

Supplemental Table 2. Branch-Point Gene Ontology Enrichment

Branching Point	GO Number	Ontology Description	Total Genes in Array	Total Genes in Cluster	P-value
1	GO:0016651	Oxidoreductase activity, acting on NADH or NADPH	49	22	7.9×10^{-20}
	GO:0006091	Energy pathways	155	34	2.3×10^{-18}
	GO:0006092	Main pathways of carbohydrate metabolism	57	14	5.0×10^{-9}
	GO:0019395	Fatty acid oxidation	15	7	2.6×10^{-7}
2	None				
3	GO:0006091	Energy pathways	155	38	5.2×10^{-7}
	GO:0006119	Oxidative phosphorylation	24	11	1.2×10^{-5}
	GO:0006941	Striated muscle contraction	19	12	4.6×10^{-8}
	GO:0015992	Proton transport	42	14	6.1×10^{-5}
4	GO:0046039	GTP metabolism	10	5	5.3×10^{-5}
	GO:0006700	C21-steroid hormone biosynthesis	4	3	4.3×10^{-4}
	GO:0046037	GMP metabolism	4	3	4.3×10^{-4}
5	GO:0007214	Gamma-aminobutyric acid signaling pathway	6	2	2.1×10^{-4}
	GO:0030594	Neurotransmitter receptor activity	33	3	2.6×10^{-4}
6	GO:0006956	Complement activation	26	10	1.3×10^{-5}
	GO:0006916	Anti-apoptosis	48	13	5.0×10^{-5}
	GO:0008610	Lipid biosynthesis	99	20	6.0×10^{-5}
7	GO:0007517	Muscle development	88	10	1.38×10^{-9}
	GO:0006941	Striated muscle contraction	19	6	4.55×10^{-9}
	GO:0008016	Regulation of heart rate	19	4	1.17×10^{-5}
8	GO:0006955	Immune response	470	116	4.0×10^{-20}
	GO:0007166	Cell surface receptor linked signal transduction	512	81	3.6×10^{-5}
	GO:0007266	Rho protein signal transduction	15	7	3.4×10^{-4}
9	GO:0000072	M-phase specific microtubule process	12	5	5.1×10^{-5}
	GO:0007588	Excretion	29	6	6.8×10^{-4}
10	GO:0030504	Inorganic diphosphate transporter activity	2	2	1.3×10^{-4}
	GO:0030500	Regulation of bone mineralization	3	2	3.9×10^{-4}
	GO:0006334	Nucleosome assembly	35	4	6.7×10^{-4}
11	GO:0007283	Spermatogenesis	60	9	5.1×10^{-7}
	GO:0009566	Fertilization	14	4	6.1×10^{-5}
	GO:0006540	Glutamate decarboxylation to succinate	2	2	2.6×10^{-4}
12	GO:0016787	Hydrolase activity	1403	25	9.1×10^{-8}
	GO:0006508	Proteolysis and peptidolysis	372	9	2.0×10^{-4}
	GO:0009405	Pathogenesis	59	4	3.0×10^{-4}
13	GO:0006412	Protein biosynthesis	318	96	1.5×10^{-9}
	GO:0006091	Energy pathways	155	50	1.5×10^{-6}
	GO:0016655	Oxidoreductase activity, acting on NADH or NADPH	38	19	2.3×10^{-6}
	GO:0006955	Immune response	470	116	5.5×10^{-6}
	GO:0004129	Cytochrome C oxidase activity	15	10	2.2×10^{-5}
14	GO:0005083	Small GTPase regulatory/interacting protein activity	94	11	1.5×10^{-4}
	GO:0016773	Phosphotransferase activity, alcohol group as acceptor	437	27	5.0×10^{-4}
	GO:0017076	Purine nucleotide binding	924	47	5.1×10^{-4}
	GO:0006511	Ubiquitin-dependent protein catabolism	111	11	6.2×10^{-4}
	GO:0004917	Interleukin-7 receptor activity	2	2	9.4×10^{-4}
15	GO:0007275	Development	936	61	6.7×10^{-4}
16	GO:0005604	Basement membrane	42	6	2.9×10^{-6}
17	GO:0008514	Organic anion transporter activity	27	2	6.7×10^{-4}
18	GO:0015078	Hydrogen ion transporter activity	95	46	7.8×10^{-13}
	GO:0006412	Protein biosynthesis	318	96	1.5×10^{-9}
	GO:0006091	Energy pathways	155	50	1.5×10^{-6}
	GO:0006955	Immune response	470	116	5.5×10^{-6}
	GO:0004129	Cytochrome c oxidase activity	15	10	2.2×10^{-5}
	GO:0006092	Main pathways of carbohydrate metabolism	57	27	7.4×10^{-8}