Table S4

metabolic, catabolic, biosynthetic processes, metabolite transport
sporulation, meiosis, reproduction, differentiation
detoxification of reactive oxygen species, response to stress and stimulus
receptor linked signal transduction
maintanence of telomere or condensed chromosome

Gene Ontology category	avg. Set1	
allantoin metabolic process	1.01550	v
allantoin catabolic process	1.01550	v
heterocycle catabolic process	1.01550	v
solute:cation symporter activity	0.99083	v
symporter activity	0.99083	v
fructose transmembrane transporter activity	0.93482	v
mannose transmembrane transporter activity	0.93482	v
aryl-alcohol dehydrogenase activity	0.93438	
sugar transmembrane transporter activity	0.89429	v
carbohydrate transmembrane transporter activity	0.85789	v
hexose transmembrane transporter activity	0.85085	v
monosaccharide transmembrane transporter activity	0.85085	v
glucose transmembrane transporter activity	0.85085	v
glucosidase activity	0.83744	v
vitamin B6 metabolic process	0.83314	v
pyridoxine metabolic process	0.83314	v
carbohydrate transport	0.81267	v
monosaccharide transport	0.79281	v
hexose transport	0.79281	v
glutathione metabolic process	0.78500	
meiotic DNA double-strand break formation	0.73417	v
cysteine-type peptidase activity	0.71318	
peroxisomal matrix	0.71278	v
siderophore transport	0.70950	
pre-autophagosomal structure	0.70850	v
aldehyde metabolic process	0.69267	
oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor	0.69233	v
ferric-chelate reductase activity	0.69233	v
heterocycle metabolic process	0.68933	
response to toxin	0.68543	
prospore membrane	0.68415	v
immature spore	0.68415	v
prospore	0.68415	v
hydrolase activity, hydrolyzing O-glycosyl compounds	0.68000	
iron ion transport	0.67556	
polyamine transmembrane transporter activity	0.67167	
secondary metabolic process	0.66617	
thiamin metabolic process	0.66565	v
DNA catabolic process, endonucleolytic	0.65825	v

aldo-keto reductase activity	0.65783	
unfolded protein binding	0.65777	
spore wall assembly (sensu Fungi)	0.65677	v
spore wall assembly	0.65677	v
reproductive sporulation	0.64264	v
sporulation (sensu Fungi)	0.64264	v
thiamin and derivative metabolic process	0.64017	v
secondary active transmembrane transporter activity	0.62729	
thiamin biosynthetic process	0.62719	v
thiamin and derivative biosynthetic process	0.62719	v
G-protein coupled receptor protein signaling pathway	0.62629	v
cell surface receptor linked signal transduction	0.62629	v
response to nutrient	0.62314	
oxidoreductase activity, oxidizing metal ions	0.62263	v
DNA catabolic process	0.62189	v
sporulation	0.61975	v
nucleobase metabolic process	0.61400	
polyamine transport	0.61129	
hydrolase activity, acting on glycosyl bonds	0.60574	
de novo pyrimidine base biosynthetic process	0.60517	
sister chromatid cohesion	0.60267	
regulation of transcription by carbon catabolites	0.60117	v
vitamin transport	0.59767	
amine transmembrane transporter activity	0.59700	
reproductive process in single-celled organism	0.59188	v
reproductive cellular process	0.59188	v
monocarboxylic acid transmembrane transporter activity	0.59175	
spore wall	0.59067	v
spore wall (sensu Fungi)	0.59067	v
vitamin biosynthetic process	0.58707	v
water-soluble vitamin biosynthetic process	0.58707	v
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as accept	0.58570	
cellular developmental process	0.58389	v
cell differentiation	0.58389	v
di-, tri-valent inorganic cation transport	0.58262	
oxidoreductase activity, acting on CH-OH group of donors	0.58129	
synapsis	0.57100	v
oxidoreductase activity, acting on peroxide as acceptor	0.57000	
peroxidase activity	0.57000	
reproductive process	0.56892	v
vitamin metabolic process	0.56298	
water-soluble vitamin metabolic process	0.56298	
glycogen metabolic process	0.56242	
NADH metabolic process	0.55783	
carboxy-lyase activity	0.55590	
reproduction of a single-celled organism	0.55397	
meiosis	0.55351	v
meiotic cell cycle	0.55351	v
M phase of meiotic cell cycle	0.55351	v

sulfur metabolic process	0.54413	
meiotic gene conversion	0.54367	v
transcription factor binding	0.54250	
sulfur compound biosynthetic process	0.54120	
active transmembrane transporter activity	0.53997	
nitrogen utilization	0.53388	
pyrimidine base biosynthetic process	0.53100	
cellular carbohydrate catabolic process	0.52968	
carbohydrate catabolic process	0.52968	
condensed nuclear chromosome	0.52944	v
transition metal ion transport	0.52924	
plasma membrane	0.52275	
RNA methyltransferase activity	0.52000	
carbon-carbon lyase activity	0.51307	
fermentation	0.50950	v
telomeric DNA binding	0.50667	v
endodeoxyribonuclease activity	0.50644	v
meiosis I	0.50587	v
transition metal ion transmembrane transporter activity	0.50308	
reproduction	0.50206	v
cell division	0.50160	
deoxyribonuclease activity	0.50127	
energy reserve metabolic process	0.50080	
O-acyltransferase activity	0.50063	