Table 5. Functional analysis of gene lists using Gene Ontology (GO) terms.

255 GO terms were analyzed for representational or directional bias in gene lists from Table 1 and PCA. Contingency tables were analyzed by Chi-squared test with Yates' continuity correction. For representational bias, genes were categorized as regulated (up or down) or not regulated. For directional bias, significant genes (only) were categorized as up or down regulated. For both analyses, genes on microarray were categorized as belonging to GO term ("term") or not belonging to GO term ("n.term"). Only microarray cDNAs assigned to official gene predictions (see Methods) were analyzed (cDNAs with EST identifier only were not assigned GO annotation and were not analyzed here). Significance levels were set to achieve similarly sized gene lists: pre-foraging maturation, hive bee-to-forager transition, and subspecies ($p < 0.001$); all treatment experiments ($p < 0.01$). For PCs, upper and lower 25% were analyzed (as "up-" and "down-regulated"); note that polarity of PCs is arbitrary. Significance of Chi-squared test is indicated by bold ($p < 0.05$) or bold/underlined ($p < 0.001$).

		Pre-foraging maturation (d1 → [d8, d12, d17])									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	924	657	830	578	0.808	495	376	429	281	0.165
0007610	behavior	81	1500	81	1327	0.498	**30**	**841**	**51**	**659**	**0.001**
0030534	adult behavior	**18**	**1563**	**6**	**1402**	**0.048**	**4**	**867**	**14**	**696**	**0.01**
0030537	larval behavior	3	1578	6	1402	0.399	0	871	3	707	0.18
0007611	learning and/or memory	14	1567	10	1398	0.741	**2**	**869**	**12**	**698**	**0.005**
0007612	learning	8	1573	7	1401	0.822	**1**	**870**	**7**	**703**	**0.038**
0007613	memory	6	1575	5	1403	0.847	2	869	4	706	0.508
0007626	locomotory behavior	61	1520	62	1346	0.511	**23**	**848**	**38**	**672**	**0.008**
0007635	chemosensory behavior	9	1572	9	1399	0.992	2	869	7	703	0.099
0007622	rhythmic behavior	8	1573	7	1401	0.822	4	867	4	706	0.947
0048512	circadian behavior	8	1573	6	1402	0.959	4	867	4	706	0.947
0009987	cellular process	853	728	775	633	0.575	459	412	394	316	0.29
0007154	cell communication	263	1318	226	1182	0.703	**107**	**764**	**156**	**554**	**4E-07**
0007155	cell adhesion	51	1530	39	1369	0.535	**17**	**854**	**34**	**676**	**0.002**
0008037	cell recognition	2	1579	0	1408	0.531	0	871	2	708	0.392
0008038	neuronal cell recognition	2	1579	0	1408	0.531	0	871	2	708	0.392
0016337	cell-cell adhesion	22	1559	17	1391	0.778	8	863	14	696	0.118
0016339	calcium-dependent cell-cell adhesion	2	1579	5	1403	0.362	1	870	1	709	0.571
0007156	homophilic cell adhesion	3	1578	6	1402	0.399	1	870	2	708	0.859
0007160	cell-matrix adhesion	6	1575	3	1405	0.621	2	869	4	706	0.508
0007267	cell-cell signaling	87	1494	69	1339	0.511	**30**	**841**	**57**	**653**	**1E-04**
0019226	transmission of nerve impulse	79	1502	59	1349	0.336	**27**	**844**	**52**	**658**	**2E-04**
0007268	synaptic transmission	59	1522	42	1366	0.303	**15**	**856**	**44**	**666**	**6E-06**
0007270	nerve-nerve synaptic transmission	10	1571	6	1402	0.603	**1**	**870**	**9**	**701**	**0.011**
0001505	regulation of neurotransmitter levels	35	1546	25	1383	0.47	**12**	**859**	**23**	**687**	**0.02**
0042133	neurotransmitter metabolism	7	1574	1	1407	0.108	3	868	4	706	0.786
0007269	neurotransmitter secretion	29	1552	24	1384	0.897	**10**	**861**	**19**	**691**	**0.039**
0007165	signal transduction	198	1383	181	1227	0.828	**83**	**788**	**115**	**595**	**9E-05**
0007166	cell surface receptor linked signal transduction	77	1504	80	1328	0.363	**33**	**838**	**44**	**666**	**0.036**
0007167	enzyme linked receptor protein signaling pathway	19	1562	27	1381	0.15	**5**	**866**	**14**	**696**	**0.021**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	7	1574	9	1399	0.629	**0**	**871**	**7**	**703**	**0.011**
0007179	transforming growth factor beta receptor signaling pathway	4	1577	5	1403	0.862	0	871	4	706	0.086
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	14	1567	18	1390	0.388	5	866	9	701	0.232
0007173	epidermal growth factor receptor signaling pathway	2	1579	6	1402	0.219	0	871	2	708	0.392
0008286	insulin receptor signaling pathway	2	1579	2	1406	0.7	0	871	2	708	0.392
0008293	torso signaling pathway	2	1579	5	1403	0.362	0	871	2	708	0.392
0007186	G-protein coupled receptor protein signaling pathway	41	1540	30	1378	0.478	17	854	24	686	0.106
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1578	2	1406	0.897	2	869	1	709	0.859
0007219	Notch signaling pathway	6	1575	7	1401	0.834	3	868	3	707	0.873
0007224	smoothened signaling pathway	4	1577	2	1406	0.789	2	869	2	708	0.766
0008063	Toll signaling pathway	1	1580	3	1405	0.537	1	870	0	710	0.918
0016055	Wnt receptor signaling pathway	9	1572	7	1401	0.985	5	866	4	706	0.758
0007242	intracellular signaling cascade	92	1489	90	1318	0.564	**41**	**830**	**51**	**659**	**0.047**
0007263	nitric oxide mediated signal transduction	2	1579	2	1406	0.7	0	871	2	708	0.392
0007243	protein kinase cascade	18	1563	23	1385	0.315	8	863	10	700	0.5
0007259	JAK-STAT cascade	3	1578	3	1405	0.789	3	868	0	710	0.325
0000165	MAPKKK cascade	15	1566	18	1390	0.493	5	866	10	700	0.149
0019932	second-messenger-mediated signaling	14	1567	8	1400	0.424	5	866	9	701	0.232
0019722	calcium-mediated signaling	10	1571	5	1403	0.417	3	868	7	703	0.2
0048015	phosphoinositide-mediated signaling	3	1578	2	1406	0.897	2	869	1	709	0.859
0007264	small GTPase mediated signal transduction	23	1558	21	1387	0.945	9	862	14	696	0.181
0007265	Ras protein signal transduction	5	1576	5	1403	0.894	1	870	4	706	0.259
0009966	regulation of signal transduction	18	1563	16	1392	0.867	10	861	8	702	0.843
0007275	development	246	1335	214	1194	0.824	**116**	**755**	**130**	**580**	**0.008**
0007568	aging	6	1575	5	1403	0.847	4	867	2	708	0.873
0030154	cell differentiation	59	1522	60	1348	0.519	25	846	34	676	0.062
0048468	cell development	40	1541	35	1373	0.968	16	855	24	686	0.075
0000904	cellular morphogenesis during differentiation	12	1569	7	1401	0.504	6	865	6	704	0.948
0042461	photoreceptor cell development	11	1570	7	1401	0.643	5	866	6	704	0.733
0042051	eye photoreceptor development (sensu Endopterygota)	11	1570	6	1402	0.462	5	866	6	704	0.733
0045165	cell fate commitment	22	1559	27	1381	0.324	10	861	12	698	0.484

		Pre-foraging maturation (d1 → [d8, d12, d17])									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	17	1564	13	1395	0.816	7	864	10	700	0.36
0007400	neuroblast cell fate determination	2	1579	6	1402	0.219	2	869	0	710	0.571
0001708	cell fate specification	3	1578	5	1403	0.604	1	870	2	708	0.859
0007349	cellularization	7	1574	4	1404	0.68	1	870	6	704	0.073
0040007	growth	18	1563	18	1390	0.856	8	863	10	700	0.5
0002164	larval development	12	1569	5	1403	0.222	6	865	6	704	0.948
0002165	larval or pupal development (sensu Insecta)	62	1519	67	1341	0.301	32	839	30	680	0.666
0007552	metamorphosis	56	1525	65	1343	0.163	29	842	27	683	0.712
0009653	morphogenesis	164	1417	155	1253	0.616	**72**	**799**	**92**	**618**	**0.003**
0002009	morphogenesis of an epithelium	19	1562	25	1383	0.251	**5**	**866**	**14**	**696**	**0.021**
0009887	organogenesis	143	1438	139	1269	0.478	**64**	**807**	**79**	**631**	**0.012**
0001654	eye morphogenesis	29	1552	28	1380	0.862	14	857	15	695	0.578
0008406	gonad development	6	1575	5	1403	0.847	5	866	1	709	0.326
0007444	imaginal disc development	41	1540	52	1356	0.105	21	850	20	690	0.729
0007494	midgut development	2	1579	3	1405	0.897	1	870	1	709	0.571
0007517	muscle development	20	1561	14	1394	0.6	7	864	13	697	0.111
0007399	neurogenesis	84	1497	78	1330	0.848	**33**	**838**	**51**	**659**	**0.004**
0007409	axonogenesis	18	1563	25	1383	0.192	**5**	**866**	**13**	**697**	**0.035**
0007411	axon guidance	13	1568	20	1388	0.165	5	866	8	702	0.352
0007417	central nervous system development	**14**	**1567**	**25**	**1383**	**0.048**	8	863	6	704	0.909
0016358	dendrite morphogenesis	6	1575	8	1400	0.627	1	870	5	705	0.138
0042063	gliogenesis	5	1576	6	1402	0.847	1	870	4	706	0.259
0007422	peripheral nervous system development	18	1563	22	1386	0.397	**5**	**866**	**13**	**697**	**0.035**
0050767	regulation of neurogenesis	3	1578	2	1406	0.897	2	869	1	709	0.859
0007424	tracheal system development (sensu Insecta)	17	1564	20	1388	0.493	5	866	12	698	0.058
0048513	organ development	145	1436	141	1267	0.472	**66**	**805**	**79**	**631**	**0.019**
0007389	pattern specification	32	1549	44	1364	0.073	12	859	20	690	0.066
0048066	pigmentation	9	1572	2	1406	0.105	5	866	4	706	0.758
0009791	post-embryonic development	12	1569	5	1403	0.222	6	865	6	704	0.948
0009790	embryonic development	51	1530	49	1359	0.776	24	847	27	683	0.303
0007530	sex determination	7	1574	3	1405	0.442	4	867	3	707	0.786
0007548	sex differentiation	13	1568	6	1402	0.259	9	862	4	706	0.454
0019827	stem cell maintenance	3	1578	5	1403	0.604	1	870	2	708	0.859
0000003	reproduction	75	1506	69	1339	0.909	**30**	**841**	**45**	**665**	**0.01**
0050793	regulation of development	22	1559	21	1387	0.94	9	862	13	697	0.258
0007582	physiological process	837	744	768	640	0.4	462	409	375	335	0.969
0008152	metabolism	605	976	561	847	0.398	**369**	**502**	**236**	**474**	**3E-04**
0009056	catabolism	**96**	**1485**	**113**	**1295**	**0.044**	52	819	44	666	0.935
0006091	energy pathways	60	1521	48	1360	0.641	**21**	**850**	**39**	**671**	**0.002**
0006118	electron transport	31	1550	24	1384	0.701	13	858	18	692	0.192
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	228	1353	204	1204	1	**157**	**714**	**71**	**639**	**9E-06**
0006259	DNA metabolism	37	1544	42	1366	0.328	**27**	**844**	**10**	**700**	**0.041**
0006350	transcription	118	1463	109	1299	0.828	**86**	**785**	**32**	**678**	**8E-05**
0043170	macromolecule metabolism	**303**	**1278**	**325**	**1083**	**0.01**	173	698	130	580	0.474
0019538	protein metabolism	**255**	**1326**	**272**	**1136**	**0.025**	147	724	108	602	0.408
0006412	protein biosynthesis	66	1515	44	1364	0.154	44	827	22	688	0.071
0006464	protein modification	**119**	**1462**	**137**	**1271**	**0.037**	73	798	46	664	0.183
0006457	protein folding	20	1561	23	1385	0.49	9	862	11	699	0.492
0005975	carbohydrate metabolism	54	1527	53	1355	0.679	27	844	27	683	0.531
0006519	amino acid and derivative metabolism	**47**	**1534**	**23**	**1385**	**0.022**	29	842	18	692	0.438
0006629	lipid metabolism	49	1532	40	1368	0.759	32	839	17	693	0.189
0009308	amine metabolism	**54**	**1527**	**27**	**1381**	**0.016**	31	840	23	687	0.835
0042440	pigment metabolism	7	1574	5	1403	0.929	5	866	2	708	0.624
0042445	hormone metabolism	4	1577	3	1405	0.878	3	868	1	709	0.766
0009058	biosynthesis	**127**	**1454**	**77**	**1331**	**0.007**	81	790	46	664	0.05
0019748	secondary metabolism	8	1573	6	1402	0.959	6	865	2	708	0.436
0019222	regulation of metabolism	119	1462	119	1289	0.387	**77**	**794**	**42**	**668**	**0.036**
0016265	death	45	1536	41	1367	0.998	27	844	18	692	0.603
0008219	cell death	39	1542	35	1373	0.933	23	848	16	694	0.741
0016271	tissue death	13	1568	14	1394	0.762	6	865	7	703	0.711
0042592	homeostasis	12	1569	17	1391	0.289	7	864	5	705	0.948
0019725	cell homeostasis	11	1570	15	1393	0.374	6	865	5	705	0.789
0050801	ion homeostasis	8	1573	6	1402	0.959	5	866	3	707	0.947
0043062	extracellular structure organization and biogenesis	10	1571	9	1399	0.836	3	868	7	703	0.2
0046903	secretion	51	1530	50	1358	0.697	**15**	**856**	**36**	**674**	**3E-04**
0048511	rhythmic process	8	1573	9	1399	0.811	4	867	4	706	0.947

		Pre-foraging maturation (d1 → [d8, d12, d17])									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	178	1403	169	1239	0.564	104	767	74	636	0.384
0050874	organismal physiological process	127	1454	105	1303	0.604	**54**	**817**	**73**	**637**	**0.004**
0050875	cellular physiological process	787	794	732	676	0.242	437	434	350	360	0.767
0006810	transport	225	1356	173	1235	0.132	**85**	**786**	**140**	**570**	**3E-08**
0006811	ion transport	**86**	**1495**	**34**	**1374**	**4E-05**	**24**	**847**	**62**	**648**	**3E-07**
0006818	hydrogen transport	13	1568	5	1403	0.158	**1**	**870**	**12**	**698**	**0.002**
0006836	neurotransmitter transport	3	1578	2	1406	0.897	0	871	3	707	0.18
0006858	extracellular transport	11	1570	4	1404	0.183	4	867	7	703	0.343
0006869	lipid transport	10	1571	6	1402	0.603	3	868	7	703	0.2
0008643	carbohydrate transport	11	1570	4	1404	0.183	7	864	4	706	0.789
0015031	protein transport	83	1498	97	1311	0.071	**31**	**840**	**52**	**658**	**0.001**
0015837	amine transport	9	1572	3	1405	0.212	4	867	5	705	0.758
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	7	1574	6	1402	0.834	5	866	2	708	0.624
0016192	vesicle-mediated transport	56	1525	63	1345	0.227	**15**	**856**	**41**	**669**	**3E-05**
0045045	secretory pathway	47	1534	48	1360	0.566	**14**	**857**	**33**	**677**	**7E-04**
0046907	intracellular transport	93	1488	105	1303	0.098	**35**	**836**	**58**	**652**	**7E-04**
0051049	regulation of transport	13	1568	5	1403	0.158	**1**	**870**	**12**	**698**	**0.002**
0008283	cell proliferation	40	1541	31	1377	0.64	21	850	19	691	0.863
0007049	cell cycle	70	1511	58	1350	0.745	37	834	33	677	0.794
0017145	stem cell division	5	1576	7	1401	0.623	3	868	2	708	0.819
0016043	cell organization and biogenesis	136	1445	139	1269	0.256	67	804	69	641	0.181
0000902	cellular morphogenesis	38	1543	42	1366	0.386	17	854	21	689	0.257
0006996	organelle organization and biogenesis	116	1465	122	1286	0.204	54	817	62	648	0.068
0007010	cytoskeleton organization and biogenesis	85	1496	85	1323	0.484	**34**	**837**	**51**	**659**	**0.006**
0006997	nuclear organization and biogenesis	3	1578	7	1401	0.256	0	871	3	707	0.18
0007028	cytoplasm organization and biogenesis	10	1571	9	1399	0.836	4	867	6	704	0.52
0016044	membrane organization and biogenesis	5	1576	4	1404	0.862	2	869	3	707	0.819
0051128	regulation of cell organization and biogenesis	6	1575	5	1403	0.847	4	867	2	708	0.873
0016049	cell growth	2	1579	7	1401	0.131	1	870	1	709	0.571
0050896	response to stimulus	88	1493	93	1315	0.266	50	821	38	672	0.822
0006950	response to stress	**19**	**1562**	**40**	**1368**	**0.002**	12	859	7	703	0.632
0009408	response to heat	**1**	**1580**	**9**	**1399**	**0.016**	1	870	0	710	0.918
0006979	response to oxidative stress	1	1580	1	1407	0.531	1	870	0	710	0.918
0051179	localization	243	1338	186	1222	0.103	**94**	**777**	**149**	**561**	**3E-08**
0006403	RNA localization	18	1563	14	1394	0.838	10	861	8	702	0.843
0008104	protein localization	94	1487	101	1307	0.2	**35**	**836**	**59**	**651**	**5E-04**
0051234	establishment of localization	228	1353	175	1233	0.124	**86**	**785**	**142**	**568**	**2E-08**
0051235	maintenance of localization	2	1579	2	1406	0.7	2	869	0	710	0.571
0050789	regulation of biological process	204	1377	199	1209	0.353	119	752	85	625	0.357
0050790	regulation of enzyme activity	6	1575	8	1400	0.627	4	867	2	708	0.873
0040029	regulation of gene expression, epigenetic	12	1569	8	1400	0.679	8	863	4	706	0.605
0006306	DNA methylation	5	1576	2	1406	0.546	4	867	1	709	0.502
0045814	negative regulation of gene expression, epigenetic	4	1577	3	1405	0.878	2	869	2	708	0.766
0006342	chromatin silencing	4	1577	3	1405	0.878	2	869	2	708	0.766
0003674	molecular_function	927	654	805	603	0.441	500	371	427	283	0.295
0016209	antioxidant activity	4	1577	5	1403	0.862	3	868	1	709	0.766
0005488	binding	527	1054	480	928	0.69	296	575	231	479	0.579
0005509	calcium ion binding	31	1550	30	1378	0.843	16	855	15	695	0.833
0030246	carbohydrate binding	11	1570	4	1404	0.183	3	868	8	702	0.119
0008289	lipid binding	17	1564	9	1399	0.278	12	859	5	705	0.295
0003676	nucleic acid binding	211	1370	178	1230	0.606	**145**	**726**	**66**	**644**	**3E-05**
0003677	DNA binding	104	1477	90	1318	0.895	**74**	**797**	**30**	**680**	**9E-04**
0003682	chromatin binding	13	1568	10	1398	0.888	11	860	2	708	0.062
0003700	transcription factor activity	48	1533	38	1370	0.659	29	842	19	691	0.545
0003723	RNA binding	70	1511	49	1359	0.219	**49**	**822**	**21**	**689**	**0.015**
0008135	translation factor activity, nucleic acid binding	19	1562	16	1392	0.996	12	859	7	703	0.632
0000166	nucleotide binding	136	1445	119	1289	0.935	75	796	61	649	0.939
0005515	protein binding	**180**	**1401**	**199**	**1209**	**0.028**	90	781	90	620	0.168
0008134	transcription factor binding	11	1570	20	1388	0.077	9	862	2	708	0.138
0008092	cytoskeletal protein binding	43	1538	45	1363	0.509	19	852	24	686	0.193
0003779	actin binding	29	1552	24	1384	0.897	14	857	15	695	0.578
0003824	catalytic activity	445	1136	394	1014	0.953	246	625	199	511	0.969
0016787	hydrolase activity	197	1384	175	1233	0.976	96	775	101	609	0.066
0003924	GTPase activity	24	1557	16	1392	0.455	9	862	15	695	0.124
0004518	nuclease activity	5	1576	10	1398	0.207	4	867	1	709	0.502

		Pre-foraging maturation (d1 → [d8, d12, d17])									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	**50**	**1531**	**68**	**1340**	**0.025**	26	845	24	686	0.763
0004721	phosphoprotein phosphatase activity	13	1568	17	1391	0.384	7	864	6	704	0.85
0016740	transferase activity	122	1459	119	1289	0.503	**80**	**791**	**42**	**668**	**0.02**
0016301	kinase activity	67	1514	68	1340	0.491	36	835	31	679	0.918
0004672	protein kinase activity	49	1532	46	1362	0.876	27	844	22	688	0.885
0030234	enzyme regulator activity	**43**	**1538**	**62**	**1346**	**0.017**	21	850	22	688	0.496
0003774	motor activity	14	1567	14	1394	0.906	4	867	10	700	0.083
0004871	signal transducer activity	145	1436	111	1297	0.234	**67**	**804**	**78**	**632**	**0.03**
0004872	receptor activity	60	1521	49	1359	0.718	**22**	**849**	**38**	**672**	**0.005**
0004879	ligand-dependent nuclear receptor activity	7	1574	2	1406	0.245	4	867	3	707	0.786
0004888	transmembrane receptor activity	38	1543	36	1372	0.88	**9**	**862**	**29**	**681**	**2E-04**
0004930	G-protein coupled receptor activity	16	1565	14	1394	0.892	**4**	**867**	**12**	**698**	**0.029**
0005057	receptor signaling protein activity	41	1540	39	1369	0.853	24	847	17	693	0.772
0005102	receptor binding	37	1544	32	1376	0.999	18	853	19	691	0.529
0005198	structural molecule activity	91	1490	71	1337	0.436	**39**	**832**	**52**	**658**	**0.021**
0030528	transcription regulator activity	98	1483	101	1307	0.32	**71**	**800**	**27**	**683**	**5E-04**
0045182	translation regulator activity	19	1562	16	1392	0.996	12	859	7	703	0.632
0005215	transporter activity	**157**	**1424**	**96**	**1312**	**0.003**	**58**	**813**	**99**	**611**	**2E-06**
0005489	electron transporter activity	18	1563	11	1397	0.419	7	864	11	699	0.249
0005216	ion channel activity	**36**	**1545**	**16**	**1392**	**0.025**	**10**	**861**	**26**	**684**	**0.002**
0005244	voltage-gated ion channel activity	18	1563	8	1400	0.139	**3**	**868**	**15**	**695**	**0.002**
0005575	cellular_component	650	931	573	835	0.846	**321**	**550**	**329**	**381**	**2E-04**
0005623	cell	587	994	525	883	0.959	**289**	**582**	**298**	**412**	**4E-04**
0005622	intracellular	436	1145	421	987	0.173	233	638	203	507	0.448
0005737	cytoplasm	230	1351	228	1180	0.232	**101**	**770**	**129**	**581**	**3E-04**
0016023	cytoplasmic vesicle	20	1561	21	1387	0.709	**6**	**865**	**14**	**696**	**0.041**
0005829	cytosol	**30**	**1551**	**49**	**1359**	**0.01**	13	858	17	693	0.262
0005783	endoplasmic reticulum	26	1555	31	1377	0.328	14	857	12	698	0.944
0005794	Golgi apparatus	9	1572	16	1392	0.134	3	868	6	704	0.327
0005815	microtubule organizing center	3	1578	6	1402	0.399	2	869	1	709	0.859
0005739	mitochondrion	60	1521	45	1363	0.43	**24**	**847**	**36**	**674**	**0.024**
0005840	ribosome	15	1566	9	1399	0.459	10	861	5	705	0.519
0005773	vacuole	8	1573	6	1402	0.959	**0**	**871**	**8**	**702**	**0.005**
0005764	lysosome	2	1579	3	1405	0.897	0	871	2	708	0.392
0005856	cytoskeleton	46	1535	39	1369	0.905	**16**	**855**	**30**	**680**	**0.008**
0005694	chromosome	22	1559	18	1390	0.913	15	856	7	703	0.304
0000228	nuclear chromosome	2	1579	3	1405	0.897	1	870	1	709	0.571
0005634	nucleus	184	1397	188	1220	0.173	**128**	**743**	**56**	**654**	**4E-05**
0005635	nuclear membrane	8	1573	9	1399	0.811	5	866	3	707	0.947
0005730	nucleolus	5	1576	6	1402	0.847	3	868	2	708	0.819
0005654	nucleoplasm	35	1546	37	1371	0.537	**26**	**845**	**9**	**701**	**0.033**
0005777	peroxisome	6	1575	3	1405	0.621	5	866	1	709	0.326
0005886	plasma membrane	89	1492	67	1341	0.324	**27**	**844**	**62**	**648**	**2E-06**
0005576	extracellular region	**53**	**1528**	**23**	**1385**	**0.004**	22	849	31	679	0.06
0005578	extracellular matrix (sensu Metazoa)	**26**	**1555**	**9**	**1399**	**0.017**	**7**	**864**	**19**	**691**	**0.007**

Hive bee-to-forager ([d8, d12, d17] ⟶ d17F)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	917	630	837	605	0.518	464	341	453	289	0.189
0007610	behavior	91	1456	71	1371	0.282	45	760	46	696	0.689
0030534	adult behavior	14	1533	10	1432	0.658	5	800	9	733	0.337
0030537	larval behavior	6	1541	3	1439	0.574	3	802	3	739	0.757
0007611	learning and/or memory	16	1531	8	1434	0.207	7	798	9	733	0.678
0007612	learning	10	1537	5	1437	0.368	4	801	6	736	0.655
0007613	memory	8	1539	3	1439	0.275	5	800	3	739	0.811
0007626	locomotory behavior	69	1478	54	1388	0.372	35	770	34	708	0.92
0007635	chemosensory behavior	11	1536	7	1435	0.575	5	800	6	736	0.892
0007622	rhythmic behavior	10	1537	5	1437	0.368	6	799	4	738	0.851
0048512	circadian behavior	10	1537	4	1438	0.227	6	799	4	738	0.851
0009987	cellular process	849	698	779	663	0.664	431	374	418	324	0.293
0007154	cell communication	271	1276	218	1224	0.085	144	661	127	615	0.74
0007155	cell adhesion	55	1492	35	1407	0.09	26	779	29	713	0.56
0008037	cell recognition	1	1546	1	1441	0.511	0	805	1	741	0.967
0008038	neuronal cell recognition	1	1546	1	1441	0.511	0	805	1	741	0.967
0016337	cell-cell adhesion	24	1523	15	1427	0.285	12	793	12	730	0.996
0016339	calcium-dependent cell-cell adhesion	4	1543	3	1439	0.926	3	802	1	741	0.675
0007156	homophilic cell adhesion	5	1542	4	1438	0.916	3	802	2	740	0.927
0007160	cell-matrix adhesion	4	1543	5	1437	0.916	1	804	3	739	0.56
0007267	cell-cell signaling	91	1456	65	1377	0.108	45	760	46	696	0.689
0019226	transmission of nerve impulse	80	1467	58	1384	0.159	38	767	42	700	0.472
0007268	synaptic transmission	57	1490	44	1398	0.392	29	776	28	714	0.965
0007270	nerve-nerve synaptic transmission	5	1542	11	1431	0.163	2	803	3	739	0.927
0001505	regulation of neurotransmitter levels	35	1512	25	1417	0.368	19	786	16	726	0.922
0042133	neurotransmitter metabolism	5	1542	3	1439	0.799	3	802	2	740	0.927
0007269	neurotransmitter secretion	30	1517	23	1419	0.566	16	789	14	728	0.967
0007165	signal transduction	208	1339	171	1271	0.212	118	687	90	652	0.167
0007166	cell surface receptor linked signal transduction	83	1464	74	1368	0.838	46	759	37	705	0.602
0007167	enzyme linked receptor protein signaling pathway	25	1522	21	1421	0.837	13	792	12	730	0.843
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	11	1536	5	1437	0.266	5	800	6	736	0.892
0007179	transforming growth factor beta receptor signaling pathway	6	1541	3	1439	0.574	4	801	2	740	0.757
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	15	1532	17	1425	0.706	8	797	7	735	0.874
0007173	epidermal growth factor receptor signaling pathway	4	1543	4	1438	0.799	3	802	1	741	0.675
0008286	insulin receptor signaling pathway	1	1546	3	1439	0.568	0	805	1	741	0.967
0008293	torso signaling pathway	3	1544	4	1438	0.926	3	802	0	742	0.277
0007186	G-protein coupled receptor protein signaling pathway	38	1509	33	1409	0.856	19	786	19	723	0.928
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1544	2	1440	0.937	1	804	2	740	0.944
0007219	Notch signaling pathway	8	1539	5	1437	0.668	5	800	3	739	0.811
0007224	smoothened signaling pathway	4	1543	2	1440	0.747	2	803	2	740	0.675
0008063	Toll signaling pathway	2	1545	2	1440	0.667	2	803	0	742	0.515
0016055	Wnt receptor signaling pathway	6	1541	10	1432	0.372	4	801	2	740	0.757
0007242	intracellular signaling cascade	**109**	**1438**	**73**	**1369**	**0.029**	62	743	47	695	0.342
0007263	nitric oxide mediated signal transduction	1	1546	3	1439	0.568	1	804	0	742	0.967
0007243	protein kinase cascade	21	1526	20	1422	0.93	12	793	9	733	0.801
0007259	JAK-STAT cascade	3	1544	3	1439	0.747	2	803	1	741	0.944
0000165	MAPKKK cascade	17	1530	16	1426	0.883	10	795	7	735	0.75
0019932	second-messenger-mediated signaling	13	1534	9	1433	0.633	5	800	8	734	0.481
0019722	calcium-mediated signaling	7	1540	8	1434	0.891	2	803	5	737	0.386
0048015	phosphoinositide-mediated signaling	3	1544	2	1440	0.937	1	804	2	740	0.944
0007264	small GTPase mediated signal transduction	22	1525	22	1420	0.934	11	794	11	731	0.982
0007265	Ras protein signal transduction	6	1541	4	1438	0.837	1	804	5	737	0.184
0009966	regulation of signal transduction	20	1527	14	1428	0.511	14	791	6	736	0.164
0007275	development	251	1296	209	1233	0.208	129	676	122	620	0.878
0007568	aging	6	1541	5	1437	0.907	4	801	2	740	0.757
0030154	cell differentiation	61	1486	58	1384	0.987	31	774	30	712	0.95
0048468	cell development	42	1505	33	1409	0.53	22	783	20	722	0.911
0000904	cellular morphogenesis during differentiation	11	1536	8	1434	0.759	9	796	2	740	0.093
0042461	photoreceptor cell development	10	1537	8	1434	0.931	8	797	2	740	0.145
0042051	eye photoreceptor development (sensu Endopterygota)	9	1538	8	1434	0.884	7	798	2	740	0.224
0045165	cell fate commitment	22	1525	27	1415	0.41	13	792	9	733	0.651

Hive bee-to-forager ([d8, d12, d17] ⟶ d17F)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	10	1537	20	1422	0.065	6	799	4	738	0.851
0007400	neuroblast cell fate determination	4	1543	4	1438	0.799	2	803	2	740	0.675
0001708	cell fate specification	2	1545	6	1436	0.245	2	803	0	742	0.515
0007349	cellularization	5	1542	6	1436	0.907	2	803	3	739	0.927
0040007	growth	21	1526	15	1427	0.531	12	793	9	733	0.801
0002164	larval development	10	1537	7	1435	0.733	7	798	3	739	0.41
0002165	larval or pupal development (sensu Insecta)	**83**	**1464**	**46**	**1396**	**0.005**	47	758	36	706	0.455
0007552	metamorphosis	**78**	**1469**	**43**	**1399**	**0.006**	45	760	33	709	0.363
0009653	morphogenesis	170	1377	149	1293	0.602	93	712	77	665	0.511
0002009	morphogenesis of an epithelium	23	1524	21	1421	0.934	13	792	10	732	0.823
0009887	organogenesis	151	1396	131	1311	0.569	82	723	69	673	0.616
0001654	eye morphogenesis	33	1514	24	1418	0.422	22	783	11	731	0.127
0008406	gonad development	5	1542	6	1436	0.907	3	802	2	740	0.927
0007444	imaginal disc development	51	1496	42	1400	0.618	31	774	20	722	0.259
0007494	midgut development	1	1546	4	1438	0.33	0	805	1	741	0.967
0007517	muscle development	15	1532	19	1423	0.469	8	797	7	735	0.874
0007399	neurogenesis	84	1463	78	1364	0.955	45	760	39	703	0.859
0007409	axonogenesis	21	1526	22	1420	0.816	10	795	11	731	0.851
0007411	axon guidance	16	1531	17	1425	0.839	9	796	7	735	0.93
0007417	central nervous system development	19	1528	20	1422	0.825	10	795	9	733	0.858
0016358	dendrite morphogenesis	4	1543	10	1432	0.141	1	804	3	739	0.56
0042063	gliogenesis	4	1543	7	1435	0.471	1	804	3	739	0.56
0007422	peripheral nervous system development	16	1531	24	1418	0.181	11	794	5	737	0.274
0050767	regulation of neurogenesis	1	1546	4	1438	0.33	0	805	1	741	0.967
0007424	tracheal system development (sensu Insecta)	17	1530	20	1422	0.585	11	794	6	736	0.419
0048513	organ development	154	1393	132	1310	0.496	84	721	70	672	0.567
0007389	pattern specification	33	1514	43	1399	0.175	18	787	15	727	0.908
0048066	pigmentation	6	1541	5	1437	0.907	5	800	1	741	0.259
0009791	post-embryonic development	10	1537	7	1435	0.733	7	798	3	739	0.41
0009790	embryonic development	49	1498	51	1391	0.646	32	773	17	725	0.081
0007530	sex determination	5	1542	5	1437	0.837	2	803	3	739	0.927
0007548	sex differentiation	9	1538	10	1432	0.878	6	799	3	739	0.585
0019827	stem cell maintenance	6	1541	2	1440	0.335	4	801	2	740	0.757
0000003	reproduction	76	1471	68	1374	0.868	41	764	35	707	0.823
0050793	regulation of development	19	1528	24	1418	0.397	10	795	9	733	0.858
0007582	physiological process	833	714	772	670	0.894	422	383	411	331	0.263
0008152	metabolism	605	942	561	881	0.939	300	505	305	437	0.135
0009056	catabolism	119	1428	90	1352	0.138	57	748	62	680	0.398
0006091	energy pathways	60	1487	48	1394	0.48	**18**	**787**	**42**	**700**	**8E-04**
0006118	electron transport	29	1518	26	1416	0.993	**8**	**797**	**21**	**721**	**0.013**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	226	1321	206	1236	0.842	123	682	103	639	0.48
0006259	DNA metabolism	42	1505	37	1405	0.889	18	787	24	718	0.293
0006350	transcription	**133**	**1414**	**94**	**1348**	**0.038**	76	729	57	685	0.253
0043170	macromolecule metabolism	322	1225	306	1136	0.82	158	647	164	578	0.256
0019538	protein metabolism	273	1274	254	1188	0.98	134	671	139	603	0.313
0006412	protein biosynthesis	52	1495	58	1384	0.389	22	783	30	712	0.198
0006464	protein modification	139	1408	117	1325	0.432	74	731	65	677	0.835
0006457	protein folding	21	1526	22	1420	0.816	13	792	8	734	0.489
0005975	carbohydrate metabolism	54	1493	53	1389	0.862	26	779	28	714	0.657
0006519	amino acid and derivative metabolism	32	1515	38	1404	0.367	17	788	15	727	0.957
0006629	lipid metabolism	41	1506	48	1394	0.326	20	785	21	721	0.791
0009308	amine metabolism	35	1512	46	1396	0.148	19	786	16	726	0.922
0042440	pigment metabolism	5	1542	7	1435	0.681	3	802	2	740	0.927
0042445	hormone metabolism	5	1542	2	1440	0.507	2	803	3	739	0.927
0009058	biosynthesis	98	1449	106	1336	0.304	45	760	53	689	0.251
0019748	secondary metabolism	7	1540	7	1435	0.892	4	801	3	739	0.914
0019222	regulation of metabolism	129	1418	109	1333	0.472	73	732	56	686	0.323
0016265	death	53	1494	33	1409	0.08	30	775	23	719	0.591
0008219	cell death	47	1500	27	1415	0.053	26	779	21	721	0.757
0016271	tissue death	**21**	**1526**	**6**	**1436**	**0.012**	11	794	10	732	0.851
0042592	homeostasis	13	1534	16	1426	0.573	7	798	6	736	0.883
0019725	cell homeostasis	12	1535	14	1428	0.706	6	799	6	736	0.882
0050801	ion homeostasis	4	1543	10	1432	0.141	3	802	1	741	0.675
0043062	extracellular structure organization and biogenesis	9	1538	10	1432	0.878	5	800	4	738	0.902
0046903	secretion	55	1492	46	1396	0.652	29	776	26	716	0.974
0048511	rhythmic process	12	1535	5	1437	0.189	6	799	6	736	0.882

Hive bee-to-forager ([d8, d12, d17] ⟶ d17F)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	191	1356	156	1286	0.213	103	702	88	654	0.63
0050874	organismal physiological process	134	1413	98	1344	0.066	67	738	67	675	0.687
0050875	cellular physiological process	788	759	731	711	0.923	400	405	388	354	0.331
0006810	transport	193	1354	205	1237	0.178	92	713	101	641	0.222
0006811	ion transport	58	1489	62	1380	0.501	24	781	34	708	0.128
0006818	hydrogen transport	13	1534	5	1437	0.132	4	801	9	733	0.207
0006836	neurotransmitter transport	3	1544	2	1440	0.937	1	804	2	740	0.944
0006858	extracellular transport	7	1540	8	1434	0.891	2	803	5	737	0.386
0006869	lipid transport	7	1540	9	1433	0.695	2	803	5	737	0.386
0008643	carbohydrate transport	6	1541	9	1433	0.513	3	802	3	739	0.757
0015031	protein transport	82	1465	98	1344	0.101	39	766	43	699	0.472
0015837	amine transport	6	1541	6	1436	0.867	2	803	4	738	0.61
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	8	1539	5	1437	0.668	5	800	3	739	0.811
0016192	vesicle-mediated transport	60	1487	59	1383	0.838	32	773	28	714	0.942
0045045	secretory pathway	50	1497	45	1397	0.945	26	779	24	718	0.89
0046907	intracellular transport	94	1453	104	1338	0.24	43	762	51	691	0.249
0051049	regulation of transport	6	1541	12	1430	0.183	2	803	4	738	0.61
0008283	cell proliferation	**48**	**1499**	**23**	**1419**	**0.01**	27	778	21	721	0.655
0007049	cell cycle	75	1472	53	1389	0.136	33	772	42	700	0.19
0017145	stem cell division	7	1540	5	1437	0.867	4	801	3	739	0.914
0016043	cell organization and biogenesis	152	1395	123	1319	0.246	75	730	77	665	0.539
0000902	cellular morphogenesis	43	1504	37	1405	0.804	25	780	18	724	0.511
0006996	organelle organization and biogenesis	131	1416	107	1335	0.322	61	744	70	672	0.223
0007010	cytoskeleton organization and biogenesis	98	1449	72	1370	0.133	44	761	54	688	0.175
0006997	nuclear organization and biogenesis	5	1542	5	1437	0.837	5	800	0	742	0.089
0007028	cytoplasm organization and biogenesis	10	1537	9	1433	0.878	8	797	2	740	0.145
0016044	membrane organization and biogenesis	8	1539	1	1441	0.058	5	800	3	739	0.811
0051128	regulation of cell organization and biogenesis	5	1542	6	1436	0.907	1	804	4	738	0.323
0016049	cell growth	5	1542	4	1438	0.916	2	803	3	739	0.927
0050896	response to stimulus	98	1449	83	1359	0.558	52	753	46	696	0.916
0006950	response to stress	37	1510	22	1420	0.117	24	781	13	729	0.157
0009408	response to heat	7	1540	3	1439	0.401	5	800	2	740	0.516
0006979	response to oxidative stress	1	1546	1	1441	0.511	1	804	0	742	0.967
0051179	localization	214	1333	215	1227	0.431	101	704	113	629	0.146
0006403	RNA localization	16	1531	16	1426	0.982	7	798	9	733	0.678
0008104	protein localization	92	1455	103	1339	0.212	44	761	48	694	0.468
0051234	establishment of localization	198	1349	205	1237	0.28	95	710	103	639	0.251
0051235	maintenance of localization	1	1546	3	1439	0.568	1	804	0	742	0.967
0050789	regulation of biological process	224	1323	179	1263	0.11	122	683	102	640	0.475
0050790	regulation of enzyme activity	7	1540	7	1435	0.892	4	801	3	739	0.914
0040029	regulation of gene expression, epigenetic	**17**	**1530**	**3**	**1439**	**0.006**	6	799	11	731	0.252
0006306	DNA methylation	**7**	**1540**	**0**	**1442**	**0.029**	3	802	4	738	0.914
0045814	negative regulation of gene expression, epigenetic	5	1542	2	1440	0.507	1	804	4	738	0.323
0006342	chromatin silencing	5	1542	2	1440	0.507	1	804	4	738	0.323
0003674	molecular_function	911	636	821	621	0.297	459	346	452	290	0.132
0016209	antioxidant activity	5	1542	4	1438	0.916	0	805	5	737	0.059
0005488	binding	529	1018	478	964	0.571	280	525	249	493	0.65
0005509	calcium ion binding	34	1513	27	1415	0.618	19	786	15	727	0.779
0030246	carbohydrate binding	8	1539	7	1435	0.891	5	800	3	739	0.811
0008289	lipid binding	15	1532	11	1431	0.681	5	800	10	732	0.231
0003676	nucleic acid binding	197	1350	192	1250	0.677	97	708	100	642	0.444
0003677	DNA binding	104	1443	90	1352	0.646	56	749	48	694	0.779
0003682	chromatin binding	11	1536	12	1430	0.866	6	799	5	737	0.892
0003700	transcription factor activity	41	1506	45	1397	0.51	26	779	15	727	0.187
0003723	RNA binding	54	1493	65	1377	0.184	22	783	32	710	0.121
0008135	translation factor activity, nucleic acid binding	14	1533	21	1421	0.219	7	798	7	735	0.908
0000166	nucleotide binding	139	1408	116	1326	0.393	72	733	67	675	0.976
0005515	protein binding	**220**	**1327**	**159**	**1283**	**0.01**	120	685	100	642	0.464
0008134	transcription factor binding	21	1526	10	1432	0.107	10	795	11	731	0.851
0008092	cytoskeletal protein binding	55	1492	33	1409	0.053	27	778	28	714	0.758
0003779	actin binding	31	1516	22	1420	0.395	15	790	16	726	0.819
0003824	catalytic activity	440	1107	399	1043	0.668	**207**	**598**	**233**	**509**	**0.015**
0016787	hydrolase activity	189	1358	183	1259	0.737	96	709	93	649	0.774
0003924	GTPase activity	19	1528	21	1421	0.702	6	799	13	729	0.118
0004518	nuclease activity	7	1540	8	1434	0.891	5	800	2	740	0.516

Hive bee-to-forager ([d8, d12, d17] ⟶ d17F)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	67	1480	51	1391	0.308	32	773	35	707	0.554
0004721	phosphoprotein phosphatase activity	10	1537	20	1422	0.065	6	799	4	738	0.851
0016740	transferase activity	137	1410	104	1338	0.114	67	738	70	672	0.497
0016301	kinase activity	79	1468	56	1386	0.128	43	762	36	706	0.748
0004672	protein kinase activity	**60**	**1487**	**35**	**1407**	**0.031**	31	774	29	713	0.942
0030234	enzyme regulator activity	60	1487	45	1397	0.305	32	773	28	714	0.942
0003774	motor activity	16	1531	12	1430	0.702	9	796	7	735	0.93
0004871	signal transducer activity	**151**	**1396**	**105**	**1337**	**0.019**	85	720	66	676	0.31
0004872	receptor activity	60	1487	49	1393	0.547	26	779	34	708	0.213
0004879	ligand-dependent nuclear receptor activity	5	1542	4	1438	0.916	3	802	2	740	0.927
0004888	transmembrane receptor activity	40	1507	34	1408	0.777	17	788	23	719	0.288
0004930	G-protein coupled receptor activity	18	1529	12	1430	0.469	8	797	10	732	0.681
0005057	receptor signaling protein activity	**54**	**1493**	**26**	**1416**	**0.006**	31	774	23	719	0.506
0005102	receptor binding	43	1504	26	1416	0.098	28	777	15	727	0.113
0005198	structural molecule activity	**97**	**1450**	**65**	**1377**	**0.041**	44	761	53	689	0.21
0030528	transcription regulator activity	114	1433	85	1357	0.123	67	738	47	695	0.162
0045182	translation regulator activity	14	1533	21	1421	0.219	7	798	7	735	0.908
0005215	transporter activity	119	1428	134	1308	0.132	**45**	**760**	**74**	**668**	**0.002**
0005489	electron transporter activity	14	1533	15	1427	0.849	**3**	**802**	**11**	**731**	**0.042**
0005216	ion channel activity	23	1524	29	1413	0.339	8	797	15	727	0.145
0005244	voltage-gated ion channel activity	14	1533	12	1430	0.986	6	799	8	734	0.673
0005575	cellular_component	630	917	593	849	0.853	**292**	**513**	**338**	**404**	**3E-04**
0005623	cell	571	976	541	901	0.76	**265**	**540**	**306**	**436**	**9E-04**
0005622	intracellular	454	1093	403	1039	0.421	**207**	**598**	**247**	**495**	**0.001**
0005737	cytoplasm	242	1305	216	1226	0.651	**88**	**717**	**154**	**588**	**2E-07**
0016023	cytoplasmic vesicle	23	1524	18	1424	0.687	12	793	11	731	0.844
0005829	cytosol	43	1504	36	1406	0.713	17	788	26	716	0.131
0005783	endoplasmic reticulum	26	1521	31	1411	0.422	10	795	16	726	0.23
0005794	Golgi apparatus	15	1532	10	1432	0.53	8	797	7	735	0.874
0005815	microtubule organizing center	4	1543	5	1437	0.916	2	803	2	740	0.675
0005739	mitochondrion	**66**	**1481**	**39**	**1403**	**0.027**	**13**	**792**	**53**	**689**	**2E-07**
0005840	ribosome	15	1532	9	1433	0.394	4	801	11	731	0.086
0005773	vacuole	8	1539	6	1436	0.892	2	803	6	736	0.238
0005764	lysosome	3	1544	2	1440	0.937	1	804	2	740	0.944
0005856	cytoskeleton	48	1499	37	1405	0.44	23	782	25	717	0.665
0005694	chromosome	24	1523	16	1426	0.373	9	796	15	727	0.218
0000228	nuclear chromosome	4	1543	1	1441	0.414	1	804	3	739	0.56
0005634	nucleus	192	1355	180	1262	0.997	103	702	89	653	0.689
0005635	nuclear membrane	7	1540	10	1432	0.527	6	799	1	741	0.159
0005730	nucleolus	6	1541	5	1437	0.907	2	803	4	738	0.61
0005654	nucleoplasm	38	1509	34	1408	0.955	20	785	18	724	0.928
0005777	peroxisome	5	1542	4	1438	0.916	2	803	3	739	0.927
0005886	plasma membrane	75	1472	81	1361	0.388	**28**	**777**	**47**	**695**	**0.013**
0005576	extracellular region	35	1512	41	1401	0.373	16	789	19	723	0.558
0005578	extracellular matrix (sensu Metazoa)	14	1533	21	1421	0.219	5	800	9	733	0.337

Hive bee-to-forager, experience independent ([d8, d12, d17] → d17F; forager not different than hive-restricted, p>0.2)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	818	544	872	642	0.193	399	284	419	260	0.236
0007610	behavior	79	1283	76	1438	0.399	39	644	40	639	0.979
0030534	adult behavior	11	1351	12	1502	0.869	4	679	7	672	0.538
0030537	larval behavior	6	1356	3	1511	0.408	3	680	3	676	0.688
0007611	learning and/or memory	12	1350	11	1503	0.799	5	678	7	672	0.764
0007612	learning	8	1354	7	1507	0.837	4	679	4	675	0.729
0007613	memory	5	1357	5	1509	0.881	3	680	2	677	0.995
0007626	locomotory behavior	60	1302	58	1456	0.496	30	653	30	649	0.913
0007635	chemosensory behavior	9	1353	9	1505	0.991	5	678	4	675	0.993
0007622	rhythmic behavior	6	1356	9	1505	0.754	5	678	1	678	0.222
0048512	circadian behavior	6	1356	8	1506	0.944	5	678	1	678	0.222
0009987	cellular process	762	600	807	707	0.166	371	312	391	288	0.246
0007154	cell communication	240	1122	226	1288	0.057	125	558	115	564	0.555
0007155	cell adhesion	46	1316	37	1477	0.167	21	662	25	654	0.638
0008037	cell recognition	1	1361	1	1513	0.526	0	683	1	678	0.998
0008038	neuronal cell recognition	1	1361	1	1513	0.526	0	683	1	678	0.998
0016337	cell-cell adhesion	20	1342	15	1499	0.319	9	674	11	668	0.811
0016339	calcium-dependent cell-cell adhesion	3	1359	3	1511	0.78	2	681	1	678	0.996
0007156	homophilic cell adhesion	3	1359	5	1509	0.838	2	681	1	678	0.996
0007160	cell-matrix adhesion	4	1358	5	1509	0.874	1	682	3	676	0.612
0007267	cell-cell signaling	82	1280	67	1447	0.065	40	643	42	637	0.888
0019226	transmission of nerve impulse	73	1289	59	1455	0.075	35	648	38	641	0.79
0007268	synaptic transmission	52	1310	47	1467	0.344	27	656	25	654	0.905
0007270	nerve-nerve synaptic transmission	5	1357	10	1504	0.406	2	681	3	676	0.995
0001505	regulation of neurotransmitter levels	32	1330	27	1487	0.348	18	665	14	665	0.603
0042133	neurotransmitter metabolism	4	1358	4	1510	0.838	3	680	1	678	0.621
0007269	neurotransmitter secretion	28	1334	24	1490	0.42	15	668	13	666	0.861
0007165	signal transduction	187	1175	174	1340	0.08	102	581	85	594	0.224
0007166	cell surface receptor linked signal transduction	77	1285	72	1442	0.317	43	640	34	645	0.362
0007167	enzyme linked receptor protein signaling pathway	21	1341	21	1493	0.849	11	672	10	669	0.989
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	8	1354	6	1508	0.641	3	680	5	674	0.717
0007179	transforming growth factor beta receptor signaling pathway	3	1359	4	1510	0.889	2	681	1	678	0.996
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	14	1348	16	1498	0.914	8	675	6	673	0.797
0007173	epidermal growth factor receptor signaling pathway	4	1358	3	1511	0.889	3	680	1	678	0.621
0008286	insulin receptor signaling pathway	1	1361	2	1512	0.927	0	683	1	678	0.998
0008293	torso signaling pathway	3	1359	4	1510	0.889	3	680	0	679	0.25
0007186	G-protein coupled receptor protein signaling pathway	37	1325	31	1483	0.291	18	665	19	660	0.986
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1359	2	1512	0.906	1	682	2	677	0.996
0007219	Notch signaling pathway	8	1354	5	1509	0.454	5	678	3	676	0.729
0007224	smoothened signaling pathway	3	1359	3	1511	0.78	2	681	1	678	0.996
0008063	Toll signaling pathway	2	1360	2	1512	0.693	2	681	0	679	0.482
0016055	Wnt receptor signaling pathway	5	1357	10	1504	0.406	4	679	1	678	0.374
0007242	intracellular signaling cascade	**96**	**1266**	**78**	**1436**	**0.04**	51	632	45	634	0.617
0007263	nitric oxide mediated signal transduction	1	1361	3	1511	0.693	1	682	0	679	0.998
0007243	protein kinase cascade	20	1342	20	1494	0.859	11	672	9	670	0.832
0007259	JAK-STAT cascade	3	1359	3	1511	0.78	2	681	1	678	0.996
0000165	MAPKKK cascade	16	1346	16	1498	0.902	9	674	7	672	0.811
0019932	second-messenger-mediated signaling	12	1350	9	1505	0.495	5	678	7	672	0.764
0019722	calcium-mediated signaling	7	1355	7	1507	0.944	2	681	5	674	0.444
0048015	phosphoinositide-mediated signaling	3	1359	2	1512	0.906	1	682	2	677	0.996
0007264	small GTPase mediated signal transduction	17	1345	25	1489	0.457	7	676	10	669	0.617
0007265	Ras protein signal transduction	5	1357	5	1509	0.881	0	683	5	674	0.072
0009966	regulation of signal transduction	17	1345	17	1497	0.89	12	671	5	674	0.146
0007275	development	220	1142	223	1291	0.315	110	573	110	569	0.979
0007568	aging	5	1357	4	1510	0.874	3	680	2	677	0.995
0030154	cell differentiation	55	1307	60	1454	0.994	29	654	26	653	0.8
0048468	cell development	37	1325	35	1479	0.566	20	663	17	662	0.753
0000904	cellular morphogenesis during differentiation	10	1352	9	1505	0.817	**9**	**674**	**1**	**678**	**0.027**
0042461	photoreceptor cell development	9	1353	9	1505	0.991	**8**	**675**	**1**	**678**	**0.046**
0042051	eye photoreceptor development (sensu Endopterygota)	8	1354	9	1505	0.827	7	676	1	678	0.078
0045165	cell fate commitment	21	1341	26	1488	0.823	13	670	8	671	0.386

Hive bee-to-forager, experience independent ([d8, d12, d17] → d17F; forager not different than hive-restricted, p>0.2)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0001709	cell fate determination	10	1352	18	1496	0.294	6	677	4	675	0.758
0007400	neuroblast cell fate determination	4	1358	4	1510	0.838	2	681	2	677	0.621
0001708	cell fate specification	2	1360	6	1508	0.361	2	681	0	679	0.482
0007349	cellularization	5	1357	6	1508	0.86	2	681	3	676	0.995
0040007	growth	18	1344	16	1498	0.629	10	673	8	671	0.822
0002164	larval development	9	1353	8	1506	0.827	6	677	3	676	0.509
0002165	larval or pupal development (sensu Insecta)	**72**	**1290**	**51**	**1463**	**0.014**	39	644	33	646	0.562
0007552	metamorphosis	**67**	**1295**	**48**	**1466**	**0.022**	37	646	30	649	0.467
0009653	morphogenesis	147	1215	158	1356	0.803	80	603	67	612	0.312
0002009	morphogenesis of an epithelium	22	1340	21	1493	0.727	12	671	10	669	0.841
0009887	organogenesis	130	1232	139	1375	0.787	70	613	60	619	0.427
0001654	eye morphogenesis	29	1333	28	1486	0.687	**21**	**662**	**8**	**671**	**0.025**
0008406	gonad development	3	1359	5	1509	0.838	1	682	2	677	0.996
0007444	imaginal disc development	45	1317	44	1470	0.612	28	655	17	662	0.135
0007494	midgut development	1	1361	3	1511	0.693	0	683	1	678	0.998
0007517	muscle development	10	1352	21	1493	0.131	4	679	6	673	0.744
0007399	neurogenesis	73	1289	82	1432	0.987	41	642	32	647	0.349
0007409	axonogenesis	20	1342	23	1491	0.967	10	673	10	669	0.832
0007411	axon guidance	15	1347	18	1496	0.964	9	674	6	673	0.612
0007417	central nervous system development	16	1346	19	1495	0.98	9	674	7	672	0.811
0016358	dendrite morphogenesis	4	1358	9	1505	0.356	1	682	3	676	0.612
0042063	gliogenesis	4	1358	7	1507	0.668	1	682	3	676	0.612
0007422	peripheral nervous system development	14	1348	25	1489	0.2	10	673	4	675	0.183
0050767	regulation of neurogenesis	1	1361	4	1510	0.437	0	683	1	678	0.998
0007424	tracheal system development (sensu Insecta)	15	1347	20	1494	0.714	9	674	6	673	0.612
0048513	organ development	133	1229	140	1374	0.682	72	611	61	618	0.38
0007389	pattern specification	30	1332	43	1471	0.334	16	667	14	665	0.866
0048066	pigmentation	5	1357	5	1509	0.881	5	678	0	679	0.074
0009791	post-embryonic development	9	1353	8	1506	0.827	6	677	3	676	0.509
0009790	embryonic development	46	1316	51	1463	0.928	29	654	17	662	0.103
0007530	sex determination	5	1357	4	1510	0.874	2	681	3	676	0.995
0007548	sex differentiation	6	1356	10	1504	0.589	3	680	3	676	0.688
0019827	stem cell maintenance	4	1358	3	1511	0.889	2	681	2	677	0.621
0000003	reproduction	70	1292	67	1447	0.418	36	647	34	645	0.922
0050793	regulation of development	17	1345	23	1491	0.645	9	674	8	671	0.99
0007582	physiological process	745	617	806	708	0.454	365	318	380	299	0.378
0008152	metabolism	543	819	580	934	0.414	**254**	**429**	**289**	**390**	**0.049**
0009056	catabolism	106	1256	93	1421	0.098	48	635	58	621	0.346
0006091	energy pathways	55	1307	51	1463	0.394	**16**	**667**	**39**	**640**	**0.002**
0006118	electron transport	27	1335	27	1487	0.799	**7**	**676**	**20**	**659**	**0.019**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	201	1161	211	1303	0.566	102	581	99	580	0.914
0006259	DNA metabolism	40	1322	33	1481	0.242	16	667	24	655	0.253
0006350	transcription	114	1248	99	1415	0.072	59	624	55	624	0.794
0043170	macromolecule metabolism	290	1072	321	1193	0.989	136	547	154	525	0.237
0019538	protein metabolism	247	1115	266	1248	0.729	114	569	133	546	0.188
0006412	protein biosynthesis	48	1314	59	1455	0.668	19	664	29	650	0.179
0006464	protein modification	129	1233	123	1391	0.226	67	616	62	617	0.738
0006457	protein folding	17	1345	25	1489	0.457	9	674	8	671	0.99
0005975	carbohydrate metabolism	47	1315	57	1457	0.726	23	660	24	655	0.984
0006519	amino acid and derivative metabolism	30	1332	40	1474	0.521	17	666	13	666	0.591
0006629	lipid metabolism	35	1327	48	1466	0.396	15	668	20	659	0.482
0009308	amine metabolism	31	1331	49	1465	0.147	18	665	13	666	0.478
0042440	pigment metabolism	5	1357	7	1507	0.916	3	680	2	677	0.995
0042445	hormone metabolism	3	1359	4	1510	0.889	1	682	2	677	0.996
0009058	biosynthesis	91	1271	109	1405	0.637	41	642	50	629	0.37
0019748	secondary metabolism	7	1355	7	1507	0.944	4	679	3	676	0.994
0019222	regulation of metabolism	111	1251	116	1398	0.678	57	626	54	625	0.868
0016265	death	43	1319	39	1475	0.411	22	661	21	658	0.984
0008219	cell death	38	1324	34	1480	0.416	19	664	19	660	0.884
0016271	tissue death	17	1345	9	1505	0.099	7	676	10	669	0.617
0042592	homeostasis	13	1349	15	1499	0.927	7	676	6	673	0.992
0019725	cell homeostasis	12	1350	13	1501	0.891	6	677	6	673	0.78
0050801	ion homeostasis	4	1358	10	1504	0.253	3	680	1	678	0.621
0043062	extracellular structure organization and biogenesis	7	1355	10	1504	0.788	4	679	3	676	0.994
0046903	secretion	51	1311	49	1465	0.522	28	655	23	656	0.583
0048511	rhythmic process	7	1355	10	1504	0.788	5	678	2	677	0.453

Hive bee-to-forager, experience independent ([d8, d12, d17] → d17F; forager not different than hive-restricted, p>0.2)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	165	1197	167	1347	0.395	83	600	82	597	0.968
0050874	organismal physiological process	118	1244	105	1409	0.097	60	623	58	621	0.95
0050875	cellular physiological process	708	654	763	751	0.417	346	337	362	317	0.354
0006810	transport	174	1188	218	1296	0.225	87	596	87	592	0.968
0006811	ion transport	52	1310	67	1447	0.47	22	661	30	649	0.312
0006818	hydrogen transport	12	1350	6	1508	0.159	4	679	8	671	0.379
0006836	neurotransmitter transport	3	1359	2	1512	0.906	1	682	2	677	0.996
0006858	extracellular transport	6	1356	9	1505	0.754	2	681	4	675	0.677
0006869	lipid transport	6	1356	8	1506	0.944	2	681	4	675	0.677
0008643	carbohydrate transport	5	1357	10	1504	0.406	3	680	2	677	0.995
0015031	protein transport	77	1285	101	1413	0.292	38	645	39	640	0.979
0015837	amine transport	6	1356	6	1508	0.916	2	681	4	675	0.677
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	7	1355	5	1509	0.636	4	679	3	676	0.994
0016192	vesicle-mediated transport	57	1305	60	1454	0.836	31	652	26	653	0.604
0045045	secretory pathway	47	1315	47	1467	0.677	25	658	22	657	0.782
0046907	intracellular transport	87	1275	109	1405	0.43	42	641	45	634	0.803
0051049	regulation of transport	6	1356	12	1502	0.338	2	681	4	675	0.677
0008283	cell proliferation	40	1322	27	1487	0.054	22	661	18	661	0.644
0007049	cell cycle	68	1294	55	1459	0.088	29	654	39	640	0.252
0017145	stem cell division	6	1356	5	1509	0.86	3	680	3	676	0.688
0016043	cell organization and biogenesis	140	1222	125	1389	0.071	69	614	71	608	0.9
0000902	cellular morphogenesis	39	1323	38	1476	0.638	23	660	16	663	0.339
0006996	organelle organization and biogenesis	121	1241	109	1405	0.111	56	627	65	614	0.426
0007010	cytoskeleton organization and biogenesis	88	1274	77	1437	0.133	39	644	49	630	0.308
0006997	nuclear organization and biogenesis	5	1357	4	1510	0.874	5	678	0	679	0.074
0007028	cytoplasm organization and biogenesis	9	1353	9	1505	0.991	7	676	2	677	0.184
0016044	membrane organization and biogenesis	7	1355	1	1513	0.055	4	679	3	676	0.994
0051128	regulation of cell organization and biogenesis	5	1357	6	1508	0.86	1	682	4	675	0.367
0016049	cell growth	5	1357	3	1511	0.614	2	681	3	676	0.995
0050896	response to stimulus	83	1279	92	1422	0.953	45	638	38	641	0.514
0006950	response to stress	30	1332	25	1489	0.346	19	664	11	668	0.202
0009408	response to heat	5	1357	4	1510	0.874	4	679	1	678	0.374
0006979	response to oxidative stress	1	1361	1	1513	0.526	1	682	0	679	0.998
0051179	localization	192	1170	230	1284	0.438	95	588	97	582	0.903
0006403	RNA localization	14	1348	16	1498	0.914	6	677	8	671	0.78
0008104	protein localization	86	1276	107	1407	0.465	43	640	43	636	0.934
0051234	establishment of localization	178	1184	219	1295	0.303	90	593	88	591	0.969
0051235	maintenance of localization	0	1362	3	1511	0.287	0	683	0	679	-
0050789	regulation of biological process	197	1165	191	1323	0.163	102	581	95	584	0.676
0050790	regulation of enzyme activity	7	1355	7	1507	0.944	4	679	3	676	0.994
0040029	regulation of gene expression, epigenetic	**17**	**1345**	**2**	**1512**	**5E-04**	6	677	11	668	0.323
0006306	DNA methylation	**7**	**1355**	**0**	**1514**	**0.016**	3	680	4	675	0.994
0045814	negative regulation of gene expression, epigenetic	5	1357	1	1513	0.175	1	682	4	675	0.367
0006342	chromatin silencing	5	1357	1	1513	0.175	1	682	4	675	0.367
0003674	molecular_function	812	550	856	658	0.103	390	293	422	257	0.065
0016209	antioxidant activity	5	1357	4	1510	0.874	0	683	5	674	0.072
0005488	binding	468	894	498	1016	0.428	232	451	236	443	0.803
0005509	calcium ion binding	31	1331	29	1485	0.586	16	667	15	664	0.987
0030246	carbohydrate binding	6	1356	8	1506	0.944	4	679	2	677	0.688
0008289	lipid binding	14	1348	11	1503	0.504	5	678	9	670	0.414
0003676	nucleic acid binding	174	1188	196	1318	0.936	75	608	99	580	0.056
0003677	DNA binding	89	1273	90	1424	0.564	41	642	48	631	0.492
0003682	chromatin binding	11	1351	11	1503	0.972	6	677	5	674	0.992
0003700	transcription factor activity	32	1330	47	1467	0.262	17	666	15	664	0.871
0003723	RNA binding	51	1311	66	1448	0.46	20	663	31	648	0.147
0008135	translation factor activity, nucleic acid binding	13	1349	22	1492	0.295	6	677	7	672	0.992
0000166	nucleotide binding	124	1238	123	1391	0.384	62	621	62	617	0.952
0005515	protein binding	**196**	**1166**	**170**	**1344**	**0.013**	103	580	93	586	0.515
0008134	transcription factor binding	**20**	**1342**	**9**	**1505**	**0.031**	9	674	11	668	0.811
0008092	cytoskeletal protein binding	**51**	**1311**	**34**	**1480**	**0.024**	23	660	28	651	0.554
0003779	actin binding	30	1332	22	1492	0.172	14	669	16	663	0.841
0003824	catalytic activity	397	965	413	1101	0.284	**179**	**504**	**218**	**461**	**0.02**
0016787	hydrolase activity	162	1200	187	1327	0.751	74	609	88	591	0.259
0003924	GTPase activity	16	1346	23	1491	0.525	4	679	12	667	0.076
0004518	nuclease activity	4	1358	8	1506	0.493	2	681	2	677	0.621

Hive bee-to-forager, experience independent ([d8, d12, d17] → d17F; forager not different than hive-restricted, p>0.2)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	59	1303	53	1461	0.292	25	658	34	645	0.277
0004721	phosphoprotein phosphatase activity	**7**	**1355**	**21**	**1493**	**0.028**	3	680	4	675	0.994
0016740	transferase activity	125	1237	108	1406	0.053	60	623	65	614	0.682
0016301	kinase activity	73	1289	61	1453	0.109	41	642	32	647	0.349
0004672	protein kinase activity	54	1308	40	1474	0.059	29	654	25	654	0.693
0030234	enzyme regulator activity	50	1312	51	1463	0.735	26	657	24	655	0.902
0003774	motor activity	13	1349	12	1502	0.79	7	676	6	673	0.992
0004871	signal transducer activity	**137**	**1225**	**108**	**1406**	**0.006**	76	607	61	618	0.221
0004872	receptor activity	57	1305	48	1466	0.177	24	659	33	646	0.269
0004879	ligand-dependent nuclear receptor activity	4	1358	5	1509	0.874	2	681	2	677	0.621
0004888	transmembrane receptor activity	38	1324	32	1482	0.292	16	667	22	657	0.4
0004930	G-protein coupled receptor activity	16	1346	11	1503	0.293	7	676	9	670	0.792
0005057	receptor signaling protein activity	**48**	**1314**	**30**	**1484**	**0.015**	28	655	20	659	0.313
0005102	receptor binding	38	1324	26	1488	0.069	24	659	14	665	0.144
0005198	structural molecule activity	**86**	**1276**	**69**	**1445**	**0.045**	37	646	49	630	0.21
0030528	transcription regulator activity	97	1265	88	1426	0.176	51	632	46	633	0.695
0045182	translation regulator activity	13	1349	22	1492	0.295	6	677	7	672	0.992
0005215	transporter activity	107	1255	141	1373	0.186	**41**	**642**	**66**	**613**	**0.014**
0005489	electron transporter activity	13	1349	15	1499	0.927	**2**	**681**	**11**	**668**	**0.025**
0005216	ion channel activity	22	1340	29	1485	0.64	8	675	14	665	0.276
0005244	voltage-gated ion channel activity	13	1349	13	1501	0.941	6	677	7	672	0.992
0005575	cellular_component	565	797	614	900	0.64	**253**	**430**	**312**	**367**	**0.001**
0005623	cell	512	850	560	954	0.767	**230**	**453**	**282**	**397**	**0.003**
0005622	intracellular	408	954	419	1095	0.191	**177**	**506**	**231**	**448**	**0.001**
0005737	cytoplasm	223	1139	226	1288	0.31	**80**	**603**	**143**	**536**	**4E-06**
0016023	cytoplasmic vesicle	21	1341	19	1495	0.62	11	672	10	669	0.989
0005829	cytosol	42	1320	37	1477	0.35	16	667	26	653	0.153
0005783	endoplasmic reticulum	26	1336	31	1483	0.895	10	673	16	663	0.315
0005794	Golgi apparatus	14	1348	11	1503	0.504	8	675	6	673	0.797
0005815	microtubule organizing center	4	1358	5	1509	0.874	2	681	2	677	0.621
0005739	mitochondrion	**62**	**1300**	**41**	**1473**	**0.011**	**12**	**671**	**50**	**629**	**1E-06**
0005840	ribosome	14	1348	9	1505	0.274	4	679	10	669	0.176
0005773	vacuole	8	1354	6	1508	0.641	2	681	6	673	0.284
0005764	lysosome	3	1359	2	1512	0.906	1	682	2	677	0.996
0005856	cytoskeleton	41	1321	39	1475	0.553	18	665	23	656	0.513
0005694	chromosome	22	1340	16	1498	0.252	8	675	14	665	0.276
0000228	nuclear chromosome	4	1358	1	1513	0.31	1	682	3	676	0.612
0005634	nucleus	168	1194	184	1330	0.927	83	600	85	594	0.902
0005635	nuclear membrane	5	1357	11	1503	0.297	5	678	0	679	0.074
0005730	nucleolus	5	1357	6	1508	0.86	2	681	3	676	0.995
0005654	nucleoplasm	33	1329	33	1481	0.756	16	667	17	662	0.986
0005777	peroxisome	5	1357	4	1510	0.874	2	681	3	676	0.995
0005886	plasma membrane	69	1293	80	1434	0.858	**26**	**657**	**43**	**636**	**0.045**
0005576	extracellular region	30	1332	43	1471	0.334	14	669	16	663	0.841
0005578	extracellular matrix (sensu Metazoa)	12	1350	22	1492	0.213	4	679	8	671	0.379

Subspecies (ligustica relative to mellifera)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	391	313	1363	922	0.058	213	160	178	153	0.417
0007610	behavior	35	669	127	2158	0.613	18	355	17	314	0.988
0030534	adult behavior	2	702	22	2263	0.128	1	372	1	330	0.532
0030537	larval behavior	1	703	8	2277	0.626	0	373	1	330	0.952
0007611	learning and/or memory	3	701	21	2264	0.298	2	371	1	330	0.917
0007612	learning	2	702	13	2272	0.529	1	372	1	330	0.532
0007613	memory	1	703	10	2275	0.437	1	372	0	331	0.952
0007626	locomotory behavior	27	677	96	2189	0.75	16	357	11	320	0.639
0007635	chemosensory behavior	3	701	15	2270	0.68	1	372	2	329	0.917
0007622	rhythmic behavior	2	702	13	2272	0.529	1	372	1	330	0.532
0048512	circadian behavior	2	702	12	2273	0.615	1	372	1	330	0.532
0009987	cellular process	**357**	**347**	**1271**	**1014**	**0.025**	198	175	159	172	0.207
0007154	cell communication	112	592	377	1908	0.755	64	309	48	283	0.391
0007155	cell adhesion	25	679	65	2220	0.405	13	360	12	319	0.917
0008037	cell recognition	0	704	2	2283	0.962	0	373	0	331	-
0008038	neuronal cell recognition	0	704	2	2283	0.962	0	373	0	331	-
0016337	cell-cell adhesion	12	692	27	2258	0.379	7	366	5	326	0.934
0016339	calcium-dependent cell-cell adhesion	3	701	4	2281	0.448	0	373	3	328	0.207
0007156	homophilic cell adhesion	4	700	5	2280	0.278	1	372	3	328	0.534
0007160	cell-matrix adhesion	5	699	4	2281	0.061	2	371	3	328	0.893
0007267	cell-cell signaling	36	668	120	2165	0.962	20	353	16	315	0.884
0019226	transmission of nerve impulse	33	671	105	2180	0.999	18	355	15	316	0.996
0007268	synaptic transmission	21	683	80	2205	0.585	12	361	9	322	0.868
0007270	nerve-nerve synaptic transmission	5	699	11	2274	0.666	2	371	3	328	0.893
0001505	regulation of neurotransmitter levels	11	693	49	2236	0.419	6	367	5	326	0.842
0042133	neurotransmitter metabolism	2	702	6	2279	0.749	0	373	2	329	0.427
0007269	neurotransmitter secretion	10	694	43	2242	0.517	6	367	4	327	0.898
0007165	signal transduction	85	619	294	1991	0.626	51	322	34	297	0.205
0007166	cell surface receptor linked signal transduction	34	670	123	2162	0.632	17	356	17	314	0.856
0007167	enzyme linked receptor protein signaling pathway	8	696	38	2247	0.414	4	369	4	327	0.852
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3	701	13	2272	0.874	2	371	1	330	0.917
0007179	transforming growth factor beta receptor signaling pathway	1	703	8	2277	0.626	0	373	1	330	0.952
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	6	698	26	2259	0.664	3	370	3	328	0.792
0007173	epidermal growth factor receptor signaling pathway	2	702	6	2279	0.749	1	372	1	330	0.532
0008286	insulin receptor signaling pathway	0	704	4	2281	0.602	0	373	0	331	-
0008293	torso signaling pathway	0	704	7	2278	0.306	0	373	0	331	-
0007186	G-protein coupled receptor protein signaling pathway	19	685	52	2233	0.615	11	362	8	323	0.84
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	701	2	2283	0.163	2	371	1	330	0.917
0007219	Notch signaling pathway	1	703	12	2273	0.306	0	373	1	330	0.952
0007224	smoothened signaling pathway	0	704	6	2279	0.379	0	373	0	331	-
0008063	Toll signaling pathway	0	704	4	2281	0.602	0	373	0	331	-
0016055	Wnt receptor signaling pathway	3	701	13	2272	0.874	2	371	1	330	0.917
0007242	intracellular signaling cascade	41	663	141	2144	0.805	28	345	13	318	0.063
0007263	nitric oxide mediated signal transduction	1	703	3	2282	0.602	1	372	0	331	0.952
0007243	protein kinase cascade	9	695	32	2253	0.954	6	367	3	328	0.623
0007259	JAK-STAT cascade	2	702	4	2281	0.933	1	372	1	330	0.532
0000165	MAPKKK cascade	7	697	26	2259	0.91	5	368	2	329	0.547
0019932	second-messenger-mediated signaling	**10**	**694**	**12**	**2273**	**0.029**	8	365	2	329	0.16
0019722	calcium-mediated signaling	7	697	8	2277	0.07	6	367	1	330	0.173
0048015	phosphoinositide-mediated signaling	3	701	2	2283	0.163	2	371	1	330	0.917
0007264	small GTPase mediated signal transduction	9	695	35	2250	0.757	7	366	2	329	0.244
0007265	Ras protein signal transduction	3	701	7	2278	0.914	2	371	1	330	0.917
0009966	regulation of signal transduction	10	694	24	2261	0.544	6	367	4	327	0.898
0007275	development	102	602	358	1927	0.485	51	322	51	280	0.585
0007568	aging	3	701	8	2277	0.948	0	373	3	328	0.207
0030154	cell differentiation	23	681	96	2189	0.318	13	360	10	321	0.894
0048468	cell development	13	691	62	2223	0.251	8	365	5	326	0.731
0000904	cellular morphogenesis during differentiation	3	701	16	2269	0.597	1	372	2	329	0.917
0042461	photoreceptor cell development	3	701	15	2270	0.68	1	372	2	329	0.917
0042051	eye photoreceptor development (sensu Endopterygota)	2	702	15	2270	0.389	1	372	1	330	0.532
0045165	cell fate commitment	11	693	38	2247	0.989	7	366	4	327	0.682

		Subspecies (ligustica relative to mellifera)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	9	695	21	2264	0.535	5	368	4	327	0.857
0007400	neuroblast cell fate determination	4	700	4	2281	0.178	3	370	1	330	0.702
0001708	cell fate specification	1	703	7	2278	0.749	0	373	1	330	0.952
0007349	cellularization	1	703	10	2275	0.437	1	372	0	331	0.952
0040007	growth	5	699	31	2254	0.239	3	370	2	329	0.893
0002164	larval development	1	703	16	2269	0.151	1	372	0	331	0.952
0002165	larval or pupal development (sensu Insecta)	25	679	104	2181	0.3	9	364	16	315	0.126
0007552	metamorphosis	24	680	97	2188	0.382	9	364	15	316	0.181
0009653	morphogenesis	78	626	241	2044	0.741	44	329	34	297	0.601
0002009	morphogenesis of an epithelium	7	697	37	2248	0.305	5	368	2	329	0.547
0009887	organogenesis	71	633	211	2074	0.547	39	334	32	299	0.825
0001654	eye morphogenesis	11	693	46	2239	0.544	7	366	4	327	0.682
0008406	gonad development	4	700	7	2278	0.517	2	371	2	329	0.702
0007444	imaginal disc development	22	682	71	2214	0.92	9	364	13	318	0.349
0007494	midgut development	2	702	3	2282	0.734	2	371	0	331	0.532
0007517	muscle development	9	695	25	2260	0.841	6	367	3	328	0.623
0007399	neurogenesis	36	668	126	2159	0.753	23	350	13	318	0.24
0007409	axonogenesis	11	693	32	2253	0.893	4	369	7	324	0.419
0007411	axon guidance	7	697	26	2259	0.91	2	371	5	326	0.358
0007417	central nervous system development	9	695	30	2255	0.905	4	369	5	326	0.857
0016358	dendrite morphogenesis	4	700	10	2275	0.898	1	372	3	328	0.534
0042063	gliogenesis	3	701	8	2277	0.948	2	371	1	330	0.917
0007422	peripheral nervous system development	7	697	33	2252	0.471	5	368	2	329	0.547
0050767	regulation of neurogenesis	3	701	2	2283	0.163	0	373	3	328	0.207
0007424	tracheal system development (sensu Insecta)	5	699	32	2253	0.21	4	369	1	330	0.444
0048513	organ development	72	632	214	2071	0.544	39	334	33	298	0.93
0007389	pattern specification	12	692	64	2221	0.139	7	366	5	326	0.934
0048066	pigmentation	3	701	8	2277	0.948	0	373	3	328	0.207
0009791	post-embryonic development	1	703	16	2269	0.151	1	372	0	331	0.952
0009790	embryonic development	**14**	**690**	**86**	**2199**	**0.03**	5	368	9	322	0.3
0007530	sex determination	3	701	7	2278	0.914	2	371	1	330	0.917
0007548	sex differentiation	5	699	14	2271	0.989	2	371	3	328	0.893
0019827	stem cell maintenance	2	702	6	2279	0.749	1	372	1	330	0.532
0000003	reproduction	27	677	117	2168	0.196	17	356	10	321	0.388
0050793	regulation of development	8	696	35	2250	0.556	2	371	6	325	0.215
0007582	physiological process	358	346	1247	1038	0.091	198	175	160	171	0.237
0008152	metabolism	259	445	907	1378	0.181	139	234	120	211	0.842
0009056	catabolism	48	656	161	2124	0.902	23	350	25	306	0.563
0006091	energy pathways	24	680	84	2201	0.829	**18**	**355**	**6**	**325**	**0.047**
0006118	electron transport	10	694	45	2240	0.431	7	366	3	328	0.443
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	90	614	342	1943	0.168	45	328	45	286	0.621
0006259	DNA metabolism	16	688	63	2222	0.571	5	368	11	320	0.131
0006350	transcription	50	654	177	2108	0.629	22	351	28	303	0.241
0043170	macromolecule metabolism	144	560	484	1801	0.718	80	293	64	267	0.549
0019538	protein metabolism	114	590	413	1872	0.276	62	311	52	279	0.822
0006412	protein biosynthesis	26	678	84	2201	0.926	13	360	13	318	0.912
0006464	protein modification	57	647	199	2086	0.667	31	342	26	305	0.934
0006457	protein folding	8	696	35	2250	0.556	5	368	3	328	0.852
0005975	carbohydrate metabolism	33	671	74	2211	0.09	20	353	13	318	0.471
0006519	amino acid and derivative metabolism	20	684	50	2235	0.39	7	366	13	318	0.159
0006629	lipid metabolism	23	681	66	2219	0.697	12	361	11	320	0.894
0009308	amine metabolism	22	682	59	2226	0.52	9	364	13	318	0.349
0042440	pigment metabolism	3	701	9	2276	0.824	0	373	3	328	0.207
0042445	hormone metabolism	0	704	7	2278	0.306	0	373	0	331	-
0009058	biosynthesis	49	655	155	2130	0.938	23	350	26	305	0.465
0019748	secondary metabolism	3	701	11	2274	0.898	0	373	3	328	0.207
0019222	regulation of metabolism	50	654	188	2097	0.376	23	350	27	304	0.379
0016265	death	19	685	67	2218	0.846	9	364	10	321	0.792
0008219	cell death	15	689	59	2226	0.593	8	365	7	324	0.815
0016271	tissue death	4	700	23	2262	0.397	2	371	2	329	0.702
0042592	homeostasis	8	696	21	2264	0.768	5	368	3	328	0.852
0019725	cell homeostasis	6	698	20	2265	0.861	4	369	2	329	0.792
0050801	ion homeostasis	4	700	10	2275	0.898	3	370	1	330	0.702
0043062	extracellular structure organization and biogenesis	3	701	16	2269	0.597	2	371	1	330	0.917
0046903	secretion	21	683	80	2205	0.585	11	362	10	321	0.868
0048511	rhythmic process	2	702	15	2270	0.389	1	372	1	330	0.532

		Subspecies (ligustica relative to mellifera)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	68	636	279	2006	0.075	34	339	34	297	0.696
0050874	organismal physiological process	60	644	172	2113	0.434	33	340	27	304	0.848
0050875	cellular physiological process	**334**	**370**	**1185**	**1100**	**0.045**	186	187	148	183	0.197
0006810	transport	81	623	317	1968	0.12	45	328	36	295	0.708
0006811	ion transport	28	676	92	2193	0.959	16	357	12	319	0.797
0006818	hydrogen transport	5	699	13	2272	0.885	3	370	2	329	0.893
0006836	neurotransmitter transport	1	703	4	2281	0.734	0	373	1	330	0.952
0006858	extracellular transport	4	700	11	2274	0.984	1	372	3	328	0.534
0006869	lipid transport	1	703	15	2270	0.18	0	373	1	330	0.952
0008643	carbohydrate transport	5	699	10	2275	0.555	1	372	4	327	0.301
0015031	protein transport	**27**	**677**	**153**	**2132**	**0.007**	17	356	10	321	0.388
0015837	amine transport	2	702	10	2275	0.824	1	372	1	330	0.532
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	2	702	11	2274	0.713	1	372	1	330	0.532
0016192	vesicle-mediated transport	24	680	95	2190	0.437	16	357	8	323	0.247
0045045	secretory pathway	19	685	76	2209	0.48	11	362	8	323	0.84
0046907	intracellular transport	**29**	**675**	**169**	**2116**	**0.003**	18	355	11	320	0.417
0051049	regulation of transport	4	700	14	2271	0.885	3	370	1	330	0.702
0008283	cell proliferation	14	690	57	2228	0.529	8	365	6	325	0.964
0007049	cell cycle	28	676	100	2185	0.726	17	356	11	320	0.52
0017145	stem cell division	3	701	9	2276	0.824	3	370	0	331	0.291
0016043	cell organization and biogenesis	63	641	212	2073	0.85	36	337	27	304	0.575
0000902	cellular morphogenesis	13	691	67	2218	0.154	9	364	4	327	0.366
0006996	organelle organization and biogenesis	55	649	183	2102	0.929	31	342	24	307	0.702
0007010	cytoskeleton organization and biogenesis	42	662	128	2157	0.786	27	346	15	316	0.176
0006997	nuclear organization and biogenesis	1	703	9	2276	0.523	0	373	1	330	0.952
0007028	cytoplasm organization and biogenesis	5	699	14	2271	0.989	4	369	1	330	0.444
0016044	membrane organization and biogenesis	1	703	8	2277	0.626	1	372	0	331	0.952
0051128	regulation of cell organization and biogenesis	4	700	7	2278	0.517	3	370	1	330	0.702
0016049	cell growth	0	704	9	2276	0.203	0	373	0	331	-
0050896	response to stimulus	49	655	132	2153	0.289	24	349	25	306	0.664
0006950	response to stress	13	691	46	2239	0.902	6	367	7	324	0.828
0009408	response to heat	1	703	9	2276	0.523	0	373	1	330	0.952
0006979	response to oxidative stress	1	703	1	2284	0.962	0	373	1	330	0.952
0051179	localization	86	618	343	1942	0.074	47	326	39	292	0.829
0006403	RNA localization	6	698	26	2259	0.664	2	371	4	327	0.577
0008104	protein localization	**28**	**676**	**167**	**2118**	**0.002**	17	356	11	320	0.52
0051234	establishment of localization	82	622	321	1964	0.117	45	328	37	294	0.804
0051235	maintenance of localization	1	703	3	2282	0.602	1	372	0	331	0.952
0050789	regulation of biological process	81	623	322	1963	0.09	39	334	42	289	0.419
0050790	regulation of enzyme activity	3	701	11	2274	0.898	0	373	3	328	0.207
0040029	regulation of gene expression, epigenetic	4	700	16	2269	0.911	2	371	2	329	0.702
0006306	DNA methylation	2	702	5	2280	0.894	1	372	1	330	0.532
0045814	negative regulation of gene expression, epigenetic	0	704	7	2278	0.306	0	373	0	331	-
0006342	chromatin silencing	0	704	7	2278	0.306	0	373	0	331	-
0003674	molecular_function	**381**	**323**	**1351**	**934**	**0.021**	209	164	172	159	0.315
0016209	antioxidant activity	2	702	7	2278	0.765	2	371	0	331	0.532
0005488	binding	218	486	789	1496	0.088	112	261	106	225	0.624
0005509	calcium ion binding	13	691	48	2237	0.791	5	368	8	323	0.436
0030246	carbohydrate binding	4	700	11	2274	0.984	3	370	1	330	0.702
0008289	lipid binding	6	698	20	2265	0.861	5	368	1	330	0.278
0003676	nucleic acid binding	77	627	312	1973	0.07	40	333	37	294	0.943
0003677	DNA binding	42	662	152	2133	0.576	21	352	21	310	0.81
0003682	chromatin binding	3	701	20	2265	0.344	2	371	1	330	0.917
0003700	transcription factor activity	19	685	67	2218	0.846	10	363	9	322	0.84
0003723	RNA binding	20	684	99	2186	0.097	13	360	7	324	0.387
0008135	translation factor activity, nucleic acid binding	5	699	30	2255	0.272	1	372	4	327	0.301
0000166	nucleotide binding	54	650	201	2084	0.391	29	344	25	306	0.975
0005515	protein binding	87	617	292	1993	0.819	49	324	38	293	0.581
0008134	transcription factor binding	6	698	25	2260	0.733	2	371	4	327	0.577
0008092	cytoskeletal protein binding	22	682	66	2219	0.844	14	359	8	323	0.424
0003779	actin binding	12	692	41	2244	0.996	7	366	5	326	0.934
0003824	catalytic activity	192	512	647	1638	0.624	110	263	82	249	0.188
0016787	hydrolase activity	79	625	293	1992	0.289	41	332	38	293	0.932
0003924	GTPase activity	9	695	31	2254	0.976	8	365	1	330	0.066
0004518	nuclease activity	3	701	12	2273	0.984	0	373	3	328	0.207

		Subspecies (ligustica relative to mellifera)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	26	678	92	2193	0.775	13	360	13	318	0.912
0004721	phosphoprotein phosphatase activity	4	700	26	2259	0.267	2	371	2	329	0.702
0016740	transferase activity	58	646	183	2102	0.907	31	342	27	304	0.95
0016301	kinase activity	31	673	104	2181	0.951	18	355	13	318	0.692
0004672	protein kinase activity	20	684	75	2210	0.645	12	361	8	323	0.681
0030234	enzyme regulator activity	26	678	79	2206	0.857	16	357	10	321	0.49
0003774	motor activity	6	698	22	2263	0.966	5	368	1	330	0.278
0004871	signal transducer activity	55	649	201	2084	0.46	32	341	23	308	0.507
0004872	receptor activity	23	681	86	2199	0.617	14	359	9	322	0.577
0004879	ligand-dependent nuclear receptor activity	1	703	8	2277	0.626	0	373	1	330	0.952
0004888	transmembrane receptor activity	14	690	60	2225	0.416	8	365	6	325	0.964
0004930	G-protein coupled receptor activity	6	698	24	2261	0.807	2	371	4	327	0.577
0005057	receptor signaling protein activity	17	687	63	2222	0.72	12	361	5	326	0.22
0005102	receptor binding	16	688	53	2232	0.943	7	366	9	322	0.62
0005198	structural molecule activity	44	660	118	2167	0.309	28	345	16	315	0.191
0030528	transcription regulator activity	41	663	158	2127	0.353	18	355	23	308	0.299
0045182	translation regulator activity	5	699	30	2255	0.272	1	372	4	327	0.301
0005215	transporter activity	51	653	202	2083	0.21	26	347	25	306	0.879
0005489	electron transporter activity	3	701	26	2259	0.143	3	370	0	331	0.291
0005216	ion channel activity	10	694	42	2243	0.565	6	367	4	327	0.898
0005244	voltage-gated ion channel activity	4	700	22	2263	0.451	2	371	2	329	0.702
0005575	cellular_component	**257**	**447**	**966**	**1319**	**0.007**	135	238	122	209	0.917
0005623	cell	**236**	**468**	**876**	**1409**	**0.023**	121	252	115	216	0.571
0005622	intracellular	**178**	**526**	**679**	**1606**	**0.026**	92	281	86	245	0.753
0005737	cytoplasm	92	612	366	1919	0.066	49	324	43	288	0.956
0016023	cytoplasmic vesicle	12	692	29	2256	0.495	7	366	5	326	0.934
0005829	cytosol	11	693	68	2217	0.056	6	367	5	326	0.842
0005783	endoplasmic reticulum	10	694	47	2238	0.357	6	367	4	327	0.898
0005794	Golgi apparatus	5	699	20	2265	0.854	1	372	4	327	0.301
0005815	microtubule organizing center	2	702	7	2278	0.765	2	371	0	331	0.532
0005739	mitochondrion	21	683	84	2201	0.449	13	360	8	323	0.542
0005840	ribosome	7	697	17	2268	0.682	4	369	3	328	0.874
0005773	vacuole	2	702	12	2273	0.615	2	371	0	331	0.532
0005764	lysosome	0	704	5	2280	0.475	0	373	0	331	-
0005856	cytoskeleton	23	681	62	2223	0.52	16	357	7	324	0.159
0005694	chromosome	8	696	32	2253	0.73	4	369	4	327	0.852
0000228	nuclear chromosome	0	704	5	2280	0.475	0	373	0	331	-
0005634	nucleus	73	631	299	1986	0.065	37	336	36	295	0.771
0005635	nuclear membrane	3	701	14	2271	0.773	2	371	1	330	0.917
0005730	nucleolus	4	700	7	2278	0.517	2	371	2	329	0.702
0005654	nucleoplasm	14	690	58	2227	0.49	6	367	8	323	0.62
0005777	peroxisome	2	702	7	2278	0.765	0	373	2	329	0.427
0005886	plasma membrane	31	673	125	2160	0.31	13	360	18	313	0.282
0005576	extracellular region	18	686	58	2227	0.913	10	363	8	323	0.986
0005578	extracellular matrix (sensu Metazoa)	10	694	25	2260	0.615	5	368	5	326	0.898

Methoprene ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	365	232	1424	1001	0.303	**208**	**153**	**157**	**79**	**0.036**
0007610	behavior	38	559	120	2305	0.197	17	344	21	215	0.06
0030534	adult behavior	6	591	17	2408	0.615	3	358	3	233	0.914
0030537	larval behavior	3	594	6	2419	0.545	2	359	1	235	0.71
0007611	learning and/or memory	7	590	17	2408	0.365	3	358	4	232	0.569
0007612	learning	4	593	11	2414	0.727	3	358	1	235	0.934
0007613	memory	4	593	7	2418	0.314	1	360	3	233	0.346
0007626	locomotory behavior	28	569	92	2333	0.375	13	348	15	221	0.174
0007635	chemosensory behavior	4	593	13	2412	0.931	2	359	2	234	0.934
0007622	rhythmic behavior	4	593	10	2415	0.621	1	360	3	233	0.346
0048512	circadian behavior	4	593	9	2416	0.515	1	360	3	233	0.346
0009987	cellular process	337	260	1324	1101	0.442	**190**	**171**	**147**	**89**	**0.025**
0007154	cell communication	101	496	386	2039	0.594	**42**	**319**	**59**	**177**	**3E-05**
0007155	cell adhesion	**27**	**570**	**58**	**2367**	**0.007**	**9**	**352**	**18**	**218**	**0.006**
0008037	cell recognition	0	597	2	2423	0.852	0	361	0	236	-
0008038	neuronal cell recognition	0	597	2	2423	0.852	0	361	0	236	-
0016337	cell-cell adhesion	**13**	**584**	**22**	**2403**	**0.017**	**3**	**358**	**10**	**226**	**0.012**
0016339	calcium-dependent cell-cell adhesion	**3**	**594**	**1**	**2424**	**0.032**	1	360	2	234	0.71
0007156	homophilic cell adhesion	**4**	**593**	**2**	**2423**	**0.018**	1	360	3	233	0.346
0007160	cell-matrix adhesion	4	593	5	2420	0.149	1	360	3	233	0.346
0007267	cell-cell signaling	35	562	119	2306	0.397	**14**	**347**	**21**	**215**	**0.018**
0019226	transmission of nerve impulse	30	567	106	2319	0.562	13	348	17	219	0.075
0007268	synaptic transmission	24	573	77	2348	0.367	11	350	13	223	0.199
0007270	nerve-nerve synaptic transmission	3	594	13	2412	0.831	0	361	3	233	0.12
0001505	regulation of neurotransmitter levels	13	584	47	2378	0.832	8	353	5	231	0.836
0042133	neurotransmitter metabolism	2	595	6	2419	0.943	1	360	1	235	0.674
0007269	neurotransmitter secretion	11	586	42	2383	0.992	7	354	4	232	0.925
0007165	signal transduction	76	521	301	2124	0.887	**29**	**332**	**47**	**189**	**4E-05**
0007166	cell surface receptor linked signal transduction	31	566	125	2300	0.948	**8**	**353**	**23**	**213**	**1E-04**
0007167	enzyme linked receptor protein signaling pathway	12	585	33	2392	0.325	**1**	**360**	**11**	**225**	**6E-04**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	2	595	13	2412	0.763	0	361	2	234	0.304
0007179	transforming growth factor beta receptor signaling pathway	1	596	8	2417	0.816	0	361	1	235	0.83
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	10	587	21	2404	0.126	**1**	**360**	**9**	**227**	**0.003**
0007173	epidermal growth factor receptor signaling pathway	1	596	6	2419	0.911	0	361	1	235	0.83
0008286	insulin receptor signaling pathway	2	595	2	2423	0.372	0	361	2	234	0.304
0008293	torso signaling pathway	2	595	5	2420	0.911	1	360	1	235	0.674
0007186	G-protein coupled receptor protein signaling pathway	11	586	60	2365	0.446	5	356	6	230	0.473
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	594	2	2423	0.089	2	359	1	235	0.71
0007219	Notch signaling pathway	2	595	11	2414	0.962	1	360	1	235	0.674
0007224	smoothened signaling pathway	2	595	4	2421	0.747	1	360	1	235	0.674
0008063	Toll signaling pathway	0	597	4	2421	0.715	0	361	0	236	-
0016055	Wnt receptor signaling pathway	3	594	11	2414	0.858	1	360	2	234	0.71
0007242	intracellular signaling cascade	27	570	159	2266	0.079	13	348	14	222	0.255
0007263	nitric oxide mediated signal transduction	0	597	3	2422	0.893	0	361	0	236	-
0007243	protein kinase cascade	**3**	**594**	**41**	**2384**	**0.048**	1	360	2	234	0.71
0007259	JAK-STAT cascade	1	596	5	2420	0.747	0	361	1	235	0.83
0000165	MAPKKK cascade	2	595	33	2392	0.059	1	360	1	235	0.674
0019932	second-messenger-mediated signaling	6	591	16	2409	0.535	5	356	1	235	0.464
0019722	calcium-mediated signaling	3	594	12	2413	0.763	3	358	0	236	0.417
0048015	phosphoinositide-mediated signaling	3	594	2	2423	0.089	2	359	1	235	0.71
0007264	small GTPase mediated signal transduction	8	589	37	2388	0.883	4	357	4	232	0.806
0007265	Ras protein signal transduction	4	593	7	2418	0.314	2	359	2	234	0.934
0009966	regulation of signal transduction	5	592	27	2398	0.714	**0**	**361**	**5**	**231**	**0.02**
0007275	development	**106**	**491**	**348**	**2077**	**0.043**	**53**	**308**	**53**	**183**	**0.02**
0007568	aging	4	593	7	2418	0.314	3	358	1	235	0.934
0030154	cell differentiation	27	570	86	2339	0.315	14	347	13	223	0.462
0048468	cell development	17	580	53	2372	0.417	11	350	6	230	0.912
0000904	cellular morphogenesis during differentiation	3	594	15	2410	0.974	3	358	0	236	0.417
0042461	photoreceptor cell development	3	594	15	2410	0.974	3	358	0	236	0.417
0042051	eye photoreceptor development (sensu Endopterygota)	3	594	14	2411	0.931	3	358	0	236	0.417
0045165	cell fate commitment	13	584	33	2392	0.203	4	357	9	227	0.054

		Methoprene (p < 0.01)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	7	590	21	2404	0.644	3	358	4	232	0.569
0007400	neuroblast cell fate determination	3	594	5	2420	0.414	1	360	2	234	0.71
0001708	cell fate specification	2	595	5	2420	0.911	1	360	1	235	0.674
0007349	cellularization	3	594	7	2418	0.676	2	359	1	235	0.71
0040007	growth	10	587	26	2399	0.315	**2**	**359**	**8**	**228**	**0.021**
0002164	larval development	6	591	11	2414	0.191	1	360	5	231	0.074
0002165	larval or pupal development (sensu Insecta)	24	573	101	2324	0.965	11	350	13	223	0.199
0007552	metamorphosis	22	575	95	2330	0.884	10	351	12	224	0.213
0009653	morphogenesis	73	524	243	2182	0.133	**31**	**330**	**42**	**194**	**0.001**
0002009	morphogenesis of an epithelium	9	588	31	2394	0.811	3	358	6	230	0.182
0009887	organogenesis	63	534	219	2206	0.286	**26**	**335**	**37**	**199**	**0.002**
0001654	eye morphogenesis	12	585	43	2382	0.828	6	355	6	230	0.652
0008406	gonad development	**5**	**592**	**5**	**2420**	**0.045**	2	359	3	233	0.631
0007444	imaginal disc development	19	578	72	2353	0.889	7	354	12	224	0.057
0007494	midgut development	2	595	2	2423	0.372	0	361	2	234	0.304
0007517	muscle development	3	594	30	2395	0.184	2	359	1	235	0.71
0007399	neurogenesis	35	562	130	2295	0.702	**15**	**346**	**20**	**216**	**0.044**
0007409	axonogenesis	7	590	40	2385	0.51	3	358	4	232	0.569
0007411	axon guidance	6	591	29	2396	0.86	3	358	3	233	0.914
0007417	central nervous system development	8	589	31	2394	0.934	5	356	3	233	0.806
0016358	dendrite morphogenesis	1	596	13	2412	0.394	1	360	0	236	0.83
0042063	gliogenesis	0	597	11	2414	0.204	0	361	0	236	-
0007422	peripheral nervous system development	8	589	32	2393	0.872	3	358	5	231	0.33
0050767	regulation of neurogenesis	1	596	5	2420	0.747	1	360	0	236	0.83
0007424	tracheal system development (sensu Insecta)	5	592	30	2395	0.546	2	359	3	233	0.631
0048513	organ development	64	533	222	2203	0.275	**27**	**334**	**37**	**199**	**0.002**
0007389	pattern specification	19	578	53	2372	0.2	12	349	7	229	0.996
0048066	pigmentation	3	594	7	2418	0.676	2	359	1	235	0.71
0009791	post-embryonic development	6	591	11	2414	0.191	1	360	5	231	0.074
0009790	embryonic development	25	572	74	2351	0.205	13	348	12	224	0.499
0007530	sex determination	2	595	8	2417	0.705	1	360	1	235	0.674
0007548	sex differentiation	**8**	**589**	**10**	**2415**	**0.019**	4	357	4	232	0.806
0019827	stem cell maintenance	2	595	6	2419	0.943	0	361	2	234	0.304
0000003	reproduction	30	567	104	2321	0.502	13	348	17	219	0.075
0050793	regulation of development	8	589	35	2390	0.998	3	358	5	231	0.33
0007582	physiological process	334	263	1305	1120	0.373	193	168	141	95	0.153
0008152	metabolism	251	346	951	1474	0.223	148	213	103	133	0.578
0009056	catabolism	46	551	157	2268	0.325	31	330	15	221	0.399
0006091	energy pathways	**41**	**556**	**67**	**2358**	**2E-06**	**34**	**327**	**7**	**229**	**0.004**
0006118	electron transport	**20**	**577**	**36**	**2389**	**0.004**	**17**	**344**	**3**	**233**	**0.04**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	75	522	359	2066	0.182	45	316	30	206	0.97
0006259	DNA metabolism	13	584	67	2358	0.512	5	356	8	228	0.176
0006350	transcription	36	561	189	2236	0.167	20	341	16	220	0.655
0043170	macromolecule metabolism	125	472	536	1889	0.574	**63**	**298**	**62**	**174**	**0.013**
0019538	protein metabolism	95	502	463	1962	0.083	**44**	**317**	**51**	**185**	**0.003**
0006412	protein biosynthesis	22	575	121	2304	0.216	**7**	**354**	**15**	**221**	**0.01**
0006464	protein modification	41	556	216	2209	0.129	**15**	**346**	**26**	**210**	**0.002**
0006457	protein folding	13	584	31	2394	0.146	5	356	8	228	0.176
0005975	carbohydrate metabolism	**32**	**565**	**76**	**2349**	**0.012**	19	342	13	223	0.956
0006519	amino acid and derivative metabolism	16	581	55	2370	0.657	9	352	7	229	0.928
0006629	lipid metabolism	**28**	**569**	**65**	**2360**	**0.016**	21	340	7	229	0.158
0009308	amine metabolism	17	580	64	2361	0.888	9	352	8	228	0.695
0042440	pigment metabolism	4	593	8	2417	0.412	4	357	0	236	0.267
0042445	hormone metabolism	2	595	5	2420	0.911	1	360	1	235	0.674
0009058	biosynthesis	48	549	194	2231	0.959	29	332	19	217	0.884
0019748	secondary metabolism	4	593	10	2415	0.621	4	357	0	236	0.267
0019222	regulation of metabolism	40	557	194	2231	0.328	22	339	18	218	0.572
0016265	death	23	574	65	2360	0.165	9	352	14	222	0.055
0008219	cell death	19	578	57	2368	0.309	**6**	**355**	**13**	**223**	**0.017**
0016271	tissue death	5	592	22	2403	0.936	3	358	2	234	0.662
0042592	homeostasis	7	590	22	2403	0.718	5	356	2	234	0.835
0019725	cell homeostasis	7	590	19	2406	0.5	5	356	2	234	0.835
0050801	ion homeostasis	4	593	9	2416	0.515	3	358	1	235	0.934
0043062	extracellular structure organization and biogenesis	1	596	18	2407	0.193	1	360	0	236	0.83
0046903	secretion	18	579	84	2341	0.676	11	350	7	229	0.851
0048511	rhythmic process	4	593	12	2413	0.831	1	360	3	233	0.346

		Methoprene ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	69	528	278	2147	0.994	35	326	34	202	0.103
0050874	organismal physiological process	**57**	**540**	**171**	**2254**	**0.047**	30	331	27	209	0.258
0050875	cellular physiological process	311	286	1242	1183	0.735	178	183	133	103	0.109
0006810	transport	86	511	315	2110	0.398	48	313	38	198	0.404
0006811	ion transport	**37**	**560**	**83**	**2342**	**0.003**	23	338	14	222	0.965
0006818	hydrogen transport	**12**	**585**	**7**	**2418**	**8E-06**	11	350	1	235	0.053
0006836	neurotransmitter transport	0	597	6	2419	0.482	0	361	0	236	-
0006858	extracellular transport	**8**	**589**	**7**	**2418**	**0.003**	3	358	5	231	0.33
0006869	lipid transport	6	591	11	2414	0.191	4	357	2	234	0.914
0008643	carbohydrate transport	**8**	**589**	**7**	**2418**	**0.003**	3	358	5	231	0.33
0015031	protein transport	**23**	**574**	**156**	**2269**	**0.022**	12	349	11	225	0.54
0015837	amine transport	4	593	9	2416	0.515	2	359	2	234	0.934
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	5	592	9	2416	0.243	3	358	2	234	0.662
0016192	vesicle-mediated transport	22	575	98	2327	0.778	15	346	7	229	0.595
0045045	secretory pathway	17	580	79	2346	0.703	11	350	6	230	0.912
0046907	intracellular transport	**24**	**573**	**175**	**2250**	**0.006**	13	348	11	225	0.666
0051049	regulation of transport	5	592	13	2412	0.575	2	359	3	233	0.631
0008283	cell proliferation	**22**	**575**	**50**	**2375**	**0.029**	11	350	11	225	0.423
0007049	cell cycle	27	570	104	2321	0.889	15	346	12	224	0.739
0017145	stem cell division	4	593	8	2417	0.412	1	360	3	233	0.346
0016043	cell organization and biogenesis	57	540	217	2208	0.706	28	333	29	207	0.089
0000902	cellular morphogenesis	18	579	56	2369	0.394	8	353	10	226	0.243
0006996	organelle organization and biogenesis	46	551	192	2233	0.93	**21**	**340**	**25**	**211**	**0.047**
0007010	cytoskeleton organization and biogenesis	37	560	129	2296	0.457	**16**	**345**	**21**	**215**	**0.041**
0006997	nuclear organization and biogenesis	1	596	8	2417	0.816	1	360	0	236	0.83
0007028	cytoplasm organization and biogenesis	4	593	13	2412	0.931	2	359	2	234	0.934
0016044	membrane organization and biogenesis	4	593	4	2421	0.088	3	358	1	235	0.934
0051128	regulation of cell organization and biogenesis	1	596	11	2414	0.527	1	360	0	236	0.83
0016049	cell growth	**5**	**592**	**4**	**2421**	**0.022**	1	360	4	232	0.162
0050896	response to stimulus	45	552	131	2294	0.058	**20**	**341**	**25**	**211**	**0.033**
0006950	response to stress	**18**	**579**	**40**	**2385**	**0.044**	**4**	**357**	**14**	**222**	**0.002**
0009408	response to heat	**6**	**591**	**5**	**2420**	**0.012**	1	360	5	231	0.074
0006979	response to oxidative stress	1	596	1	2424	0.852	0	361	1	235	0.83
0051179	localization	93	504	336	2089	0.31	51	310	42	194	0.274
0006403	RNA localization	6	591	23	2402	0.915	3	358	3	233	0.914
0008104	protein localization	**26**	**571**	**166**	**2259**	**0.032**	13	348	13	223	0.362
0051234	establishment of localization	87	510	319	2106	0.399	48	313	39	197	0.33
0051235	maintenance of localization	2	595	1	2424	0.188	2	359	0	236	0.674
0050789	regulation of biological process	77	520	325	2100	0.797	**38**	**323**	**39**	**197**	**0.044**
0050790	regulation of enzyme activity	2	595	13	2412	0.763	1	360	1	235	0.674
0040029	regulation of gene expression, epigenetic	5	592	15	2410	0.757	3	358	2	234	0.662
0006306	DNA methylation	2	595	5	2420	0.911	1	360	1	235	0.674
0045814	negative regulation of gene expression, epigenetic	0	597	7	2418	0.401	0	361	0	236	-
0006342	chromatin silencing	0	597	7	2418	0.401	0	361	0	236	-
0003674	molecular_function	356	241	1408	1017	0.515	204	157	152	84	0.066
0016209	antioxidant activity	1	596	7	2418	0.943	1	360	0	236	0.83
0005488	binding	195	402	847	1578	0.32	**102**	**259**	**93**	**143**	**0.006**
0005509	calcium ion binding	14	583	44	2381	0.497	8	353	6	230	0.985
0030246	carbohydrate binding	2	595	12	2413	0.858	1	360	1	235	0.674
0008289	lipid binding	5	592	21	2404	0.857	3	358	2	234	0.662
0003676	nucleic acid binding	**58**	**539**	**366**	**2059**	**9E-04**	**27**	**334**	**31**	**205**	**0.032**
0003677	DNA binding	32	565	163	2262	0.263	18	343	14	222	0.752
0003682	chromatin binding	4	593	20	2405	0.901	2	359	2	234	0.934
0003700	transcription factor activity	11	586	76	2349	0.12	7	354	4	232	0.925
0003723	RNA binding	**15**	**582**	**108**	**2317**	**0.042**	5	356	10	226	0.056
0008135	translation factor activity, nucleic acid binding	5	592	29	2396	0.598	2	359	3	233	0.631
0000166	nucleotide binding	53	544	203	2222	0.752	25	336	28	208	0.054
0005515	protein binding	79	518	303	2122	0.676	**38**	**323**	**41**	**195**	**0.022**
0008134	transcription factor binding	5	592	24	2401	0.915	2	359	3	233	0.631
0008092	cytoskeletal protein binding	25	572	64	2361	0.062	12	349	13	223	0.274
0003779	actin binding	16	581	38	2387	0.096	10	351	6	230	0.928
0003824	catalytic activity	**190**	**407**	**650**	**1775**	**0.016**	120	241	70	166	0.408
0016787	hydrolase activity	83	514	277	2148	0.108	56	305	27	209	0.199
0003924	GTPase activity	5	592	31	2394	0.497	2	359	3	233	0.631
0004518	nuclease activity	1	596	13	2412	0.394	1	360	0	236	0.83

		Methoprene ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	23	574	90	2335	0.966	17	344	6	230	0.26
0004721	phosphoprotein phosphatase activity	4	593	25	2400	0.565	3	358	1	235	0.934
0016740	transferase activity	51	546	196	2229	0.776	27	334	24	212	0.317
0016301	kinase activity	27	570	113	2312	0.973	14	347	13	223	0.462
0004672	protein kinase activity	18	579	78	2347	0.904	8	353	10	226	0.243
0030234	enzyme regulator activity	20	577	91	2334	0.729	11	350	9	227	0.782
0003774	motor activity	5	592	22	2403	0.936	4	357	1	235	0.662
0004871	signal transducer activity	46	551	205	2220	0.609	**17**	**344**	**29**	**207**	**0.001**
0004872	receptor activity	20	577	84	2341	0.991	**4**	**357**	**16**	**220**	**4E-04**
0004879	ligand-dependent nuclear receptor activity	2	595	7	2418	0.816	1	360	1	235	0.674
0004888	transmembrane receptor activity	12	585	59	2366	0.645	**2**	**359**	**10**	**226**	**0.005**
0004930	G-protein coupled receptor activity	4	593	25	2400	0.565	2	359	2	234	0.934
0005057	receptor signaling protein activity	14	583	68	2357	0.633	9	352	5	231	0.985
0005102	receptor binding	13	584	54	2371	0.935	6	355	7	229	0.435
0005198	structural molecule activity	37	560	157	2268	0.878	17	344	20	216	0.091
0030528	transcription regulator activity	**28**	**569**	**170**	**2255**	**0.05**	17	344	11	225	0.864
0045182	translation regulator activity	5	592	29	2396	0.598	2	359	3	233	0.631
0005215	transporter activity	**75**	**522**	**176**	**2249**	**4E-05**	48	313	27	209	0.587
0005489	electron transporter activity	**11**	**586**	**18**	**2407**	**0.025**	9	352	2	234	0.25
0005216	ion channel activity	10	587	41	2384	0.88	**2**	**359**	**8**	**228**	**0.021**
0005244	voltage-gated ion channel activity	5	592	21	2404	0.857	1	360	4	232	0.162
0005575	cellular_component	251	346	998	1427	0.727	**137**	**224**	**114**	**122**	**0.015**
0005623	cell	225	372	918	1507	0.977	126	235	99	137	0.099
0005622	intracellular	173	424	722	1703	0.741	103	258	70	166	0.838
0005737	cytoplasm	**121**	**476**	**371**	**2054**	**0.004**	76	285	45	191	0.627
0016023	cytoplasmic vesicle	9	588	34	2391	0.998	6	355	3	233	0.968
0005829	cytosol	21	576	91	2334	0.88	13	348	8	228	0.928
0005783	endoplasmic reticulum	**18**	**579**	**39**	**2386**	**0.036**	12	349	6	230	0.763
0005794	Golgi apparatus	9	588	17	2408	0.096	5	356	4	232	0.968
0005815	microtubule organizing center	4	593	5	2420	0.149	**0**	**361**	**4**	**232**	**0.049**
0005739	mitochondrion	29	568	80	2345	0.088	20	341	9	227	0.444
0005840	ribosome	5	592	52	2373	0.053	2	359	3	233	0.631
0005773	vacuole	**9**	**588**	**7**	**2418**	**8E-04**	8	353	1	235	0.157
0005764	lysosome	1	596	5	2420	0.747	0	361	1	235	0.83
0005856	cytoskeleton	21	576	63	2362	0.278	8	353	13	223	0.056
0005694	chromosome	8	589	30	2395	0.998	3	358	5	231	0.33
0000228	nuclear chromosome	0	597	5	2420	0.583	0	361	0	236	-
0005634	nucleus	63	534	313	2112	0.136	37	324	26	210	0.871
0005635	nuclear membrane	3	594	15	2410	0.974	1	360	2	234	0.71
0005730	nucleolus	1	596	10	2415	0.61	0	361	1	235	0.83
0005654	nucleoplasm	10	587	64	2361	0.223	5	356	5	231	0.721
0005777	peroxisome	3	594	6	2419	0.545	2	359	1	235	0.71
0005886	plasma membrane	29	568	118	2307	0.922	**9**	**352**	**20**	**216**	**0.002**
0005576	extracellular region	18	579	52	2373	0.265	8	353	10	226	0.243
0005578	extracellular matrix (sensu Metazoa)	9	588	26	2399	0.498	**1**	**360**	**8**	**228**	**0.007**

		Manganese (p < 0.01)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	534	328	1255	905	0.057	210	123	324	205	0.644
0007610	behavior	55	807	103	2057	0.088	**37**	**296**	**18**	**511**	**1E-05**
0030534	adult behavior	5	857	18	2142	0.623	4	329	1	528	0.149
0030537	larval behavior	5	857	4	2156	0.153	4	329	1	528	0.149
0007611	learning and/or memory	5	857	19	2141	0.541	3	330	2	527	0.601
0007612	learning	4	858	11	2149	0.899	3	330	1	528	0.326
0007613	memory	2	860	9	2151	0.67	1	332	1	528	0.692
0007626	locomotory behavior	43	819	77	2083	0.088	**27**	**306**	**16**	**513**	**0.001**
0007635	chemosensory behavior	4	858	13	2147	0.851	3	330	1	528	0.326
0007622	rhythmic behavior	5	857	9	2151	0.764	**5**	**328**	**0**	**529**	**0.018**
0048512	circadian behavior	4	858	9	2151	0.898	**4**	**329**	**0**	**529**	**0.044**
0009987	cellular process	495	367	1166	994	0.093	203	130	292	237	0.111
0007154	cell communication	145	717	342	1818	0.54	**100**	**233**	**45**	**484**	**4E-16**
0007155	cell adhesion	25	837	60	2100	0.951	**16**	**317**	**9**	**520**	**0.015**
0008037	cell recognition	2	860	0	2160	0.145	2	331	0	529	0.29
0008038	neuronal cell recognition	2	860	0	2160	0.145	2	331	0	529	0.29
0016337	cell-cell adhesion	9	853	26	2134	0.856	5	328	4	525	0.481
0016339	calcium-dependent cell-cell adhesion	1	861	3	2157	0.691	0	333	1	528	0.815
0007156	homophilic cell adhesion	3	859	3	2157	0.475	2	331	1	528	0.685
0007160	cell-matrix adhesion	3	859	6	2154	0.96	2	331	1	528	0.685
0007267	cell-cell signaling	54	808	100	2060	0.079	**42**	**291**	**12**	**517**	**3E-09**
0019226	transmission of nerve impulse	46	816	90	2070	0.192	**35**	**298**	**11**	**518**	**2E-07**
0007268	synaptic transmission	34	828	67	2093	0.293	**27**	**306**	**7**	**522**	**2E-06**
0007270	nerve-nerve synaptic transmission	3	859	13	2147	0.555	3	330	0	529	0.111
0001505	regulation of neurotransmitter levels	22	840	38	2122	0.205	**17**	**316**	**5**	**524**	**4E-04**
0042133	neurotransmitter metabolism	4	858	4	2156	0.34	**4**	**329**	**0**	**529**	**0.044**
0007269	neurotransmitter secretion	18	844	35	2125	0.465	**13**	**320**	**5**	**524**	**0.007**
0007165	signal transduction	105	757	272	1888	0.804	**69**	**264**	**36**	**493**	**2E-09**
0007166	cell surface receptor linked signal transduction	54	808	102	2058	0.101	**36**	**297**	**18**	**511**	**2E-05**
0007167	enzyme linked receptor protein signaling pathway	14	848	31	2129	0.825	**11**	**322**	**3**	**526**	**0.005**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	4	858	11	2149	0.899	3	330	1	528	0.326
0007179	transforming growth factor beta receptor signaling pathway	3	859	6	2154	0.96	3	330	0	529	0.111
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	11	851	20	2140	0.508	**9**	**324**	**2**	**527**	**0.008**
0007173	epidermal growth factor receptor signaling pathway	3	859	4	2156	0.673	2	331	1	528	0.685
0008286	insulin receptor signaling pathway	0	862	4	2156	0.478	0	333	0	529	-
0008293	torso signaling pathway	3	859	4	2156	0.673	2	331	1	528	0.685
0007186	G-protein coupled receptor protein signaling pathway	24	838	47	2113	0.388	14	319	10	519	0.072
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	2	860	3	2157	0.942	2	331	0	529	0.29
0007219	Notch signaling pathway	6	856	7	2153	0.27	5	328	1	528	0.066
0007224	smoothened signaling pathway	1	861	5	2155	0.848	1	332	0	529	0.815
0008063	Toll signaling pathway	2	860	2	2158	0.691	0	333	2	527	0.692
0016055	Wnt receptor signaling pathway	6	856	8	2152	0.371	**6**	**327**	**0**	**529**	**0.007**
0007242	intracellular signaling cascade	52	810	134	2026	0.926	**33**	**300**	**19**	**510**	**3E-04**
0007263	nitric oxide mediated signal transduction	0	862	3	2157	0.649	0	333	0	529	-
0007243	protein kinase cascade	13	849	31	2129	0.986	7	326	6	523	0.396
0007259	JAK-STAT cascade	2	860	4	2156	0.848	1	332	1	528	0.692
0000165	MAPKKK cascade	10	852	25	2135	0.856	6	327	4	525	0.285
0019932	second-messenger-mediated signaling	4	858	18	2142	0.4	**4**	**329**	**0**	**529**	**0.044**
0019722	calcium-mediated signaling	2	860	13	2147	0.308	2	331	0	529	0.29
0048015	phosphoinositide-mediated signaling	2	860	3	2157	0.942	2	331	0	529	0.29
0007264	small GTPase mediated signal transduction	9	853	36	2124	0.267	3	330	6	523	0.987
0007265	Ras protein signal transduction	0	862	11	2149	0.078	0	333	0	529	-
0009966	regulation of signal transduction	8	854	24	2136	0.805	6	327	2	527	0.079
0007275	development	133	729	321	1839	0.735	**82**	**251**	**51**	**478**	**5E-09**
0007568	aging	2	860	9	2151	0.67	0	333	2	527	0.692
0030154	cell differentiation	36	826	77	2083	0.488	**25**	**308**	**11**	**518**	**2E-04**
0048468	cell development	20	842	50	2110	0.9	**13**	**320**	**7**	**522**	**0.027**
0000904	cellular morphogenesis during differentiation	5	857	13	2147	0.848	4	329	1	528	0.149
0042461	photoreceptor cell development	5	857	13	2147	0.848	4	329	1	528	0.149
0042051	eye photoreceptor development (sensu Endopterygota)	4	858	13	2147	0.851	3	330	1	528	0.326
0045165	cell fate commitment	17	845	29	2131	0.266	**13**	**320**	**4**	**525**	**0.003**

Manganese ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	9	853	19	2141	0.829	**7**	**326**	**2**	**527**	**0.037**
0007400	neuroblast cell fate determination	4	858	4	2156	0.34	2	331	2	527	0.963
0001708	cell fate specification	0	862	7	2153	0.21	0	333	0	529	-
0007349	cellularization	2	860	8	2152	0.805	0	333	2	527	0.692
0040007	growth	9	853	27	2133	0.775	3	330	6	523	0.987
0002164	larval development	4	858	13	2147	0.851	1	332	3	526	0.963
0002165	larval or pupal development (sensu Insecta)	36	826	89	2071	0.975	**24**	**309**	**12**	**517**	**8E-04**
0007552	metamorphosis	34	828	83	2077	0.979	**24**	**309**	**10**	**519**	**2E-04**
0009653	morphogenesis	93	769	223	1937	0.756	**65**	**268**	**28**	**501**	**1E-10**
0002009	morphogenesis of an epithelium	8	854	32	2128	0.305	2	331	6	523	0.667
0009887	organogenesis	85	777	197	1963	0.574	**62**	**271**	**23**	**506**	**2E-11**
0001654	eye morphogenesis	17	845	38	2122	0.807	**12**	**321**	**5**	**524**	**0.013**
0008406	gonad development	5	857	5	2155	0.248	4	329	1	528	0.149
0007444	imaginal disc development	23	839	68	2092	0.562	**19**	**314**	**4**	**525**	**3E-05**
0007494	midgut development	0	862	4	2156	0.478	0	333	0	529	-
0007517	muscle development	11	851	22	2138	0.673	**9**	**324**	**2**	**527**	**0.008**
0007399	neurogenesis	**60**	**802**	**105**	**2055**	**0.027**	**44**	**289**	**16**	**513**	**2E-08**
0007409	axonogenesis	19	843	28	2132	0.097	**14**	**319**	**5**	**524**	**0.003**
0007411	axon guidance	15	847	20	2140	0.089	**12**	**321**	**3**	**526**	**0.002**
0007417	central nervous system development	13	849	26	2134	0.623	**10**	**323**	**3**	**526**	**0.01**
0016358	dendrite morphogenesis	3	859	11	2149	0.77	2	331	1	528	0.685
0042063	gliogenesis	3	859	8	2152	0.808	2	331	1	528	0.685
0007422	peripheral nervous system development	12	850	28	2132	0.975	7	326	5	524	0.266
0050767	regulation of neurogenesis	2	860	4	2156	0.848	1	332	1	528	0.692
0007424	tracheal system development (sensu Insecta)	11	851	24	2136	0.846	**8**	**325**	**3**	**526**	**0.043**
0048513	organ development	86	776	200	1960	0.589	**62**	**271**	**24**	**505**	**4E-11**
0007389	pattern specification	19	843	53	2107	0.784	**12**	**321**	**7**	**522**	**0.047**
0048066	pigmentation	3	859	7	2153	0.805	2	331	1	528	0.685
0009791	post-embryonic development	4	858	13	2147	0.851	1	332	3	526	0.963
0009790	embryonic development	34	828	65	2095	0.234	**22**	**311**	**12**	**517**	**0.003**
0007530	sex determination	3	859	7	2153	0.805	3	330	0	529	0.111
0007548	sex differentiation	7	855	11	2149	0.475	5	328	2	527	0.162
0019827	stem cell maintenance	2	860	6	2154	0.864	2	331	0	529	0.29
0000003	reproduction	36	826	98	2062	0.736	**23**	**310**	**13**	**516**	**0.003**
0050793	regulation of development	13	849	30	2130	0.936	6	327	7	522	0.784
0007582	physiological process	492	370	1147	1013	0.052	189	144	303	226	0.936
0008152	metabolism	356	506	846	1314	0.298	**117**	**216**	**239**	**290**	**0.004**
0009056	catabolism	55	807	148	2012	0.699	20	313	35	494	0.831
0006091	energy pathways	37	825	71	2089	0.217	**3**	**330**	**34**	**495**	**2E-04**
0006118	electron transport	18	844	38	2122	0.648	**2**	**331**	**16**	**513**	**0.029**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	112	750	322	1838	0.194	52	281	60	469	0.087
0006259	DNA metabolism	17	845	63	2097	0.182	7	326	10	519	0.973
0006350	transcription	57	805	168	1992	0.305	**38**	**295**	**19**	**510**	**1E-05**
0043170	macromolecule metabolism	200	662	461	1699	0.286	**55**	**278**	**145**	**384**	**3E-04**
0019538	protein metabolism	156	706	402	1758	0.782	49	284	107	422	0.05
0006412	protein biosynthesis	51	811	92	2068	0.065	**1**	**332**	**50**	**479**	**7E-08**
0006464	protein modification	**59**	**803**	**198**	**1962**	**0.046**	25	308	34	495	0.636
0006457	protein folding	15	847	29	2131	0.512	6	327	9	520	0.875
0005975	carbohydrate metabolism	**42**	**820**	**66**	**2094**	**0.02**	**7**	**326**	**35**	**494**	**0.005**
0006519	amino acid and derivative metabolism	**30**	**832**	**41**	**2119**	**0.014**	9	324	21	508	0.425
0006629	lipid metabolism	30	832	63	2097	0.488	7	326	23	506	0.119
0009308	amine metabolism	**33**	**829**	**48**	**2112**	**0.019**	10	323	23	506	0.412
0042440	pigment metabolism	4	858	8	2152	0.961	1	332	3	526	0.963
0042445	hormone metabolism	3	859	4	2156	0.673	2	331	1	528	0.685
0009058	biosynthesis	**86**	**776**	**156**	**2004**	**0.014**	**9**	**324**	**77**	**452**	**3E-08**
0019748	secondary metabolism	5	857	9	2151	0.764	2	331	3	526	0.691
0019222	regulation of metabolism	61	801	173	1987	0.429	**39**	**294**	**22**	**507**	**5E-05**
0016265	death	24	838	64	2096	0.885	10	323	14	515	0.923
0008219	cell death	21	841	55	2105	0.963	9	324	12	517	0.86
0016271	tissue death	6	856	21	2139	0.607	3	330	3	526	0.878
0042592	homeostasis	8	854	21	2139	0.925	4	329	4	525	0.765
0019725	cell homeostasis	7	855	19	2141	0.971	3	330	4	525	0.874
0050801	ion homeostasis	3	859	10	2150	0.898	2	331	1	528	0.685
0043062	extracellular structure organization and biogenesis	8	854	11	2149	0.289	5	328	3	526	0.304
0046903	secretion	**39**	**823**	**63**	**2097**	**0.036**	19	314	20	509	0.248
0048511	rhythmic process	6	856	10	2150	0.603	**6**	**327**	**0**	**529**	**0.007**

Manganese ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	90	772	257	1903	0.284	**53**	**280**	**37**	**492**	**5E-05**
0050874	organismal physiological process	72	790	156	2004	0.324	**47**	**286**	**25**	**504**	**2E-06**
0050875	cellular physiological process	463	399	1090	1070	0.116	179	154	284	245	0.96
0006810	transport	127	735	274	1886	0.15	55	278	72	457	0.283
0006811	ion transport	39	823	81	2079	0.378	18	315	21	508	0.413
0006818	hydrogen transport	6	856	13	2147	0.967	0	333	6	523	0.126
0006836	neurotransmitter transport	**5**	**857**	**1**	**2159**	**0.012**	**5**	**328**	**0**	**529**	**0.018**
0006858	extracellular transport	**9**	**853**	**6**	**2154**	**0.016**	2	331	7	522	0.501
0006869	lipid transport	4	858	13	2147	0.851	1	332	3	526	0.963
0008643	carbohydrate transport	5	857	10	2150	0.899	2	331	3	526	0.691
0015031	protein transport	55	807	124	2036	0.557	19	314	36	493	0.617
0015837	amine transport	**8**	**854**	**5**	**2155**	**0.02**	5	328	3	526	0.304
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	**0**	**862**	**14**	**2146**	**0.038**	0	333	0	529	-
0016192	vesicle-mediated transport	40	822	80	2080	0.277	20	313	20	509	0.178
0045045	secretory pathway	36	826	60	2100	0.062	16	317	20	509	0.578
0046907	intracellular transport	59	803	140	2020	0.778	21	312	38	491	0.72
0051049	regulation of transport	6	856	12	2148	0.848	3	330	3	526	0.878
0008283	cell proliferation	22	840	50	2110	0.799	**15**	**318**	**7**	**522**	**0.008**
0007049	cell cycle	35	827	96	2064	0.712	**21**	**312**	**14**	**515**	**0.013**
0017145	stem cell division	4	858	8	2152	0.961	2	331	2	527	0.963
0016043	cell organization and biogenesis	77	785	197	1963	0.927	**49**	**284**	**28**	**501**	**4E-06**
0000902	cellular morphogenesis	21	841	53	2107	0.919	**15**	**318**	**6**	**523**	**0.004**
0006996	organelle organization and biogenesis	63	799	175	1985	0.512	**36**	**297**	**27**	**502**	**0.003**
0007010	cytoskeleton organization and biogenesis	50	812	116	2044	0.704	**29**	**304**	**21**	**508**	**0.006**
0006997	nuclear organization and biogenesis	2	860	7	2153	0.96	1	332	1	528	0.692
0007028	cytoplasm organization and biogenesis	8	854	9	2151	0.153	3	330	5	524	0.765
0016044	membrane organization and biogenesis	3	859	5	2155	0.864	2	331	1	528	0.685
0051128	regulation of cell organization and biogenesis	1	861	11	2149	0.218	0	333	1	528	0.815
0016049	cell growth	1	861	8	2152	0.43	0	333	1	528	0.815
0050896	response to stimulus	55	807	121	2039	0.46	27	306	28	501	0.133
0006950	response to stress	20	842	38	2122	0.385	9	324	11	518	0.719
0009408	response to heat	5	857	6	2154	0.362	4	329	1	528	0.149
0006979	response to oxidative stress	0	862	2	2158	0.912	0	333	0	529	-
0051179	localization	133	729	296	1864	0.242	59	274	74	455	0.168
0006403	RNA localization	**3**	**859**	**26**	**2134**	**0.049**	2	331	1	528	0.685
0008104	protein localization	56	806	136	2024	0.904	19	314	37	492	0.545
0051234	establishment of localization	130	732	276	1884	0.106	58	275	72	457	0.155
0051235	maintenance of localization	1	861	2	2158	0.649	1	332	0	529	0.815
0050789	regulation of biological process	103	759	299	1861	0.185	**60**	**273**	**43**	**486**	**2E-05**
0050790	regulation of enzyme activity	3	859	12	2148	0.655	1	332	2	527	0.685
0040029	regulation of gene expression, epigenetic	**1**	**861**	**19**	**2141**	**0.037**	1	332	0	529	0.815
0006306	DNA methylation	1	861	6	2154	0.677	1	332	0	529	0.815
0045814	negative regulation of gene expression, epigenetic	0	862	7	2153	0.21	0	333	0	529	-
0006342	chromatin silencing	0	862	7	2153	0.21	0	333	0	529	-
0003674	molecular_function	**528**	**334**	**1236**	**924**	**0.047**	208	125	320	209	0.612
0016209	antioxidant activity	1	861	7	2153	0.54	0	333	1	528	0.815
0005488	binding	304	558	738	1422	0.595	**139**	**194**	**165**	**364**	**0.002**
0005509	calcium ion binding	21	841	37	2123	0.245	11	322	10	519	0.279
0030246	carbohydrate binding	5	857	9	2151	0.764	1	332	4	525	0.691
0008289	lipid binding	9	853	17	2143	0.636	4	329	5	524	0.987
0003676	nucleic acid binding	124	738	300	1860	0.767	48	285	76	453	0.936
0003677	DNA binding	49	813	146	2014	0.315	**37**	**296**	**12**	**517**	**1E-07**
0003682	chromatin binding	3	859	21	2139	0.129	2	331	1	528	0.685
0003700	transcription factor activity	24	838	63	2097	0.939	**21**	**312**	**3**	**526**	**2E-06**
0003723	RNA binding	35	827	88	2072	0.933	**5**	**328**	**30**	**499**	**0.004**
0008135	translation factor activity, nucleic acid binding	11	851	23	2137	0.759	**0**	**333**	**11**	**518**	**0.019**
0000166	nucleotide binding	67	795	189	1971	0.424	30	303	37	492	0.345
0005515	protein binding	119	743	263	1897	0.248	**71**	**262**	**48**	**481**	**7E-07**
0008134	transcription factor binding	7	855	22	2138	0.75	**6**	**327**	**1**	**528**	**0.029**
0008092	cytoskeletal protein binding	33	829	56	2104	0.09	**19**	**314**	**14**	**515**	**0.036**
0003779	actin binding	**23**	**839**	**31**	**2129**	**0.031**	10	323	13	516	0.79
0003824	catalytic activity	237	625	603	1557	0.85	**71**	**262**	**166**	**363**	**0.002**
0016787	hydrolase activity	93	769	267	1893	0.253	37	296	56	473	0.897
0003924	GTPase activity	11	851	25	2135	0.932	2	331	9	520	0.276
0004518	nuclease activity	6	856	8	2152	0.371	0	333	6	523	0.126

Manganese ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	27	835	86	2074	0.315	13	320	14	515	0.406
0004721	phosphoprotein phosphatase activity	4	858	25	2135	0.119	3	330	1	528	0.326
0016740	transferase activity	67	795	180	1980	0.664	23	310	44	485	0.534
0016301	kinase activity	38	824	102	2058	0.783	18	315	20	509	0.337
0004672	protein kinase activity	24	838	72	2088	0.508	13	320	11	518	0.17
0030234	enzyme regulator activity	31	831	80	2080	0.972	17	316	14	515	0.089
0003774	motor activity	6	856	21	2139	0.607	4	329	2	527	0.32
0004871	signal transducer activity	67	795	184	1976	0.55	**42**	**291**	**25**	**504**	**4E-05**
0004872	receptor activity	27	835	77	2083	0.632	**18**	**315**	**9**	**520**	**0.005**
0004879	ligand-dependent nuclear receptor activity	4	858	5	2155	0.49	3	330	1	528	0.326
0004888	transmembrane receptor activity	14	848	57	2103	0.126	**11**	**322**	**3**	**526**	**0.005**
0004930	G-protein coupled receptor activity	6	856	23	2137	0.464	5	328	1	528	0.066
0005057	receptor signaling protein activity	18	844	64	2096	0.225	10	323	8	521	0.213
0005102	receptor binding	21	841	46	2114	0.704	**15**	**318**	**6**	**523**	**0.004**
0005198	structural molecule activity	**68**	**794**	**126**	**2034**	**0.046**	23	310	45	484	0.472
0030528	transcription regulator activity	52	810	146	2014	0.517	**37**	**296**	**15**	**514**	**1E-06**
0045182	translation regulator activity	11	851	23	2137	0.759	**0**	**333**	**11**	**518**	**0.019**
0005215	transporter activity	**86**	**776**	**165**	**1995**	**0.042**	30	303	56	473	0.525
0005489	electron transporter activity	10	852	19	2141	0.612	1	332	9	520	0.123
0005216	ion channel activity	13	849	38	2122	0.743	**10**	**323**	**3**	**526**	**0.01**
0005244	voltage-gated ion channel activity	9	853	17	2143	0.636	**8**	**325**	**1**	**528**	**0.006**
0005575	cellular_component	376	486	873	1287	0.116	140	193	236	293	0.503
0005623	cell	350	512	793	1367	0.051	129	204	221	308	0.416
0005622	intracellular	267	595	628	1532	0.323	**84**	**249**	**183**	**346**	**0.005**
0005737	cytoplasm	**166**	**696**	**326**	**1834**	**0.006**	**30**	**303**	**136**	**393**	**2E-09**
0016023	cytoplasmic vesicle	18	844	25	2135	0.075	9	324	9	520	0.449
0005829	cytosol	**43**	**819**	**69**	**2091**	**0.024**	**0**	**333**	**43**	**486**	**2E-07**
0005783	endoplasmic reticulum	16	846	41	2119	0.943	**0**	**333**	**16**	**513**	**0.003**
0005794	Golgi apparatus	6	856	20	2140	0.689	2	331	4	525	0.878
0005815	microtubule organizing center	3	859	6	2154	0.96	3	330	0	529	0.111
0005739	mitochondrion	38	824	71	2089	0.166	**3**	**330**	**35**	**494**	**1E-04**
0005840	ribosome	**28**	**834**	**29**	**2131**	**9E-04**	**0**	**333**	**28**	**501**	**5E-05**
0005773	vacuole	5	857	11	2149	0.972	0	333	5	524	0.187
0005764	lysosome	1	861	5	2155	0.848	0	333	1	528	0.815
0005856	cytoskeleton	21	841	63	2097	0.547	**14**	**319**	**7**	**522**	**0.015**
0005694	chromosome	6	856	32	2128	0.117	5	328	1	528	0.066
0000228	nuclear chromosome	1	861	4	2156	0.942	1	332	0	529	0.815
0005634	nucleus	96	766	280	1880	0.189	**53**	**280**	**43**	**486**	**6E-04**
0005635	nuclear membrane	3	859	15	2145	0.392	1	332	2	527	0.685
0005730	nucleolus	4	858	7	2153	0.808	1	332	3	526	0.963
0005654	nucleoplasm	14	848	60	2100	0.085	4	329	10	519	0.615
0005777	peroxisome	4	858	5	2155	0.49	0	333	4	525	0.282
0005886	plasma membrane	50	812	97	2063	0.156	**34**	**299**	**16**	**513**	**2E-05**
0005576	extracellular region	19	843	51	2109	0.9	**16**	**317**	**3**	**526**	**1E-04**
0005578	extracellular matrix (sensu Metazoa)	9	853	26	2134	0.856	**9**	**324**	**0**	**529**	**5E-04**

		cGMP ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	294	211	1495	1022	0.658	154	125	140	86	0.15
0007610	behavior	33	472	125	2392	0.182	16	263	17	209	0.531
0030534	adult behavior	3	502	20	2497	0.847	1	278	2	224	0.855
0030537	larval behavior	2	503	7	2510	0.997	0	279	2	224	0.389
0007611	learning and/or memory	7	498	17	2500	0.171	3	276	4	222	0.779
0007612	learning	**6**	**499**	**9**	**2508**	**0.038**	3	276	3	223	0.878
0007613	memory	2	503	9	2508	0.784	1	278	1	225	0.574
0007626	locomotory behavior	22	483	98	2419	0.718	11	268	11	215	0.774
0007635	chemosensory behavior	5	500	12	2505	0.279	3	276	2	224	0.813
0007622	rhythmic behavior	**7**	**498**	**7**	**2510**	**0.003**	3	276	4	222	0.779
0048512	circadian behavior	**6**	**499**	**7**	**2510**	**0.013**	2	277	4	222	0.501
0009987	cellular process	273	232	1388	1129	0.69	143	136	130	96	0.188
0007154	cell communication	96	409	391	2126	0.061	62	217	34	192	0.054
0007155	cell adhesion	**22**	**483**	**63**	**2454**	**0.031**	15	264	7	219	0.304
0008037	cell recognition	1	504	1	2516	0.753	1	278	0	226	0.916
0008038	neuronal cell recognition	1	504	1	2516	0.753	1	278	0	226	0.916
0016337	cell-cell adhesion	10	495	25	2492	0.096	6	273	4	222	0.987
0016339	calcium-dependent cell-cell adhesion	2	503	2	2515	0.265	1	278	1	225	0.574
0007156	homophilic cell adhesion	3	502	3	2514	0.101	2	277	1	225	0.855
0007160	cell-matrix adhesion	0	505	9	2508	0.369	0	279	0	226	-
0007267	cell-cell signaling	29	476	125	2392	0.54	19	260	10	216	0.34
0019226	transmission of nerve impulse	27	478	109	2408	0.375	18	261	9	217	0.304
0007268	synaptic transmission	22	483	79	2438	0.21	15	264	7	219	0.304
0007270	nerve-nerve synaptic transmission	1	504	15	2502	0.43	0	279	1	225	0.916
0001505	regulation of neurotransmitter levels	16	489	44	2473	0.056	12	267	4	222	0.174
0042133	neurotransmitter metabolism	**4**	**501**	**4**	**2513**	**0.04**	3	276	1	225	0.77
0007269	neurotransmitter secretion	12	493	41	2476	0.326	9	270	3	223	0.272
0007165	signal transduction	70	435	307	2210	0.337	42	237	28	198	0.464
0007166	cell surface receptor linked signal transduction	31	474	125	2392	0.329	16	263	15	211	0.815
0007167	enzyme linked receptor protein signaling pathway	**14**	**491**	**31**	**2486**	**0.016**	5	274	9	217	0.223
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3	502	12	2505	0.996	1	278	2	224	0.855
0007179	transforming growth factor beta receptor signaling pathway	2	503	7	2510	0.997	1	278	1	225	0.574
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	**11**	**494**	**20**	**2497**	**0.01**	4	275	7	219	0.334
0007173	epidermal growth factor receptor signaling pathway	3	502	4	2513	0.177	0	279	3	223	0.178
0008286	insulin receptor signaling pathway	0	505	4	2513	0.821	0	279	0	226	-
0008293	torso signaling pathway	**4**	**501**	**3**	**2514**	**0.018**	1	278	3	223	0.474
0007186	G-protein coupled receptor protein signaling pathway	9	496	62	2455	0.447	8	271	1	225	0.087
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	1	504	4	2513	0.687	1	278	0	226	0.916
0007219	Notch signaling pathway	4	501	9	2508	0.323	2	277	2	224	0.77
0007224	smoothened signaling pathway	1	504	5	2512	0.586	0	279	1	225	0.916
0008063	Toll signaling pathway	2	503	2	2515	0.265	1	278	1	225	0.574
0016055	Wnt receptor signaling pathway	**6**	**499**	**8**	**2509**	**0.023**	2	277	4	222	0.501
0007242	intracellular signaling cascade	38	467	148	2369	0.193	25	254	13	213	0.234
0007263	nitric oxide mediated signal transduction	0	505	3	2514	0.998	0	279	0	226	-
0007243	protein kinase cascade	12	493	32	2485	0.091	6	273	6	220	0.939
0007259	JAK-STAT cascade	1	504	5	2512	0.586	0	279	1	225	0.916
0000165	MAPKKK cascade	**11**	**494**	**24**	**2493**	**0.034**	6	273	5	221	0.795
0019932	second-messenger-mediated signaling	2	503	20	2497	0.5	2	277	0	226	0.574
0019722	calcium-mediated signaling	0	505	15	2502	0.164	0	279	0	226	-
0048015	phosphoinositide-mediated signaling	1	504	4	2513	0.687	1	278	0	226	0.916
0007264	small GTPase mediated signal transduction	9	496	36	2481	0.693	6	273	3	223	0.721
0007265	Ras protein signal transduction	4	501	7	2510	0.178	4	275	0	226	0.193
0009966	regulation of signal transduction	8	497	24	2493	0.305	3	276	5	221	0.51
0007275	development	**94**	**411**	**360**	**2157**	**0.016**	50	229	44	182	0.742
0007568	aging	2	503	9	2508	0.784	1	278	1	225	0.574
0030154	cell differentiation	20	485	93	2424	0.874	10	269	10	216	0.801
0048468	cell development	11	494	59	2458	0.949	7	272	4	222	0.795
0000904	cellular morphogenesis during differentiation	1	504	17	2500	0.339	1	278	0	226	0.916
0042461	photoreceptor cell development	1	504	17	2500	0.339	1	278	0	226	0.916
0042051	eye photoreceptor development (sensu Endopterygota)	1	504	16	2501	0.382	1	278	0	226	0.916
0045165	cell fate commitment	9	496	37	2480	0.746	**1**	**278**	**8**	**218**	**0.019**

		cGMP ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	4	501	24	2493	0.927	1	278	3	223	0.474
0007400	neuroblast cell fate determination	2	503	6	2511	0.877	1	278	1	225	0.574
0001708	cell fate specification	0	505	7	2510	0.497	0	279	0	226	-
0007349	cellularization	2	503	8	2509	0.885	0	279	2	224	0.389
0040007	growth	5	500	31	2486	0.817	2	277	3	223	0.813
0002164	larval development	5	500	12	2505	0.279	2	277	3	223	0.813
0002165	larval or pupal development (sensu Insecta)	25	480	100	2417	0.377	13	266	12	214	0.898
0007552	metamorphosis	24	481	93	2424	0.318	12	267	12	214	0.749
0009653	morphogenesis	**69**	**436**	**247**	**2270**	**0.012**	38	241	31	195	0.921
0002009	morphogenesis of an epithelium	11	494	29	2488	0.104	4	275	7	219	0.334
0009887	organogenesis	**60**	**445**	**222**	**2295**	**0.038**	31	248	29	197	0.648
0001654	eye morphogenesis	9	496	46	2471	0.91	3	276	6	220	0.319
0008406	gonad development	4	501	6	2511	0.12	2	277	2	224	0.77
0007444	imaginal disc development	16	489	75	2442	0.933	6	273	10	216	0.232
0007494	midgut development	1	504	3	2514	0.821	1	278	0	226	0.916
0007517	muscle development	6	499	27	2490	0.995	6	273	0	226	0.071
0007399	neurogenesis	35	470	130	2387	0.137	17	262	18	208	0.518
0007409	axonogenesis	6	499	41	2476	0.594	3	276	3	223	0.878
0007411	axon guidance	5	500	30	2487	0.874	3	276	2	224	0.813
0007417	central nervous system development	10	495	29	2488	0.198	4	275	6	220	0.51
0016358	dendrite morphogenesis	1	504	13	2504	0.547	0	279	1	225	0.916
0042063	gliogenesis	2	503	9	2508	0.784	2	277	0	226	0.574
0007422	peripheral nervous system development	8	497	32	2485	0.728	3	276	5	221	0.51
0050767	regulation of neurogenesis	1	504	5	2512	0.586	0	279	1	225	0.916
0007424	tracheal system development (sensu Insecta)	**12**	**493**	**23**	**2494**	**0.01**	6	273	6	220	0.939
0048513	organ development	60	445	226	2291	0.051	31	248	29	197	0.648
0007389	pattern specification	18	487	54	2463	0.08	9	270	9	217	0.83
0048066	pigmentation	4	501	6	2511	0.12	2	277	2	224	0.77
0009791	post-embryonic development	5	500	12	2505	0.279	2	277	3	223	0.813
0009790	embryonic development	**31**	**474**	**68**	**2449**	**1E-04**	16	263	15	211	0.815
0007530	sex determination	2	503	8	2509	0.885	1	278	1	225	0.574
0007548	sex differentiation	4	501	14	2503	0.755	2	277	2	224	0.77
0019827	stem cell maintenance	3	502	5	2512	0.27	1	278	2	224	0.855
0000003	reproduction	22	483	112	2405	0.98	8	271	14	212	0.109
0050793	regulation of development	4	501	39	2478	0.269	2	277	2	224	0.77
0007582	physiological process	266	239	1373	1144	0.47	**135**	**144**	**131**	**95**	**0.04**
0008152	metabolism	201	304	1001	1516	0.971	**98**	**181**	**103**	**123**	**0.022**
0009056	catabolism	29	476	174	2343	0.389	19	260	10	216	0.34
0006091	energy pathways	20	485	88	2429	0.703	14	265	6	220	0.261
0006118	electron transport	6	499	50	2467	0.301	4	275	2	224	0.878
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	73	432	361	2156	0.997	46	233	27	199	0.188
0006259	DNA metabolism	13	492	67	2450	0.968	9	270	4	222	0.456
0006350	transcription	33	472	192	2325	0.446	**25**	**254**	**8**	**218**	**0.023**
0043170	macromolecule metabolism	115	390	546	1971	0.634	**50**	**229**	**65**	**161**	**0.005**
0019538	protein metabolism	92	413	466	2051	0.925	**40**	**239**	**52**	**174**	**0.017**
0006412	protein biosynthesis	20	485	123	2394	0.435	10	269	10	216	0.801
0006464	protein modification	45	460	212	2305	0.786	21	258	24	202	0.291
0006457	protein folding	12	493	32	2485	0.091	**0**	**279**	**12**	**214**	**3E-04**
0005975	carbohydrate metabolism	26	479	82	2435	0.05	11	268	15	211	0.246
0006519	amino acid and derivative metabolism	14	491	57	2460	0.599	**3**	**276**	**11**	**215**	**0.021**
0006629	lipid metabolism	18	487	75	2442	0.58	**5**	**274**	**13**	**213**	**0.032**
0009308	amine metabolism	17	488	64	2453	0.371	**4**	**275**	**13**	**213**	**0.015**
0042440	pigment metabolism	2	503	10	2507	0.701	1	278	1	225	0.574
0042445	hormone metabolism	**4**	**501**	**3**	**2514**	**0.018**	2	277	2	224	0.77
0009058	biosynthesis	40	465	202	2315	0.991	18	261	22	204	0.233
0019748	secondary metabolism	2	503	12	2505	0.908	1	278	1	225	0.574
0019222	regulation of metabolism	39	466	195	2322	0.942	**28**	**251**	**11**	**215**	**0.046**
0016265	death	14	491	74	2443	0.952	6	273	8	218	0.501
0008219	cell death	12	493	64	2453	0.95	5	274	7	219	0.507
0016271	tissue death	6	499	21	2496	0.609	4	275	2	224	0.878
0042592	homeostasis	8	497	21	2496	0.184	4	275	4	222	0.954
0019725	cell homeostasis	7	498	19	2498	0.255	3	276	4	222	0.779
0050801	ion homeostasis	5	500	8	2509	0.083	2	277	3	223	0.813
0043062	extracellular structure organization and biogenesis	3	502	16	2501	0.841	2	277	1	225	0.855
0046903	secretion	17	488	85	2432	0.902	11	268	6	220	0.582
0048511	rhythmic process	**7**	**498**	**9**	**2508**	**0.01**	3	276	4	222	0.779

cGMP ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	57	448	290	2227	0.941	34	245	23	203	0.57
0050874	organismal physiological process	41	464	187	2330	0.658	25	254	16	210	0.545
0050875	cellular physiological process	250	255	1303	1214	0.379	127	152	123	103	0.057
0006810	transport	64	441	337	2180	0.718	32	247	32	194	0.442
0006811	ion transport	25	480	95	2422	0.267	13	266	12	214	0.898
0006818	hydrogen transport	6	499	13	2504	0.152	5	274	1	225	0.328
0006836	neurotransmitter transport	1	504	5	2512	0.586	1	278	0	226	0.916
0006858	extracellular transport	3	502	12	2505	0.996	0	279	3	223	0.178
0006869	lipid transport	3	502	14	2503	0.824	1	278	2	224	0.855
0008643	carbohydrate transport	4	501	11	2506	0.491	2	277	2	224	0.77
0015031	protein transport	22	483	157	2360	0.126	11	268	11	215	0.774
0015837	amine transport	2	503	11	2506	0.807	0	279	2	224	0.389
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	2	503	12	2505	0.908	1	278	1	225	0.574
0016192	vesicle-mediated transport	17	488	103	2414	0.524	10	269	7	219	0.957
0045045	secretory pathway	17	488	79	2438	0.899	11	268	6	220	0.582
0046907	intracellular transport	25	480	174	2343	0.127	14	265	11	215	0.898
0051049	regulation of transport	4	501	14	2503	0.755	1	278	3	223	0.474
0008283	cell proliferation	14	491	58	2459	0.639	7	272	7	219	0.898
0007049	cell cycle	23	482	108	2409	0.884	13	266	10	216	0.929
0017145	stem cell division	4	501	8	2509	0.247	2	277	2	224	0.77
0016043	cell organization and biogenesis	49	456	225	2292	0.645	30	249	19	207	0.463
0000902	cellular morphogenesis	12	493	62	2455	0.966	7	272	5	221	0.939
0006996	organelle organization and biogenesis	44	461	194	2323	0.5	25	254	19	207	0.952
0007010	cytoskeleton organization and biogenesis	33	472	133	2384	0.308	19	260	14	212	0.923
0006997	nuclear organization and biogenesis	0	505	9	2508	0.369	0	279	0	226	-
0007028	cytoplasm organization and biogenesis	3	502	14	2503	0.824	1	278	2	224	0.855
0016044	membrane organization and biogenesis	0	505	8	2509	0.427	0	279	0	226	-
0051128	regulation of cell organization and biogenesis	2	503	10	2507	0.701	1	278	1	225	0.574
0016049	cell growth	1	504	8	2509	0.997	0	279	1	225	0.916
0050896	response to stimulus	39	466	137	2380	0.058	18	261	21	205	0.307
0006950	response to stress	**16**	**489**	**42**	**2475**	**0.039**	**2**	**277**	**14**	**212**	**0.001**
0009408	response to heat	**6**	**499**	**5**	**2512**	**0.003**	**0**	**279**	**6**	**220**	**0.02**
0006979	response to oxidative stress	0	505	2	2515	0.753	0	279	0	226	-
0051179	localization	69	436	360	2157	0.76	33	246	36	190	0.229
0006403	RNA localization	3	502	26	2491	0.501	1	278	2	224	0.855
0008104	protein localization	24	481	168	2349	0.129	11	268	13	213	0.459
0051234	establishment of localization	64	441	342	2175	0.632	32	247	32	194	0.442
0051235	maintenance of localization	1	504	2	2515	0.998	1	278	0	226	0.916
0050789	regulation of biological process	71	434	331	2186	0.633	40	239	31	195	0.944
0050790	regulation of enzyme activity	4	501	11	2506	0.491	2	277	2	224	0.77
0040029	regulation of gene expression, epigenetic	3	502	17	2500	0.924	1	278	2	224	0.855
0006306	DNA methylation	1	504	6	2511	0.738	1	278	0	226	0.916
0045814	negative regulation of gene expression, epigenetic	1	504	6	2511	0.738	0	279	1	225	0.916
0006342	chromatin silencing	1	504	6	2511	0.738	0	279	1	225	0.916
0003674	molecular_function	285	220	1479	1038	0.359	147	132	138	88	0.072
0016209	antioxidant activity	0	505	8	2509	0.427	0	279	0	226	-
0005488	binding	176	329	866	1651	0.888	93	186	83	143	0.483
0005509	calcium ion binding	7	498	51	2466	0.436	4	275	3	223	0.779
0030246	carbohydrate binding	1	504	13	2504	0.547	0	279	1	225	0.916
0008289	lipid binding	5	500	21	2496	0.935	4	275	1	225	0.505
0003676	nucleic acid binding	68	437	356	2161	0.741	41	238	27	199	0.442
0003677	DNA binding	30	475	165	2352	0.679	21	258	9	217	0.137
0003682	chromatin binding	7	498	17	2500	0.171	3	276	4	222	0.779
0003700	transcription factor activity	13	492	74	2443	0.762	10	269	3	223	0.19
0003723	RNA binding	21	484	102	2415	0.989	10	269	11	215	0.621
0008135	translation factor activity, nucleic acid binding	7	498	27	2490	0.705	2	277	5	221	0.295
0000166	nucleotide binding	49	456	207	2310	0.316	**17**	**262**	**32**	**194**	**0.004**
0005515	protein binding	70	435	312	2205	0.406	38	241	32	194	0.964
0008134	transcription factor binding	7	498	22	2495	0.408	4	275	3	223	0.779
0008092	cytoskeletal protein binding	16	489	73	2444	0.856	11	268	5	221	0.396
0003779	actin binding	7	498	47	2470	0.575	4	275	3	223	0.779
0003824	catalytic activity	137	368	703	1814	0.755	**64**	**215**	**73**	**153**	**0.024**
0016787	hydrolase activity	54	451	306	2211	0.394	31	248	23	203	0.847
0003924	GTPase activity	5	500	31	2486	0.817	2	277	3	223	0.813
0004518	nuclease activity	2	503	12	2505	0.908	2	277	0	226	0.574

cGMP ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	12	493	101	2416	0.101	10	269	2	224	0.092
0004721	phosphoprotein phosphatase activity	5	500	24	2493	0.863	3	276	2	224	0.813
0016740	transferase activity	44	461	203	2314	0.692	20	259	24	202	0.227
0016301	kinase activity	23	482	117	2400	0.981	10	269	13	213	0.343
0004672	protein kinase activity	19	486	77	2440	0.494	9	270	10	216	0.639
0030234	enzyme regulator activity	25	480	86	2431	0.123	15	264	10	216	0.776
0003774	motor activity	3	502	24	2493	0.6	1	278	2	224	0.855
0004871	signal transducer activity	35	470	216	2301	0.255	20	259	15	211	0.954
0004872	receptor activity	**8**	**497**	**96**	**2421**	**0.018**	4	275	4	222	0.954
0004879	ligand-dependent nuclear receptor activity	0	505	9	2508	0.369	0	279	0	226	-
0004888	transmembrane receptor activity	7	498	64	2453	0.16	4	275	3	223	0.779
0004930	G-protein coupled receptor activity	2	503	27	2490	0.241	2	277	0	226	0.574
0005057	receptor signaling protein activity	13	492	69	2448	0.951	6	273	7	219	0.7
0005102	receptor binding	14	491	53	2464	0.446	10	269	4	222	0.336
0005198	structural molecule activity	30	475	164	2353	0.703	18	261	12	214	0.726
0030528	transcription regulator activity	30	475	168	2349	0.61	20	259	10	216	0.268
0045182	translation regulator activity	7	498	27	2490	0.705	2	277	5	221	0.295
0005215	transporter activity	44	461	207	2310	0.783	24	255	20	206	0.952
0005489	electron transporter activity	1	504	28	2489	0.094	1	278	0	226	0.916
0005216	ion channel activity	7	498	44	2473	0.699	2	277	5	221	0.295
0005244	voltage-gated ion channel activity	5	500	21	2496	0.935	2	277	3	223	0.813
0005575	cellular_component	201	304	1048	1469	0.475	107	172	94	132	0.517
0005623	cell	186	319	957	1560	0.651	100	179	86	140	0.675
0005622	intracellular	144	361	751	1766	0.589	78	201	66	160	0.834
0005737	cytoplasm	73	432	419	2098	0.25	38	241	35	191	0.641
0016023	cytoplasmic vesicle	7	498	36	2481	0.897	5	274	2	224	0.628
0005829	cytosol	12	493	100	2417	0.109	4	275	8	218	0.211
0005783	endoplasmic reticulum	4	501	53	2464	0.072	0	279	4	222	0.084
0005794	Golgi apparatus	4	501	22	2495	0.935	2	277	2	224	0.77
0005815	microtubule organizing center	2	503	7	2510	0.997	1	278	1	225	0.574
0005739	mitochondrion	18	487	91	2426	0.941	9	270	9	217	0.83
0005840	ribosome	6	499	51	2466	0.278	4	275	2	224	0.878
0005773	vacuole	3	502	13	2504	0.907	2	277	1	225	0.855
0005764	lysosome	1	504	5	2512	0.586	0	279	1	225	0.916
0005856	cytoskeleton	16	489	68	2449	0.664	8	271	8	218	0.862
0005694	chromosome	9	496	29	2488	0.347	3	276	6	220	0.319
0000228	nuclear chromosome	1	504	4	2513	0.687	0	279	1	225	0.916
0005634	nucleus	62	443	314	2203	0.961	36	243	26	200	0.734
0005635	nuclear membrane	2	503	16	2501	0.748	1	278	1	225	0.574
0005730	nucleolus	2	503	9	2508	0.784	1	278	1	225	0.574
0005654	nucleoplasm	13	492	61	2456	0.966	5	274	8	218	0.342
0005777	peroxisome	1	504	8	2509	0.997	0	279	1	225	0.916
0005886	plasma membrane	21	484	126	2391	0.487	10	269	11	215	0.621
0005576	extracellular region	11	494	59	2458	0.949	6	273	5	221	0.795
0005578	extracellular matrix (sensu Metazoa)	6	499	29	2488	0.874	4	275	2	224	0.878

		cAMP (p < 0.01)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	123	90	1666	1143	0.708	65	59	58	31	0.086
0007610	behavior	7	206	151	2658	0.246	3	121	4	85	0.654
0030534	adult behavior	1	212	22	2787	0.921	1	123	0	89	0.867
0030537	larval behavior	0	213	9	2800	0.861	0	124	0	89	-
0007611	learning and/or memory	0	213	24	2785	0.34	0	124	0	89	-
0007612	learning	0	213	15	2794	0.573	0	124	0	89	-
0007613	memory	0	213	11	2798	0.745	0	124	0	89	-
0007626	locomotory behavior	4	209	116	2693	0.15	2	122	2	87	0.861
0007635	chemosensory behavior	0	213	17	2792	0.507	0	124	0	89	-
0007622	rhythmic behavior	3	210	11	2798	0.113	1	123	2	87	0.771
0048512	circadian behavior	3	210	10	2799	0.085	1	123	2	87	0.771
0009987	cellular process	111	102	1550	1259	0.426	**57**	**67**	**54**	**35**	**0.048**
0007154	cell communication	34	179	453	2356	0.973	18	106	16	73	0.624
0007155	cell adhesion	7	206	78	2731	0.827	7	117	0	89	0.059
0008037	cell recognition	0	213	2	2807	0.321	0	124	0	89	-
0008038	neuronal cell recognition	0	213	2	2807	0.321	0	124	0	89	-
0016337	cell-cell adhesion	4	209	31	2778	0.493	4	120	0	89	0.231
0016339	calcium-dependent cell-cell adhesion	**2**	**211**	**2**	**2807**	**0.017**	2	122	0	89	0.629
0007156	homophilic cell adhesion	**3**	**210**	**3**	**2806**	**9E-04**	3	121	0	89	0.374
0007160	cell-matrix adhesion	1	212	8	2801	0.861	1	123	0	89	0.867
0007267	cell-cell signaling	13	200	141	2668	0.595	5	119	8	81	0.23
0019226	transmission of nerve impulse	13	200	123	2686	0.318	5	119	8	81	0.23
0007268	synaptic transmission	10	203	91	2718	0.346	4	120	6	83	0.385
0007270	nerve-nerve synaptic transmission	1	212	15	2794	0.715	0	124	1	88	0.867
0001505	regulation of neurotransmitter levels	7	206	53	2756	0.247	4	120	3	86	0.741
0042133	neurotransmitter metabolism	1	212	7	2802	0.93	0	124	1	88	0.867
0007269	neurotransmitter secretion	6	207	47	2762	0.339	4	120	2	87	0.995
0007165	signal transduction	22	191	355	2454	0.381	12	112	10	79	0.888
0007166	cell surface receptor linked signal transduction	9	204	147	2662	0.631	4	120	5	84	0.61
0007167	enzyme linked receptor protein signaling pathway	3	210	42	2767	0.847	1	123	2	87	0.771
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	0	213	15	2794	0.573	0	124	0	89	-
0007179	transforming growth factor beta receptor signaling pathway	0	213	9	2800	0.861	0	124	0	89	-
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	3	210	28	2781	0.824	1	123	2	87	0.771
0007173	epidermal growth factor receptor signaling pathway	1	212	6	2803	0.992	0	124	1	88	0.867
0008286	insulin receptor signaling pathway	0	213	4	2805	0.67	0	124	0	89	-
0008293	torso signaling pathway	1	212	6	2803	0.992	0	124	1	88	0.867
0007186	G-protein coupled receptor protein signaling pathway	3	210	68	2741	0.48	1	123	2	87	0.771
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	1	212	4	2805	0.796	0	124	1	88	0.867
0007219	Notch signaling pathway	0	213	13	2796	0.651	0	124	0	89	-
0007224	smoothened signaling pathway	0	213	6	2803	0.902	0	124	0	89	-
0008063	Toll signaling pathway	1	212	3	2806	0.67	1	123	0	89	0.867
0016055	Wnt receptor signaling pathway	2	211	12	2797	0.591	1	123	1	88	0.629
0007242	intracellular signaling cascade	11	202	175	2634	0.634	5	119	6	83	0.57
0007263	nitric oxide mediated signal transduction	0	213	3	2806	0.515	0	124	0	89	-
0007243	protein kinase cascade	2	211	42	2767	0.721	1	123	1	88	0.629
0007259	JAK-STAT cascade	0	213	6	2803	0.902	0	124	0	89	-
0000165	MAPKKK cascade	2	211	33	2776	0.982	1	123	1	88	0.629
0019932	second-messenger-mediated signaling	1	212	21	2788	0.966	0	124	1	88	0.867
0019722	calcium-mediated signaling	0	213	15	2794	0.573	0	124	0	89	-
0048015	phosphoinositide-mediated signaling	1	212	4	2805	0.796	0	124	1	88	0.867
0007264	small GTPase mediated signal transduction	1	212	44	2765	0.327	0	124	1	88	0.867
0007265	Ras protein signal transduction	0	213	11	2798	0.745	0	124	0	89	-
0009966	regulation of signal transduction	2	211	30	2779	0.865	1	123	1	88	0.629
0007275	development	32	181	422	2387	0.921	15	109	17	72	0.224
0007568	aging	0	213	11	2798	0.745	0	124	0	89	-
0030154	cell differentiation	4	209	109	2700	0.194	1	123	3	86	0.396
0048468	cell development	2	211	68	2741	0.25	1	123	1	88	0.629
0000904	cellular morphogenesis during differentiation	1	212	17	2792	0.831	0	124	1	88	0.867
0042461	photoreceptor cell development	1	212	17	2792	0.831	0	124	1	88	0.867
0042051	eye photoreceptor development (sensu Endopterygota)	1	212	16	2793	0.774	0	124	1	88	0.867
0045165	cell fate commitment	1	212	45	2764	0.312	0	124	1	88	0.867

		cAMP (p < 0.01)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0001709	cell fate determination	0	213	28	2781	0.274	0	124	0	89	-
0007400	neuroblast cell fate determination	0	213	8	2801	0.93	0	124	0	89	-
0001708	cell fate specification	0	213	7	2802	0.992	0	124	0	89	-
0007349	cellularization	0	213	10	2799	0.8	0	124	0	89	-
0040007	growth	3	210	33	2776	0.98	1	123	2	87	0.771
0002164	larval development	2	211	15	2794	0.774	1	123	1	88	0.629
0002165	larval or pupal development (sensu Insecta)	14	199	111	2698	0.094	5	119	9	80	0.137
0007552	metamorphosis	14	199	103	2706	0.053	5	119	9	80	0.137
0009653	morphogenesis	24	189	292	2517	0.776	11	113	13	76	0.277
0002009	morphogenesis of an epithelium	2	211	38	2771	0.843	2	122	0	89	0.629
0009887	organogenesis	21	192	261	2548	0.879	8	116	13	76	0.083
0001654	eye morphogenesis	4	209	51	2758	0.841	0	124	4	85	0.061
0008406	gonad development	0	213	10	2799	0.8	0	124	0	89	-
0007444	imaginal disc development	9	204	82	2727	0.386	2	122	7	82	0.059
0007494	midgut development	0	213	4	2805	0.67	0	124	0	89	-
0007517	muscle development	1	212	32	2777	0.572	1	123	0	89	0.867
0007399	neurogenesis	7	206	158	2651	0.196	3	121	4	85	0.654
0007409	axonogenesis	1	212	46	2763	0.298	0	124	1	88	0.867
0007411	axon guidance	1	212	34	2775	0.521	0	124	1	88	0.867
0007417	central nervous system development	1	212	38	2771	0.432	0	124	1	88	0.867
0016358	dendrite morphogenesis	0	213	14	2795	0.61	0	124	0	89	-
0042063	gliogenesis	0	213	11	2798	0.745	0	124	0	89	-
0007422	peripheral nervous system development	2	211	38	2771	0.843	0	124	2	87	0.339
0050767	regulation of neurogenesis	1	212	5	2804	0.902	0	124	1	88	0.867
0007424	tracheal system development (sensu Insecta)	1	212	34	2775	0.521	0	124	1	88	0.867
0048513	organ development	21	192	265	2544	0.934	8	116	13	76	0.083
0007389	pattern specification	4	209	68	2741	0.789	3	121	1	88	0.861
0048066	pigmentation	0	213	10	2799	0.8	0	124	0	89	-
0009791	post-embryonic development	2	211	15	2794	0.774	1	123	1	88	0.629
0009790	embryonic development	6	207	93	2716	0.849	4	120	2	87	0.995
0007530	sex determination	0	213	10	2799	0.8	0	124	0	89	-
0007548	sex differentiation	0	213	18	2791	0.478	0	124	0	89	-
0019827	stem cell maintenance	0	213	8	2801	0.93	0	124	0	89	-
0000003	reproduction	6	207	128	2681	0.309	2	122	4	85	0.404
0050793	regulation of development	3	210	40	2769	0.778	0	124	3	86	0.142
0007582	physiological process	114	99	1525	1284	0.884	59	65	55	34	0.056
0008152	metabolism	86	127	1116	1693	0.91	43	81	43	46	0.063
0009056	catabolism	14	199	189	2620	0.957	9	115	5	84	0.845
0006091	energy pathways	7	206	101	2708	0.966	7	117	0	89	0.059
0006118	electron transport	4	209	52	2757	0.814	4	120	0	89	0.231
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	25	188	409	2400	0.302	14	110	11	78	0.981
0006259	DNA metabolism	1	212	79	2730	0.067	0	124	1	88	0.867
0006350	transcription	12	201	213	2596	0.363	6	118	6	83	0.77
0043170	macromolecule metabolism	55	158	606	2203	0.174	28	96	27	62	0.264
0019538	protein metabolism	48	165	510	2299	0.135	23	101	25	64	0.14
0006412	protein biosynthesis	14	199	129	2680	0.252	10	114	4	85	0.449
0006464	protein modification	18	195	239	2570	0.922	8	116	10	79	0.323
0006457	protein folding	**10**	**203**	**34**	**2775**	**1E-04**	**0**	**124**	**10**	**79**	**5E-04**
0005975	carbohydrate metabolism	8	205	100	2709	0.966	5	119	3	86	0.909
0006519	amino acid and derivative metabolism	7	206	64	2745	0.483	**1**	**123**	**6**	**83**	**0.045**
0006629	lipid metabolism	4	209	89	2720	0.398	3	121	1	88	0.861
0009308	amine metabolism	7	206	74	2735	0.728	**1**	**123**	**6**	**83**	**0.045**
0042440	pigment metabolism	0	213	12	2797	0.696	0	124	0	89	-
0042445	hormone metabolism	2	211	5	2804	0.137	1	123	1	88	0.629
0009058	biosynthesis	21	192	221	2588	0.367	14	110	7	82	0.553
0019748	secondary metabolism	0	213	14	2795	0.61	0	124	0	89	-
0019222	regulation of metabolism	12	201	222	2587	0.288	6	118	6	83	0.77
0016265	death	8	205	80	2729	0.583	2	122	6	83	0.115
0008219	cell death	8	205	68	2741	0.331	2	122	6	83	0.115
0016271	tissue death	4	209	23	2786	0.228	1	123	3	86	0.396
0042592	homeostasis	1	212	28	2781	0.692	0	124	1	88	0.867
0019725	cell homeostasis	1	212	25	2784	0.798	0	124	1	88	0.867
0050801	ion homeostasis	1	212	12	2797	0.651	0	124	1	88	0.867
0043062	extracellular structure organization and biogenesis	0	213	19	2790	0.451	0	124	0	89	-
0046903	secretion	10	203	92	2717	0.363	7	117	3	86	0.656
0048511	rhythmic process	3	210	13	2796	0.179	1	123	2	87	0.771

cAMP ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	21	192	326	2483	0.51	9	115	12	77	0.204
0050874	organismal physiological process	22	191	206	2603	0.144	11	113	11	78	0.551
0050875	cellular physiological process	105	108	1448	1361	0.573	**53**	**71**	**52**	**37**	**0.034**
0006810	transport	29	184	372	2437	0.961	16	108	13	76	0.877
0006811	ion transport	11	202	109	2700	0.457	6	118	5	84	0.952
0006818	hydrogen transport	3	210	16	2793	0.297	3	121	0	89	0.374
0006836	neurotransmitter transport	0	213	6	2803	0.902	0	124	0	89	-
0006858	extracellular transport	1	212	14	2795	0.654	0	124	1	88	0.867
0006869	lipid transport	0	213	17	2792	0.507	0	124	0	89	-
0008643	carbohydrate transport	3	210	12	2797	0.145	2	122	1	88	0.771
0015031	protein transport	8	205	171	2638	0.215	5	119	3	86	0.909
0015837	amine transport	2	211	11	2798	0.526	1	123	1	88	0.629
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	2	211	12	2797	0.591	1	123	1	88	0.629
0016192	vesicle-mediated transport	8	205	112	2697	0.988	5	119	3	86	0.909
0045045	secretory pathway	8	205	88	2721	0.766	5	119	3	86	0.909
0046907	intracellular transport	11	202	188	2621	0.469	7	117	4	85	0.952
0051049	regulation of transport	**4**	**209**	**14**	**2795**	**0.039**	2	122	2	87	0.861
0008283	cell proliferation	7	206	65	2744	0.507	3	121	4	85	0.654
0007049	cell cycle	10	203	121	2688	0.926	4	120	6	83	0.385
0017145	stem cell division	0	213	12	2797	0.696	0	124	0	89	-
0016043	cell organization and biogenesis	13	200	261	2548	0.15	5	119	8	81	0.23
0000902	cellular morphogenesis	4	209	70	2739	0.742	1	123	3	86	0.396
0006996	organelle organization and biogenesis	10	203	228	2581	0.098	4	120	6	83	0.385
0007010	cytoskeleton organization and biogenesis	7	206	159	2650	0.19	3	121	4	85	0.654
0006997	nuclear organization and biogenesis	0	213	9	2800	0.861	0	124	0	89	-
0007028	cytoplasm organization and biogenesis	0	213	17	2792	0.507	0	124	0	89	-
0016044	membrane organization and biogenesis	0	213	8	2801	0.93	0	124	0	89	-
0051128	regulation of cell organization and biogenesis	0	213	12	2797	0.696	0	124	0	89	-
0016049	cell growth	0	213	9	2800	0.861	0	124	0	89	-
0050896	response to stimulus	**22**	**191**	**154**	**2655**	**0.006**	**8**	**116**	**14**	**75**	**0.049**
0006950	response to stress	**10**	**203**	**48**	**2761**	**0.005**	**1**	**123**	**9**	**80**	**0.005**
0009408	response to heat	**3**	**210**	**8**	**2801**	**0.042**	0	124	3	86	0.142
0006979	response to oxidative stress	0	213	2	2807	0.321	0	124	0	89	-
0051179	localization	30	183	399	2410	0.957	17	107	13	76	0.989
0006403	RNA localization	1	212	28	2781	0.692	1	123	0	89	0.867
0008104	protein localization	9	204	183	2626	0.24	6	118	3	86	0.857
0051234	establishment of localization	30	183	376	2433	0.854	17	107	13	76	0.989
0051235	maintenance of localization	0	213	3	2806	0.515	0	124	0	89	-
0050789	regulation of biological process	23	190	379	2430	0.312	10	114	13	76	0.196
0050790	regulation of enzyme activity	0	213	15	2794	0.573	0	124	0	89	-
0040029	regulation of gene expression, epigenetic	0	213	20	2789	0.425	0	124	0	89	-
0006306	DNA methylation	0	213	7	2802	0.992	0	124	0	89	-
0045814	negative regulation of gene expression, epigenetic	0	213	7	2802	0.992	0	124	0	89	-
0006342	chromatin silencing	0	213	7	2802	0.992	0	124	0	89	-
0003674	molecular_function	122	91	1642	1167	0.792	**63**	**61**	**59**	**30**	**0.035**
0016209	antioxidant activity	0	213	8	2801	0.93	0	124	0	89	-
0005488	binding	66	147	976	1833	0.299	**31**	**93**	**35**	**54**	**0.038**
0005509	calcium ion binding	4	209	54	2755	0.831	3	121	1	88	0.861
0030246	carbohydrate binding	0	213	14	2795	0.61	0	124	0	89	-
0008289	lipid binding	3	210	23	2786	0.608	1	123	2	87	0.771
0003676	nucleic acid binding	23	190	401	2408	0.191	13	111	10	79	0.961
0003677	DNA binding	12	201	183	2626	0.719	6	118	6	83	0.77
0003682	chromatin binding	1	212	23	2786	0.878	0	124	1	88	0.867
0003700	transcription factor activity	5	208	82	2727	0.788	2	122	3	86	0.706
0003723	RNA binding	5	208	118	2691	0.254	2	122	3	86	0.706
0008135	translation factor activity, nucleic acid binding	1	212	33	2776	0.546	0	124	1	88	0.867
0000166	nucleotide binding	17	196	239	2570	0.89	**5**	**119**	**12**	**77**	**0.024**
0005515	protein binding	22	191	360	2449	0.344	9	115	13	76	0.131
0008134	transcription factor binding	2	211	27	2782	0.74	1	123	1	88	0.629
0008092	cytoskeletal protein binding	4	209	85	2724	0.456	3	121	1	88	0.861
0003779	actin binding	2	211	52	2757	0.484	1	123	1	88	0.629
0003824	catalytic activity	66	147	774	2035	0.318	34	90	32	57	0.239
0016787	hydrolase activity	29	184	331	2478	0.493	16	108	13	76	0.877
0003924	GTPase activity	2	211	34	2775	0.98	0	124	2	87	0.339
0004518	nuclease activity	0	213	14	2795	0.61	0	124	0	89	-

		cAMP ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	11	202	102	2707	0.342	7	117	4	85	0.952
0004721	phosphoprotein phosphatase activity	2	211	27	2782	0.74	1	123	1	88	0.629
0016740	transferase activity	21	192	226	2583	0.423	10	114	11	78	0.421
0016301	kinase activity	9	204	131	2678	0.901	4	120	5	84	0.61
0004672	protein kinase activity	6	207	90	2719	0.914	3	121	3	86	0.995
0030234	enzyme regulator activity	4	209	107	2702	0.209	2	122	2	87	0.861
0003774	motor activity	2	211	25	2784	0.761	2	122	0	89	0.629
0004871	signal transducer activity	12	201	239	2570	0.181	7	117	5	84	0.77
0004872	receptor activity	5	208	99	2710	0.476	3	121	2	87	0.706
0004879	ligand-dependent nuclear receptor activity	0	213	9	2800	0.861	0	124	0	89	-
0004888	transmembrane receptor activity	3	210	68	2741	0.48	2	122	1	88	0.771
0004930	G-protein coupled receptor activity	0	213	29	2780	0.26	0	124	0	89	-
0005057	receptor signaling protein activity	4	209	78	2731	0.576	1	123	3	86	0.396
0005102	receptor binding	3	210	64	2745	0.555	3	121	0	89	0.374
0005198	structural molecule activity	16	197	178	2631	0.596	13	111	3	86	0.093
0030528	transcription regulator activity	9	204	189	2620	0.201	4	120	5	84	0.61
0045182	translation regulator activity	1	212	33	2776	0.546	0	124	1	88	0.867
0005215	transporter activity	22	191	229	2580	0.327	13	111	9	80	0.888
0005489	electron transporter activity	2	211	27	2782	0.74	2	122	0	89	0.629
0005216	ion channel activity	3	210	48	2761	0.958	0	124	3	86	0.142
0005244	voltage-gated ion channel activity	1	212	25	2784	0.798	0	124	1	88	0.867
0005575	cellular_component	81	132	1168	1641	0.346	49	75	32	57	0.7
0005623	cell	75	138	1068	1741	0.458	46	78	29	60	0.593
0005622	intracellular	58	155	837	1972	0.476	36	88	22	67	0.588
0005737	cytoplasm	36	177	456	2353	0.874	26	98	10	79	0.092
0016023	cytoplasmic vesicle	3	210	40	2769	0.778	2	122	1	88	0.771
0005829	cytosol	8	205	104	2705	0.882	6	118	2	87	0.538
0005783	endoplasmic reticulum	1	212	56	2753	0.188	1	123	0	89	0.867
0005794	Golgi apparatus	4	209	22	2787	0.199	3	121	1	88	0.861
0005815	microtubule organizing center	1	212	8	2801	0.861	0	124	1	88	0.867
0005739	mitochondrion	7	206	102	2707	0.944	4	120	3	86	0.741
0005840	ribosome	6	207	51	2758	0.439	6	118	0	89	0.092
0005773	vacuole	2	211	14	2795	0.715	2	122	0	89	0.629
0005764	lysosome	0	213	6	2803	0.902	0	124	0	89	-
0005856	cytoskeleton	8	205	76	2733	0.495	6	118	2	87	0.538
0005694	chromosome	2	211	36	2773	0.909	1	123	1	88	0.629
0000228	nuclear chromosome	0	213	5	2804	0.796	0	124	0	89	-
0005634	nucleus	23	190	353	2456	0.518	10	114	13	76	0.196
0005635	nuclear membrane	1	212	17	2792	0.831	1	123	0	89	0.867
0005730	nucleolus	0	213	11	2798	0.745	0	124	0	89	-
0005654	nucleoplasm	4	209	70	2739	0.742	1	123	3	86	0.396
0005777	peroxisome	1	212	8	2801	0.861	1	123	0	89	0.867
0005886	plasma membrane	4	209	143	2666	0.053	2	122	2	87	0.861
0005576	extracellular region	4	209	66	2743	0.838	3	121	1	88	0.861
0005578	extracellular matrix (sensu Metazoa)	3	210	32	2777	0.982	2	122	1	88	0.771

		cGMP vs. cAMP (p < 0.01; "up" means higher in cGMP)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	255	170	1534	1063	0.757	126	89	129	81	0.621
0007610	behavior	24	401	134	2463	0.764	15	200	9	201	0.321
0030534	adult behavior	5	420	18	2579	0.446	2	213	3	207	0.979
0030537	larval behavior	1	424	8	2589	0.822	0	215	1	209	0.991
0007611	learning and/or memory	3	422	21	2576	0.941	1	214	2	208	0.984
0007612	learning	2	423	13	2584	0.771	1	214	1	209	0.489
0007613	memory	2	423	9	2588	0.967	1	214	1	209	0.489
0007626	locomotory behavior	19	406	101	2496	0.663	11	204	8	202	0.677
0007635	chemosensory behavior	1	424	16	2581	0.533	1	214	0	210	0.991
0007622	rhythmic behavior	5	420	9	2588	0.051	3	212	2	208	0.979
0048512	circadian behavior	4	421	9	2588	0.181	2	213	2	208	0.632
0009987	cellular process	236	189	1425	1172	0.841	118	97	118	92	0.862
0007154	cell communication	**88**	**337**	**399**	**2198**	**0.007**	**62**	**153**	**26**	**184**	**5E-05**
0007155	cell adhesion	18	407	67	2530	0.079	11	204	7	203	0.502
0008037	cell recognition	1	424	1	2596	0.656	1	214	0	210	0.991
0008038	neuronal cell recognition	1	424	1	2596	0.656	1	214	0	210	0.991
0016337	cell-cell adhesion	8	417	27	2570	0.207	4	211	4	206	0.746
0016339	calcium-dependent cell-cell adhesion	2	423	2	2595	0.177	1	214	1	209	0.489
0007156	homophilic cell adhesion	3	422	3	2594	0.052	2	213	1	209	0.984
0007160	cell-matrix adhesion	3	422	6	2591	0.236	1	214	2	208	0.984
0007267	cell-cell signaling	27	398	127	2470	0.249	**20**	**195**	**7**	**203**	**0.02**
0019226	transmission of nerve impulse	24	401	112	2485	0.27	**18**	**197**	**6**	**204**	**0.024**
0007268	synaptic transmission	20	405	81	2516	0.123	**16**	**199**	**4**	**206**	**0.014**
0007270	nerve-nerve synaptic transmission	2	423	14	2583	0.857	2	213	0	210	0.489
0001505	regulation of neurotransmitter levels	13	412	47	2550	0.128	10	205	3	207	0.1
0042133	neurotransmitter metabolism	3	422	5	2592	0.161	3	212	0	210	0.255
0007269	neurotransmitter secretion	10	415	43	2554	0.415	7	208	3	207	0.356
0007165	signal transduction	65	360	312	2285	0.069	**43**	**172**	**22**	**188**	**0.01**
0007166	cell surface receptor linked signal transduction	22	403	134	2463	0.917	16	199	6	204	0.056
0007167	enzyme linked receptor protein signaling pathway	9	416	36	2561	0.348	6	209	3	207	0.523
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	2	423	13	2584	0.771	1	214	1	209	0.489
0007179	transforming growth factor beta receptor signaling pathway	2	423	7	2590	0.822	1	214	1	209	0.489
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	7	418	24	2573	0.266	5	210	2	208	0.465
0007173	epidermal growth factor receptor signaling pathway	2	423	5	2592	0.575	1	214	1	209	0.489
0008286	insulin receptor signaling pathway	0	425	4	2593	0.928	0	215	0	210	-
0008293	torso signaling pathway	2	423	5	2592	0.575	1	214	1	209	0.489
0007186	G-protein coupled receptor protein signaling pathway	7	418	64	2533	0.391	6	209	1	209	0.135
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	1	424	4	2593	0.794	1	214	0	210	0.991
0007219	Notch signaling pathway	3	422	10	2587	0.591	1	214	2	208	0.984
0007224	smoothened signaling pathway	0	425	6	2591	0.686	0	215	0	210	-
0008063	Toll signaling pathway	1	424	3	2594	0.928	1	214	0	210	0.991
0016055	Wnt receptor signaling pathway	3	422	11	2586	0.682	2	213	1	209	0.984
0007242	intracellular signaling cascade	**39**	**386**	**147**	**2450**	**0.007**	**28**	**187**	**11**	**199**	**0.009**
0007263	nitric oxide mediated signal transduction	1	424	2	2595	0.897	0	215	1	209	0.991
0007243	protein kinase cascade	10	415	34	2563	0.148	**9**	**206**	**1**	**209**	**0.028**
0007259	JAK-STAT cascade	1	424	5	2592	0.686	1	214	0	210	0.991
0000165	MAPKKK cascade	8	417	27	2570	0.207	7	208	1	209	0.08
0019932	second-messenger-mediated signaling	4	421	18	2579	0.803	2	213	2	208	0.632
0019722	calcium-mediated signaling	2	423	13	2584	0.771	0	215	2	208	0.468
0048015	phosphoinositide-mediated signaling	1	424	4	2593	0.794	1	214	0	210	0.991
0007264	small GTPase mediated signal transduction	7	418	38	2559	0.941	5	210	2	208	0.465
0007265	Ras protein signal transduction	2	423	9	2588	0.967	2	213	0	210	0.489
0009966	regulation of signal transduction	8	417	24	2573	0.125	6	209	2	208	0.3
0007275	development	**84**	**341**	**370**	**2227**	**0.004**	49	166	35	175	0.143
0007568	aging	2	423	9	2588	0.967	1	214	1	209	0.489
0030154	cell differentiation	14	411	99	2498	0.701	7	208	7	203	0.82
0048468	cell development	7	418	63	2534	0.415	4	211	3	207	0.975
0000904	cellular morphogenesis during differentiation	2	423	16	2581	0.983	2	213	0	210	0.489
0042461	photoreceptor cell development	2	423	16	2581	0.983	2	213	0	210	0.489
0042051	eye photoreceptor development (sensu Endopterygota)	2	423	15	2582	0.939	2	213	0	210	0.489
0045165	cell fate commitment	4	421	42	2555	0.4	1	214	3	207	0.599

		cGMP vs. cAMP ($p < 0.01$; "up" means higher in cGMP)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	2	423	26	2571	0.432	1	214	1	209	0.489
0007400	neuroblast cell fate determination	1	424	7	2590	0.703	1	214	0	210	0.991
0001708	cell fate specification	0	425	7	2590	0.598	0	215	0	210	-
0007349	cellularization	0	425	10	2587	0.409	0	215	0	210	-
0040007	growth	4	421	32	2565	0.786	1	214	3	207	0.599
0002164	larval development	2	423	15	2582	0.939	1	214	1	209	0.489
0002165	larval or pupal development (sensu Insecta)	25	400	100	2497	0.069	16	199	9	201	0.239
0007552	metamorphosis	**25**	**400**	**92**	**2505**	**0.029**	16	199	9	201	0.239
0009653	morphogenesis	**62**	**363**	**254**	**2343**	**0.004**	37	178	25	185	0.158
0002009	morphogenesis of an epithelium	8	417	32	2565	0.391	3	212	5	205	0.696
0009887	organogenesis	**55**	**370**	**227**	**2370**	**0.008**	32	183	23	187	0.288
0001654	eye morphogenesis	5	420	50	2547	0.382	3	212	2	208	0.979
0008406	gonad development	2	423	8	2589	0.932	1	214	1	209	0.489
0007444	imaginal disc development	15	410	76	2521	0.602	9	206	6	204	0.632
0007494	midgut development	2	423	2	2595	0.177	2	213	0	210	0.489
0007517	muscle development	4	421	29	2568	0.943	3	212	1	209	0.632
0007399	neurogenesis	28	397	137	2460	0.323	16	199	12	198	0.602
0007409	axonogenesis	5	420	42	2555	0.639	5	210	0	210	0.076
0007411	axon guidance	5	420	30	2567	0.836	5	210	0	210	0.076
0007417	central nervous system development	5	420	34	2563	0.994	2	213	3	207	0.979
0016358	dendrite morphogenesis	1	424	13	2584	0.718	0	215	1	209	0.991
0042063	gliogenesis	3	422	8	2589	0.408	2	213	1	209	0.984
0007422	peripheral nervous system development	8	417	32	2565	0.391	3	212	5	205	0.696
0050767	regulation of neurogenesis	1	424	5	2592	0.686	0	215	1	209	0.991
0007424	tracheal system development (sensu Insecta)	9	416	26	2571	0.08	6	209	3	207	0.523
0048513	organ development	**56**	**369**	**230**	**2367**	**0.006**	33	182	23	187	0.232
0007389	pattern specification	10	415	62	2535	0.898	6	209	4	206	0.778
0048066	pigmentation	2	423	8	2589	0.932	1	214	1	209	0.489
0009791	post-embryonic development	2	423	15	2582	0.939	1	214	1	209	0.489
0009790	embryonic development	**22**	**403**	**77**	**2520**	**0.026**	13	202	9	201	0.548
0007530	sex determination	1	424	9	2588	0.932	1	214	0	210	0.991
0007548	sex differentiation	2	423	16	2581	0.983	1	214	1	209	0.489
0019827	stem cell maintenance	1	424	7	2590	0.703	1	214	0	210	0.991
0000003	reproduction	17	408	117	2480	0.732	8	207	9	201	0.961
0050793	regulation of development	4	421	39	2558	0.494	1	214	3	207	0.599
0007582	physiological process	228	197	1411	1186	0.834	107	108	121	89	0.127
0008152	metabolism	166	259	1036	1561	0.786	75	140	91	119	0.092
0009056	catabolism	22	403	181	2416	0.206	13	202	9	201	0.548
0006091	energy pathways	17	408	91	2506	0.712	7	208	10	200	0.586
0006118	electron transport	6	419	50	2547	0.594	**0**	**215**	**6**	**204**	**0.037**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	64	361	370	2227	0.713	36	179	28	182	0.397
0006259	DNA metabolism	13	412	67	2530	0.684	9	206	4	206	0.278
0006350	transcription	33	392	192	2405	0.864	**26**	**189**	**7**	**203**	**0.001**
0043170	macromolecule metabolism	90	335	571	2026	0.756	37	178	53	157	0.057
0019538	protein metabolism	66	359	492	2105	0.106	28	187	38	172	0.19
0006412	protein biosynthesis	14	411	129	2468	0.167	5	210	9	201	0.39
0006464	protein modification	31	394	226	2371	0.384	15	200	16	194	0.946
0006457	protein folding	8	417	36	2561	0.567	1	214	7	203	0.069
0005975	carbohydrate metabolism	**27**	**398**	**81**	**2516**	**0.001**	11	204	16	194	0.39
0006519	amino acid and derivative metabolism	12	413	59	2538	0.601	4	211	8	202	0.358
0006629	lipid metabolism	18	407	75	2522	0.18	**3**	**212**	**15**	**195**	**0.007**
0009308	amine metabolism	14	411	67	2530	0.495	5	210	9	201	0.39
0042440	pigment metabolism	3	422	9	2588	0.499	2	213	1	209	0.984
0042445	hormone metabolism	2	423	5	2592	0.575	1	214	1	209	0.489
0009058	biosynthesis	30	395	212	2385	0.496	11	204	19	191	0.164
0019748	secondary metabolism	3	422	11	2586	0.682	2	213	1	209	0.984
0019222	regulation of metabolism	33	392	201	2396	0.936	**27**	**188**	**6**	**204**	**4E-04**
0016265	death	14	411	74	2523	0.726	8	207	6	204	0.82
0008219	cell death	12	413	64	2533	0.786	7	208	5	205	0.801
0016271	tissue death	6	419	21	2576	0.344	4	211	2	208	0.702
0042592	homeostasis	7	418	22	2575	0.194	4	211	3	207	0.975
0019725	cell homeostasis	6	419	20	2577	0.296	3	212	3	207	0.702
0050801	ion homeostasis	3	422	10	2587	0.591	2	213	1	209	0.984
0043062	extracellular structure organization and biogenesis	2	423	17	2580	0.909	1	214	1	209	0.489
0046903	secretion	13	412	89	2508	0.807	8	207	5	205	0.603
0048511	rhythmic process	5	420	11	2586	0.105	3	212	2	208	0.979

cGMP vs. cAMP ($p < 0.01$; "up" means higher in cGMP)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	47	378	300	2297	0.831	**32**	**183**	**15**	**195**	**0.017**
0050874	organismal physiological process	38	387	190	2407	0.282	24	191	14	196	0.146
0050875	cellular physiological process	210	215	1343	1254	0.408	100	115	110	100	0.266
0006810	transport	53	372	348	2249	0.655	25	190	28	182	0.7
0006811	ion transport	16	409	104	2493	0.92	7	208	9	201	0.762
0006818	hydrogen transport	1	424	18	2579	0.438	1	214	0	210	0.991
0006836	neurotransmitter transport	1	424	5	2592	0.686	1	214	0	210	0.991
0006858	extracellular transport	3	422	12	2585	0.771	0	215	3	207	0.238
0006869	lipid transport	3	422	14	2583	0.939	0	215	3	207	0.238
0008643	carbohydrate transport	4	421	11	2586	0.301	1	214	3	207	0.599
0015031	protein transport	21	404	158	2439	0.415	11	204	10	200	0.956
0015837	amine transport	3	422	10	2587	0.591	1	214	2	208	0.984
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	0	425	14	2583	0.258	0	215	0	210	-
0016192	vesicle-mediated transport	12	413	108	2489	0.241	8	207	4	206	0.402
0045045	secretory pathway	12	413	84	2513	0.765	8	207	4	206	0.402
0046907	intracellular transport	23	402	176	2421	0.344	12	203	11	199	0.954
0051049	regulation of transport	2	423	16	2581	0.983	0	215	2	208	0.468
0008283	cell proliferation	16	409	56	2541	0.065	10	205	6	204	0.474
0007049	cell cycle	20	405	111	2486	0.782	9	206	11	199	0.777
0017145	stem cell division	2	423	10	2587	0.876	2	213	0	210	0.489
0016043	cell organization and biogenesis	42	383	232	2365	0.589	25	190	17	193	0.29
0000902	cellular morphogenesis	7	418	67	2530	0.325	5	210	2	208	0.465
0006996	organelle organization and biogenesis	36	389	202	2395	0.693	20	195	16	194	0.654
0007010	cytoskeleton organization and biogenesis	24	401	142	2455	0.972	14	201	10	200	0.568
0006997	nuclear organization and biogenesis	0	425	9	2588	0.462	0	215	0	210	-
0007028	cytoplasm organization and biogenesis	3	422	14	2583	0.939	1	214	2	208	0.984
0016044	membrane organization and biogenesis	0	425	8	2589	0.524	0	215	0	210	-
0051128	regulation of cell organization and biogenesis	1	424	11	2586	0.876	0	215	1	209	0.991
0016049	cell growth	0	425	9	2588	0.462	0	215	0	210	-
0050896	response to stimulus	29	396	147	2450	0.402	15	200	14	196	0.948
0006950	response to stress	9	416	49	2548	0.896	3	212	6	204	0.478
0009408	response to heat	2	423	9	2588	0.967	0	215	2	208	0.468
0006979	response to oxidative stress	0	425	2	2595	0.656	0	215	0	210	-
0051179	localization	54	371	375	2222	0.382	25	190	29	181	0.596
0006403	RNA localization	1	424	28	2569	0.166	0	215	1	209	0.991
0008104	protein localization	21	404	171	2426	0.238	11	204	10	200	0.956
0051234	establishment of localization	53	372	353	2244	0.581	25	190	28	182	0.7
0051235	maintenance of localization	0	425	3	2594	0.897	0	215	0	210	-
0050789	regulation of biological process	58	367	344	2253	0.882	**38**	**177**	**20**	**190**	**0.021**
0050790	regulation of enzyme activity	2	423	13	2584	0.771	1	214	1	209	0.489
0040029	regulation of gene expression, epigenetic	4	421	16	2581	0.657	2	213	2	208	0.632
0006306	DNA methylation	1	424	6	2591	0.598	1	214	0	210	0.991
0045814	negative regulation of gene expression, epigenetic	1	424	6	2591	0.598	0	215	1	209	0.991
0006342	chromatin silencing	1	424	6	2591	0.598	0	215	1	209	0.991
0003674	molecular_function	246	179	1518	1079	0.867	121	94	125	85	0.563
0016209	antioxidant activity	0	425	8	2589	0.524	0	215	0	210	-
0005488	binding	162	263	880	1717	0.1	88	127	74	136	0.268
0005509	calcium ion binding	11	414	47	2550	0.372	4	211	7	203	0.515
0030246	carbohydrate binding	2	423	12	2585	0.718	1	214	1	209	0.489
0008289	lipid binding	6	419	20	2577	0.296	3	212	3	207	0.702
0003676	nucleic acid binding	52	373	372	2225	0.283	31	184	21	189	0.214
0003677	DNA binding	29	396	166	2431	0.819	**21**	**194**	**8**	**202**	**0.025**
0003682	chromatin binding	6	419	18	2579	0.21	3	212	3	207	0.702
0003700	transcription factor activity	14	411	73	2524	0.692	9	206	5	205	0.441
0003723	RNA binding	13	412	110	2487	0.315	3	212	10	200	0.083
0008135	translation factor activity, nucleic acid binding	4	421	30	2567	0.889	2	213	2	208	0.632
0000166	nucleotide binding	41	384	215	2382	0.398	17	198	24	186	0.287
0005515	protein binding	**69**	**356**	**313**	**2284**	**0.02**	39	176	30	180	0.344
0008134	transcription factor binding	6	419	23	2574	0.445	5	210	1	209	0.228
0008092	cytoskeletal protein binding	16	409	73	2524	0.356	10	205	6	204	0.474
0003779	actin binding	6	419	48	2549	0.666	3	212	3	207	0.702
0003824	catalytic activity	122	303	718	1879	0.694	**50**	**165**	**72**	**138**	**0.016**
0016787	hydrolase activity	47	378	313	2284	0.613	23	192	24	186	0.932
0003924	GTPase activity	4	421	32	2565	0.786	3	212	1	209	0.632
0004518	nuclease activity	2	423	12	2585	0.718	2	213	0	210	0.489

cGMP vs. cAMP (p < 0.01; "up" means higher in cGMP)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	11	414	102	2495	0.226	6	209	5	205	0.968
0004721	phosphoprotein phosphatase activity	4	421	25	2572	0.821	3	212	1	209	0.632
0016740	transferase activity	40	385	207	2390	0.363	18	197	22	188	0.564
0016301	kinase activity	20	405	120	2477	0.962	11	204	9	201	0.861
0004672	protein kinase activity	16	409	80	2517	0.551	9	206	7	203	0.836
0030234	enzyme regulator activity	18	407	93	2504	0.599	12	203	6	204	0.249
0003774	motor activity	5	420	22	2575	0.696	0	215	5	205	0.068
0004871	signal transducer activity	34	391	217	2380	0.88	23	192	11	199	0.058
0004872	receptor activity	10	415	94	2503	0.236	7	208	3	207	0.356
0004879	ligand-dependent nuclear receptor activity	1	424	8	2589	0.822	0	215	1	209	0.991
0004888	transmembrane receptor activity	7	418	64	2533	0.391	6	209	1	209	0.135
0004930	G-protein coupled receptor activity	2	423	27	2570	0.397	2	213	0	210	0.489
0005057	receptor signaling protein activity	13	412	69	2528	0.755	8	207	5	205	0.603
0005102	receptor binding	11	414	56	2541	0.702	8	207	3	207	0.237
0005198	structural molecule activity	28	397	166	2431	0.963	12	203	16	194	0.515
0030528	transcription regulator activity	31	394	167	2430	0.575	21	194	10	200	0.072
0045182	translation regulator activity	4	421	30	2567	0.889	2	213	2	208	0.632
0005215	transporter activity	33	392	218	2379	0.733	14	201	19	191	0.426
0005489	electron transporter activity	1	424	28	2569	0.166	0	215	1	209	0.991
0005216	ion channel activity	5	420	46	2551	0.497	3	212	2	208	0.979
0005244	voltage-gated ion channel activity	3	422	23	2574	0.929	2	213	1	209	0.984
0005575	cellular_component	162	263	1087	1510	0.162	83	132	79	131	0.913
0005623	cell	151	274	992	1605	0.318	78	137	73	137	0.822
0005622	intracellular	111	314	784	1813	0.1	53	162	58	152	0.558
0005737	cytoplasm	59	366	433	2164	0.17	26	189	33	177	0.348
0016023	cytoplasmic vesicle	8	417	35	2562	0.521	5	210	3	207	0.746
0005829	cytosol	9	416	103	2494	0.083	2	213	7	203	0.167
0005783	endoplasmic reticulum	5	420	52	2545	0.333	0	215	5	205	0.068
0005794	Golgi apparatus	1	424	25	2572	0.222	1	214	0	210	0.991
0005815	microtubule organizing center	1	424	8	2589	0.822	1	214	0	210	0.991
0005739	mitochondrion	11	414	98	2499	0.283	4	211	7	203	0.515
0005840	ribosome	4	421	53	2544	0.176	2	213	2	208	0.632
0005773	vacuole	1	424	15	2582	0.589	0	215	1	209	0.991
0005764	lysosome	1	424	5	2592	0.686	0	215	1	209	0.991
0005856	cytoskeleton	14	411	70	2527	0.591	6	209	8	202	0.752
0005694	chromosome	6	419	32	2565	0.942	2	213	4	206	0.66
0000228	nuclear chromosome	0	425	5	2592	0.794	0	215	0	210	-
0005634	nucleus	51	374	325	2272	0.827	28	187	23	187	0.612
0005635	nuclear membrane	2	423	16	2581	0.983	0	215	2	208	0.468
0005730	nucleolus	0	425	11	2586	0.363	0	215	0	210	-
0005654	nucleoplasm	9	416	65	2532	0.759	3	212	6	204	0.478
0005777	peroxisome	1	424	8	2589	0.822	0	215	1	209	0.991
0005886	plasma membrane	19	406	128	2469	0.775	14	201	5	205	0.068
0005576	extracellular region	**17**	**408**	**53**	**2544**	**0.021**	9	206	8	202	0.961
0005578	extracellular matrix (sensu Metazoa)	**10**	**415**	**25**	**2572**	**0.025**	5	210	5	205	0.778

		All Treatments vs. Control ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	263	176	1526	1057	0.784	133	106	130	70	0.058
0007610	behavior	21	418	137	2446	0.736	13	226	8	192	0.632
0030534	adult behavior	2	437	21	2562	0.617	1	238	1	199	0.558
0030537	larval behavior	1	438	8	2575	0.855	0	239	1	199	0.929
0007611	learning and/or memory	3	436	21	2562	0.994	2	237	1	199	0.877
0007612	learning	2	437	13	2570	0.814	2	237	0	200	0.558
0007613	memory	2	437	9	2574	0.933	1	238	1	199	0.558
0007626	locomotory behavior	16	423	104	2479	0.805	10	229	6	194	0.686
0007635	chemosensory behavior	2	437	15	2568	0.983	2	237	0	200	0.558
0007622	rhythmic behavior	5	434	9	2574	0.061	2	237	3	197	0.841
0048512	circadian behavior	**5**	**434**	**8**	**2575**	**0.039**	2	237	3	197	0.841
0009987	cellular process	249	190	1412	1171	0.454	126	113	123	77	0.08
0007154	cell communication	83	356	404	2179	0.099	51	188	32	168	0.193
0007155	cell adhesion	**20**	**419**	**65**	**2518**	**0.026**	11	228	9	191	0.858
0008037	cell recognition	1	438	1	2582	0.674	1	238	0	200	0.929
0008038	neuronal cell recognition	1	438	1	2582	0.674	1	238	0	200	0.929
0016337	cell-cell adhesion	**10**	**429**	**25**	**2558**	**0.033**	5	234	5	195	0.971
0016339	calcium-dependent cell-cell adhesion	2	437	2	2581	0.192	1	238	1	199	0.558
0007156	homophilic cell adhesion	3	436	3	2580	0.059	2	237	1	199	0.877
0007160	cell-matrix adhesion	2	437	7	2576	0.855	1	238	1	199	0.558
0007267	cell-cell signaling	30	409	124	2459	0.094	18	221	12	188	0.657
0019226	transmission of nerve impulse	28	411	108	2475	0.054	17	222	11	189	0.622
0007268	synaptic transmission	**22**	**417**	**79**	**2504**	**0.05**	14	225	8	192	0.504
0007270	nerve-nerve synaptic transmission	1	438	15	2568	0.558	0	239	1	199	0.929
0001505	regulation of neurotransmitter levels	**15**	**424**	**45**	**2538**	**0.032**	11	228	4	196	0.218
0042133	neurotransmitter metabolism	3	436	5	2578	0.179	2	237	1	199	0.877
0007269	neurotransmitter secretion	12	427	41	2542	0.135	9	230	3	197	0.248
0007165	signal transduction	57	382	320	2263	0.786	32	207	25	175	0.894
0007166	cell surface receptor linked signal transduction	21	418	135	2448	0.786	11	228	10	190	0.976
0007167	enzyme linked receptor protein signaling pathway	7	432	38	2545	0.987	3	236	4	196	0.812
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	2	437	13	2570	0.814	1	238	1	199	0.558
0007179	transforming growth factor beta receptor signaling pathway	2	437	7	2576	0.855	1	238	1	199	0.558
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	5	434	26	2557	0.999	2	237	3	197	0.841
0007173	epidermal growth factor receptor signaling pathway	1	438	6	2577	0.604	0	239	1	199	0.929
0008286	insulin receptor signaling pathway	0	439	4	2579	0.908	0	239	0	200	-
0008293	torso signaling pathway	2	437	5	2578	0.604	0	239	2	198	0.402
0007186	G-protein coupled receptor protein signaling pathway	8	431	63	2520	0.536	6	233	2	198	0.412
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	2	437	3	2580	0.326	2	237	0	200	0.558
0007219	Notch signaling pathway	2	437	11	2572	0.759	1	238	1	199	0.558
0007224	smoothened signaling pathway	0	439	6	2577	0.666	0	239	0	200	-
0008063	Toll signaling pathway	2	437	2	2581	0.192	1	238	1	199	0.558
0016055	Wnt receptor signaling pathway	5	434	9	2574	0.061	2	237	3	197	0.841
0007242	intracellular signaling cascade	28	411	158	2425	0.918	17	222	11	189	0.622
0007263	nitric oxide mediated signal transduction	0	439	3	2580	0.916	0	239	0	200	-
0007243	protein kinase cascade	6	433	38	2545	0.963	4	235	2	198	0.847
0007259	JAK-STAT cascade	0	439	6	2577	0.666	0	239	0	200	-
0000165	MAPKKK cascade	6	433	29	2554	0.841	4	235	2	198	0.847
0019932	second-messenger-mediated signaling	4	435	18	2565	0.853	4	235	0	200	0.182
0019722	calcium-mediated signaling	2	437	13	2570	0.814	2	237	0	200	0.558
0048015	phosphoinositide-mediated signaling	2	437	3	2580	0.326	2	237	0	200	0.558
0007264	small GTPase mediated signal transduction	7	432	38	2545	0.987	3	236	4	196	0.812
0007265	Ras protein signal transduction	2	437	9	2574	0.933	1	238	1	199	0.558
0009966	regulation of signal transduction	6	433	26	2557	0.668	1	238	5	195	0.145
0007275	development	**82**	**357**	**372**	**2211**	**0.025**	44	195	38	162	0.972
0007568	aging	2	437	9	2574	0.933	1	238	1	199	0.558
0030154	cell differentiation	18	421	95	2488	0.768	10	229	8	192	0.885
0048468	cell development	9	430	61	2522	0.818	7	232	2	198	0.279
0000904	cellular morphogenesis during differentiation	0	439	18	2565	0.156	0	239	0	200	-
0042461	photoreceptor cell development	0	439	18	2565	0.156	0	239	0	200	-
0042051	eye photoreceptor development (sensu Endopterygota)	0	439	17	2566	0.174	0	239	0	200	-
0045165	cell fate commitment	10	429	36	2547	0.235	3	236	7	193	0.212

		All Treatments vs. Control ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	5	434	23	2560	0.816	2	237	3	197	0.841
0007400	neuroblast cell fate determination	3	436	5	2578	0.179	1	238	2	198	0.877
0001708	cell fate specification	0	439	7	2576	0.579	0	239	0	200	-
0007349	cellularization	2	437	8	2575	0.966	1	238	1	199	0.558
0040007	growth	5	434	31	2552	0.898	2	237	3	197	0.841
0002164	larval development	4	435	13	2570	0.477	2	237	2	198	0.745
0002165	larval or pupal development (sensu Insecta)	21	418	104	2479	0.544	11	228	10	190	0.976
0007552	metamorphosis	20	419	97	2486	0.503	10	229	10	190	0.858
0009653	morphogenesis	55	384	261	2322	0.147	31	208	24	176	0.872
0002009	morphogenesis of an epithelium	8	431	32	2551	0.445	4	235	4	196	0.917
0009887	organogenesis	49	390	233	2350	0.181	25	214	24	176	0.72
0001654	eye morphogenesis	7	432	48	2535	0.85	2	237	5	195	0.316
0008406	gonad development	3	436	7	2576	0.346	2	237	1	199	0.877
0007444	imaginal disc development	14	425	77	2506	0.932	5	234	9	191	0.247
0007494	midgut development	1	438	3	2580	0.908	1	238	0	200	0.929
0007517	muscle development	4	435	29	2554	0.884	4	235	0	200	0.182
0007399	neurogenesis	29	410	136	2447	0.303	15	224	14	186	0.911
0007409	axonogenesis	5	434	42	2541	0.58	2	237	3	197	0.841
0007411	axon guidance	3	436	32	2551	0.445	2	237	1	199	0.877
0007417	central nervous system development	6	433	33	2550	0.94	3	236	3	197	0.847
0016358	dendrite morphogenesis	2	437	12	2571	0.723	1	238	1	199	0.558
0042063	gliogenesis	2	437	9	2574	0.933	2	237	0	200	0.558
0007422	peripheral nervous system development	7	432	33	2550	0.756	2	237	5	195	0.316
0050767	regulation of neurogenesis	1	438	5	2578	0.666	0	239	1	199	0.929
0007424	tracheal system development (sensu Insecta)	9	430	26	2557	0.099	6	233	3	197	0.685
0048513	organ development	50	389	236	2347	0.161	26	213	24	176	0.828
0007389	pattern specification	**17**	**422**	**55**	**2528**	**0.041**	12	227	5	195	0.265
0048066	pigmentation	3	436	7	2576	0.346	2	237	1	199	0.877
0009791	post-embryonic development	4	435	13	2570	0.477	2	237	2	198	0.745
0009790	embryonic development	**27**	**412**	**72**	**2511**	**4E-04**	16	223	11	189	0.749
0007530	sex determination	1	438	9	2574	0.966	1	238	0	200	0.929
0007548	sex differentiation	3	436	15	2568	0.939	2	237	1	199	0.877
0019827	stem cell maintenance	2	437	6	2577	0.734	1	238	1	199	0.558
0000003	reproduction	21	418	113	2470	0.795	12	227	9	191	0.976
0050793	regulation of development	4	435	39	2544	0.446	2	237	2	198	0.745
0007582	physiological process	239	200	1400	1183	0.966	**118**	**121**	**121**	**79**	**0.025**
0008152	metabolism	176	263	1026	1557	0.925	**81**	**158**	**95**	**105**	**0.005**
0009056	catabolism	26	413	177	2406	0.538	17	222	9	191	0.341
0006091	energy pathways	13	426	95	2488	0.543	8	231	5	195	0.811
0006118	electron transport	6	433	50	2533	0.531	3	236	3	197	0.847
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	61	378	373	2210	0.82	35	204	26	174	0.721
0006259	DNA metabolism	13	426	67	2516	0.778	6	233	7	193	0.744
0006350	transcription	29	410	196	2387	0.531	21	218	8	192	0.069
0043170	macromolecule metabolism	90	349	571	2012	0.49	**33**	**206**	**57**	**143**	**2E-04**
0019538	protein metabolism	73	366	485	2098	0.315	**27**	**212**	**46**	**154**	**0.002**
0006412	protein biosynthesis	14	425	129	2454	0.127	4	235	10	190	0.089
0006464	protein modification	30	409	227	2356	0.206	11	228	19	181	0.066
0006457	protein folding	**12**	**427**	**32**	**2551**	**0.028**	**0**	**239**	**12**	**188**	**4E-04**
0005975	carbohydrate metabolism	21	418	87	2496	0.181	8	231	13	187	0.188
0006519	amino acid and derivative metabolism	14	425	57	2526	0.278	4	235	10	190	0.089
0006629	lipid metabolism	16	423	77	2506	0.552	7	232	9	191	0.536
0009308	amine metabolism	16	423	65	2518	0.233	5	234	11	189	0.101
0042440	pigment metabolism	1	438	11	2572	0.842	1	238	0	200	0.929
0042445	hormone metabolism	3	436	4	2579	0.111	2	237	1	199	0.877
0009058	biosynthesis	27	412	215	2368	0.145	11	228	16	184	0.202
0019748	secondary metabolism	1	438	13	2570	0.685	1	238	0	200	0.929
0019222	regulation of metabolism	31	408	203	2380	0.63	21	218	10	190	0.175
0016265	death	13	426	75	2508	0.931	5	234	8	192	0.373
0008219	cell death	11	428	65	2518	0.88	4	235	7	193	0.361
0016271	tissue death	5	434	22	2561	0.751	2	237	3	197	0.841
0042592	homeostasis	6	433	23	2560	0.495	3	236	3	197	0.847
0019725	cell homeostasis	5	434	21	2562	0.686	2	237	3	197	0.841
0050801	ion homeostasis	**5**	**434**	**8**	**2575**	**0.039**	2	237	3	197	0.841
0043062	extracellular structure organization and biogenesis	2	437	17	2566	0.865	2	237	0	200	0.558
0046903	secretion	17	422	85	2498	0.631	11	228	6	194	0.536
0048511	rhythmic process	5	434	11	2572	0.122	2	237	3	197	0.841

All Treatments vs. Control ($p < 0.01$)

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	50	389	297	2286	0.988	28	211	22	178	0.933
0050874	organismal physiological process	**46**	**393**	**182**	**2401**	**0.016**	28	211	18	182	0.442
0050875	cellular physiological process	222	217	1331	1252	0.749	**110**	**129**	**112**	**88**	**0.047**
0006810	transport	63	376	338	2245	0.518	33	206	30	170	0.827
0006811	ion transport	24	415	96	2487	0.109	14	225	10	190	0.855
0006818	hydrogen transport	4	435	15	2568	0.629	3	236	1	199	0.745
0006836	neurotransmitter transport	0	439	6	2577	0.666	0	239	0	200	-
0006858	extracellular transport	4	435	11	2572	0.332	1	238	3	197	0.494
0006869	lipid transport	3	436	14	2569	0.983	0	239	3	197	0.187
0008643	carbohydrate transport	**6**	**433**	**9**	**2574**	**0.015**	2	237	4	196	0.527
0015031	protein transport	19	420	160	2423	0.155	10	229	9	191	0.941
0015837	amine transport	4	435	9	2574	0.204	2	237	2	198	0.745
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	3	436	11	2572	0.723	2	237	1	199	0.877
0016192	vesicle-mediated transport	17	422	103	2480	0.986	11	228	6	194	0.536
0045045	secretory pathway	16	423	80	2503	0.647	10	229	6	194	0.686
0046907	intracellular transport	24	415	175	2408	0.359	13	226	11	189	0.855
0051049	regulation of transport	4	435	14	2569	0.553	1	238	3	197	0.494
0008283	cell proliferation	**17**	**422**	**55**	**2528**	**0.041**	9	230	8	192	0.903
0007049	cell cycle	23	416	108	2475	0.379	14	225	9	191	0.674
0017145	stem cell division	4	435	8	2575	0.149	2	237	2	198	0.745
0016043	cell organization and biogenesis	44	395	230	2353	0.506	26	213	18	182	0.622
0000902	cellular morphogenesis	8	431	66	2517	0.452	4	235	4	196	0.917
0006996	organelle organization and biogenesis	38	401	200	2383	0.575	20	219	18	182	0.949
0007010	cytoskeleton organization and biogenesis	28	411	138	2445	0.443	16	223	12	188	0.92
0006997	nuclear organization and biogenesis	1	438	8	2575	0.855	1	238	0	200	0.929
0007028	cytoplasm organization and biogenesis	5	434	12	2571	0.161	3	236	2	198	0.841
0016044	membrane organization and biogenesis	2	437	6	2577	0.734	2	237	0	200	0.558
0051128	regulation of cell organization and biogenesis	1	438	11	2572	0.842	0	239	1	199	0.929
0016049	cell growth	1	438	8	2575	0.855	0	239	1	199	0.929
0050896	response to stimulus	**37**	**402**	**139**	**2444**	**0.016**	18	221	19	181	0.571
0006950	response to stress	**15**	**424**	**43**	**2540**	**0.022**	**2**	**237**	**13**	**187**	**0.003**
0009408	response to heat	**5**	**434**	**6**	**2577**	**0.013**	**0**	**239**	**5**	**195**	**0.045**
0006979	response to oxidative stress	0	439	2	2581	0.674	0	239	0	200	-
0051179	localization	69	370	360	2223	0.361	35	204	34	166	0.587
0006403	RNA localization	4	435	25	2558	0.879	2	237	2	198	0.745
0008104	protein localization	22	417	170	2413	0.254	11	228	11	189	0.834
0051234	establishment of localization	64	375	342	2241	0.494	34	205	30	170	0.926
0051235	maintenance of localization	1	438	2	2581	0.916	1	238	0	200	0.929
0050789	regulation of biological process	59	380	343	2240	0.988	31	208	28	172	0.862
0050790	regulation of enzyme activity	1	438	14	2569	0.618	1	238	0	200	0.929
0040029	regulation of gene expression, epigenetic	5	434	15	2568	0.31	1	238	4	196	0.27
0006306	DNA methylation	2	437	5	2578	0.604	1	238	1	199	0.558
0045814	negative regulation of gene expression, epigenetic	1	438	6	2577	0.604	0	239	1	199	0.929
0006342	chromatin silencing	1	438	6	2577	0.604	0	239	1	199	0.929
0003674	molecular_function	252	187	1512	1071	0.694	**125**	**114**	**127**	**73**	**0.023**
0016209	antioxidant activity	0	439	8	2575	0.506	0	239	0	200	-
0005488	binding	147	292	895	1688	0.674	70	169	77	123	0.053
0005509	calcium ion binding	10	429	48	2535	0.686	6	233	4	196	0.971
0030246	carbohydrate binding	2	437	12	2571	0.723	1	238	1	199	0.558
0008289	lipid binding	4	435	22	2561	0.877	1	238	3	197	0.494
0003676	nucleic acid binding	54	385	370	2213	0.292	26	213	28	172	0.398
0003677	DNA binding	30	409	165	2418	0.805	19	220	11	189	0.41
0003682	chromatin binding	4	435	20	2563	0.994	1	238	3	197	0.494
0003700	transcription factor activity	10	429	77	2506	0.509	8	231	2	198	0.187
0003723	RNA binding	15	424	108	2475	0.536	5	234	10	190	0.16
0008135	translation factor activity, nucleic acid binding	4	435	30	2553	0.83	0	239	4	196	0.091
0000166	nucleotide binding	42	397	214	2369	0.424	**14**	**225**	**28**	**172**	**0.006**
0005515	protein binding	58	381	324	2259	0.755	32	207	26	174	0.983
0008134	transcription factor binding	3	436	26	2557	0.706	1	238	2	198	0.877
0008092	cytoskeletal protein binding	17	422	72	2511	0.276	11	228	6	194	0.536
0003779	actin binding	10	429	44	2539	0.519	7	232	3	197	0.498
0003824	catalytic activity	126	313	714	1869	0.689	61	178	65	135	0.133
0016787	hydrolase activity	63	376	297	2286	0.104	36	203	27	173	0.743
0003924	GTPase activity	5	434	31	2552	0.898	1	238	4	196	0.27
0004518	nuclease activity	1	438	13	2570	0.685	1	238	0	200	0.929

		All Treatments vs. Control ($p < 0.01$)									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	14	425	99	2484	0.602	11	228	3	197	0.116
0004721	phosphoprotein phosphatase activity	5	434	24	2559	0.879	3	236	2	198	0.841
0016740	transferase activity	35	404	212	2371	0.943	14	225	21	179	0.107
0016301	kinase activity	14	425	126	2457	0.152	7	232	7	193	0.947
0004672	protein kinase activity	9	430	87	2496	0.191	4	235	5	195	0.787
0030234	enzyme regulator activity	15	424	96	2487	0.864	9	230	6	194	0.86
0003774	motor activity	3	436	24	2559	0.817	2	237	1	199	0.877
0004871	signal transducer activity	29	410	222	2361	0.193	15	224	14	186	0.911
0004872	receptor activity	11	428	93	2490	0.307	3	236	8	192	0.127
0004879	ligand-dependent nuclear receptor activity	0	439	9	2574	0.444	0	239	0	200	-
0004888	transmembrane receptor activity	8	431	63	2520	0.536	3	236	5	195	0.54
0004930	G-protein coupled receptor activity	3	436	26	2557	0.706	2	237	1	199	0.877
0005057	receptor signaling protein activity	7	432	75	2508	0.161	4	235	3	197	0.812
0005102	receptor binding	12	427	55	2528	0.536	8	231	4	196	0.57
0005198	structural molecule activity	29	410	165	2418	0.947	17	222	12	188	0.784
0030528	transcription regulator activity	25	414	173	2410	0.496	17	222	8	192	0.232
0045182	translation regulator activity	4	435	30	2553	0.83	0	239	4	196	0.091
0005215	transporter activity	43	396	208	2375	0.259	22	217	21	179	0.769
0005489	electron transporter activity	3	436	26	2557	0.706	2	237	1	199	0.877
0005216	ion channel activity	6	433	45	2538	0.716	2	237	4	196	0.527
0005244	voltage-gated ion channel activity	3	436	23	2560	0.877	2	237	1	199	0.877
0005575	cellular_component	179	260	1070	1513	0.839	91	148	88	112	0.246
0005623	cell	163	276	980	1603	0.787	84	155	79	121	0.4
0005622	intracellular	124	315	771	1812	0.533	63	176	61	139	0.394
0005737	cytoplasm	69	370	423	2160	0.783	36	203	33	167	0.779
0016023	cytoplasmic vesicle	6	433	37	2546	0.912	4	235	2	198	0.847
0005829	cytosol	11	428	101	2482	0.192	5	234	6	194	0.764
0005783	endoplasmic reticulum	7	432	50	2533	0.767	2	237	5	195	0.316
0005794	Golgi apparatus	7	432	19	2564	0.128	4	235	3	197	0.812
0005815	microtubule organizing center	3	436	6	2577	0.259	1	238	2	198	0.877
0005739	mitochondrion	14	425	95	2488	0.712	6	233	8	192	0.541
0005840	ribosome	**2**	**437**	**55**	**2528**	**0.028**	2	237	0	200	0.558
0005773	vacuole	4	435	12	2571	0.403	3	236	1	199	0.745
0005764	lysosome	1	438	5	2578	0.666	0	239	1	199	0.929
0005856	cytoskeleton	16	423	68	2515	0.3	9	230	7	193	0.914
0005694	chromosome	7	432	31	2552	0.65	2	237	5	195	0.316
0000228	nuclear chromosome	0	439	5	2578	0.774	0	239	0	200	-
0005634	nucleus	53	386	323	2260	0.861	29	210	24	176	0.917
0005635	nuclear membrane	3	436	15	2568	0.939	1	238	2	198	0.877
0005730	nucleolus	1	438	10	2573	0.933	0	239	1	199	0.929
0005654	nucleoplasm	11	428	63	2520	0.933	3	236	8	192	0.127
0005777	peroxisome	1	438	8	2575	0.855	0	239	1	199	0.929
0005886	plasma membrane	21	418	126	2457	0.972	11	228	10	190	0.976
0005576	extracellular region	15	424	55	2528	0.137	9	230	6	194	0.86
0005578	extracellular matrix (sensu Metazoa)	**10**	**429**	**25**	**2558**	**0.033**	4	235	6	194	0.544

PC1

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	871	606	883	629	0.779	421	273	450	333	0.233
0007610	behavior	87	1390	75	1437	0.297	48	646	39	744	0.143
0030534	adult behavior	12	1465	12	1500	0.883	**10**	**684**	**2**	**781**	**0.025**
0030537	larval behavior	6	1471	3	1509	0.482	3	691	3	780	0.794
0007611	learning and/or memory	**20**	**1457**	**4**	**1508**	**0.002**	14	680	6	777	0.064
0007612	learning	**12**	**1465**	**3**	**1509**	**0.034**	9	685	3	780	0.097
0007613	memory	8	1469	3	1509	0.212	4	690	4	779	0.854
0007626	locomotory behavior	64	1413	59	1453	0.616	34	660	30	753	0.38
0007635	chemosensory behavior	12	1465	6	1506	0.218	8	686	4	779	0.28
0007622	rhythmic behavior	7	1470	8	1504	0.964	4	690	3	780	0.873
0048512	circadian behavior	6	1471	8	1504	0.823	3	691	3	780	0.794
0009987	cellular process	808	669	820	692	0.824	391	303	417	366	0.256
0007154	cell communication	**265**	**1212**	**224**	**1288**	**0.024**	**148**	**546**	**117**	**666**	**0.002**
0007155	cell adhesion	48	1429	42	1470	0.517	27	667	21	762	0.246
0008037	cell recognition	2	1475	0	1512	0.469	2	692	0	783	0.427
0008038	neuronal cell recognition	2	1475	0	1512	0.469	2	692	0	783	0.427
0016337	cell-cell adhesion	20	1457	19	1493	0.941	12	682	8	775	0.343
0016339	calcium-dependent cell-cell adhesion	5	1472	2	1510	0.431	2	692	3	780	0.892
0007156	homophilic cell adhesion	6	1471	3	1509	0.482	3	691	3	780	0.794
0007160	cell-matrix adhesion	6	1471	3	1509	0.482	4	690	2	781	0.577
0007267	cell-cell signaling	**90**	**1387**	**66**	**1446**	**0.041**	**52**	**642**	**38**	**745**	**0.045**
0019226	transmission of nerve impulse	**80**	**1397**	**58**	**1454**	**0.049**	**47**	**647**	**33**	**750**	**0.04**
0007268	synaptic transmission	60	1417	41	1471	0.052	**38**	**656**	**22**	**761**	**0.014**
0007270	nerve-nerve synaptic transmission	9	1468	7	1505	0.766	6	688	3	780	0.394
0001505	regulation of neurotransmitter levels	35	1442	25	1487	0.206	19	675	16	767	0.481
0042133	neurotransmitter metabolism	5	1472	3	1509	0.699	3	691	2	781	0.892
0007269	neurotransmitter secretion	30	1447	23	1489	0.359	16	678	14	769	0.604
0007165	signal transduction	201	1276	178	1334	0.146	**108**	**586**	**93**	**690**	**0.047**
0007166	cell surface receptor linked signal transduction	76	1401	81	1431	0.859	41	653	35	748	0.258
0007167	enzyme linked receptor protein signaling pathway	23	1454	23	1489	0.945	**16**	**678**	**7**	**776**	**0.048**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	11	1466	5	1507	0.193	8	686	3	780	0.157
0007179	transforming growth factor beta receptor signaling pathway	5	1472	4	1508	0.972	3	691	2	781	0.892
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	13	1464	19	1493	0.411	9	685	4	779	0.182
0007173	epidermal growth factor receptor signaling pathway	5	1472	3	1509	0.699	2	692	3	780	0.892
0008286	insulin receptor signaling pathway	1	1476	3	1509	0.633	1	693	0	783	0.952
0008293	torso signaling pathway	3	1474	4	1508	0.975	1	693	2	781	0.917
0007186	G-protein coupled receptor protein signaling pathway	35	1442	36	1476	0.92	18	676	17	766	0.718
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1474	2	1510	0.979	1	693	2	781	0.917
0007219	Notch signaling pathway	7	1470	6	1506	0.966	3	691	4	779	0.873
0007224	smoothened signaling pathway	5	1472	1	1511	0.21	3	691	2	781	0.892
0008063	Toll signaling pathway	1	1476	3	1509	0.633	0	694	1	782	0.952
0016055	Wnt receptor signaling pathway	8	1469	8	1504	0.839	4	690	4	779	0.854
0007242	intracellular signaling cascade	100	1377	82	1430	0.143	53	641	47	736	0.253
0007263	nitric oxide mediated signal transduction	1	1476	3	1509	0.633	1	693	0	783	0.952
0007243	protein kinase cascade	19	1458	22	1490	0.811	11	683	8	775	0.467
0007259	JAK-STAT cascade	2	1475	4	1508	0.704	0	694	2	781	0.533
0000165	MAPKKK cascade	16	1461	17	1495	0.946	10	684	6	777	0.318
0019932	second-messenger-mediated signaling	14	1463	8	1504	0.261	9	685	5	778	0.301
0019722	calcium-mediated signaling	9	1468	6	1506	0.573	7	687	2	781	0.128
0048015	phosphoinositide-mediated signaling	3	1474	2	1510	0.979	1	693	2	781	0.917
0007264	small GTPase mediated signal transduction	20	1457	24	1488	0.706	12	682	8	775	0.343
0007265	Ras protein signal transduction	7	1470	3	1509	0.323	6	688	1	782	0.093
0009966	regulation of signal transduction	21	1456	13	1499	0.202	10	684	11	772	0.872
0007275	development	235	1242	225	1287	0.466	118	576	117	666	0.313
0007568	aging	7	1470	4	1508	0.52	3	691	4	779	0.873
0030154	cell differentiation	63	1414	56	1456	0.489	33	661	30	753	0.455
0048468	cell development	42	1435	33	1479	0.299	23	671	19	764	0.386
0000904	cellular morphogenesis during differentiation	10	1467	9	1503	0.959	3	691	7	776	0.446
0042461	photoreceptor cell development	9	1468	9	1503	0.852	3	691	6	777	0.625
0042051	eye photoreceptor development (sensu Endopterygota)	8	1469	9	1503	0.961	3	691	5	778	0.854
0045165	cell fate commitment	23	1454	26	1486	0.837	11	683	12	771	0.897

PC1

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	15	1462	15	1497	0.905	8	686	7	776	0.814
0007400	neuroblast cell fate determination	3	1474	5	1507	0.748	2	692	1	782	0.917
0001708	cell fate specification	4	1473	4	1508	0.748	2	692	2	781	0.703
0007349	cellularization	8	1469	3	1509	0.212	6	688	2	781	0.216
0040007	growth	16	1461	20	1492	0.665	8	686	8	775	0.993
0002164	larval development	9	1468	8	1504	0.961	3	691	6	777	0.625
0002165	larval or pupal development (sensu Insecta)	68	1409	61	1451	0.499	31	663	37	746	0.911
0007552	metamorphosis	64	1413	57	1455	0.491	29	665	35	748	0.884
0009653	morphogenesis	162	1315	157	1355	0.647	83	611	79	704	0.287
0002009	morphogenesis of an epithelium	17	1460	27	1485	0.197	9	685	8	775	0.802
0009887	organogenesis	144	1333	138	1374	0.603	72	622	72	711	0.5
0001654	eye morphogenesis	31	1446	26	1486	0.532	12	682	19	764	0.452
0008406	gonad development	5	1472	6	1506	0.969	1	693	4	779	0.446
0007444	imaginal disc development	49	1428	44	1468	0.592	22	672	27	756	0.879
0007494	midgut development	3	1474	2	1510	0.979	2	692	1	782	0.917
0007517	muscle development	18	1459	16	1496	0.809	10	684	8	775	0.62
0007399	neurogenesis	78	1399	84	1428	0.802	41	653	37	746	0.369
0007409	axonogenesis	20	1457	23	1489	0.818	12	682	8	775	0.343
0007411	axon guidance	15	1462	18	1494	0.778	7	687	8	775	0.814
0007417	central nervous system development	19	1458	20	1492	0.941	9	685	10	773	0.843
0016358	dendrite morphogenesis	6	1471	8	1504	0.823	3	691	3	780	0.794
0042063	gliogenesis	6	1471	5	1507	0.969	4	690	2	781	0.577
0007422	peripheral nervous system development	21	1456	19	1493	0.815	11	683	10	773	0.781
0050767	regulation of neurogenesis	1	1476	4	1508	0.385	0	694	1	782	0.952
0007424	tracheal system development (sensu Insecta)	17	1460	20	1492	0.795	7	687	10	773	0.812
0048513	organ development	147	1330	139	1373	0.52	73	621	74	709	0.55
0007389	pattern specification	36	1441	40	1472	0.806	19	675	17	766	0.592
0048066	pigmentation	5	1472	6	1506	0.969	1	693	4	779	0.446
0009791	post-embryonic development	9	1468	8	1504	0.961	3	691	6	777	0.625
0009790	embryonic development	47	1430	53	1459	0.697	18	676	29	754	0.287
0007530	sex determination	4	1473	6	1506	0.78	2	692	2	781	0.703
0007548	sex differentiation	11	1466	8	1504	0.609	4	690	7	776	0.685
0019827	stem cell maintenance	3	1474	5	1507	0.748	2	692	1	782	0.917
0000003	reproduction	76	1401	68	1444	0.458	41	653	35	748	0.258
0050793	regulation of development	17	1460	26	1486	0.249	9	685	8	775	0.802
0007582	physiological process	790	687	815	697	0.849	374	320	416	367	0.81
0008152	metabolism	555	922	611	901	0.121	245	449	310	473	0.1
0009056	catabolism	92	1385	117	1395	0.122	44	650	48	735	0.953
0006091	energy pathways	57	1420	51	1461	0.539	**40**	**654**	**17**	**766**	**6E-04**
0006118	electron transport	29	1448	26	1486	0.719	18	676	11	772	0.145
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	209	1268	223	1289	0.68	**74**	**620**	**135**	**648**	**4E-04**
0006259	DNA metabolism	**27**	**1450**	**52**	**1460**	**0.009**	8	686	19	764	0.103
0006350	transcription	118	1359	109	1403	0.462	**39**	**655**	**79**	**704**	**0.002**
0043170	macromolecule metabolism	**278**	**1199**	**350**	**1162**	**0.004**	134	560	144	639	0.701
0019538	protein metabolism	**233**	**1244**	**294**	**1218**	**0.01**	111	583	122	661	0.884
0006412	protein biosynthesis	49	1428	61	1451	0.345	23	671	26	757	0.89
0006464	protein modification	123	1354	133	1379	0.695	51	643	72	711	0.235
0006457	protein folding	17	1460	26	1486	0.249	8	686	9	774	0.812
0005975	carbohydrate metabolism	50	1427	57	1455	0.64	27	667	23	760	0.386
0006519	amino acid and derivative metabolism	36	1441	34	1478	0.826	14	680	22	761	0.414
0006629	lipid metabolism	44	1433	45	1467	0.918	17	677	27	756	0.33
0009308	amine metabolism	41	1436	40	1472	0.915	18	676	23	760	0.808
0042440	pigment metabolism	4	1473	8	1504	0.408	1	693	3	780	0.703
0042445	hormone metabolism	3	1474	4	1508	0.975	1	693	2	781	0.917
0009058	biosynthesis	102	1375	102	1410	0.92	43	651	59	724	0.363
0019748	secondary metabolism	5	1472	9	1503	0.447	1	693	4	779	0.446
0019222	regulation of metabolism	121	1356	117	1395	0.696	47	647	74	709	0.075
0016265	death	44	1433	42	1470	0.826	19	675	25	758	0.719
0008219	cell death	37	1440	37	1475	0.987	16	678	21	762	0.768
0016271	tissue death	15	1462	12	1500	0.654	7	687	8	775	0.814
0042592	homeostasis	13	1464	16	1496	0.757	5	689	8	775	0.734
0019725	cell homeostasis	12	1465	14	1498	0.891	5	689	7	776	0.936
0050801	ion homeostasis	5	1472	9	1503	0.447	1	693	4	779	0.446
0043062	extracellular structure organization and biogenesis	6	1471	13	1499	0.184	4	690	2	781	0.577
0046903	secretion	55	1422	46	1466	0.353	33	661	22	761	0.067
0048511	rhythmic process	9	1468	8	1504	0.961	6	688	3	780	0.394

		PC1									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	166	1311	181	1331	0.57	72	622	94	689	0.364
0050874	organismal physiological process	**134**	**1343**	**98**	**1414**	**0.01**	72	622	62	721	0.121
0050875	cellular physiological process	747	730	772	740	0.82	353	341	394	389	0.875
0006810	transport	214	1263	184	1328	0.07	**127**	**567**	**87**	**696**	**1E-04**
0006811	ion transport	**71**	**1406**	**49**	**1463**	**0.037**	**49**	**645**	**22**	**761**	**2E-04**
0006818	hydrogen transport	13	1464	5	1507	0.088	**11**	**683**	**2**	**781**	**0.014**
0006836	neurotransmitter transport	4	1473	1	1511	0.357	3	691	1	782	0.534
0006858	extracellular transport	6	1471	9	1503	0.637	4	690	2	781	0.577
0006869	lipid transport	7	1470	9	1503	0.839	5	689	2	781	0.358
0008643	carbohydrate transport	8	1469	7	1505	0.964	3	691	5	778	0.854
0015031	protein transport	88	1389	92	1420	0.945	**53**	**641**	**35**	**748**	**0.014**
0015837	amine transport	9	1468	3	1509	0.137	5	689	4	779	0.856
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	6	1471	7	1505	0.966	2	692	4	779	0.794
0016192	vesicle-mediated transport	62	1415	57	1455	0.614	37	657	25	758	0.055
0045045	secretory pathway	52	1425	43	1469	0.342	**32**	**662**	**20**	**763**	**0.046**
0046907	intracellular transport	99	1378	99	1413	0.923	**60**	**634**	**39**	**744**	**0.007**
0051049	regulation of transport	11	1466	7	1505	0.448	**9**	**685**	**2**	**781**	**0.043**
0008283	cell proliferation	**45**	**1432**	**26**	**1486**	**0.024**	17	677	28	755	0.269
0007049	cell cycle	64	1413	64	1448	0.964	33	661	31	752	0.534
0017145	stem cell division	5	1472	7	1505	0.804	3	691	2	781	0.892
0016043	cell organization and biogenesis	128	1349	147	1365	0.35	63	631	65	718	0.662
0000902	cellular morphogenesis	36	1441	44	1468	0.492	18	676	18	765	0.843
0006996	organelle organization and biogenesis	109	1368	129	1383	0.273	56	638	53	730	0.393
0007010	cytoskeleton organization and biogenesis	87	1390	83	1429	0.693	50	644	37	746	0.056
0006997	nuclear organization and biogenesis	3	1474	7	1505	0.361	0	694	3	780	0.292
0007028	cytoplasm organization and biogenesis	**4**	**1473**	**15**	**1497**	**0.024**	1	693	3	780	0.703
0016044	membrane organization and biogenesis	5	1472	4	1508	0.972	2	692	3	780	0.892
0051128	regulation of cell organization and biogenesis	5	1472	6	1506	0.969	3	691	2	781	0.892
0016049	cell growth	3	1474	6	1506	0.527	2	692	1	782	0.917
0050896	response to stimulus	86	1391	95	1417	0.652	39	655	47	736	0.84
0006950	response to stress	26	1451	33	1479	0.485	9	685	17	766	0.281
0009408	response to heat	4	1473	6	1506	0.78	2	692	2	781	0.703
0006979	response to oxidative stress	1	1476	1	1511	0.49	0	694	1	782	0.952
0051179	localization	231	1246	198	1314	0.053	**136**	**558**	**95**	**688**	**1E-04**
0006403	RNA localization	15	1462	17	1495	0.912	7	687	8	775	0.814
0008104	protein localization	96	1381	99	1413	0.983	**58**	**636**	**38**	**745**	**0.009**
0051234	establishment of localization	217	1260	186	1326	0.063	**128**	**566**	**89**	**694**	**2E-04**
0051235	maintenance of localization	2	1475	2	1510	0.633	0	694	2	781	0.533
0050789	regulation of biological process	196	1281	207	1305	0.777	84	610	112	671	0.243
0050790	regulation of enzyme activity	9	1468	5	1507	0.397	2	692	7	776	0.247
0040029	regulation of gene expression, epigenetic	10	1467	10	1502	0.864	5	689	5	778	0.899
0006306	DNA methylation	3	1474	4	1508	0.975	1	693	2	781	0.917
0045814	negative regulation of gene expression, epigenetic	2	1475	5	1507	0.468	1	693	1	782	0.533
0006342	chromatin silencing	2	1475	5	1507	0.468	1	693	1	782	0.533
0003674	molecular_function	866	611	866	646	0.475	424	270	442	341	0.079
0016209	antioxidant activity	5	1472	4	1508	0.972	4	690	1	782	0.302
0005488	binding	499	978	508	1004	0.945	231	463	268	515	0.744
0005509	calcium ion binding	33	1444	28	1484	0.542	18	676	15	768	0.482
0030246	carbohydrate binding	7	1470	8	1504	0.964	5	689	2	781	0.358
0008289	lipid binding	15	1462	11	1501	0.515	6	688	9	774	0.776
0003676	nucleic acid binding	189	1288	200	1312	0.767	77	617	112	671	0.078
0003677	DNA binding	100	1377	94	1418	0.589	**33**	**661**	**67**	**716**	**0.005**
0003682	chromatin binding	7	1470	16	1496	0.106	1	693	6	777	0.174
0003700	transcription factor activity	44	1433	42	1470	0.826	**13**	**681**	**31**	**752**	**0.028**
0003723	RNA binding	51	1426	68	1444	0.172	24	670	27	756	0.895
0008135	translation factor activity, nucleic acid binding	16	1461	19	1493	0.787	9	685	7	776	0.621
0000166	nucleotide binding	133	1344	122	1390	0.395	67	627	66	717	0.466
0005515	protein binding	188	1289	191	1321	0.981	96	598	92	691	0.262
0008134	transcription factor binding	15	1462	16	1496	0.948	6	688	9	774	0.776
0008092	cytoskeletal protein binding	46	1431	42	1470	0.663	25	669	21	762	0.386
0003779	actin binding	24	1453	29	1483	0.639	13	681	11	772	0.614
0003824	catalytic activity	400	1077	439	1073	0.251	201	493	199	584	0.141
0016787	hydrolase activity	175	1302	197	1315	0.356	89	605	86	697	0.312
0003924	GTPase activity	17	1460	23	1489	0.471	**13**	**681**	**4**	**779**	**0.027**
0004518	nuclease activity	**3**	**1474**	**12**	**1500**	**0.043**	0	694	3	780	0.292

PC1

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	54	1423	64	1448	0.474	25	669	29	754	0.972
0004721	phosphoprotein phosphatase activity	11	1466	19	1493	0.222	4	690	7	776	0.685
0016740	transferase activity	117	1360	124	1388	0.831	51	643	66	717	0.502
0016301	kinase activity	73	1404	62	1450	0.308	36	658	37	746	0.773
0004672	protein kinase activity	55	1422	40	1472	0.115	28	666	27	756	0.648
0030234	enzyme regulator activity	58	1419	47	1465	0.265	29	665	29	754	0.738
0003774	motor activity	19	1458	9	1503	0.077	12	682	7	776	0.234
0004871	signal transducer activity	139	1338	117	1395	0.117	70	624	69	714	0.455
0004872	receptor activity	58	1419	51	1461	0.478	32	662	26	757	0.254
0004879	ligand-dependent nuclear receptor activity	7	1470	2	1510	0.17	2	692	5	778	0.549
0004888	transmembrane receptor activity	37	1440	37	1475	0.987	**24**	**670**	**13**	**770**	**0.041**
0004930	G-protein coupled receptor activity	16	1461	14	1498	0.804	10	684	6	777	0.318
0005057	receptor signaling protein activity	47	1430	33	1479	0.114	21	673	26	757	0.862
0005102	receptor binding	35	1442	34	1478	0.922	16	678	19	764	0.985
0005198	structural molecule activity	82	1395	80	1432	0.815	**48**	**646**	**34**	**749**	**0.041**
0030528	transcription regulator activity	104	1373	95	1417	0.448	**33**	**661**	**71**	**712**	**0.002**
0045182	translation regulator activity	16	1461	19	1493	0.787	9	685	7	776	0.621
0005215	transporter activity	**142**	**1335**	**111**	**1401**	**0.03**	**91**	**603**	**51**	**732**	**3E-05**
0005489	electron transporter activity	12	1465	17	1495	0.495	8	686	4	779	0.28
0005216	ion channel activity	30	1447	22	1490	0.287	**23**	**671**	**7**	**776**	**0.002**
0005244	voltage-gated ion channel activity	16	1461	10	1502	0.296	**12**	**682**	**4**	**779**	**0.045**
0005575	cellular_component	613	864	610	902	0.544	**328**	**366**	**285**	**498**	**3E-05**
0005623	cell	559	918	553	959	0.495	**297**	**397**	**262**	**521**	**3E-04**
0005622	intracellular	428	1049	429	1083	0.745	**222**	**472**	**206**	**577**	**0.019**
0005737	cytoplasm	228	1249	230	1282	0.904	**143**	**551**	**85**	**698**	**3E-07**
0016023	cytoplasmic vesicle	21	1456	20	1492	0.94	12	682	9	774	0.472
0005829	cytosol	34	1443	45	1467	0.301	21	673	13	770	0.116
0005783	endoplasmic reticulum	25	1452	32	1480	0.476	13	681	12	771	0.761
0005794	Golgi apparatus	13	1464	12	1500	0.953	6	688	7	776	0.827
0005815	microtubule organizing center	3	1474	6	1506	0.527	1	693	2	781	0.917
0005739	mitochondrion	62	1415	43	1469	0.056	**46**	**648**	**16**	**767**	**2E-05**
0005840	ribosome	9	1468	15	1497	0.333	6	688	3	780	0.394
0005773	vacuole	7	1470	7	1505	0.823	**7**	**687**	**0**	**783**	**0.015**
0005764	lysosome	1	1476	4	1508	0.385	1	693	0	783	0.952
0005856	cytoskeleton	46	1431	39	1473	0.441	26	668	20	763	0.243
0005694	chromosome	**13**	**1464**	**27**	**1485**	**0.046**	5	689	8	775	0.734
0000228	nuclear chromosome	1	1476	4	1508	0.385	0	694	1	782	0.952
0005634	nucleus	178	1299	194	1318	0.555	**63**	**631**	**115**	**668**	**0.001**
0005635	nuclear membrane	10	1467	7	1505	0.593	2	692	8	775	0.162
0005730	nucleolus	3	1474	8	1504	0.242	1	693	2	781	0.917
0005654	nucleoplasm	29	1448	43	1469	0.147	9	685	20	763	0.121
0005777	peroxisome	4	1473	5	1507	0.972	1	693	3	780	0.703
0005886	plasma membrane	77	1400	79	1433	0.946	**52**	**642**	**25**	**758**	**3E-04**
0005576	extracellular region	42	1435	34	1478	0.359	**28**	**666**	**14**	**769**	**0.015**
0005578	extracellular matrix (sensu Metazoa)	21	1456	14	1498	0.276	**16**	**678**	**5**	**778**	**0.013**

PC2

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	867	628	887	607	0.467	467	341	400	287	0.909
0007610	behavior	91	1404	71	1423	0.126	**39**	**769**	**52**	**635**	**0.036**
0030534	adult behavior	15	1480	9	1485	0.306	5	803	10	677	0.175
0030537	larval behavior	6	1489	3	1491	0.505	1	807	5	682	0.153
0007611	learning and/or memory	17	1478	7	1487	0.065	7	801	10	677	0.409
0007612	learning	**12**	**1483**	**3**	**1491**	**0.038**	5	803	7	680	0.566
0007613	memory	6	1489	5	1489	0.999	3	805	3	684	0.833
0007626	locomotory behavior	65	1430	58	1436	0.583	28	780	37	650	0.092
0007635	chemosensory behavior	**14**	**1481**	**4**	**1490**	**0.033**	6	802	8	679	0.566
0007622	rhythmic behavior	4	1491	11	1483	0.12	3	805	1	686	0.734
0048512	circadian behavior	4	1491	10	1484	0.18	3	805	1	686	0.734
0009987	cellular process	802	693	826	668	0.387	434	374	368	319	0.996
0007154	cell communication	258	1237	231	1263	0.201	**108**	**700**	**150**	**537**	**2E-05**
0007155	cell adhesion	51	1444	39	1455	0.24	**20**	**788**	**31**	**656**	**0.043**
0008037	cell recognition	2	1493	0	1494	0.48	0	808	2	685	0.409
0008038	neuronal cell recognition	2	1493	0	1494	0.48	0	808	2	685	0.409
0016337	cell-cell adhesion	24	1471	15	1479	0.198	10	798	14	673	0.308
0016339	calcium-dependent cell-cell adhesion	3	1492	4	1490	0.999	1	807	2	685	0.888
0007156	homophilic cell adhesion	5	1490	4	1490	0.999	2	806	3	684	0.856
0007160	cell-matrix adhesion	6	1489	3	1491	0.505	2	806	4	683	0.542
0007267	cell-cell signaling	82	1413	74	1420	0.568	**31**	**777**	**51**	**636**	**0.003**
0019226	transmission of nerve impulse	69	1426	69	1425	0.934	**26**	**782**	**43**	**644**	**0.008**
0007268	synaptic transmission	51	1444	50	1444	0.997	**16**	**792**	**35**	**652**	**0.002**
0007270	nerve-nerve synaptic transmission	6	1489	10	1484	0.451	1	807	5	682	0.153
0001505	regulation of neurotransmitter levels	30	1465	30	1464	0.898	**8**	**800**	**22**	**665**	**0.004**
0042133	neurotransmitter metabolism	4	1491	4	1490	0.724	1	807	3	684	0.506
0007269	neurotransmitter secretion	26	1469	27	1467	0.998	**7**	**801**	**19**	**668**	**0.009**
0007165	signal transduction	199	1296	180	1314	0.326	**84**	**724**	**115**	**572**	**4E-04**
0007166	cell surface receptor linked signal transduction	75	1420	82	1412	0.62	33	775	42	645	0.094
0007167	enzyme linked receptor protein signaling pathway	29	1466	17	1477	0.103	12	796	17	670	0.232
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	12	1483	4	1490	0.08	4	804	8	679	0.248
0007179	transforming growth factor beta receptor signaling pathway	7	1488	2	1492	0.182	1	807	6	681	0.083
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	18	1477	14	1480	0.595	8	800	10	677	0.559
0007173	epidermal growth factor receptor signaling pathway	6	1489	2	1492	0.289	1	807	5	682	0.153
0008286	insulin receptor signaling pathway	1	1494	3	1491	0.616	1	807	0	687	0.935
0008293	torso signaling pathway	3	1492	4	1490	0.999	0	808	3	684	0.193
0007186	G-protein coupled receptor protein signaling pathway	30	1465	41	1453	0.229	13	795	17	670	0.315
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	1	1494	4	1490	0.37	1	807	0	687	0.935
0007219	Notch signaling pathway	8	1487	5	1489	0.579	4	804	4	683	0.9
0007224	smoothened signaling pathway	1	1494	5	1489	0.22	1	807	0	687	0.935
0008063	Toll signaling pathway	1	1494	3	1491	0.616	0	808	1	686	0.935
0016055	Wnt receptor signaling pathway	9	1486	7	1487	0.803	4	804	5	682	0.807
0007242	intracellular signaling cascade	90	1405	92	1402	0.935	42	766	48	639	0.18
0007263	nitric oxide mediated signal transduction	3	1492	1	1493	0.617	0	808	3	684	0.193
0007243	protein kinase cascade	20	1475	21	1473	0.998	10	798	10	677	0.889
0007259	JAK-STAT cascade	3	1492	3	1491	0.683	3	805	0	687	0.308
0000165	MAPKKK cascade	16	1479	17	1477	0.998	6	802	10	677	0.279
0019932	second-messenger-mediated signaling	11	1484	11	1483	0.832	7	801	4	683	0.736
0019722	calcium-mediated signaling	9	1486	6	1488	0.606	6	802	3	684	0.67
0048015	phosphoinositide-mediated signaling	1	1494	4	1490	0.37	1	807	0	687	0.935
0007264	small GTPase mediated signal transduction	23	1472	21	1473	0.881	11	797	12	675	0.695
0007265	Ras protein signal transduction	4	1491	6	1488	0.751	3	805	1	686	0.734
0009966	regulation of signal transduction	18	1477	16	1478	0.865	7	801	11	676	0.289
0007275	development	224	1271	236	1258	0.572	111	697	113	574	0.164
0007568	aging	5	1490	6	1488	0.999	3	805	2	685	0.856
0030154	cell differentiation	60	1435	59	1435	0.997	27	781	33	654	0.193
0048468	cell development	33	1462	42	1452	0.348	14	794	19	668	0.239
0000904	cellular morphogenesis during differentiation	9	1486	10	1484	0.999	2	806	7	680	0.113
0042461	photoreceptor cell development	9	1486	9	1485	0.814	2	806	7	680	0.113
0042051	eye photoreceptor development (sensu Endopterygota)	8	1487	9	1485	0.999	2	806	6	681	0.195
0045165	cell fate commitment	26	1469	23	1471	0.775	10	798	16	671	0.158

PC2

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	13	1482	17	1477	0.581	4	804	9	678	0.158
0007400	neuroblast cell fate determination	4	1491	4	1490	0.724	3	805	1	686	0.734
0001708	cell fate specification	4	1491	4	1490	0.724	1	807	3	684	0.506
0007349	cellularization	5	1490	6	1488	0.999	1	807	4	683	0.28
0040007	growth	19	1476	17	1477	0.868	10	798	9	678	0.915
0002164	larval development	13	1482	4	1490	0.052	6	802	7	680	0.769
0002165	larval or pupal development (sensu Insecta)	69	1426	60	1434	0.474	36	772	33	654	0.845
0007552	metamorphosis	63	1432	58	1436	0.713	33	775	30	657	0.887
0009653	morphogenesis	159	1336	160	1334	0.995	74	734	85	602	0.054
0002009	morphogenesis of an epithelium	27	1468	17	1477	0.172	10	798	17	670	0.111
0009887	organogenesis	144	1351	138	1356	0.759	68	740	76	611	0.101
0001654	eye morphogenesis	31	1464	26	1468	0.594	15	793	16	671	0.648
0008406	gonad development	6	1489	5	1489	0.999	4	804	2	685	0.833
0007444	imaginal disc development	51	1444	42	1452	0.401	25	783	26	661	0.555
0007494	midgut development	3	1492	2	1492	0.999	2	806	1	686	0.888
0007517	muscle development	18	1477	16	1478	0.865	6	802	12	675	0.124
0007399	neurogenesis	89	1406	73	1421	0.227	40	768	49	638	0.095
0007409	axonogenesis	20	1475	23	1471	0.757	9	799	11	676	0.554
0007411	axon guidance	15	1480	18	1476	0.725	7	801	8	679	0.752
0007417	central nervous system development	18	1477	21	1473	0.746	10	798	8	679	0.913
0016358	dendrite morphogenesis	6	1489	8	1486	0.788	2	806	4	683	0.542
0042063	gliogenesis	7	1488	4	1490	0.546	3	805	4	683	0.829
0007422	peripheral nervous system development	18	1477	22	1472	0.631	7	801	11	676	0.289
0050767	regulation of neurogenesis	2	1493	3	1491	0.999	1	807	1	686	0.552
0007424	tracheal system development (sensu Insecta)	21	1474	16	1478	0.509	**6**	**802**	**15**	**672**	**0.032**
0048513	organ development	146	1349	140	1354	0.76	69	739	77	610	0.1
0007389	pattern specification	36	1459	40	1454	0.725	16	792	20	667	0.317
0048066	pigmentation	7	1488	4	1490	0.546	3	805	4	683	0.829
0009791	post-embryonic development	13	1482	4	1490	0.052	6	802	7	680	0.769
0009790	embryonic development	53	1442	47	1447	0.613	**21**	**787**	**32**	**655**	**0.045**
0007530	sex determination	6	1489	4	1490	0.752	5	803	1	686	0.302
0007548	sex differentiation	10	1485	9	1485	0.999	6	802	4	683	0.952
0019827	stem cell maintenance	7	1488	1	1493	0.077	3	805	4	683	0.829
0000003	reproduction	77	1418	67	1427	0.444	33	775	44	643	0.057
0050793	regulation of development	22	1473	21	1473	0.998	10	798	12	675	0.549
0007582	physiological process	783	712	822	672	0.157	434	374	349	338	0.284
0008152	metabolism	577	918	589	905	0.669	**348**	**460**	**229**	**458**	**1E-04**
0009056	catabolism	100	1395	109	1385	0.563	60	748	40	647	0.257
0006091	energy pathways	50	1445	58	1436	0.49	29	779	21	666	0.67
0006118	electron transport	30	1465	25	1469	0.588	17	791	13	674	0.916
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	212	1283	220	1274	0.71	127	681	85	602	0.076
0006259	DNA metabolism	41	1454	38	1456	0.822	25	783	16	671	0.457
0006350	transcription	122	1373	105	1389	0.272	72	736	50	637	0.292
0043170	macromolecule metabolism	316	1179	312	1182	0.9	185	623	131	556	0.081
0019538	protein metabolism	270	1225	257	1237	0.57	**161**	**647**	**109**	**578**	**0.049**
0006412	protein biosynthesis	59	1436	51	1443	0.499	**40**	**768**	**19**	**668**	**0.042**
0006464	protein modification	132	1363	124	1370	0.651	77	731	55	632	0.345
0006457	protein folding	**12**	**1483**	**31**	**1463**	**0.006**	8	800	4	683	0.555
0005975	carbohydrate metabolism	52	1443	55	1439	0.841	27	781	25	662	0.864
0006519	amino acid and derivative metabolism	32	1463	38	1456	0.543	19	789	13	674	0.666
0006629	lipid metabolism	49	1446	40	1454	0.391	**35**	**773**	**14**	**673**	**0.019**
0009308	amine metabolism	38	1457	43	1451	0.65	20	788	18	669	0.99
0042440	pigment metabolism	5	1490	7	1487	0.771	4	804	1	686	0.473
0042445	hormone metabolism	3	1492	4	1490	0.999	3	805	0	687	0.308
0009058	biosynthesis	99	1396	105	1389	0.713	**64**	**744**	**35**	**652**	**0.037**
0019748	secondary metabolism	7	1488	7	1487	0.79	5	803	2	685	0.586
0019222	regulation of metabolism	121	1374	117	1377	0.844	69	739	52	635	0.555
0016265	death	45	1450	41	1453	0.745	28	780	17	670	0.334
0008219	cell death	40	1455	34	1460	0.558	25	783	15	672	0.354
0016271	tissue death	15	1480	12	1482	0.7	9	799	6	681	0.838
0042592	homeostasis	**22**	**1473**	**7**	**1487**	**0.009**	14	794	8	679	0.488
0019725	cell homeostasis	**20**	**1475**	**6**	**1488**	**0.01**	13	795	7	680	0.445
0050801	ion homeostasis	**12**	**1483**	**2**	**1492**	**0.016**	8	800	4	683	0.555
0043062	extracellular structure organization and biogenesis	13	1482	6	1488	0.168	4	804	9	678	0.158
0046903	secretion	46	1449	55	1439	0.416	**14**	**794**	**32**	**655**	**0.002**
0048511	rhythmic process	6	1489	11	1483	0.33	5	803	1	686	0.302

PC2

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	170	1325	177	1317	0.727	95	713	75	612	0.668
0050874	organismal physiological process	119	1376	113	1381	0.736	57	751	62	625	0.191
0050875	cellular physiological process	739	756	780	714	0.138	411	397	328	359	0.25
0006810	transport	192	1303	206	1288	0.48	**85**	**723**	**107**	**580**	**0.005**
0006811	ion transport	65	1430	55	1439	0.404	**26**	**782**	**39**	**648**	**0.028**
0006818	hydrogen transport	7	1488	11	1483	0.477	2	806	5	682	0.329
0006836	neurotransmitter transport	5	1490	0	1494	0.074	1	807	4	683	0.28
0006858	extracellular transport	10	1485	5	1489	0.301	4	804	6	681	0.565
0006869	lipid transport	10	1485	6	1488	0.453	5	803	5	682	0.952
0008643	carbohydrate transport	8	1487	7	1487	0.999	4	804	4	683	0.9
0015031	protein transport	77	1418	103	1391	0.054	34	774	43	644	0.095
0015837	amine transport	6	1489	6	1488	0.773	4	804	2	685	0.833
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	6	1489	7	1487	0.999	3	805	3	684	0.833
0016192	vesicle-mediated transport	56	1439	63	1431	0.572	**18**	**790**	**38**	**649**	**0.001**
0045045	secretory pathway	42	1453	53	1441	0.296	**13**	**795**	**29**	**658**	**0.004**
0046907	intracellular transport	86	1409	112	1382	0.065	40	768	46	641	0.183
0051049	regulation of transport	7	1488	11	1483	0.477	1	807	6	681	0.083
0008283	cell proliferation	42	1453	29	1465	0.15	23	785	19	668	0.95
0007049	cell cycle	64	1431	64	1430	0.931	34	774	30	657	0.982
0017145	stem cell division	7	1488	5	1489	0.773	4	804	3	684	0.829
0016043	cell organization and biogenesis	**121**	**1374**	**154**	**1340**	**0.042**	62	746	59	628	0.582
0000902	cellular morphogenesis	37	1458	43	1451	0.569	17	791	20	667	0.404
0006996	organelle organization and biogenesis	105	1390	133	1361	0.067	54	754	51	636	0.648
0007010	cytoskeleton organization and biogenesis	75	1420	95	1399	0.132	36	772	39	648	0.337
0006997	nuclear organization and biogenesis	4	1491	6	1488	0.751	1	807	3	684	0.506
0007028	cytoplasm organization and biogenesis	10	1485	9	1485	0.999	3	805	7	680	0.225
0016044	membrane organization and biogenesis	3	1492	6	1488	0.504	2	806	1	686	0.888
0051128	regulation of cell organization and biogenesis	6	1489	5	1489	0.999	4	804	2	685	0.833
0016049	cell growth	5	1490	4	1490	0.999	4	804	1	686	0.473
0050896	response to stimulus	91	1404	90	1404	0.996	55	753	36	651	0.248
0006950	response to stress	26	1469	33	1461	0.429	14	794	12	675	0.859
0009408	response to heat	5	1490	5	1489	0.752	3	805	2	685	0.856
0006979	response to oxidative stress	0	1495	2	1492	0.479	0	808	0	687	-
0051179	localization	208	1287	221	1273	0.526	**93**	**715**	**115**	**572**	**0.005**
0006403	RNA localization	15	1480	17	1477	0.857	7	801	8	679	0.752
0008104	protein localization	**82**	**1413**	**113**	**1381**	**0.026**	**35**	**773**	**47**	**640**	**0.044**
0051234	establishment of localization	196	1299	207	1287	0.587	**86**	**722**	**110**	**577**	**0.003**
0051235	maintenance of localization	3	1492	1	1493	0.617	2	806	1	686	0.888
0050789	regulation of biological process	196	1299	207	1287	0.587	105	703	91	596	0.947
0050790	regulation of enzyme activity	3	1492	11	1483	0.061	2	806	1	686	0.888
0040029	regulation of gene expression, epigenetic	13	1482	7	1487	0.263	8	800	5	682	0.791
0006306	DNA methylation	6	1489	1	1493	0.13	4	804	2	685	0.833
0045814	negative regulation of gene expression, epigenetic	4	1491	3	1491	0.999	2	806	2	685	0.734
0006342	chromatin silencing	4	1491	3	1491	0.999	2	806	2	685	0.734
0003674	molecular_function	859	636	873	621	0.615	466	342	393	294	0.897
0016209	antioxidant activity	7	1488	2	1492	0.182	**7**	**801**	**0**	**687**	**0.039**
0005488	binding	510	985	497	997	0.652	275	533	235	452	0.988
0005509	calcium ion binding	37	1458	24	1470	0.121	17	791	20	667	0.404
0030246	carbohydrate binding	9	1486	6	1488	0.606	2	806	7	680	0.113
0008289	lipid binding	11	1484	15	1479	0.553	8	800	3	684	0.345
0003676	nucleic acid binding	200	1295	189	1305	0.592	**124**	**684**	**76**	**611**	**0.019**
0003677	DNA binding	100	1395	94	1400	0.714	57	751	43	644	0.61
0003682	chromatin binding	7	1488	16	1478	0.094	5	803	2	685	0.586
0003700	transcription factor activity	41	1454	45	1449	0.74	19	789	22	665	0.398
0003723	RNA binding	61	1434	58	1436	0.855	**43**	**765**	**18**	**669**	**0.012**
0008135	translation factor activity, nucleic acid binding	13	1482	22	1472	0.173	9	799	4	683	0.41
0000166	nucleotide binding	120	1375	135	1359	0.356	70	738	50	637	0.375
0005515	protein binding	186	1309	193	1301	0.736	92	716	94	593	0.207
0008134	transcription factor binding	21	1474	10	1484	0.071	14	794	7	680	0.343
0008092	cytoskeletal protein binding	39	1456	49	1445	0.329	17	791	22	665	0.244
0003779	actin binding	22	1473	31	1463	0.266	11	797	11	676	0.866
0003824	catalytic activity	421	1074	418	1076	0.944	**251**	**557**	**170**	**517**	**0.008**
0016787	hydrolase activity	185	1310	187	1307	0.95	99	709	86	601	0.939
0003924	GTPase activity	19	1476	21	1473	0.872	10	798	9	678	0.915
0004518	nuclease activity	5	1490	10	1484	0.3	1	807	4	683	0.28

		PC2									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	62	1433	56	1438	0.641	37	771	25	662	0.436
0004721	phosphoprotein phosphatase activity	16	1479	14	1480	0.856	8	800	8	679	0.941
0016740	transferase activity	127	1368	114	1380	0.423	**82**	**726**	**45**	**642**	**0.017**
0016301	kinase activity	66	1429	69	1425	0.857	37	771	29	658	0.834
0004672	protein kinase activity	51	1444	44	1450	0.534	30	778	21	666	0.58
0030234	enzyme regulator activity	47	1448	58	1436	0.319	22	786	25	662	0.388
0003774	motor activity	**7**	**1488**	**21**	**1473**	**0.014**	2	806	5	682	0.329
0004871	signal transducer activity	137	1358	119	1375	0.269	**62**	**746**	**75**	**612**	**0.038**
0004872	receptor activity	55	1440	54	1440	0.997	27	781	28	659	0.539
0004879	ligand-dependent nuclear receptor activity	4	1491	5	1489	0.999	3	805	1	686	0.734
0004888	transmembrane receptor activity	39	1456	35	1459	0.726	16	792	23	664	0.136
0004930	G-protein coupled receptor activity	14	1481	16	1478	0.853	6	802	8	679	0.566
0005057	receptor signaling protein activity	43	1452	37	1457	0.573	26	782	17	670	0.483
0005102	receptor binding	40	1455	29	1465	0.224	**14**	**794**	**26**	**661**	**0.022**
0005198	structural molecule activity	81	1414	81	1413	0.939	35	773	46	641	0.058
0030528	transcription regulator activity	102	1393	97	1397	0.773	58	750	44	643	0.625
0045182	translation regulator activity	13	1482	22	1472	0.173	9	799	4	683	0.41
0005215	transporter activity	132	1363	121	1373	0.515	64	744	68	619	0.211
0005489	electron transporter activity	17	1478	12	1482	0.457	9	799	8	679	0.879
0005216	ion channel activity	29	1466	23	1471	0.486	13	795	16	671	0.413
0005244	voltage-gated ion channel activity	16	1479	10	1484	0.326	6	802	10	677	0.279
0005575	cellular_component	603	892	620	874	0.542	319	489	284	403	0.498
0005623	cell	541	954	571	923	0.266	284	524	257	430	0.394
0005622	intracellular	409	1086	448	1046	0.121	230	578	179	508	0.325
0005737	cytoplasm	212	1283	246	1248	0.092	125	683	87	600	0.14
0016023	cytoplasmic vesicle	15	1480	26	1468	0.115	**3**	**805**	**12**	**675**	**0.016**
0005829	cytosol	37	1458	42	1452	0.646	25	783	12	675	0.133
0005783	endoplasmic reticulum	23	1472	34	1460	0.18	16	792	7	680	0.196
0005794	Golgi apparatus	13	1482	12	1482	0.999	5	803	8	679	0.394
0005815	microtubule organizing center	4	1491	5	1489	0.999	2	806	2	685	0.734
0005739	mitochondrion	47	1448	58	1436	0.319	31	777	16	671	0.129
0005840	ribosome	**20**	**1475**	**4**	**1490**	**0.002**	13	795	7	680	0.445
0005773	vacuole	6	1489	8	1486	0.788	2	806	4	683	0.542
0005764	lysosome	2	1493	3	1491	0.999	1	807	1	686	0.552
0005856	cytoskeleton	36	1459	49	1445	0.186	15	793	21	666	0.18
0005694	chromosome	25	1470	15	1479	0.153	15	793	10	677	0.689
0000228	nuclear chromosome	3	1492	2	1492	0.999	2	806	1	686	0.888
0005634	nucleus	178	1317	194	1300	0.402	106	702	72	615	0.136
0005635	nuclear membrane	8	1487	9	1485	0.999	2	806	6	681	0.195
0005730	nucleolus	4	1491	7	1487	0.545	3	805	1	686	0.734
0005654	nucleoplasm	41	1454	31	1463	0.284	24	784	17	670	0.67
0005777	peroxisome	7	1488	2	1492	0.182	5	803	2	685	0.586
0005886	plasma membrane	82	1413	74	1420	0.568	36	772	46	641	0.075
0005576	extracellular region	44	1451	32	1462	0.202	**16**	**792**	**28**	**659**	**0.025**
0005578	extracellular matrix (sensu Metazoa)	21	1474	14	1480	0.309	**4**	**804**	**17**	**670**	**0.003**

PC3

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	805	579	949	656	0.62	374	281	431	298	0.479
0007610	behavior	**89**	**1295**	**73**	**1532**	**0.029**	47	608	42	687	0.336
0030534	adult behavior	10	1374	14	1591	0.801	3	652	7	722	0.433
0030537	larval behavior	4	1380	5	1600	0.824	1	654	3	726	0.693
0007611	learning and/or memory	9	1375	15	1590	0.507	5	650	4	725	0.872
0007612	learning	5	1379	10	1595	0.453	3	652	2	727	0.905
0007613	memory	5	1379	6	1599	0.805	2	653	3	726	0.905
0007626	locomotory behavior	68	1316	55	1550	0.051	33	622	35	694	0.937
0007635	chemosensory behavior	7	1377	11	1594	0.692	5	650	2	727	0.368
0007622	rhythmic behavior	8	1376	7	1598	0.773	3	652	5	724	0.839
0048512	circadian behavior	8	1376	6	1599	0.585	3	652	5	724	0.839
0009987	cellular process	749	635	879	726	0.751	344	311	405	324	0.281
0007154	cell communication	245	1139	244	1361	0.073	114	541	131	598	0.838
0007155	cell adhesion	49	1335	41	1564	0.143	22	633	27	702	0.841
0008037	cell recognition	1	1383	1	1604	0.546	0	655	1	728	0.957
0008038	neuronal cell recognition	1	1383	1	1604	0.546	0	655	1	728	0.957
0016337	cell-cell adhesion	21	1363	18	1587	0.43	9	646	12	717	0.847
0016339	calcium-dependent cell-cell adhesion	4	1380	3	1602	0.844	3	652	1	728	0.543
0007156	homophilic cell adhesion	6	1378	3	1602	0.372	3	652	3	726	0.781
0007160	cell-matrix adhesion	5	1379	4	1601	0.824	3	652	2	727	0.905
0007267	cell-cell signaling	**92**	**1292**	**64**	**1541**	**0.001**	45	610	47	682	0.836
0019226	transmission of nerve impulse	**80**	**1304**	**58**	**1547**	**0.006**	39	616	41	688	0.883
0007268	synaptic transmission	56	1328	45	1560	0.076	25	630	31	698	0.784
0007270	nerve-nerve synaptic transmission	11	1373	5	1600	0.12	6	649	5	724	0.858
0001505	regulation of neurotransmitter levels	27	1357	33	1572	0.941	10	645	17	712	0.375
0042133	neurotransmitter metabolism	3	1381	5	1600	0.885	3	652	0	729	0.211
0007269	neurotransmitter secretion	25	1359	28	1577	0.991	8	647	17	712	0.178
0007165	signal transduction	185	1199	194	1411	0.321	81	574	104	625	0.338
0007166	cell surface receptor linked signal transduction	69	1315	88	1517	0.599	37	618	32	697	0.342
0007167	enzyme linked receptor protein signaling pathway	18	1366	28	1577	0.404	12	643	6	723	0.157
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	8	1376	8	1597	0.963	4	651	4	725	0.839
0007179	transforming growth factor beta receptor signaling pathway	5	1379	4	1601	0.824	3	652	2	727	0.905
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	11	1373	21	1584	0.237	8	647	3	726	0.164
0007173	epidermal growth factor receptor signaling pathway	2	1382	6	1599	0.393	1	654	1	728	0.527
0008286	insulin receptor signaling pathway	1	1383	3	1602	0.724	1	654	0	729	0.957
0008293	torso signaling pathway	**0**	**1384**	**7**	**1598**	**0.037**	0	655	0	729	-
0007186	G-protein coupled receptor protein signaling pathway	36	1348	35	1570	0.527	20	635	16	713	0.405
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	4	1380	1	1604	0.288	1	654	3	726	0.693
0007219	Notch signaling pathway	5	1379	8	1597	0.772	3	652	2	727	0.905
0007224	smoothened signaling pathway	0	1384	6	1599	0.062	0	655	0	729	-
0008063	Toll signaling pathway	1	1383	3	1602	0.724	0	655	1	728	0.957
0016055	Wnt receptor signaling pathway	6	1378	10	1595	0.648	1	654	5	724	0.272
0007242	intracellular signaling cascade	89	1295	93	1512	0.517	36	619	53	676	0.217
0007263	nitric oxide mediated signal transduction	3	1381	1	1604	0.516	0	655	3	726	0.287
0007243	protein kinase cascade	22	1362	19	1586	0.428	10	645	12	717	0.97
0007259	JAK-STAT cascade	3	1381	3	1602	0.82	2	653	1	728	0.926
0000165	MAPKKK cascade	18	1366	15	1590	0.436	7	648	11	718	0.628
0019932	second-messenger-mediated signaling	14	1370	8	1597	0.155	4	651	10	719	0.253
0019722	calcium-mediated signaling	10	1374	5	1600	0.185	3	652	7	722	0.433
0048015	phosphoinositide-mediated signaling	4	1380	1	1604	0.288	1	654	3	726	0.693
0007264	small GTPase mediated signal transduction	20	1364	24	1581	0.969	8	647	12	717	0.663
0007265	Ras protein signal transduction	3	1381	7	1598	0.473	2	653	1	728	0.926
0009966	regulation of signal transduction	17	1367	17	1588	0.793	6	649	11	718	0.45
0007275	development	217	1167	243	1362	0.722	106	549	111	618	0.678
0007568	aging	3	1381	8	1597	0.334	3	652	0	729	0.211
0030154	cell differentiation	48	1336	71	1534	0.216	21	634	27	702	0.72
0048468	cell development	29	1355	46	1559	0.22	11	644	18	711	0.403
0000904	cellular morphogenesis during differentiation	9	1375	10	1595	0.891	3	652	6	723	0.611
0042461	photoreceptor cell development	8	1376	10	1595	0.937	3	652	5	724	0.839
0042051	eye photoreceptor development (sensu Endopterygota)	8	1376	9	1596	0.856	3	652	5	724	0.839
0045165	cell fate commitment	21	1363	28	1577	0.731	10	645	11	718	0.847

PC3

GO#	GO term	Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
		term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	13	1371	17	1588	0.886	7	648	6	723	0.846
0007400	neuroblast cell fate determination	6	1378	2	1603	0.202	2	653	4	725	0.781
0001708	cell fate specification	3	1381	5	1600	0.885	2	653	1	728	0.926
0007349	cellularization	7	1377	4	1601	0.394	4	651	3	726	0.887
0040007	growth	16	1368	20	1585	0.955	9	646	7	722	0.64
0002164	larval development	6	1378	11	1594	0.503	3	652	3	726	0.781
0002165	larval or pupal development (sensu Insecta)	54	1330	75	1530	0.345	29	626	25	704	0.413
0007552	metamorphosis	52	1332	69	1536	0.512	27	628	25	704	0.593
0009653	morphogenesis	160	1224	159	1446	0.161	71	584	89	640	0.477
0002009	morphogenesis of an epithelium	19	1365	25	1580	0.79	7	648	12	717	0.49
0009887	organogenesis	142	1242	140	1465	0.17	63	592	79	650	0.511
0001654	eye morphogenesis	23	1361	34	1571	0.438	7	648	16	713	0.154
0008406	gonad development	5	1379	6	1599	0.805	3	652	2	727	0.905
0007444	imaginal disc development	41	1343	52	1553	0.741	22	633	19	710	0.506
0007494	midgut development	4	1380	1	1604	0.288	2	653	2	727	0.693
0007517	muscle development	20	1364	14	1591	0.194	8	647	12	717	0.663
0007399	neurogenesis	84	1300	78	1527	0.169	35	620	49	680	0.337
0007409	axonogenesis	26	1358	17	1588	0.085	16	639	10	719	0.205
0007411	axon guidance	20	1364	13	1592	0.138	13	642	7	722	0.171
0007417	central nervous system development	19	1365	20	1585	0.886	10	645	9	720	0.814
0016358	dendrite morphogenesis	9	1375	5	1600	0.278	**8**	**647**	**1**	**728**	**0.03**
0042063	gliogenesis	4	1380	7	1598	0.719	2	653	2	727	0.693
0007422	peripheral nervous system development	20	1364	20	1585	0.755	9	646	11	718	0.988
0050767	regulation of neurogenesis	**5**	**1379**	**0**	**1605**	**0.05**	5	650	0	729	0.056
0007424	tracheal system development (sensu Insecta)	15	1369	22	1583	0.588	4	651	11	718	0.177
0048513	organ development	145	1239	141	1464	0.132	65	590	80	649	0.583
0007389	pattern specification	**25**	**1359**	**51**	**1554**	**0.024**	12	643	13	716	0.893
0048066	pigmentation	5	1379	6	1599	0.805	4	651	1	728	0.309
0009791	post-embryonic development	6	1378	11	1594	0.503	3	652	3	726	0.781
0009790	embryonic development	39	1345	61	1544	0.165	19	636	20	709	0.989
0007530	sex determination	5	1379	5	1600	0.934	2	653	3	726	0.905
0007548	sex differentiation	9	1375	10	1595	0.891	5	650	4	725	0.872
0019827	stem cell maintenance	2	1382	6	1599	0.393	1	654	1	728	0.527
0000003	reproduction	56	1328	88	1517	0.081	26	629	30	699	0.999
0050793	regulation of development	20	1364	23	1582	0.899	**15**	**640**	**5**	**724**	**0.023**
0007582	physiological process	734	650	871	734	0.524	338	317	396	333	0.338
0008152	metabolism	517	867	649	956	0.092	244	411	273	456	0.984
0009056	catabolism	94	1290	115	1490	0.744	46	609	48	681	0.828
0006091	energy pathways	43	1341	65	1540	0.201	17	638	26	703	0.376
0006118	electron transport	19	1365	36	1569	0.103	9	646	10	719	0.82
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	190	1194	242	1363	0.32	89	566	101	628	0.948
0006259	DNA metabolism	32	1352	47	1558	0.351	**22**	**633**	**10**	**719**	**0.023**
0006350	transcription	103	1281	124	1481	0.824	54	601	49	680	0.33
0043170	macromolecule metabolism	285	1099	343	1262	0.634	128	527	157	572	0.396
0019538	protein metabolism	241	1143	286	1319	0.809	108	547	133	596	0.43
0006412	protein biosynthesis	47	1337	63	1542	0.504	22	633	25	704	0.939
0006464	protein modification	114	1270	142	1463	0.597	54	601	60	669	0.929
0006457	protein folding	20	1364	23	1582	0.899	5	650	15	714	0.074
0005975	carbohydrate metabolism	47	1337	60	1545	0.686	20	635	27	702	0.604
0006519	amino acid and derivative metabolism	37	1347	33	1572	0.321	19	636	18	711	0.741
0006629	lipid metabolism	39	1345	50	1555	0.712	20	635	19	710	0.734
0009308	amine metabolism	40	1344	41	1564	0.652	20	635	20	709	0.855
0042440	pigment metabolism	6	1378	6	1599	0.974	5	650	1	728	0.174
0042445	hormone metabolism	3	1381	4	1601	0.844	1	654	2	727	0.926
0009058	biosynthesis	82	1302	122	1483	0.082	38	617	44	685	0.944
0019748	secondary metabolism	8	1376	6	1599	0.585	6	649	2	727	0.224
0019222	regulation of metabolism	106	1278	132	1473	0.616	56	599	50	679	0.28
0016265	death	38	1346	48	1557	0.772	16	639	22	707	0.625
0008219	cell death	34	1350	40	1565	0.956	13	642	21	708	0.368
0016271	tissue death	12	1372	15	1590	0.999	4	651	8	721	0.493
0042592	homeostasis	12	1372	17	1588	0.728	4	651	8	721	0.493
0019725	cell homeostasis	10	1374	16	1589	0.543	3	652	7	722	0.433
0050801	ion homeostasis	6	1378	8	1597	0.992	2	653	4	725	0.781
0043062	extracellular structure organization and biogenesis	8	1376	11	1594	0.891	4	651	4	725	0.839
0046903	secretion	51	1333	50	1555	0.448	21	634	30	699	0.451
0048511	rhythmic process	9	1375	8	1597	0.759	4	651	5	724	0.872

PC3

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	162	1222	185	1420	0.924	82	573	80	649	0.419
0050874	organismal physiological process	**126**	**1258**	**106**	**1499**	**0.013**	60	595	66	663	0.98
0050875	cellular physiological process	693	691	826	779	0.47	316	339	377	352	0.217
0006810	transport	182	1202	216	1389	0.847	83	572	99	630	0.675
0006811	ion transport	55	1329	65	1540	0.99	25	630	30	699	0.884
0006818	hydrogen transport	6	1378	12	1593	0.384	3	652	3	726	0.781
0006836	neurotransmitter transport	2	1382	3	1602	0.868	1	654	1	728	0.527
0006858	extracellular transport	6	1378	9	1596	0.817	3	652	3	726	0.781
0006869	lipid transport	7	1377	9	1596	0.963	4	651	3	726	0.887
0008643	carbohydrate transport	7	1377	8	1597	0.817	5	650	2	727	0.368
0015031	protein transport	80	1304	100	1505	0.661	34	621	46	683	0.438
0015837	amine transport	7	1377	5	1600	0.584	2	653	5	724	0.537
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	**2**	**1382**	**11**	**1594**	**0.05**	0	655	2	727	0.527
0016192	vesicle-mediated transport	57	1327	62	1543	0.793	**19**	**636**	**38**	**691**	**0.043**
0045045	secretory pathway	46	1338	49	1556	0.752	18	637	28	701	0.326
0046907	intracellular transport	85	1299	113	1492	0.362	38	617	47	682	0.698
0051049	regulation of transport	12	1372	6	1599	0.133	5	650	7	722	0.917
0008283	cell proliferation	38	1346	33	1572	0.265	17	638	21	708	0.873
0007049	cell cycle	59	1325	69	1536	0.966	26	629	33	696	0.705
0017145	stem cell division	5	1379	7	1598	0.974	1	654	4	725	0.437
0016043	cell organization and biogenesis	136	1248	139	1466	0.3	70	585	66	663	0.353
0000902	cellular morphogenesis	41	1343	39	1566	0.432	16	639	25	704	0.356
0006996	organelle organization and biogenesis	118	1266	120	1485	0.323	64	591	54	675	0.14
0007010	cytoskeleton organization and biogenesis	83	1301	87	1518	0.549	42	613	41	688	0.615
0006997	nuclear organization and biogenesis	3	1381	7	1598	0.473	1	654	2	727	0.926
0007028	cytoplasm organization and biogenesis	12	1372	7	1598	0.212	3	652	9	720	0.206
0016044	membrane organization and biogenesis	5	1379	4	1601	0.824	2	653	3	726	0.905
0051128	regulation of cell organization and biogenesis	8	1376	3	1602	0.145	5	650	3	726	0.612
0016049	cell growth	2	1382	7	1598	0.264	2	653	0	729	0.433
0050896	response to stimulus	84	1300	97	1508	0.962	39	616	45	684	0.954
0006950	response to stress	21	1363	38	1567	0.125	8	647	13	716	0.526
0009408	response to heat	3	1381	7	1598	0.473	1	654	2	727	0.926
0006979	response to oxidative stress	1	1383	1	1604	0.546	1	654	0	729	0.957
0051179	localization	197	1187	232	1373	0.905	91	564	106	623	0.789
0006403	RNA localization	12	1372	20	1585	0.409	6	649	6	723	0.917
0008104	protein localization	88	1296	107	1498	0.79	39	616	49	680	0.636
0051234	establishment of localization	186	1198	217	1388	0.991	85	570	101	628	0.69
0051235	maintenance of localization	1	1383	3	1602	0.724	0	655	1	728	0.957
0050789	regulation of biological process	186	1198	217	1388	0.991	96	559	90	639	0.238
0050790	regulation of enzyme activity	3	1381	11	1594	0.109	3	652	0	729	0.211
0040029	regulation of gene expression, epigenetic	9	1375	11	1594	0.914	7	648	2	727	0.133
0006306	DNA methylation	3	1381	4	1601	0.844	1	654	2	727	0.926
0045814	negative regulation of gene expression, epigenetic	3	1381	4	1601	0.844	3	652	0	729	0.211
0006342	chromatin silencing	3	1381	4	1601	0.844	3	652	0	729	0.211
0003674	molecular_function	792	592	940	665	0.482	379	276	413	316	0.689
0016209	antioxidant activity	3	1381	6	1599	0.655	2	653	1	728	0.926
0005488	binding	460	924	547	1058	0.654	224	431	236	493	0.508
0005509	calcium ion binding	32	1352	29	1576	0.398	20	635	12	717	0.119
0030246	carbohydrate binding	5	1379	10	1595	0.453	1	654	4	725	0.437
0008289	lipid binding	14	1370	12	1593	0.564	5	650	9	720	0.545
0003676	nucleic acid binding	167	1217	222	1383	0.169	81	574	86	643	0.809
0003677	DNA binding	86	1298	108	1497	0.62	42	613	44	685	0.859
0003682	chromatin binding	**3**	**1381**	**20**	**1585**	**0.003**	2	653	1	728	0.926
0003700	transcription factor activity	41	1343	45	1560	0.881	18	637	23	706	0.774
0003723	RNA binding	**43**	**1341**	**76**	**1529**	**0.03**	21	634	22	707	0.963
0008135	translation factor activity, nucleic acid binding	13	1371	22	1583	0.356	3	652	10	719	0.139
0000166	nucleotide binding	118	1266	137	1468	0.955	51	604	67	662	0.402
0005515	protein binding	182	1202	197	1408	0.508	86	569	96	633	0.954
0008134	transcription factor binding	11	1373	20	1585	0.301	8	647	3	726	0.164
0008092	cytoskeletal protein binding	45	1339	43	1562	0.415	23	632	22	707	0.715
0003779	actin binding	27	1357	26	1579	0.586	15	640	12	717	0.503
0003824	catalytic activity	375	1009	464	1141	0.289	183	472	192	537	0.543
0016787	hydrolase activity	165	1219	207	1398	0.453	80	575	85	644	0.815
0003924	GTPase activity	22	1362	18	1587	0.342	11	644	11	718	0.97
0004518	nuclease activity	5	1379	10	1595	0.453	4	651	1	728	0.309

PC3

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	52	1332	66	1539	0.687	24	631	28	701	0.975
0004721	phosphoprotein phosphatase activity	10	1374	20	1585	0.212	5	650	5	724	0.882
0016740	transferase activity	111	1273	130	1475	0.99	56	599	55	674	0.556
0016301	kinase activity	62	1322	73	1532	0.999	26	629	36	693	0.459
0004672	protein kinase activity	43	1341	52	1553	0.919	18	637	25	704	0.566
0030234	enzyme regulator activity	53	1331	52	1553	0.439	19	636	34	695	0.117
0003774	motor activity	13	1371	15	1590	0.859	3	652	10	719	0.139
0004871	signal transducer activity	**136**	**1248**	**120**	**1485**	**0.026**	61	594	75	654	0.604
0004872	receptor activity	58	1326	51	1554	0.169	31	624	27	702	0.412
0004879	ligand-dependent nuclear receptor activity	4	1380	5	1600	0.824	2	653	2	727	0.693
0004888	transmembrane receptor activity	35	1349	39	1566	0.956	22	633	13	716	0.091
0004930	G-protein coupled receptor activity	15	1369	15	1590	0.823	11	644	4	725	0.077
0005057	receptor signaling protein activity	40	1344	40	1565	0.576	13	642	27	702	0.081
0005102	receptor binding	35	1349	34	1571	0.533	16	639	19	710	0.982
0005198	structural molecule activity	86	1298	76	1529	0.089	41	614	45	684	0.964
0030528	transcription regulator activity	89	1295	110	1495	0.697	46	609	43	686	0.458
0045182	translation regulator activity	13	1371	22	1583	0.356	3	652	10	719	0.139
0005215	transporter activity	110	1274	143	1462	0.381	54	601	56	673	0.774
0005489	electron transporter activity	9	1375	20	1585	0.142	4	651	5	724	0.872
0005216	ion channel activity	29	1355	23	1582	0.215	16	639	13	716	0.505
0005244	voltage-gated ion channel activity	11	1373	15	1590	0.831	7	648	4	725	0.433
0005575	cellular_component	**536**	**848**	**687**	**918**	**0.026**	265	390	271	458	0.231
0005623	cell	493	891	619	986	0.105	244	411	249	480	0.252
0005622	intracellular	**368**	**1016**	**489**	**1116**	**0.022**	183	472	185	544	0.31
0005737	cytoplasm	**192**	**1192**	**266**	**1339**	**0.046**	98	557	94	635	0.302
0016023	cytoplasmic vesicle	20	1364	21	1584	0.871	8	647	12	717	0.663
0005829	cytosol	29	1355	50	1555	0.105	9	646	20	709	0.112
0005783	endoplasmic reticulum	20	1364	37	1568	0.114	9	646	11	718	0.988
0005794	Golgi apparatus	13	1371	12	1593	0.71	7	648	6	723	0.846
0005815	microtubule organizing center	2	1382	7	1598	0.264	1	654	1	728	0.527
0005739	mitochondrion	46	1338	59	1546	0.673	24	631	22	707	0.603
0005840	ribosome	11	1373	13	1592	0.874	6	649	5	724	0.858
0005773	vacuole	4	1380	10	1595	0.287	2	653	2	727	0.693
0005764	lysosome	1	1383	4	1601	0.464	1	654	0	729	0.957
0005856	cytoskeleton	44	1340	41	1564	0.361	20	635	24	705	0.921
0005694	chromosome	**9**	**1375**	**31**	**1574**	**0.004**	6	649	3	726	0.406
0000228	nuclear chromosome	3	1381	2	1603	0.868	3	652	0	729	0.211
0005634	nucleus	**149**	**1235**	**223**	**1382**	**0.011**	72	583	77	652	0.864
0005635	nuclear membrane	7	1377	10	1595	0.856	3	652	4	725	0.887
0005730	nucleolus	5	1379	6	1599	0.805	2	653	3	726	0.905
0005654	nucleoplasm	28	1356	44	1561	0.247	16	639	12	717	0.39
0005777	peroxisome	5	1379	4	1601	0.824	5	650	0	729	0.056
0005886	plasma membrane	83	1301	73	1532	0.09	**49**	**606**	**34**	**695**	**0.037**
0005576	extracellular region	33	1351	43	1562	0.694	15	640	18	711	0.967
0005578	extracellular matrix (sensu Metazoa)	19	1365	16	1589	0.434	9	646	10	719	0.82

PC4

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	841	589	913	646	0.92	510	362	331	227	0.797
0007610	behavior	69	1361	93	1466	0.196	47	825	22	536	0.263
0030534	adult behavior	7	1423	17	1542	0.102	5	867	2	556	0.857
0030537	larval behavior	2	1428	7	1552	0.228	1	871	1	557	0.684
0007611	learning and/or memory	12	1418	12	1547	0.994	8	864	4	554	0.914
0007612	learning	8	1422	7	1552	0.867	6	866	2	556	0.651
0007613	memory	4	1426	7	1552	0.645	2	870	2	556	0.95
0007626	locomotory behavior	51	1379	72	1487	0.176	32	840	19	539	0.907
0007635	chemosensory behavior	9	1421	9	1550	0.958	7	865	2	556	0.488
0007622	rhythmic behavior	6	1424	9	1550	0.726	5	867	1	557	0.48
0048512	circadian behavior	5	1425	9	1550	0.521	4	868	1	557	0.679
0009987	cellular process	787	643	841	718	0.575	468	404	319	239	0.214
0007154	cell communication	237	1193	252	1307	0.801	148	724	89	469	0.664
0007155	cell adhesion	42	1388	48	1511	0.905	27	845	15	543	0.775
0008037	cell recognition	0	1430	2	1557	0.518	0	872	0	558	-
0008038	neuronal cell recognition	0	1430	2	1557	0.518	0	872	0	558	-
0016337	cell-cell adhesion	19	1411	20	1539	0.959	12	860	7	551	0.968
0016339	calcium-dependent cell-cell adhesion	3	1427	4	1555	0.909	1	871	2	556	0.696
0007156	homophilic cell adhesion	4	1426	5	1554	0.897	2	870	2	556	0.95
0007160	cell-matrix adhesion	5	1425	4	1555	0.897	4	868	1	557	0.679
0007267	cell-cell signaling	70	1360	86	1473	0.496	46	826	24	534	0.479
0019226	transmission of nerve impulse	63	1367	75	1484	0.66	41	831	22	536	0.582
0007268	synaptic transmission	43	1387	58	1501	0.329	26	846	17	541	0.929
0007270	nerve-nerve synaptic transmission	9	1421	7	1552	0.671	4	868	5	553	0.498
0001505	regulation of neurotransmitter levels	26	1404	34	1525	0.565	15	857	11	547	0.886
0042133	neurotransmitter metabolism	3	1427	5	1554	0.817	1	871	2	556	0.696
0007269	neurotransmitter secretion	24	1406	29	1530	0.812	14	858	10	548	0.955
0007165	signal transduction	189	1241	190	1369	0.43	117	755	72	486	0.841
0007166	cell surface receptor linked signal transduction	82	1348	75	1484	0.294	53	819	29	529	0.56
0007167	enzyme linked receptor protein signaling pathway	26	1404	20	1539	0.299	15	857	11	547	0.886
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	10	1420	6	1553	0.354	4	868	6	552	0.299
0007179	transforming growth factor beta receptor signaling pathway	6	1424	3	1556	0.425	2	870	4	554	0.331
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	18	1412	14	1545	0.436	11	861	7	551	0.817
0007173	epidermal growth factor receptor signaling pathway	7	1423	1	1558	0.058	5	867	2	556	0.857
0008286	insulin receptor signaling pathway	3	1427	1	1558	0.557	2	870	1	557	0.696
0008293	torso signaling pathway	4	1426	3	1556	0.909	2	870	2	556	0.95
0007186	G-protein coupled receptor protein signaling pathway	37	1393	34	1525	0.543	24	848	13	545	0.749
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	2	1428	3	1556	0.923	0	872	2	556	0.297
0007219	Notch signaling pathway	7	1423	6	1553	0.876	6	866	1	557	0.339
0007224	smoothened signaling pathway	2	1428	4	1555	0.762	1	871	1	557	0.684
0008063	Toll signaling pathway	3	1427	1	1558	0.557	1	871	2	556	0.696
0016055	Wnt receptor signaling pathway	9	1421	7	1552	0.671	8	864	1	557	0.168
0007242	intracellular signaling cascade	88	1342	94	1465	0.948	56	816	32	526	0.678
0007263	nitric oxide mediated signal transduction	4	1426	0	1559	0.112	4	868	0	558	0.276
0007243	protein kinase cascade	20	1410	21	1538	0.971	9	863	11	547	0.213
0007259	JAK-STAT cascade	2	1428	4	1555	0.762	2	870	0	558	0.684
0000165	MAPKKK cascade	16	1414	17	1542	0.92	7	865	9	549	0.245
0019932	second-messenger-mediated signaling	8	1422	14	1545	0.386	3	869	5	553	0.316
0019722	calcium-mediated signaling	6	1424	9	1550	0.726	3	869	3	555	0.894
0048015	phosphoinositide-mediated signaling	2	1428	3	1556	0.923	0	872	2	556	0.297
0007264	small GTPase mediated signal transduction	24	1406	20	1539	0.456	15	857	9	549	0.955
0007265	Ras protein signal transduction	6	1424	4	1555	0.65	3	869	3	555	0.894
0009966	regulation of signal transduction	19	1411	15	1544	0.441	13	859	6	552	0.665
0007275	development	237	1193	223	1336	0.096	146	726	91	467	0.886
0007568	aging	4	1426	7	1552	0.645	2	870	2	556	0.95
0030154	cell differentiation	**68**	**1362**	**51**	**1508**	**0.048**	39	833	29	529	0.617
0048468	cell development	38	1392	37	1522	0.705	21	851	17	541	0.573
0000904	cellular morphogenesis during differentiation	7	1423	12	1547	0.464	3	869	4	554	0.551
0042461	photoreceptor cell development	7	1423	11	1548	0.599	3	869	4	554	0.551
0042051	eye photoreceptor development (sensu Endopterygota)	7	1423	10	1549	0.758	3	869	4	554	0.551
0045165	cell fate commitment	**31**	**1399**	**18**	**1541**	**0.042**	18	854	13	545	0.881

PC4

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	18	1412	12	1547	0.248	12	860	6	552	0.799
0007400	neuroblast cell fate determination	4	1426	4	1555	0.817	4	868	0	558	0.276
0001708	cell fate specification	4	1426	4	1555	0.817	3	869	1	557	0.95
0007349	cellularization	5	1425	6	1553	0.886	2	870	3	555	0.614
0040007	growth	17	1413	19	1540	0.926	13	859	4	554	0.286
0002164	larval development	10	1420	7	1552	0.506	4	868	6	552	0.299
0002165	larval or pupal development (sensu Insecta)	65	1365	64	1495	0.616	35	837	30	528	0.282
0007552	metamorphosis	58	1372	63	1496	0.942	33	839	25	533	0.608
0009653	morphogenesis	162	1268	157	1402	0.292	103	769	59	499	0.525
0002009	morphogenesis of an epithelium	23	1407	21	1538	0.659	13	859	10	548	0.821
0009887	organogenesis	144	1286	138	1421	0.282	91	781	53	505	0.628
0001654	eye morphogenesis	29	1401	28	1531	0.742	13	859	16	542	0.108
0008406	gonad development	4	1426	7	1552	0.645	2	870	2	556	0.95
0007444	imaginal disc development	50	1380	43	1516	0.291	30	842	20	538	0.998
0007494	midgut development	3	1427	2	1557	0.923	1	871	2	556	0.696
0007517	muscle development	13	1417	21	1538	0.339	10	862	3	555	0.369
0007399	neurogenesis	85	1345	77	1482	0.258	59	813	26	532	0.126
0007409	axonogenesis	19	1411	24	1535	0.742	12	860	7	551	0.968
0007411	axon guidance	16	1414	17	1542	0.92	10	862	6	552	0.895
0007417	central nervous system development	19	1411	20	1539	0.959	15	857	4	554	0.168
0016358	dendrite morphogenesis	7	1423	7	1552	0.915	4	868	3	555	0.857
0042063	gliogenesis	4	1426	7	1552	0.645	3	869	1	557	0.95
0007422	peripheral nervous system development	22	1408	18	1541	0.451	16	856	6	552	0.359
0050767	regulation of neurogenesis	2	1428	3	1556	0.923	1	871	1	557	0.684
0007424	tracheal system development (sensu Insecta)	19	1411	18	1541	0.791	13	859	6	552	0.665
0048513	organ development	147	1283	139	1420	0.229	93	779	54	504	0.61
0007389	pattern specification	40	1390	36	1523	0.465	27	845	13	545	0.488
0048066	pigmentation	4	1426	7	1552	0.645	3	869	1	557	0.95
0009791	post-embryonic development	10	1420	7	1552	0.506	4	868	6	552	0.299
0009790	embryonic development	**59**	**1371**	**41**	**1518**	**0.03**	34	838	25	533	0.687
0007530	sex determination	6	1424	4	1555	0.65	5	867	1	557	0.48
0007548	sex differentiation	8	1422	11	1548	0.786	5	867	3	555	0.783
0019827	stem cell maintenance	5	1425	3	1556	0.634	3	869	2	556	0.679
0000003	reproduction	68	1362	76	1483	0.946	41	831	27	531	0.993
0050793	regulation of development	22	1408	21	1538	0.775	17	855	5	553	0.174
0007582	physiological process	773	657	832	727	0.734	460	412	313	245	0.237
0008152	metabolism	574	856	592	967	0.24	333	539	241	317	0.068
0009056	catabolism	97	1333	112	1447	0.721	**43**	**829**	**54**	**504**	**7E-04**
0006091	energy pathways	45	1385	63	1496	0.226	**18**	**854**	**27**	**531**	**0.005**
0006118	electron transport	23	1407	32	1527	0.443	11	861	12	546	0.277
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	**230**	**1200**	**202**	**1357**	**0.017**	140	732	90	468	0.971
0006259	DNA metabolism	42	1388	37	1522	0.398	28	844	14	544	0.544
0006350	transcription	120	1310	107	1452	0.132	73	799	47	511	0.949
0043170	macromolecule metabolism	296	1134	332	1227	0.723	**153**	**719**	**143**	**415**	**3E-04**
0019538	protein metabolism	256	1174	271	1288	0.746	**128**	**744**	**128**	**430**	**9E-05**
0006412	protein biosynthesis	51	1379	59	1500	0.827	30	842	21	537	0.861
0006464	protein modification	121	1309	135	1424	0.898	**61**	**811**	**60**	**498**	**0.017**
0006457	protein folding	17	1413	26	1533	0.345	7	865	10	548	0.152
0005975	carbohydrate metabolism	45	1385	62	1497	0.262	29	843	16	542	0.742
0006519	amino acid and derivative metabolism	30	1400	40	1519	0.469	19	853	11	547	0.938
0006629	lipid metabolism	42	1388	47	1512	0.986	31	841	11	547	0.116
0009308	amine metabolism	34	1396	47	1512	0.338	21	851	13	545	0.934
0042440	pigment metabolism	3	1427	9	1550	0.194	2	870	1	557	0.696
0042445	hormone metabolism	2	1428	5	1554	0.52	1	871	1	557	0.684
0009058	biosynthesis	90	1340	114	1445	0.303	56	816	34	524	0.89
0019748	secondary metabolism	4	1426	10	1549	0.239	2	870	2	556	0.95
0019222	regulation of metabolism	119	1311	119	1440	0.531	71	801	48	510	0.834
0016265	death	45	1385	41	1518	0.462	25	847	20	538	0.547
0008219	cell death	41	1389	33	1526	0.23	23	849	18	540	0.626
0016271	tissue death	9	1421	18	1541	0.186	5	867	4	554	0.993
0042592	homeostasis	15	1415	14	1545	0.815	8	864	7	551	0.731
0019725	cell homeostasis	14	1416	12	1547	0.676	7	865	7	551	0.568
0050801	ion homeostasis	9	1421	5	1554	0.334	3	869	6	552	0.173
0043062	extracellular structure organization and biogenesis	5	1425	14	1545	0.098	3	869	2	556	0.679
0046903	secretion	46	1384	55	1504	0.712	27	845	19	539	0.866
0048511	rhythmic process	8	1422	9	1550	0.858	6	866	2	556	0.651

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		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	**184**	**1246**	**163**	**1396**	**0.046**	105	767	79	479	0.278
0050874	organismal physiological process	102	1328	130	1429	0.245	67	805	35	523	0.365
0050875	cellular physiological process	733	697	786	773	0.672	429	443	304	254	0.058
0006810	transport	183	1247	215	1344	0.456	111	761	72	486	0.988
0006811	ion transport	58	1372	62	1497	0.987	36	836	22	536	0.971
0006818	hydrogen transport	9	1421	9	1550	0.958	**1**	**871**	**8**	**550**	**0.006**
0006836	neurotransmitter transport	2	1428	3	1556	0.923	1	871	1	557	0.684
0006858	extracellular transport	9	1421	6	1553	0.493	7	865	2	556	0.488
0006869	lipid transport	9	1421	7	1552	0.671	8	864	1	557	0.168
0008643	carbohydrate transport	9	1421	6	1553	0.493	6	866	3	555	0.993
0015031	protein transport	81	1349	99	1460	0.477	46	826	35	523	0.497
0015837	amine transport	6	1424	6	1553	0.889	4	868	2	556	0.894
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	5	1425	8	1551	0.689	2	870	3	555	0.614
0016192	vesicle-mediated transport	53	1377	66	1493	0.52	31	841	22	536	0.814
0045045	secretory pathway	45	1385	50	1509	0.992	26	846	19	539	0.77
0046907	intracellular transport	90	1340	108	1451	0.534	52	820	38	520	0.595
0051049	regulation of transport	11	1419	7	1552	0.371	7	865	4	554	0.897
0008283	cell proliferation	42	1388	29	1530	0.07	28	844	14	544	0.544
0007049	cell cycle	63	1367	65	1494	0.819	39	833	24	534	0.982
0017145	stem cell division	6	1424	6	1553	0.889	6	866	0	558	0.123
0016043	cell organization and biogenesis	136	1294	139	1420	0.618	79	793	57	501	0.526
0000902	cellular morphogenesis	40	1390	40	1519	0.781	25	847	15	543	0.972
0006996	organelle organization and biogenesis	119	1311	119	1440	0.531	71	801	48	510	0.834
0007010	cytoskeleton organization and biogenesis	84	1346	86	1473	0.732	51	821	33	525	0.949
0006997	nuclear organization and biogenesis	6	1424	4	1555	0.65	3	869	3	555	0.894
0007028	cytoplasm organization and biogenesis	8	1422	11	1548	0.786	5	867	3	555	0.783
0016044	membrane organization and biogenesis	3	1427	6	1553	0.59	2	870	1	557	0.696
0051128	regulation of cell organization and biogenesis	5	1425	6	1553	0.886	3	869	2	556	0.679
0016049	cell growth	6	1424	3	1556	0.425	6	866	0	558	0.123
0050896	response to stimulus	79	1351	102	1457	0.276	52	820	27	531	0.43
0006950	response to stress	29	1401	30	1529	0.943	20	852	9	549	0.485
0009408	response to heat	5	1425	5	1554	0.857	3	869	2	556	0.679
0006979	response to oxidative stress	0	1430	2	1557	0.518	0	872	0	558	-
0051179	localization	199	1231	230	1329	0.549	122	750	77	481	0.981
0006403	RNA localization	15	1415	17	1542	0.946	10	862	5	553	0.851
0008104	protein localization	89	1341	106	1453	0.574	52	820	37	521	0.691
0051234	establishment of localization	184	1246	219	1340	0.373	112	760	72	486	0.961
0051235	maintenance of localization	3	1427	1	1558	0.557	1	871	2	556	0.696
0050789	regulation of biological process	206	1224	197	1362	0.173	121	751	85	473	0.525
0050790	regulation of enzyme activity	4	1426	10	1549	0.239	4	868	0	558	0.276
0040029	regulation of gene expression, epigenetic	8	1422	12	1547	0.631	5	867	3	555	0.783
0006306	DNA methylation	2	1428	5	1554	0.52	2	870	0	558	0.684
0045814	negative regulation of gene expression, epigenetic	4	1426	3	1556	0.909	3	869	1	557	0.95
0006342	chromatin silencing	4	1426	3	1556	0.909	3	869	1	557	0.95
0003674	molecular_function	833	597	899	660	0.774	499	373	334	224	0.353
0016209	antioxidant activity	3	1427	6	1553	0.59	1	871	2	556	0.696
0005488	binding	488	942	519	1040	0.657	300	572	188	370	0.826
0005509	calcium ion binding	24	1406	37	1522	0.225	14	858	10	548	0.955
0030246	carbohydrate binding	6	1424	9	1550	0.726	4	868	2	556	0.894
0008289	lipid binding	10	1420	16	1543	0.445	6	866	4	554	0.794
0003676	nucleic acid binding	204	1226	185	1374	0.058	123	749	81	477	0.889
0003677	DNA binding	99	1331	95	1464	0.398	61	811	38	520	0.978
0003682	chromatin binding	11	1419	12	1547	0.835	9	863	2	556	0.266
0003700	transcription factor activity	42	1388	44	1515	0.938	22	850	20	538	0.318
0003723	RNA binding	62	1368	57	1502	0.392	40	832	22	536	0.652
0008135	translation factor activity, nucleic acid binding	20	1410	15	1544	0.348	**7**	**865**	**13**	**545**	**0.03**
0000166	nucleotide binding	122	1308	133	1426	0.948	74	798	48	510	0.984
0005515	protein binding	184	1246	195	1364	0.811	115	757	69	489	0.71
0008134	transcription factor binding	17	1413	14	1545	0.546	11	861	6	552	0.947
0008092	cytoskeletal protein binding	35	1395	53	1506	0.153	25	847	10	548	0.268
0003779	actin binding	20	1410	33	1526	0.178	12	860	8	550	0.888
0003824	catalytic activity	397	1033	442	1117	0.751	**223**	**649**	**174**	**384**	**0.024**
0016787	hydrolase activity	183	1247	189	1370	0.616	**94**	**778**	**89**	**469**	**0.006**
0003924	GTPase activity	20	1410	20	1539	0.908	12	860	8	550	0.888
0004518	nuclease activity	7	1423	8	1551	0.867	7	865	0	558	0.083

PC4

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	55	1375	63	1496	0.858	**18**	**854**	**37**	**521**	**2E-05**
0004721	phosphoprotein phosphatase activity	16	1414	14	1545	0.673	8	864	8	550	0.517
0016740	transferase activity	110	1320	131	1428	0.519	72	800	38	520	0.368
0016301	kinase activity	59	1371	76	1483	0.37	40	832	19	539	0.337
0004672	protein kinase activity	41	1389	54	1505	0.41	26	846	15	543	0.871
0030234	enzyme regulator activity	42	1388	63	1496	0.124	26	846	16	542	0.972
0003774	motor activity	17	1413	11	1548	0.238	13	859	4	554	0.286
0004871	signal transducer activity	132	1298	124	1435	0.238	87	785	45	513	0.261
0004872	receptor activity	59	1371	50	1509	0.215	41	831	18	540	0.218
0004879	ligand-dependent nuclear receptor activity	6	1424	3	1556	0.425	4	868	2	556	0.894
0004888	transmembrane receptor activity	43	1387	31	1528	0.094	29	843	14	544	0.469
0004930	G-protein coupled receptor activity	19	1411	11	1548	0.128	11	861	8	550	0.968
0005057	receptor signaling protein activity	38	1392	42	1517	0.959	23	849	15	543	0.912
0005102	receptor binding	30	1400	39	1520	0.54	19	853	11	547	0.938
0005198	structural molecule activity	75	1355	87	1472	0.746	52	820	23	535	0.161
0030528	transcription regulator activity	104	1326	95	1464	0.223	63	809	41	517	0.986
0045182	translation regulator activity	20	1410	15	1544	0.348	**7**	**865**	**13**	**545**	**0.03**
0005215	transporter activity	115	1315	138	1421	0.466	62	810	53	505	0.128
0005489	electron transporter activity	14	1416	15	1544	0.889	5	867	9	549	0.094
0005216	ion channel activity	23	1407	29	1530	0.7	16	856	7	551	0.525
0005244	voltage-gated ion channel activity	13	1417	13	1546	0.981	11	861	2	556	0.142
0005575	cellular_component	601	829	622	937	0.252	352	520	249	309	0.125
0005623	cell	555	875	557	1002	0.088	327	545	228	330	0.224
0005622	intracellular	425	1005	432	1127	0.241	**239**	**633**	**186**	**372**	**0.02**
0005737	cytoplasm	212	1218	246	1313	0.501	**101**	**771**	**111**	**447**	**2E-05**
0016023	cytoplasmic vesicle	16	1414	25	1534	0.327	7	865	9	549	0.245
0005829	cytosol	**47**	**1383**	**32**	**1527**	**0.047**	**17**	**855**	**30**	**528**	**7E-04**
0005783	endoplasmic reticulum	31	1399	26	1533	0.387	**9**	**863**	**22**	**536**	**5E-04**
0005794	Golgi apparatus	10	1420	15	1544	0.557	8	864	2	556	0.362
0005815	microtubule organizing center	2	1428	7	1552	0.228	1	871	1	557	0.684
0005739	mitochondrion	43	1387	62	1497	0.18	20	852	23	535	0.069
0005840	ribosome	7	1423	17	1542	0.102	5	867	2	556	0.857
0005773	vacuole	9	1421	5	1554	0.334	3	869	6	552	0.173
0005764	lysosome	3	1427	2	1557	0.923	3	869	0	558	0.427
0005856	cytoskeleton	42	1388	43	1516	0.854	**34**	**838**	**8**	**550**	**0.011**
0005694	chromosome	22	1408	18	1541	0.451	15	857	7	551	0.633
0000228	nuclear chromosome	2	1428	3	1556	0.923	1	871	1	557	0.684
0005634	nucleus	**201**	**1229**	**171**	**1388**	**0.012**	114	758	87	471	0.208
0005635	nuclear membrane	8	1422	9	1550	0.858	7	865	1	557	0.239
0005730	nucleolus	4	1426	7	1552	0.645	1	871	3	555	0.335
0005654	nucleoplasm	35	1395	37	1522	0.99	24	848	11	547	0.449
0005777	peroxisome	3	1427	6	1553	0.59	2	870	1	557	0.696
0005886	plasma membrane	84	1346	72	1487	0.144	52	820	32	526	0.949
0005576	extracellular region	36	1394	40	1519	0.974	22	850	14	544	0.876
0005578	extracellular matrix (sensu Metazoa)	20	1410	15	1544	0.348	13	859	7	551	0.888

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		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	**971**	**623**	**783**	**612**	**0.009**	370	251	601	372	0.412
0007610	behavior	83	1511	79	1316	0.639	**54**	**567**	**29**	**944**	**1E-06**
0030534	adult behavior	11	1583	13	1382	0.594	**9**	**612**	**2**	**971**	**0.009**
0030537	larval behavior	4	1590	5	1390	0.841	2	619	2	971	0.952
0007611	learning and/or memory	11	1583	13	1382	0.594	**9**	**612**	**2**	**971**	**0.009**
0007612	learning	9	1585	6	1389	0.795	**7**	**614**	**2**	**971**	**0.04**
0007613	memory	4	1590	7	1388	0.408	3	618	1	972	0.334
0007626	locomotory behavior	63	1531	60	1335	0.699	**41**	**580**	**22**	**951**	**3E-05**
0007635	chemosensory behavior	10	1584	8	1387	0.963	**8**	**613**	**2**	**971**	**0.019**
0007622	rhythmic behavior	9	1585	6	1389	0.795	**7**	**614**	**2**	**971**	**0.04**
0048512	circadian behavior	8	1586	6	1389	0.985	6	615	2	971	0.083
0009987	cellular process	**904**	**690**	**724**	**671**	**0.009**	349	272	555	418	0.781
0007154	cell communication	248	1346	241	1154	0.224	**157**	**464**	**91**	**882**	**2E-17**
0007155	cell adhesion	**38**	**1556**	**52**	**1343**	**0.042**	20	601	18	955	0.114
0008037	cell recognition	2	1592	0	1395	0.539	2	619	0	973	0.296
0008038	neuronal cell recognition	2	1592	0	1395	0.539	2	619	0	973	0.296
0016337	cell-cell adhesion	15	1579	24	1371	0.087	7	614	8	965	0.727
0016339	calcium-dependent cell-cell adhesion	2	1592	5	1390	0.35	1	620	1	972	0.685
0007156	homophilic cell adhesion	3	1591	6	1389	0.384	2	619	1	972	0.695
0007160	cell-matrix adhesion	2	1592	7	1388	0.124	1	620	1	972	0.685
0007267	cell-cell signaling	89	1505	67	1328	0.382	**62**	**559**	**27**	**946**	**2E-09**
0019226	transmission of nerve impulse	77	1517	61	1334	0.612	**54**	**567**	**23**	**950**	**2E-08**
0007268	synaptic transmission	59	1535	42	1353	0.347	**43**	**578**	**16**	**957**	**1E-07**
0007270	nerve-nerve synaptic transmission	11	1583	5	1390	0.323	**10**	**611**	**1**	**972**	**0.001**
0001505	regulation of neurotransmitter levels	34	1560	26	1369	0.694	**24**	**597**	**10**	**963**	**3E-04**
0042133	neurotransmitter metabolism	5	1589	3	1392	0.868	**5**	**616**	**0**	**973**	**0.019**
0007269	neurotransmitter secretion	30	1564	23	1372	0.731	**20**	**601**	**10**	**963**	**0.003**
0007165	signal transduction	187	1407	192	1203	0.107	**117**	**504**	**70**	**903**	**3E-12**
0007166	cell surface receptor linked signal transduction	75	1519	82	1313	0.176	**54**	**567**	**21**	**952**	**4E-09**
0007167	enzyme linked receptor protein signaling pathway	21	1573	25	1370	0.367	**16**	**605**	**5**	**968**	**1E-03**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	9	1585	7	1388	0.987	**7**	**614**	**2**	**971**	**0.04**
0007179	transforming growth factor beta receptor signaling pathway	5	1589	4	1391	0.841	3	618	2	971	0.612
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	13	1581	19	1376	0.204	**10**	**611**	**3**	**970**	**0.011**
0007173	epidermal growth factor receptor signaling pathway	2	1592	6	1389	0.21	2	619	0	973	0.296
0008286	insulin receptor signaling pathway	1	1593	3	1392	0.525	0	621	1	972	0.821
0008293	torso signaling pathway	4	1590	3	1392	0.86	3	618	1	972	0.334
0007186	G-protein coupled receptor protein signaling pathway	35	1559	36	1359	0.569	**24**	**597**	**11**	**962**	**5E-04**
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	5	1589	0	1395	0.1	4	617	1	972	0.154
0007219	Notch signaling pathway	7	1587	6	1389	0.809	**6**	**615**	**1**	**972**	**0.031**
0007224	smoothened signaling pathway	5	1589	1	1394	0.287	3	618	2	971	0.612
0008063	Toll signaling pathway	0	1594	4	1391	0.101	0	621	0	973	-
0016055	Wnt receptor signaling pathway	6	1588	10	1385	0.307	5	616	1	972	0.07
0007242	intracellular signaling cascade	98	1496	84	1311	0.946	**65**	**556**	**33**	**940**	**2E-08**
0007263	nitric oxide mediated signal transduction	3	1591	1	1394	0.713	3	618	0	973	0.115
0007243	protein kinase cascade	23	1571	18	1377	0.841	**16**	**605**	**7**	**966**	**0.005**
0007259	JAK-STAT cascade	2	1592	4	1391	0.567	0	621	2	971	0.685
0000165	MAPKKK cascade	19	1575	14	1381	0.752	**14**	**607**	**5**	**968**	**0.004**
0019932	second-messenger-mediated signaling	11	1583	11	1384	0.921	7	614	4	969	0.169
0019722	calcium-mediated signaling	6	1588	9	1386	0.437	3	618	3	970	0.892
0048015	phosphoinositide-mediated signaling	5	1589	0	1395	0.1	4	617	1	972	0.154
0007264	small GTPase mediated signal transduction	27	1567	17	1378	0.355	**16**	**605**	**11**	**962**	**0.047**
0007265	Ras protein signal transduction	6	1588	4	1391	0.915	4	617	2	971	0.33
0009966	regulation of signal transduction	17	1577	17	1378	0.827	**13**	**608**	**4**	**969**	**0.003**
0007275	development	236	1358	224	1171	0.371	**128**	**493**	**108**	**865**	**3E-07**
0007568	aging	6	1588	5	1390	0.825	2	619	4	969	0.892
0030154	cell differentiation	60	1534	59	1336	0.579	**36**	**585**	**24**	**949**	**0.001**
0048468	cell development	35	1559	40	1355	0.292	18	603	17	956	0.176
0000904	cellular morphogenesis during differentiation	11	1583	8	1387	0.865	6	615	5	968	0.451
0042461	photoreceptor cell development	11	1583	7	1388	0.669	6	615	5	968	0.451
0042051	eye photoreceptor development (sensu Endopterygota)	10	1584	7	1388	0.832	5	616	5	968	0.694
0045165	cell fate commitment	22	1572	27	1368	0.294	**14**	**607**	**8**	**965**	**0.03**

PC5

GO#	GO term	Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
		term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	14	1580	16	1379	0.581	7	614	7	966	0.565
0007400	neuroblast cell fate determination	2	1592	6	1389	0.21	2	619	0	973	0.296
0001708	cell fate specification	3	1591	5	1390	0.587	2	619	1	972	0.695
0007349	cellularization	7	1587	4	1391	0.701	3	618	4	969	0.86
0040007	growth	22	1572	14	1381	0.439	10	611	12	961	0.683
0002164	larval development	10	1584	7	1388	0.832	5	616	5	968	0.694
0002165	larval or pupal development (sensu Insecta)	75	1519	54	1341	0.303	**44**	**577**	**31**	**942**	**5E-04**
0007552	metamorphosis	71	1523	50	1345	0.267	**42**	**579**	**29**	**944**	**6E-04**
0009653	morphogenesis	157	1437	162	1233	0.134	**96**	**525**	**61**	**912**	**3E-09**
0002009	morphogenesis of an epithelium	21	1573	23	1372	0.55	11	610	10	963	0.296
0009887	organogenesis	135	1459	147	1248	0.062	**86**	**535**	**49**	**924**	**1E-09**
0001654	eye morphogenesis	27	1567	30	1365	0.437	**17**	**604**	**10**	**963**	**0.017**
0008406	gonad development	5	1589	6	1389	0.825	4	617	1	972	0.154
0007444	imaginal disc development	52	1542	41	1354	0.688	**36**	**585**	**16**	**957**	**1E-05**
0007494	midgut development	2	1592	3	1392	0.881	1	620	1	972	0.685
0007517	muscle development	16	1578	18	1377	0.573	**12**	**609**	**4**	**969**	**0.007**
0007399	neurogenesis	78	1516	84	1311	0.201	**54**	**567**	**24**	**949**	**4E-08**
0007409	axonogenesis	28	1566	15	1380	0.16	**22**	**599**	**6**	**967**	**3E-05**
0007411	axon guidance	22	1572	11	1384	0.171	**19**	**602**	**3**	**970**	**1E-05**
0007417	central nervous system development	20	1574	19	1376	0.923	**16**	**605**	**4**	**969**	**4E-04**
0016358	dendrite morphogenesis	9	1585	5	1390	0.579	5	616	4	969	0.496
0042063	gliogenesis	8	1586	3	1392	0.323	4	617	4	969	0.781
0007422	peripheral nervous system development	23	1571	17	1378	0.709	**16**	**605**	**7**	**966**	**0.005**
0050767	regulation of neurogenesis	3	1591	2	1393	0.881	2	619	1	972	0.695
0007424	tracheal system development (sensu Insecta)	17	1577	20	1375	0.459	9	612	8	965	0.348
0048513	organ development	138	1456	148	1247	0.081	**87**	**534**	**51**	**922**	**2E-09**
0007389	pattern specification	35	1559	41	1354	0.241	**26**	**595**	**9**	**964**	**3E-05**
0048066	pigmentation	4	1590	7	1388	0.408	2	619	2	971	0.952
0009791	post-embryonic development	10	1584	7	1388	0.832	5	616	5	968	0.694
0009790	embryonic development	**43**	**1551**	**57**	**1338**	**0.045**	**28**	**593**	**15**	**958**	**7E-04**
0007530	sex determination	4	1590	6	1389	0.597	1	620	3	970	0.952
0007548	sex differentiation	11	1583	8	1387	0.865	**8**	**613**	**3**	**970**	**0.046**
0019827	stem cell maintenance	3	1591	5	1390	0.587	2	619	1	972	0.695
0000003	reproduction	71	1523	73	1322	0.365	**37**	**584**	**34**	**939**	**0.028**
0050793	regulation of development	22	1572	21	1374	0.894	13	608	9	964	0.084
0007582	physiological process	**892**	**702**	**713**	**682**	**0.009**	331	290	561	412	0.098
0008152	metabolism	642	952	524	871	0.139	**215**	**406**	**427**	**546**	**3E-04**
0009056	catabolism	**127**	**1467**	**82**	**1313**	**0.031**	**35**	**586**	**92**	**881**	**0.008**
0006091	energy pathways	**85**	**1509**	**23**	**1372**	**1E-07**	**15**	**606**	**70**	**903**	**6E-05**
0006118	electron transport	**41**	**1553**	**14**	**1381**	**0.002**	**9**	**612**	**32**	**941**	**0.036**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	218	1376	214	1181	0.215	90	531	128	845	0.494
0006259	DNA metabolism	36	1558	43	1352	0.198	12	609	24	949	0.598
0006350	transcription	**104**	**1490**	**123**	**1272**	**0.022**	**56**	**565**	**48**	**925**	**0.002**
0043170	macromolecule metabolism	**368**	**1226**	**260**	**1135**	**0.003**	**111**	**510**	**257**	**716**	**1E-04**
0019538	protein metabolism	297	1297	230	1165	0.137	**97**	**524**	**200**	**773**	**0.016**
0006412	protein biosynthesis	69	1525	41	1354	0.055	**7**	**614**	**62**	**911**	**1E-06**
0006464	protein modification	142	1452	114	1281	0.514	59	562	83	890	0.567
0006457	protein folding	26	1568	17	1378	0.429	11	610	15	958	0.88
0005975	carbohydrate metabolism	**73**	**1521**	**34**	**1361**	**0.002**	**15**	**606**	**58**	**915**	**0.001**
0006519	amino acid and derivative metabolism	37	1557	33	1362	0.967	13	608	24	949	0.755
0006629	lipid metabolism	52	1542	37	1358	0.384	14	607	38	935	0.096
0009308	amine metabolism	44	1550	37	1358	0.945	14	607	30	943	0.408
0042440	pigment metabolism	6	1588	6	1389	0.954	2	619	4	969	0.892
0042445	hormone metabolism	4	1590	3	1392	0.86	3	618	1	972	0.334
0009058	biosynthesis	120	1474	84	1311	0.119	**22**	**599**	**98**	**875**	**2E-06**
0019748	secondary metabolism	6	1588	8	1387	0.604	2	619	4	969	0.892
0019222	regulation of metabolism	116	1478	122	1273	0.158	**56**	**565**	**60**	**913**	**0.042**
0016265	death	45	1549	41	1354	0.937	24	597	21	952	0.064
0008219	cell death	38	1556	36	1359	0.82	21	600	17	956	0.055
0016271	tissue death	18	1576	9	1386	0.229	9	612	9	964	0.47
0042592	homeostasis	18	1576	11	1384	0.447	7	614	11	962	0.813
0019725	cell homeostasis	17	1577	9	1386	0.298	6	615	11	962	0.951
0050801	ion homeostasis	10	1584	4	1391	0.275	4	617	6	967	0.797
0043062	extracellular structure organization and biogenesis	8	1586	11	1384	0.451	6	615	2	971	0.083
0046903	secretion	62	1532	39	1356	0.121	26	595	36	937	0.721
0048511	rhythmic process	9	1585	8	1387	0.832	**7**	**614**	**2**	**971**	**0.04**

PC5

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	176	1418	171	1224	0.328	**88**	**533**	**88**	**885**	**0.002**
0050874	organismal physiological process	127	1467	105	1290	0.704	**76**	**545**	**51**	**922**	**8E-07**
0050875	cellular physiological process	**849**	**745**	**670**	**725**	**0.005**	314	307	535	438	0.094
0006810	transport	**234**	**1360**	**164**	**1231**	**0.022**	103	518	131	842	0.1
0006811	ion transport	71	1523	49	1346	0.224	35	586	36	937	0.089
0006818	hydrogen transport	**17**	**1577**	**1**	**1394**	**0.001**	3	618	14	959	0.118
0006836	neurotransmitter transport	4	1590	1	1394	0.455	3	618	1	972	0.334
0006858	extracellular transport	10	1584	5	1390	0.436	4	617	6	967	0.797
0006869	lipid transport	12	1582	4	1391	0.136	3	618	9	964	0.485
0008643	carbohydrate transport	5	1589	10	1385	0.195	1	620	4	969	0.681
0015031	protein transport	105	1489	75	1320	0.19	39	582	66	907	0.771
0015837	amine transport	10	1584	2	1393	0.072	7	614	3	970	0.09
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	8	1586	5	1390	0.752	1	620	7	966	0.24
0016192	vesicle-mediated transport	72	1522	47	1348	0.132	32	589	40	933	0.394
0045045	secretory pathway	59	1535	36	1359	0.101	25	596	34	939	0.68
0046907	intracellular transport	117	1477	81	1314	0.108	42	579	75	898	0.544
0051049	regulation of transport	13	1581	5	1390	0.169	7	614	6	967	0.412
0008283	cell proliferation	42	1552	29	1366	0.381	**23**	**598**	**19**	**954**	**0.049**
0007049	cell cycle	78	1516	50	1345	0.094	30	591	48	925	0.979
0017145	stem cell division	**2**	**1592**	**10**	**1385**	**0.024**	1	620	1	972	0.685
0016043	cell organization and biogenesis	139	1455	136	1259	0.364	**70**	**551**	**69**	**904**	**0.005**
0000902	cellular morphogenesis	40	1554	40	1355	0.623	**25**	**596**	**15**	**958**	**0.003**
0006996	organelle organization and biogenesis	119	1475	119	1276	0.315	**59**	**562**	**60**	**913**	**0.018**
0007010	cytoskeleton organization and biogenesis	93	1501	77	1318	0.771	**51**	**570**	**42**	**931**	**0.002**
0006997	nuclear organization and biogenesis	6	1588	4	1391	0.915	2	619	4	969	0.892
0007028	cytoplasm organization and biogenesis	**5**	**1589**	**14**	**1381**	**0.033**	4	617	1	972	0.154
0016044	membrane organization and biogenesis	6	1588	3	1392	0.639	2	619	4	969	0.892
0051128	regulation of cell organization and biogenesis	6	1588	5	1390	0.825	3	618	3	970	0.892
0016049	cell growth	4	1590	5	1390	0.841	2	619	2	971	0.952
0050896	response to stimulus	99	1495	82	1313	0.761	**59**	**562**	**40**	**933**	**2E-05**
0006950	response to stress	32	1562	27	1368	0.992	16	605	16	957	0.267
0009408	response to heat	3	1591	7	1388	0.245	3	618	0	973	0.115
0006979	response to oxidative stress	1	1593	1	1394	0.539	1	620	0	973	0.821
0051179	localization	247	1347	182	1213	0.064	110	511	137	836	0.06
0006403	RNA localization	18	1576	14	1381	0.877	7	614	11	962	0.813
0008104	protein localization	110	1484	85	1310	0.413	41	580	69	904	0.784
0051234	establishment of localization	**236**	**1358**	**167**	**1228**	**0.027**	104	517	132	841	0.095
0051235	maintenance of localization	2	1592	2	1393	0.713	2	619	0	973	0.296
0050789	regulation of biological process	203	1391	200	1195	0.22	**102**	**519**	**101**	**872**	**6E-04**
0050790	regulation of enzyme activity	6	1588	8	1387	0.604	3	618	3	970	0.892
0040029	regulation of gene expression, epigenetic	8	1586	12	1383	0.33	2	619	6	967	0.654
0006306	DNA methylation	3	1591	4	1391	0.86	0	621	3	970	0.428
0045814	negative regulation of gene expression, epigenetic	3	1591	4	1391	0.86	1	620	2	971	0.695
0006342	chromatin silencing	3	1591	4	1391	0.86	1	620	2	971	0.695
0003674	molecular_function	**970**	**624**	**762**	**633**	**7E-04**	374	247	596	377	0.721
0016209	antioxidant activity	8	1586	1	1394	0.071	0	621	8	965	0.057
0005488	binding	555	1039	452	943	0.175	230	391	325	648	0.152
0005509	calcium ion binding	32	1562	29	1366	0.994	14	607	18	955	0.705
0030246	carbohydrate binding	6	1588	9	1386	0.437	0	621	6	967	0.123
0008289	lipid binding	12	1582	14	1381	0.59	5	616	7	966	0.917
0003676	nucleic acid binding	211	1383	178	1217	0.74	80	541	131	842	0.796
0003677	DNA binding	**88**	**1506**	**106**	**1289**	**0.026**	**49**	**572**	**39**	**934**	**0.001**
0003682	chromatin binding	8	1586	15	1380	0.114	5	616	3	970	0.315
0003700	transcription factor activity	**33**	**1561**	**53**	**1342**	**0.007**	**21**	**600**	**12**	**961**	**0.006**
0003723	RNA binding	**79**	**1515**	**40**	**1355**	**0.005**	**21**	**600**	**58**	**915**	**0.028**
0008135	translation factor activity, nucleic acid binding	**26**	**1568**	**9**	**1386**	**0.02**	**2**	**619**	**24**	**949**	**0.002**
0000166	nucleotide binding	149	1445	106	1289	0.101	59	562	90	883	0.936
0005515	protein binding	200	1394	179	1216	0.859	**110**	**511**	**90**	**883**	**1E-06**
0008134	transcription factor binding	16	1578	15	1380	0.991	10	611	6	967	0.092
0008092	cytoskeletal protein binding	48	1546	40	1355	0.902	22	599	26	947	0.4
0003779	actin binding	24	1570	29	1366	0.296	9	612	15	958	0.95
0003824	catalytic activity	**484**	**1110**	**355**	**1040**	**0.003**	**145**	**476**	**339**	**634**	**2E-06**
0016787	hydrolase activity	207	1387	165	1230	0.367	**66**	**555**	**141**	**832**	**0.031**
0003924	GTPase activity	25	1569	15	1380	0.312	8	613	17	956	0.608
0004518	nuclease activity	10	1584	5	1390	0.436	2	619	8	965	0.364

		PC5									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	67	1527	51	1344	0.501	**17**	**604**	**50**	**923**	**0.028**
0004721	phosphoprotein phosphatase activity	16	1578	14	1381	0.854	8	613	8	965	0.514
0016740	transferase activity	126	1468	115	1280	0.785	51	570	75	898	0.788
0016301	kinase activity	77	1517	58	1337	0.426	**40**	**581**	**37**	**936**	**0.023**
0004672	protein kinase activity	51	1543	44	1351	0.973	**33**	**588**	**18**	**955**	**2E-04**
0030234	enzyme regulator activity	59	1535	46	1349	0.618	30	591	29	944	0.076
0003774	motor activity	16	1578	12	1383	0.829	8	613	8	965	0.514
0004871	signal transducer activity	132	1462	124	1271	0.598	**88**	**533**	**44**	**929**	**2E-11**
0004872	receptor activity	58	1536	51	1344	0.942	**41**	**580**	**17**	**956**	**9E-07**
0004879	ligand-dependent nuclear receptor activity	6	1588	3	1392	0.639	5	616	1	972	0.07
0004888	transmembrane receptor activity	36	1558	38	1357	0.484	**26**	**595**	**10**	**963**	**7E-05**
0004930	G-protein coupled receptor activity	13	1581	17	1378	0.358	**10**	**611**	**3**	**970**	**0.011**
0005057	receptor signaling protein activity	45	1549	35	1360	0.676	**31**	**590**	**14**	**959**	**6E-05**
0005102	receptor binding	29	1565	40	1355	0.075	**20**	**601**	**9**	**964**	**0.002**
0005198	structural molecule activity	83	1511	79	1316	0.639	31	590	52	921	0.847
0030528	transcription regulator activity	**87**	**1507**	**112**	**1283**	**0.006**	**50**	**571**	**37**	**936**	**4E-04**
0045182	translation regulator activity	**26**	**1568**	**9**	**1386**	**0.02**	**2**	**619**	**24**	**949**	**0.002**
0005215	transporter activity	**152**	**1442**	**101**	**1294**	**0.029**	62	559	90	883	0.69
0005489	electron transporter activity	**23**	**1571**	**6**	**1389**	**0.009**	6	615	17	956	0.289
0005216	ion channel activity	28	1566	24	1371	0.948	**21**	**600**	**7**	**966**	**2E-04**
0005244	voltage-gated ion channel activity	15	1579	11	1384	0.802	**12**	**609**	**3**	**970**	**0.003**
0005575	cellular_component	**692**	**902**	**531**	**864**	**0.003**	**250**	**371**	**442**	**531**	**0.048**
0005623	cell	**629**	**965**	**483**	**912**	**0.007**	228	393	401	572	0.082
0005622	intracellular	**495**	**1099**	**362**	**1033**	**0.002**	**150**	**471**	**345**	**628**	**3E-06**
0005737	cytoplasm	**301**	**1293**	**157**	**1238**	**1E-08**	**60**	**561**	**241**	**732**	**9E-14**
0016023	cytoplasmic vesicle	24	1570	17	1378	0.606	12	609	12	961	0.365
0005829	cytosol	**54**	**1540**	**25**	**1370**	**0.009**	**3**	**618**	**51**	**922**	**6E-07**
0005783	endoplasmic reticulum	37	1557	20	1375	0.102	**2**	**619**	**35**	**938**	**5E-05**
0005794	Golgi apparatus	12	1582	13	1382	0.738	2	619	10	963	0.196
0005815	microtubule organizing center	8	1586	1	1394	0.071	4	617	4	969	0.781
0005739	mitochondrion	**83**	**1511**	**22**	**1373**	**1E-07**	**5**	**616**	**78**	**895**	**6E-10**
0005840	ribosome	18	1576	6	1389	0.053	**1**	**620**	**17**	**956**	**0.007**
0005773	vacuole	**13**	**1581**	**1**	**1394**	**0.007**	**0**	**621**	**13**	**960**	**0.009**
0005764	lysosome	5	1589	0	1395	0.1	0	621	5	968	0.184
0005856	cytoskeleton	51	1543	34	1361	0.254	24	597	27	946	0.289
0005694	chromosome	18	1576	22	1373	0.366	10	611	8	965	0.227
0000228	nuclear chromosome	3	1591	2	1393	0.881	0	621	3	970	0.428
0005634	nucleus	184	1410	188	1207	0.123	78	543	106	867	0.35
0005635	nuclear membrane	6	1588	11	1384	0.211	3	618	3	970	0.892
0005730	nucleolus	6	1588	5	1390	0.825	1	620	5	968	0.482
0005654	nucleoplasm	33	1561	39	1356	0.242	13	608	20	953	0.898
0005777	peroxisome	8	1586	1	1394	0.071	0	621	8	965	0.057
0005886	plasma membrane	83	1511	73	1322	0.96	**56**	**565**	**27**	**946**	**9E-08**
0005576	extracellular region	42	1552	34	1361	0.821	22	599	20	953	0.099
0005578	extracellular matrix (sensu Metazoa)	18	1576	17	1378	0.955	10	611	8	965	0.227

PC6

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	**927**	**588**	**827**	**647**	**0.005**	615	373	312	215	0.27
0007610	behavior	82	1433	80	1394	0.95	**37**	**951**	**45**	**482**	**1E-04**
0030534	adult behavior	12	1503	12	1462	0.891	5	983	7	520	0.157
0030537	larval behavior	4	1511	5	1469	0.967	3	985	1	526	0.909
0007611	learning and/or memory	12	1503	12	1462	0.891	**4**	**984**	**8**	**519**	**0.043**
0007612	learning	5	1510	10	1464	0.276	3	985	2	525	0.822
0007613	memory	5	1510	6	1468	0.964	1	987	4	523	0.098
0007626	locomotory behavior	63	1452	60	1414	0.977	**28**	**960**	**35**	**492**	**7E-04**
0007635	chemosensory behavior	6	1509	12	1462	0.215	2	986	4	523	0.225
0007622	rhythmic behavior	7	1508	8	1466	0.958	5	983	2	525	0.959
0048512	circadian behavior	7	1508	7	1467	0.829	5	983	2	525	0.959
0009987	cellular process	**872**	**643**	**756**	**718**	**7E-04**	580	408	292	235	0.237
0007154	cell communication	253	1262	236	1238	0.646	**136**	**852**	**117**	**410**	**4E-05**
0007155	cell adhesion	37	1478	53	1421	0.082	**17**	**971**	**20**	**507**	**0.021**
0008037	cell recognition	0	1515	2	1472	0.467	0	988	0	527	-
0008038	neuronal cell recognition	0	1515	2	1472	0.467	0	988	0	527	-
0016337	cell-cell adhesion	**12**	**1503**	**27**	**1447**	**0.019**	5	983	7	520	0.157
0016339	calcium-dependent cell-cell adhesion	2	1513	5	1469	0.428	0	988	2	525	0.232
0007156	homophilic cell adhesion	3	1512	6	1468	0.478	0	988	3	524	0.077
0007160	cell-matrix adhesion	2	1513	7	1467	0.169	1	987	1	526	0.771
0007267	cell-cell signaling	88	1427	68	1406	0.166	**44**	**944**	**44**	**483**	**0.003**
0019226	transmission of nerve impulse	79	1436	59	1415	0.136	**39**	**949**	**40**	**487**	**0.004**
0007268	synaptic transmission	58	1457	43	1431	0.202	31	957	27	500	0.075
0007270	nerve-nerve synaptic transmission	10	1505	6	1468	0.486	5	983	5	522	0.496
0001505	regulation of neurotransmitter levels	33	1482	27	1447	0.586	20	968	13	514	0.706
0042133	neurotransmitter metabolism	3	1512	5	1469	0.694	2	986	1	526	0.58
0007269	neurotransmitter secretion	30	1485	23	1451	0.465	18	970	12	515	0.68
0007165	signal transduction	194	1321	185	1289	0.878	**108**	**880**	**86**	**441**	**0.004**
0007166	cell surface receptor linked signal transduction	86	1429	71	1403	0.331	50	938	36	491	0.193
0007167	enzyme linked receptor protein signaling pathway	25	1490	21	1453	0.725	**10**	**978**	**15**	**512**	**0.014**
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	10	1505	6	1468	0.486	4	984	6	521	0.178
0007179	transforming growth factor beta receptor signaling pathway	**8**	**1507**	**1**	**1473**	**0.05**	4	984	4	523	0.594
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	15	1500	17	1457	0.798	6	982	9	518	0.074
0007173	epidermal growth factor receptor signaling pathway	2	1513	6	1468	0.271	0	988	2	525	0.232
0008286	insulin receptor signaling pathway	2	1513	2	1472	0.636	0	988	2	525	0.232
0008293	torso signaling pathway	2	1513	5	1469	0.428	1	987	1	526	0.771
0007186	G-protein coupled receptor protein signaling pathway	41	1474	30	1444	0.278	25	963	16	511	0.681
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1512	2	1472	0.976	2	986	1	526	0.58
0007219	Notch signaling pathway	6	1509	7	1467	0.96	4	984	2	525	0.723
0007224	smoothened signaling pathway	3	1512	3	1471	0.708	2	986	1	526	0.58
0008063	Toll signaling pathway	3	1512	1	1473	0.636	2	986	1	526	0.58
0016055	Wnt receptor signaling pathway	8	1507	8	1466	0.845	6	982	2	525	0.833
0007242	intracellular signaling cascade	96	1419	86	1388	0.619	57	931	39	488	0.258
0007263	nitric oxide mediated signal transduction	2	1513	2	1472	0.636	1	987	1	526	0.771
0007243	protein kinase cascade	23	1492	18	1456	0.589	14	974	9	518	0.826
0007259	JAK-STAT cascade	1	1514	5	1469	0.208	1	987	0	527	0.749
0000165	MAPKKK cascade	21	1494	12	1462	0.186	12	976	9	518	0.581
0019932	second-messenger-mediated signaling	11	1504	11	1463	0.881	4	984	7	520	0.089
0019722	calcium-mediated signaling	7	1508	8	1466	0.958	2	986	5	522	0.1
0048015	phosphoinositide-mediated signaling	3	1512	2	1472	0.976	2	986	1	526	0.58
0007264	small GTPase mediated signal transduction	22	1493	22	1452	0.952	12	976	10	517	0.405
0007265	Ras protein signal transduction	5	1510	5	1469	0.785	1	987	4	523	0.098
0009966	regulation of signal transduction	15	1500	19	1455	0.55	8	980	7	520	0.485
0007275	development	239	1276	221	1253	0.588	**130**	**858**	**109**	**418**	**2E-04**
0007568	aging	7	1508	4	1470	0.576	6	982	1	526	0.457
0030154	cell differentiation	56	1459	63	1411	0.475	31	957	25	502	0.151
0048468	cell development	32	1483	43	1431	0.197	22	966	10	517	0.813
0000904	cellular morphogenesis during differentiation	7	1508	12	1462	0.327	5	983	2	525	0.959
0042461	photoreceptor cell development	7	1508	11	1463	0.443	5	983	2	525	0.959
0042051	eye photoreceptor development (sensu Endopterygota)	6	1509	11	1463	0.303	5	983	1	526	0.614
0045165	cell fate commitment	23	1492	26	1448	0.7	12	976	11	516	0.27

PC6

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	12	1503	18	1456	0.321	6	982	6	521	0.42
0007400	neuroblast cell fate determination	5	1510	3	1471	0.753	2	986	3	524	0.474
0001708	cell fate specification	3	1512	5	1469	0.694	1	987	2	525	0.58
0007349	cellularization	9	1506	2	1472	0.077	5	983	4	523	0.795
0040007	growth	20	1495	16	1458	0.674	**8**	**980**	**12**	**515**	**0.032**
0002164	larval development	10	1505	7	1467	0.667	6	982	4	523	0.989
0002165	larval or pupal development (sensu Insecta)	65	1450	64	1410	0.983	**34**	**954**	**31**	**496**	**0.036**
0007552	metamorphosis	60	1455	61	1413	0.878	**30**	**958**	**30**	**497**	**0.017**
0009653	morphogenesis	160	1355	159	1315	0.888	**80**	**908**	**80**	**447**	**3E-05**
0002009	morphogenesis of an epithelium	22	1493	22	1452	0.952	11	977	11	516	0.199
0009887	organogenesis	138	1377	144	1330	0.579	**70**	**918**	**68**	**459**	**3E-04**
0001654	eye morphogenesis	26	1489	31	1443	0.522	14	974	12	515	0.308
0008406	gonad development	7	1508	4	1470	0.576	3	985	4	523	0.397
0007444	imaginal disc development	39	1476	54	1420	0.108	**18**	**970**	**21**	**506**	**0.018**
0007494	midgut development	3	1512	2	1472	0.976	1	987	2	525	0.58
0007517	muscle development	17	1498	17	1457	0.927	9	979	8	519	0.417
0007399	neurogenesis	87	1428	75	1399	0.478	**44**	**944**	**43**	**484**	**0.005**
0007409	axonogenesis	27	1488	16	1458	0.148	**11**	**977**	**16**	**511**	**0.013**
0007411	axon guidance	21	1494	12	1462	0.186	9	979	12	515	0.053
0007417	central nervous system development	19	1496	20	1454	0.931	9	979	10	517	0.161
0016358	dendrite morphogenesis	9	1506	5	1469	0.452	3	985	6	521	0.096
0042063	gliogenesis	5	1510	6	1468	0.964	3	985	2	525	0.822
0007422	peripheral nervous system development	16	1499	24	1450	0.229	8	980	8	519	0.307
0050767	regulation of neurogenesis	3	1512	2	1472	0.976	2	986	1	526	0.58
0007424	tracheal system development (sensu Insecta)	17	1498	20	1454	0.678	12	976	5	522	0.832
0048513	organ development	139	1376	147	1327	0.497	**71**	**917**	**68**	**459**	**3E-04**
0007389	pattern specification	**26**	**1489**	**50**	**1424**	**0.005**	17	971	9	518	0.85
0048066	pigmentation	5	1510	6	1468	0.964	4	984	1	526	0.822
0009791	post-embryonic development	10	1505	7	1467	0.667	6	982	4	523	0.989
0009790	embryonic development	54	1461	46	1428	0.567	30	958	24	503	0.17
0007530	sex determination	5	1510	5	1469	0.785	3	985	2	525	0.822
0007548	sex differentiation	10	1505	9	1465	0.952	5	983	5	522	0.496
0019827	stem cell maintenance	6	1509	2	1472	0.306	5	983	1	526	0.614
0000003	reproduction	66	1449	78	1396	0.268	37	951	29	498	0.143
0050793	regulation of development	24	1491	19	1455	0.6	**8**	**980**	**16**	**511**	**0.002**
0007582	physiological process	**860**	**655**	**745**	**729**	**7E-04**	**581**	**407**	**279**	**248**	**0.032**
0008152	metabolism	**630**	**885**	**536**	**938**	**0.004**	**442**	**546**	**188**	**339**	**8E-04**
0009056	catabolism	117	1398	92	1382	0.13	**92**	**896**	**25**	**502**	**0.002**
0006091	energy pathways	**80**	**1435**	**28**	**1446**	**1E-06**	**69**	**919**	**11**	**516**	**8E-05**
0006118	electron transport	**38**	**1477**	**17**	**1457**	**0.009**	**32**	**956**	**6**	**521**	**0.02**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	224	1291	208	1266	0.637	144	844	80	447	0.81
0006259	DNA metabolism	40	1475	39	1435	0.917	26	962	14	513	0.889
0006350	transcription	110	1405	117	1357	0.529	**59**	**929**	**51**	**476**	**0.011**
0043170	macromolecule metabolism	**346**	**1169**	**282**	**1192**	**0.015**	**252**	**736**	**94**	**433**	**9E-04**
0019538	protein metabolism	286	1229	241	1233	0.078	**202**	**786**	**84**	**443**	**0.039**
0006412	protein biosynthesis	49	1466	61	1413	0.224	34	954	15	512	0.638
0006464	protein modification	**150**	**1365**	**106**	**1368**	**0.01**	100	888	50	477	0.762
0006457	protein folding	24	1491	19	1455	0.6	18	970	6	521	0.425
0005975	carbohydrate metabolism	60	1455	47	1427	0.3	**51**	**937**	**9**	**518**	**0.002**
0006519	amino acid and derivative metabolism	40	1475	30	1444	0.331	29	959	11	516	0.417
0006629	lipid metabolism	38	1477	51	1423	0.155	26	962	12	515	0.804
0009308	amine metabolism	43	1472	38	1436	0.745	30	958	13	514	0.636
0042440	pigment metabolism	5	1510	7	1467	0.736	5	983	0	527	0.244
0042445	hormone metabolism	2	1513	5	1469	0.428	2	986	0	527	0.771
0009058	biosynthesis	99	1416	105	1369	0.572	**77**	**911**	**22**	**505**	**0.009**
0019748	secondary metabolism	5	1510	9	1465	0.392	5	983	0	527	0.244
0019222	regulation of metabolism	119	1396	119	1355	0.878	**60**	**928**	**59**	**468**	**6E-04**
0016265	death	50	1465	36	1438	0.196	33	955	17	510	0.974
0008219	cell death	42	1473	32	1442	0.347	26	962	16	511	0.77
0016271	tissue death	17	1498	10	1464	0.276	10	978	7	520	0.764
0042592	homeostasis	15	1500	14	1460	0.941	11	977	4	523	0.696
0019725	cell homeostasis	14	1501	12	1462	0.899	11	977	3	524	0.44
0050801	ion homeostasis	7	1508	7	1467	0.829	6	982	1	526	0.457
0043062	extracellular structure organization and biogenesis	11	1504	8	1466	0.689	6	982	5	522	0.669
0046903	secretion	61	1454	40	1434	0.059	42	946	19	508	0.637
0048511	rhythmic process	8	1507	9	1465	0.955	6	982	2	525	0.833

PC6

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	179	1336	168	1306	0.765	**95**	**893**	**84**	**443**	**4E-04**
0050874	organismal physiological process	117	1398	115	1359	0.99	**57**	**931**	**60**	**467**	**1E-04**
0050875	cellular physiological process	**820**	**695**	**699**	**775**	**3E-04**	**556**	**432**	**264**	**263**	**0.025**
0006810	transport	**221**	**1294**	**177**	**1297**	**0.043**	149	839	72	455	0.504
0006811	ion transport	**75**	**1440**	**45**	**1429**	**0.011**	48	940	27	500	0.919
0006818	hydrogen transport	**14**	**1501**	**4**	**1470**	**0.038**	13	975	1	526	0.057
0006836	neurotransmitter transport	3	1512	2	1472	0.976	1	987	2	525	0.58
0006858	extracellular transport	10	1505	5	1469	0.326	5	983	5	522	0.496
0006869	lipid transport	8	1507	8	1466	0.845	7	981	1	526	0.34
0008643	carbohydrate transport	8	1507	7	1467	0.958	7	981	1	526	0.34
0015031	protein transport	102	1413	78	1396	0.114	69	919	33	494	0.67
0015837	amine transport	7	1508	5	1469	0.809	5	983	2	525	0.959
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	7	1508	6	1468	0.96	6	982	1	526	0.457
0016192	vesicle-mediated transport	**74**	**1441**	**45**	**1429**	**0.014**	53	935	21	506	0.289
0045045	secretory pathway	**59**	**1456**	**36**	**1438**	**0.031**	41	947	18	509	0.573
0046907	intracellular transport	107	1408	91	1383	0.366	74	914	33	494	0.433
0051049	regulation of transport	9	1506	9	1465	0.859	5	983	4	523	0.795
0008283	cell proliferation	35	1480	36	1438	0.907	22	966	13	514	0.907
0007049	cell cycle	60	1455	68	1406	0.429	40	948	20	507	0.918
0017145	stem cell division	7	1508	5	1469	0.809	5	983	2	525	0.959
0016043	cell organization and biogenesis	131	1384	144	1330	0.318	**70**	**918**	**61**	**466**	**0.004**
0000902	cellular morphogenesis	44	1471	36	1438	0.503	**22**	**966**	**22**	**505**	**0.047**
0006996	organelle organization and biogenesis	113	1402	125	1349	0.335	**60**	**928**	**53**	**474**	**0.007**
0007010	cytoskeleton organization and biogenesis	82	1433	88	1386	0.563	**41**	**947**	**41**	**486**	**0.004**
0006997	nuclear organization and biogenesis	4	1511	6	1468	0.719	3	985	1	526	0.909
0007028	cytoplasm organization and biogenesis	10	1505	9	1465	0.952	8	980	2	525	0.514
0016044	membrane organization and biogenesis	6	1509	3	1471	0.531	5	983	1	526	0.614
0051128	regulation of cell organization and biogenesis	8	1507	3	1471	0.245	3	985	5	522	0.201
0016049	cell growth	5	1510	4	1470	0.967	2	986	3	524	0.474
0050896	response to stimulus	82	1433	99	1375	0.156	**43**	**945**	**39**	**488**	**0.017**
0006950	response to stress	24	1491	35	1439	0.155	15	973	9	518	0.948
0009408	response to heat	3	1512	7	1467	0.32	1	987	2	525	0.58
0006979	response to oxidative stress	1	1514	1	1473	0.491	0	988	1	526	0.749
0051179	localization	236	1279	193	1281	0.06	157	831	79	448	0.7
0006403	RNA localization	14	1501	18	1456	0.541	11	977	3	524	0.44
0008104	protein localization	110	1405	85	1389	0.114	73	915	37	490	0.874
0051234	establishment of localization	223	1292	180	1294	0.051	150	838	73	454	0.535
0051235	maintenance of localization	2	1513	2	1472	0.636	1	987	1	526	0.771
0050789	regulation of biological process	208	1307	195	1279	0.729	**113**	**875**	**95**	**432**	**5E-04**
0050790	regulation of enzyme activity	9	1506	5	1469	0.452	8	980	1	526	0.252
0040029	regulation of gene expression, epigenetic	10	1505	10	1464	0.871	6	982	4	523	0.989
0006306	DNA methylation	3	1512	4	1470	0.971	3	985	0	527	0.51
0045814	negative regulation of gene expression, epigenetic	3	1512	4	1470	0.971	1	987	2	525	0.58
0006342	chromatin silencing	3	1512	4	1470	0.971	1	987	2	525	0.58
0003674	molecular_function	**912**	**603**	**820**	**654**	**0.013**	608	380	304	223	0.16
0016209	antioxidant activity	5	1510	4	1470	0.967	5	983	0	527	0.244
0005488	binding	521	994	486	988	0.435	**317**	**671**	**204**	**323**	**0.011**
0005509	calcium ion binding	28	1487	33	1441	0.531	14	974	14	513	0.132
0030246	carbohydrate binding	8	1507	7	1467	0.958	3	985	5	522	0.201
0008289	lipid binding	13	1502	13	1461	0.899	5	983	8	519	0.082
0003676	nucleic acid binding	191	1324	198	1276	0.538	**109**	**879**	**82**	**445**	**0.014**
0003677	DNA binding	95	1420	99	1375	0.674	**47**	**941**	**48**	**479**	**0.001**
0003682	chromatin binding	9	1506	14	1460	0.366	4	984	5	522	0.336
0003700	transcription factor activity	43	1472	43	1431	0.984	**19**	**969**	**24**	**503**	**0.006**
0003723	RNA binding	61	1454	58	1416	0.973	37	951	24	503	0.531
0008135	translation factor activity, nucleic acid binding	17	1498	18	1456	0.935	15	973	2	525	0.08
0000166	nucleotide binding	142	1373	113	1361	0.109	100	888	42	485	0.202
0005515	protein binding	184	1331	195	1279	0.403	**102**	**886**	**82**	**445**	**0.004**
0008134	transcription factor binding	10	1505	21	1453	0.06	4	984	6	521	0.178
0008092	cytoskeletal protein binding	41	1474	47	1427	0.502	**19**	**969**	**22**	**505**	**0.016**
0003779	actin binding	24	1491	29	1445	0.512	13	975	11	516	0.353
0003824	catalytic activity	**453**	**1062**	**386**	**1088**	**0.027**	**332**	**656**	**121**	**406**	**2E-05**
0016787	hydrolase activity	196	1319	176	1298	0.441	**150**	**838**	**46**	**481**	**5E-04**
0003924	GTPase activity	17	1498	23	1451	0.377	13	975	4	523	0.469
0004518	nuclease activity	5	1510	10	1464	0.276	4	984	1	526	0.822

PC6

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	67	1448	51	1423	0.209	**54**	**934**	**13**	**514**	**0.01**
0004721	phosphoprotein phosphatase activity	18	1497	12	1462	0.4	11	977	7	520	0.905
0016740	transferase activity	130	1385	111	1363	0.324	93	895	37	490	0.137
0016301	kinase activity	80	1435	55	1419	0.051	51	937	29	498	0.871
0004672	protein kinase activity	56	1459	39	1435	0.125	32	956	24	503	0.25
0030234	enzyme regulator activity	**65**	**1450**	**40**	**1434**	**0.025**	44	944	21	506	0.768
0003774	motor activity	16	1499	12	1462	0.619	8	980	8	519	0.307
0004871	signal transducer activity	134	1381	122	1352	0.624	**72**	**916**	**62**	**465**	**0.005**
0004872	receptor activity	57	1458	52	1422	0.807	**27**	**961**	**30**	**497**	**0.006**
0004879	ligand-dependent nuclear receptor activity	5	1510	4	1470	0.967	3	985	2	525	0.822
0004888	transmembrane receptor activity	39	1476	35	1439	0.815	20	968	19	508	0.093
0004930	G-protein coupled receptor activity	16	1499	14	1460	0.914	10	978	6	521	0.972
0005057	receptor signaling protein activity	48	1467	32	1442	0.115	29	959	19	508	0.579
0005102	receptor binding	35	1480	34	1440	0.908	19	969	16	511	0.233
0005198	structural molecule activity	78	1437	84	1390	0.56	**41**	**947**	**37**	**490**	**0.022**
0030528	transcription regulator activity	93	1422	106	1368	0.28	**48**	**940**	**45**	**482**	**0.006**
0045182	translation regulator activity	17	1498	18	1456	0.935	15	973	2	525	0.08
0005215	transporter activity	**156**	**1359**	**97**	**1377**	**3E-04**	112	876	44	483	0.083
0005489	electron transporter activity	19	1496	10	1464	0.156	16	972	3	524	0.132
0005216	ion channel activity	31	1484	21	1453	0.246	**13**	**975**	**18**	**509**	**0.01**
0005244	voltage-gated ion channel activity	14	1501	12	1462	0.899	**3**	**985**	**11**	**516**	**0.002**
0005575	cellular_component	**647**	**868**	**576**	**898**	**0.048**	429	559	218	309	0.474
0005623	cell	585	930	527	947	0.114	391	597	194	333	0.319
0005622	intracellular	448	1067	409	1065	0.288	**316**	**672**	**132**	**395**	**0.006**
0005737	cytoplasm	**267**	**1248**	**191**	**1283**	**5E-04**	**206**	**782**	**61**	**466**	**9E-06**
0016023	cytoplasmic vesicle	**28**	**1487**	**13**	**1461**	**0.035**	20	968	8	519	0.619
0005829	cytosol	**52**	**1463**	**27**	**1447**	**0.009**	**42**	**946**	**10**	**517**	**0.025**
0005783	endoplasmic reticulum	34	1481	23	1451	0.218	**29**	**959**	**5**	**522**	**0.021**
0005794	Golgi apparatus	15	1500	10	1464	0.463	11	977	4	523	0.696
0005815	microtubule organizing center	3	1512	6	1468	0.478	1	987	2	525	0.58
0005739	mitochondrion	**66**	**1449**	**39**	**1435**	**0.015**	**57**	**931**	**9**	**518**	**4E-04**
0005840	ribosome	9	1506	15	1459	0.275	7	981	2	525	0.658
0005773	vacuole	**13**	**1502**	**1**	**1473**	**0.004**	12	976	1	526	0.077
0005764	lysosome	4	1511	1	1473	0.387	3	985	1	526	0.909
0005856	cytoskeleton	38	1477	47	1427	0.313	19	969	19	508	0.068
0005694	chromosome	14	1501	26	1448	0.066	7	981	7	520	0.358
0000228	nuclear chromosome	0	1515	5	1469	0.069	0	988	0	527	-
0005634	nucleus	179	1336	193	1281	0.316	114	874	65	462	0.709
0005635	nuclear membrane	7	1508	10	1464	0.587	4	984	3	524	0.959
0005730	nucleolus	4	1511	7	1467	0.516	4	984	0	527	0.349
0005654	nucleoplasm	37	1478	35	1439	0.999	27	961	10	517	0.407
0005777	peroxisome	4	1511	5	1469	0.967	3	985	1	526	0.909
0005886	plasma membrane	84	1431	72	1402	0.466	**40**	**948**	**44**	**483**	**8E-04**
0005576	extracellular region	37	1478	39	1435	0.812	21	967	16	511	0.358
0005578	extracellular matrix (sensu Metazoa)	20	1495	15	1459	0.549	9	979	11	516	0.094

PC7

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008150	biological_process	885	617	869	618	0.818	304	233	581	384	0.193
0007610	behavior	82	1420	80	1407	0.988	25	512	57	908	0.366
0030534	adult behavior	10	1492	14	1473	0.522	7	530	3	962	0.053
0030537	larval behavior	6	1496	3	1484	0.514	4	533	2	963	0.248
0007611	learning and/or memory	11	1491	13	1474	0.818	2	535	9	956	0.366
0007612	learning	8	1494	7	1480	0.984	1	536	7	958	0.314
0007613	memory	2	1500	9	1478	0.067	0	537	2	963	0.751
0007626	locomotory behavior	58	1444	65	1422	0.542	19	518	39	926	0.73
0007635	chemosensory behavior	9	1493	9	1478	0.83	2	535	7	958	0.617
0007622	rhythmic behavior	6	1496	9	1478	0.591	2	535	4	961	0.762
0048512	circadian behavior	5	1497	9	1478	0.411	2	535	3	962	0.788
0009987	cellular process	815	687	813	674	0.849	273	264	542	423	0.053
0007154	cell communication	252	1250	237	1250	0.568	92	445	160	805	0.84
0007155	cell adhesion	46	1456	44	1443	0.953	16	521	30	935	0.987
0008037	cell recognition	2	1500	0	1487	0.484	0	537	2	963	0.751
0008038	neuronal cell recognition	2	1500	0	1487	0.484	0	537	2	963	0.751
0016337	cell-cell adhesion	20	1482	19	1468	0.975	9	528	11	954	0.526
0016339	calcium-dependent cell-cell adhesion	2	1500	5	1482	0.441	2	535	0	965	0.247
0007156	homophilic cell adhesion	3	1499	6	1481	0.495	2	535	1	964	0.606
0007160	cell-matrix adhesion	4	1498	5	1482	0.988	3	534	1	964	0.264
0007267	cell-cell signaling	74	1428	82	1405	0.522	31	506	43	922	0.315
0019226	transmission of nerve impulse	68	1434	70	1417	0.883	29	508	39	926	0.278
0007268	synaptic transmission	45	1457	56	1431	0.288	**24**	**513**	**21**	**944**	**0.019**
0007270	nerve-nerve synaptic transmission	7	1495	9	1478	0.787	**7**	**530**	**0**	**965**	**0.002**
0001505	regulation of neurotransmitter levels	28	1474	32	1455	0.667	13	524	15	950	0.322
0042133	neurotransmitter metabolism	4	1498	4	1483	0.734	**4**	**533**	**0**	**965**	**0.031**
0007269	neurotransmitter secretion	25	1477	28	1459	0.753	10	527	15	950	0.813
0007165	signal transduction	198	1304	181	1306	0.438	70	467	128	837	0.963
0007166	cell surface receptor linked signal transduction	85	1417	72	1415	0.358	25	512	60	905	0.255
0007167	enzyme linked receptor protein signaling pathway	21	1481	25	1462	0.631	5	532	16	949	0.357
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	9	1493	7	1480	0.818	2	535	7	958	0.617
0007179	transforming growth factor beta receptor signaling pathway	5	1497	4	1483	0.988	1	536	4	961	0.788
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	14	1488	18	1469	0.574	3	534	11	954	0.399
0007173	epidermal growth factor receptor signaling pathway	4	1498	4	1483	0.734	0	537	4	961	0.331
0008286	insulin receptor signaling pathway	1	1501	3	1484	0.61	0	537	1	964	0.766
0008293	torso signaling pathway	2	1500	5	1482	0.441	1	536	1	964	0.751
0007186	G-protein coupled receptor protein signaling pathway	41	1461	30	1457	0.247	14	523	27	938	0.958
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	4	1498	1	1486	0.377	1	536	3	962	0.942
0007219	Notch signaling pathway	9	1493	4	1483	0.274	1	536	8	957	0.231
0007224	smoothened signaling pathway	3	1499	3	1484	0.692	0	537	3	962	0.49
0008063	Toll signaling pathway	2	1500	2	1485	0.624	0	537	2	963	0.751
0016055	Wnt receptor signaling pathway	9	1493	7	1480	0.818	1	536	8	957	0.231
0007242	intracellular signaling cascade	98	1404	84	1403	0.355	31	506	67	898	0.441
0007263	nitric oxide mediated signal transduction	2	1500	2	1485	0.624	1	536	1	964	0.751
0007243	protein kinase cascade	25	1477	16	1471	0.22	6	531	19	946	0.305
0007259	JAK-STAT cascade	3	1499	3	1484	0.692	0	537	3	962	0.49
0000165	MAPKKK cascade	22	1480	11	1476	0.085	6	531	16	949	0.541
0019932	second-messenger-mediated signaling	12	1490	10	1477	0.849	7	530	5	960	0.181
0019722	calcium-mediated signaling	8	1494	7	1480	0.984	6	531	2	963	0.051
0048015	phosphoinositide-mediated signaling	4	1498	1	1486	0.377	1	536	3	962	0.942
0007264	small GTPase mediated signal transduction	28	1474	16	1471	0.102	11	526	17	948	0.846
0007265	Ras protein signal transduction	5	1497	5	1482	0.764	2	535	3	962	0.788
0009966	regulation of signal transduction	20	1482	14	1473	0.405	5	532	15	950	0.438
0007275	development	229	1273	231	1256	0.867	75	462	154	811	0.34
0007568	aging	5	1497	6	1481	0.987	2	535	3	962	0.788
0030154	cell differentiation	63	1439	56	1431	0.613	17	520	46	919	0.177
0048468	cell development	39	1463	36	1451	0.849	13	524	26	939	0.881
0000904	cellular morphogenesis during differentiation	9	1493	10	1477	0.982	4	533	5	960	0.844
0042461	photoreceptor cell development	9	1493	9	1478	0.83	4	533	5	960	0.844
0042051	eye photoreceptor development (sensu Endopterygota)	9	1493	8	1479	0.983	4	533	5	960	0.844
0045165	cell fate commitment	24	1478	25	1462	0.972	7	530	17	948	0.643

PC7

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	16	1486	14	1473	0.876	4	533	12	953	0.522
0007400	neuroblast cell fate determination	6	1496	2	1485	0.295	1	536	5	960	0.582
0001708	cell fate specification	2	1500	6	1481	0.282	0	537	2	963	0.751
0007349	cellularization	7	1495	4	1483	0.557	2	535	5	960	0.998
0040007	growth	14	1488	22	1465	0.229	4	533	10	955	0.777
0002164	larval development	12	1490	5	1482	0.15	4	533	8	957	0.899
0002165	larval or pupal development (sensu Insecta)	67	1435	62	1425	0.763	**14**	**523**	**53**	**912**	**0.014**
0007552	metamorphosis	60	1442	61	1426	0.955	**11**	**526**	**49**	**916**	**0.006**
0009653	morphogenesis	157	1345	162	1325	0.74	48	489	109	856	0.179
0002009	morphogenesis of an epithelium	24	1478	20	1467	0.673	4	533	20	945	0.08
0009887	organogenesis	139	1363	143	1344	0.782	42	495	97	868	0.181
0001654	eye morphogenesis	24	1478	33	1454	0.268	6	531	18	947	0.372
0008406	gonad development	4	1498	7	1480	0.535	2	535	2	963	0.942
0007444	imaginal disc development	43	1459	50	1437	0.496	**7**	**530**	**36**	**929**	**0.011**
0007494	midgut development	1	1501	4	1483	0.365	0	537	1	964	0.766
0007517	muscle development	16	1486	18	1469	0.84	6	531	10	955	0.908
0007399	neurogenesis	**95**	**1407**	**67**	**1420**	**0.034**	27	510	68	897	0.153
0007409	axonogenesis	25	1477	18	1469	0.374	4	533	21	944	0.062
0007411	axon guidance	17	1485	16	1471	0.977	4	533	13	952	0.422
0007417	central nervous system development	21	1481	18	1469	0.771	8	529	13	952	0.997
0016358	dendrite morphogenesis	8	1494	6	1481	0.803	3	534	5	960	0.79
0042063	gliogenesis	7	1495	4	1483	0.557	0	537	7	958	0.113
0007422	peripheral nervous system development	25	1477	15	1472	0.161	8	529	17	948	0.854
0050767	regulation of neurogenesis	3	1499	2	1485	0.991	1	536	2	963	0.606
0007424	tracheal system development (sensu Insecta)	20	1482	17	1470	0.764	6	531	14	951	0.76
0048513	organ development	141	1361	145	1342	0.783	42	495	99	866	0.144
0007389	pattern specification	35	1467	41	1446	0.532	9	528	26	939	0.282
0048066	pigmentation	5	1497	6	1481	0.987	3	534	2	963	0.506
0009791	post-embryonic development	12	1490	5	1482	0.15	4	533	8	957	0.899
0009790	embryonic development	51	1451	49	1438	0.96	14	523	37	928	0.267
0007530	sex determination	6	1496	4	1483	0.764	1	536	5	960	0.582
0007548	sex differentiation	6	1496	13	1474	0.161	3	534	3	962	0.762
0019827	stem cell maintenance	4	1498	4	1483	0.734	0	537	4	961	0.331
0000003	reproduction	68	1434	76	1411	0.509	**15**	**522**	**53**	**912**	**0.023**
0050793	regulation of development	19	1483	24	1463	0.517	3	534	16	949	0.113
0007582	physiological process	804	698	801	686	0.882	**268**	**269**	**536**	**429**	**0.041**
0008152	metabolism	567	935	599	888	0.167	192	345	375	590	0.257
0009056	catabolism	105	1397	104	1383	0.946	38	499	67	898	0.993
0006091	energy pathways	57	1445	51	1436	0.662	**36**	**501**	**21**	**944**	**2E-05**
0006118	electron transport	31	1471	24	1463	0.436	**17**	**520**	**14**	**951**	**0.04**
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	**196**	**1306**	**236**	**1251**	**0.032**	63	474	133	832	0.293
0006259	DNA metabolism	37	1465	42	1445	0.616	11	526	26	939	0.548
0006350	transcription	113	1389	114	1373	0.937	**30**	**507**	**83**	**882**	**0.043**
0043170	macromolecule metabolism	303	1199	325	1162	0.278	**82**	**455**	**221**	**744**	**5E-04**
0019538	protein metabolism	254	1248	273	1214	0.322	**61**	**476**	**193**	**772**	**3E-05**
0006412	protein biosynthesis	53	1449	57	1430	0.73	14	523	39	926	0.194
0006464	protein modification	122	1380	134	1353	0.422	**29**	**508**	**93**	**872**	**0.005**
0006457	protein folding	22	1480	21	1466	0.974	5	532	17	948	0.289
0005975	carbohydrate metabolism	51	1451	56	1431	0.655	21	516	30	935	0.501
0006519	amino acid and derivative metabolism	35	1467	35	1452	0.937	15	522	20	945	0.478
0006629	lipid metabolism	42	1460	47	1440	0.632	13	524	29	936	0.621
0009308	amine metabolism	40	1462	41	1446	0.963	16	521	24	941	0.688
0042440	pigment metabolism	6	1496	6	1481	0.786	4	533	2	963	0.248
0042445	hormone metabolism	3	1499	4	1483	0.989	1	536	2	963	0.606
0009058	biosynthesis	104	1398	100	1387	0.886	42	495	62	903	0.36
0019748	secondary metabolism	7	1495	7	1480	0.803	5	532	2	963	0.114
0019222	regulation of metabolism	120	1382	118	1369	0.99	**28**	**509**	**92**	**873**	**0.004**
0016265	death	48	1454	38	1449	0.348	11	526	37	928	0.083
0008219	cell death	42	1460	32	1455	0.31	**8**	**529**	**34**	**931**	**0.033**
0016271	tissue death	17	1485	10	1477	0.257	4	533	13	952	0.422
0042592	homeostasis	17	1485	12	1475	0.472	8	529	9	956	0.469
0019725	cell homeostasis	14	1488	12	1475	0.864	7	530	7	958	0.402
0050801	ion homeostasis	8	1494	6	1481	0.803	4	533	4	961	0.636
0043062	extracellular structure organization and biogenesis	10	1492	9	1478	0.982	1	536	9	956	0.169
0046903	secretion	57	1445	44	1443	0.245	19	518	38	927	0.804
0048511	rhythmic process	7	1495	10	1477	0.612	2	535	5	960	0.998

PC7

GO#	GO term	Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
		term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	189	1313	158	1329	0.107	**41**	**496**	**148**	**817**	**2E-05**
0050874	organismal physiological process	115	1387	117	1370	0.882	49	488	66	899	0.135
0050875	cellular physiological process	756	746	763	724	0.618	**248**	**289**	**508**	**457**	**0.019**
0006810	transport	196	1306	202	1285	0.706	67	470	129	836	0.681
0006811	ion transport	58	1444	62	1425	0.737	**34**	**503**	**24**	**941**	**4E-04**
0006818	hydrogen transport	9	1493	9	1478	0.83	**8**	**529**	**1**	**964**	**0.003**
0006836	neurotransmitter transport	1	1501	4	1483	0.365	1	536	0	965	0.766
0006858	extracellular transport	5	1497	10	1477	0.291	3	534	2	963	0.506
0006869	lipid transport	7	1495	9	1478	0.787	1	536	6	959	0.428
0008643	carbohydrate transport	6	1496	9	1478	0.591	1	536	5	960	0.582
0015031	protein transport	98	1404	82	1405	0.278	**20**	**517**	**78**	**887**	**0.002**
0015837	amine transport	3	1499	9	1478	0.143	2	535	1	964	0.606
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	4	1498	9	1478	0.258	1	536	3	962	0.942
0016192	vesicle-mediated transport	65	1437	54	1433	0.379	20	517	45	920	0.469
0045045	secretory pathway	55	1447	40	1447	0.159	18	519	37	928	0.739
0046907	intracellular transport	103	1399	95	1392	0.659	**22**	**515**	**81**	**884**	**0.002**
0051049	regulation of transport	**15**	**1487**	**3**	**1484**	**0.01**	5	532	10	955	0.941
0008283	cell proliferation	36	1466	35	1452	0.966	9	528	27	938	0.235
0007049	cell cycle	59	1443	69	1418	0.384	**7**	**530**	**52**	**913**	**2E-04**
0017145	stem cell division	8	1494	4	1483	0.395	1	536	7	958	0.314
0016043	cell organization and biogenesis	140	1362	135	1352	0.868	**36**	**501**	**104**	**861**	**0.012**
0000902	cellular morphogenesis	41	1461	39	1448	0.946	13	524	28	937	0.702
0006996	organelle organization and biogenesis	119	1383	119	1368	0.99	**24**	**513**	**95**	**870**	**3E-04**
0007010	cytoskeleton organization and biogenesis	83	1419	87	1400	0.761	**19**	**518**	**64**	**901**	**0.017**
0006997	nuclear organization and biogenesis	4	1498	6	1481	0.739	0	537	4	961	0.331
0007028	cytoplasm organization and biogenesis	9	1493	10	1477	0.982	3	534	6	959	0.844
0016044	membrane organization and biogenesis	4	1498	5	1482	0.988	0	537	4	961	0.331
0051128	regulation of cell organization and biogenesis	5	1497	6	1481	0.987	0	537	5	960	0.229
0016049	cell growth	2	1500	7	1480	0.177	1	536	1	964	0.751
0050896	response to stimulus	89	1413	92	1395	0.824	30	507	59	906	0.763
0006950	response to stress	32	1470	27	1460	0.626	9	528	23	942	0.469
0009408	response to heat	8	1494	2	1485	0.117	4	533	4	961	0.636
0006979	response to oxidative stress	1	1501	1	1486	0.484	0	537	1	964	0.766
0051179	localization	210	1292	219	1268	0.596	72	465	138	827	0.689
0006403	RNA localization	15	1487	17	1470	0.837	6	531	9	956	0.941
0008104	protein localization	107	1395	88	1399	0.207	**22**	**515**	**85**	**880**	**1E-03**
0051234	establishment of localization	198	1304	205	1282	0.667	68	469	130	835	0.716
0051235	maintenance of localization	2	1500	2	1485	0.624	1	536	1	964	0.751
0050789	regulation of biological process	220	1282	183	1304	0.069	**52**	**485**	**168**	**797**	**7E-05**
0050790	regulation of enzyme activity	6	1496	8	1479	0.774	2	535	4	961	0.762
0040029	regulation of gene expression, epigenetic	10	1492	10	1477	0.84	3	534	7	958	0.96
0006306	DNA methylation	2	1500	5	1482	0.441	2	535	0	965	0.247
0045814	negative regulation of gene expression, epigenetic	5	1497	2	1485	0.457	1	536	4	961	0.788
0006342	chromatin silencing	5	1497	2	1485	0.457	1	536	4	961	0.788
0003674	molecular_function	870	632	862	625	0.991	303	234	567	398	0.411
0016209	antioxidant activity	7	1495	2	1485	0.187	4	533	3	962	0.43
0005488	binding	496	1006	511	976	0.461	**148**	**389**	**348**	**617**	**1E-03**
0005509	calcium ion binding	36	1466	25	1462	0.21	17	520	19	946	0.201
0030246	carbohydrate binding	10	1492	5	1482	0.31	1	536	9	956	0.169
0008289	lipid binding	10	1492	16	1471	0.312	3	534	7	958	0.96
0003676	nucleic acid binding	177	1325	212	1275	0.051	**47**	**490**	**130**	**835**	**0.008**
0003677	DNA binding	85	1417	109	1378	0.075	27	510	58	907	0.501
0003682	chromatin binding	16	1486	7	1480	0.099	4	533	12	953	0.522
0003700	transcription factor activity	36	1466	50	1437	0.142	16	521	20	945	0.355
0003723	RNA binding	58	1444	61	1426	0.808	**10**	**527**	**48**	**917**	**0.004**
0008135	translation factor activity, nucleic acid binding	20	1482	15	1472	0.516	5	532	15	950	0.438
0000166	nucleotide binding	136	1366	119	1368	0.335	42	495	94	871	0.251
0005515	protein binding	185	1317	194	1293	0.586	**41**	**496**	**144**	**821**	**5E-05**
0008134	transcription factor binding	15	1487	16	1471	0.978	**1**	**536**	**14**	**951**	**0.036**
0008092	cytoskeletal protein binding	43	1459	45	1442	0.876	11	526	32	933	0.211
0003779	actin binding	30	1472	23	1464	0.427	8	529	22	943	0.392
0003824	catalytic activity	446	1056	393	1094	0.052	159	378	287	678	0.996
0016787	hydrolase activity	**207**	**1295**	**165**	**1322**	**0.03**	67	470	140	825	0.309
0003924	GTPase activity	**29**	**1473**	**11**	**1476**	**0.007**	11	526	18	947	0.959
0004518	nuclease activity	5	1497	10	1477	0.291	0	537	5	960	0.229

		PC7									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	62	1440	56	1431	0.679	18	519	44	921	0.321
0004721	phosphoprotein phosphatase activity	17	1485	13	1474	0.601	2	535	15	950	0.069
0016740	transferase activity	120	1382	121	1366	0.935	39	498	81	884	0.499
0016301	kinase activity	74	1428	61	1426	0.319	22	515	52	913	0.325
0004672	protein kinase activity	48	1454	47	1440	0.96	14	523	34	931	0.415
0030234	enzyme regulator activity	53	1449	52	1435	0.958	18	519	35	930	0.896
0003774	motor activity	15	1487	13	1474	0.87	7	530	8	957	0.538
0004871	signal transducer activity	133	1369	123	1364	0.614	53	484	80	885	0.348
0004872	receptor activity	54	1448	55	1432	0.957	**29**	**508**	**25**	**940**	**0.008**
0004879	ligand-dependent nuclear receptor activity	4	1498	5	1482	0.988	2	535	2	963	0.942
0004888	transmembrane receptor activity	36	1466	38	1449	0.872	18	519	18	947	0.103
0004930	G-protein coupled receptor activity	15	1487	15	1472	0.876	8	529	7	958	0.247
0005057	receptor signaling protein activity	35	1467	45	1442	0.287	10	527	25	940	0.472
0005102	receptor binding	34	1468	35	1452	0.966	11	526	23	942	0.812
0005198	structural molecule activity	79	1423	83	1404	0.758	27	510	52	913	0.858
0030528	transcription regulator activity	96	1406	103	1384	0.608	26	511	70	895	0.085
0045182	translation regulator activity	20	1482	15	1472	0.516	5	532	15	950	0.438
0005215	transporter activity	128	1374	125	1362	0.962	**62**	**475**	**66**	**899**	**0.002**
0005489	electron transporter activity	16	1486	13	1474	0.729	7	530	9	956	0.683
0005216	ion channel activity	24	1478	28	1459	0.648	**14**	**523**	**10**	**955**	**0.035**
0005244	voltage-gated ion channel activity	10	1492	16	1471	0.312	5	532	5	960	0.54
0005575	cellular_component	608	894	615	872	0.652	204	333	404	561	0.158
0005623	cell	550	952	562	925	0.53	188	349	362	603	0.363
0005622	intracellular	428	1074	429	1058	0.862	**136**	**401**	**292**	**673**	**0.049**
0005737	cytoplasm	240	1262	218	1269	0.342	84	453	156	809	0.848
0016023	cytoplasmic vesicle	20	1482	21	1466	0.974	8	529	12	953	0.87
0005829	cytosol	42	1460	37	1450	0.681	9	528	33	932	0.072
0005783	endoplasmic reticulum	**37**	**1465**	**20**	**1467**	**0.036**	**4**	**533**	**33**	**932**	**0.002**
0005794	Golgi apparatus	12	1490	13	1474	0.98	2	535	10	955	0.279
0005815	microtubule organizing center	3	1499	6	1481	0.495	0	537	3	962	0.49
0005739	mitochondrion	55	1447	50	1437	0.73	**35**	**502**	**20**	**945**	**2E-05**
0005840	ribosome	9	1493	15	1472	0.294	4	533	5	960	0.844
0005773	vacuole	7	1495	7	1480	0.803	4	533	3	962	0.43
0005764	lysosome	2	1500	3	1484	0.991	0	537	2	963	0.751
0005856	cytoskeleton	38	1464	47	1440	0.354	11	526	27	938	0.475
0005694	chromosome	24	1478	16	1471	0.279	7	530	17	948	0.643
0000228	nuclear chromosome	1	1501	4	1483	0.365	1	536	0	965	0.766
0005634	nucleus	180	1322	192	1295	0.476	**44**	**493**	**136**	**829**	**1E-03**
0005635	nuclear membrane	11	1491	6	1481	0.341	1	536	10	955	0.125
0005730	nucleolus	2	1500	9	1478	0.067	0	537	2	963	0.751
0005654	nucleoplasm	35	1467	37	1450	0.871	13	524	22	943	0.996
0005777	peroxisome	6	1496	3	1484	0.514	1	536	5	960	0.582
0005886	plasma membrane	84	1418	72	1415	0.401	35	502	49	916	0.295
0005576	extracellular region	42	1460	34	1453	0.442	17	520	25	940	0.628
0005578	extracellular matrix (sensu Metazoa)	21	1481	14	1473	0.322	12	525	9	956	0.067

PC8

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	955	620	799	615	0.024	**324**	**289**	**631**	**331**	**6E-07**
0007610	behavior	**71**	**1504**	**91**	**1323**	**0.025**	25	588	46	916	0.595
0030534	adult behavior	12	1563	12	1402	0.952	4	609	8	954	0.919
0030537	larval behavior	7	1568	2	1412	0.24	4	609	3	959	0.547
0007611	learning and/or memory	11	1564	13	1401	0.638	6	607	5	957	0.449
0007612	learning	6	1569	9	1405	0.467	3	610	3	959	0.89
0007613	memory	4	1571	7	1407	0.433	1	612	3	959	0.953
0007626	locomotory behavior	**50**	**1525**	**73**	**1341**	**0.008**	19	594	31	931	0.991
0007635	chemosensory behavior	7	1568	11	1403	0.347	2	611	5	957	0.862
0007622	rhythmic behavior	10	1565	5	1409	0.408	2	611	8	954	0.365
0048512	circadian behavior	9	1566	5	1409	0.547	2	611	7	955	0.492
0009987	cellular process	879	696	749	665	0.129	**298**	**315**	**581**	**381**	**6E-06**
0007154	cell communication	**235**	**1340**	**254**	**1160**	**0.028**	**116**	**497**	**119**	**843**	**5E-04**
0007155	cell adhesion	**32**	**1543**	**58**	**1356**	**0.001**	17	596	15	947	0.138
0008037	cell recognition	1	1574	1	1413	0.527	0	613	1	961	0.82
0008038	neuronal cell recognition	1	1574	1	1413	0.527	0	613	1	961	0.82
0016337	cell-cell adhesion	**13**	**1562**	**26**	**1388**	**0.023**	**10**	**603**	**3**	**959**	**0.011**
0016339	calcium-dependent cell-cell adhesion	1	1574	6	1408	0.097	1	612	0	962	0.82
0007156	homophilic cell adhesion	2	1573	7	1407	0.134	1	612	1	961	0.686
0007160	cell-matrix adhesion	3	1572	6	1408	0.406	3	610	0	962	0.114
0007267	cell-cell signaling	73	1502	83	1331	0.152	**39**	**574**	**34**	**928**	**0.013**
0019226	transmission of nerve impulse	68	1507	70	1344	0.462	**38**	**575**	**30**	**932**	**0.005**
0007268	synaptic transmission	48	1527	53	1361	0.339	**28**	**585**	**20**	**942**	**0.008**
0007270	nerve-nerve synaptic transmission	10	1565	6	1408	0.591	6	607	4	958	0.295
0001505	regulation of neurotransmitter levels	28	1547	32	1382	0.416	15	598	13	949	0.159
0042133	neurotransmitter metabolism	5	1570	3	1411	0.84	4	609	1	961	0.153
0007269	neurotransmitter secretion	24	1551	29	1385	0.341	11	602	13	949	0.625
0007165	signal transduction	192	1383	187	1227	0.427	**89**	**524**	**103**	**859**	**0.03**
0007166	cell surface receptor linked signal transduction	75	1500	82	1332	0.235	31	582	44	918	0.751
0007167	enzyme linked receptor protein signaling pathway	20	1555	26	1388	0.266	8	605	12	950	0.896
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	10	1565	6	1408	0.591	1	612	9	953	0.12
0007179	transforming growth factor beta receptor signaling pathway	5	1570	4	1410	0.871	0	613	5	957	0.184
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	**10**	**1565**	**22**	**1392**	**0.024**	7	606	3	959	0.09
0007173	epidermal growth factor receptor signaling pathway	1	1574	7	1407	0.054	1	612	0	962	0.82
0008286	insulin receptor signaling pathway	2	1573	2	1412	0.694	1	612	1	961	0.686
0008293	torso signaling pathway	3	1572	4	1410	0.886	1	612	2	960	0.694
0007186	G-protein coupled receptor protein signaling pathway	34	1541	37	1377	0.484	17	596	17	945	0.245
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	3	1572	2	1412	0.904	1	612	2	960	0.694
0007219	Notch signaling pathway	6	1569	7	1407	0.845	1	612	5	957	0.483
0007224	smoothened signaling pathway	5	1570	1	1413	0.273	1	612	4	958	0.682
0008063	Toll signaling pathway	3	1572	1	1413	0.694	1	612	2	960	0.694
0016055	Wnt receptor signaling pathway	**4**	**1571**	**12**	**1402**	**0.048**	2	611	2	960	0.953
0007242	intracellular signaling cascade	87	1488	95	1319	0.198	40	573	47	915	0.202
0007263	nitric oxide mediated signal transduction	0	1575	4	1410	0.107	0	613	0	962	-
0007243	protein kinase cascade	19	1556	22	1392	0.507	8	605	11	951	0.96
0007259	JAK-STAT cascade	3	1572	3	1411	0.782	0	613	3	959	0.429
0000165	MAPKKK cascade	16	1559	17	1397	0.755	8	605	8	954	0.512
0019932	second-messenger-mediated signaling	14	1561	8	1406	0.414	6	607	8	954	0.978
0019722	calcium-mediated signaling	11	1564	4	1410	0.178	5	608	6	956	0.892
0048015	phosphoinositide-mediated signaling	3	1572	2	1412	0.904	1	612	2	960	0.694
0007264	small GTPase mediated signal transduction	22	1553	22	1392	0.835	8	605	14	948	0.978
0007265	Ras protein signal transduction	4	1571	6	1408	0.625	2	611	2	960	0.953
0009966	regulation of signal transduction	16	1559	18	1396	0.625	7	606	9	953	0.888
0007275	development	232	1343	228	1186	0.315	80	533	152	810	0.153
0007568	aging	8	1567	3	1411	0.303	2	611	6	956	0.656
0030154	cell differentiation	54	1521	65	1349	0.124	18	595	36	926	0.475
0048468	cell development	33	1542	42	1372	0.159	9	604	24	938	0.228
0000904	cellular morphogenesis during differentiation	8	1567	11	1403	0.486	3	610	5	957	0.779
0042461	photoreceptor cell development	8	1567	10	1404	0.641	3	610	5	957	0.779
0042051	eye photoreceptor development (sensu Endopterygota)	7	1568	10	1404	0.478	3	610	4	958	0.862
0045165	cell fate commitment	19	1556	30	1384	0.068	7	606	12	950	0.96

PC8

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	12	1563	18	1396	0.224	5	608	7	955	0.919
0007400	neuroblast cell fate determination	4	1571	4	1410	0.84	2	611	2	960	0.953
0001708	cell fate specification	3	1572	5	1409	0.612	1	612	2	960	0.694
0007349	cellularization	6	1569	5	1409	0.858	1	612	5	957	0.483
0040007	growth	17	1558	19	1395	0.622	3	610	14	948	0.119
0002164	larval development	9	1566	8	1406	0.823	1	612	8	954	0.17
0002165	larval or pupal development (sensu Insecta)	66	1509	63	1351	0.79	**15**	**598**	**51**	**911**	**0.009**
0007552	metamorphosis	61	1514	60	1354	0.675	**14**	**599**	**47**	**915**	**0.013**
0009653	morphogenesis	158	1417	161	1253	0.255	56	557	102	860	0.39
0002009	morphogenesis of an epithelium	20	1555	24	1390	0.414	**2**	**611**	**18**	**944**	**0.015**
0009887	organogenesis	137	1438	145	1269	0.164	53	560	84	878	0.974
0001654	eye morphogenesis	25	1550	32	1382	0.224	7	606	18	944	0.356
0008406	gonad development	3	1572	8	1406	0.165	1	612	2	960	0.694
0007444	imaginal disc development	**37**	**1538**	**56**	**1358**	**0.015**	9	604	28	934	0.094
0007494	midgut development	4	1571	1	1413	0.438	3	610	1	961	0.333
0007517	muscle development	19	1556	15	1399	0.84	8	605	11	951	0.96
0007399	neurogenesis	**70**	**1505**	**92**	**1322**	**0.016**	30	583	40	922	0.572
0007409	axonogenesis	**15**	**1560**	**28**	**1386**	**0.028**	5	608	10	952	0.857
0007411	axon guidance	**10**	**1565**	**23**	**1391**	**0.016**	3	610	7	955	0.799
0007417	central nervous system development	19	1556	20	1394	0.735	9	604	10	952	0.601
0016358	dendrite morphogenesis	5	1570	9	1405	0.314	2	611	3	959	0.682
0042063	gliogenesis	4	1571	7	1407	0.433	3	610	1	961	0.333
0007422	peripheral nervous system development	18	1557	22	1392	0.411	6	607	12	950	0.806
0050767	regulation of neurogenesis	3	1572	2	1412	0.904	1	612	2	960	0.694
0007424	tracheal system development (sensu Insecta)	21	1554	16	1398	0.74	6	607	15	947	0.451
0048513	organ development	140	1435	146	1268	0.204	55	558	85	877	0.998
0007389	pattern specification	**31**	**1544**	**45**	**1369**	**0.047**	9	604	22	940	0.34
0048066	pigmentation	6	1569	5	1409	0.858	4	609	2	960	0.329
0009791	post-embryonic development	9	1566	8	1406	0.823	1	612	8	954	0.17
0009790	embryonic development	46	1529	54	1360	0.207	15	598	31	931	0.461
0007530	sex determination	3	1572	7	1407	0.262	1	612	2	960	0.694
0007548	sex differentiation	8	1567	11	1403	0.486	3	610	5	957	0.779
0019827	stem cell maintenance	3	1572	5	1409	0.612	0	613	3	959	0.429
0000003	reproduction	67	1508	77	1337	0.152	18	595	49	913	0.052
0050793	regulation of development	20	1555	23	1391	0.507	5	608	15	947	0.292
0007582	physiological process	**873**	**702**	**732**	**682**	**0.049**	**291**	**322**	**582**	**380**	**5E-07**
0008152	metabolism	635	940	531	883	0.131	**195**	**418**	**440**	**522**	**5E-08**
0009056	catabolism	121	1454	88	1326	0.136	**34**	**579**	**87**	**875**	**0.015**
0006091	energy pathways	**72**	**1503**	**36**	**1378**	**0.004**	22	591	50	912	0.172
0006118	electron transport	36	1539	19	1395	0.076	9	604	27	935	0.119
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	222	1353	210	1204	0.593	**67**	**546**	**155**	**807**	**0.005**
0006259	DNA metabolism	39	1536	40	1374	0.627	14	599	25	937	0.821
0006350	transcription	**103**	**1472**	**124**	**1290**	**0.026**	37	576	66	896	0.588
0043170	macromolecule metabolism	**357**	**1218**	**271**	**1143**	**0.021**	**89**	**524**	**268**	**694**	**1E-09**
0019538	protein metabolism	296	1279	231	1183	0.087	**75**	**538**	**221**	**741**	**2E-07**
0006412	protein biosynthesis	**73**	**1502**	**37**	**1377**	**0.005**	**12**	**601**	**61**	**901**	**9E-05**
0006464	protein modification	120	1455	136	1278	0.06	37	576	83	879	0.073
0006457	protein folding	27	1548	16	1398	0.237	**3**	**610**	**24**	**938**	**0.005**
0005975	carbohydrate metabolism	66	1509	41	1373	0.072	**17**	**596**	**49**	**913**	**0.035**
0006519	amino acid and derivative metabolism	41	1534	29	1385	0.381	16	597	25	937	0.882
0006629	lipid metabolism	50	1525	39	1375	0.575	18	595	32	930	0.777
0009308	amine metabolism	46	1529	35	1379	0.525	17	596	29	933	0.901
0042440	pigment metabolism	7	1568	5	1409	0.918	3	610	4	958	0.862
0042445	hormone metabolism	4	1571	3	1411	0.886	2	611	2	960	0.953
0009058	biosynthesis	**126**	**1449**	**78**	**1336**	**0.009**	**33**	**580**	**93**	**869**	**0.003**
0019748	secondary metabolism	8	1567	6	1408	0.947	3	610	5	957	0.779
0019222	regulation of metabolism	117	1458	121	1293	0.284	37	576	80	882	0.113
0016265	death	49	1526	37	1377	0.485	**11**	**602**	**38**	**924**	**0.024**
0008219	cell death	41	1534	33	1381	0.722	**9**	**604**	**32**	**930**	**0.036**
0016271	tissue death	18	1557	9	1405	0.205	3	610	15	947	0.088
0042592	homeostasis	16	1559	13	1401	0.935	8	605	8	954	0.512
0019725	cell homeostasis	15	1560	11	1403	0.752	7	606	8	954	0.725
0050801	ion homeostasis	10	1565	4	1410	0.255	7	606	3	959	0.09
0043062	extracellular structure organization and biogenesis	10	1565	9	1405	0.822	4	609	6	956	0.799
0046903	secretion	58	1517	43	1371	0.386	16	597	42	920	0.096
0048511	rhythmic process	11	1564	6	1408	0.452	2	611	9	953	0.269

PC8

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	**165**	**1410**	**182**	**1232**	**0.047**	**49**	**564**	**116**	**846**	**0.013**
0050874	organismal physiological process	121	1454	111	1303	0.918	**64**	**549**	**57**	**905**	**0.001**
0050875	cellular physiological process	826	749	693	721	0.066	**271**	**342**	**555**	**407**	**2E-07**
0006810	transport	**230**	**1345**	**168**	**1246**	**0.033**	**104**	**509**	**126**	**836**	**0.041**
0006811	ion transport	71	1504	49	1365	0.175	**54**	**559**	**17**	**945**	**1E-10**
0006818	hydrogen transport	10	1565	8	1406	0.994	6	607	4	958	0.295
0006836	neurotransmitter transport	3	1572	2	1412	0.904	3	610	0	962	0.114
0006858	extracellular transport	10	1565	5	1409	0.408	6	607	4	958	0.295
0006869	lipid transport	8	1567	8	1406	0.972	2	611	6	956	0.656
0008643	carbohydrate transport	8	1567	7	1407	0.834	3	610	5	957	0.779
0015031	protein transport	107	1468	73	1341	0.073	**31**	**582**	**76**	**886**	**0.037**
0015837	amine transport	5	1570	7	1407	0.633	3	610	2	960	0.611
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	8	1567	5	1409	0.718	3	610	5	957	0.779
0016192	vesicle-mediated transport	65	1510	54	1360	0.737	22	591	43	919	0.467
0045045	secretory pathway	54	1521	41	1373	0.472	15	598	39	923	0.117
0046907	intracellular transport	114	1461	84	1330	0.177	**31**	**582**	**83**	**879**	**0.01**
0051049	regulation of transport	8	1567	10	1404	0.641	2	611	6	956	0.656
0008283	cell proliferation	**27**	**1548**	**44**	**1370**	**0.017**	10	603	17	945	0.997
0007049	cell cycle	**56**	**1519**	**72**	**1342**	**0.048**	**14**	**599**	**42**	**920**	**0.042**
0017145	stem cell division	7	1568	5	1409	0.918	1	612	6	956	0.341
0016043	cell organization and biogenesis	**128**	**1447**	**147**	**1267**	**0.038**	41	572	87	875	0.116
0000902	cellular morphogenesis	36	1539	44	1370	0.199	9	604	27	935	0.119
0006996	organelle organization and biogenesis	**110**	**1465**	**128**	**1286**	**0.044**	**32**	**581**	**78**	**884**	**0.037**
0007010	cytoskeleton organization and biogenesis	78	1497	92	1322	0.08	22	591	56	906	0.061
0006997	nuclear organization and biogenesis	5	1570	5	1409	0.884	0	613	5	957	0.184
0007028	cytoplasm organization and biogenesis	9	1566	10	1404	0.814	2	611	7	955	0.492
0016044	membrane organization and biogenesis	2	1573	7	1407	0.134	1	612	1	961	0.686
0051128	regulation of cell organization and biogenesis	6	1569	5	1409	0.858	1	612	5	957	0.483
0016049	cell growth	4	1571	5	1409	0.871	2	611	2	960	0.953
0050896	response to stimulus	91	1484	90	1324	0.552	39	574	52	910	0.495
0006950	response to stress	30	1545	29	1385	0.877	**5**	**608**	**25**	**937**	**0.02**
0009408	response to heat	5	1570	5	1409	0.884	0	613	5	957	0.184
0006979	response to oxidative stress	2	1573	0	1414	0.527	1	612	1	961	0.686
0051179	localization	**251**	**1324**	**178**	**1236**	**0.011**	109	504	142	820	0.127
0006403	RNA localization	17	1558	15	1399	0.898	4	609	13	949	0.29
0008104	protein localization	115	1460	80	1334	0.081	**32**	**581**	**83**	**879**	**0.015**
0051234	establishment of localization	**234**	**1341**	**169**	**1245**	**0.023**	105	508	129	833	0.051
0051235	maintenance of localization	2	1573	2	1412	0.694	0	613	2	960	0.686
0050789	regulation of biological process	**191**	**1384**	**212**	**1202**	**0.025**	**59**	**554**	**132**	**830**	**0.019**
0050790	regulation of enzyme activity	5	1570	9	1405	0.314	1	612	4	958	0.682
0040029	regulation of gene expression, epigenetic	11	1564	9	1405	0.986	5	608	6	956	0.892
0006306	DNA methylation	5	1570	2	1412	0.539	2	611	3	959	0.682
0045814	negative regulation of gene expression, epigenetic	4	1571	3	1411	0.886	2	611	2	960	0.953
0006342	chromatin silencing	4	1571	3	1411	0.886	2	611	2	960	0.953
0003674	molecular_function	934	641	798	616	0.122	**318**	**295**	**616**	**346**	**2E-06**
0016209	antioxidant activity	7	1568	2	1412	0.24	2	611	5	957	0.862
0005488	binding	533	1042	474	940	0.884	**165**	**448**	**368**	**594**	**5E-06**
0005509	calcium ion binding	26	1549	35	1379	0.144	13	600	13	949	0.334
0030246	carbohydrate binding	5	1570	10	1404	0.213	1	612	4	958	0.682
0008289	lipid binding	10	1565	16	1398	0.207	6	607	4	958	0.295
0003676	nucleic acid binding	220	1355	169	1245	0.114	**59**	**554**	**161**	**801**	**1E-04**
0003677	DNA binding	91	1484	103	1311	0.111	36	577	55	907	0.985
0003682	chromatin binding	9	1566	14	1400	0.272	5	608	4	958	0.494
0003700	transcription factor activity	41	1534	45	1369	0.403	21	592	20	942	0.14
0003723	RNA binding	**74**	**1501**	**45**	**1369**	**0.043**	**13**	**600**	**61**	**901**	**2E-04**
0008135	translation factor activity, nucleic acid binding	**31**	**1544**	**4**	**1410**	**4E-05**	**3**	**610**	**28**	**934**	**0.001**
0000166	nucleotide binding	139	1436	116	1298	0.588	**40**	**573**	**99**	**863**	**0.013**
0005515	protein binding	191	1384	188	1226	0.366	**51**	**562**	**140**	**822**	**3E-04**
0008134	transcription factor binding	15	1560	16	1398	0.763	**1**	**612**	**14**	**948**	**0.021**
0008092	cytoskeletal protein binding	43	1532	45	1369	0.534	**10**	**603**	**33**	**929**	**0.048**
0003779	actin binding	26	1549	27	1387	0.692	**4**	**609**	**22**	**940**	**0.023**
0003824	catalytic activity	450	1125	389	1025	0.546	**142**	**471**	**308**	**654**	**2E-04**
0016787	hydrolase activity	202	1373	170	1244	0.543	**62**	**551**	**140**	**822**	**0.013**
0003924	GTPase activity	21	1554	19	1395	0.893	8	605	13	949	0.883
0004518	nuclease activity	8	1567	7	1407	0.834	3	610	5	957	0.779

PC8

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	70	1505	48	1366	0.168	**18**	**595**	**52**	**910**	**0.028**
0004721	phosphoprotein phosphatase activity	11	1564	19	1395	0.113	4	609	7	955	0.892
0016740	transferase activity	119	1456	122	1292	0.313	41	572	78	884	0.346
0016301	kinase activity	**58**	**1517**	**77**	**1337**	**0.026**	23	590	35	927	0.984
0004672	protein kinase activity	**38**	**1537**	**57**	**1357**	**0.016**	16	597	22	940	0.811
0030234	enzyme regulator activity	58	1517	47	1367	0.666	21	592	37	925	0.768
0003774	motor activity	10	1565	18	1396	0.106	3	610	7	955	0.799
0004871	signal transducer activity	128	1447	128	1286	0.403	59	554	69	893	0.101
0004872	receptor activity	55	1520	54	1360	0.705	27	586	28	934	0.152
0004879	ligand-dependent nuclear receptor activity	3	1572	6	1408	0.406	1	612	2	960	0.694
0004888	transmembrane receptor activity	38	1537	36	1378	0.907	19	594	19	943	0.211
0004930	G-protein coupled receptor activity	16	1559	14	1400	0.91	6	607	10	952	0.888
0005057	receptor signaling protein activity	38	1537	42	1372	0.407	16	597	22	940	0.811
0005102	receptor binding	34	1541	35	1379	0.65	12	601	22	940	0.794
0005198	structural molecule activity	82	1493	80	1334	0.643	26	587	56	906	0.208
0030528	transcription regulator activity	93	1482	106	1308	0.095	33	580	60	902	0.554
0045182	translation regulator activity	**31**	**1544**	**4**	**1410**	**4E-05**	**3**	**610**	**28**	**934**	**0.001**
0005215	transporter activity	**153**	**1422**	**100**	**1314**	**0.012**	**77**	**536**	**76**	**886**	**0.003**
0005489	electron transporter activity	20	1555	9	1405	0.115	5	608	15	947	0.292
0005216	ion channel activity	28	1547	24	1390	0.978	**23**	**590**	**5**	**957**	**6E-06**
0005244	voltage-gated ion channel activity	14	1561	12	1402	0.937	**11**	**602**	**3**	**959**	**0.005**
0005575	cellular_component	671	904	552	862	0.052	**216**	**397**	**455**	**507**	**3E-06**
0005623	cell	**617**	**958**	**495**	**919**	**0.021**	**198**	**415**	**419**	**543**	**1E-05**
0005622	intracellular	475	1100	382	1032	0.063	**116**	**497**	**359**	**603**	**1E-14**
0005737	cytoplasm	**277**	**1298**	**181**	**1233**	**3E-04**	**51**	**562**	**226**	**736**	**2E-14**
0016023	cytoplasmic vesicle	25	1550	16	1398	0.362	6	607	19	943	0.182
0005829	cytosol	**63**	**1512**	**16**	**1398**	**2E-06**	**5**	**608**	**58**	**904**	**5E-07**
0005783	endoplasmic reticulum	**43**	**1532**	**14**	**1400**	**8E-04**	**6**	**607**	**37**	**925**	**0.001**
0005794	Golgi apparatus	11	1564	14	1400	0.501	1	612	10	952	0.084
0005815	microtubule organizing center	5	1570	4	1410	0.871	1	612	4	958	0.682
0005739	mitochondrion	**69**	**1506**	**36**	**1378**	**0.009**	**13**	**600**	**56**	**906**	**7E-04**
0005840	ribosome	14	1561	10	1404	0.726	3	610	11	951	0.283
0005773	vacuole	7	1568	7	1407	0.947	5	608	2	960	0.168
0005764	lysosome	2	1573	3	1411	0.904	0	613	2	960	0.686
0005856	cytoskeleton	40	1535	45	1369	0.344	10	603	30	932	0.096
0005694	chromosome	**13**	**1562**	**27**	**1387**	**0.016**	4	609	9	953	0.749
0000228	nuclear chromosome	3	1572	2	1412	0.904	2	611	1	961	0.694
0005634	nucleus	192	1383	180	1234	0.696	**52**	**561**	**140**	**822**	**4E-04**
0005635	nuclear membrane	7	1568	10	1404	0.478	1	612	6	956	0.341
0005730	nucleolus	7	1568	4	1410	0.67	0	613	7	955	0.084
0005654	nucleoplasm	33	1542	39	1375	0.289	11	602	22	940	0.628
0005777	peroxisome	6	1569	3	1411	0.612	0	613	6	956	0.124
0005886	plasma membrane	79	1496	77	1337	0.656	**48**	**565**	**31**	**931**	**7E-05**
0005576	extracellular region	38	1537	38	1376	0.719	20	593	18	944	0.113
0005578	extracellular matrix (sensu Metazoa)	20	1555	15	1399	0.719	12	601	8	954	0.086

PC9

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	p	term	n.term	term	n.term	p
0008150	biological_process	862	613	892	622	0.82	444	321	418	292	0.786
0007610	behavior	72	1403	90	1424	0.229	**46**	**719**	**26**	**684**	**0.049**
0030534	adult behavior	11	1464	13	1501	0.888	8	757	3	707	0.277
0030537	larval behavior	2	1473	7	1507	0.195	1	764	1	709	0.512
0007611	learning and/or memory	10	1465	14	1500	0.582	7	758	3	707	0.404
0007612	learning	6	1469	9	1505	0.64	3	762	3	707	0.751
0007613	memory	4	1471	7	1507	0.575	2	763	2	708	0.67
0007626	locomotory behavior	56	1419	67	1447	0.439	36	729	20	690	0.078
0007635	chemosensory behavior	8	1467	10	1504	0.856	5	760	3	707	0.803
0007622	rhythmic behavior	8	1467	7	1507	0.96	2	763	6	704	0.242
0048512	circadian behavior	8	1467	6	1508	0.751	2	763	6	704	0.242
0009987	cellular process	796	679	832	682	0.613	418	347	378	332	0.626
0007154	cell communication	245	1230	244	1270	0.752	123	642	122	588	0.617
0007155	cell adhesion	44	1431	46	1468	0.985	25	740	19	691	0.607
0008037	cell recognition	1	1474	1	1513	0.491	1	764	0	710	0.97
0008038	neuronal cell recognition	1	1474	1	1513	0.491	1	764	0	710	0.97
0016337	cell-cell adhesion	19	1456	20	1494	0.935	11	754	8	702	0.765
0016339	calcium-dependent cell-cell adhesion	2	1473	5	1509	0.47	2	763	0	710	0.512
0007156	homophilic cell adhesion	3	1472	6	1508	0.53	3	762	0	710	0.275
0007160	cell-matrix adhesion	4	1471	5	1509	0.969	2	763	2	708	0.67
0007267	cell-cell signaling	82	1393	74	1440	0.457	41	724	41	669	0.815
0019226	transmission of nerve impulse	72	1403	66	1448	0.553	38	727	34	676	0.97
0007268	synaptic transmission	51	1424	50	1464	0.894	27	738	24	686	0.989
0007270	nerve-nerve synaptic transmission	8	1467	8	1506	0.843	3	762	5	705	0.645
0001505	regulation of neurotransmitter levels	31	1444	29	1485	0.816	16	749	15	695	0.878
0042133	neurotransmitter metabolism	4	1471	4	1510	0.751	2	763	2	708	0.67
0007269	neurotransmitter secretion	27	1448	26	1488	0.924	14	751	13	697	0.847
0007165	signal transduction	186	1289	193	1321	0.954	94	671	92	618	0.757
0007166	cell surface receptor linked signal transduction	82	1393	75	1439	0.509	40	725	42	668	0.645
0007167	enzyme linked receptor protein signaling pathway	24	1451	22	1492	0.812	11	754	13	697	0.696
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	8	1467	8	1506	0.843	5	760	3	707	0.803
0007179	transforming growth factor beta receptor signaling pathway	5	1470	4	1510	0.969	2	763	3	707	0.933
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	17	1458	15	1499	0.801	7	758	10	700	0.52
0007173	epidermal growth factor receptor signaling pathway	3	1472	5	1509	0.751	2	763	1	709	0.948
0008286	insulin receptor signaling pathway	1	1474	3	1511	0.635	1	764	0	710	0.97
0008293	torso signaling pathway	4	1471	3	1511	0.972	1	764	3	707	0.565
0007186	G-protein coupled receptor protein signaling pathway	35	1440	36	1478	0.911	15	750	20	690	0.364
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	1	1474	4	1510	0.386	0	765	1	709	0.97
0007219	Notch signaling pathway	6	1469	7	1507	0.962	3	762	3	707	0.751
0007224	smoothened signaling pathway	3	1472	3	1511	0.706	2	763	1	709	0.948
0008063	Toll signaling pathway	2	1473	2	1512	0.635	1	764	1	709	0.512
0016055	Wnt receptor signaling pathway	7	1468	9	1505	0.843	6	759	1	709	0.156
0007242	intracellular signaling cascade	89	1386	93	1421	0.962	46	719	43	667	0.941
0007263	nitric oxide mediated signal transduction	2	1473	2	1512	0.635	0	765	2	708	0.447
0007243	protein kinase cascade	22	1453	19	1495	0.69	11	754	11	699	0.969
0007259	JAK-STAT cascade	1	1474	5	1509	0.232	1	764	0	710	0.97
0000165	MAPKKK cascade	19	1456	14	1500	0.438	10	755	9	701	0.87
0019932	second-messenger-mediated signaling	11	1464	11	1503	0.879	6	759	5	705	0.901
0019722	calcium-mediated signaling	8	1467	7	1507	0.96	6	759	2	708	0.338
0048015	phosphoinositide-mediated signaling	1	1474	4	1510	0.386	0	765	1	709	0.97
0007264	small GTPase mediated signal transduction	24	1451	20	1494	0.587	11	754	13	697	0.696
0007265	Ras protein signal transduction	5	1470	5	1509	0.783	4	761	1	709	0.416
0009966	regulation of signal transduction	17	1458	17	1497	0.924	8	757	9	701	0.877
0007275	development	229	1246	231	1283	0.879	124	641	105	605	0.496
0007568	aging	6	1469	5	1509	0.965	2	763	4	706	0.616
0030154	cell differentiation	62	1413	57	1457	0.603	32	733	30	680	0.929
0048468	cell development	33	1442	42	1472	0.412	17	748	16	694	0.892
0000904	cellular morphogenesis during differentiation	8	1467	11	1503	0.687	5	760	3	707	0.803
0042461	photoreceptor cell development	8	1467	10	1504	0.856	5	760	3	707	0.803
0042051	eye photoreceptor development (sensu Endopterygota)	8	1467	9	1505	0.957	5	760	3	707	0.803
0045165	cell fate commitment	29	1446	20	1494	0.213	14	751	15	695	0.839

PC9

		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0001709	cell fate determination	18	1457	12	1502	0.322	8	757	10	700	0.692
0007400	neuroblast cell fate determination	4	1471	4	1510	0.751	2	763	2	708	0.67
0001708	cell fate specification	4	1471	4	1510	0.751	1	764	3	707	0.565
0007349	cellularization	5	1470	6	1508	0.965	3	762	2	708	0.933
0040007	growth	14	1461	22	1492	0.273	8	757	6	704	0.898
0002164	larval development	7	1468	10	1504	0.665	3	762	4	706	0.921
0002165	larval or pupal development (sensu Insecta)	62	1413	67	1447	0.835	35	730	27	683	0.543
0007552	metamorphosis	59	1416	62	1452	0.969	35	730	24	686	0.3
0009653	morphogenesis	163	1312	156	1358	0.547	91	674	72	638	0.322
0002009	morphogenesis of an epithelium	28	1447	16	1498	0.079	16	749	12	698	0.709
0009887	organogenesis	143	1332	139	1375	0.676	76	689	67	643	0.814
0001654	eye morphogenesis	30	1445	27	1487	0.714	16	749	14	696	0.983
0008406	gonad development	3	1472	8	1506	0.244	1	764	2	708	0.948
0007444	imaginal disc development	45	1430	48	1466	0.934	28	737	17	693	0.207
0007494	midgut development	4	1471	1	1513	0.355	1	764	3	707	0.565
0007517	muscle development	14	1461	20	1494	0.432	6	759	8	702	0.683
0007399	neurogenesis	82	1393	80	1434	0.801	39	726	43	667	0.491
0007409	axonogenesis	20	1455	23	1491	0.825	13	752	7	703	0.338
0007411	axon guidance	18	1457	15	1499	0.67	13	752	5	705	0.133
0007417	central nervous system development	21	1454	18	1496	0.686	9	756	12	698	0.54
0016358	dendrite morphogenesis	6	1469	8	1506	0.827	3	762	3	707	0.751
0042063	gliogenesis	4	1471	7	1507	0.575	4	761	0	710	0.153
0007422	peripheral nervous system development	16	1459	24	1490	0.302	5	760	11	699	0.159
0050767	regulation of neurogenesis	3	1472	2	1512	0.977	3	762	0	710	0.275
0007424	tracheal system development (sensu Insecta)	16	1459	21	1493	0.561	10	755	6	704	0.545
0048513	organ development	144	1331	142	1372	0.769	77	688	67	643	0.75
0007389	pattern specification	35	1440	41	1473	0.641	17	748	18	692	0.823
0048066	pigmentation	5	1470	6	1508	0.965	1	764	4	706	0.327
0009791	post-embryonic development	7	1468	10	1504	0.665	3	762	4	706	0.921
0009790	embryonic development	54	1421	46	1468	0.398	29	736	25	685	0.891
0007530	sex determination	4	1471	6	1508	0.783	2	763	2	708	0.67
0007548	sex differentiation	7	1468	12	1502	0.388	2	763	5	705	0.391
0019827	stem cell maintenance	4	1471	4	1510	0.751	2	763	2	708	0.67
0000003	reproduction	64	1411	80	1434	0.262	39	726	25	685	0.175
0050793	regulation of development	19	1456	24	1490	0.597	12	753	7	703	0.447
0007582	physiological process	784	691	821	693	0.581	414	351	370	340	0.472
0008152	metabolism	**546**	**929**	**620**	**894**	**0.03**	290	475	256	454	0.495
0009056	catabolism	96	1379	113	1401	0.341	53	712	43	667	0.567
0006091	energy pathways	50	1425	58	1456	0.584	19	746	31	679	0.064
0006118	electron transport	26	1449	29	1485	0.861	10	755	16	694	0.237
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolis	212	1263	220	1294	0.943	**130**	**635**	**82**	**628**	**0.004**
0006259	DNA metabolism	42	1433	37	1477	0.566	**30**	**735**	**12**	**698**	**0.016**
0006350	transcription	111	1364	116	1398	0.943	**70**	**695**	**41**	**669**	**0.018**
0043170	macromolecule metabolism	**284**	**1191**	**344**	**1170**	**0.023**	151	614	133	577	0.672
0019538	protein metabolism	242	1233	285	1229	0.092	133	632	109	601	0.325
0006412	protein biosynthesis	49	1426	61	1453	0.353	31	734	18	692	0.139
0006464	protein modification	117	1358	139	1375	0.248	59	706	58	652	0.82
0006457	protein folding	23	1452	20	1494	0.694	10	755	13	697	0.548
0005975	carbohydrate metabolism	**42**	**1433**	**65**	**1449**	**0.042**	20	745	22	688	0.688
0006519	amino acid and derivative metabolism	34	1441	36	1478	0.992	16	749	18	692	0.694
0006629	lipid metabolism	38	1437	51	1463	0.243	15	750	23	687	0.166
0009308	amine metabolism	36	1439	45	1469	0.434	17	748	19	691	0.692
0042440	pigment metabolism	7	1468	5	1509	0.738	3	762	4	706	0.921
0042445	hormone metabolism	4	1471	3	1511	0.972	1	764	3	707	0.565
0009058	biosynthesis	88	1387	116	1398	0.077	49	716	39	671	0.529
0019748	secondary metabolism	8	1467	6	1508	0.751	3	762	5	705	0.645
0019222	regulation of metabolism	117	1358	121	1393	0.994	**75**	**690**	**42**	**668**	**0.008**
0016265	death	44	1431	42	1472	0.816	22	743	22	688	0.922
0008219	cell death	38	1437	36	1478	0.817	20	745	18	692	0.945
0016271	tissue death	11	1464	16	1498	0.481	7	758	4	706	0.63
0042592	homeostasis	16	1459	13	1501	0.657	7	758	9	701	0.688
0019725	cell homeostasis	15	1460	11	1503	0.511	6	759	9	701	0.506
0050801	ion homeostasis	9	1466	5	1509	0.394	4	761	5	705	0.911
0043062	extracellular structure organization and biogenesis	7	1468	12	1502	0.388	4	761	3	707	0.921
0046903	secretion	50	1425	51	1463	0.945	25	740	25	685	0.901
0048511	rhythmic process	9	1466	8	1506	0.957	3	762	6	704	0.435

		PC9									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0050791	regulation of physiological process	172	1303	175	1339	0.976	**105**	**660**	**67**	**643**	**0.013**
0050874	organismal physiological process	111	1364	121	1393	0.683	56	709	55	655	0.833
0050875	cellular physiological process	740	735	779	735	0.506	396	369	344	366	0.223
0006810	transport	207	1268	191	1323	0.277	111	654	96	614	0.637
0006811	ion transport	62	1413	58	1456	0.671	**23**	**742**	**39**	**671**	**0.025**
0006818	hydrogen transport	8	1467	10	1504	0.856	3	762	5	705	0.645
0006836	neurotransmitter transport	4	1471	1	1513	0.355	2	763	2	708	0.67
0006858	extracellular transport	11	1464	4	1510	0.109	3	762	8	702	0.182
0006869	lipid transport	6	1469	10	1504	0.484	2	763	4	706	0.616
0008643	carbohydrate transport	5	1470	10	1504	0.325	2	763	3	707	0.933
0015031	protein transport	98	1377	82	1432	0.182	58	707	40	670	0.163
0015837	amine transport	7	1468	5	1509	0.738	2	763	5	705	0.391
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	10	1465	3	1511	0.086	8	757	2	708	0.142
0016192	vesicle-mediated transport	66	1409	53	1461	0.205	32	733	34	676	0.663
0045045	secretory pathway	48	1427	47	1467	0.897	24	741	24	686	0.908
0046907	intracellular transport	110	1365	88	1426	0.083	67	698	43	667	0.061
0051049	regulation of transport	9	1466	9	1505	0.856	6	759	3	707	0.578
0008283	cell proliferation	36	1439	35	1479	0.911	22	743	14	696	0.339
0007049	cell cycle	66	1409	62	1452	0.673	41	724	25	685	0.114
0017145	stem cell division	5	1470	7	1507	0.807	2	763	3	707	0.933
0016043	cell organization and biogenesis	141	1334	134	1380	0.544	**88**	**677**	**53**	**657**	**0.011**
0000902	cellular morphogenesis	41	1434	39	1475	0.817	**29**	**736**	**12**	**698**	**0.022**
0006996	organelle organization and biogenesis	122	1353	116	1398	0.584	**76**	**689**	**46**	**664**	**0.021**
0007010	cytoskeleton organization and biogenesis	90	1385	80	1434	0.376	54	711	36	674	0.137
0006997	nuclear organization and biogenesis	7	1468	3	1511	0.321	5	760	2	708	0.51
0007028	cytoplasm organization and biogenesis	**4**	**1471**	**15**	**1499**	**0.025**	3	762	1	709	0.67
0016044	membrane organization and biogenesis	5	1470	4	1510	0.969	5	760	0	710	0.087
0051128	regulation of cell organization and biogenesis	7	1468	4	1510	0.517	5	760	2	708	0.51
0016049	cell growth	4	1471	5	1509	0.969	3	762	1	709	0.67
0050896	response to stimulus	90	1385	91	1423	0.978	43	722	47	663	0.489
0006950	response to stress	26	1449	33	1481	0.492	11	754	15	695	0.432
0009408	response to heat	6	1469	4	1510	0.72	2	763	4	706	0.616
0006979	response to oxidative stress	1	1474	1	1513	0.491	0	765	1	709	0.97
0051179	localization	220	1255	209	1305	0.416	115	650	105	605	0.954
0006403	RNA localization	16	1459	16	1498	0.918	8	757	8	702	0.919
0008104	protein localization	103	1372	92	1422	0.353	60	705	43	667	0.214
0051234	establishment of localization	209	1266	194	1320	0.302	112	653	97	613	0.643
0051235	maintenance of localization	1	1474	3	1511	0.635	0	765	1	709	0.97
0050789	regulation of biological process	196	1279	207	1307	0.8	**117**	**648**	**79**	**631**	**0.023**
0050790	regulation of enzyme activity	4	1471	10	1504	0.197	4	761	0	710	0.153
0040029	regulation of gene expression, epigenetic	8	1467	12	1502	0.539	7	758	1	709	0.095
0006306	DNA methylation	4	1471	3	1511	0.972	3	762	1	709	0.67
0045814	negative regulation of gene expression, epigenetic	2	1473	5	1509	0.47	2	763	0	710	0.512
0006342	chromatin silencing	2	1473	5	1509	0.47	2	763	0	710	0.512
0003674	molecular_function	842	633	890	624	0.366	435	330	407	303	0.9
0016209	antioxidant activity	6	1469	3	1511	0.48	2	763	4	706	0.616
0005488	binding	476	999	531	983	0.114	**271**	**494**	**205**	**505**	**0.008**
0005509	calcium ion binding	29	1446	32	1482	0.876	15	750	14	696	0.863
0030246	carbohydrate binding	6	1469	9	1505	0.64	3	762	3	707	0.751
0008289	lipid binding	14	1461	12	1502	0.792	8	757	6	704	0.898
0003676	nucleic acid binding	192	1283	197	1317	0.96	**119**	**646**	**73**	**637**	**0.003**
0003677	DNA binding	101	1374	93	1421	0.479	62	703	39	671	0.06
0003682	chromatin binding	14	1461	9	1505	0.368	10	755	4	706	0.229
0003700	transcription factor activity	39	1436	47	1467	0.52	21	744	18	692	0.929
0003723	RNA binding	57	1418	62	1452	0.819	37	728	20	690	0.061
0008135	translation factor activity, nucleic acid binding	19	1456	16	1498	0.676	14	751	5	705	0.092
0000166	nucleotide binding	127	1348	128	1386	0.931	75	690	52	658	0.109
0005515	protein binding	177	1298	202	1312	0.295	100	665	77	633	0.217
0008134	transcription factor binding	19	1456	12	1502	0.248	13	752	6	704	0.221
0008092	cytoskeletal protein binding	43	1432	45	1469	0.987	26	739	17	693	0.322
0003779	actin binding	28	1447	25	1489	0.709	18	747	10	700	0.255
0003824	catalytic activity	392	1083	447	1067	0.08	205	560	187	523	0.888
0016787	hydrolase activity	173	1302	199	1315	0.264	101	664	72	638	0.081
0003924	GTPase activity	19	1456	21	1493	0.939	8	757	11	699	0.531
0004518	nuclease activity	**12**	**1463**	**3**	**1511**	**0.034**	7	758	5	705	0.873

		PC9									
		Representational bias					Directional bias				
		regulated		not regulated			up-reg.		down-reg.		
GO#	GO term	term	n.term	term	n.term	*p*	term	n.term	term	n.term	*p*
0008233	peptidase activity	54	1421	64	1450	0.483	31	734	23	687	0.489
0004721	phosphoprotein phosphatase activity	13	1462	17	1497	0.632	10	755	3	707	0.124
0016740	transferase activity	117	1358	124	1390	0.848	67	698	50	660	0.262
0016301	kinase activity	62	1413	73	1441	0.468	37	728	25	685	0.259
0004672	protein kinase activity	47	1428	48	1466	0.937	28	737	19	691	0.354
0030234	enzyme regulator activity	51	1424	54	1460	0.95	23	742	28	682	0.4
0003774	motor activity	15	1460	13	1501	0.795	7	758	8	702	0.885
0004871	signal transducer activity	132	1343	124	1390	0.499	71	694	61	649	0.71
0004872	receptor activity	58	1417	51	1463	0.469	29	736	29	681	0.876
0004879	ligand-dependent nuclear receptor activity	6	1469	3	1511	0.48	3	762	3	707	0.751
0004888	transmembrane receptor activity	37	1438	37	1477	0.997	18	747	19	691	0.818
0004930	G-protein coupled receptor activity	15	1460	15	1499	0.911	7	758	8	702	0.885
0005057	receptor signaling protein activity	41	1434	39	1475	0.817	**29**	**736**	**12**	**698**	**0.022**
0005102	receptor binding	38	1437	31	1483	0.401	19	746	19	691	0.945
0005198	structural molecule activity	76	1399	86	1428	0.578	42	723	34	676	0.623
0030528	transcription regulator activity	93	1382	106	1408	0.49	**58**	**707**	**35**	**675**	**0.047**
0045182	translation regulator activity	19	1456	16	1498	0.676	14	751	5	705	0.092
0005215	transporter activity	122	1353	131	1383	0.757	53	712	69	641	0.064
0005489	electron transporter activity	14	1461	15	1499	0.944	4	761	10	700	0.138
0005216	ion channel activity	22	1453	30	1484	0.376	9	756	13	697	0.412
0005244	voltage-gated ion channel activity	12	1463	14	1500	0.896	7	758	5	705	0.873
0005575	cellular_component	597	878	626	888	0.654	310	455	287	423	0.989
0005623	cell	544	931	568	946	0.748	291	474	253	457	0.367
0005622	intracellular	418	1057	439	1075	0.721	231	534	187	523	0.113
0005737	cytoplasm	222	1253	236	1278	0.721	116	649	106	604	0.958
0016023	cytoplasmic vesicle	23	1452	18	1496	0.476	9	756	14	696	0.307
0005829	cytosol	39	1436	40	1474	0.912	25	740	14	696	0.165
0005783	endoplasmic reticulum	22	1453	35	1479	0.132	15	750	7	703	0.184
0005794	Golgi apparatus	14	1461	11	1503	0.64	9	756	5	705	0.505
0005815	microtubule organizing center	6	1469	3	1511	0.48	3	762	3	707	0.751
0005739	mitochondrion	44	1431	61	1453	0.146	17	748	27	683	0.103
0005840	ribosome	9	1466	15	1499	0.337	3	762	6	704	0.435
0005773	vacuole	5	1470	9	1505	0.45	0	765	5	705	0.061
0005764	lysosome	1	1474	4	1510	0.386	0	765	1	709	0.97
0005856	cytoskeleton	41	1434	44	1470	0.922	24	741	17	693	0.479
0005694	chromosome	21	1454	19	1495	0.809	**17**	**748**	**4**	**706**	**0.014**
0000228	nuclear chromosome	1	1474	4	1510	0.386	1	764	0	710	0.97
0005634	nucleus	184	1291	188	1326	0.994	**116**	**649**	**68**	**642**	**0.002**
0005635	nuclear membrane	9	1466	8	1506	0.957	7	758	2	708	0.22
0005730	nucleolus	3	1472	8	1506	0.244	1	764	2	708	0.948
0005654	nucleoplasm	37	1438	35	1479	0.817	24	741	13	697	0.151
0005777	peroxisome	6	1469	3	1511	0.48	5	760	1	709	0.256
0005886	plasma membrane	78	1397	78	1436	0.932	41	724	37	673	0.991
0005576	extracellular region	**25**	**1450**	**51**	**1463**	**0.005**	9	756	16	694	0.162
0005578	extracellular matrix (sensu Metazoa)	13	1462	22	1492	0.2	5	760	8	702	0.489