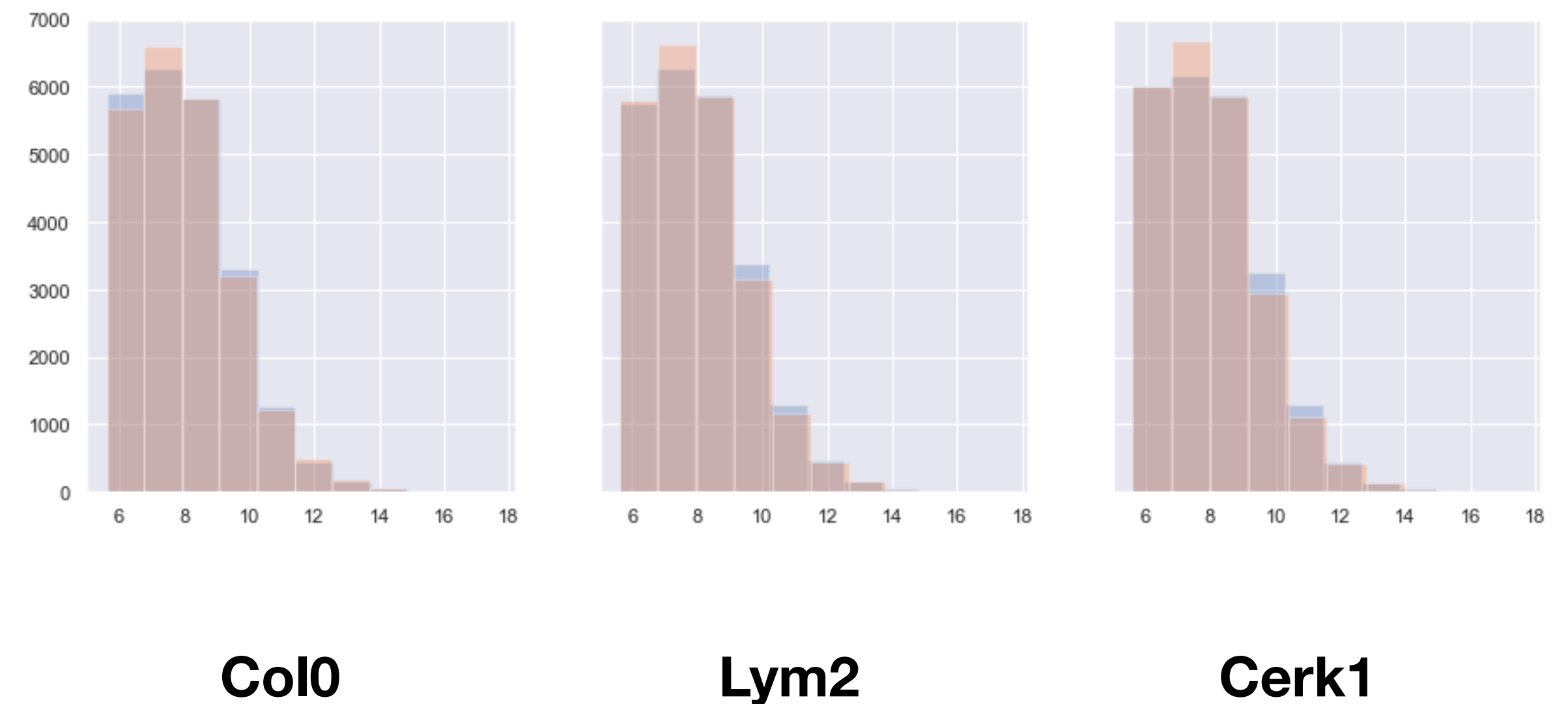# Normalised counts:

DESeq2 uses median of ratios:

counts divided by sample-specific size factors determined by median ratio of gene counts relative to geometric mean per gene

This fixes the issues of seq read depth and RNA composition; **NOT FOR USE WHEN COMPARING BETWEEN SAMPLES**

Sample counts are normalised means we can compare effectively

Col0   **Lym2**   **Cerk1**
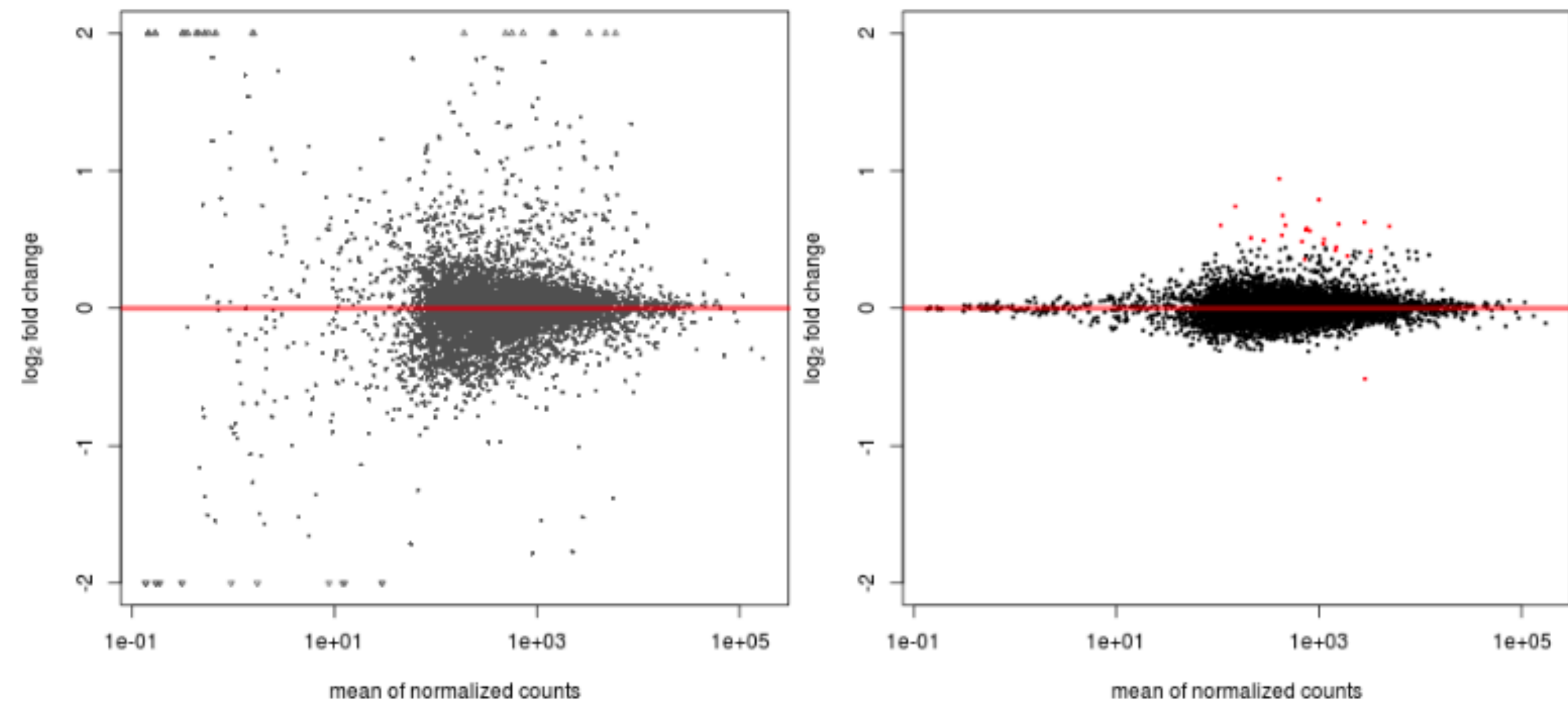
Log2foldChanges

DESeq2 applies shrinkage estimation:

This is done to centre small or insignificant changes towards zero

Needed because:

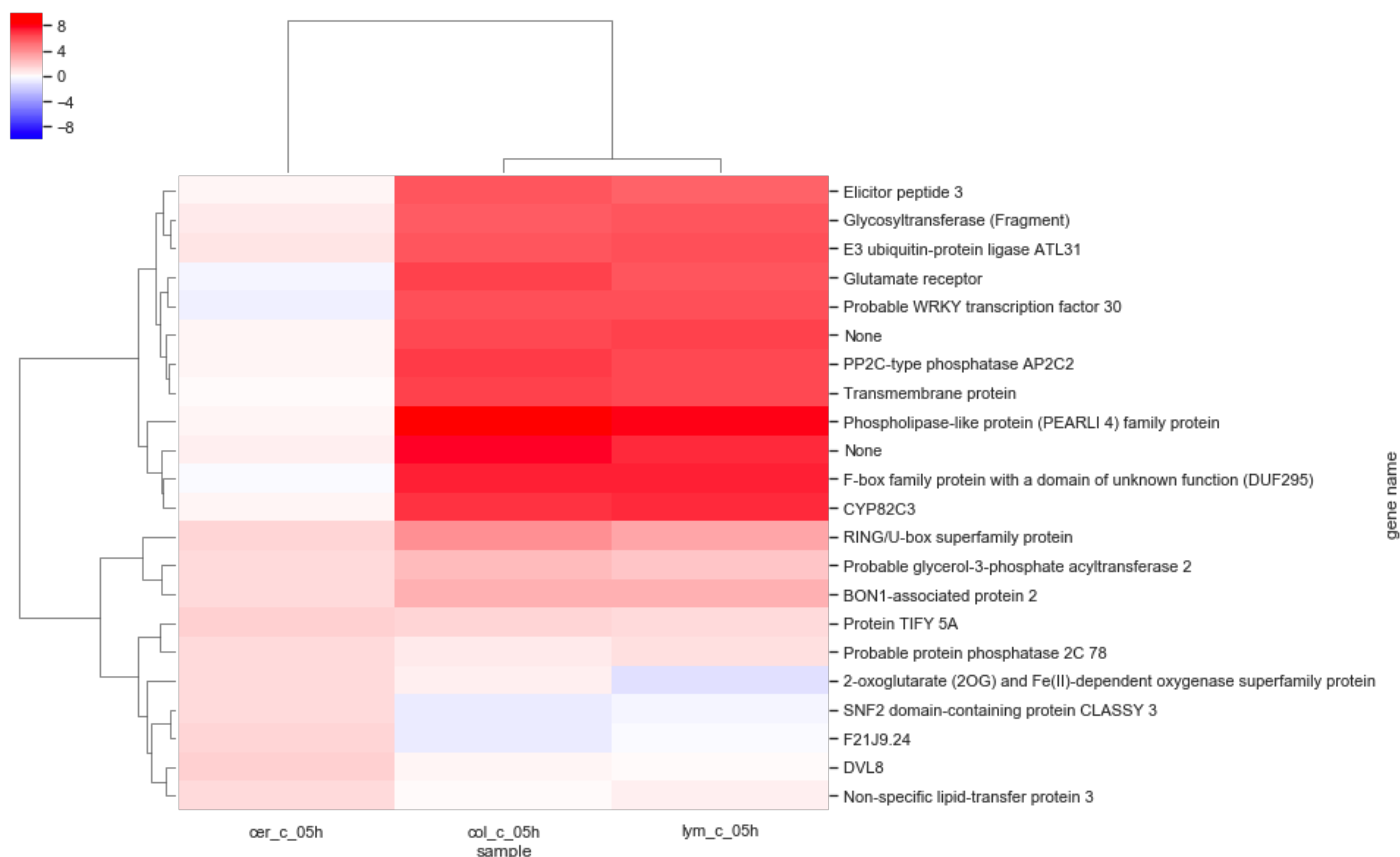Lowly expressed genes have high variability and shrinkage can reduce it

Example from DESeq2 documents; left shows without shrinkage, right with
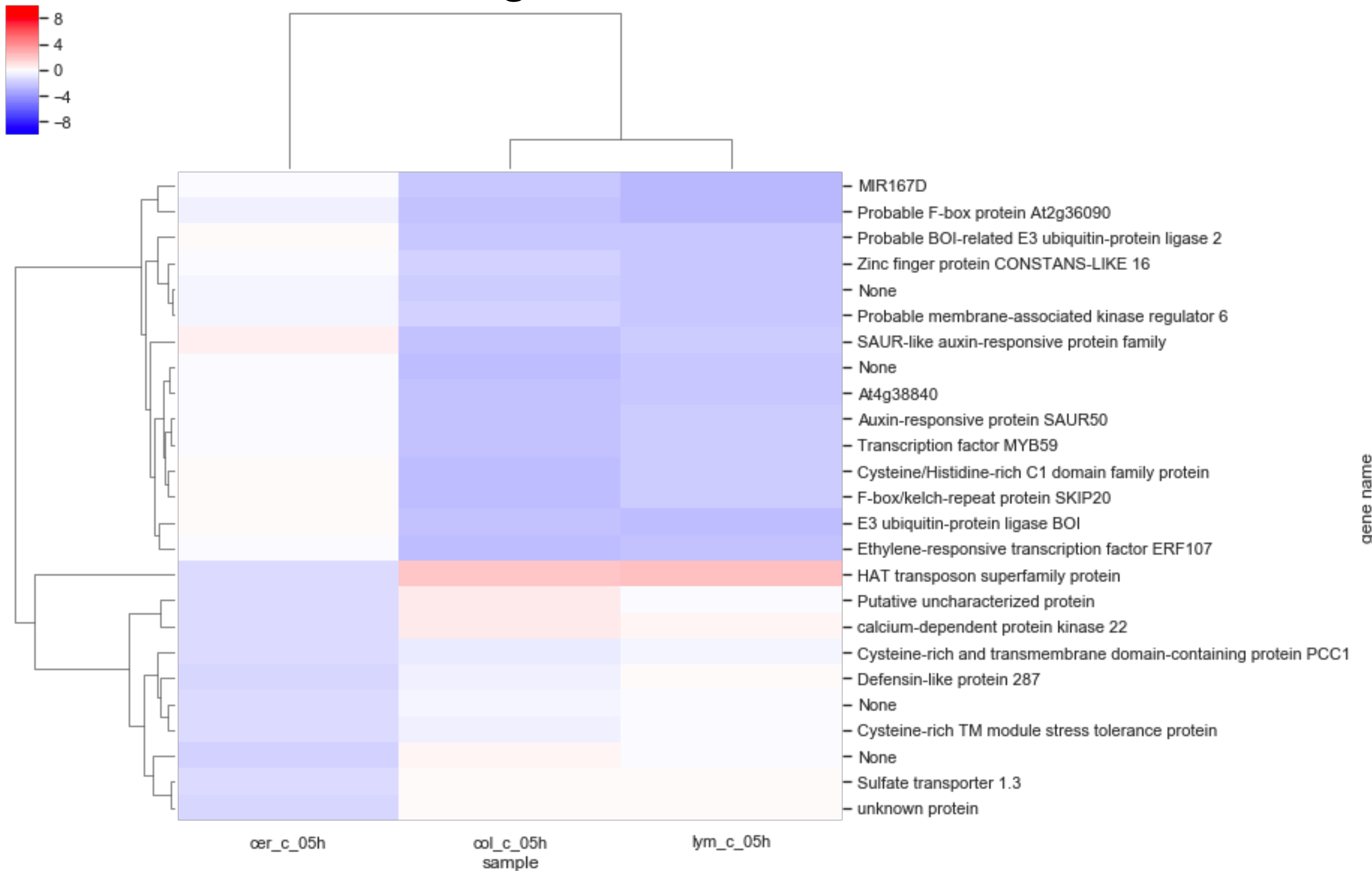
Heatmaps info

Each presented heat map is not cross compared with its neighbouring columns, but rather with their logical comparable - i.e. col0 water is compared to col0 chitin
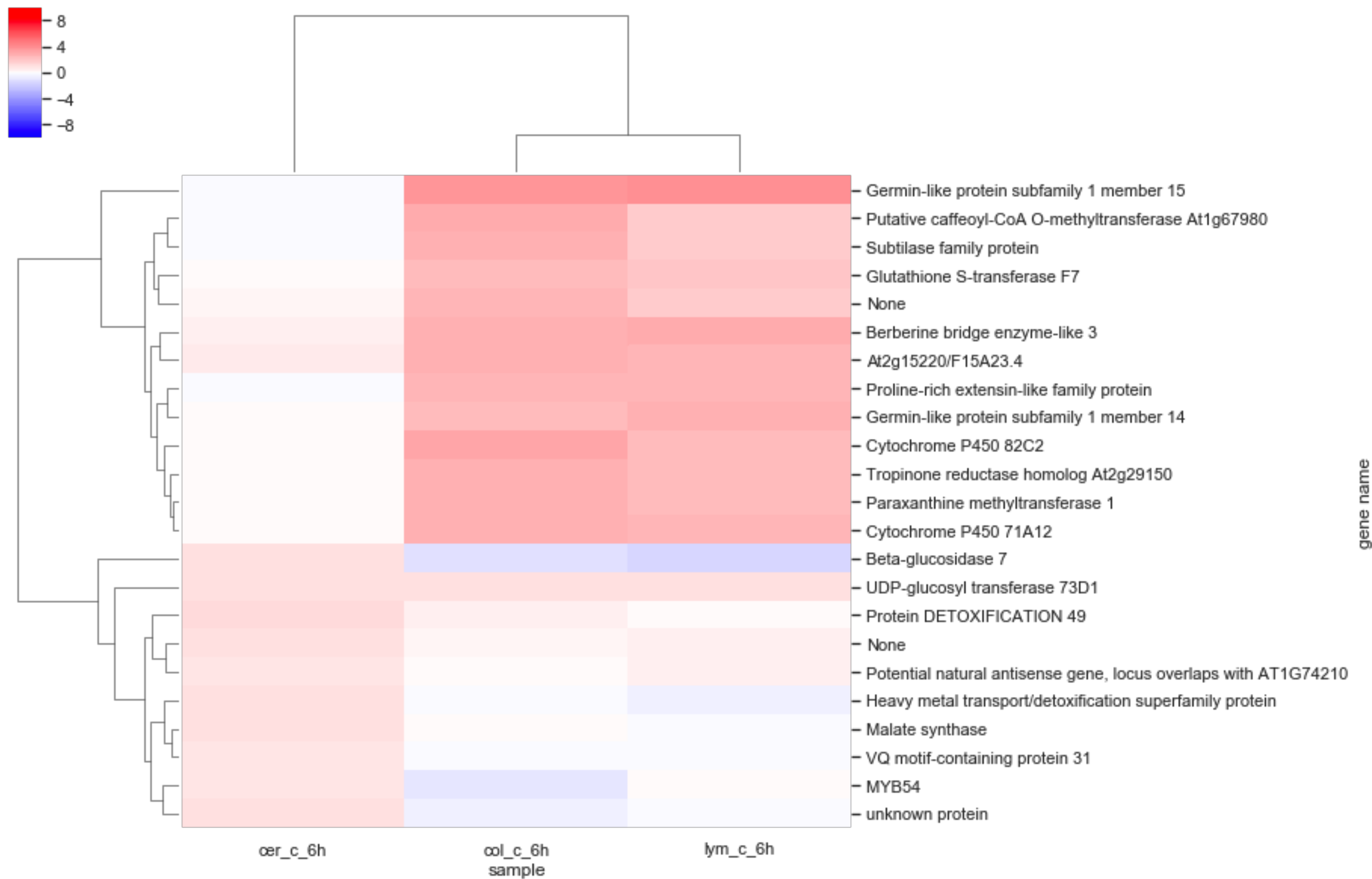
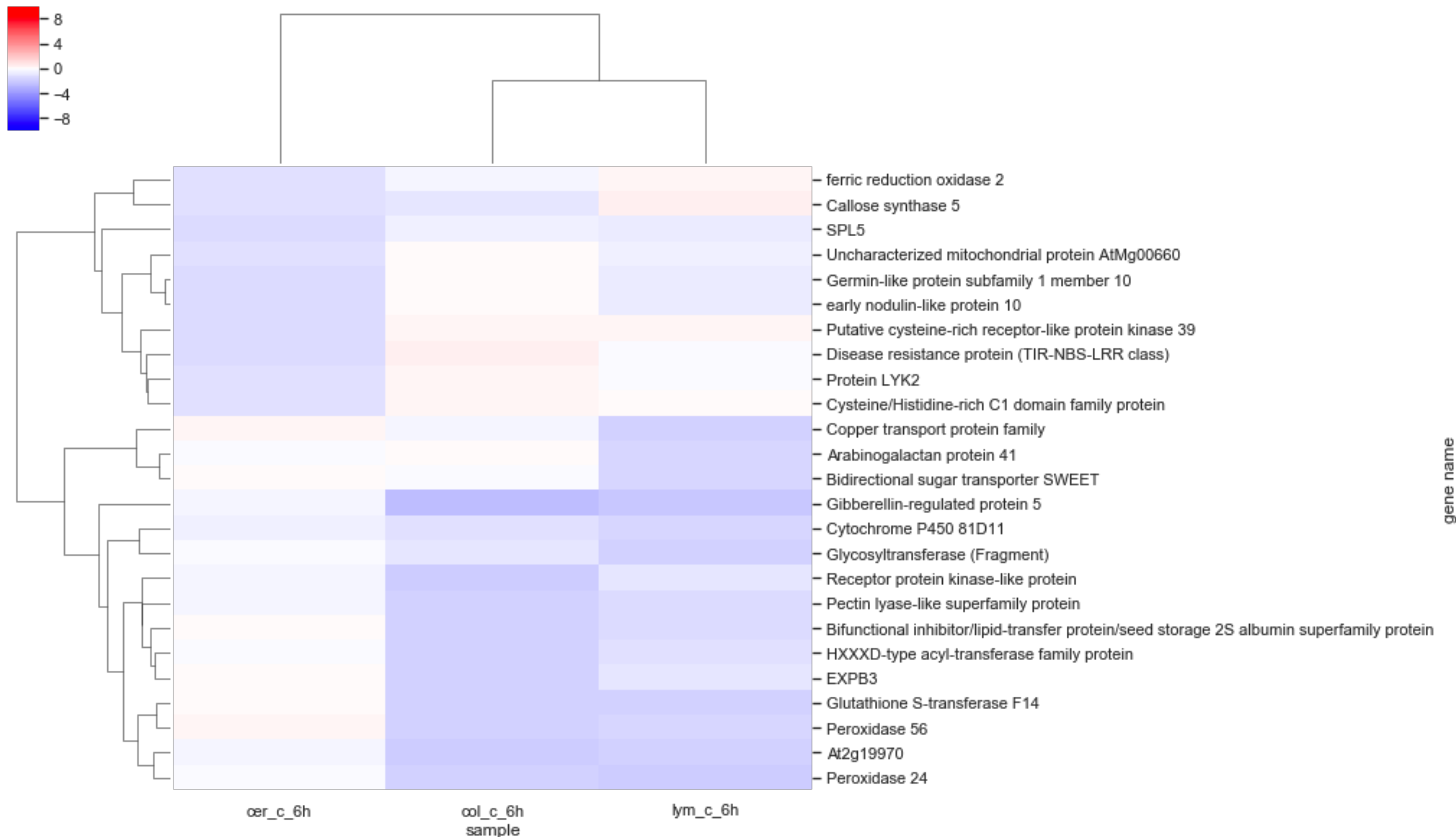Most up-regulated Genes for C/W at 05hr

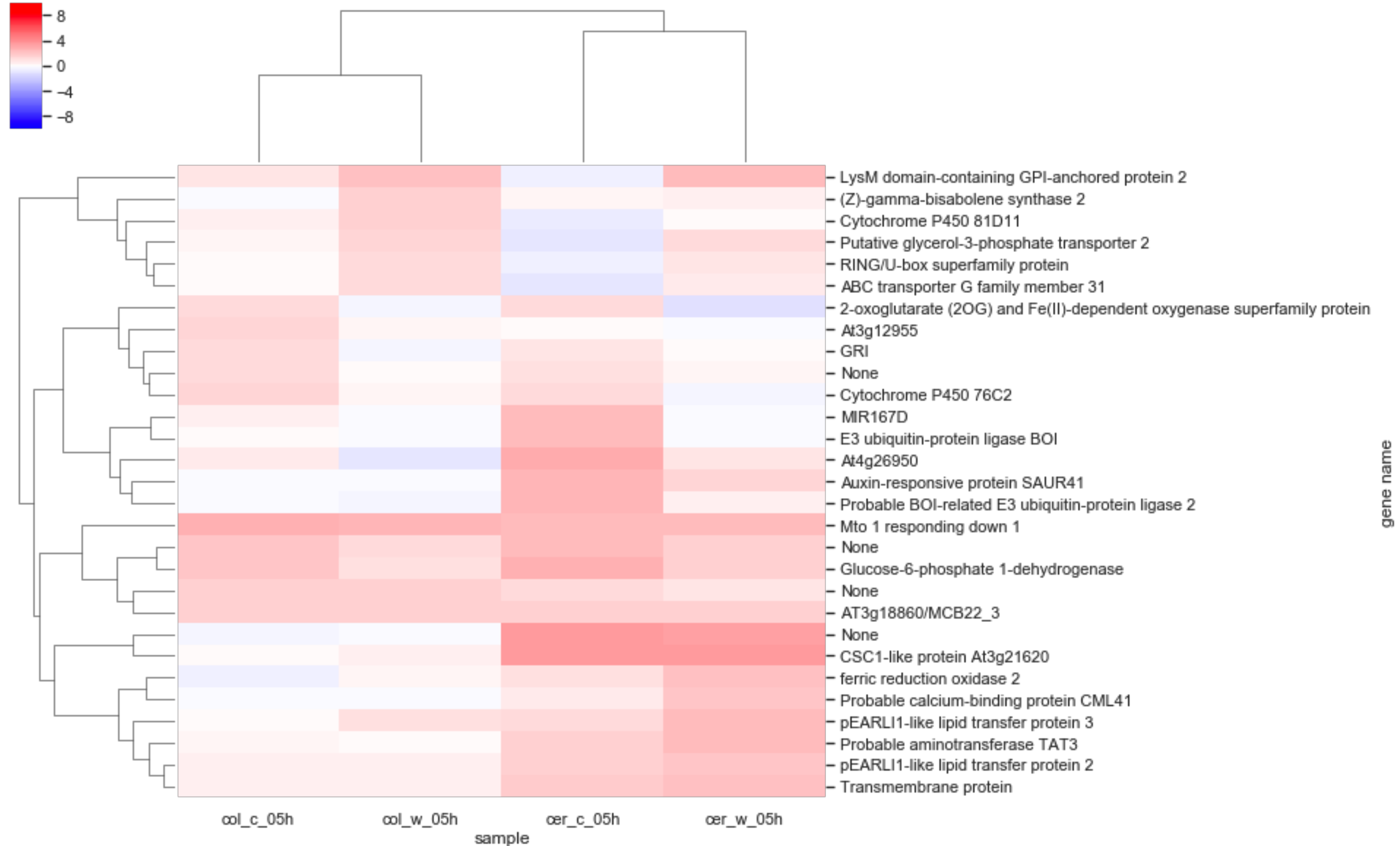Most down-regulated Genes for C/W at 05hr

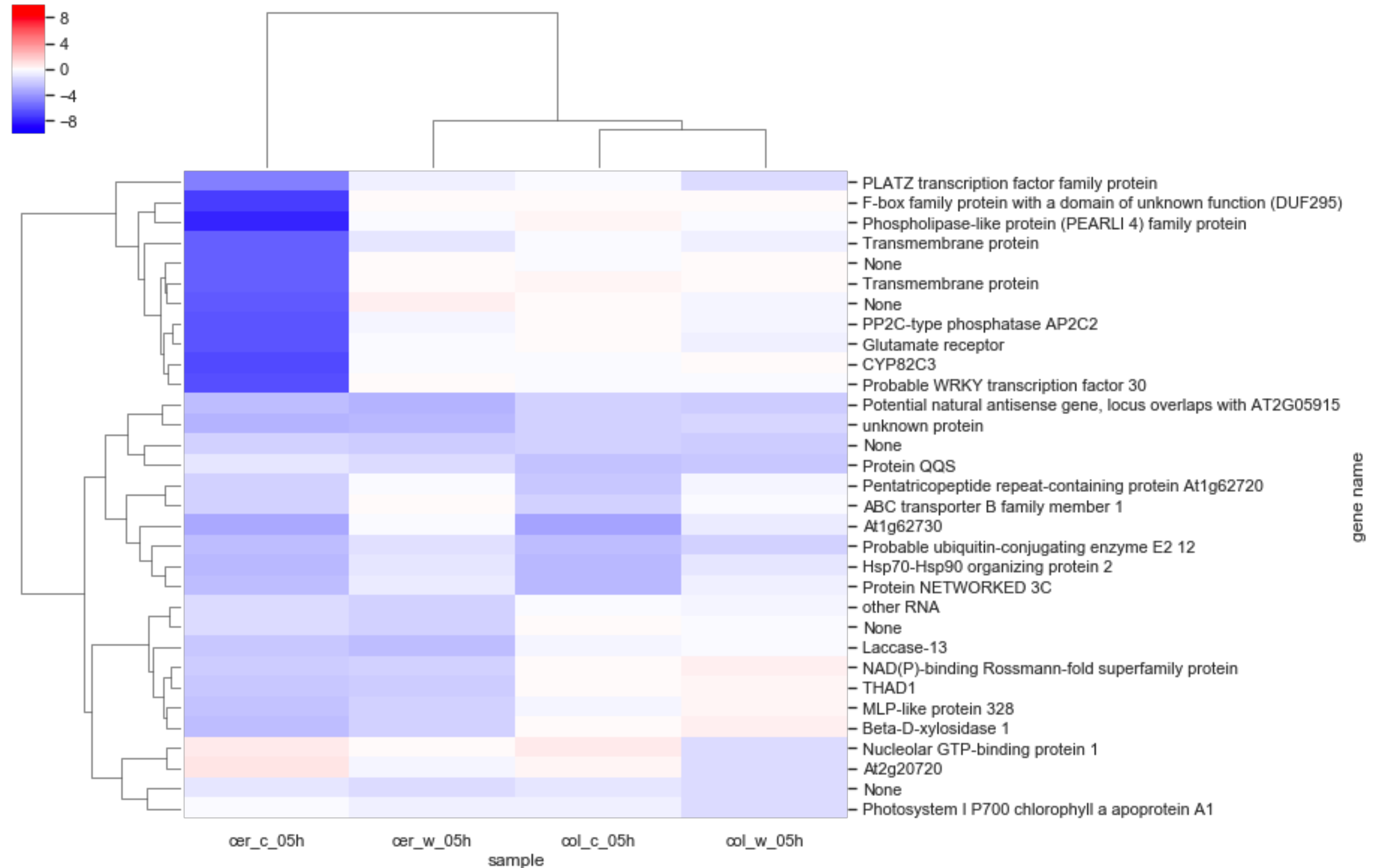Most up-regulated Genes for C/W at 6hr

Most down-regulated Genes for C/W at 6hr

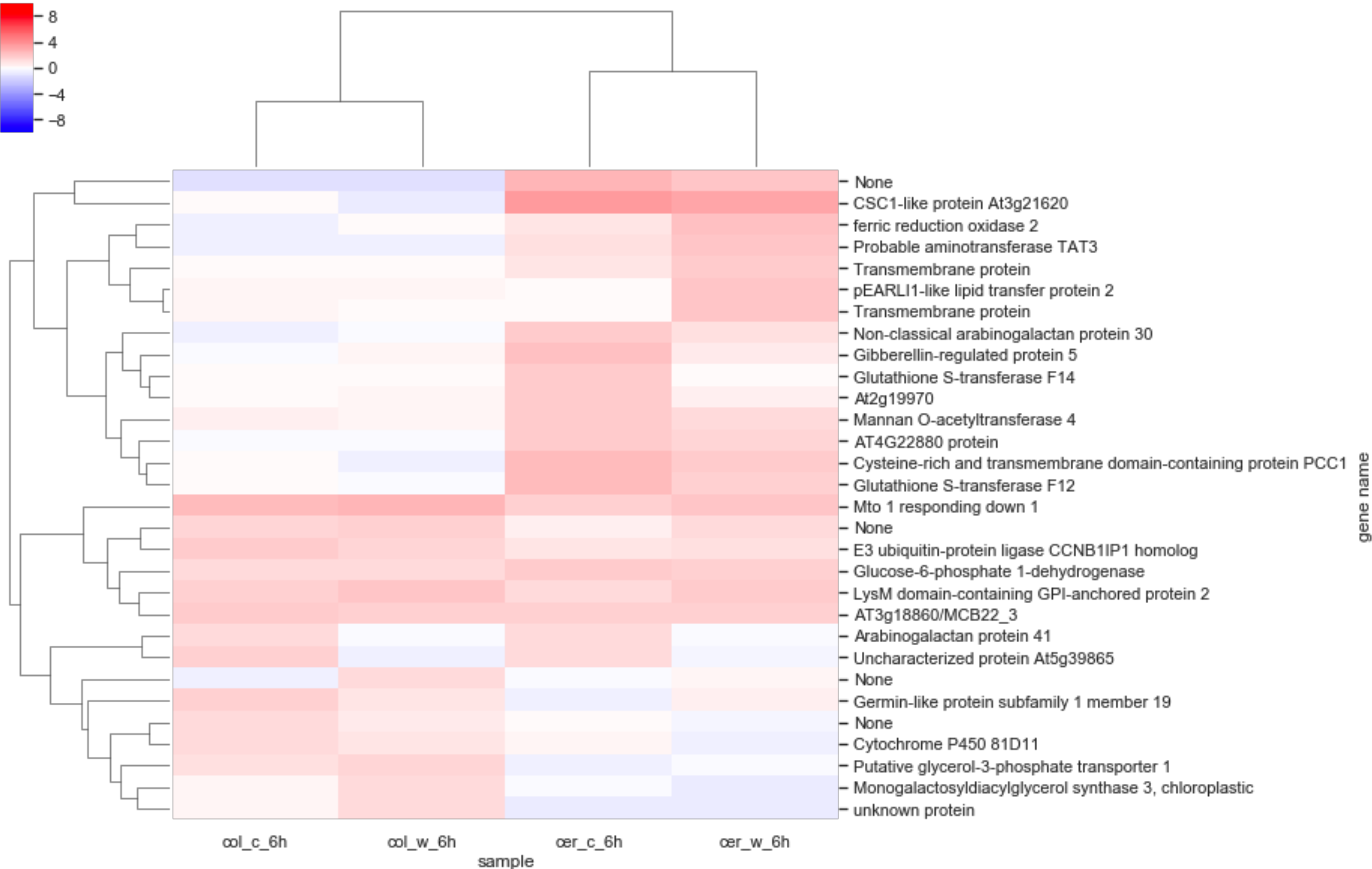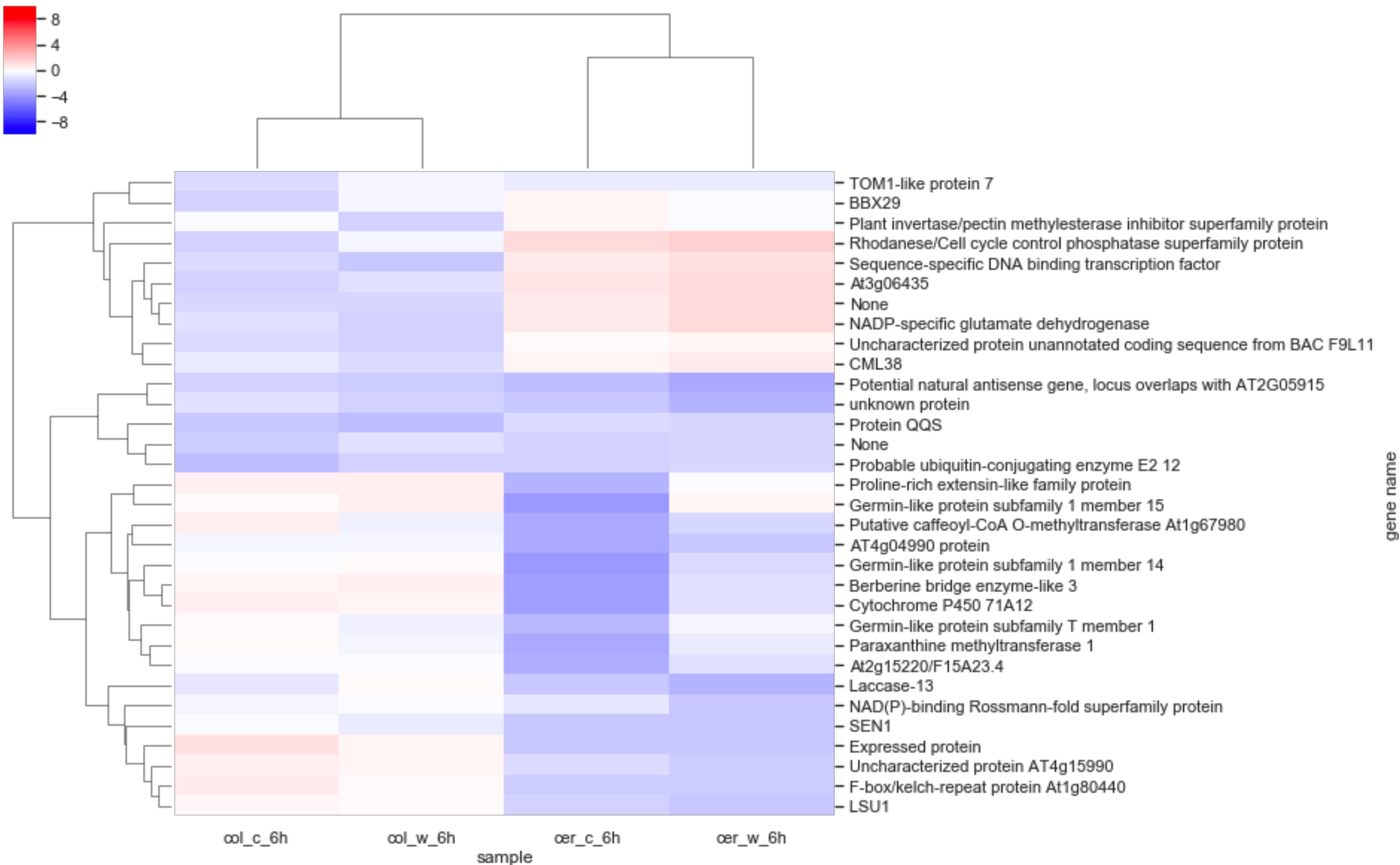Most up-regulated Genes for compared to Lym at 05hr

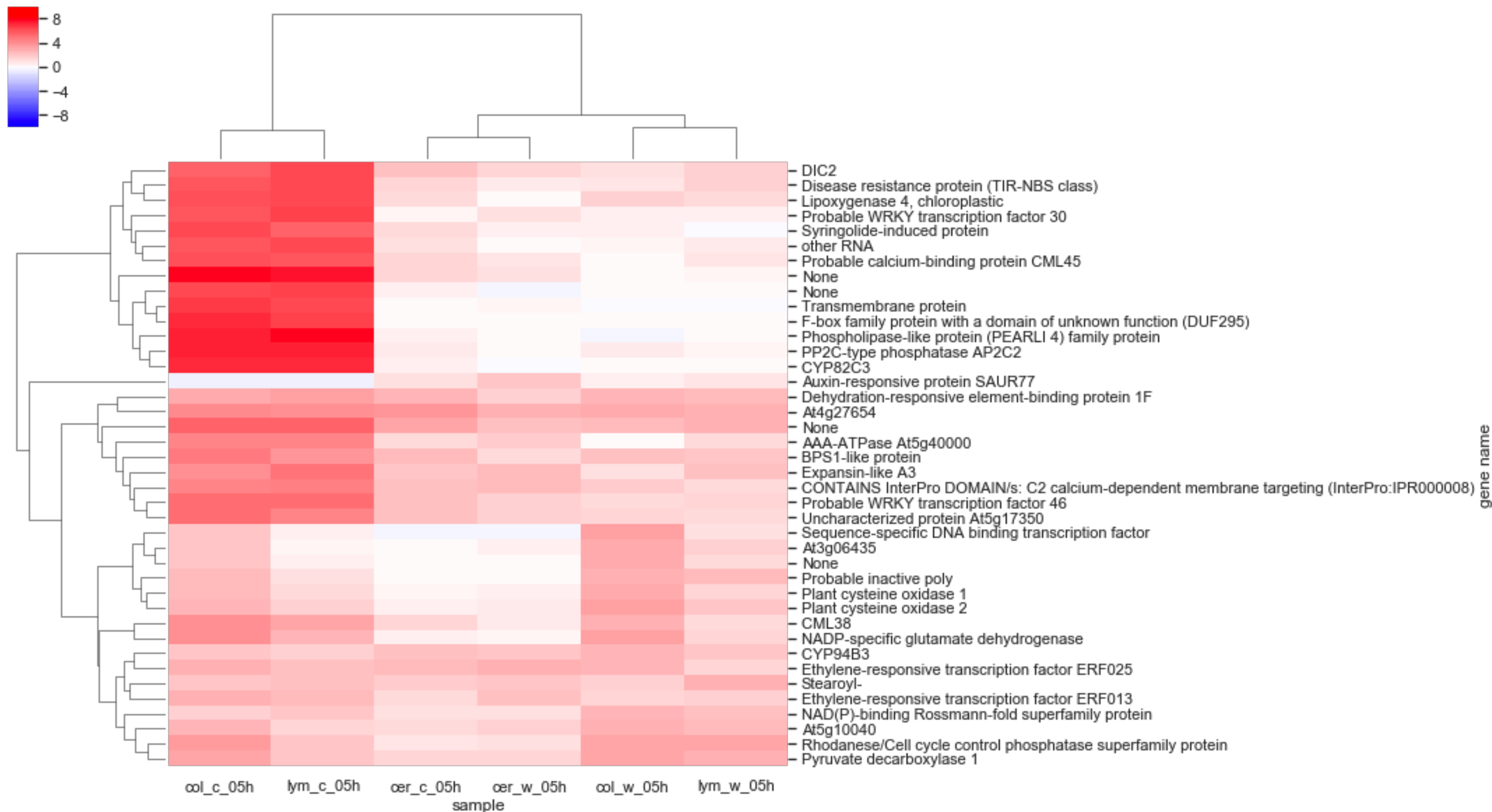Most down-regulated Genes for compared to Lym at 05hr

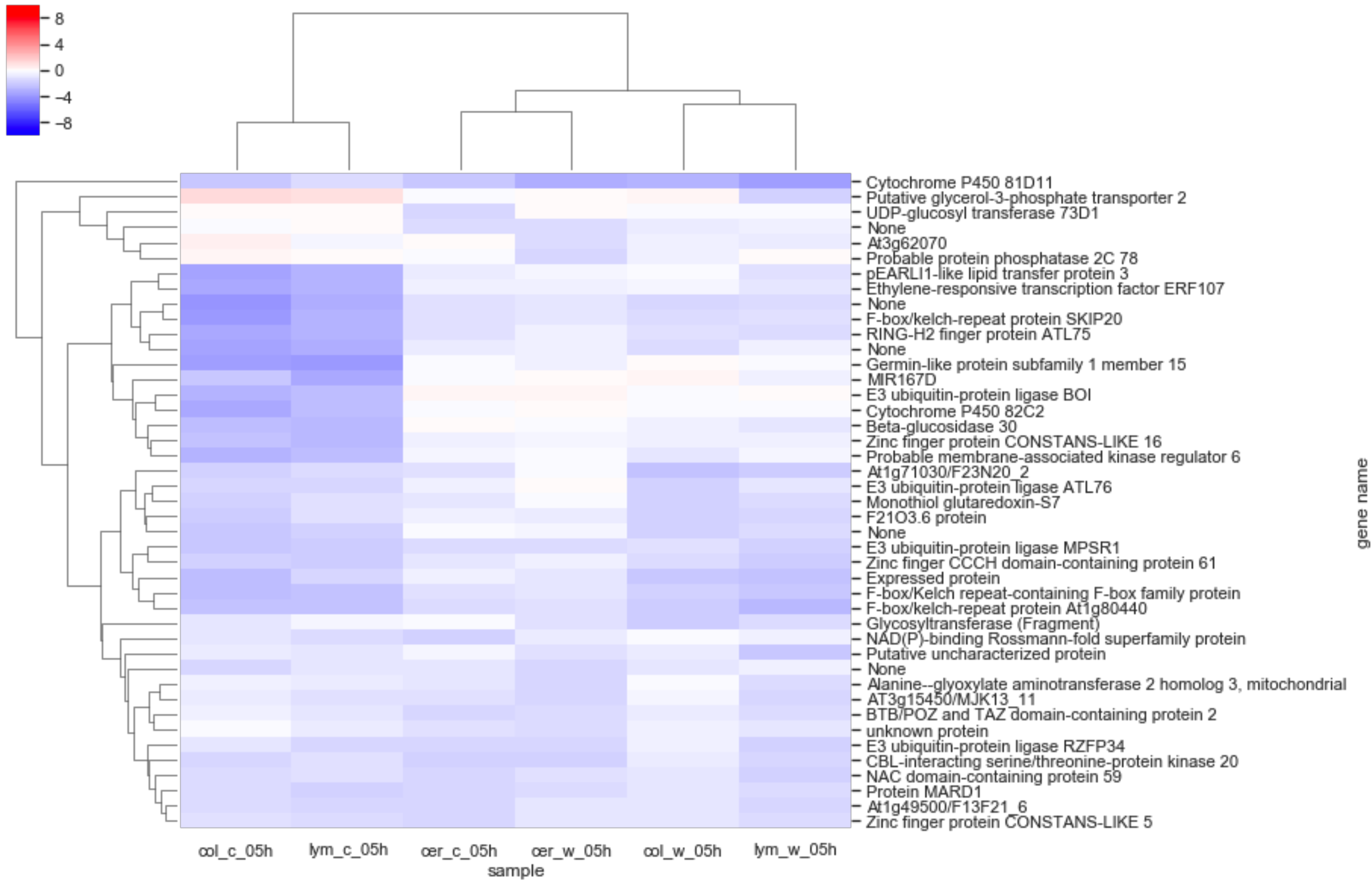# Most up-regulated Genes for compared to Lym at 6hr
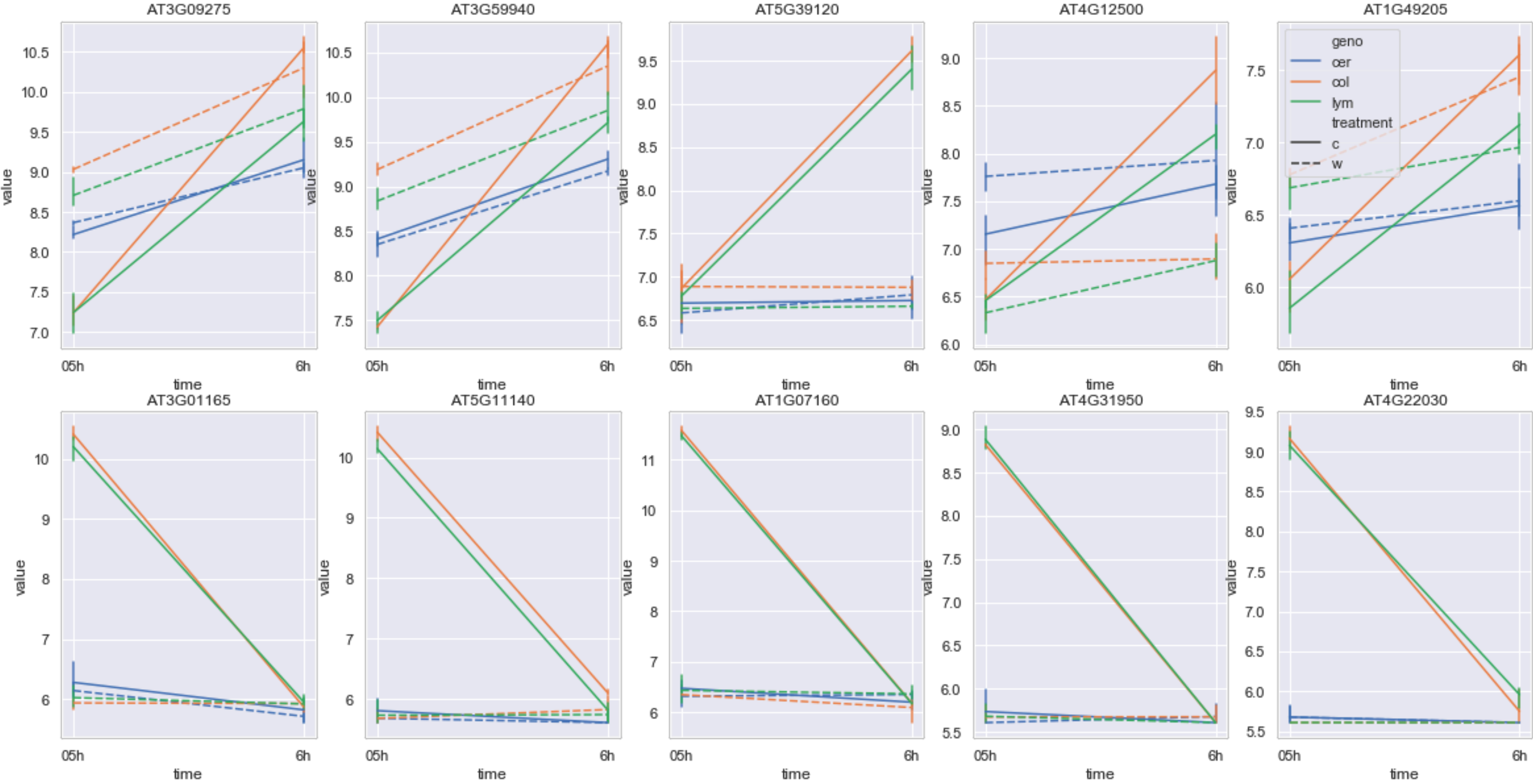
Most down-regulated Genes for compared to Lym at 6hr

Most up-regulated Genes across time

Most down-regulated Genes across time

Most different genes across time for Col0; up-regulated on top row, down on bottom

Gene selection via modeling

Selecting 25 genes in Col0 C/W

	incoming	name	description
0	AT1G68520	COL6	Zinc finger protein CONSTANS-LIKE 6
1	AT5G25350	EBF2	EIN3-binding F-box protein 2
2	AT2G37430	ZAT11	ZAT11
3	AT4G19700	BOI	E3 ubiquitin-protein ligase BOI
4	AT3G09275	AT3G09275	None
5	AT1G72520	LOX4	Lipoxygenase 4, chloroplastic
6	AT3G59940	SKIP20	F-box/kelch-repeat protein SKIP20
7	AT5G24110	WRKY30	Probable WRKY transcription factor 30
8	AT1G07160	AT1G07160	PP2C-type phosphatase AP2C2
9	AT1G25440	COL16	Zinc finger protein CONSTANS-LIKE 16
10	AT1G66090	AT1G66090	Disease resistance protein (TIR-NBS class)
11	AT2G18440	GUT15	GUT15 (GENE WITH UNSTABLE TRANSCRIPT 15)
12	AT5G11140	AT5G11140	Phospholipase-like protein (PEARLI 4) family protein
13	AT1G56242	AT1G56242	other RNA
14	AT2G21210	AT2G21210	SAUR-like auxin-responsive protein family
15	AT5G37260	RVE2	Protein REVEILLE 2
16	AT4G38840	AT4G38840	At4g38840
17	AT5G27420	ATL31	E3 ubiquitin-protein ligase ATL31
18	AT1G56240	PP2B13	F-box protein PP2-B13
19	AT5G47230	ERF5	ERF5
20	AT5G60390	A1	Elongation factor 1-alpha 4
21	AT5G61590	ERF107	Ethylene-responsive transcription factor ERF107
22	AT1G14540	PER4	Peroxidase
23	AT3G02840	AT3G02840	ARM repeat superfamily protein
24	AT5G59780	MYB59	Transcription factor MYB59
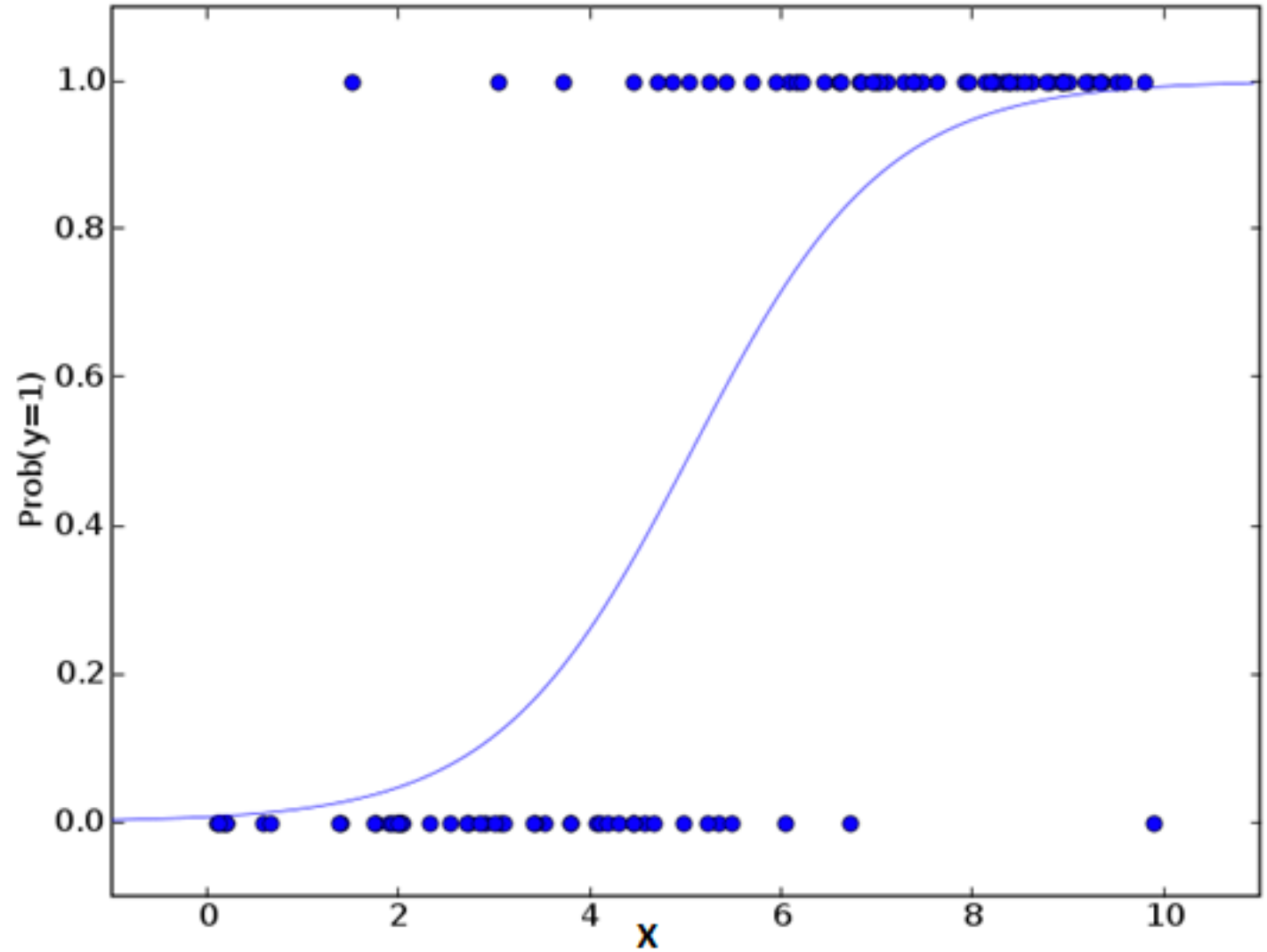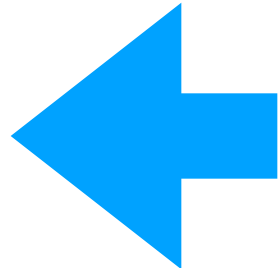
Ranking 25 genes in Col0 C/W
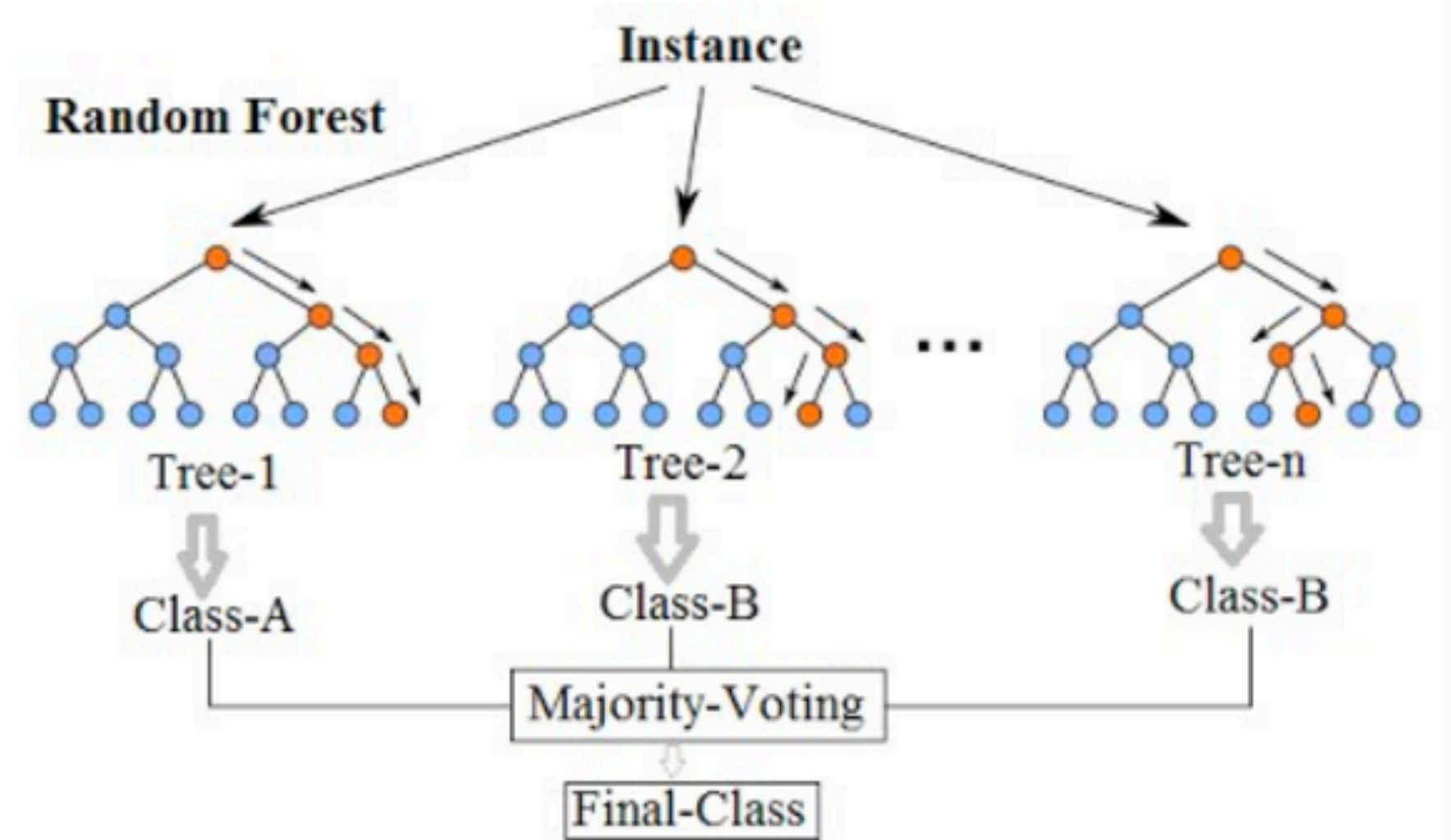
gene	importance	name	description
AT5G20620	0.0597047	UBQ4	Polyubiquitin 4
AT4G08950	0.0537518	EXO	Protein EXORDIUM
AT3G06355	0.0523239	AT3G06355	None
AT4G24110	0.050203	AT4G24110	NADP-specific glutamate dehydrogenase
AT3G28740	0.0500793	CYP81D11	Cytochrome P450 81D11
AT5G21940	0.0497868	AT5G21940	At5g21940
AT3G09440	0.0488543	HSP70-3	Heat shock protein 70 (Hsp 70) family protein
AT1G02930	0.0474558	GSTF6	Glutathione S-transferase F6
AT5G63160	0.0452281	BT1	BTB/POZ and TAZ domain-containing protein 1
AT1G24280	0.0446611	G6PD3	Glucose-6-phosphate 1-dehydrogenase
AT3G50770	0.0424266	CML41	Probable calcium-binding protein CML41
AT2G17120	0.0422194	LYM2	LysM domain-containing GPI-anchored protein 2
AT5G49360	0.042113	BXL1	Beta-D-xylosidase 1
AT1G62740	0.0403225	HOP2	Hsp70-Hsp90 organizing protein 2
AT4G35180	0.039032	LHT7	Lysine histidine transporter-like 7
AT4G29780	0.0352248	AT4G29780	Nuclease
AT3G47420	0.0331851	ATPS3	Putative glycerol-3-phosphate transporter 1
AT1G62730	0.0326117	AT1G62730	At1g62730
AT1G26380	0.0320114	FOX1	Berberine bridge enzyme-like 3
AT4G24570	0.031677	PUMP4	DIC2
AT1G56660	0.0298262	AT1G56660	F25P12.91 protein
AT1G26240	0.0285357	AT1G26240	Proline-rich extensin-like family protein
AT5G24110	0.0254376	WRKY30	Probable WRKY transcription factor 30
AT3G44860	0.0226285	FAMT	Farnesoic acid carboxyl-O-methyltransferase
AT4G23680	0.0206998	AT4G23680	AT4g23680/F9D16_150

Example Tree:
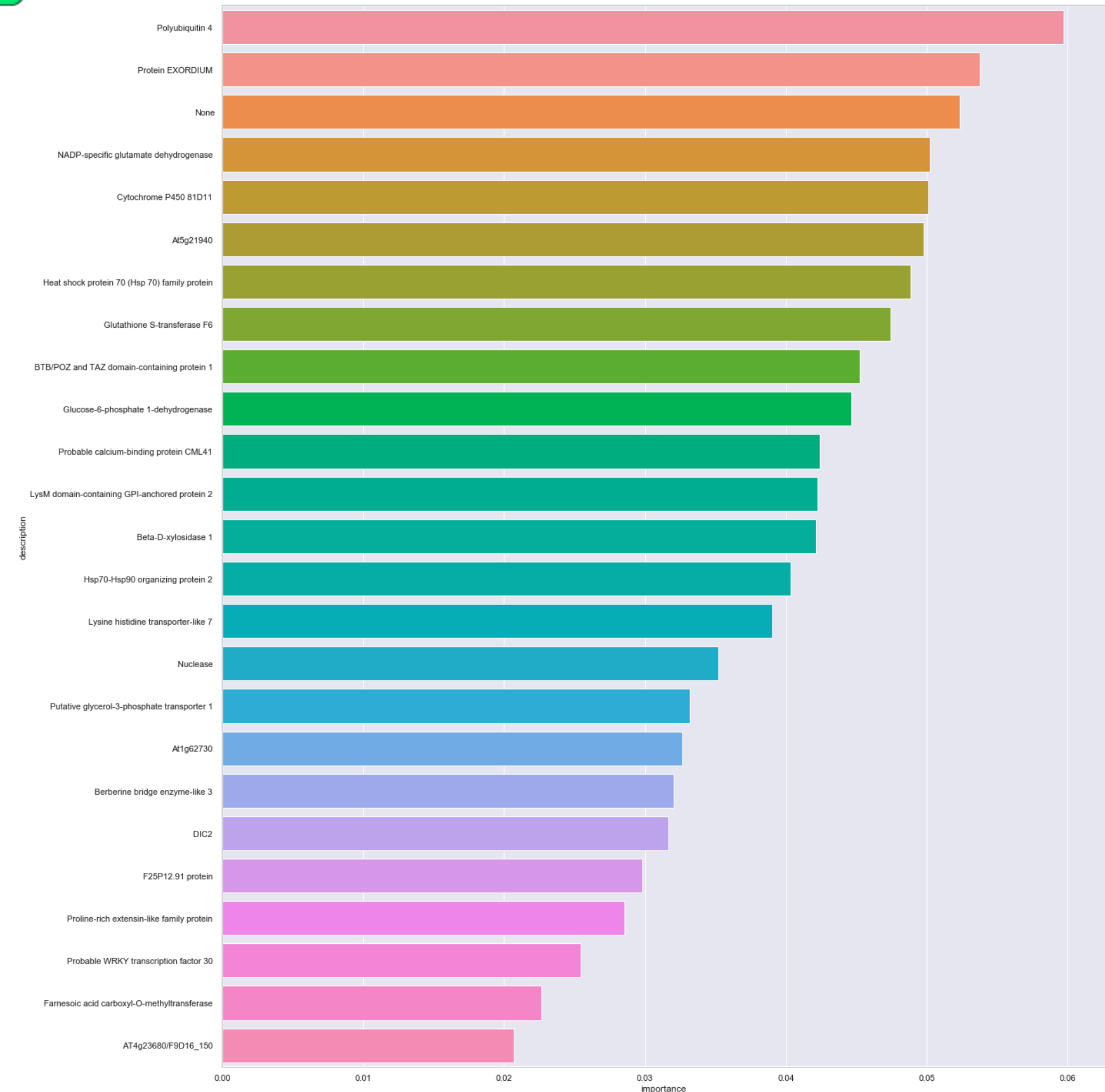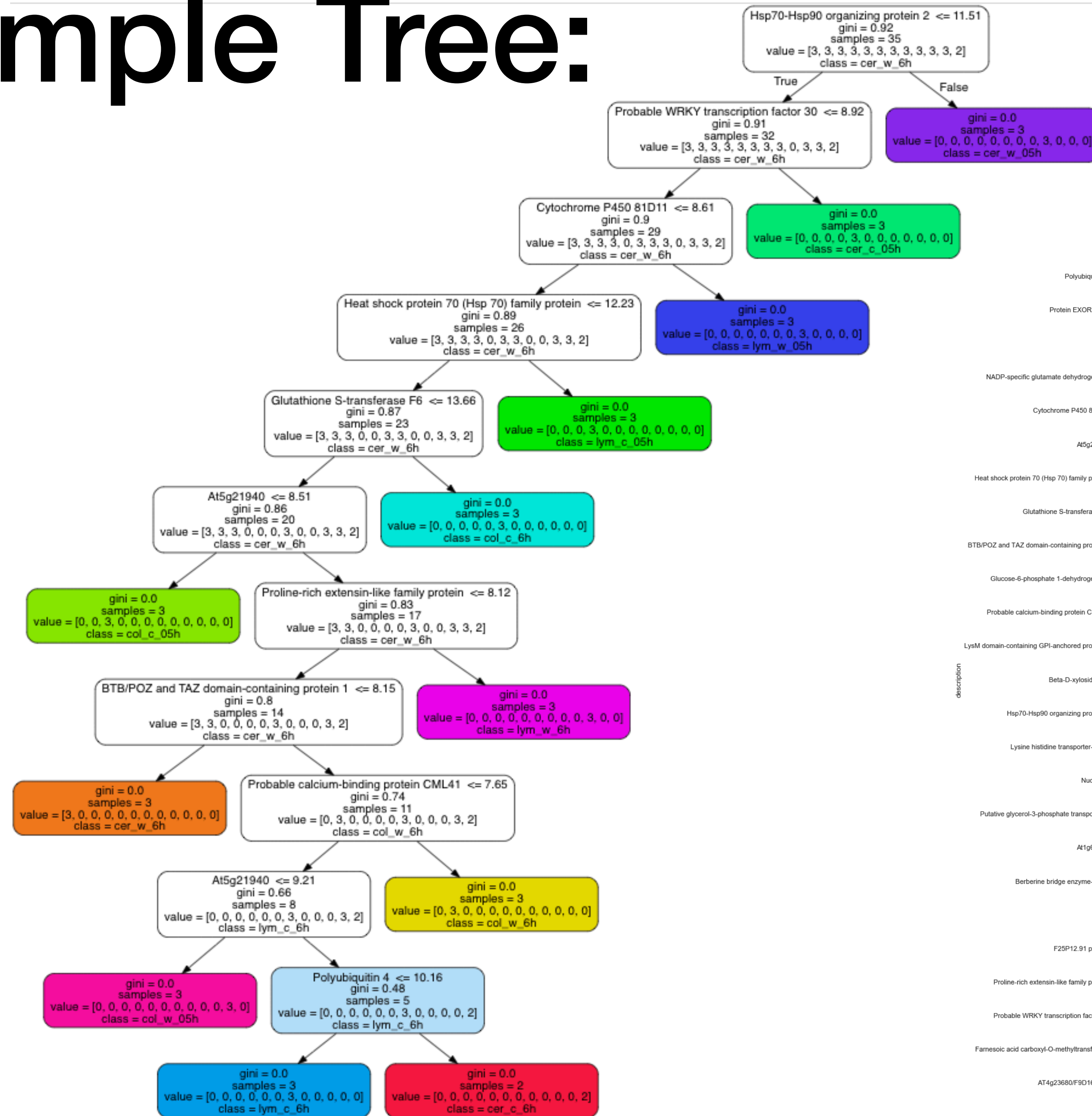
Grouping genes by trends

Grouping based on modelling significance