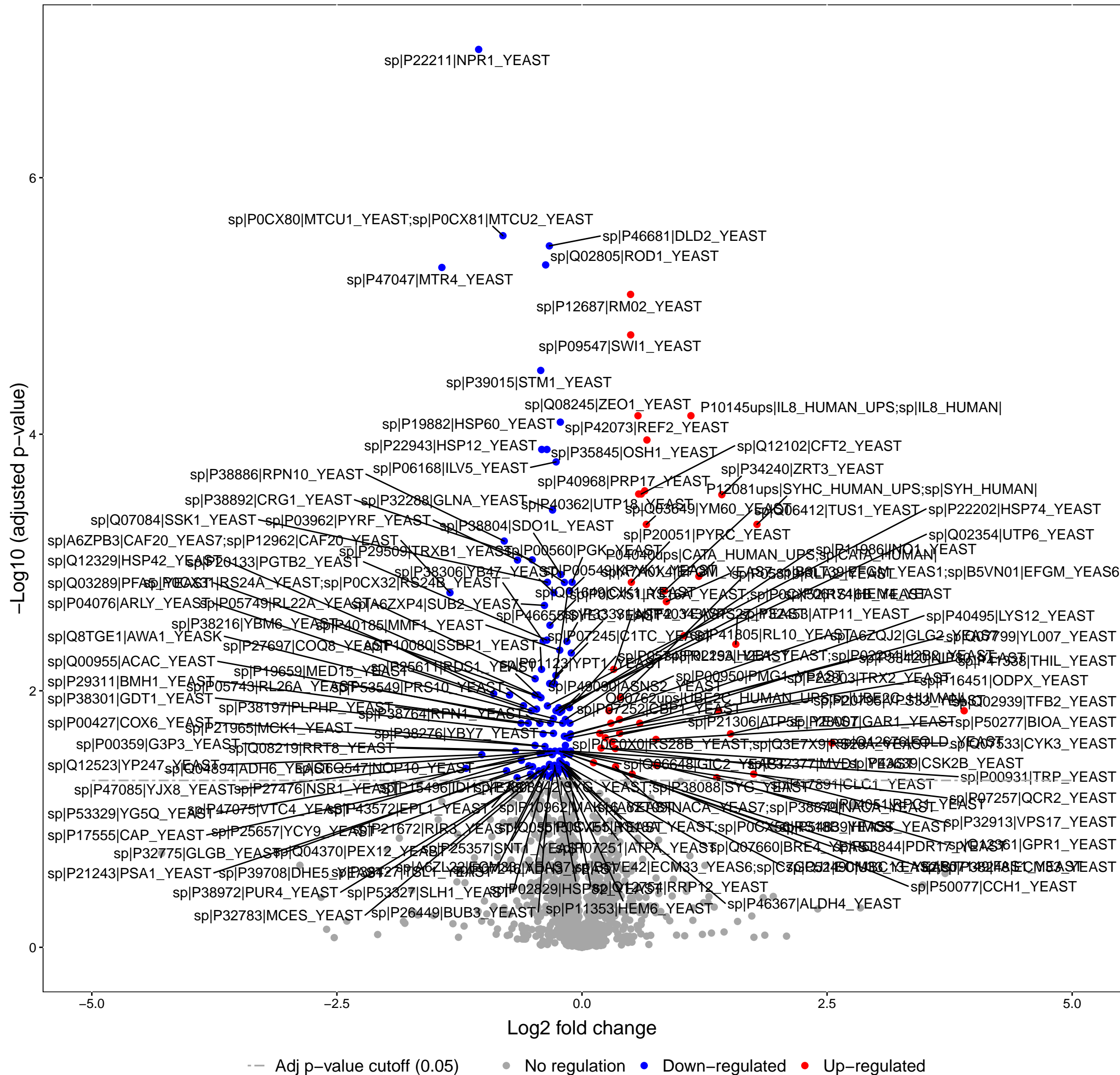
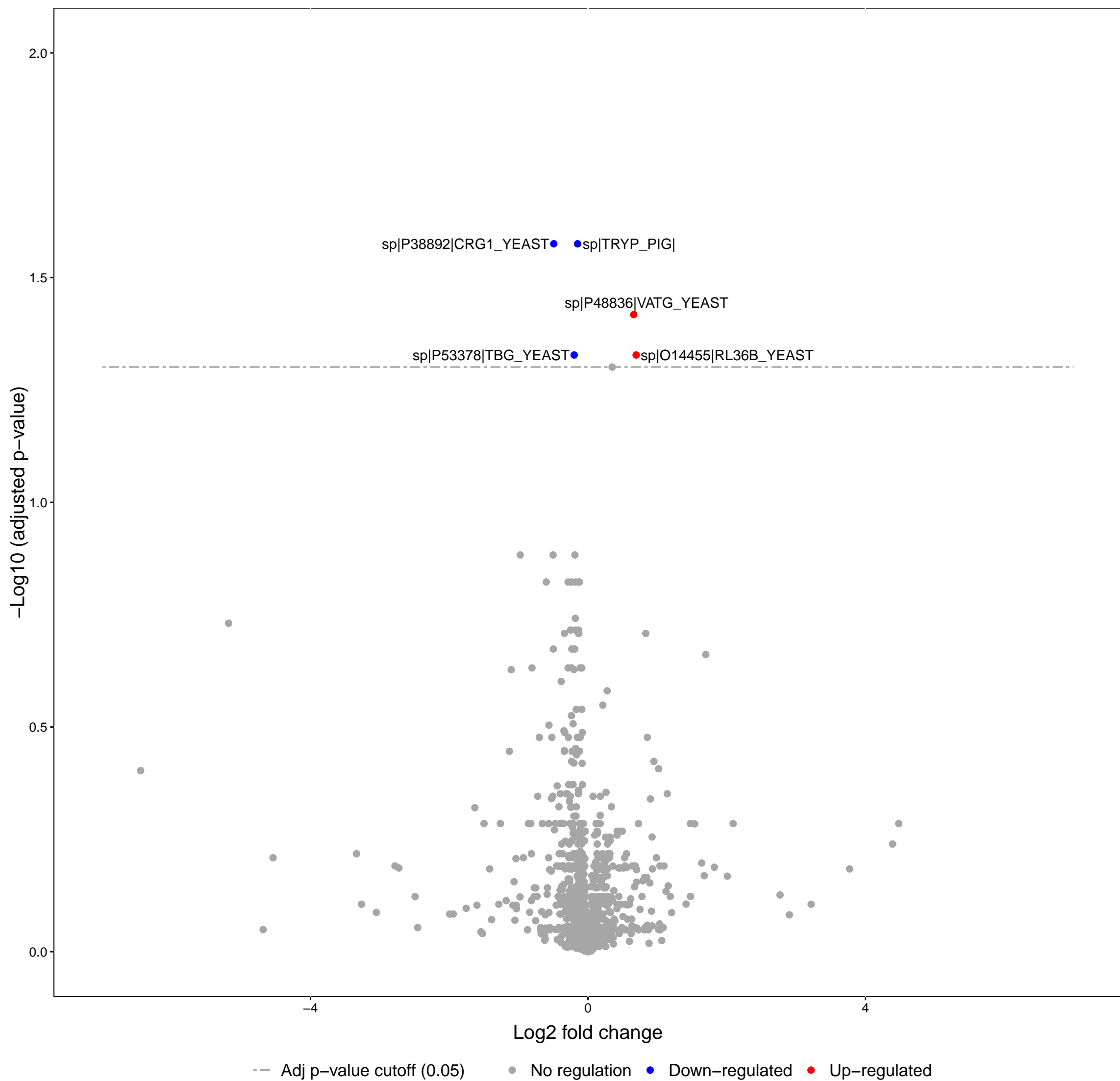


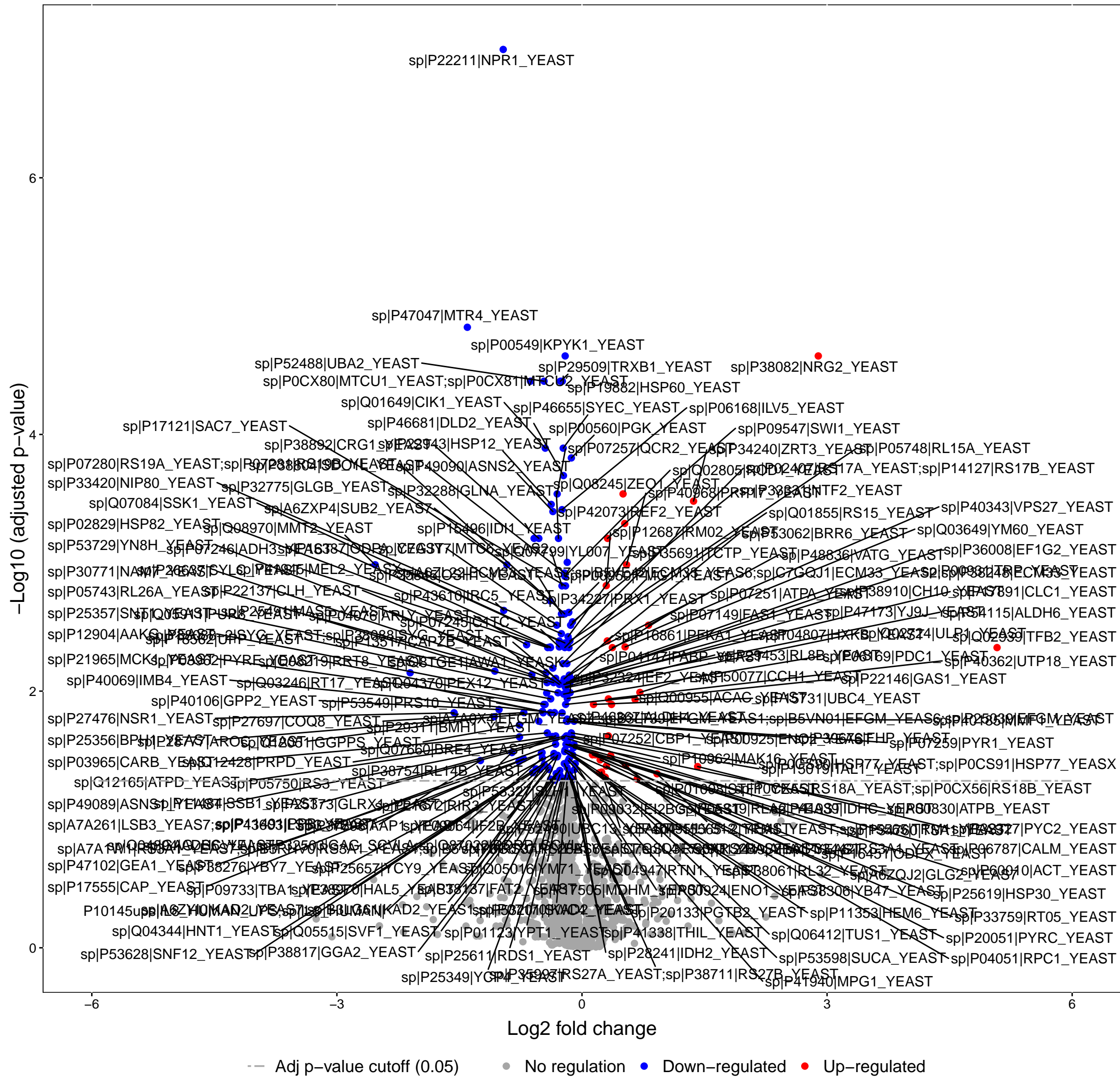
125 amol–12500 amol



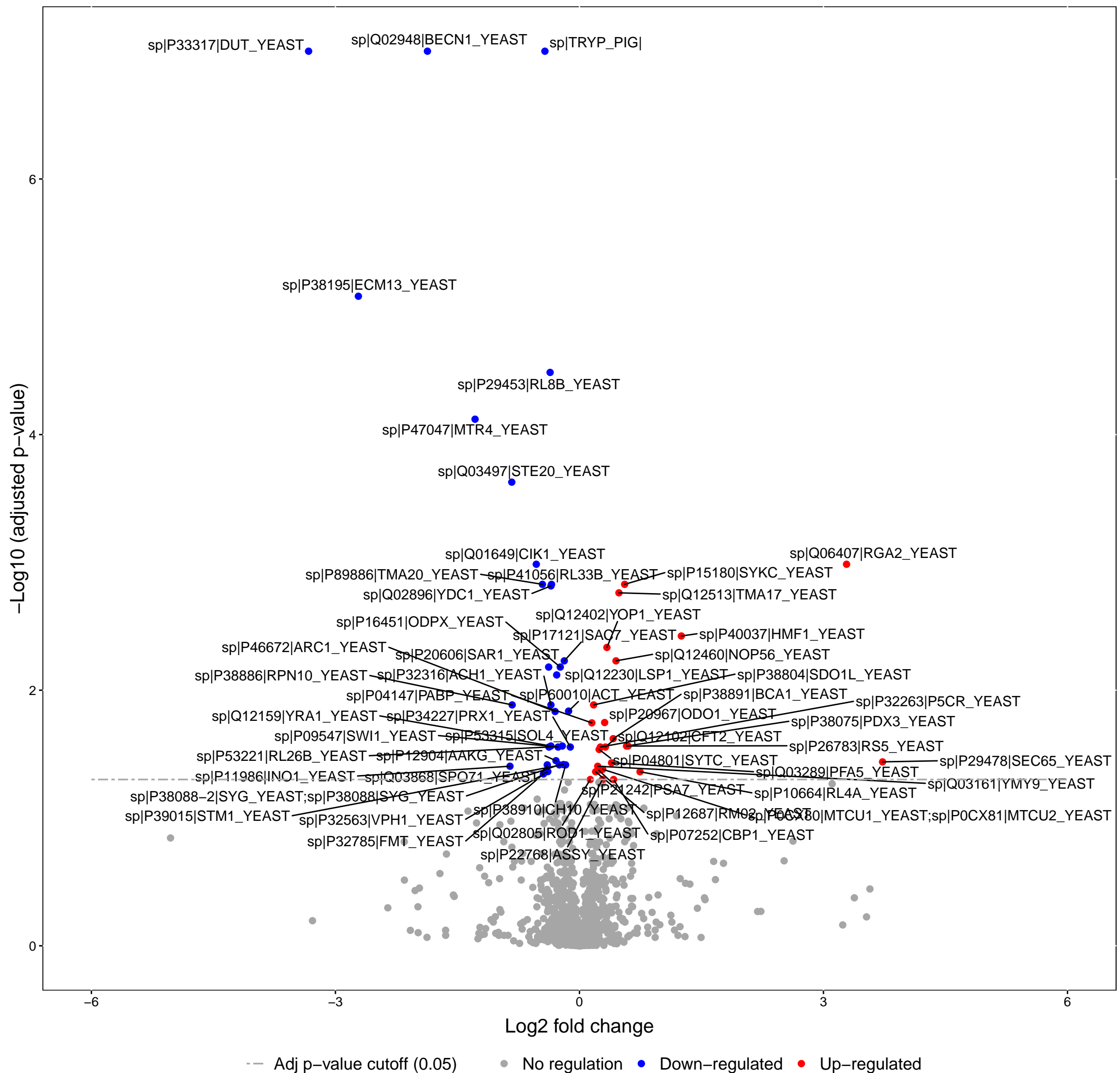
125 amol–250 amol



125 amol–2500 amol

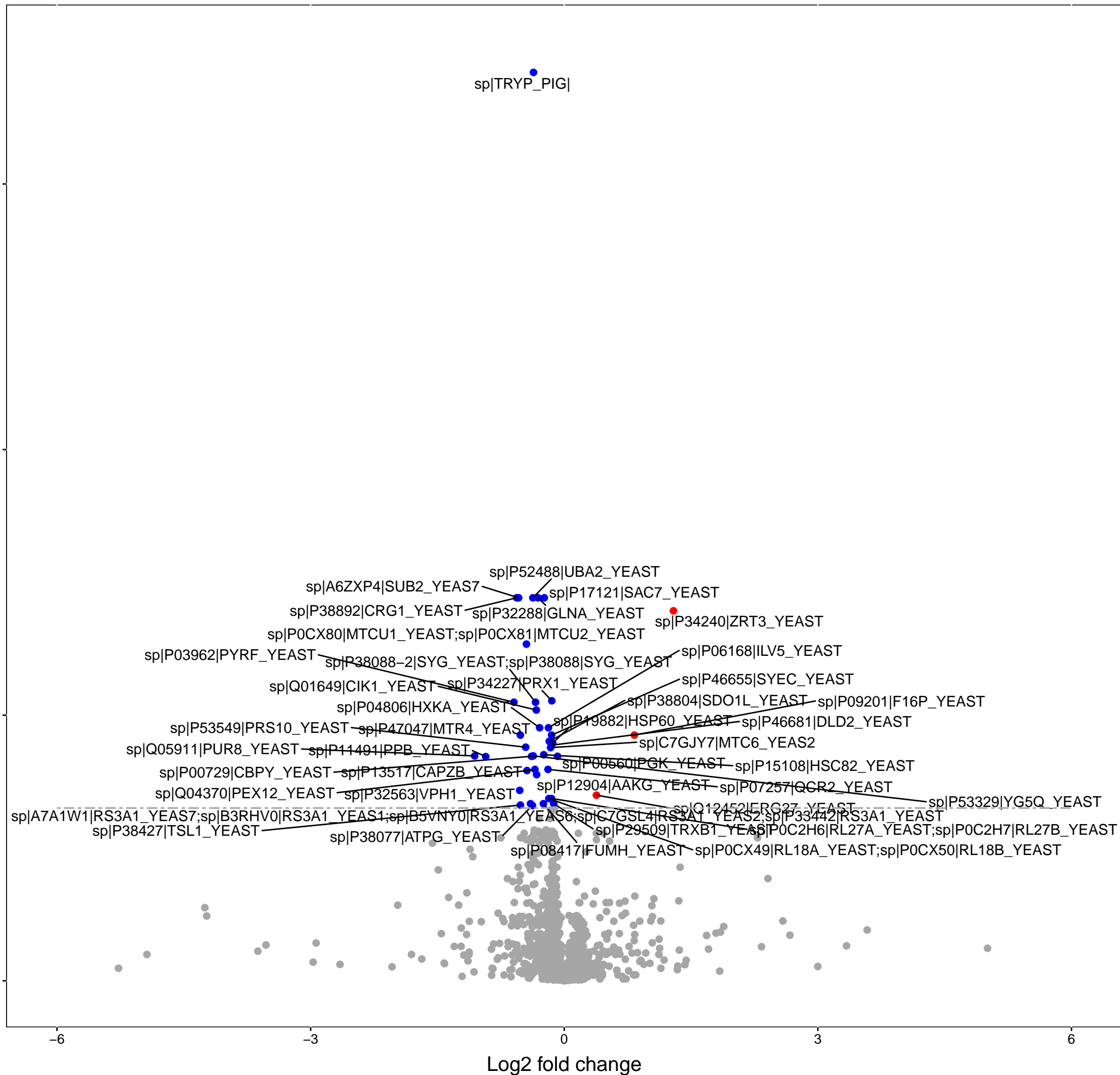


125 amol–50 amol



125 amol–500 amol

–Log10 (adjusted p–value)



-- Adj p–value cutoff (0.05)

● No regulation

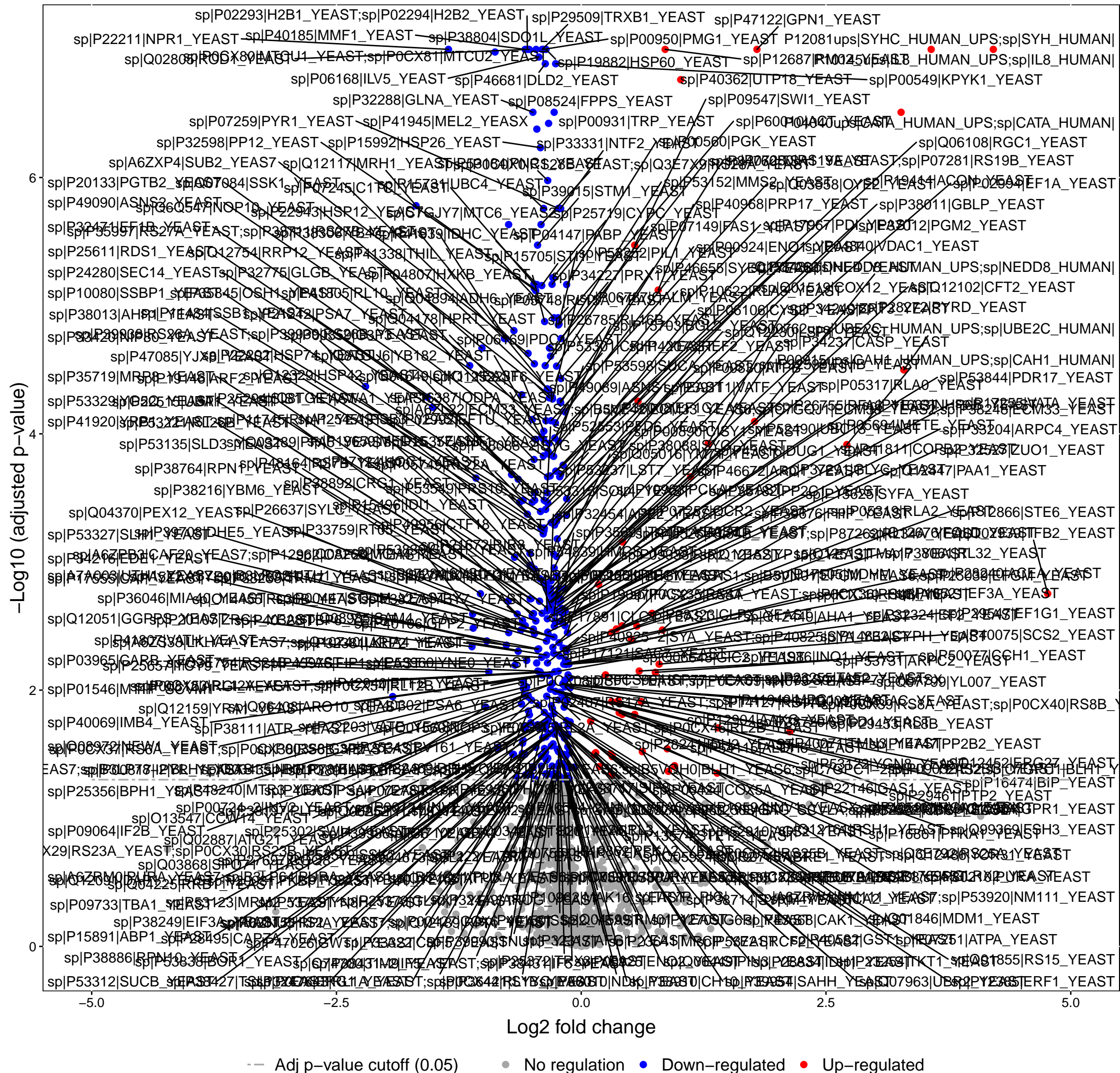
● Down–regulated

● Up–regulated

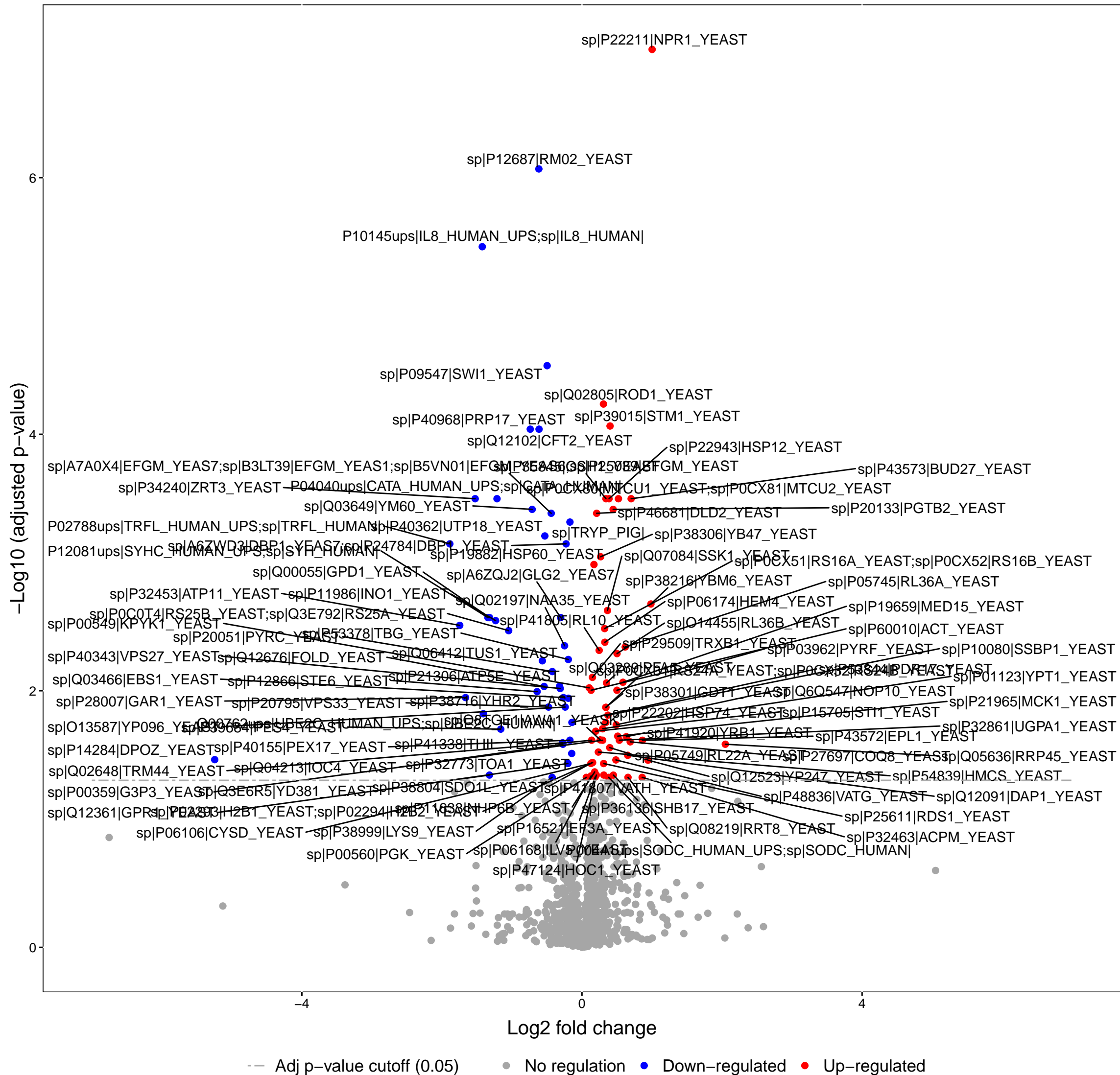
[illegible]

- Up-regulated

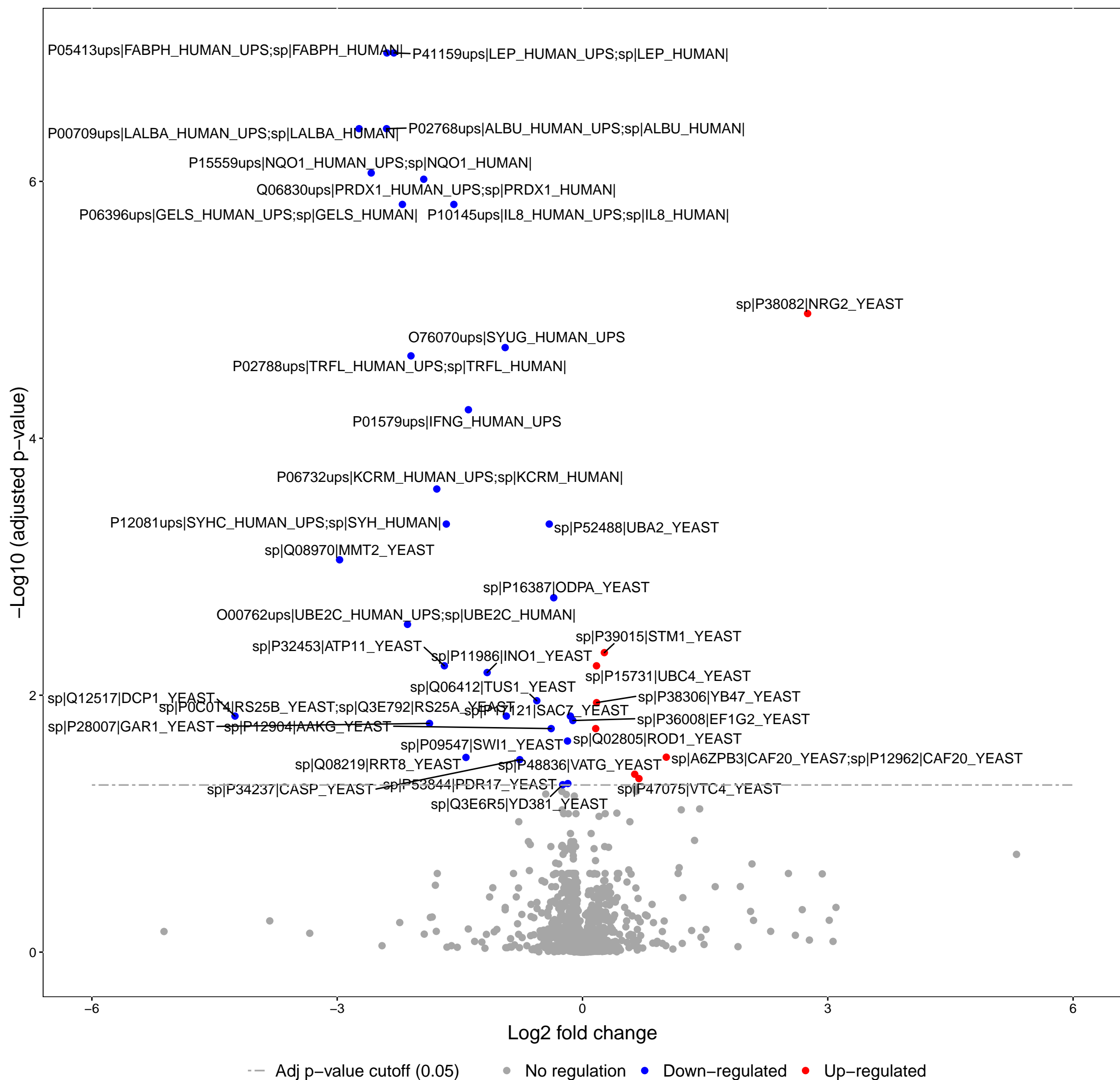
125 amol–50000 amol



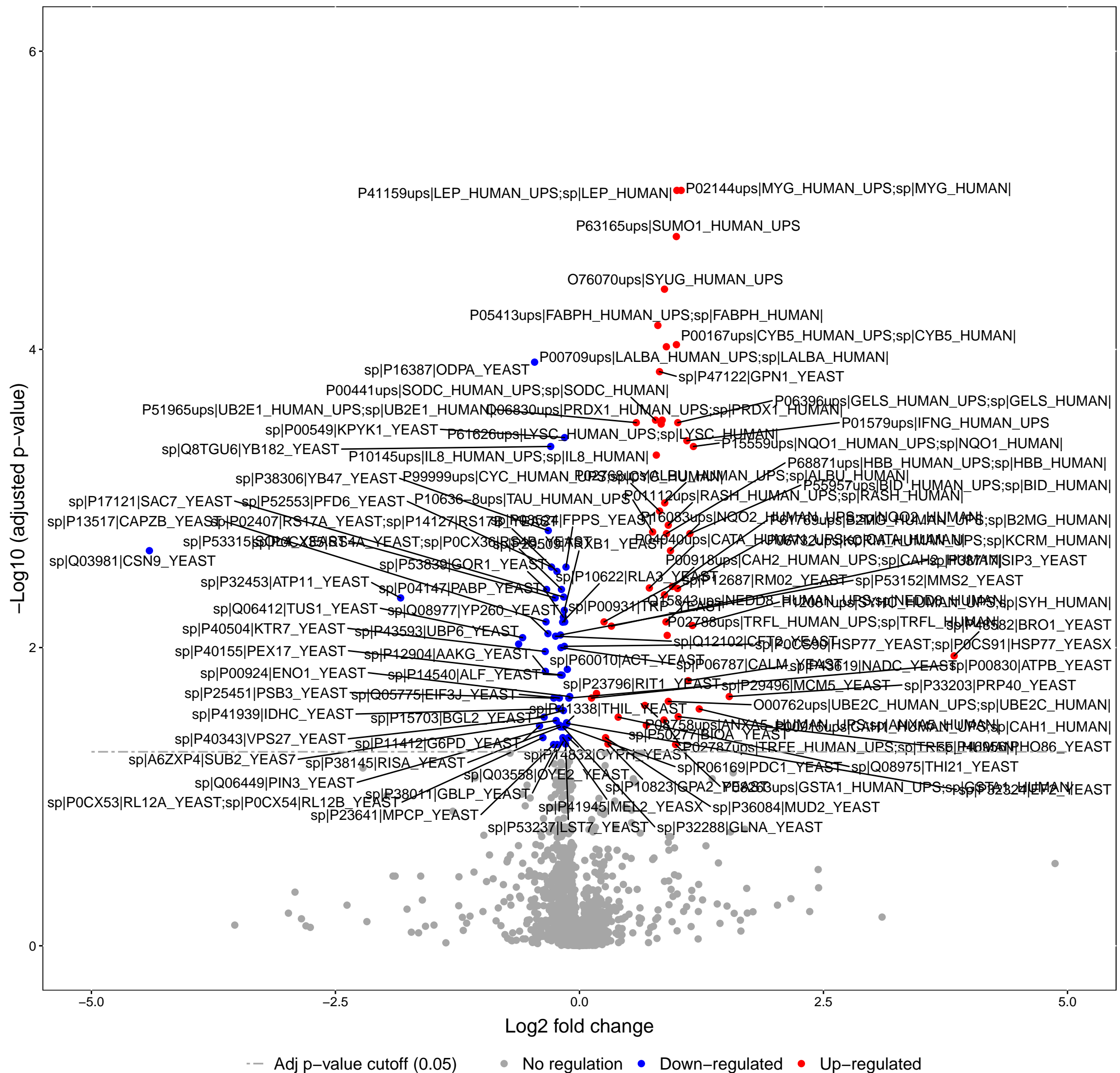
12500 amol–250 amol



12500 amol–2500 amol



12500 amol–25000 amol

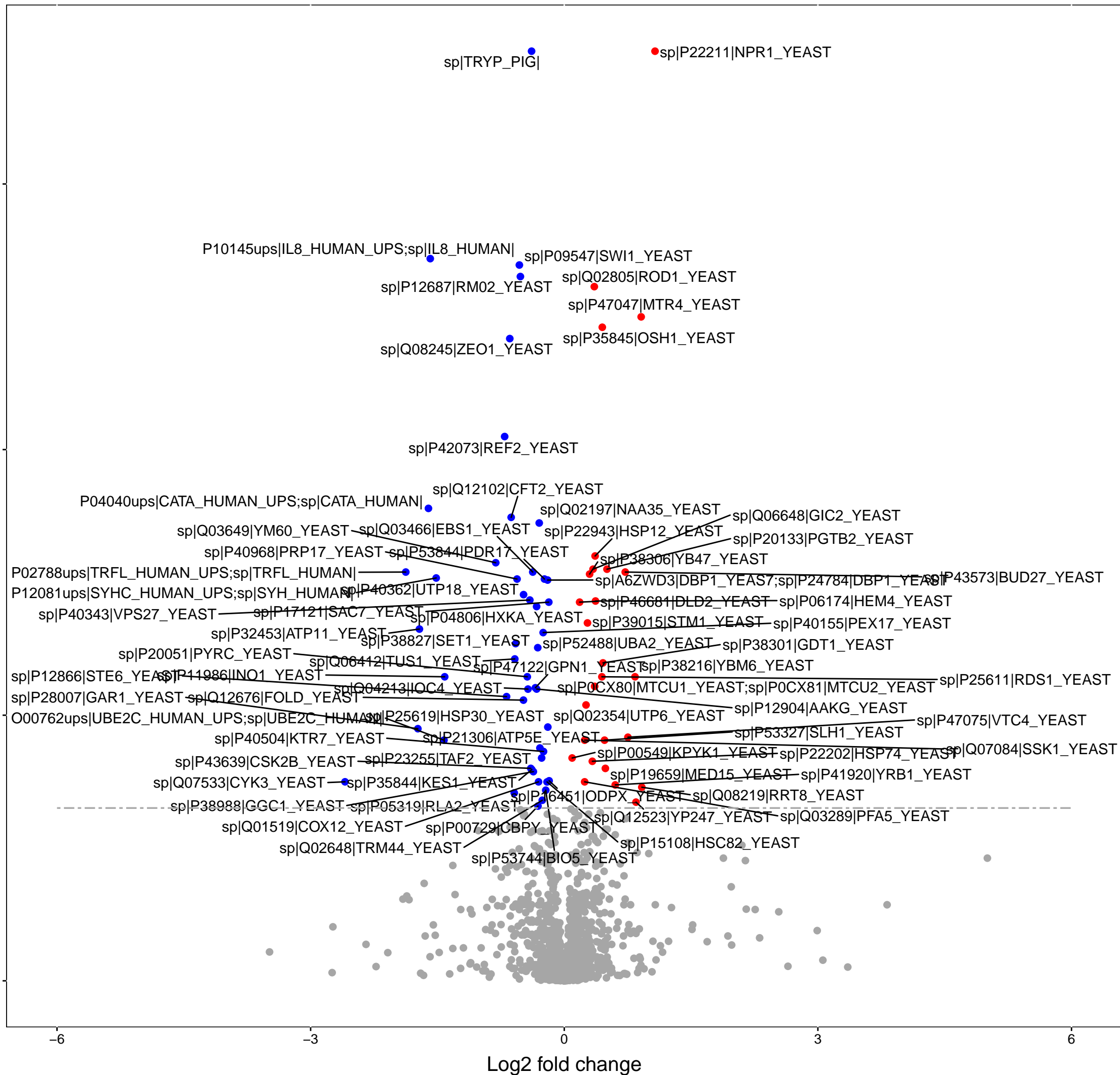


[illegible]

- Up-regulated

12500 amol–500 amol

–Log10 (adjusted p–value)



-- Adj p–value cutoff (0.05)

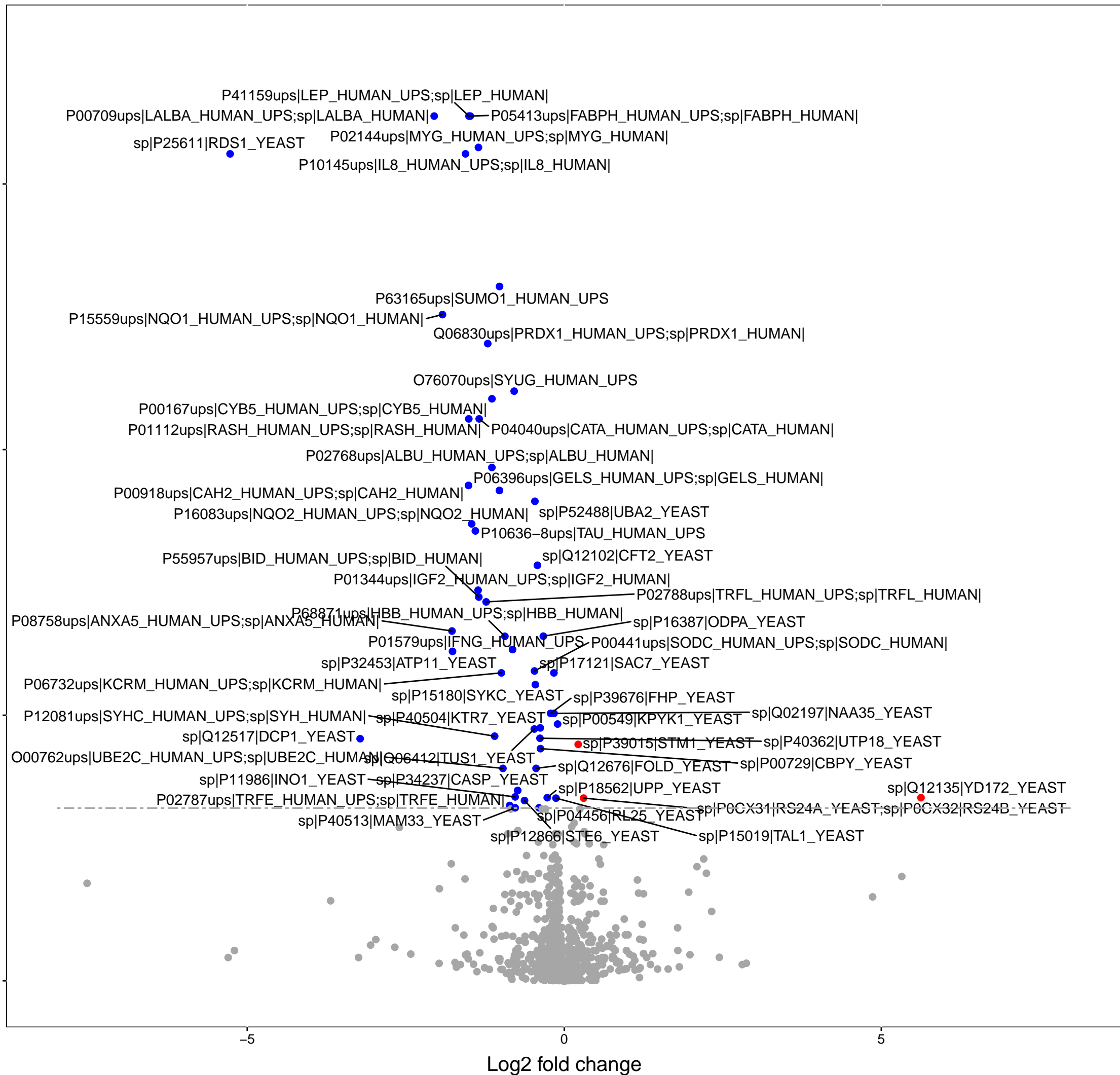
● No regulation

● Down–regulated

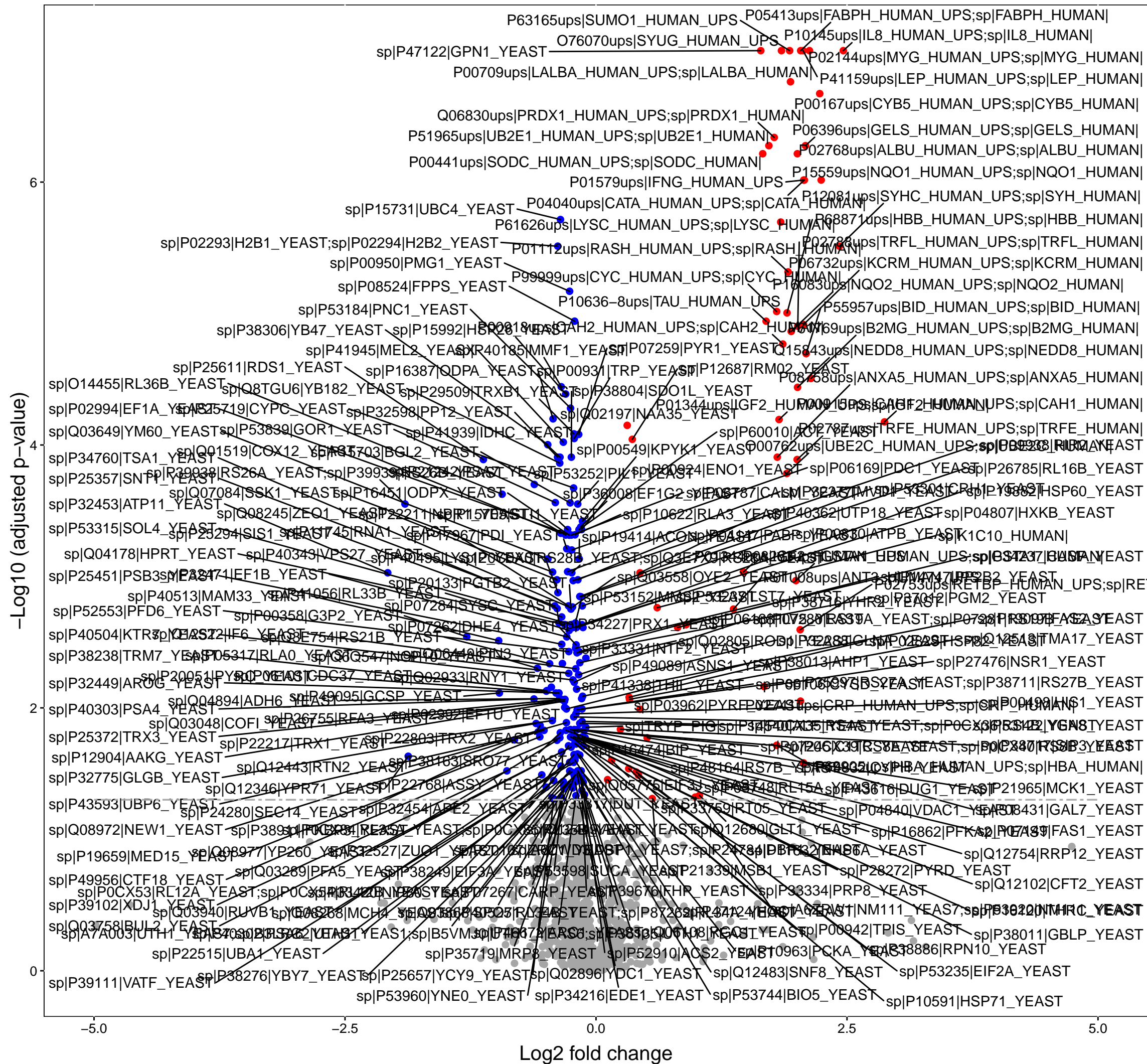
● Up–regulated

12500 amol–5000 amol

–Log10 (adjusted p–value)



12500 amol–50000 amol



Volcano plot showing Log2 fold change (X-axis) versus -Log10(p-value) (Y-axis). The plot displays a dense cluster of grey points at the bottom, indicating non-significant changes. Points are colored blue for downregulated proteins (Log2 fold change < -1) and red for upregulated proteins (Log2 fold change > 1). Labeled points include:

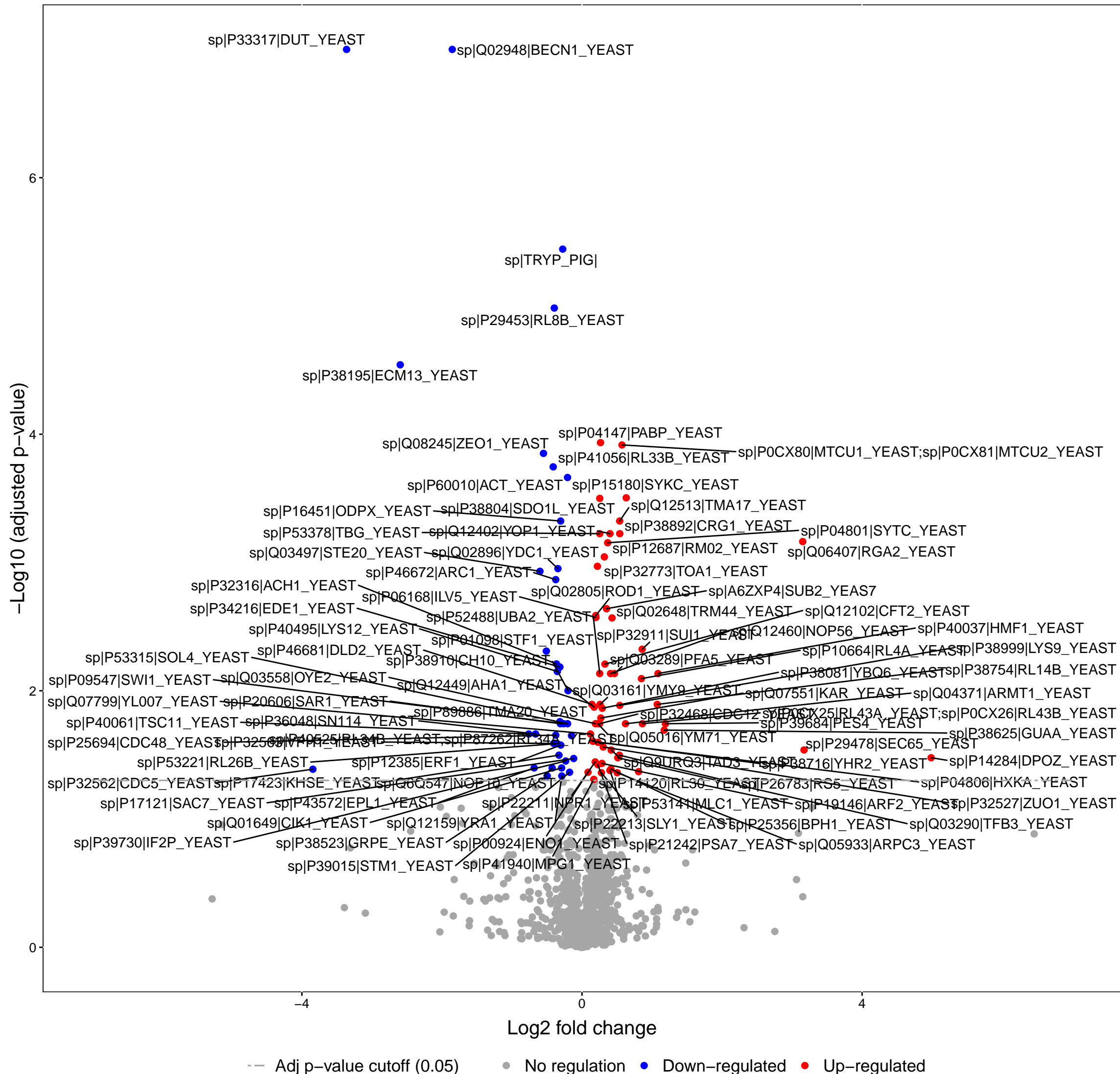
- sp|P22211|NPR1_YEAST
- sp|P38082|NRG2_YEAST
- sp|P00549|KPYK1_YEAST
- sp|P12687|RM02_YEAST
- sp|P29509|TRXB1_YEAST
- sp|P40968|PRP17_YEAST
- sp|P43573|BUD27_YEAST
- sp|P19882|HSP60_YEAST
- sp|P34240|ZRT3_YEAST
- sp|Q08970|MMT2_YEAST
- sp|P52488|UBA2_YEAST
- sp|P22943|HSP12_YEAST
- sp|A6ZWD3|DBP1_YEAST
- sp|P24784|IDBP1_YEAST
- sp|P09547|SWI1_YEAST
- sp|P60010|ACT_YEAST
- sp|B3139|EFGM_YEAST
- sp|B5VN01|EFGM_YEAST
- sp|P25039|EFGM_YEAST
- sp|P43610|IRC5_YEAST
- sp|P07257|QCR2_YEAST
- sp|P38716|YHR2_YEAST
- sp|P35845|OSH1_YEAST
- sp|P53378|TBG_YEAST
- sp|P00560|PGK_YEAST
- sp|P15496|IDI1_YEAST
- sp|P20133|PGTB2_YEAST
- sp|P38910|CH10_YEAST
- sp|P29453|RL8B_YEAST
- sp|P35691|TCTP_YEAST
- sp|P53062|BRR6_YEAST
- sp|Q12374|NCA2_YEAST
- sp|P25491|MAS52B0519A_YEAST
- sp|P07281|P3327_YEAST
- sp|Q03649|YM60_YEAST
- sp|P49090|ASNS2_YEAST
- sp|P46655|SYEC_YEAST
- sp|Q07084|SSK1_YEAST
- sp|P00950|PMG1_YEAST
- sp|P15731|UBC4_YEAST
- sp|P38216|YBM6_YEAST
- sp|P32751|PQCX80_YEAST
- sp|P0CX81|MTCU2_YEAST
- sp|C7GJY7|MTC6_YEAST
- sp|P00950|PMG1_YEAST
- sp|P15731|UBC4_YEAST
- sp|Q12165|ATPD_YEAST
- sp|Q08219|IRRT8_YEAST
- sp|P21965|MCK1_YEAST
- sp|Q08TGL1|AWA1_YEAST
- sp|A6ZQJ2|GLG2_YEAST
- sp|P22146|GAS1_YEAST
- sp|Q12517|DCP1_YEAST
- sp|P40825-2|SYA_YEAST
- sp|P40825|SYA_YEAST
- sp|P47121|SAC7_YEAST
- sp|A6Z4J1|MYO3_YEAST
- sp|P30006|MYO3_YEAST
- sp|P0CS91|HSP77_YEAST
- sp|P02829|HSP82_YEAST
- sp|Q03246|RT17_YEAST
- sp|P15705|STI1_YEAST
- sp|P06106|CYSD_YEAST
- sp|P32324|EF2_YEAST
- sp|P06169|PDC1_YEAST
- sp|P25694|CDC48_YEAST
- sp|P13517|CAPZB_YEAST
- sp|P09733|TBA1_YEAST
- sp|P89105|CTR9_YEAST
- sp|Q02197|NAA35_YEAST
- sp|P33420|NIP80_YEAST
- sp|P06102|NOT3_YEAST
- sp|P04076|ARLY_YEAST
- sp|P38804|SDO1L_YEAST
- sp|P19097|FAS2_YEAST
- sp|Q02981|YP109_YEAST
- sp|P28777|AROC_YEAST
- sp|Q05636|RRP45_YEAST
- sp|Q04370|PEX12_YEAST
- sp|P38061|RL32_YEAST
- sp|P38306|YB47_YEAST
- sp|P00931|TRP_YEAST
- sp|P05745|RL36A_YEAST
- sp|P46367|ALDH4_YEAST
- sp|Q01649|CK1_YEAST
- sp|Q03290|TFB3_YEAST
- sp|P40362|UTP18_YEAST
- sp|P16387|ODPA_YEAST
- sp|P03965|CARB_YEAST
- sp|P41945|MEL2_YEAST
- sp|P41805|RL10_YEAST

- Up-regulated

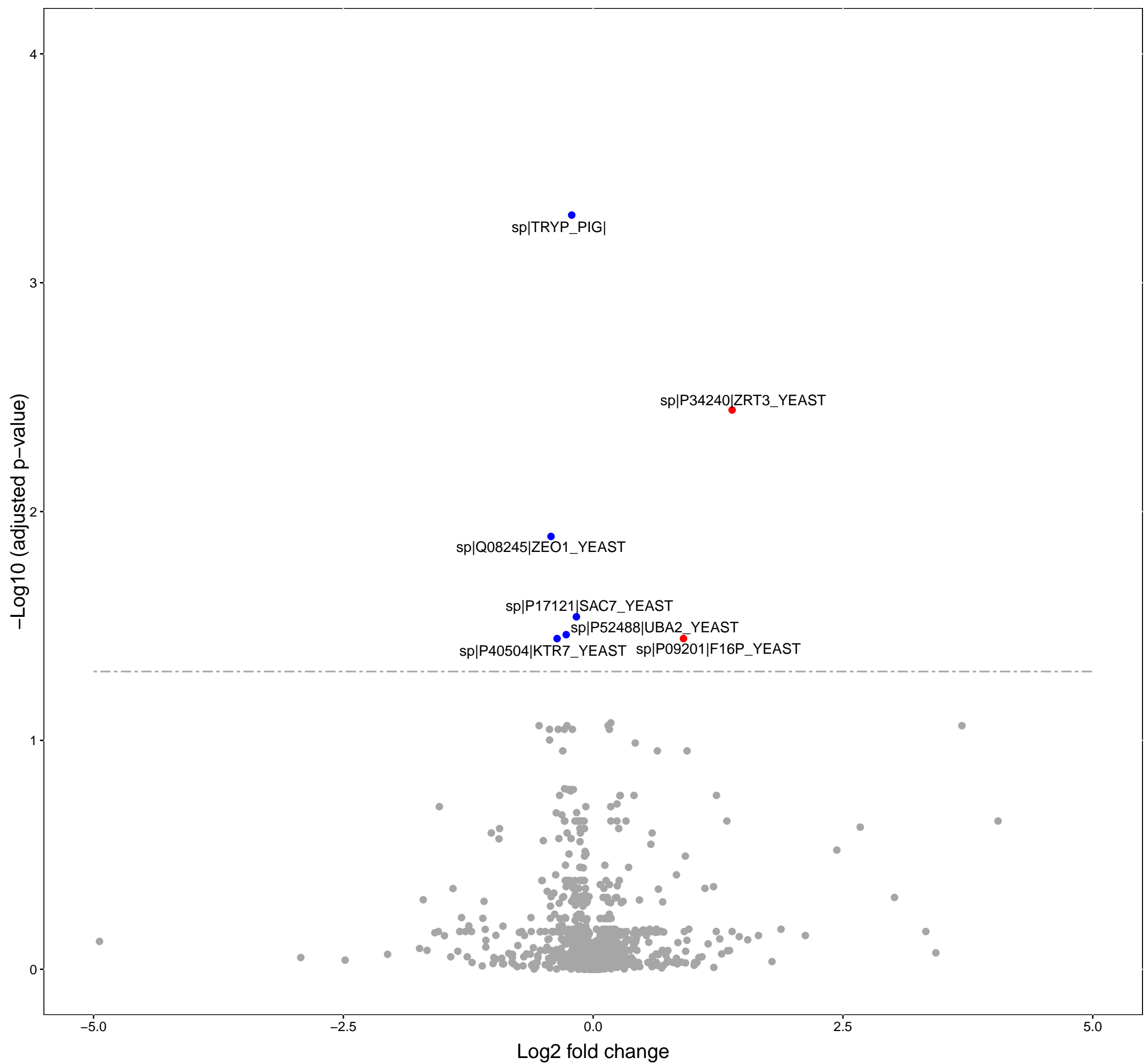
[illegible]

- Up-regulated

250 amol–50 amol

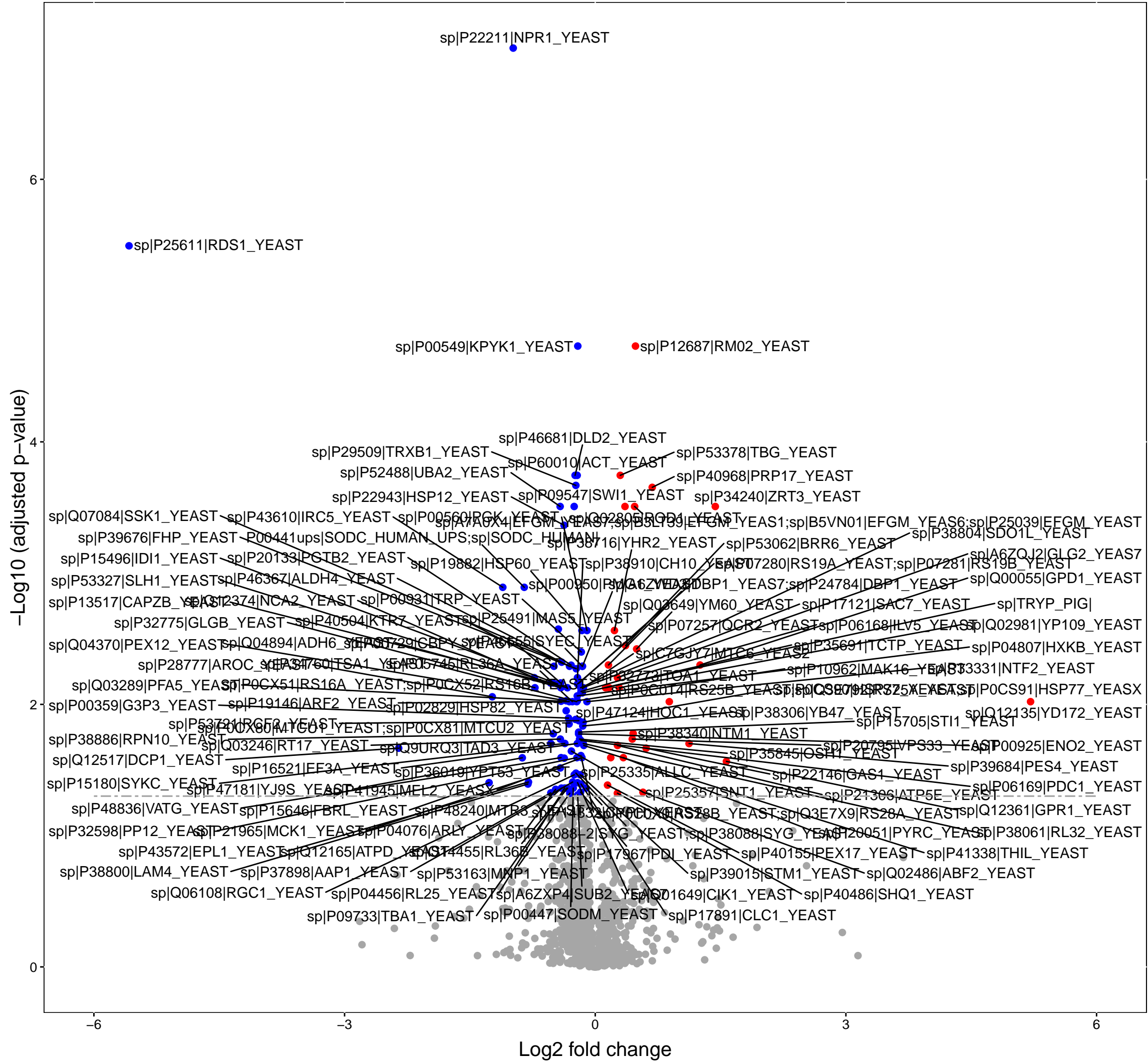


250 amol–500 amol

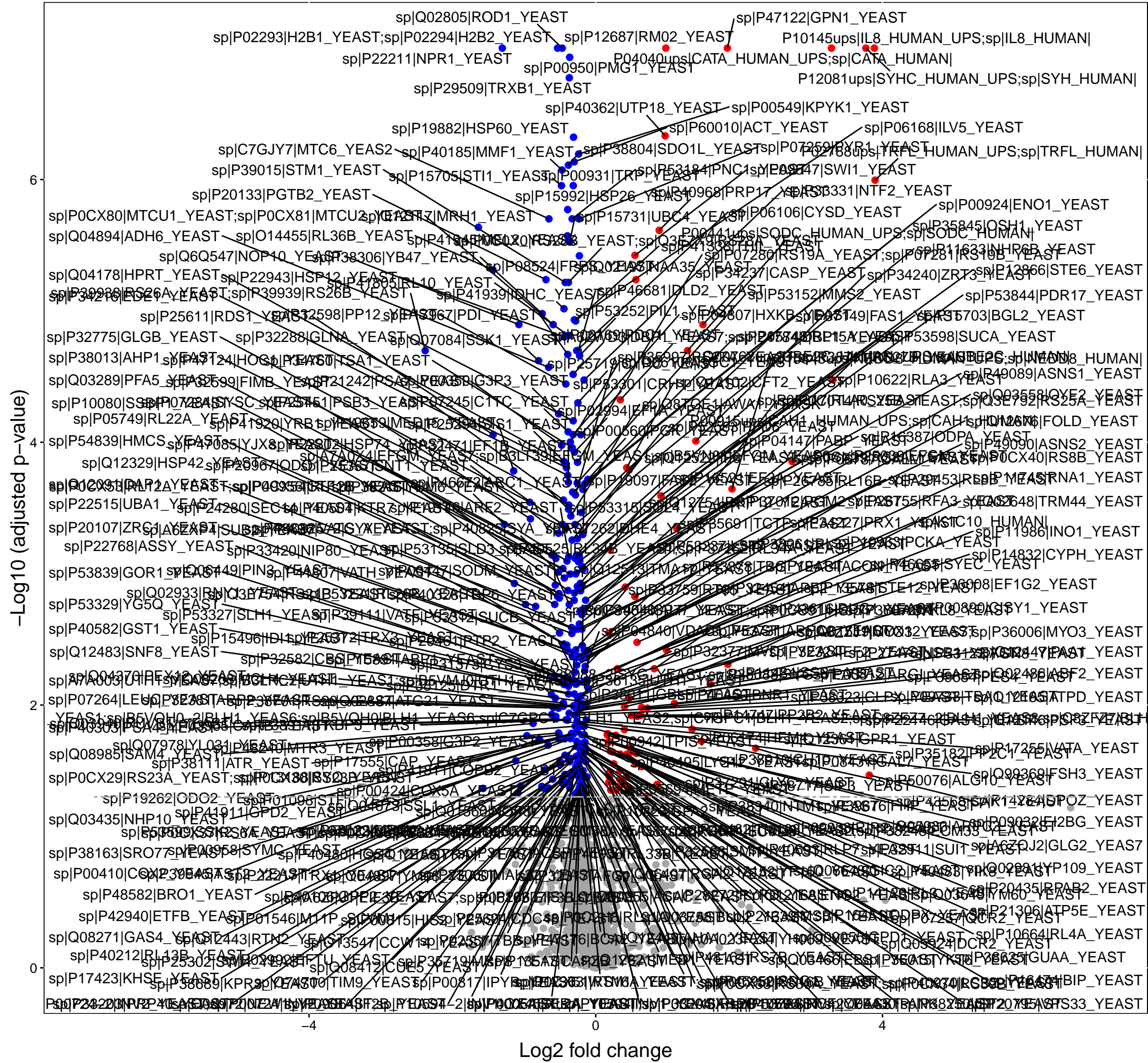


-- Adj p-value cutoff (0.05) ● No regulation ● Down-regulated ● Up-regulated

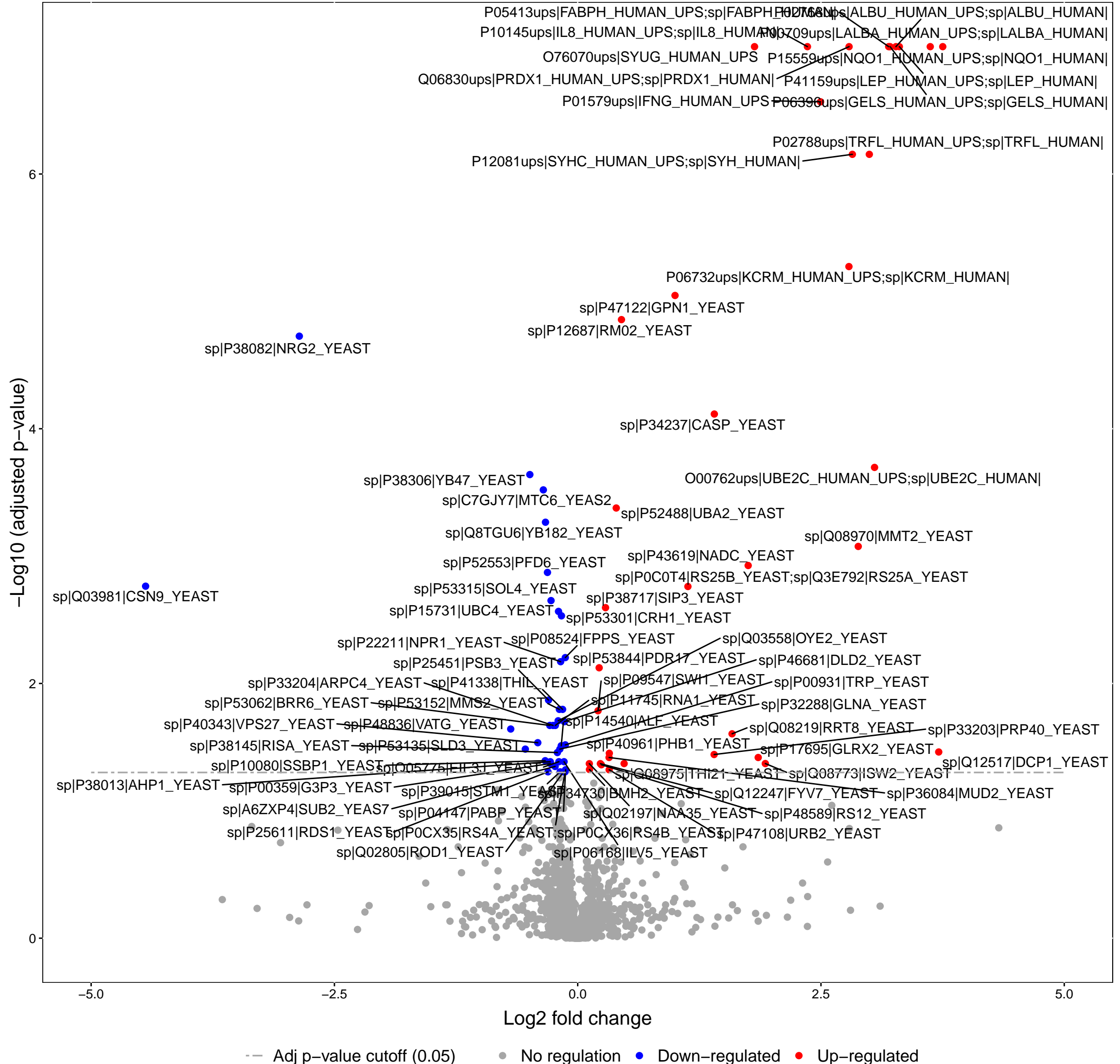
250 amol–5000 amol



250 amol–50000 amol

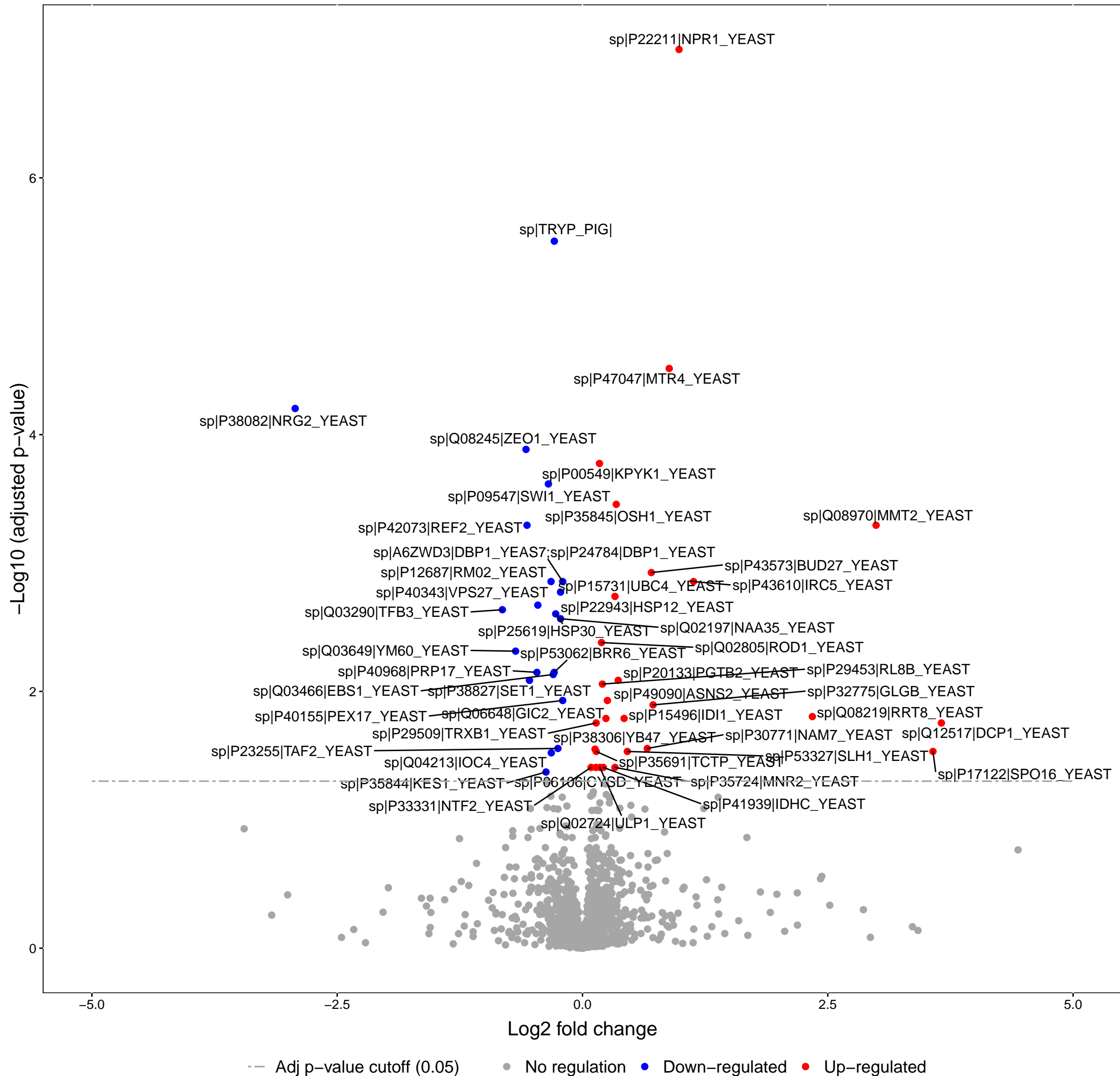


2500 amol–25000 amol

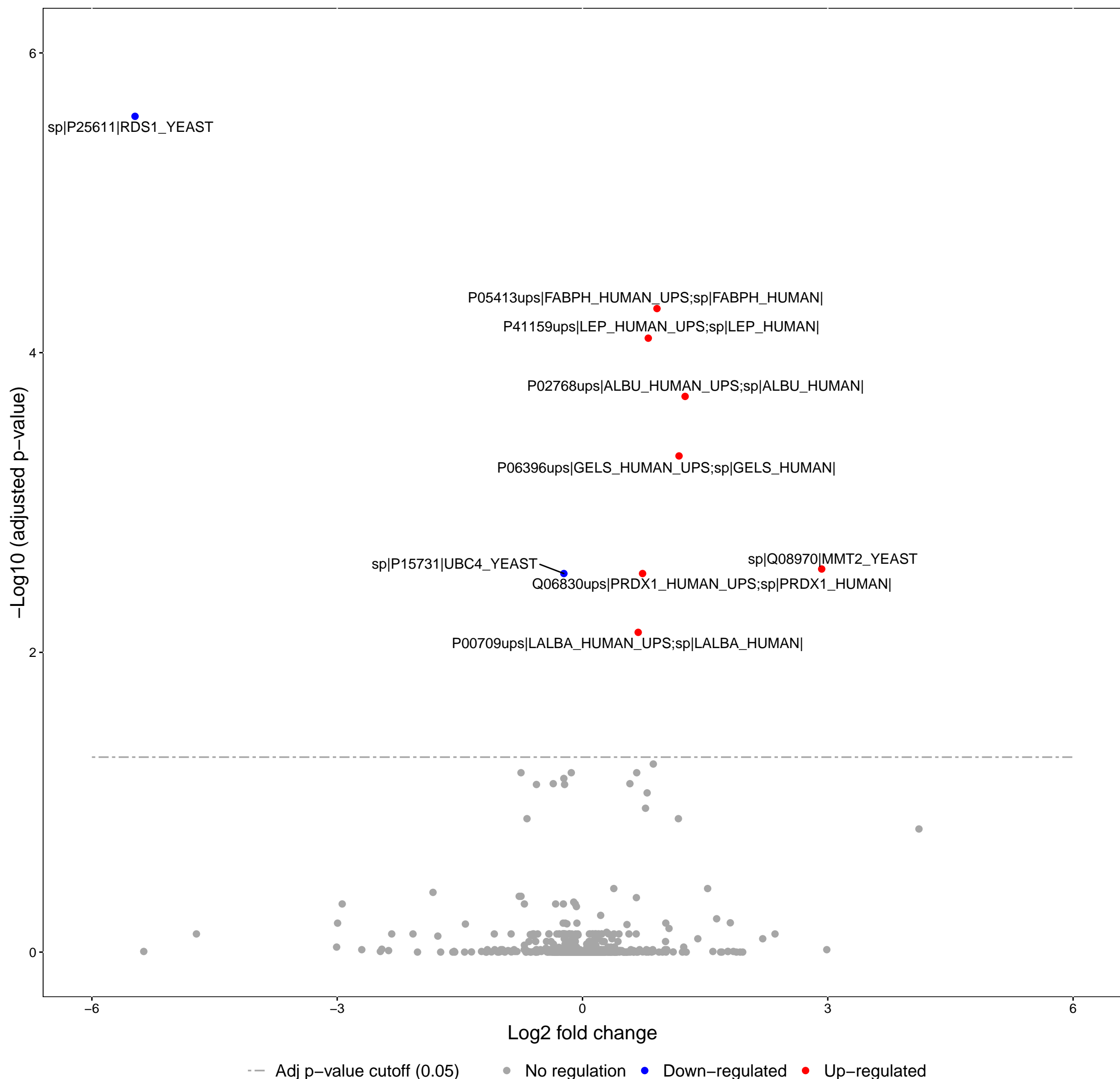


- Up-regulated

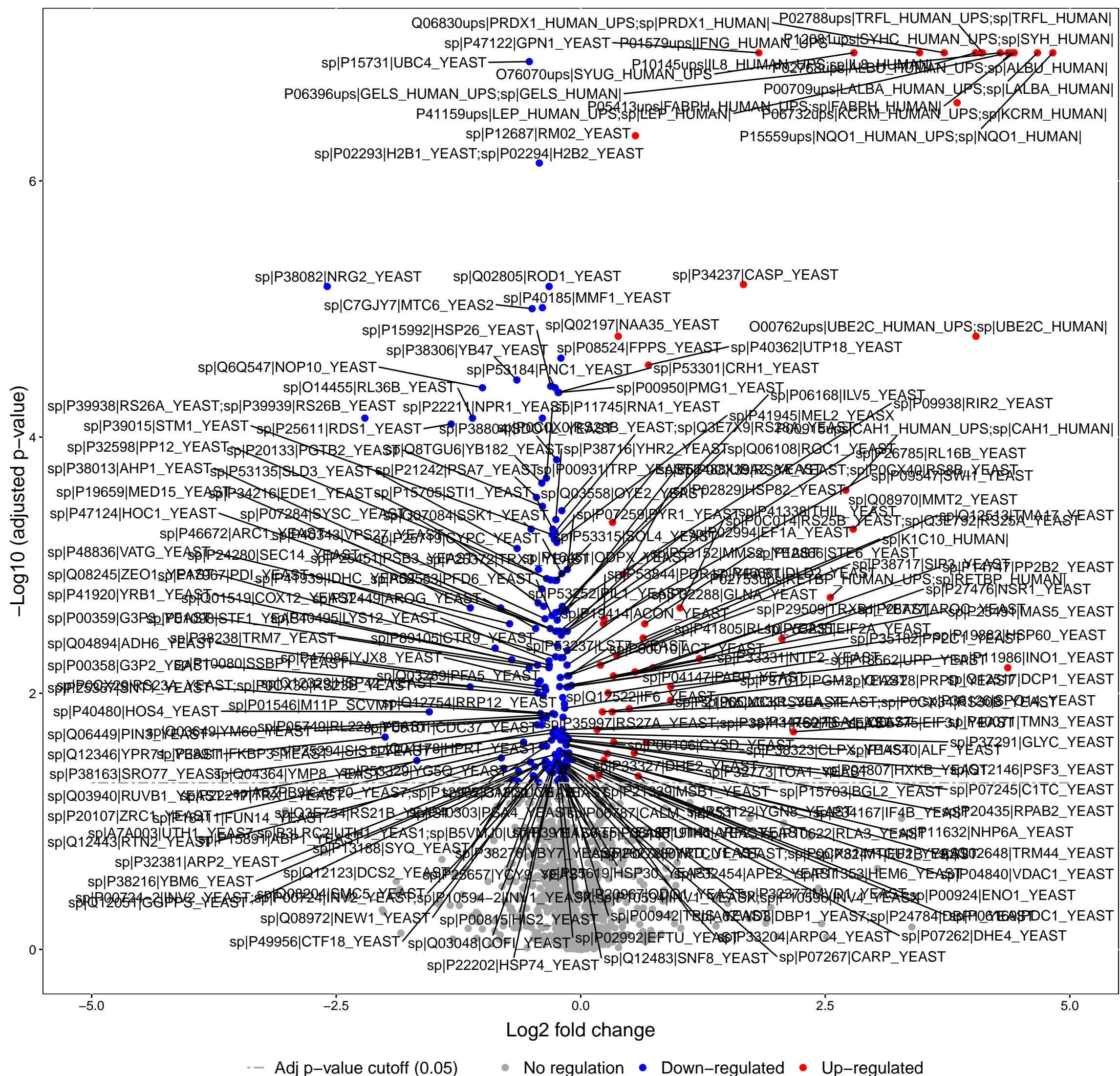
2500 amol–500 amol



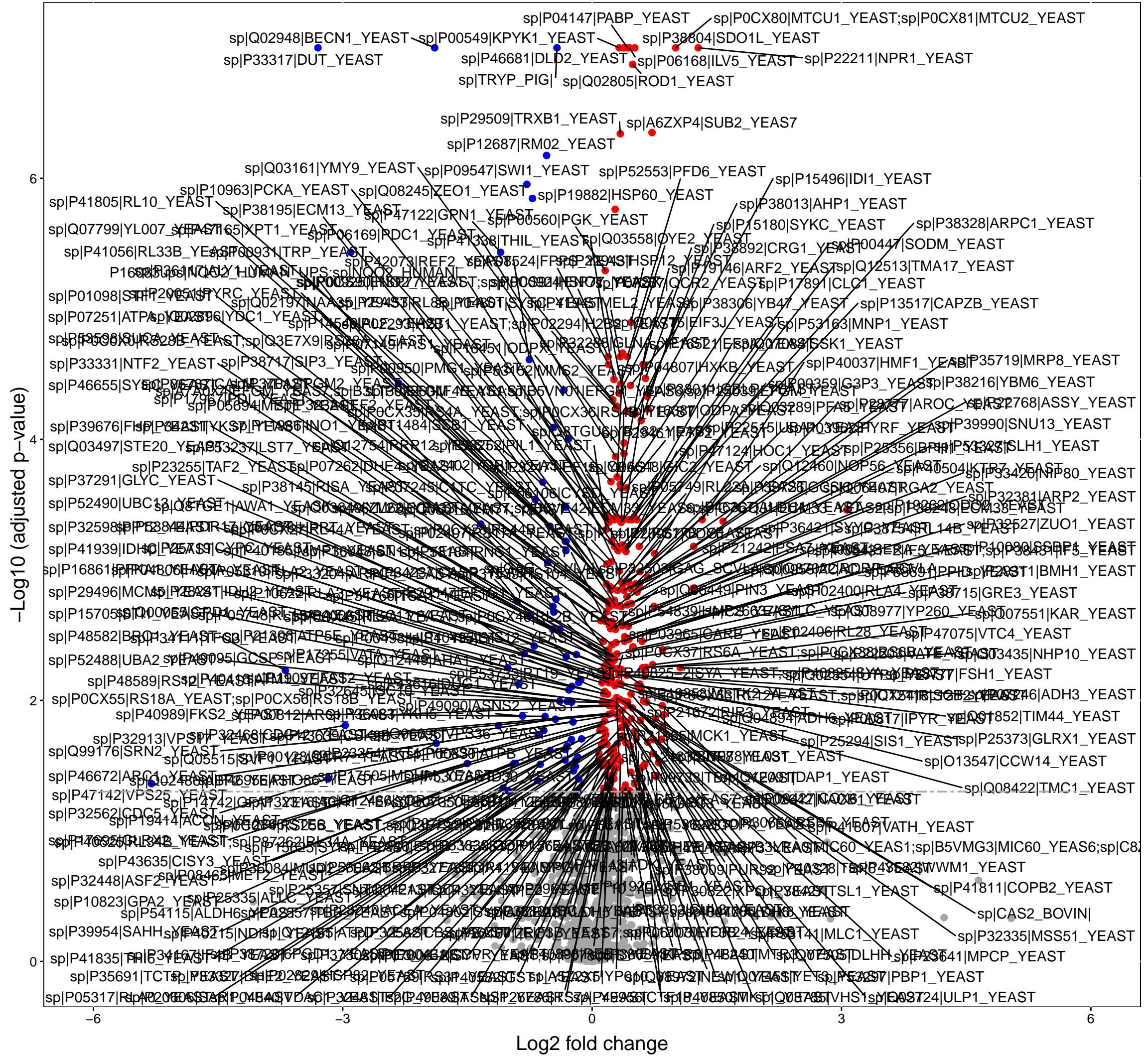
2500 amol–5000 amol



2500 amol–50000 amol



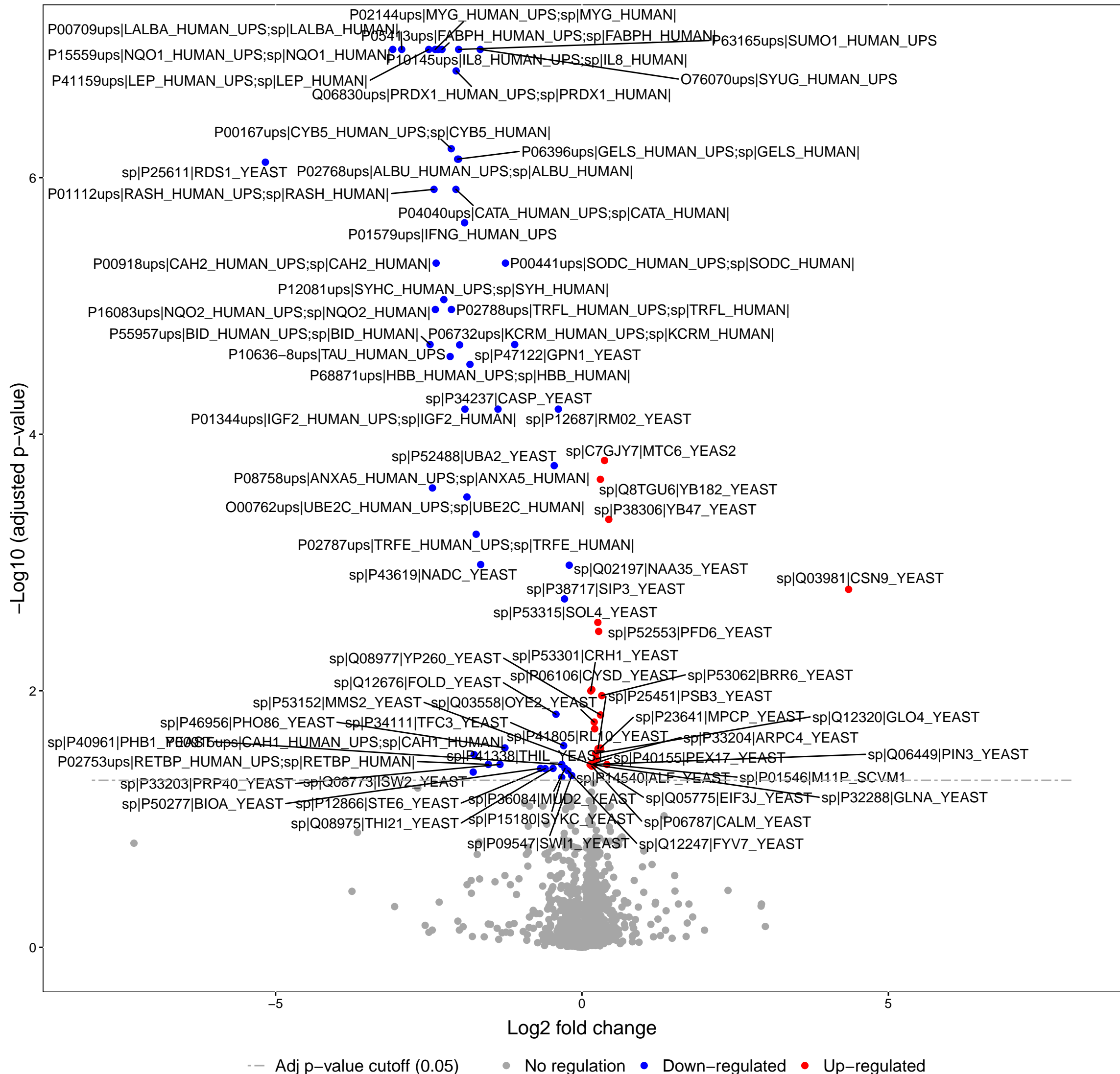
25000 amol–50 amol



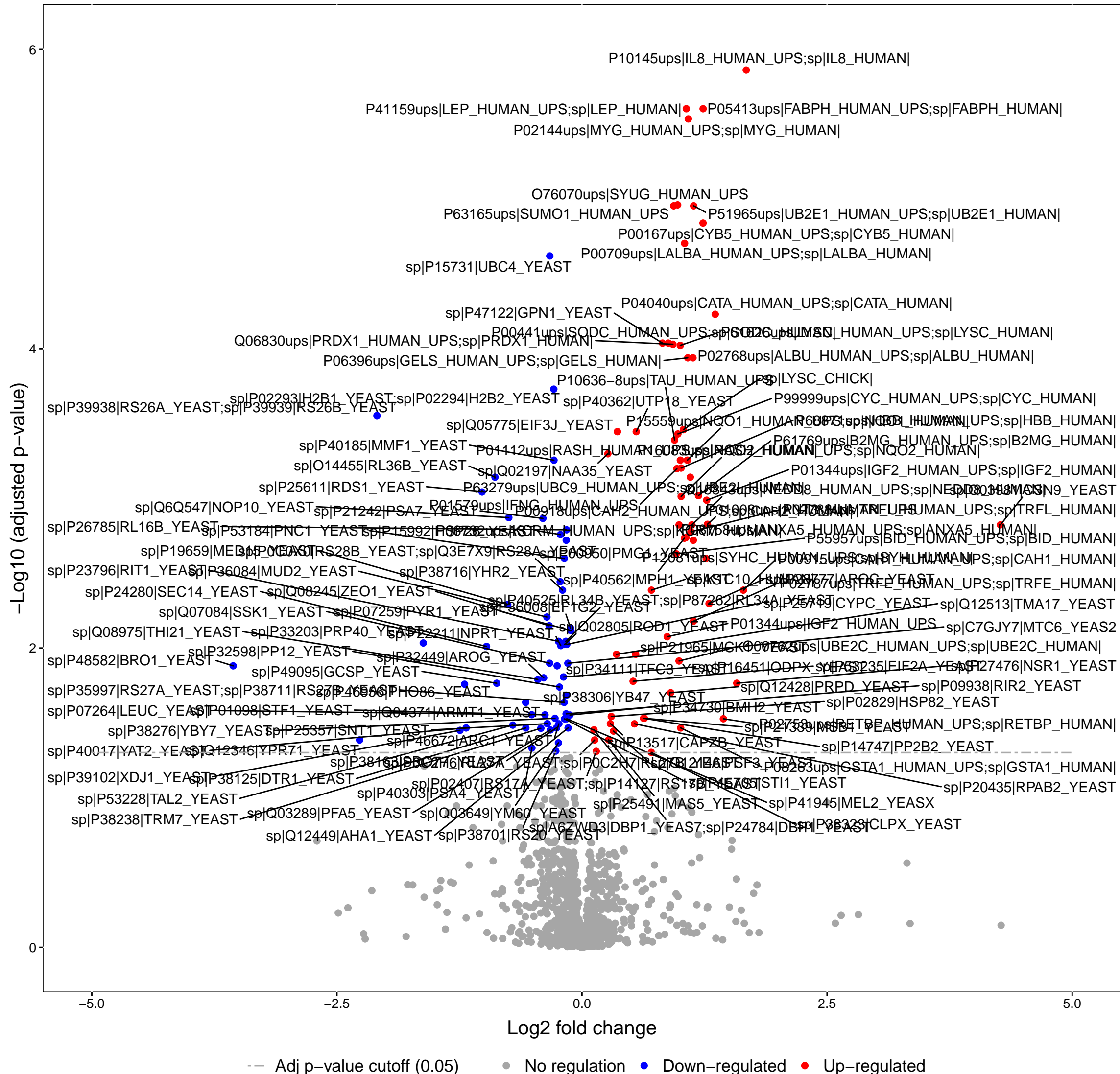
-- Adj p-value cutoff (0.05) ● No regulation ● Down-regulated ● Up-regulated

- Up-regulated

25000 amol–5000 amol



25000 amol–50000 amol



Volcano plot showing Log2 fold change (X-axis) versus -Log10 adjusted p-value (Y-axis). The plot displays a large number of genes, with a dense cluster of points around the center (Log2 fold change near 0, -Log10 adjusted p-value near 1.3). Genes with significant up-regulation (red dots) and down-regulation (blue dots) are highlighted. The legend indicates the color coding: red for up-regulated, blue for down-regulated, and grey for no regulation. A dashed line represents the adjusted p-value cutoff (0.05).

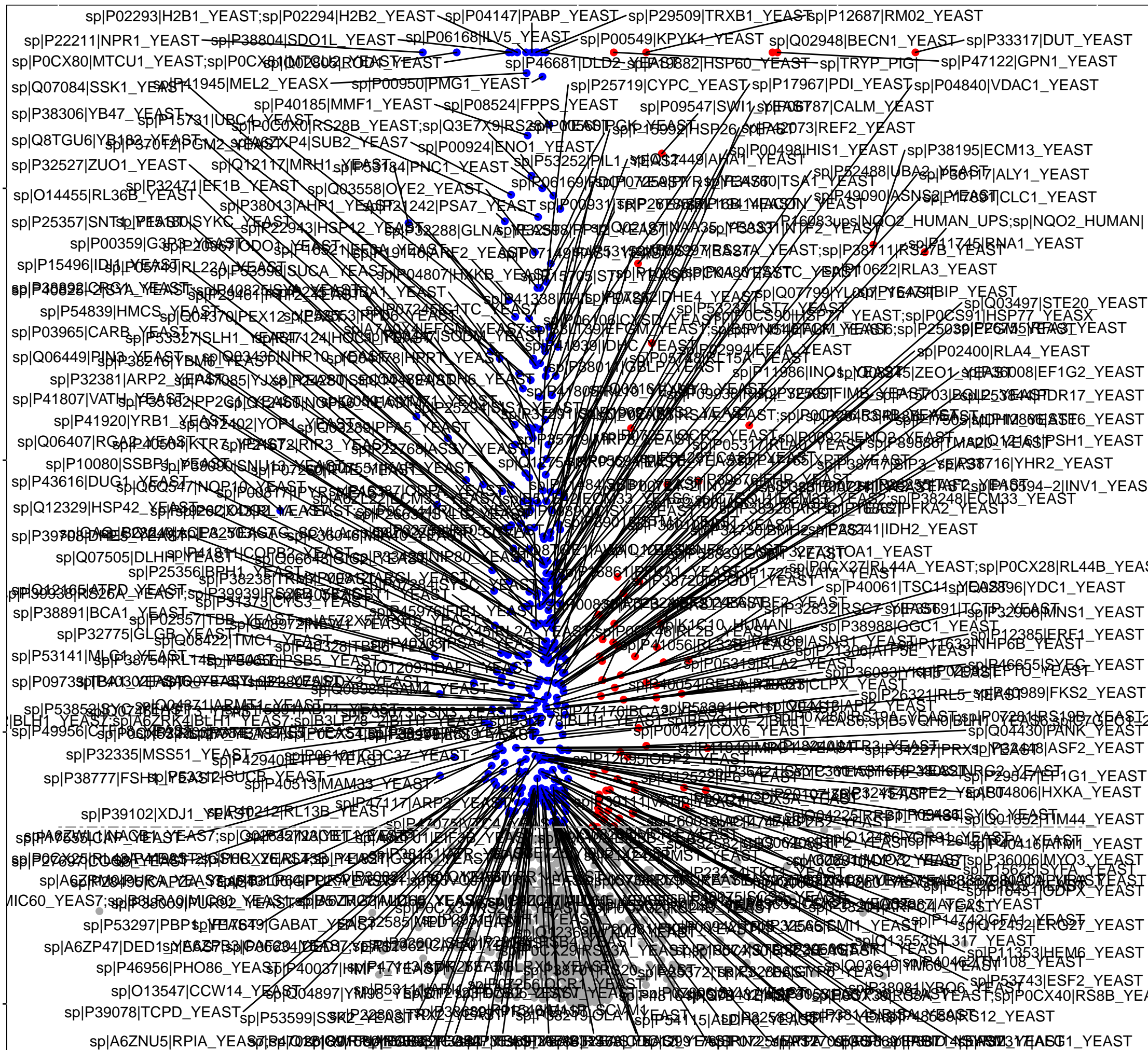
Legend:

- Adj p-value cutoff (0.05)
- No regulation
- Down-regulated
- Up-regulated

- Up-regulated

[illegible]

- Up-regulated



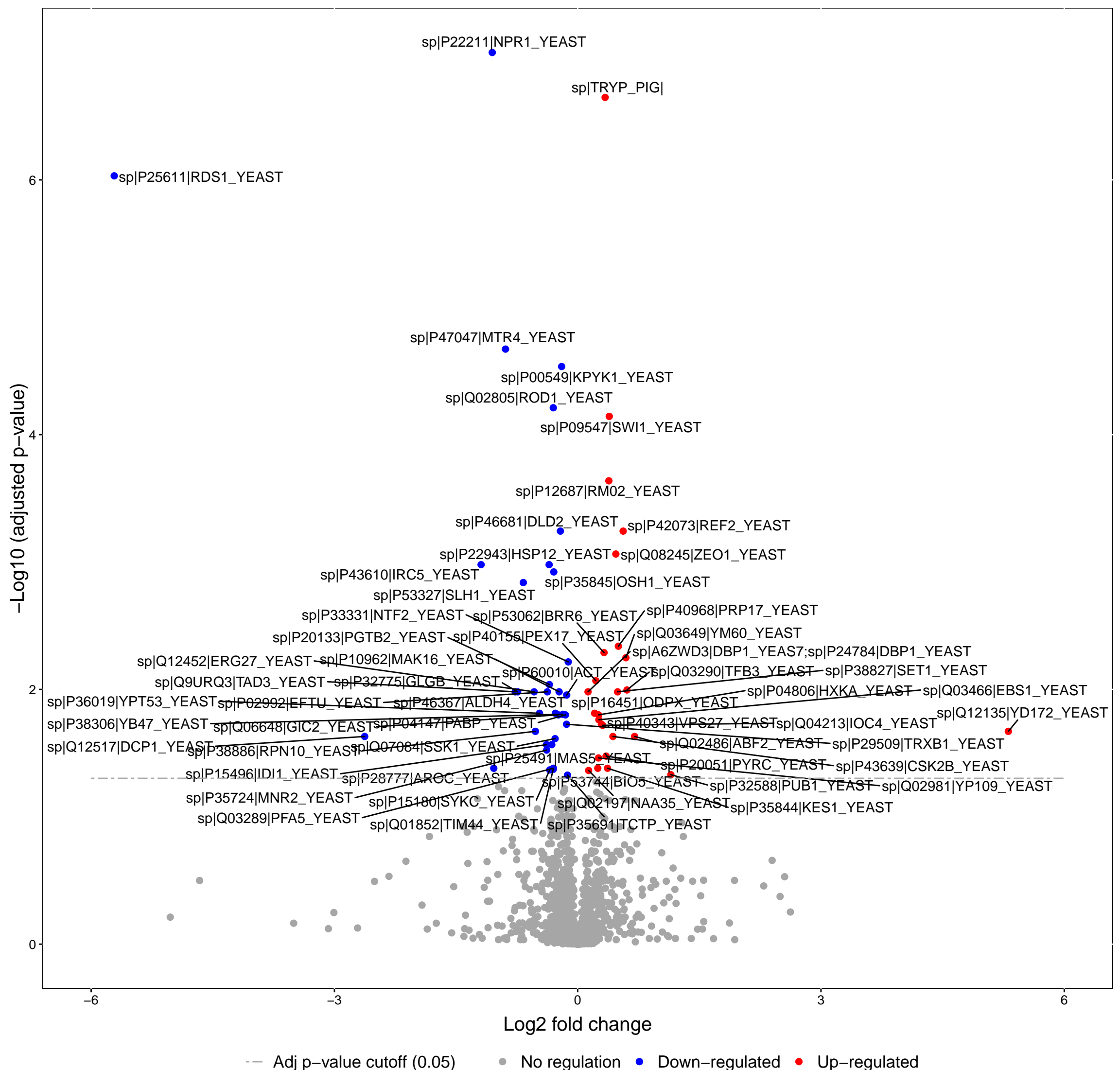
- Adj p-value cutoff (0.05)

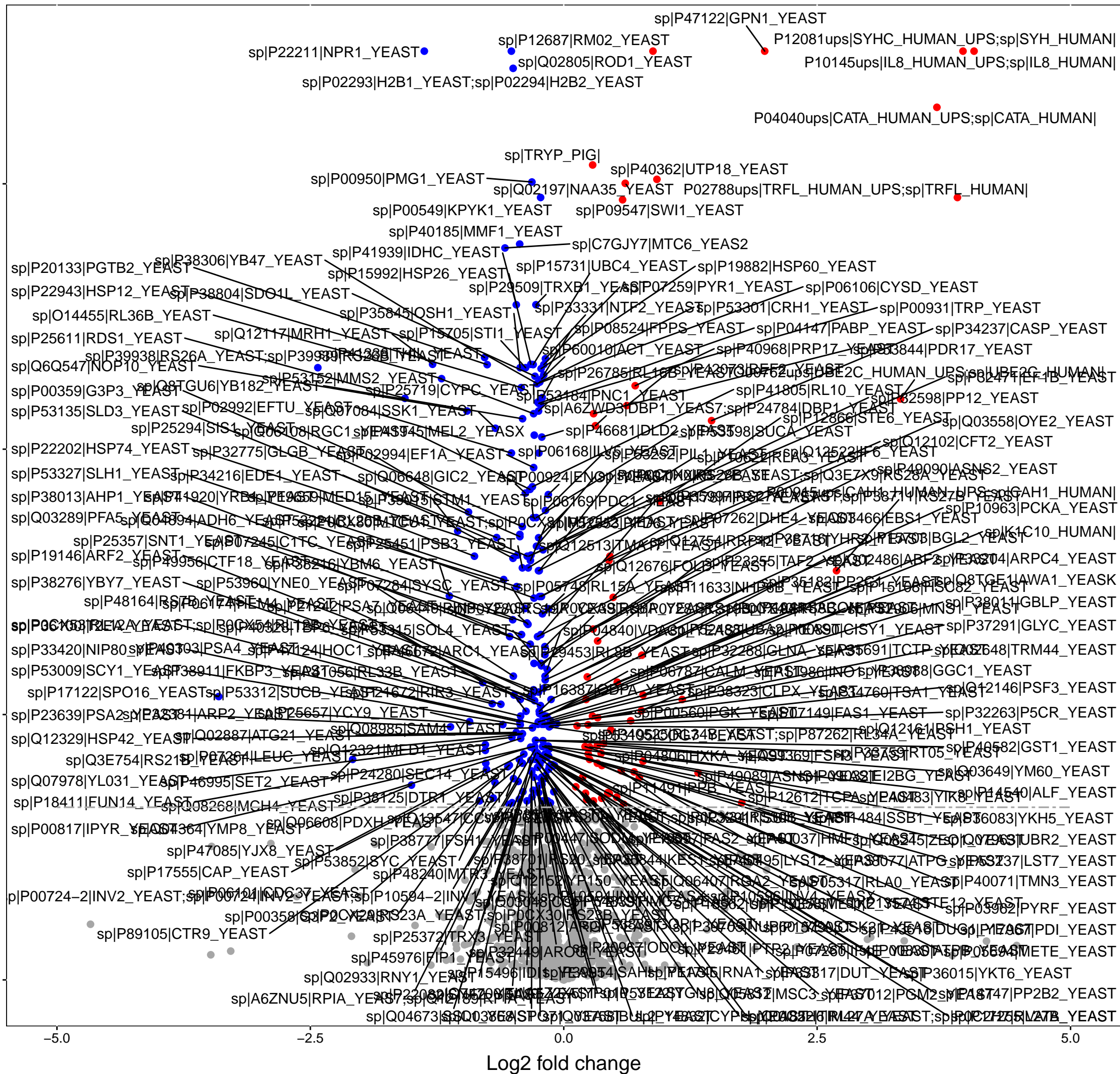
- No regulation

- Down-regulated

- Up-regulated

500 amol–5000 amol





- Up-regulated