Putting it all together with fission yeast: Data connections within and beyond PomBase

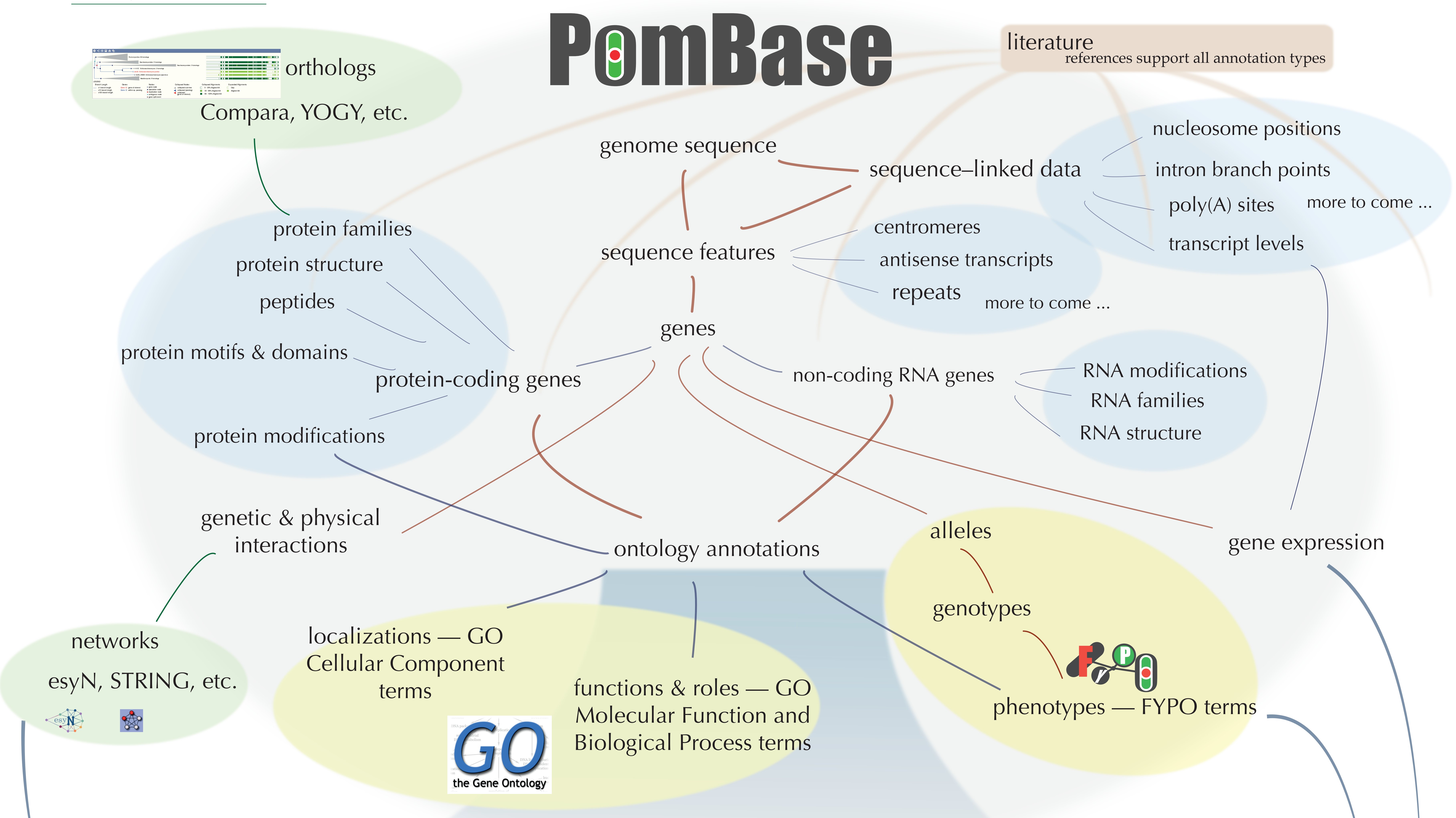
Midori A. Harris[1], Antonia Lock[2], Kim Rutherford[1], Mark McDowall[3], Jürg Bähler[2], Paul Kersey[3], Stephen G. Oliver[1] and Valerie Wood[1]

[1]Department of Biochemistry and Cambridge Systems Biology Centre, University of Cambridge, Sanger Building, 80 Tennis Court Road, Cambridge CB2 1GA, UK; [2]Department of Genetics, Evolution & Environment and UCL Genetics Institute, University College London, London WC1E 6BT, UK; [3]EMBL—European Bioinformatics Institute, Hinxton, Cambridge CB10 1SD, UK

Summary

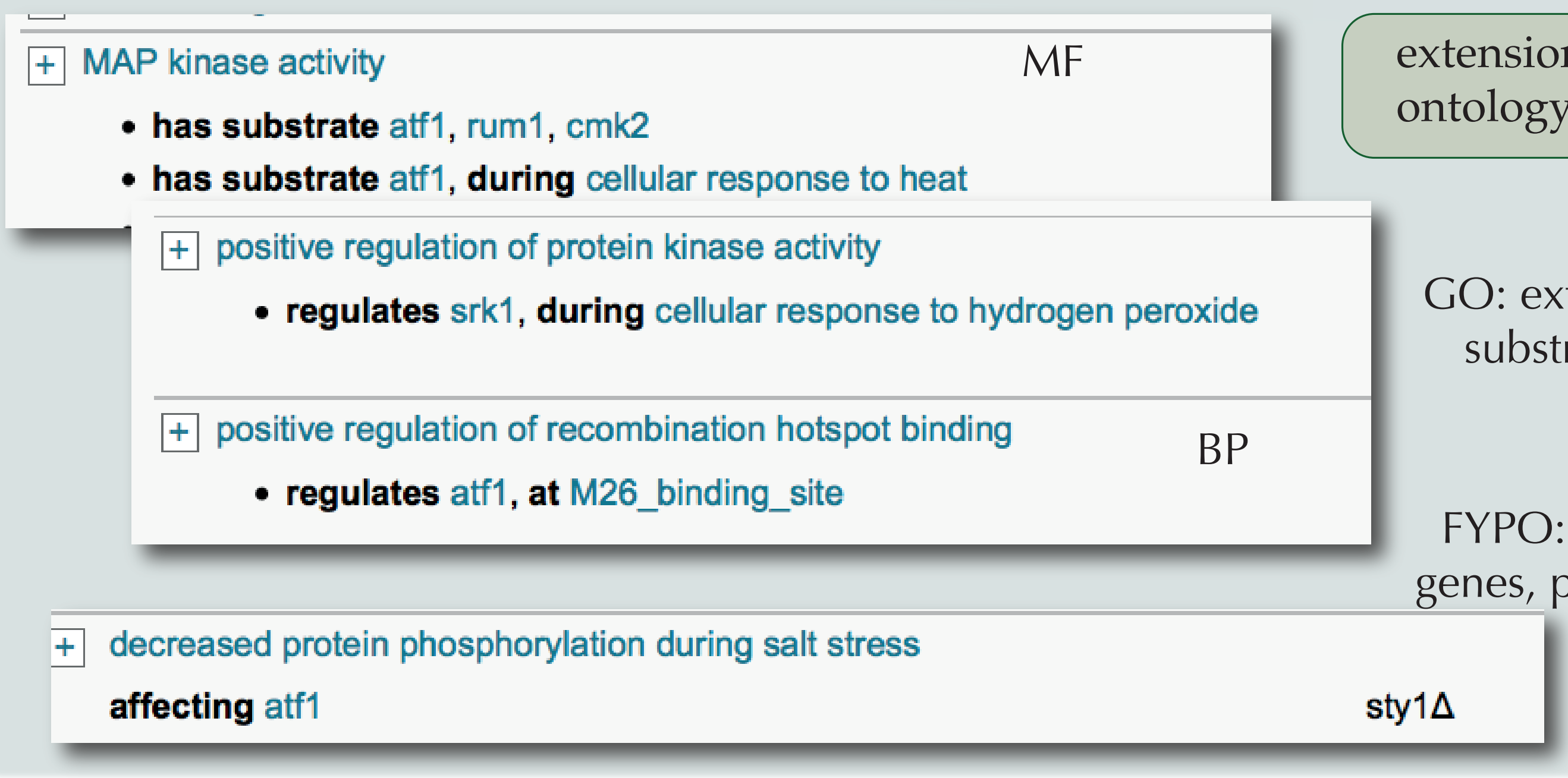
The fission yeast model organism database, PomBase, gathers and integrates a wide range of data about *Schizosaccharomyces pombe* biology. Annotations of function, phenotype, modification, expression, and sequence and structural features use ontologies to facilitate integration with data from other species as well as to capture links between different types of observations and inferences. By exploring the interconnections among different data types and databases, researchers can guide the interpretation of experimental and computational results, and discover promising topics and approaches for further study. We provide a graphical summary of data types and connections within and beyond PomBase.

Data types and links



Finding connections between data types

ontology annotation extensions



+ MAP kinase activity
- **has substrate** atf1, rum1, cmk2
- **has substrate** atf1, **during** cellular response to heat

+ positive regulation of protein kinase activity
- **regulates** srk1, **during** cellular response to hydrogen peroxide

+ positive regulation of recombination hotspot binding
- **regulates** atf1, **at** M26_binding_site

+ decreased protein phosphorylation during salt stress

affecting atf1 sty1Δ

extensions refer to other ontology terms or genes

GO: extensions identify substrates or timing

FYPO: extensions identify genes, proteins, etc. affected in a mutant

ontology term definitions

logical definitions in one ontology refer to other ontologies

abnormal actomyosin contractile ring assembly

quality—a PATO term

entity—a GO biological process term

FYPO

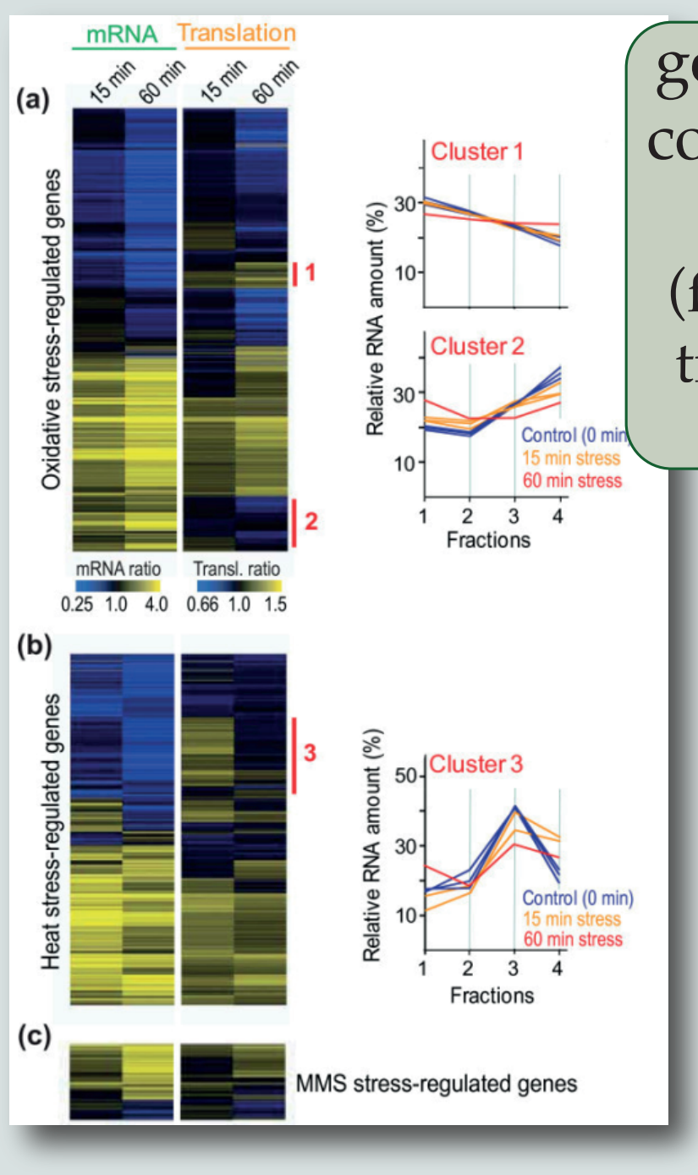
glucose metabolic process

substance—a ChEBI term

a general GO biological process term

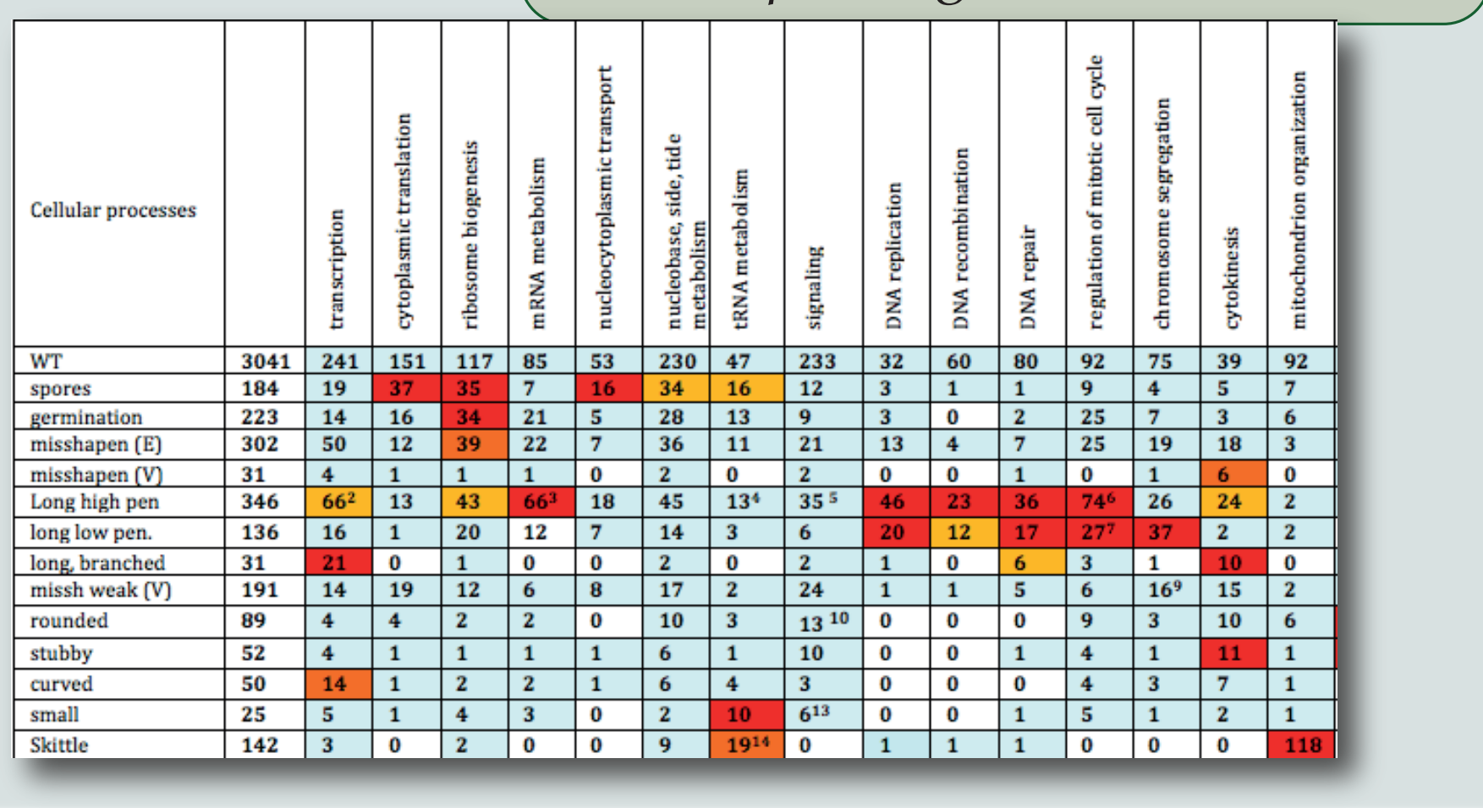
GO

ontology term enrichment analysis



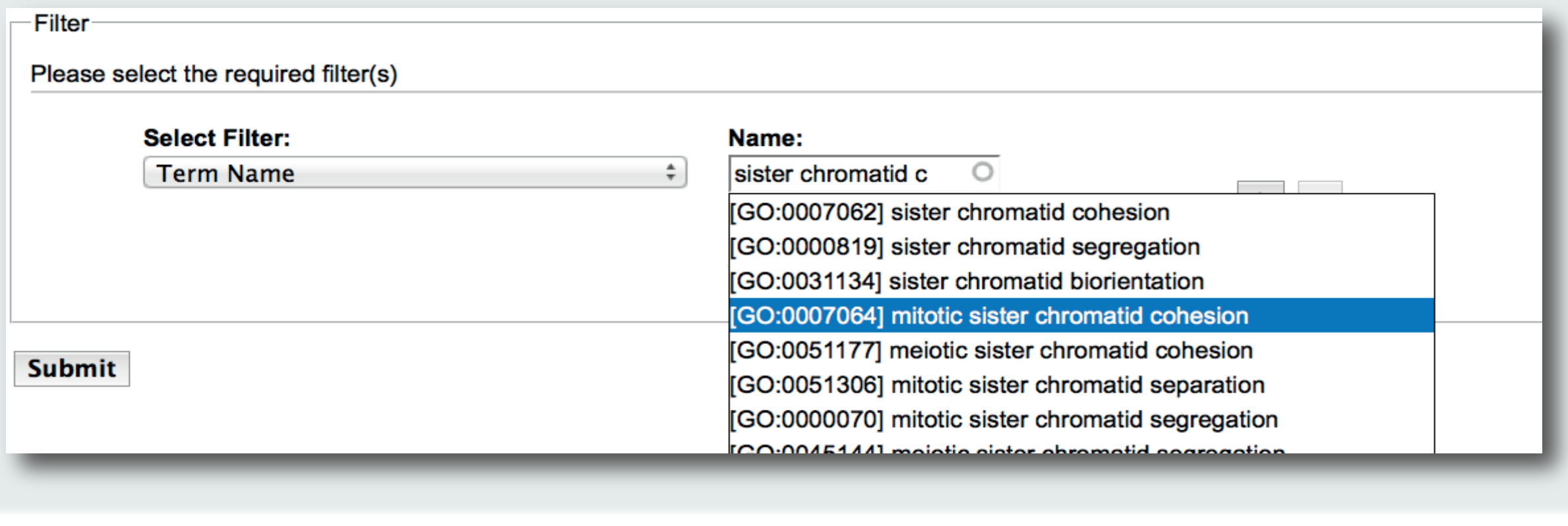
gene expression data correlated with annotated GO terms (future: also use additional ontologies, e.g. FYPO)

correlations between annotated GO and FYPO terms (*S. pombe* gene deletions)



Cellular processes		transcription	cytoplasmic translation	ribosome biogenesis	mRNA metabolism	nucleocytoplasmic transport	nucleobase, side, tide metabolism	tRNA metabolism	signaling	DNA replication	DNA recombination	DNA repair	regulation of mitotic cell cycle	chromosome segregation	cytokinesis	mitochondrion organization
WT	3041	241	151	117	85	53	230	47	233	32	60	80	92	75	39	92
spores	184	19	37	35	7	16	34	16	12	3	1	1	9	4	5	7
germination	223	14	16	34	21	5	28	13	9	3	0	2	25	7	3	6
misshapen (E)	302	50	12	39	22	7	36	11	21	13	4	7	25	19	18	3
misshapen (V)	31	4	1	1	1	0	2	0	2	0	0	1	0	1	6	0
Long high pen	346	66[2]	13	43	66[3]	18	45	13[4]	35 [5]	46	23	36	74[6]	26	24	2
long low pen.	136	16	1	20	12	7	14	3	6	20	12	17	27[7]	37	2	2
long, branched	31	21	0	1	0	0	2	0	2	1	0	6	3	1	10	0
missh weak (V)	191	14	19	12	6	8	17	2	24	1	1	5	6	16[9]	15	2
rounded	89	4	4	2	2	0	10	3	13 [10]	0	0	0	9	3	10	6
stubby	52	4	1	1	1	1	6	1	10	0	0	1	4	1	11	1
curved	50	14	1	2	2	1	6	4	3	0	0	0	4	3	7	1
small	25	5	1	4	3	0	2	10	6[13]	0	0	1	5	1	2	1
Skittle	142	3	0	2	0	0	9	19[14]	0	1	1	1	0	0	0	118

querying PomBase



Filter

Please select the required filter(s)

Select Filter: Term Name

Name: sister chromatid c

[GO:0007062] sister chromatid cohesion
[GO:0000819] sister chromatid segregation
[GO:0031134] sister chromatid biorientation
[GO:0007064] mitotic sister chromatid cohesion
[GO:0051177] meiotic sister chromatid cohesion
[GO:0051306] mitotic sister chromatid separation
[GO:0000070] mitotic sister chromatid segregation

retrieve genes annotated to an ontology term

future: retrieve other annotations for genes in results set

Acknowledgements

PomBase is funded by the Wellcome Trust, and is run by a consortium comprising the University of Cambridge, the European Bioinformatics Institute and University College London. FYPO logo: Jonathan Lawson. Gene expression figure: Lackner, D.H. *et al.* (2012). *Genome Biology* **13(4)**: R25.