

Additional file 11. GO enriched categories for a) top 0.5% highly differentiated SNPs, b) top 0.5% highly differentiated SNPs differentially fixed between populations 1-4 and population 6.

a)

term ID	description	frequency	log10 p-value
GO:0051179	localization	17.86%	-1.4177
GO:0010467	gene expression	16.70%	-2.2774
GO:0016070	RNA metabolic process	13.71%	-1.5186
GO:0019538	protein metabolic process	12.33%	-1.511
GO:0007154	cell communication	4.36%	-1.6099
GO:0006812	cation transport	3.98%	-3.3979
GO:0023052	signaling	3.84%	-1.5547
GO:0006508	proteolysis	3.71%	-2.2269
GO:0006396	RNA processing	2.78%	-1.5196
GO:0008610	lipid biosynthetic process	2.21%	-2.7852
GO:0006310	DNA recombination	1.84%	-1.7484
GO:0009057	macromolecule catabolic process	1.64%	-1.5659
GO:0051641	cellular localization	1.64%	-1.4074
GO:0008643	carbohydrate transport	1.47%	-3.8861
GO:0051301	cell division	1.36%	-1.6692
GO:0048519	negative regulation of biological process	1.24%	-2.062
GO:0006022	aminoglycan metabolic process	1.10%	-1.769
GO:0042254	ribosome biogenesis	1.03%	-1.9531
GO:0016072	rRNA metabolic process	0.76%	-1.4634
GO:0006023	aminoglycan biosynthetic process	0.73%	-1.4852
GO:0022402	cell cycle process	0.53%	-2.1463
GO:0009311	oligosaccharide metabolic process	0.51%	-1.4671
GO:0016071	mRNA metabolic process	0.49%	-1.6899
GO:0006928	cellular component movement	0.49%	-1.4689
GO:0007059	chromosome segregation	0.37%	-1.6189
GO:0009894	regulation of catabolic process	0.28%	-1.7404
GO:0006413	translational initiation	0.27%	-1.4244
GO:0031329	regulation of cellular catabolic process	0.26%	-1.4595
GO:1901701	cellular response to oxygen-containing compound	0.23%	-2.8794
GO:0000003	reproduction	0.21%	-2.7799
GO:0007017	microtubule-based process	0.17%	-1.8159
GO:0052646	alditol phosphate metabolic process	0.15%	-1.3021
GO:0006072	glycerol-3-phosphate metabolic process	0.14%	-1.3021
GO:0000272	polysaccharide catabolic process	0.14%	-2.3063
GO:0019954	asexual reproduction	0.14%	-1.8404
GO:0006298	mismatch repair	0.14%	-3.0862
GO:1901071	glucosamine-containing compound metabolic process	0.13%	-2.0878
GO:0016567	protein ubiquitination	0.11%	-1.5885
GO:0010876	lipid localization	0.10%	-1.4618
GO:0040007	growth	0.08%	-2.0357
GO:0003006	developmental process involved in reproduction	0.08%	-2.2874
GO:0000280	nuclear division	0.06%	-1.7701

term_ID	description	frequency	log10 p-value
GO:0006816	calcium ion transport	0.05%	-1.5516
GO:0005992	trehalose biosynthetic process	0.05%	-2.1707
GO:0010565	regulation of cellular ketone metabolic process	0.04%	-1.4852
GO:0051235	maintenance of location	0.03%	-2.1643
GO:0006888	ER to Golgi vesicle-mediated transport	0.02%	-2.0878
GO:0015914	phospholipid transport	0.02%	-1.7364
GO:0032507	maintenance of protein location in cell	0.02%	-1.8196
GO:0006271	DNA strand elongation involved in DNA replication	0.01%	-1.4852
GO:0022616	DNA strand elongation	0.01%	-1.4852
GO:0006487	protein N-linked glycosylation	0.01%	-2.3063
GO:0018022	peptidyl-lysine methylation	0.00%	-1.3021
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	0.00%	-1.7364
GO:0030447	filamentous growth	0.00%	-1.5596
GO:0042762	regulation of sulfur metabolic process	0.00%	-1.9248
GO:0034248	regulation of cellular amide metabolic process	0.00%	-1.5516
GO:0042318	penicillin biosynthetic process	0.00%	-2.1707
GO:1900549	N';N";N"'-triacylfusarinine C metabolic process	0.00%	-1.7364
GO:1900551	N';N";N"'-triacylfusarinine C biosynthetic process	0.00%	-1.7364
GO:0051278	fungal-type cell wall polysaccharide biosynthetic process	0.00%	-2.1707
GO:0036184	asperthecin biosynthetic process	0.00%	-1.3021

b)

term_ID	description	frequency	log10 p-value
GO:0010467	gene expression	16.70%	-1.6542
GO:0019538	protein metabolic process	12.33%	-1.7167
GO:0031326	regulation of cellular biosynthetic process	9.00%	-2.4962
GO:0044248	cellular catabolic process	7.95%	-1.3343
GO:0006412	translation	4.70%	-1.3155
GO:0006396	RNA processing	2.78%	-2.0969
GO:0008643	carbohydrate transport	1.47%	-3.8539
GO:0005976	polysaccharide metabolic process	1.08%	-1.9169
GO:0042254	ribosome biogenesis	1.03%	-2.1226
GO:0016071	mRNA metabolic process	0.49%	-1.7849
GO:0006928	cellular component movement	0.49%	-1.6946
GO:0052803	imidazole-containing compound metabolic process	0.46%	-1.5038
GO:0006547	histidine metabolic process	0.45%	-1.5038
GO:0090502	RNA phosphodiester bond hydrolysis; endonucleolytic	0.42%	-1.4405
GO:0006397	mRNA processing	0.37%	-1.547
GO:0009628	response to abiotic stimulus	0.31%	-1.5632
GO:1901700	response to oxygen-containing compound	0.31%	-1.5117
GO:0000272	polysaccharide catabolic process	0.14%	-1.7897
GO:0019954	asexual reproduction	0.14%	-2.0921
GO:0006298	mismatch repair	0.14%	-2.7852
GO:0006112	energy reserve metabolic process	0.13%	-1.326
GO:0048646	anatomical structure formation involved in morphogenesis	0.13%	-2.4609
GO:0022414	reproductive process	0.12%	-1.4034

term ID	description	frequency	log10 p-value
GO:0051056	regulation of small GTPase mediated signal transduction	0.11%	-1.534
GO:0016567	protein ubiquitination	0.11%	-2.0737
GO:0046854	phosphatidylinositol phosphorylation	0.11%	-2.585
GO:0040007	growth	0.08%	-1.6003
GO:1903047	mitotic cell cycle process	0.08%	-2.9957
GO:0044703	multi-organism reproductive process	0.07%	-1.7724
GO:0005992	trehalose biosynthetic process	0.05%	-3.2757
GO:0016049	cell growth	0.04%	-1.6112
GO:0006888	ER to Golgi vesicle-mediated transport	0.02%	-2.9245
GO:0006487	protein N-linked glycosylation	0.01%	-2.6655
GO:0030010	establishment of cell polarity	0.01%	-2.15
GO:0051784	negative regulation of nuclear division	0.01%	-2.1284
GO:0071852	fungus-type cell wall organization or biogenesis	0.00%	-1.534
GO:0033244	regulation of penicillin metabolic process	0.00%	-2.6198
GO:0045460	sterigmatocystin metabolic process	0.00%	-1.326