29	375/18723	0.01981033	0.128113766	0.090943995
GO:0006000	fructose met	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0021984	adenohypoph	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0032905	transforming	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0036302	atrioventricul	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0051481	negative regu	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0051988	regulation of	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0060213	positive regul	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0097154	GABAergic ne	1/29	13/18723	0.019955929	0.128113766	0.090943995
GO:0030900	forebrain dev	3/29	379/18723	0.02036871	0.128113766	0.090943995
GO:0048880	sensory syste	3/29	381/18723	0.020651169	0.128113766	0.090943995
GO:0001890	placenta dev	2/29	144/18723	0.020821778	0.128113766	0.090943995
GO:0061351	neural precu	2/29	145/18723	0.021092932	0.128113766	0.090943995
GO:0007043	cell-cell juncti	2/29	146/18723	0.021365572	0.128113766	0.090943995
GO:0001711	endodermal c	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0002467	germinal cent	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0007100	mitotic centr	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0007638	mechanosens	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0010457	centriole-cen	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0031115	negative regu	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0033604	negative regu	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0035810	positive regul	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0035815	positive regul	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0048148	behavioral re	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0055057	neuroblast di	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0070307	lens fiber cell	1/29	14/18723	0.021474971	0.128113766	0.090943995
GO:0071456	cellular respo	2/29	151/18723	0.022750894	0.128113766	0.090943995
GO:0006570	tyrosine met	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0010763	positive regul	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0010820	positive regul	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0030252	growth horm	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0042754	negative regu	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0051299	centrosome s	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0060211	regulation of	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0070071	proton-transp	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0072044	collecting duc	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0099170	postsynaptic	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:1900029	positive regul	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:1900153	positive regul	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:1904424	regulation of	1/29	15/18723	0.02299174	0.128113766	0.090943995
GO:0006349	regulation of	1/29	16/18723	0.024506238	0.131673636	0.093471036
GO:0010819	regulation of	1/29	16/18723	0.024506238	0.131673636	0.093471036
GO:0033631	cell-cell adhe	1/29	16/18723	0.024506238	0.131673636	0.093471036

GO:0071361	cellular respo	1/29	16/18723	0.024506238	0.131673636	0.093471036
GO:0097284	hepatocyte a	1/29	16/18723	0.024506238	0.131673636	0.093471036
GO:0036294	cellular respo	2/29	161/18723	0.025630201	0.131673636	0.093471036
GO:0002031	G protein-co	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0007625	grooming beh	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0021756	striatum dev	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0030903	notochord de	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0033623	regulation of	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0048521	negative regu	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0051580	regulation of	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0060033	anatomical st	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0071371	cellular respo	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0072673	lamellipodiun	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0090494	dopamine up	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:1904355	positive regul	1/29	17/18723	0.02601847	0.131673636	0.093471036
GO:0032102	negative regu	3/29	420/18723	0.026595686	0.131673636	0.093471036
GO:0043112	receptor met	2/29	166/18723	0.027122986	0.131673636	0.093471036
GO:0048608	reproductive	3/29	424/18723	0.027252388	0.131673636	0.093471036
GO:0002223	stimulatory C	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0002544	chronic inflan	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0033189	response to v	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0045187	regulation of	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0045953	negative regu	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0060438	trachea devel	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0072234	metanephric	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0090493	catecholamin	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:1900151	regulation of	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:1990840	response to k	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:1990858	cellular respo	1/29	18/18723	0.027528438	0.131673636	0.093471036
GO:0061458	reproductive	3/29	427/18723	0.027750652	0.132151784	0.093810458
GO:0043254	regulation of	3/29	428/18723	0.027917833	0.132364812	0.093961681
GO:0002716	negative regu	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:0010002	cardioblast di	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:0014067	negative regu	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:0045780	positive regul	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:0140131	positive regul	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:2000738	positive regul	1/29	19/18723	0.029036146	0.134137068	0.09521975
GO:0048732	gland develop	3/29	436/18723	0.029274934	0.134664697	0.095594298
GO:0001659	temperature	2/29	174/18723	0.029583232	0.134934488	0.095785814
GO:0048639	positive regul	2/29	174/18723	0.029583232	0.134934488	0.095785814
GO:0030324	lung developr	2/29	177/18723	0.030528193	0.135309288	0.096051873
GO:0051302	regulation of	2/29	177/18723	0.030528193	0.135309288	0.096051873
GO:0071453	cellular respo	2/29	177/18723	0.030528193	0.135309288	0.096051873
GO:0006346	DNA methyla	1/29	20/18723	0.030541597	0.135309288	0.096051873
GO:0007194	negative regu	1/29	20/18723	0.030541597	0.135309288	0.096051873
GO:0043046	DNA methyla	1/29	20/18723	0.030541597	0.135309288	0.096051873
GO:1901386	negative regu	1/29	20/18723	0.030541597	0.135309288	0.096051873
GO:0030323	respiratory tu	2/29	181/18723	0.031806799	0.135781502	0.096387083
GO:0023019	signal transdu	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0033630	positive regul	1/29	21/18723	0.032044794	0.135781502	0.096387083

GO:0035813	regulation of	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0050802	circadian slee	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0072170	metanephric	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0072243	metanephric	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0150105	protein locali	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:1905209	positive regul	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:2000291	regulation of	1/29	21/18723	0.032044794	0.135781502	0.096387083
GO:0009314	response to r	3/29	456/18723	0.032820298	0.135781502	0.096387083
GO:0051896	regulation of	2/29	185/18723	0.033106459	0.135781502	0.096387083
GO:0002029	desensitizati	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0002220	innate immur	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0014821	phasic smoot	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0022401	negative adaç	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0035809	regulation of	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0042749	regulation of	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0048169	regulation of	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0060713	labyrinthine l	1/29	22/18723	0.03354574	0.135781502	0.096387083
GO:0002758	innate immur	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0016338	calcium-indeç	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0021544	subpallium de	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0021871	forebrain regi	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0021895	cerebral corte	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0023058	adaptation of	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0031280	negative regu	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0035812	renal sodium	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0042438	melanin biosy	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0051590	positive regul	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0060487	lung epithelia	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0060575	intestinal epit	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0071514	genetic impri	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0071636	positive regul	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:1900273	positive regul	1/29	23/18723	0.035044439	0.135781502	0.096387083
GO:0050777	negative regu	2/29	194/18723	0.036106182	0.136680647	0.097025359
GO:0001911	negative regu	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0003148	outflow tract	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0006582	melanin metç	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0010288	response to lç	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0022410	circadian slee	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0044062	regulation of	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0060479	lung cell diffe	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:2000209	regulation of	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:2001026	regulation of	1/29	24/18723	0.036540895	0.136680647	0.097025359
GO:0001763	morphogeneç	2/29	196/18723	0.036786735	0.137125726	0.097341306
GO:0001964	startle respor	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0010996	response to a	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0021846	cell proliferat	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0033622	integrin activi	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0044550	secondary mç	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0051450	myoblast pro	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0072207	metanephric	1/29	25/18723	0.038035109	0.137972996	0.097942757

GO:1901623	regulation of	1/29	25/18723	0.038035109	0.137972996	0.097942757
GO:0045216	cell-cell juncti	2/29	200/18723	0.038162793	0.137973174	0.097942883
GO:0060541	respiratory sy	2/29	203/18723	0.039207781	0.13828084	0.098161286
GO:0001963	synaptic tran	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0002092	positive regul	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0002710	negative regu	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0045745	positive regul	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0045954	positive regul	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0051350	negative regu	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0060669	embryonic pl	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0071880	adenylate cyc	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:1904353	regulation of	1/29	26/18723	0.039527086	0.13828084	0.098161286
GO:0001958	endochondra	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0007628	adult walking	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0032781	positive regul	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0034698	response to g	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0036075	replacement	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0042745	circadian slee	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0051953	negative regu	1/29	27/18723	0.041016828	0.140313896	0.09960449
GO:0043491	protein kinas	2/29	211/18723	0.042047707	0.143137667	0.101608997
GO:0010818	T cell chemot	1/29	28/18723	0.04250434	0.143137667	0.101608997
GO:0031342	negative regu	1/29	28/18723	0.04250434	0.143137667	0.101608997
GO:0032801	receptor cata	1/29	28/18723	0.04250434	0.143137667	0.101608997
GO:0090659	walking beha	1/29	28/18723	0.04250434	0.143137667	0.101608997
GO:0000289	nuclear-trans	1/29	29/18723	0.043989623	0.145867431	0.103546772
GO:0003309	type B pancre	1/29	29/18723	0.043989623	0.145867431	0.103546772
GO:0006734	NADH metab	1/29	29/18723	0.043989623	0.145867431	0.103546772
GO:0040018	positive regul	1/29	29/18723	0.043989623	0.145867431	0.103546772
GO:2000406	positive regul	1/29	29/18723	0.043989623	0.145867431	0.103546772
GO:0007163	establishmen	2/29	218/18723	0.044594879	0.146734236	0.10416209
GO:0045088	regulation of	2/29	218/18723	0.044594879	0.146734236	0.10416209
GO:0003299	muscle hyper	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0009072	aromatic ami	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0014887	cardiac muscl	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0014898	cardiac muscl	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0019674	NAD metabol	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0031365	N-terminal pr	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0034508	centromere c	1/29	30/18723	0.045472682	0.146734236	0.10416209
GO:0002717	positive regul	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:0050482	arachidonic a	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:0060045	positive regul	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:0060795	cell fate comr	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:1900027	regulation of	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:1903963	arachidonate	1/29	31/18723	0.046953519	0.148846786	0.105661724
GO:0050769	positive regul	2/29	225/18723	0.047198624	0.149186294	0.10590273
GO:0003338	metanephros	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0010039	response to ii	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0030431	sleep	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0035767	endothelial c	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0035883	enteroendocr	1/29	32/18723	0.048432138	0.150014732	0.106490812

GO:0045761	regulation of	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0071875	adrenergic re	1/29	32/18723	0.048432138	0.150014732	0.106490812
GO:0001975	response to a	1/29	33/18723	0.049908542	0.153270268	0.108801816
GO:0018345	protein palmi	1/29	33/18723	0.049908542	0.153270268	0.108801816
GO:0032228	regulation of	1/29	33/18723	0.049908542	0.153270268	0.108801816
GO:0007160	cell-matrix ad	2/29	233/18723	0.050241778	0.153856549	0.109217999
GO:0007616	long-term me	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0014072	response to i	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0032212	positive regul	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0043276	anoikis	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0043278	response to n	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0051482	positive regul	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0051973	positive regul	1/29	34/18723	0.051382734	0.154290933	0.109526355
GO:0031334	positive regul	2/29	237/18723	0.051789711	0.15508221	0.110088058
GO:0007020	microtubule r	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:0008608	attachment o	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:0098801	regulation of	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:0098810	neurotransmi	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:1905207	regulation of	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:2000403	positive regul	1/29	35/18723	0.052854718	0.155683788	0.110515099
GO:0010762	regulation of	1/29	36/18723	0.054324496	0.158287817	0.112363619
GO:0014046	dopamine sec	1/29	36/18723	0.054324496	0.158287817	0.112363619
GO:0014059	regulation of	1/29	36/18723	0.054324496	0.158287817	0.112363619
GO:0070306	lens fiber cell	1/29	36/18723	0.054324496	0.158287817	0.112363619
GO:0003161	cardiac cond	1/29	37/18723	0.055792072	0.160402207	0.113864559
GO:0042178	xenobiotic ca	1/29	37/18723	0.055792072	0.160402207	0.113864559
GO:0051954	positive regul	1/29	37/18723	0.055792072	0.160402207	0.113864559
GO:1902745	positive regul	1/29	37/18723	0.055792072	0.160402207	0.113864559
GO:1904358	positive regul	1/29	37/18723	0.055792072	0.160402207	0.113864559
GO:0035886	vascular asso	1/29	38/18723	0.057257449	0.163744185	0.116236926
GO:0046676	negative regu	1/29	38/18723	0.057257449	0.163744185	0.116236926
GO:0097305	response to a	2/29	253/18723	0.058151169	0.165736294	0.117651062
GO:0001914	regulation of	1/29	39/18723	0.05872063	0.165736294	0.117651062
GO:0016233	telomere cap	1/29	39/18723	0.05872063	0.165736294	0.117651062
GO:0031507	heterochrom	1/29	39/18723	0.05872063	0.165736294	0.117651062
GO:0042417	dopamine me	1/29	39/18723	0.05872063	0.165736294	0.117651062
GO:0043547	positive regul	2/29	255/18723	0.058964924	0.165992404	0.117832867
GO:0031111	negative regu	1/29	40/18723	0.060181618	0.167702921	0.11904711
GO:1901020	negative regu	1/29	40/18723	0.060181618	0.167702921	0.11904711
GO:0031348	negative regu	2/29	258/18723	0.060193093	0.167702921	0.11904711
GO:0045165	cell fate com	2/29	258/18723	0.060193093	0.167702921	0.11904711
GO:0045927	positive regul	2/29	259/18723	0.060604476	0.16841501	0.119552599
GO:0048286	lung alveolus	1/29	41/18723	0.061640416	0.169120025	0.120053068
GO:0055023	positive regul	1/29	41/18723	0.061640416	0.169120025	0.120053068
GO:0071634	regulation of	1/29	41/18723	0.061640416	0.169120025	0.120053068
GO:1900026	positive regul	1/29	41/18723	0.061640416	0.169120025	0.120053068
GO:1901385	regulation of	1/29	41/18723	0.061640416	0.169120025	0.120053068
GO:0009636	response to t	2/29	262/18723	0.061844555	0.169250542	0.120145718
GO:0007212	dopamine rec	1/29	42/18723	0.063097028	0.171376602	0.121654942
GO:0032467	positive regul	1/29	42/18723	0.063097028	0.171376602	0.121654942



GO:2000404	regulation of	1/29	42/18723	0.063097028	0.171376602	0.121654942
GO:0001504	neurotransmi	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0001709	cell fate dete	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0021983	pituitary glan	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0045776	negative regu	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0046717	acid secretior	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0071604	transforming	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0090278	negative regu	1/29	43/18723	0.064551457	0.172296606	0.122308024
GO:0002792	negative regu	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0008542	visual learnin	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0032007	negative regu	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0042269	regulation of	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0045124	regulation of	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0048066	development	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0060711	labyrinthine l	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0097178	ruffle assemb	1/29	44/18723	0.066003706	0.172440985	0.122410515
GO:0051962	positive regul	2/29	272/18723	0.066041228	0.172440985	0.122410515
GO:0032309	icosanoid sec	1/29	45/18723	0.067453778	0.174443861	0.123832294
GO:0035987	endodermal c	1/29	45/18723	0.067453778	0.174443861	0.123832294
GO:0046189	phenol-conta	1/29	45/18723	0.067453778	0.174443861	0.123832294
GO:0060421	positive regul	1/29	45/18723	0.067453778	0.174443861	0.123832294
GO:0007548	sex differenti	2/29	276/18723	0.067746476	0.174782674	0.124072807
GO:0031018	endocrine pa	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:0035094	response to n	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:0043462	regulation of	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:0060976	coronary vasc	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:0070828	heterochrom	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:1900271	regulation of	1/29	46/18723	0.068901676	0.175253439	0.124406989
GO:0010761	fibroblast mi	1/29	47/18723	0.070347403	0.177262338	0.125833044
GO:0048512	circadian beh	1/29	47/18723	0.070347403	0.177262338	0.125833044
GO:0051972	regulation of	1/29	47/18723	0.070347403	0.177262338	0.125833044
GO:1903170	negative regu	1/29	47/18723	0.070347403	0.177262338	0.125833044
GO:0002715	regulation of	1/29	48/18723	0.071790963	0.180060398	0.1278193
GO:0033628	regulation of	1/29	48/18723	0.071790963	0.180060398	0.1278193
GO:0001913	T cell mediat	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0007622	rhythmic beh	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0014075	response to a	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0018198	peptidyl-cyst	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0048168	regulation of	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0051932	synaptic tran	1/29	49/18723	0.073232359	0.18115373	0.128595422
GO:0007632	visual behavi	1/29	50/18723	0.074671593	0.183038531	0.129933385
GO:0015872	dopamine tra	1/29	50/18723	0.074671593	0.183038531	0.129933385
GO:0045814	negative regu	1/29	50/18723	0.074671593	0.183038531	0.129933385
GO:0060425	lung morpho	1/29	50/18723	0.074671593	0.183038531	0.129933385
GO:0006636	unsaturated f	1/29	51/18723	0.076108669	0.184056984	0.130656352
GO:0021872	forebrain gen	1/29	51/18723	0.076108669	0.184056984	0.130656352
GO:0046850	regulation of	1/29	51/18723	0.076108669	0.184056984	0.130656352
GO:0048013	ephrin recept	1/29	51/18723	0.076108669	0.184056984	0.130656352
GO:0051339	regulation of	1/29	51/18723	0.076108669	0.184056984	0.130656352
GO:0060043	regulation of	1/29	51/18723	0.076108669	0.184056984	0.130656352

GO:0002218	activation of i	1/29	52/18723	0.077543591	0.185863906	0.13193903
GO:0032206	positive regul	1/29	52/18723	0.077543591	0.185863906	0.13193903
GO:0043392	negative regu	1/29	52/18723	0.077543591	0.185863906	0.13193903
GO:0048260	positive regul	1/29	52/18723	0.077543591	0.185863906	0.13193903
GO:0002707	negative regu	1/29	53/18723	0.07897636	0.186924615	0.132691995
GO:0031279	regulation of	1/29	53/18723	0.07897636	0.186924615	0.132691995
GO:0032210	regulation of	1/29	53/18723	0.07897636	0.186924615	0.132691995
GO:0045744	negative regu	1/29	53/18723	0.07897636	0.186924615	0.132691995
GO:0071715	icosanoid tra	1/29	53/18723	0.07897636	0.186924615	0.132691995
GO:0090287	regulation of	2/29	304/18723	0.080085579	0.186924615	0.132691995
GO:0001706	endoderm fo	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0002823	negative regu	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0006584	catecholamin	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0009712	catechol-cont	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0014888	striated musc	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0060350	endochondra	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:1902743	regulation of	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:2000300	regulation of	1/29	54/18723	0.08040698	0.186924615	0.132691995
GO:0002067	glandular epit	1/29	55/18723	0.081835455	0.188297055	0.133666248
GO:0031113	regulation of	1/29	55/18723	0.081835455	0.188297055	0.133666248
GO:0022604	regulation of	2/29	309/18723	0.082359475	0.188297055	0.133666248
GO:0070372	regulation of	2/29	309/18723	0.082359475	0.188297055	0.133666248
GO:0060326	cell chemota	2/29	310/18723	0.082816699	0.188297055	0.133666248
GO:0000288	nuclear-trans	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0001912	positive regul	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0002090	regulation of	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0022029	telencephalo	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0031529	ruffle organiz	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0046622	positive regul	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0050433	regulation of	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:0055078	sodium ion h	1/29	56/18723	0.083261788	0.188297055	0.133666248
GO:1900024	regulation of	1/29	57/18723	0.084685981	0.191118048	0.135668783
GO:0043666	regulation of	1/29	58/18723	0.086108037	0.193117817	0.137088358
GO:0050432	catecholamin	1/29	58/18723	0.086108037	0.193117817	0.137088358
GO:2000736	regulation of	1/29	58/18723	0.086108037	0.193117817	0.137088358
GO:0007204	positive regul	2/29	319/18723	0.086967631	0.193888781	0.137635641
GO:0009416	response to li	2/29	320/18723	0.087432774	0.193888781	0.137635641
GO:0002820	negative regu	1/29	59/18723	0.08752796	0.193888781	0.137635641
GO:0019369	arachidonic a	1/29	59/18723	0.08752796	0.193888781	0.137635641
GO:0021885	forebrain cell	1/29	59/18723	0.08752796	0.193888781	0.137635641
GO:2001258	negative regu	1/29	59/18723	0.08752796	0.193888781	0.137635641
GO:0060038	cardiac muscl	1/29	60/18723	0.088945753	0.196626502	0.139579064
GO:0008544	epidermis de	2/29	324/18723	0.089301051	0.197009052	0.139850625
GO:0019748	secondary m	1/29	61/18723	0.090361419	0.197334736	0.140081817
GO:0030199	collagen fibril	1/29	61/18723	0.090361419	0.197334736	0.140081817
GO:0040014	regulation of	1/29	61/18723	0.090361419	0.197334736	0.140081817
GO:1904356	regulation of	1/29	61/18723	0.090361419	0.197334736	0.140081817
GO:2000401	regulation of	1/29	61/18723	0.090361419	0.197334736	0.140081817
GO:0007588	excretion	1/29	62/18723	0.091774961	0.199176868	0.14138949
GO:0046148	pigment bios	1/29	62/18723	0.091774961	0.199176868	0.14138949

GO:0060393	regulation of	1/29	62/18723	0.091774961	0.199176868	0.14138949
GO:0048638	regulation of	2/29	330/18723	0.092126211	0.199176868	0.14138949
GO:0070371	ERK1 and ERk	2/29	330/18723	0.092126211	0.199176868	0.14138949
GO:0002704	negative regu	1/29	63/18723	0.093186382	0.200666293	0.142446787
GO:0031343	positive regul	1/29	63/18723	0.093186382	0.200666293	0.142446787
GO:0046888	negative regu	1/29	64/18723	0.094595685	0.202490962	0.143742062
GO:0048247	lymphocyte c	1/29	64/18723	0.094595685	0.202490962	0.143742062
GO:0070542	response to f	1/29	64/18723	0.094595685	0.202490962	0.143742062
GO:0015909	long-chain fat	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0045453	bone resorpti	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0048645	animal organ	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0060389	pathway-rest	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0071677	positive regul	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0090307	mitotic spindl	1/29	65/18723	0.096002873	0.203090227	0.144167462
GO:0050922	negative regu	1/29	66/18723	0.09740795	0.204462124	0.145141329
GO:0071300	cellular respo	1/29	66/18723	0.09740795	0.204462124	0.145141329
GO:0072678	T cell migratic	1/29	66/18723	0.09740795	0.204462124	0.145141329
GO:2000573	positive regul	1/29	66/18723	0.09740795	0.204462124	0.145141329
GO:0001933	negative regu	2/29	342/18723	0.097855849	0.204607684	0.145244658
GO:0045765	regulation of	2/29	342/18723	0.097855849	0.204607684	0.145244658
GO:0061180	mammary gla	1/29	67/18723	0.098810918	0.205829007	0.146111637
GO:0030336	negative regu	2/29	344/18723	0.098820772	0.205829007	0.146111637
GO:0032922	circadian regt	1/29	68/18723	0.10021178	0.207129893	0.147035096
GO:0042267	natural killer	1/29	68/18723	0.10021178	0.207129893	0.147035096
GO:0051926	negative regu	1/29	68/18723	0.10021178	0.207129893	0.147035096
GO:0060411	cardiac septu	1/29	68/18723	0.10021178	0.207129893	0.147035096
GO:0043087	regulation of	2/29	348/18723	0.100758948	0.207467472	0.147274733
GO:1901342	regulation of	2/29	348/18723	0.100758948	0.207467472	0.147274733
GO:0007004	telomere mai	1/29	69/18723	0.101610539	0.207638928	0.147396444
GO:0045669	positive regul	1/29	69/18723	0.101610539	0.207638928	0.147396444
GO:0050805	negative regu	1/29	69/18723	0.101610539	0.207638928	0.147396444
GO:0051966	regulation of	1/29	69/18723	0.101610539	0.207638928	0.147396444
GO:0031346	positive regul	2/29	353/18723	0.103197031	0.210086611	0.149133979
GO:0051480	regulation of	2/29	353/18723	0.103197031	0.210086611	0.149133979
GO:0002228	natural killer	1/29	71/18723	0.104401762	0.210950103	0.149746945
GO:0008344	adult locomo	1/29	71/18723	0.104401762	0.210950103	0.149746945
GO:0050795	regulation of	1/29	71/18723	0.104401762	0.210950103	0.149746945
GO:0071230	cellular respo	1/29	71/18723	0.104401762	0.210950103	0.149746945
GO:0002460	adaptive imm	2/29	356/18723	0.104667926	0.211093336	0.149848621
GO:0001818	negative regu	2/29	357/18723	0.105159547	0.211392912	0.150061281
GO:0030032	lamellipodiun	1/29	72/18723	0.105794232	0.211392912	0.150061281
GO:0033627	cell adhesion	1/29	72/18723	0.105794232	0.211392912	0.150061281
GO:0050709	negative regu	1/29	72/18723	0.105794232	0.211392912	0.150061281
GO:0055021	regulation of	1/29	72/18723	0.105794232	0.211392912	0.150061281
GO:2000146	negative regu	2/29	359/18723	0.106144754	0.211701991	0.150280687
GO:0051145	smooth musc	1/29	73/18723	0.107184612	0.212599203	0.15091759
GO:0051937	catecholamin	1/29	73/18723	0.107184612	0.212599203	0.15091759
GO:0072089	stem cell prol	1/29	73/18723	0.107184612	0.212599203	0.15091759
GO:0031589	cell-substrate	2/29	363/18723	0.108122946	0.213676243	0.151682147
GO:0051098	regulation of	2/29	363/18723	0.108122946	0.213676243	0.151682147

GO:0003151	outflow tract	1/29	74/18723	0.108572904	0.213874761	0.151823069
GO:0050767	regulation of	2/29	364/18723	0.108619097	0.213874761	0.151823069
GO:0006278	RNA-depende	1/29	75/18723	0.109959111	0.215634723	0.153072412
GO:0043627	response to e	1/29	75/18723	0.109959111	0.215634723	0.153072412
GO:0051271	negative regu	2/29	367/18723	0.110111348	0.215634723	0.153072412
GO:0006305	DNA alkylatio	1/29	76/18723	0.111343238	0.216478489	0.153671375
GO:0006306	DNA methyla	1/29	76/18723	0.111343238	0.216478489	0.153671375
GO:0014855	striated musc	1/29	76/18723	0.111343238	0.216478489	0.153671375
GO:0021536	diencephalon	1/29	76/18723	0.111343238	0.216478489	0.153671375
GO:0007492	endoderm de	1/29	77/18723	0.112725286	0.217989327	0.154743872
GO:0031016	pancreas dev	1/29	77/18723	0.112725286	0.217989327	0.154743872
GO:0032418	lysosome loci	1/29	77/18723	0.112725286	0.217989327	0.154743872
GO:0010038	response to n	2/29	373/18723	0.113112678	0.218347867	0.154998388
GO:0007193	adenylate cyc	1/29	78/18723	0.114105258	0.219090202	0.155525349
GO:0008306	associative le	1/29	78/18723	0.114105258	0.219090202	0.155525349
GO:0070373	negative regu	1/29	78/18723	0.114105258	0.219090202	0.155525349
GO:0010770	positive regul	1/29	79/18723	0.115483158	0.220950963	0.156846246
GO:0060420	regulation of	1/29	79/18723	0.115483158	0.220950963	0.156846246
GO:0001570	vasculogenes	1/29	80/18723	0.116858989	0.222011541	0.157599117
GO:0032204	regulation of	1/29	80/18723	0.116858989	0.222011541	0.157599117
GO:0032272	negative regu	1/29	80/18723	0.116858989	0.222011541	0.157599117
GO:0071229	cellular respo	1/29	80/18723	0.116858989	0.222011541	0.157599117
GO:0006096	glycolytic pro	1/29	81/18723	0.118232753	0.222664819	0.158062859
GO:0010833	telomere mai	1/29	81/18723	0.118232753	0.222664819	0.158062859
GO:0021954	central nervo	1/29	81/18723	0.118232753	0.222664819	0.158062859
GO:0030512	negative regu	1/29	81/18723	0.118232753	0.222664819	0.158062859
GO:0048144	fibroblast pro	1/29	81/18723	0.118232753	0.222664819	0.158062859
GO:0042326	negative regu	2/29	385/18723	0.119180438	0.222917957	0.158242554
GO:0001892	embryonic pl	1/29	82/18723	0.119604454	0.222917957	0.158242554
GO:0001910	regulation of	1/29	82/18723	0.119604454	0.222917957	0.158242554
GO:0006757	ATP generatic	1/29	82/18723	0.119604454	0.222917957	0.158242554
GO:0008543	fibroblast gro	1/29	82/18723	0.119604454	0.222917957	0.158242554
GO:2001252	positive regul	1/29	82/18723	0.119604454	0.222917957	0.158242554
GO:0046785	microtubule	1/29	83/18723	0.120974095	0.22469587	0.159504639
GO:0048678	response to a	1/29	83/18723	0.120974095	0.22469587	0.159504639
GO:0006631	fatty acid me	2/29	390/18723	0.12173335	0.224917269	0.159661803
GO:0040013	negative regu	2/29	391/18723	0.122245623	0.224917269	0.159661803
GO:0010921	regulation of	1/29	84/18723	0.122341678	0.224917269	0.159661803
GO:0015844	monoamine t	1/29	84/18723	0.122341678	0.224917269	0.159661803
GO:0042440	pigment met	1/29	84/18723	0.122341678	0.224917269	0.159661803
GO:0061157	mRNA destab	1/29	84/18723	0.122341678	0.224917269	0.159661803
GO:0001656	metanephros	1/29	85/18723	0.123707207	0.22627325	0.160624372
GO:0002709	regulation of	1/29	85/18723	0.123707207	0.22627325	0.160624372
GO:0098773	skin epidermi	1/29	85/18723	0.123707207	0.22627325	0.160624372
GO:0015908	fatty acid trar	1/29	86/18723	0.125070684	0.22722926	0.161303014
GO:0032413	negative regu	1/29	86/18723	0.125070684	0.22722926	0.161303014
GO:0034103	regulation of	1/29	86/18723	0.125070684	0.22722926	0.161303014
GO:0046928	regulation of	1/29	86/18723	0.125070684	0.22722926	0.161303014
GO:0048041	focal adhesio	1/29	87/18723	0.126432113	0.22893319	0.162512581
GO:0061014	positive regul	1/29	87/18723	0.126432113	0.22893319	0.162512581

GO:0031110	regulation of	1/29	88/18723	0.127791497	0.23023768	0.163438598
GO:0050779	RNA destabili	1/29	88/18723	0.127791497	0.23023768	0.163438598
GO:0070098	chemokine-r	1/29	88/18723	0.127791497	0.23023768	0.163438598
GO:0046330	positive regul	1/29	89/18723	0.129148837	0.232031207	0.164711768
GO:0002028	regulation of	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0035278	miRNA media	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0035304	regulation of	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0040033	negative regu	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0046031	ADP metaboli	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0046849	bone remode	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0097581	lamellipodiun	1/29	90/18723	0.130504139	0.232031207	0.164711768
GO:0001503	ossification	2/29	408/18723	0.131037246	0.232525046	0.165062328
GO:0002065	columnar/cut	1/29	91/18723	0.131857403	0.232525046	0.165062328
GO:0045974	regulation of	1/29	91/18723	0.131857403	0.232525046	0.165062328
GO:0051952	regulation of	1/29	91/18723	0.131857403	0.232525046	0.165062328
GO:0072080	nephron tubu	1/29	91/18723	0.131857403	0.232525046	0.165062328
GO:0006497	protein lipida	1/29	92/18723	0.133208634	0.233384982	0.16567277
GO:0032465	regulation of	1/29	92/18723	0.133208634	0.233384982	0.16567277
GO:0035249	synaptic tran	1/29	92/18723	0.133208634	0.233384982	0.16567277
GO:1903351	cellular respo	1/29	92/18723	0.133208634	0.233384982	0.16567277
GO:0033273	response to v	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:0060349	bone morphic	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:0060993	kidney morpt	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:0097306	cellular respo	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:1901019	regulation of	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:1903350	response to d	1/29	93/18723	0.134557834	0.233478361	0.165739058
GO:0002690	positive regul	1/29	94/18723	0.135905007	0.234685803	0.166596183
GO:0061326	renal tubule c	1/29	94/18723	0.135905007	0.234685803	0.166596183
GO:1902414	protein locali	1/29	94/18723	0.135905007	0.234685803	0.166596183
GO:0007044	cell-substrate	1/29	95/18723	0.137250155	0.236630649	0.167976769
GO:0003073	regulation of	1/29	96/18723	0.13859328	0.237431594	0.168545335
GO:0010769	regulation of	1/29	96/18723	0.13859328	0.237431594	0.168545335
GO:0042158	lipoprotein bi	1/29	96/18723	0.13859328	0.237431594	0.168545335
GO:0055017	cardiac muscl	1/29	96/18723	0.13859328	0.237431594	0.168545335
GO:0010596	negative regu	1/29	97/18723	0.139934387	0.238219011	0.169104299
GO:0120162	positive regul	1/29	97/18723	0.139934387	0.238219011	0.169104299
GO:1990868	response to c	1/29	97/18723	0.139934387	0.238219011	0.169104299
GO:1990869	cellular respo	1/29	97/18723	0.139934387	0.238219011	0.169104299
GO:0050808	synapse organ	2/29	426/18723	0.140506606	0.238817046	0.169528824
GO:0032103	positive regul	2/29	427/18723	0.141037222	0.238967456	0.169635596
GO:0048568	embryonic or	2/29	427/18723	0.141037222	0.238967456	0.169635596
GO:0003300	cardiac muscl	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0006165	nucleoside di	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0007631	feeding beha	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0015837	amine transp	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0031341	regulation of	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0060291	long-term syr	1/29	99/18723	0.142610555	0.239382003	0.16992987
GO:0044728	DNA methylat	1/29	100/18723	0.143945622	0.240131509	0.170461921
GO:0045807	positive regul	1/29	100/18723	0.143945622	0.240131509	0.170461921
GO:0051588	regulation of	1/29	100/18723	0.143945622	0.240131509	0.170461921

GO:0060079	excitatory po	1/29	100/18723	0.143945622	0.240131509	0.170461921
GO:0002683	negative regu	2/29	434/18723	0.144764293	0.24086849	0.170985082
GO:0006576	cellular bioge	1/29	101/18723	0.145278683	0.24086849	0.170985082
GO:0046939	nucleotide pt	1/29	101/18723	0.145278683	0.24086849	0.170985082
GO:0150115	cell-substrate	1/29	101/18723	0.145278683	0.24086849	0.170985082
GO:0045785	positive regul	2/29	437/18723	0.146368303	0.241143916	0.171180598
GO:0014897	striated musc	1/29	102/18723	0.146609738	0.241143916	0.171180598
GO:1904063	negative regu	1/29	102/18723	0.146609738	0.241143916	0.171180598
GO:0002027	regulation of	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0003279	cardiac septu	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0009135	purine nuclec	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0009179	purine ribonu	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0030593	neutrophil ch	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0090277	positive regul	1/29	103/18723	0.147938792	0.241143916	0.171180598
GO:0045936	negative regu	2/29	441/18723	0.148513067	0.241143916	0.171180598
GO:0010563	negative regu	2/29	442/18723	0.149050328	0.241143916	0.171180598
GO:0007200	phospholipas	1/29	104/18723	0.149265848	0.241143916	0.171180598
GO:0014896	muscle hyper	1/29	104/18723	0.149265848	0.241143916	0.171180598
GO:0032006	regulation of	1/29	104/18723	0.149265848	0.241143916	0.171180598
GO:0060419	heart growth	1/29	104/18723	0.149265848	0.241143916	0.171180598
GO:0051960	regulation of	2/29	443/18723	0.149588012	0.241143916	0.171180598
GO:0016055	Wnt signaling	2/29	444/18723	0.150126116	0.241143916	0.171180598
GO:0016079	synaptic vesic	1/29	105/18723	0.150590908	0.241143916	0.171180598
GO:0040029	regulation of	1/29	105/18723	0.150590908	0.241143916	0.171180598
GO:0120034	positive regul	1/29	105/18723	0.150590908	0.241143916	0.171180598
GO:0198738	cell-cell signa	2/29	446/18723	0.151203577	0.241143916	0.171180598
GO:0001824	blastocyst de	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0002793	positive regul	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0006090	pyruvate met	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0006906	vesicle fusion	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0009185	ribonucleosid	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0046620	regulation of	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0099565	chemical syna	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:2000278	regulation of	1/29	106/18723	0.151913975	0.241143916	0.171180598
GO:0006874	cellular calciu	2/29	448/18723	0.15228269	0.241374762	0.171344468
GO:0021761	limbic system	1/29	107/18723	0.153235052	0.241820571	0.171660934
GO:0071868	cellular respo	1/29	107/18723	0.153235052	0.241820571	0.171660934
GO:0071870	cellular respo	1/29	107/18723	0.153235052	0.241820571	0.171660934
GO:0003012	muscle syster	2/29	452/18723	0.154445796	0.24319218	0.172634597
GO:0034446	substrate adh	1/29	108/18723	0.154554142	0.24319218	0.172634597
GO:0002456	T cell mediatε	1/29	109/18723	0.155871248	0.243377814	0.172766372
GO:0032410	negative regu	1/29	109/18723	0.155871248	0.243377814	0.172766372
GO:0034766	negative regu	1/29	109/18723	0.155871248	0.243377814	0.172766372
GO:0043266	regulation of	1/29	109/18723	0.155871248	0.243377814	0.172766372
GO:0072009	nephron epitl	1/29	109/18723	0.155871248	0.243377814	0.172766372
GO:0002698	negative regu	1/29	110/18723	0.157186373	0.243377814	0.172766372
GO:0003014	renal system	1/29	110/18723	0.157186373	0.243377814	0.172766372
GO:0006939	smooth musc	1/29	110/18723	0.157186373	0.243377814	0.172766372
GO:0007088	regulation of	1/29	110/18723	0.157186373	0.243377814	0.172766372
GO:0048259	regulation of	1/29	110/18723	0.157186373	0.243377814	0.172766372

GO:0090174	organelle me	1/29	110/18723	0.157186373	0.243377814	0.172766372
GO:0006805	xenobiotic m	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0014066	regulation of	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0015718	monocarboxy	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0071867	response to n	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0071869	response to c	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0090288	negative regu	1/29	111/18723	0.15849952	0.243377814	0.172766372
GO:0055074	calcium ion h	2/29	460/18723	0.158790988	0.243479514	0.172838567
GO:0000956	nuclear-trans	1/29	112/18723	0.159810691	0.244004741	0.173211409
GO:0001676	long-chain fat	1/29	112/18723	0.159810691	0.244004741	0.173211409
GO:0010633	negative regu	1/29	112/18723	0.159810691	0.244004741	0.173211409
GO:0002708	positive regul	1/29	113/18723	0.161119889	0.244965682	0.173893551
GO:0031623	receptor inte	1/29	113/18723	0.161119889	0.244965682	0.173893551
GO:0044106	cellular amin	1/29	113/18723	0.161119889	0.244965682	0.173893551
GO:0007041	lysosomal tra	1/29	114/18723	0.162427118	0.246542289	0.175012735
GO:0001819	positive regul	2/29	467/18723	0.162612999	0.246542289	0.175012735
GO:0006417	regulation of	2/29	468/18723	0.163160472	0.246854536	0.17523439
GO:0051209	release of sec	1/29	115/18723	0.163732379	0.246854536	0.17523439
GO:0071675	regulation of	1/29	115/18723	0.163732379	0.246854536	0.17523439
GO:0090630	activation of	1/29	115/18723	0.163732379	0.246854536	0.17523439
GO:0043200	response to a	1/29	116/18723	0.165035677	0.248127353	0.176137923
GO:0051283	negative regu	1/29	116/18723	0.165035677	0.248127353	0.176137923
GO:0051225	spindle assen	1/29	117/18723	0.166337013	0.249264015	0.176944804
GO:0072676	lymphocyte n	1/29	117/18723	0.166337013	0.249264015	0.176944804
GO:0001667	ameboidal-ty	2/29	475/18723	0.167002757	0.249264015	0.176944804
GO:0007613	memory	1/29	118/18723	0.167636391	0.249264015	0.176944804
GO:0009308	amine metab	1/29	118/18723	0.167636391	0.249264015	0.176944804
GO:0051101	regulation of	1/29	118/18723	0.167636391	0.249264015	0.176944804
GO:0051282	regulation of	1/29	118/18723	0.167636391	0.249264015	0.176944804
GO:1903313	positive regul	1/29	118/18723	0.167636391	0.249264015	0.176944804
GO:0043410	positive regul	2/29	480/18723	0.169757636	0.252071435	0.178937705
GO:0006304	DNA modific	1/29	120/18723	0.170229283	0.252079254	0.178943255
GO:0007052	mitotic spindl	1/29	120/18723	0.170229283	0.252079254	0.178943255
GO:0001704	formation of	1/29	121/18723	0.171522803	0.252266871	0.179076439
GO:0003206	cardiac cham	1/29	121/18723	0.171522803	0.252266871	0.179076439
GO:0042752	regulation of	1/29	121/18723	0.171522803	0.252266871	0.179076439
GO:0043500	muscle adapt	1/29	121/18723	0.171522803	0.252266871	0.179076439
GO:1904019	epithelial cell	1/29	121/18723	0.171522803	0.252266871	0.179076439
GO:0002688	regulation of	1/29	122/18723	0.172814376	0.252790718	0.179448302
GO:0031109	microtubule	1/29	122/18723	0.172814376	0.252790718	0.179448302
GO:0051208	sequestering	1/29	122/18723	0.172814376	0.252790718	0.179448302
GO:1990266	neutrophil mi	1/29	122/18723	0.172814376	0.252790718	0.179448302
GO:0072503	cellular divale	2/29	486/18723	0.173074473	0.252829061	0.17947552
GO:0006690	icosanoid me	1/29	123/18723	0.174104005	0.253647479	0.18005649
GO:0010811	positive regul	1/29	123/18723	0.174104005	0.253647479	0.18005649
GO:0001909	leukocyte me	1/29	124/18723	0.175391692	0.254836585	0.180900599
GO:0009132	nucleoside di	1/29	124/18723	0.175391692	0.254836585	0.180900599
GO:0055007	cardiac muscl	1/29	125/18723	0.176677441	0.256016506	0.181738189
GO:0071621	granulocyte c	1/29	125/18723	0.176677441	0.256016506	0.181738189
GO:0031929	TOR signaling	1/29	126/18723	0.177961254	0.25718732	0.182569313

GO:0032874	positive regul	1/29	126/18723	0.177961254	0.25718732	0.182569313
GO:0048565	digestive trac	1/29	127/18723	0.179243134	0.258349104	0.183394028
GO:0051224	negative regu	1/29	127/18723	0.179243134	0.258349104	0.183394028
GO:0017015	regulation of	1/29	128/18723	0.180523084	0.259157309	0.183967747
GO:0035303	regulation of	1/29	128/18723	0.180523084	0.259157309	0.183967747
GO:0070304	positive regul	1/29	128/18723	0.180523084	0.259157309	0.183967747
GO:0007098	centrosome c	1/29	130/18723	0.183077205	0.262127759	0.186076378
GO:0030534	adult behavic	1/29	130/18723	0.183077205	0.262127759	0.186076378
GO:0000723	telomere mai	1/29	131/18723	0.184351381	0.262215583	0.186138721
GO:0045089	positive regul	1/29	131/18723	0.184351381	0.262215583	0.186138721
GO:0090101	negative regu	1/29	131/18723	0.184351381	0.262215583	0.186138721
GO:1903844	regulation of	1/29	131/18723	0.184351381	0.262215583	0.186138721
GO:1904950	negative regu	1/29	131/18723	0.184351381	0.262215583	0.186138721
GO:0035264	multicellular	1/29	132/18723	0.185623638	0.263332222	0.186931389
GO:0045667	regulation of	1/29	132/18723	0.185623638	0.263332222	0.186931389
GO:0046328	regulation of	1/29	133/18723	0.18689398	0.264440304	0.187717982
GO:0046887	positive regul	1/29	133/18723	0.18689398	0.264440304	0.187717982
GO:0002705	positive regul	1/29	134/18723	0.188162408	0.265193693	0.18825279
GO:0008277	regulation of	1/29	134/18723	0.188162408	0.265193693	0.18825279
GO:0032147	activation of	1/29	134/18723	0.188162408	0.265193693	0.18825279
GO:0001101	response to a	1/29	135/18723	0.189428925	0.26593853	0.188781526
GO:0002687	positive regul	1/29	135/18723	0.189428925	0.26593853	0.188781526
GO:0042157	lipoprotein m	1/29	135/18723	0.189428925	0.26593853	0.188781526
GO:0045727	positive regul	1/29	136/18723	0.190693534	0.266674917	0.189304264
GO:0072073	kidney epithe	1/29	136/18723	0.190693534	0.266674917	0.189304264
GO:1903305	regulation of	1/29	136/18723	0.190693534	0.266674917	0.189304264
GO:0030879	mammary gla	1/29	137/18723	0.191956239	0.267402956	0.189821077
GO:0055123	digestive syst	1/29	137/18723	0.191956239	0.267402956	0.189821077
GO:0060078	regulation of	1/29	137/18723	0.191956239	0.267402956	0.189821077
GO:0007224	smoothened	1/29	138/18723	0.193217041	0.268812897	0.190821951
GO:0051783	regulation of	1/29	139/18723	0.194475944	0.270216575	0.191818378
GO:0008584	male gonad d	1/29	141/18723	0.196988061	0.271959252	0.19305545
GO:0031333	negative regu	1/29	141/18723	0.196988061	0.271959252	0.19305545
GO:0032355	response to e	1/29	141/18723	0.196988061	0.271959252	0.19305545
GO:0048284	organelle fusi	1/29	141/18723	0.196988061	0.271959252	0.19305545
GO:0050921	positive regul	1/29	141/18723	0.196988061	0.271959252	0.19305545
GO:0046546	development	1/29	142/18723	0.198241282	0.272644817	0.193542111
GO:0072006	nephron dev	1/29	142/18723	0.198241282	0.272644817	0.193542111
GO:0097553	calcium ion tr	1/29	142/18723	0.198241282	0.272644817	0.193542111
GO:0030010	establishmen	1/29	143/18723	0.199492614	0.27332258	0.194023235
GO:0031023	microtubule	1/29	143/18723	0.199492614	0.27332258	0.194023235
GO:0034763	negative regu	1/29	143/18723	0.199492614	0.27332258	0.194023235
GO:0007612	learning	1/29	144/18723	0.200742061	0.273647122	0.194253617
GO:0014065	phosphatidyli	1/29	144/18723	0.200742061	0.273647122	0.194253617
GO:0106106	cold-induced	1/29	144/18723	0.200742061	0.273647122	0.194253617
GO:0120161	regulation of	1/29	144/18723	0.200742061	0.273647122	0.194253617
GO:0007269	neurotransmi	1/29	145/18723	0.201989624	0.274655074	0.194969131
GO:0099643	signal release	1/29	145/18723	0.201989624	0.274655074	0.194969131
GO:0007189	adenylate cyc	1/29	146/18723	0.203235307	0.276001717	0.195925071
GO:0001889	liver develop	1/29	147/18723	0.204479113	0.276253973	0.196104139



GO:0016331	morphogene: 1/29	147/18723	0.204479113	0.276253973	0.196104139
GO:1902850	microtubule c 1/29	147/18723	0.204479113	0.276253973	0.196104139
GO:1903531	negative regu 1/29	147/18723	0.204479113	0.276253973	0.196104139
GO:0010212	response to ic 1/29	148/18723	0.205721043	0.276253973	0.196104139
GO:0050905	neuromusculi 1/29	148/18723	0.205721043	0.276253973	0.196104139
GO:0051384	response to g 1/29	148/18723	0.205721043	0.276253973	0.196104139
GO:0070507	regulation of 1/29	148/18723	0.205721043	0.276253973	0.196104139
GO:0097530	granulocyte n 1/29	148/18723	0.205721043	0.276253973	0.196104139
GO:0061008	hepaticobiliar 1/29	150/18723	0.208199291	0.27923503	0.1982203
GO:0055067	monovalent i 1/29	151/18723	0.209435614	0.280545104	0.199150281
GO:0120254	olefinic comp 1/29	153/18723	0.21190267	0.283498498	0.201246804
GO:0016052	carbohydrate 1/29	154/18723	0.213133409	0.284792602	0.202165448
GO:0001764	neuron migra 1/29	156/18723	0.215589322	0.287363819	0.203990676
GO:0035051	cardiocyte dif 1/29	156/18723	0.215589322	0.287363819	0.203990676
GO:0007030	Golgi organiz: 1/29	157/18723	0.216814502	0.287931789	0.20439386
GO:0007034	vacuolar tran 1/29	157/18723	0.216814502	0.287931789	0.20439386
GO:1990845	adaptive ther 1/29	157/18723	0.216814502	0.287931789	0.20439386
GO:0043488	regulation of 1/29	158/18723	0.218037834	0.289201102	0.205294906
GO:0032200	telomere org: 1/29	159/18723	0.219259321	0.290109334	0.205939631
GO:1903169	regulation of 1/29	159/18723	0.219259321	0.290109334	0.205939631
GO:0043271	negative regu 1/29	160/18723	0.220478965	0.291010698	0.206579481
GO:0060402	calcium ion tr 1/29	160/18723	0.220478965	0.291010698	0.206579481
GO:0003205	cardiac cham 1/29	161/18723	0.22169677	0.29226123	0.207467195
GO:0021953	central nervo 1/29	162/18723	0.222912738	0.292793037	0.207844709
GO:0034250	positive regul 1/29	162/18723	0.222912738	0.292793037	0.207844709
GO:0051100	negative regu 1/29	162/18723	0.222912738	0.292793037	0.207844709
GO:0006633	fatty acid bio: 1/29	163/18723	0.224126871	0.293318581	0.208217776
GO:0051494	negative regu 1/29	163/18723	0.224126871	0.293318581	0.208217776
GO:0061025	membrane fu 1/29	163/18723	0.224126871	0.293318581	0.208217776
GO:0050806	positive regul 1/29	164/18723	0.225339173	0.294548544	0.209090889
GO:0046661	male sex diffε 1/29	165/18723	0.226549646	0.294705375	0.209202219
GO:0050796	regulation of 1/29	165/18723	0.226549646	0.294705375	0.209202219
GO:0071772	response to E 1/29	165/18723	0.226549646	0.294705375	0.209202219
GO:0071773	cellular respo 1/29	165/18723	0.226549646	0.294705375	0.209202219
GO:0061013	regulation of 1/29	166/18723	0.227758292	0.295921531	0.21006553
GO:0007254	JNK cascade 1/29	167/18723	0.228965115	0.296420705	0.210419879
GO:0031960	response to c 1/29	167/18723	0.228965115	0.296420705	0.210419879
GO:1902904	negative regu 1/29	167/18723	0.228965115	0.296420705	0.210419879
GO:0000070	mitotic sister 1/29	168/18723	0.230170116	0.296560067	0.210518807
GO:0002706	regulation of 1/29	168/18723	0.230170116	0.296560067	0.210518807
GO:0002822	regulation of 1/29	168/18723	0.230170116	0.296560067	0.210518807
GO:0002833	positive regul 1/29	168/18723	0.230170116	0.296560067	0.210518807
GO:0043487	regulation of 1/29	170/18723	0.232574667	0.299301447	0.212464828
GO:0051048	negative regu 1/29	171/18723	0.233774222	0.300487436	0.213306725
GO:0000910	cytokinesis 1/29	173/18723	0.236167902	0.303203684	0.215234905
GO:0007584	response to n 1/29	174/18723	0.237362033	0.304375276	0.216066582
GO:0048771	tissue remodel 1/29	175/18723	0.238554362	0.305541783	0.216894649
GO:0071466	cellular respo 1/29	177/18723	0.240933621	0.308223958	0.218798642
GO:0035265	organ growth 1/29	178/18723	0.242120558	0.309011007	0.219357344
GO:0048015	phosphatidyli 1/29	178/18723	0.242120558	0.309011007	0.219357344

GO:0007416	synapse assem	1/29	179/18723	0.243305702	0.309792066	0.219911794
GO:0007626	locomotory b	1/29	179/18723	0.243305702	0.309792066	0.219911794
GO:0043409	negative regul	1/29	180/18723	0.244489057	0.310567181	0.220462023
GO:0071897	DNA biosynth	1/29	180/18723	0.244489057	0.310567181	0.220462023
GO:0045766	positive regul	1/29	181/18723	0.245670626	0.310971834	0.220749274
GO:0099504	synaptic vesic	1/29	181/18723	0.245670626	0.310971834	0.220749274
GO:1904018	positive regul	1/29	181/18723	0.245670626	0.310971834	0.220749274
GO:0048017	inositol lipid-r	1/29	182/18723	0.246850409	0.311735155	0.221291132
GO:0060401	cytosolic calci	1/29	182/18723	0.246850409	0.311735155	0.221291132
GO:0002819	regulation of	1/29	183/18723	0.248028412	0.312857308	0.222087714
GO:0007051	spindle organ	1/29	184/18723	0.249204635	0.313609092	0.222621382
GO:2001257	regulation of	1/29	184/18723	0.249204635	0.313609092	0.222621382
GO:0007369	gastrulation	1/29	185/18723	0.250379081	0.314720682	0.223410465
GO:0008217	regulation of	1/29	186/18723	0.251551754	0.315461074	0.223936047
GO:0120032	regulation of	1/29	186/18723	0.251551754	0.315461074	0.223936047
GO:0033044	regulation of	1/29	187/18723	0.252722655	0.316562214	0.224717711
GO:0001906	cell killing	1/29	188/18723	0.253891788	0.317291356	0.225235307
GO:0060491	regulation of	1/29	188/18723	0.253891788	0.317291356	0.225235307
GO:0051216	cartilage devel	1/29	190/18723	0.256224757	0.319837139	0.22704248
GO:0032872	regulation of	1/29	192/18723	0.258550683	0.322368268	0.228839249
GO:0030073	insulin secret	1/29	195/18723	0.262026408	0.325575342	0.231115852
GO:0070302	regulation of	1/29	195/18723	0.262026408	0.325575342	0.231115852
GO:1901605	alpha-amino acid	1/29	195/18723	0.262026408	0.325575342	0.231115852
GO:0071674	mononuclear	1/29	196/18723	0.263181483	0.326260531	0.231602247
GO:0090276	regulation of	1/29	196/18723	0.263181483	0.326260531	0.231602247
GO:0007179	transforming	1/29	198/18723	0.265486399	0.328364757	0.233095971
GO:0048167	regulation of	1/29	198/18723	0.265486399	0.328364757	0.233095971
GO:0002791	regulation of	1/29	200/18723	0.267784353	0.330450783	0.234576776
GO:0099003	vesicle-media	1/29	200/18723	0.267784353	0.330450783	0.234576776
GO:0051054	positive regul	1/29	201/18723	0.268930725	0.331010736	0.23497427
GO:0065004	protein-DNA int	1/29	201/18723	0.268930725	0.331010736	0.23497427
GO:0000819	sister chroma	1/29	202/18723	0.270075365	0.331010736	0.23497427
GO:0009913	epidermal cell	1/29	202/18723	0.270075365	0.331010736	0.23497427
GO:0017157	regulation of	1/29	202/18723	0.270075365	0.331010736	0.23497427
GO:0090087	regulation of	1/29	202/18723	0.270075365	0.331010736	0.23497427
GO:0060348	bone develop	1/29	205/18723	0.27349891	0.334827091	0.237683382
GO:0008016	regulation of	1/29	206/18723	0.274636642	0.335460125	0.238132753
GO:0048863	stem cell diff	1/29	206/18723	0.274636642	0.335460125	0.238132753
GO:0006836	neurotransmi	1/29	208/18723	0.276906949	0.33785148	0.239830303
GO:0071222	cellular respo	1/29	209/18723	0.278039528	0.338850879	0.240539744
GO:0002685	regulation of	1/29	210/18723	0.279170394	0.339463662	0.24097474
GO:0007623	circadian rhyt	1/29	210/18723	0.279170394	0.339463662	0.24097474
GO:0030100	regulation of	1/29	211/18723	0.280299549	0.340071619	0.24140631
GO:0050807	regulation of	1/29	211/18723	0.280299549	0.340071619	0.24140631
GO:0001505	regulation of	1/29	213/18723	0.282552739	0.342420977	0.243074047
GO:0051651	maintenance	1/29	214/18723	0.283676779	0.343014092	0.24349508
GO:0072330	monocarboxy	1/29	214/18723	0.283676779	0.343014092	0.24349508
GO:0007601	visual percep	1/29	215/18723	0.284799118	0.343986421	0.244185307
GO:0009612	response to n	1/29	216/18723	0.285919759	0.344954531	0.244872538
GO:0070374	positive regul	1/29	217/18723	0.287038705	0.345918439	0.245556787

GO:0050803	regulation of 1/29	218/18723	0.288155957	0.346878163	0.246238065
GO:0050953	sensory perce 1/29	219/18723	0.28927152	0.347833718	0.246916384
GO:0002064	epithelial cell 1/29	220/18723	0.290385394	0.348011763	0.247042773
GO:0048705	skeletal syste 1/29	220/18723	0.290385394	0.348011763	0.247042773
GO:0097529	myeloid leuko 1/29	220/18723	0.290385394	0.348011763	0.247042773
GO:0008406	gonad develo 1/29	221/18723	0.291497582	0.348186615	0.247166894
GO:0010810	regulation of 1/29	221/18723	0.291497582	0.348186615	0.247166894
GO:0071219	cellular respo 1/29	221/18723	0.291497582	0.348186615	0.247166894
GO:0050920	regulation of 1/29	223/18723	0.293716912	0.350450311	0.248773822
GO:0010001	glial cell diffe 1/29	225/18723	0.295929529	0.352701016	0.250371528
GO:0002703	regulation of 1/29	226/18723	0.297033327	0.353626681	0.251028629
GO:0045137	development 1/29	227/18723	0.298135453	0.35376995	0.251130331
GO:0046777	protein autoo 1/29	227/18723	0.298135453	0.35376995	0.251130331
GO:0098657	import into c 1/29	227/18723	0.298135453	0.35376995	0.251130331
GO:0001649	osteoblast dif 1/29	229/18723	0.300334703	0.355988831	0.252705446
GO:0030595	leukocyte che 1/29	230/18723	0.301431832	0.356507451	0.253073598
GO:0045055	regulated exc 1/29	230/18723	0.301431832	0.356507451	0.253073598
GO:0006402	mRNA catabo 1/29	232/18723	0.303621108	0.358312683	0.254355076
GO:0010594	regulation of 1/29	232/18723	0.303621108	0.358312683	0.254355076
GO:0007188	adenylate cyc 1/29	233/18723	0.30471326	0.35881812	0.25471387
GO:0032271	regulation of 1/29	233/18723	0.30471326	0.35881812	0.25471387
GO:0060560	development 1/29	234/18723	0.305803758	0.359710405	0.255347276
GO:0002699	positive regul 1/29	235/18723	0.306892605	0.360598811	0.255977928
GO:0030072	peptide horm 1/29	236/18723	0.307979803	0.360700073	0.256049811
GO:0048738	cardiac muscl 1/29	236/18723	0.307979803	0.360700073	0.256049811
GO:0090068	positive regul 1/29	236/18723	0.307979803	0.360700073	0.256049811
GO:0019318	hexose metal 1/29	237/18723	0.309065354	0.361188809	0.256396749
GO:1901617	organic hydrc 1/29	237/18723	0.309065354	0.361188809	0.256396749
GO:0051403	stress-activat 1/29	239/18723	0.311231526	0.363327516	0.257914951
GO:0032886	regulation of 1/29	240/18723	0.312312152	0.364195724	0.258531265
GO:0006813	potassium ior 1/29	241/18723	0.313391141	0.364275079	0.258587597
GO:0060047	heart contrac 1/29	241/18723	0.313391141	0.364275079	0.258587597
GO:0071824	protein-DNA 1/29	241/18723	0.313391141	0.364275079	0.258587597
GO:0002790	peptide secre 1/29	242/18723	0.314468495	0.36513474	0.259197844
GO:0043543	protein acylat 1/29	243/18723	0.315544217	0.365990663	0.259805437
GO:0006898	receptor-mec 1/29	244/18723	0.316618308	0.366842863	0.260410387
GO:0006814	sodium ion tr 1/29	245/18723	0.317690773	0.367298102	0.260733547
GO:0017148	negative regu 1/29	245/18723	0.317690773	0.367298102	0.260733547
GO:0003007	heart morpho 1/29	246/18723	0.318761612	0.367749523	0.261053997
GO:0071216	cellular respo 1/29	246/18723	0.318761612	0.367749523	0.261053997
GO:0031098	stress-activat 1/29	247/18723	0.319830829	0.368589686	0.261650403
GO:0021537	telencephalo 1/29	248/18723	0.320898425	0.369033188	0.261965231
GO:0033002	muscle cell pr 1/29	248/18723	0.320898425	0.369033188	0.261965231
GO:0046883	regulation of 1/29	249/18723	0.321964403	0.369865589	0.262556127
GO:0071560	cellular respo 1/29	250/18723	0.323028765	0.370694369	0.263144452
GO:0003015	heart process 1/29	251/18723	0.324091514	0.371519541	0.263730216
GO:0061448	connective tis 1/29	252/18723	0.325152653	0.37234112	0.26431343
GO:0007611	learning or m 1/29	255/18723	0.328326426	0.375180619	0.266329102
GO:0051924	regulation of 1/29	255/18723	0.328326426	0.375180619	0.266329102
GO:0071559	response to t 1/29	256/18723	0.329381144	0.375196013	0.26634003

GO:0090092	regulation of	1/29	256/18723	0.329381144	0.375196013	0.26634003
GO:1903522	regulation of	1/29	256/18723	0.329381144	0.375196013	0.26634003
GO:0005996	monosacchar	1/29	257/18723	0.330434263	0.375999408	0.266910335
GO:0051321	meiotic cell c	1/29	261/18723	0.334630793	0.380374224	0.270015881
GO:0043588	skin developr	1/29	263/18723	0.336719524	0.382346434	0.271415892
GO:0015833	peptide trans	1/29	264/18723	0.337761514	0.383127174	0.271970115
GO:0032412	regulation of	1/29	267/18723	0.340878009	0.386256948	0.274191845
GO:0001894	tissue homeo	1/29	268/18723	0.341913691	0.386619979	0.274449549
GO:0050708	regulation of	1/29	268/18723	0.341913691	0.386619979	0.274449549
GO:0034249	negative regu	1/29	273/18723	0.347068574	0.391221198	0.277715812
GO:0046942	carboxylic aci	1/29	273/18723	0.347068574	0.391221198	0.277715812
GO:0098742	cell-cell adhe:	1/29	273/18723	0.347068574	0.391221198	0.277715812
GO:0043270	positive regul	1/29	275/18723	0.349119592	0.393123208	0.27906599
GO:0046034	ATP metaboli	1/29	277/18723	0.351164389	0.39492884	0.280347752
GO:0006401	RNA catabolic	1/29	278/18723	0.35218446	0.39492884	0.280347752
GO:0022898	regulation of	1/29	278/18723	0.35218446	0.39492884	0.280347752
GO:0031349	positive regul	1/29	278/18723	0.35218446	0.39492884	0.280347752
GO:0043542	endothelial c	1/29	279/18723	0.353202983	0.395660544	0.280867166
GO:0006470	protein deph	1/29	281/18723	0.355235392	0.397114228	0.281899092
GO:0098813	nuclear chror	1/29	281/18723	0.355235392	0.397114228	0.281899092
GO:1903532	positive regul	1/29	282/18723	0.356249283	0.397836234	0.282411621
GO:0051146	striated musc	1/29	283/18723	0.357261634	0.398449091	0.28284667
GO:0006520	cellular aminc	1/29	284/18723	0.358272448	0.398449091	0.28284667
GO:0015850	organic hydrc	1/29	284/18723	0.358272448	0.398449091	0.28284667
GO:0022409	positive regul	1/29	284/18723	0.358272448	0.398449091	0.28284667
GO:0140014	mitotic nucle:	1/29	287/18723	0.36129569	0.401398398	0.284940291
GO:1903311	regulation of	1/29	288/18723	0.362300378	0.402101343	0.28543929
GO:0002429	immune resp	1/29	291/18723	0.365305294	0.404191426	0.286922975
GO:0002757	immune resp	1/29	291/18723	0.365305294	0.404191426	0.286922975
GO:0016236	macroautoph	1/29	291/18723	0.365305294	0.404191426	0.286922975
GO:0010632	regulation of	1/29	292/18723	0.366303892	0.404881909	0.287413128
GO:0001822	kidney develc	1/29	293/18723	0.367300972	0.405569306	0.28790109
GO:0010948	negative regu	1/29	294/18723	0.368296538	0.40625363	0.28838687
GO:0046879	hormone secr	1/29	295/18723	0.36929059	0.406934891	0.288870476
GO:0050890	cognition	1/29	296/18723	0.370283133	0.407613103	0.289351918
GO:0051258	protein polyn	1/29	297/18723	0.371274167	0.408288275	0.289831202
GO:0048511	rhythmic pro	1/29	298/18723	0.372263696	0.408960422	0.290308338
GO:0016050	vesicle organi	1/29	300/18723	0.374238243	0.410542866	0.291431666
GO:0030198	extracellular	1/29	301/18723	0.375223267	0.410542866	0.291431666
GO:0042063	gliogenesis	1/29	301/18723	0.375223267	0.410542866	0.291431666
GO:0042886	amide transp	1/29	301/18723	0.375223267	0.410542866	0.291431666
GO:0043062	extracellular	1/29	302/18723	0.376206793	0.410787418	0.291605266
GO:0072001	renal system	1/29	302/18723	0.376206793	0.410787418	0.291605266
GO:0015849	organic acid t	1/29	303/18723	0.377188825	0.411029354	0.291777009
GO:0060070	canonical Wn	1/29	303/18723	0.377188825	0.411029354	0.291777009
GO:0045229	external enca	1/29	304/18723	0.378169364	0.411682862	0.292240914
GO:0009914	hormone trar	1/29	306/18723	0.380125972	0.413396555	0.293457411
GO:0032409	regulation of	1/29	310/18723	0.38402137	0.416794278	0.29586935
GO:0051047	positive regul	1/29	310/18723	0.38402137	0.416794278	0.29586935
GO:0070588	calcium ion tr	1/29	312/18723	0.385960196	0.418478407	0.297064861

GO:0045787	positive regul	1/29	313/18723	0.386927398	0.41910673	0.297510888
GO:0046394	carboxylic aci	1/29	314/18723	0.387893129	0.419312472	0.297656938
GO:0060249	anatomical st	1/29	314/18723	0.387893129	0.419312472	0.297656938
GO:0002768	immune resp	1/29	315/18723	0.388857391	0.419934904	0.298098783
GO:0016053	organic acid k	1/29	316/18723	0.389820186	0.420135215	0.298240978
GO:0043414	macromolecu	1/29	316/18723	0.389820186	0.420135215	0.298240978
GO:0051235	maintenance	1/29	327/18723	0.400314744	0.431016173	0.305965033
GO:0003002	regionalizatio	1/29	331/18723	0.404087565	0.434645431	0.30854133
GO:0001655	urogenital sys	1/29	338/18723	0.410634925	0.440932908	0.313004615
GO:0002697	regulation of	1/29	339/18723	0.411564574	0.440932908	0.313004615
GO:0007568	aging	1/29	339/18723	0.411564574	0.440932908	0.313004615
GO:0048545	response to s	1/29	339/18723	0.411564574	0.440932908	0.313004615
GO:0032496	response to li	1/29	343/18723	0.415269029	0.444461208	0.315509247
GO:0007059	chromosome	1/29	346/18723	0.418032584	0.446976482	0.317294761
GO:0006936	muscle contr	1/29	347/18723	0.418950963	0.447515801	0.317677608
GO:0010639	negative regu	1/29	348/18723	0.419867943	0.448052563	0.318058638
GO:0002449	lymphocyte n	1/29	350/18723	0.421697713	0.449118451	0.318815279
GO:0042742	defense resp	1/29	350/18723	0.421697713	0.449118451	0.318815279
GO:0006887	exocytosis	1/29	352/18723	0.42352191	0.450617307	0.319879271
GO:0015711	organic anion	1/29	354/18723	0.42534055	0.452107311	0.320936978
GO:0007178	transmembra	1/29	355/18723	0.426247792	0.452626585	0.321305594
GO:0010631	epithelial cell	1/29	357/18723	0.428058129	0.453657683	0.32203754
GO:1904062	regulation of	1/29	357/18723	0.428058129	0.453657683	0.32203754
GO:0009306	protein secre	1/29	359/18723	0.42986295	0.454678912	0.322762478
GO:0051052	regulation of	1/29	359/18723	0.42986295	0.454678912	0.322762478
GO:0035592	establishmen	1/29	360/18723	0.430763297	0.454741332	0.322806788
GO:0090132	epithelium m	1/29	360/18723	0.430763297	0.454741332	0.322806788
GO:0002237	response to n	1/29	363/18723	0.433456109	0.457137613	0.324507834
GO:0032259	methylation	1/29	364/18723	0.434350977	0.457634899	0.324860841
GO:0090130	tissue migrati	1/29	365/18723	0.43524448	0.458129779	0.325212141
GO:0140694	non-membra	1/29	367/18723	0.437027399	0.459558968	0.326226678
GO:0009150	purine ribonu	1/29	368/18723	0.43791682	0.45960008	0.326255863
GO:0071692	protein locali	1/29	368/18723	0.43791682	0.45960008	0.326255863
GO:0050900	leukocyte mi	1/29	369/18723	0.438804884	0.460085431	0.326600399
GO:0002253	activation of	1/29	375/18723	0.444104886	0.465191262	0.330224869
GO:0050878	regulation of	1/29	379/18723	0.447611337	0.468410315	0.332509976
GO:0006644	phospholipid	1/29	383/18723	0.451096428	0.47023085	0.333802317
GO:0032535	regulation of	1/29	383/18723	0.451096428	0.47023085	0.333802317
GO:1902903	regulation of	1/29	383/18723	0.451096428	0.47023085	0.333802317
GO:0014706	striated musc	1/29	384/18723	0.451964378	0.47023085	0.333802317
GO:0022412	cellular proce	1/29	384/18723	0.451964378	0.47023085	0.333802317
GO:0042692	muscle cell di	1/29	384/18723	0.451964378	0.47023085	0.333802317
GO:0009259	ribonucleotid	1/29	385/18723	0.452831003	0.47023085	0.333802317
GO:0045786	negative regu	1/29	385/18723	0.452831003	0.47023085	0.333802317
GO:0045860	positive regul	1/29	386/18723	0.453696305	0.47067726	0.33411921
GO:0006163	purine nuclec	1/29	396/18723	0.46227697	0.478660349	0.339786158
GO:0019693	ribose phospl	1/29	396/18723	0.46227697	0.478660349	0.339786158
GO:0006869	lipid transpor	1/29	398/18723	0.463977418	0.479961329	0.340709683
GO:0060537	muscle tissue	1/29	403/18723	0.468205854	0.483872398	0.34348603
GO:0010959	regulation of	1/29	406/18723	0.470727438	0.486013716	0.345006085

GO:0034655	nucleobase-c	1/29	407/18723	0.471565397	0.486414308	0.345290453
GO:0006325	chromatin org	1/29	409/18723	0.473237475	0.487673699	0.346184456
GO:0072521	purine-contai	1/29	416/18723	0.479049614	0.493192983	0.350102424
GO:0016311	dephosphory	1/29	417/18723	0.479874848	0.493572512	0.35037184
GO:0007409	axonogenesis	1/29	418/18723	0.48069882	0.493950023	0.350639824
GO:0006816	calcium ion tr	1/29	422/18723	0.483982122	0.496851542	0.352699522
GO:0031331	positive regul	1/29	427/18723	0.488058072	0.500560509	0.355332403
GO:0042391	regulation of	1/29	434/18723	0.493712217	0.505879532	0.359108212
GO:0007389	pattern speci	1/29	436/18723	0.495316581	0.507042825	0.359933998
GO:0000280	nuclear divisi	1/29	439/18723	0.497713926	0.508386748	0.360888008
GO:0050804	modulation o	1/29	439/18723	0.497713926	0.508386748	0.360888008
GO:0002443	leukocyte me	1/29	440/18723	0.498510595	0.508386748	0.360888008
GO:0099177	regulation of	1/29	440/18723	0.498510595	0.508386748	0.360888008
GO:0046700	heterocycle c	1/29	445/18723	0.502475675	0.511947412	0.363415613
GO:0010876	lipid localizati	1/29	448/18723	0.504840175	0.513388739	0.364438766
GO:0022407	regulation of	1/29	448/18723	0.504840175	0.513388739	0.364438766
GO:0044270	cellular nitro	1/29	451/18723	0.507193824	0.515297485	0.365793725
GO:0007608	sensory perce	1/29	456/18723	0.511092588	0.518770974	0.368259448
GO:0007346	regulation of	1/29	457/18723	0.511868758	0.519071415	0.368472721
GO:0023061	signal release	1/29	463/18723	0.51650086	0.523277816	0.371458715
GO:0019439	aromatic corr	1/29	467/18723	0.519565319	0.524906644	0.37261497
GO:0033674	positive regul	1/29	467/18723	0.519565319	0.524906644	0.37261497
GO:0061564	axon develop	1/29	467/18723	0.519565319	0.524906644	0.37261497
GO:0002764	immune resp	1/29	468/18723	0.520328498	0.525186841	0.372813873
GO:0051051	negative regu	1/29	470/18723	0.521851347	0.526232562	0.373556198
GO:0019221	cytokine-mec	1/29	472/18723	0.523369528	0.527271631	0.374293801
GO:0031667	response to n	1/29	474/18723	0.524883054	0.528304079	0.375026704
GO:0048285	organelle fiss	1/29	488/18723	0.535348554	0.538336546	0.382148442
GO:0009117	nucleotide m	1/29	489/18723	0.536087512	0.538578625	0.382320286
GO:0006091	generation of	1/29	490/18723	0.536825335	0.538819115	0.382491002
GO:0034765	regulation of	1/29	491/18723	0.537562025	0.539058023	0.382660596
GO:0009896	positive regul	1/29	492/18723	0.538297583	0.539295354	0.38282907
GO:1901361	organic cyclic	1/29	495/18723	0.540497487	0.540997948	0.384037688
GO:0006753	nucleoside ph	1/29	497/18723	0.541958463	0.541958463	0.384719528

## Supplementary table 2

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue
GO:0002052	positive regul	2/29	23/18723	0.000574358	0.128113766	0.090943995
GO:0019730	antimicrobial	3月29日	122/18723	0.000871494	0.128113766	0.090943995
GO:1902692	regulation of	2/29	33/18723	0.001187209	0.128113766	0.090943995
GO:0060428	lung epitheliu	2/29	37/18723	0.001491766	0.128113766	0.090943995
GO:0002920	regulation of	2/29	45/18723	0.002200544	0.128113766	0.090943995
GO:2000179	positive regul	2/29	54/18723	0.003153471	0.128113766	0.090943995
GO:0042220	response to c	2/29	55/18723	0.003269337	0.128113766	0.090943995
GO:0051898	negative regu	2/29	55/18723	0.003269337	0.128113766	0.090943995
GO:0007405	neuroblast pr	2/29	58/18723	0.00362876	0.128113766	0.090943995
GO:0034329	cell junction	4月29日	420/18723	0.003802407	0.128113766	0.090943995
GO:0006500	N-terminal pr	1月29日	3/18723	0.004639745	0.128113766	0.090943995
GO:0021769	orbitofrontal	1月29日	3/18723	0.004639745	0.128113766	0.090943995

geneID	Count
DRD2/DCT	2
CXCL13/CXCL	3
DRD2/DCT	2
WNT7B/GAT4	2
CXCL13/GAT4	2
DRD2/DCT	2
DRD2/DNMT3A	2
DRD2/CRYBA	2
DRD2/DCT	2
MPP7/ARHGAP25	4
HHAT	1
DRD2	1
NEK2	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
WNT7B	1
WNT7B	1
DRD2	1
DRD2	1
SCD	1
MPP7/CLDN7	2
CYP2U1/GAT4	4
KLRD1/DRD2	2
MPP7/CLDN7	2
WNT7B	1
DRD2	1
GATA6	1
WNT7B	1
DNMT3A	1
DRD2	1
GATA6	1
CXCL13	1
MPP7/CLDN7	2
CXCL13/CXCL	2
MPP7/CLDN7	2
WNT7B/CRYE	2
ALDOB	1
DCT	1
DCT	1
DRD2	1
DRD2	1
GATA6	1
CXCL13	1
DRD2/DCT	2
FGF5/DRD2	2

DRD2	1
DRD2	1
DRD2	1
DNMT3A	1
GATA6	1
CXCL13	1
GATA6	1
WNT7B	1
ALDOB	1
MPP7	1
DRD2/DCT	2
ARHGEF7/DR	3
GATA6	1
HHAT	1
DCT	1
DRD2	1
WNT7B	1
WNT7B	1
GATA6	1
GATA6	1
DRD2	1
CRYBA1	1
ARHGEF7	1
CXCL13	1
GATA6/DRD2	3
WNT7B/GAT/	2
KLRD1/DRD2	2
GATA6	1
WNT7B	1
CXCL13	1
DNMT3A	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1
DRD2	1
DRD2	1
PLEKHM1	1
ALDOB	1
GATA6	1
DNMT3A	1
DRD2	1
DRD2/DCT	2
CXCL13/CXCL	3
CXCL13/FGF5	2
GATA6/DRD2	3
WNT7B/DRD:	3
DRD2/DNMT:	2
KLRD1/GATA/	3
CYP2U1/SCD	2



DRD2	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1
GATA6	1
NEK2	1
GATA6	1
DRD2	1
DRD2	1
GATA6	1
WNT7B	1
CYP2U1	1
PLEKHM1	1
CXCL13/FGF5	2
KLRD1	1
ARHGEF7	1
ALDOB	1
CXCL13	1
GATA6	1
DRD2	1
DRD2	1
WNT7B	1
GATA6	1
GATA6	1
WNT7B	1
GATA6	1
CXCL13	1
GATA6/DRD2	3
GATA6/DRD2	2
GATA6	1
DRD2	1
DRD2	1
DRD2	1
WNT7B	1
CXCL13	1
CXCL13	1
DRD2	1
CXCL13	1
DRD2	1
WNT7B	1
WNT7B	1
CXCL13	1
ARHGEF7	1
DRD2	1
DRD2	1
WNT7B	1
GATA6	1
DRD2	1
DRD2	1

DRD2	1
DRD2	1
SNX25	1
GATA6	1
WNT7B/NEK2	3
DRD2/DNMT:	2
WNT7B/DRD:	3
WNT7B/DRD:	3
ALDOB	1
DRD2	1
GATA6	1
GATA6	1
DRD2	1
NEK2	1
TNRC6C	1
DRD2	1
WNT7B/DRD:	3
WNT7B/DRD:	3
PLAC1/WNT7	2
DRD2/DCT	2
MPP7/CLDN7	2
GATA6	1
CXCL13	1
NEK2	1
DRD2	1
NEK2	1
ARHGEF7	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
DCT	1
WNT7B	1
GATA6/DNM	2
DCT	1
ARHGEF7	1
CXCL13	1
DRD2	1
DRD2	1
NEK2	1
TNRC6C	1
ALDOB	1
WNT7B	1
DRD2	1
PLEKHM1	1
TNRC6C	1
ARHGEF7	1
DNMT3A	1
CXCL13	1
CXCL13	1

DNMT3A	1
DNMT3A	1
GATA6/DNM	2
DRD2	1
DRD2	1
DRD2	1
COL13A1	1
CXCL13	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1
ARHGEF7	1
DRD2	1
NEK2	1
CXCL13/KLRD	3
SNX25/DRD2	2
PLAC1/WNT7	3
KLRD1	1
CXCL13	1
DNMT3A	1
DRD2	1
KLRD1	1
WNT7B	1
WNT7B	1
DRD2	1
TNRC6C	1
KLRD1	1
KLRD1	1
PLAC1/WNT7	3
MPP7/CXCL1	3
KLRD1	1
GATA6	1
CRYBA1	1
PLEKHM1	1
CXCL13	1
GATA6	1
WNT7B/GAT/	3
SCD/DRD2	2
GATA6/DRD2	2
WNT7B/GAT/	2
FGF5/DRD2	2
GATA6/DNM	2
DNMT3A	1
DRD2	1
DNMT3A	1
DRD2	1
WNT7B/GAT/	2
FGF5	1
CXCL13	1

DRD2	1
DRD2	1
WNT7B	1
WNT7B	1
MPP7	1
GATA6	1
GATA6	1
DRD2/DNMT3	3
DRD2/CRYBA	2
DRD2	1
KLRD1	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
WNT7B	1
KLRD1	1
CLDN7	1
DRD2	1
WNT7B	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
DCT	1
DRD2	1
GATA6	1
GATA6	1
DNMT3A	1
GATA6	1
DRD2	1
KLRD1/DRD2	2
KLRD1	1
GATA6	1
DCT	1
DNMT3A	1
DRD2	1
DRD2	1
GATA6	1
CRYBA1	1
CXCL13	1
DRD2/COL13	2
DRD2	1
DRD2	1
DCT	1
CXCL13	1
DCT	1
GATA6	1
WNT7B	1

CXCL13	1
MPP7/CLDN7	2
WNT7B/GAT4	2
DRD2	1
DRD2	1
KLRD1	1
DRD2	1
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WNT7B	1
DRD2	1
NEK2	1
COL13A1	1
DRD2	1
ALDOB	1
GATA6	1
COL13A1	1
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DRD2	1
DRD2/CRYBA	2
CXCL13	1
KLRD1	1
SNX25	1
DRD2	1
TNRC6C	1
GATA6	1
ALDOB	1
DRD2	1
CXCL13	1
MPP7/WNT7	2
KLRD1/DRD2	2
GATA6	1
DCT	1
GATA6	1
GATA6	1
ALDOB	1
HHAT	1
CENPI	1
KLRD1	1
DRD2	1
GATA6	1
GATA6	1
PLEKHM1	1
DRD2	1
DRD2/DCT	2
WNT7B	1
DRD2	1
DRD2	1
CXCL13	1
GATA6	1

DRD2	1
DRD2	1
DRD2	1
HHAT	1
DRD2	1
ARHGEF7/CO	2
DRD2	1
DRD2	1
NEK2	1
CRYBA1	1
DRD2	1
DRD2	1
NEK2	1
MPP7/CXCL1:	2
ARHGEF7	1
NEK2	1
DRD2	1
DRD2	1
GATA6	1
CXCL13	1
ARHGEF7	1
DRD2	1
DRD2	1
WNT7B	1
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CYP2U1	1
DRD2	1
ARHGEF7	1
NEK2	1
GATA6	1
DRD2	1
DRD2/DNMT:	2
KLRD1	1
NEK2	1
DNMT3A	1
DRD2	1
CXCL13/ARHC	2
ARHGEF7	1
DRD2	1
KLRD1/DRD2	2
WNT7B/GAT/	2
GATA6/DRD2	2
GATA6	1
GATA6	1
GATA6	1
ARHGEF7	1
DRD2	1
DRD2/DNMT:	2
DRD2	1
DRD2	1

CXCL13	1
DRD2	1
GATA6	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1
DRD2	1
DRD2	1
DRD2	1
CRYBA1	1
KLRD1	1
PLEKHM1	1
DCT	1
WNT7B	1
PLEKHM1	1
DRD2/DCT	2
DRD2	1
GATA6	1
DCT	1
GATA6	1
GATA6/CENP	2
GATA6	1
DRD2	1
ALDOB	1
GATA6	1
DNMT3A	1
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DRD2	1
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DRD2	1
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WNT7B	1
SCD	1
DCT	1
PLEKHM1	1
ARHGEF7	1
DRD2	1
GATA6	1

KLRD1	1
NEK2	1
NEK2	1
DRD2	1
KLRD1	1
DRD2	1
NEK2	1
DRD2	1
DRD2	1
SNX25/CXCL1	2
GATA6	1
KLRD1	1
DRD2	1
DRD2	1
GATA6	1
COL13A1	1
ARHGEF7	1
DRD2	1
GATA6	1
ARHGEF7	1
LARP4/ARHG	2
DRD2/CRYBA	2
CXCL13/CXCL	2
TNRC6C	1
KLRD1	1
DRD2	1
DRD2	1
PLEKHM1	1
GATA6	1
DRD2	1
DRD2	1
ARHGEF7	1
DRD2	1
DRD2	1
GATA6	1
CXCL13/DRD:	2
DRD2/DCT	2
KLRD1	1
CYP2U1	1
DRD2	1
DRD2	1
GATA6	1
GATA6/DCT	2
DCT	1
COL13A1	1
DRD2	1
NEK2	1
CXCL13	1
DRD2	1
DCT	1



SNX25	1
GATA6/DRD2	2
DRD2/CRYBA	2
KLRD1	1
KLRD1	1
DRD2	1
CXCL13	1
SCD	1
DRD2	1
PLEKHM1	1
GATA6	1
SNX25	1
CXCL13	1
NEK2	1
CXCL13	1
WNT7B	1
CXCL13	1
NEK2	1
SNX25/DRD2	2
CXCL13/GATA6	2
WNT7B	1
CXCL13/DRD2	2
DRD2	1
KLRD1	1
DRD2	1
GATA6	1
CXCL13/ARHGGEF7	2
CXCL13/GATA6	2
NEK2	1
WNT7B	1
DRD2	1
DRD2	1
PLEKHM1/ARHGGEF7	2
CXCL13/DRD2	2
KLRD1	1
DRD2	1
DRD2	1
DNMT3A	1
CXCL13/KLRD1	2
GATA6/CRYBA	2
ARHGGEF7	1
CXCL13	1
DRD2	1
GATA6	1
CXCL13/DRD2	2
GATA6	1
DRD2	1
WNT7B	1
ARHGGEF7/CRYBA	2
ARHGGEF7/NEK2	2

GATA6	1
DRD2/DCT	2
NEK2	1
GATA6	1
CXCL13/DRD:	2
DNMT3A	1
DNMT3A	1
GATA6	1
DRD2	1
GATA6	1
GATA6	1
PLEKHM1	1
DRD2/DNMT:	2
DRD2	1
DRD2	1
CRYBA1	1
ARHGEF7	1
GATA6	1
WNT7B	1
NEK2	1
ARHGEF7	1
DNMT3A	1
ALDOB	1
NEK2	1
DRD2	1
SNX25	1
WNT7B	1
SNX25/DRD2	2
WNT7B	1
KLRD1	1
ALDOB	1
FGF5	1
NEK2	1
ARHGEF7	1
DRD2	1
CYP2U1/SCD	2
CXCL13/DRD:	2
DRD2	1
DRD2	1
DCT	1
TNRC6C	1
WNT7B	1
KLRD1	1
GATA6	1
DRD2	1
DRD2	1
PLEKHM1	1
DRD2	1
ARHGEF7	1
TNRC6C	1

ARHGEF7	1
TNRC6C	1
CXCL13	1
WNT7B	1
DRD2	1
TNRC6C	1
DRD2	1
TNRC6C	1
ALDOB	1
PLEKHM1	1
ARHGEF7	1
WNT7B/COL1	2
GATA6	1
TNRC6C	1
DRD2	1
WNT7B	1
HHAT	1
DRD2	1
DRD2	1
DRD2	1
DNMT3A	1
COL13A1	1
WNT7B	1
DNMT3A	1
DRD2	1
DRD2	1
CXCL13	1
WNT7B	1
MPP7	1
ARHGEF7	1
DRD2	1
ARHGEF7	1
HHAT	1
GATA6	1
CXCL13	1
SCD	1
CXCL13	1
CXCL13	1
WNT7B/DRD:	2
CXCL13/KLRD	2
WNT7B/COL1	2
GATA6	1
ALDOB	1
DRD2	1
DRD2	1
KLRD1	1
DRD2	1
DNMT3A	1
DRD2	1
DRD2	1

DRD2	1
KLRD1/DRD2	2
DRD2	1
ALDOB	1
ARHGEF7	1
CXCL13/ARHGEF7	2
GATA6	1
DRD2	1
DRD2	1
GATA6	1
ALDOB	1
ALDOB	1
CXCL13	1
DRD2	1
SNX25/DRD2	2
SNX25/DRD2	2
DRD2	1
GATA6	1
CRYBA1	1
GATA6	1
DRD2/DCT	2
WNT7B/DRD2	2
DRD2	1
DNMT3A	1
PLEKHM1	1
WNT7B/DRD2	2
NEK2	1
DRD2	1
ALDOB	1
PLEKHM1	1
ALDOB	1
GATA6	1
DRD2	1
NEK2	1
CXCL13/DRD2	2
DRD2	1
DRD2	1
DRD2	1
GATA6/DRD2	2
ARHGEF7	1
KLRD1	1
DRD2	1
DRD2	1
DRD2	1
WNT7B	1
KLRD1	1
DRD2	1
DRD2	1
NEK2	1
DRD2	1

PLEKHM1	1
CYP2U1	1
CRYBA1	1
DRD2	1
DRD2	1
DRD2	1
CXCL13	1
CXCL13/DRD2	2
TNRC6C	1
CYP2U1	1
CXCL13	1
KLRD1	1
DRD2	1
DRD2	1
PLEKHM1	1
GATA6/DRD2	2
LARP4/TNRC6C	2
DRD2	1
CXCL13	1
CXCL13	1
DNMT3A	1
DRD2	1
NEK2	1
CXCL13	1
CXCL13/ARHGGEF7	2
DRD2	1
DRD2	1
NEK2	1
DRD2	1
TNRC6C	1
WNT7B/DRD2	2
DNMT3A	1
NEK2	1
GATA6	1
GATA6	1
DRD2	1
GATA6	1
DNMT3A	1
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ARHGGEF7	1
DRD2	1
CXCL13	1
CXCL13/DRD2	2
CYP2U1	1
ARHGGEF7	1
KLRD1	1
ALDOB	1
GATA6	1
CXCL13	1
CRYBA1	1

WNT7B	1
GATA6	1
DRD2	1
SNX25	1
DRD2	1
WNT7B	1
NEK2	1
DRD2	1
NEK2	1
KLRD1	1
SNX25	1
SNX25	1
DRD2	1
DRD2	1
WNT7B	1
WNT7B	1
DRD2	1
KLRD1	1
DRD2	1
DRD2	1
DNMT3A	1
CXCL13	1
HHAT	1
LARP4	1
WNT7B	1
DRD2	1
WNT7B	1
GATA6	1
DRD2	1
HHAT	1
NEK2	1
GATA6	1
ARHGEF7	1
DNMT3A	1
PLEKHM1	1
CXCL13	1
GATA6	1
WNT7B	1
DRD2	1
MPP7	1
NEK2	1
DRD2	1
DRD2	1
CRYBA1	1
SCD	1
SCD	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1

WNT7B	1
NEK2	1
DRD2	1
DNMT3A	1
DRD2	1
WNT7B	1
ARHGEF7	1
CXCL13	1
GATA6	1
DRD2	1
CYP2U1	1
ALDOB	1
DRD2	1
GATA6	1
ARHGEF7	1
PLEKHM1	1
SCD	1
TNRC6C	1
NEK2	1
DRD2	1
DRD2	1
DRD2	1
GATA6	1
DRD2	1
LARP4	1
NEK2	1
SCD	1
ARHGEF7	1
PLEKHM1	1
DRD2	1
GATA6	1
DRD2	1
GATA6	1
GATA6	1
TNRC6C	1
WNT7B	1
WNT7B	1
ARHGEF7	1
NEK2	1
KLRD1	1
KLRD1	1
KLRD1	1
TNRC6C	1
DRD2	1
DRD2	1
DNMT3A	1
PLEKHM1	1
CYP2U1	1
GATA6	1
CRYBA1	1

DRD2	1
DRD2	1
CRYBA1	1
NEK2	1
GATA6	1
DRD2	1
GATA6	1
CRYBA1	1
DRD2	1
KLRD1	1
NEK2	1
DRD2	1
GATA6	1
DRD2	1
PLEKHM1	1
NEK2	1
KLRD1	1
PLEKHM1	1
WNT7B	1
WNT7B	1
DRD2	1
WNT7B	1
DCT	1
CXCL13	1
DRD2	1
SNX25	1
DRD2	1
DRD2	1
DRD2	1
NEK2	1
CENPI	1
NEK2	1
GATA6	1
DRD2	1
DRD2	1
COL13A1	1
DRD2	1
GATA6	1
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CXCL13	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1
SCD	1
CRYBA1	1
DRD2	1
DRD2	1



DRD2	1
CRYBA1	1
WNT7B	1
COL13A1	1
CXCL13	1
GATA6	1
ARHGEF7	1
CXCL13	1
CXCL13	1
FGF5	1
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GATA6	1
NEK2	1
DRD2	1
WNT7B	1
CXCL13	1
DRD2	1
TNRC6C	1
CXCL13	1
DRD2	1
ARHGEF7	1
WNT7B	1
KLRD1	1
DRD2	1
GATA6	1
DRD2	1
ALDOB	1
DCT	1
WNT7B	1
ARHGEF7	1
DRD2	1
DRD2	1
CENPI	1
DRD2	1
HHAT	1
DRD2	1
DRD2	1
TNRC6C	1
GATA6	1
CXCL13	1
WNT7B	1
DRD2	1
GATA6	1
DRD2	1
SNX25	1
DRD2	1
WNT7B	1
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DRD2	1
SNX25	1

SNX25	1
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NEK2	1
GATA6	1
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DRD2	1
PLEKHM1	1
DRD2	1
TNRC6C	1
DRD2	1
CLDN7	1
DRD2	1
ALDOB	1
TNRC6C	1
DRD2	1
KLRD1	1
CXCL13	1
DRD2	1
NEK2	1
DRD2	1
GATA6	1
DCT	1
DRD2	1
CXCL13	1
NEK2	1
TNRC6C	1
KLRD1	1
KLRD1	1
PLEKHM1	1
CXCL13	1
WNT7B	1
NEK2	1
DRD2	1
DRD2	1
ARHGEF7	1
DRD2	1
PLEKHM1	1
COL13A1	1
FGF5	1
DRD2	1
COL13A1	1
WNT7B	1
DRD2	1
WNT7B	1
COL13A1	1
DRD2	1
DRD2	1
DRD2	1
DRD2	1

DRD2	1
SCD	1
PLEKHM1	1
KLRD1	1
SCD	1
DNMT3A	1
DRD2	1
WNT7B	1
WNT7B	1
KLRD1	1
DNMT3A	1
WNT7B	1
CXCL13	1
NEK2	1
DRD2	1
ARHGEF7	1
KLRD1	1
CXCL13	1
DRD2	1
DRD2	1
SNX25	1
CXCL13	1
DRD2	1
DRD2	1
NEK2	1
DRD2	1
CXCL13	1
CXCL13	1
DNMT3A	1
CXCL13	1
NEK2	1
ALDOB	1
DRD2	1
CXCL13	1
KLRD1	1
DRD2	1
GATA6	1
WNT7B	1
ARHGEF7	1
GATA6	1
DNMT3A	1
GATA6	1
ALDOB	1
NEK2	1
DRD2	1
ALDOB	1
ALDOB	1
DRD2	1
GATA6	1
DRD2	1

TNRC6C	1
DNMT3A	1
ALDOB	1
DRD2	1
DRD2	1
DRD2	1
TNRC6C	1
DRD2	1
WNT7B	1
NEK2	1
DRD2	1
KLRD1	1
DRD2	1
TNRC6C	1
DRD2	1
CXCL13	1
TNRC6C	1
DRD2	1
NEK2	1
DRD2	1
TNRC6C	1
DRD2	1
DRD2	1
KLRD1	1
DRD2	1
CXCL13	1
DNMT3A	1
NEK2	1
ALDOB	1
ALDOB	1
DRD2	1
TNRC6C	1
TNRC6C	1
ALDOB	1

geneID	Count
DRD2/DCT	2
CXCL13/CXCL	3
DRD2/DCT	2
WNT7B/GAT#	2
CXCL13/GAT#	2
DRD2/DCT	2
DRD2/DNMT:	2
DRD2/CRYBA	2
DRD2/DCT	2
MPP7/ARHG#	4
HHAT	1
DRD2	1