

Supplementary Table 1: List of top 20 significantly overrepresented GO categories derived from BINGO analyses output based on our data. The list has been arranged in ascending order of the Node size.

Name	Description	Average Shortest Path Length	Betweenness Centrality	Closeness Centrality	Neighborhood Connectivity	Node Size	No. of Genes	adjusted P Value
65007	biological regulation	3.72	0.138077	0.268817	8.333333	16.12452	65	0.00348
50789	regulation of biological process	2.68254	0.263324	0.372781	4.090909	15.87451	63	0.0027
50794	regulation of cellular process	2.605263	0.131545	0.383838	4.2	15.74802	62	0.0024
19222	regulation of metabolic process	2.125	0.039602	0.470588	4.75	12.49	39	0.0216
31323	regulation of cellular metabolic process	0	0	0	7	12	36	0.0449
23052	signaling	2.625	0.012372	0.380952	5.666667	12	36	0.00789
32502	developmental process	2.858824	0.112328	0.349794	7	11.6619	34	0.0216
7275	multicellular organismal development	3.904762	0.175373	0.256098	5	11.31371	32	0.0216
10468	regulation of gene expression	1.333333	0.015726	0.75	3	11.13553	31	0.0299
48856	anatomical structure development	2.426471	0.066427	0.412121	5.428571	10.77033	29	0.0295
16043	cellular component organization	2.625	0.017086	0.380952	5.2	10.77033	29	0.0207
48731	system development	3.531915	0.30602	0.283133	5.125	10.58301	28	0.0194
23033	signaling pathway	1.5	0.007868	0.666667	2.5	10.3923	27	0.0113
48869	cellular developmental process	2.774194	0.143077	0.360465	6.166667	9.591663	23	0.0143
48523	negative regulation of cellular process	3	0.074143	0.333333	5.25	9.380832	22	0.0371
30154	cell differentiation	2.615385	0.069689	0.382353	4	9.380832	22	0.0184
48513	organ development	2.827586	0.199668	0.353659	5.375	9.165151	21	0.0482
7166	cell surface receptor linked signaling pathway	1	0.005863	1	1.5	8.944272	20	0.00875
51239	regulation of multicellular organismal process	1.9375	0.058335	0.516129	4.285714	8.485281	18	0.0083
35466	regulation of signaling pathway	0	0	0	11	7.745967	15	0.0299