

Constructing AGR GO slim

1. Experimental GO annotations from

- Human
- Mouse
- Rat
- Zebrafish
- Fly
- C elegans
- Yeast

Filter out NOTs, dual taxa

Include inferred annotations using all relationships

2. Consider number of annotations to term, depth in DAG, information content

Select terms

Eliminate parent-child terms

Analyze what terms and objects are in and out

3. Manual review of terms displayed graphically

Revise

Go to step 2

What is included/excluded from slim?

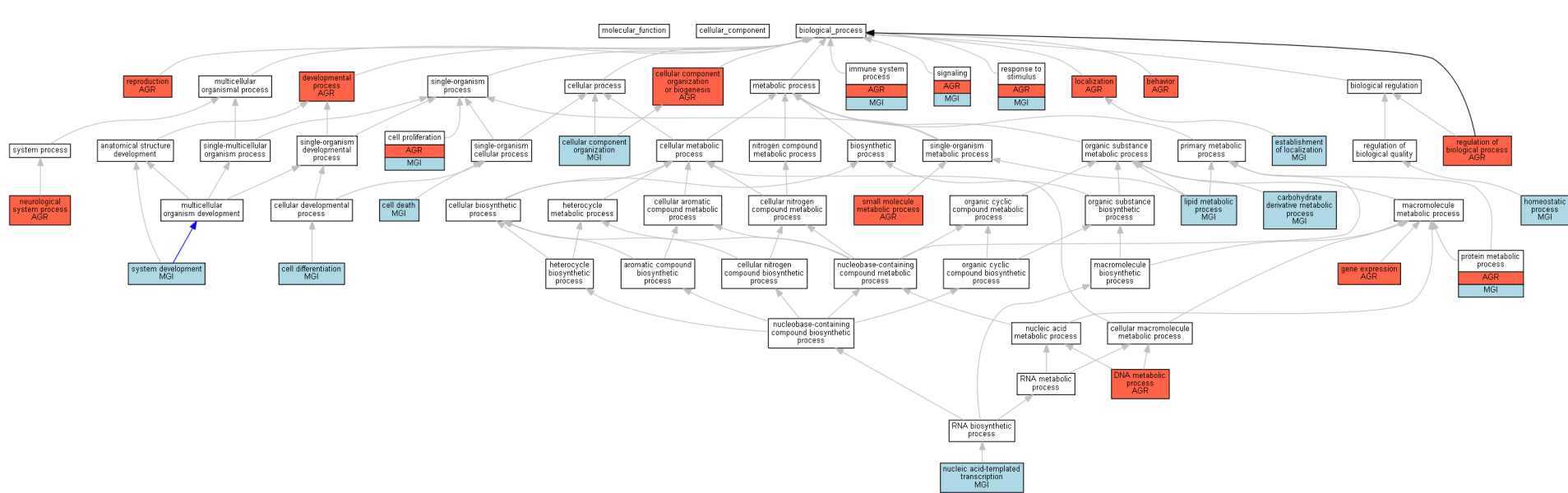
genes			
DB	genes_all	genes_out	
FB	7361	307	4%
MGI	11088	816	7%
RGD	5395	372	7%
SGD	5398	211	4%
UniProtKB	11980	1965	16%
WB	3305	574	17%
ZFIN	4421	322	7%

go_terms				
Aspect	go_id_all	go_id_in	go_id_out	
C	1863	1532	331	18%
F	4295	3550	745	17%
P	14084	12690	1394	10%

Compare MGI slim and initial proposed AGR slim

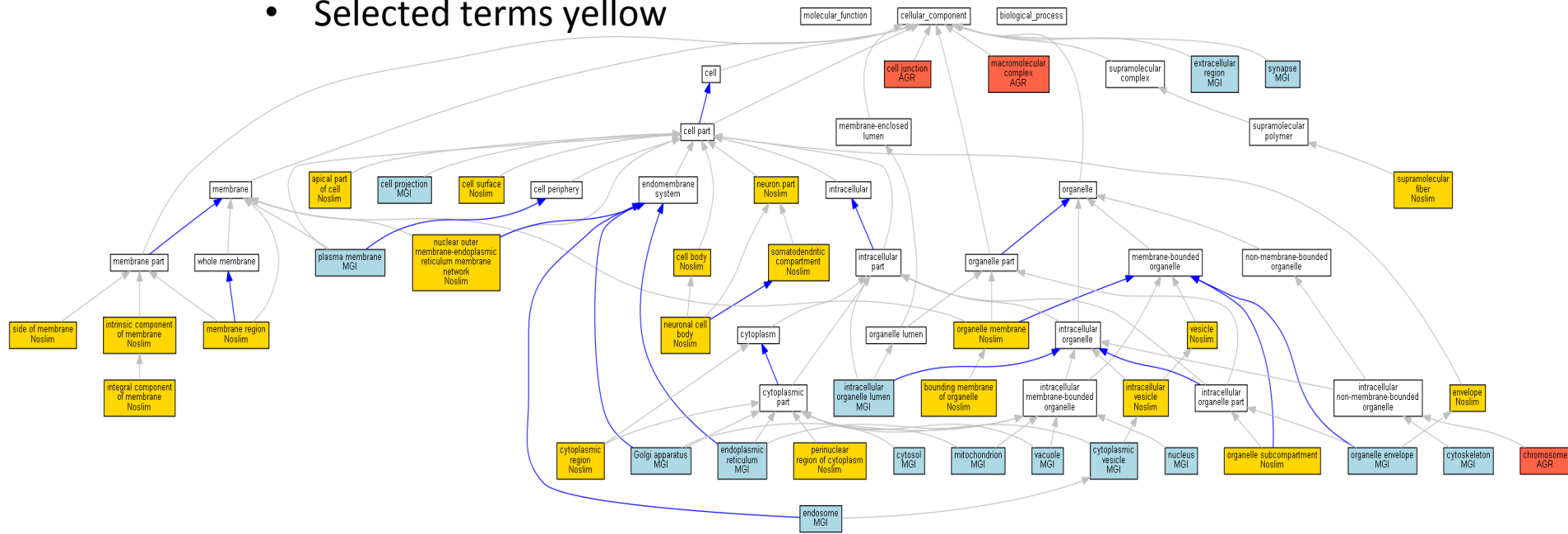
Biological Process

- MGI blue
- AGR red



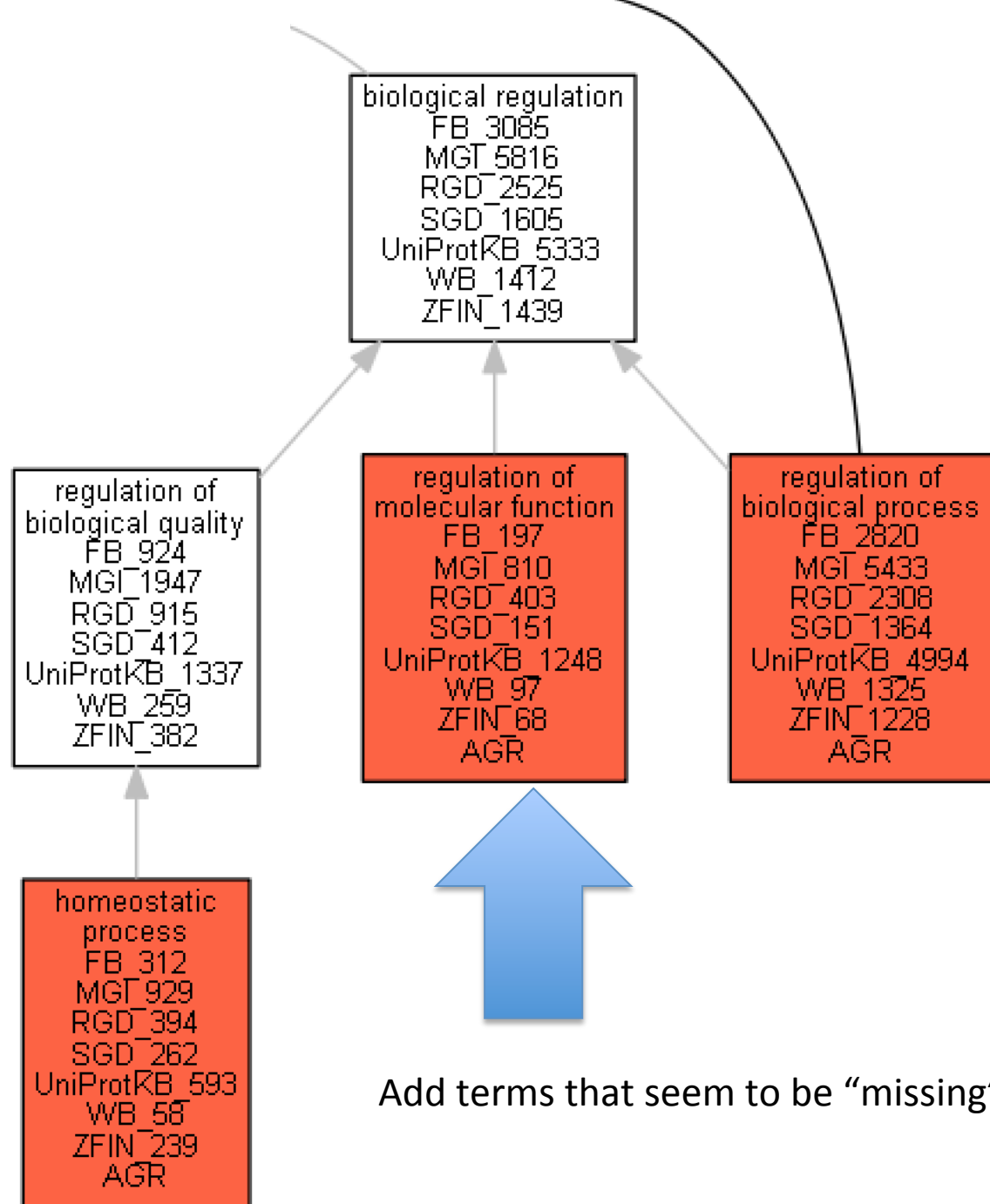
Compare refined MGI-AGR slim Cellular Component

- MGI blue
- AGR red
- Selected terms yellow

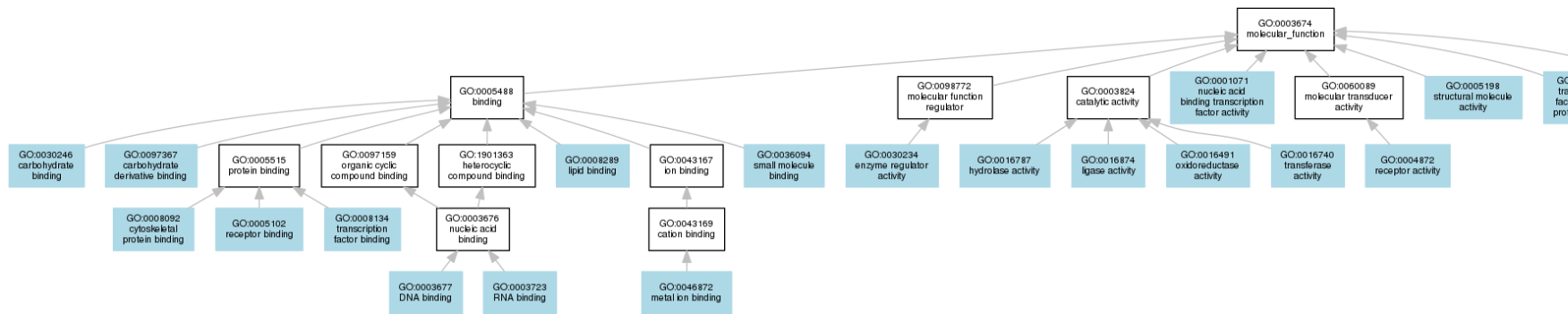




Some terms do not include annotations from all organisms



Molecular Function



Biological Process

