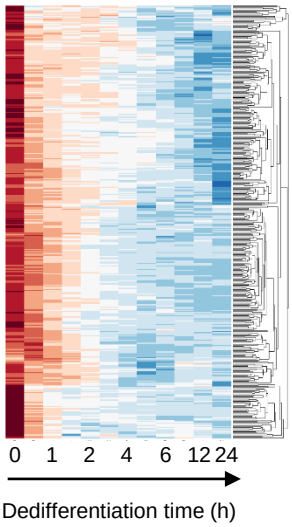
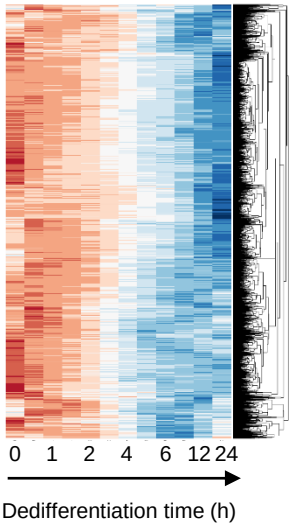
A



GO biological process complete	FC	p-value
spore wall assembly	15.5	6.8·10-5
culmination involved in sorocarp development	3.47	0.00011

B



GO biological process complete	FC	p-value
regulation of cell-cell adhesion	6.22	0.00251
phosphorelay signal transduction system	5.19	7.6·10-6
response to differentiation-inducing factor 1	4.84	1.4·10-7
cell-cell adhesion via plasma-membrane adhesion molecules	4.47	0.00215
cAMP-mediated signaling	4.36	3.4·10-5
sorocarp spore cell differentiation	4.27	0.00079
protein autophosphorylation	4.15	0.00029
peptidyl-threonine phosphorylation	4.09	0.00182
slug development involved in sorocarp development	3.84	0.00248
response to purine-containing compound	3.63	0.00073
positive regulation of chemorepellent activity	3.63	0.00200
signal transduction by protein phosphorylation	3.63	7.5·10-7
peptidyl-serine phosphorylation	3.52	0.00013
negative regulation of hydrolase activity	3.51	0.00035
peptidyl-tyrosine phosphorylation	3.49	0.00096
actin filament bundle assembly	3.28	0.00060
sorocarp stalk cell differentiation	3.2	0.00266
stress-activated protein kinase signaling cascade	3.11	0.00059
regulation of cell differentiation	3.11	1.6·10-5
activation of GTPase activity	3.04	0.00022
activation of protein kinase activity	2.96	6.3·10-5
sporulation resulting in formation of a cellular spore	2.89	4.1·10-6
aggregation involved in sorocarp development	2.86	3.4·10-9
chemotaxis to cAMP	2.78	1.2·10-6
regulation of Rho protein signal transduction	2.72	0.00083
regulation of protein serine/threonine kinase activity	2.54	0.00084
response to light stimulus	2.52	0.00197
multicellular organism development	2.48	9.8·10-5
cell motility	2.42	3.9·10-5
regulation of sorocarp development	2.42	5.3·10-5
protein dephosphorylation	2.36	0.00031
mitotic cytokinesis	2.3	0.00013
response to drug	2.03	0.00104
small GTPase mediated signal transduction	1.99	0.00022
regulation of cytoskeleton organization	1.92	0.00168
protein ubiquitination	1.76	0.00184