Supplementary Table 3

mating, sporulation, filamentous growth, meiosis, reproduction, differentiation
signal transduction (during conjugation, receptor linked), DNA repair
response to stress and stimulus, detoxification of reactive oxygen species
metabolic, catabolic, biosynthetic processes, metabolite transport
maintanence of telomere or condensed chromosome

Gene Ontology category	avg. Sir2/3/4	
regulation of conjugation with cellular fusion	1.53010	
signal transduction during conjugation with cellular fusion	1.53010	
pheromone-dependent signal transduction during conjugation with cellular fusion	1.53010	
regulation of conjugation	1.53010	
G-protein coupled receptor protein signaling pathway	1.30935	v
response to pheromone during conjugation with cellular fusion	1.17459	
vitamin B6 metabolic process	1.03496	v
pyridoxine metabolic process	1.03496	v
response to pheromone	1.02318	
cell surface receptor linked signal transduction	0.98881	v
extracellular region	0.98801	
meiotic DNA double-strand break formation	0.95308	v
DNA catabolic process, endonucleolytic	0.90907	v
mating projection tip	0.89150	
sexual reproduction	0.85914	
conjugation	0.85914	
conjugation with cellular fusion	0.85914	
peroxisomal matrix	0.83553	v
oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor	0.82392	v
ferric-chelate reductase activity	0.82392	v
cell projection part	0.81648	
cell projection	0.80118	
mating projection	0.80118	
DNA catabolic process	0.78156	v
multi-organism process	0.77759	
thiamin biosynthetic process	0.73795	v
synapsis	0.73622	v
meiotic recombination	0.71632	
thiamin and derivative biosynthetic process	0.71347	v
thiamin metabolic process	0.71081	v
spore wall assembly (sensu Fungi)	0.70596	v
spore wall assembly	0.70596	v
meiosis I	0.68582	v
meiotic gene conversion	0.68109	v
telomeric DNA binding	0.67857	v
thiamin and derivative metabolic process	0.67684	v
mating type determination	0.66550	
reproductive developmental process	0.66550	
sex determination	0.66550	
invasive growth (sensu Saccharomyces)	0.66305	
pre-autophagosomal structure	0.65584	v
integral to plasma membrane	0.65265	

microtubule binding	0.64240	
mating type switching	0.63819	
intrinsic to plasma membrane	0.63248	
reproduction	0.63065	v
meiosis	0.62981	v
meiotic cell cycle	0.62981	v
M phase of meiotic cell cycle	0.62981	v
fructose transmembrane transporter activity	0.62916	v
mannose transmembrane transporter activity	0.62916	v
gene conversion at mating-type locus	0.62712	
plasma membrane part	0.62681	
double-strand break repair via homologous recombination	0.62353	
allantoin metabolic process	0.61981	v
allantoin catabolic process	0.61981	v
heterocycle catabolic process	0.61981	v
sugar transmembrane transporter activity	0.61602	v
signal transducer activity	0.61517	
molecular transducer activity	0.61517	
hexose transmembrane transporter activity	0.61455	v
monosaccharide transmembrane transporter activity	0.61455	v
oxidoreductase activity, oxidizing metal ions	0.60956	v
monosaccharide transport	0.60572	v
hexose transport	0.60572	v
DNA-directed DNA polymerase activity	0.60097	
external encapsulating structure	0.59973	
chitin- and beta-glucan-containing cell wall	0.59973	
cell wall	0.59973	
spore wall	0.59382	v
spore wall (sensu Fungi)	0.59382	v
solute:cation symporter activity	0.59236	v
symporter activity	0.59236	v
recombinational repair	0.58350	
DNA recombination	0.57732	
peroxisomal part	0.57709	
microbody part	0.57709	
glucose transmembrane transporter activity	0.57429	v
integral to peroxisomal membrane	0.56602	
intrinsic to peroxisomal membrane	0.56602	
double-strand break repair via single-strand annealing	0.56598	
phosphoinositide-mediated signaling	0.55709	
inositol lipid-mediated signaling	0.55709	
double-stranded DNA binding	0.55621	
cell development	0.55476	
fatty acid beta-oxidation	0.55108	
carbohydrate transport	0.54848	v
mitotic recombination	0.54654	
vitamin biosynthetic process	0.54637	v
water-soluble vitamin biosynthetic process	0.54637	v

double-strand break repair via nonhomologous end joining	0.54532	
carbohydrate transmembrane transporter activity	0.54512	v
reproductive process	0.54510	v
cell communication	0.54001	
extrinsic to membrane	0.53978	
nitrogen compound catabolic process	0.53789	
amine catabolic process	0.53789	
signal transduction	0.53766	
condensed chromosome	0.53646	
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0.53581	
peroxisome	0.53481	
microbody	0.53481	
anaphase-promoting complex	0.53266	
nonprotein amino acid metabolic process	0.53155	
cellular developmental process	0.53077	v
cell differentiation	0.53077	v
establishment of organelle localization	0.52967	
prospore membrane	0.52830	v
immature spore	0.52830	v
prospore	0.52830	v
nuclear chromosome, telomeric region	0.52686	
fermentation	0.52647	v
glucosidase activity	0.52557	v
cellular response to extracellular stimulus	0.52504	
cellular response to starvation	0.52504	
response to starvation	0.52504	
cellular response to nutrient levels	0.52504	
reproductive sporulation	0.52308	v
sporulation (sensu Fungi)	0.52308	v
non-recombinational repair	0.52275	
microtubule associated complex	0.52257	
regulation of a molecular function	0.52234	
sporulation	0.52229	v
response to chemical stimulus	0.52163	
reproductive process in single-celled organism	0.52029	v
reproductive cellular process	0.52029	v
condensed nuclear chromosome	0.51698	v
M phase	0.51536	
regulation of catalytic activity	0.51398	
filamentous growth	0.51356	
regulation of transcription by carbon catabolites	0.51318	v
multidrug transporter activity	0.51294	
deacetylase activity	0.51230	
response to external stimulus	0.51186	
response to extracellular stimulus	0.51186	
response to nutrient levels	0.51186	
hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	0.50700	
telomere maintenance via recombination	0.50532	
fatty acid oxidation	0.50512	
endodeoxyribonuclease activity	0.50498	v
cellular response to stress	0.50192	
cellular response to stimulus	0.50192	