

Additional File 6

Genes and Gene Expression Modules Associated with Caloric Restriction and Aging in the Laboratory Mouse

William R. Swindell

University of Michigan, Departments of Pathology and Geriatrics

Gene Expression Modules Regulated by CR

This file provides a description of gene expression modules regulated by CR in multiple tissue types. Gene expression modules of varying size are displayed, including those with 2, 3, 5, 10, 20 and 40 member genes. The value of M associated with each module is directly related to the overall responsiveness of member genes to CR across tissue types (see Methods). The p-value associated with each value of M is generated by a simulation analysis, in which modules of the same size are formed at random, without reference to observed co-expression patterns (see Methods).

A dendrogram is shown for each module, which represents the co-expression patterns of member genes. This was generated based upon an average linkage hierarchical cluster analysis, in which similarity between genes was based upon the absolute value of Pearson's correlation coefficient (r) (see Methods). Additionally, for each module, a grid is shown that displays the differential expression patterns associated with member genes. Symbols have the following interpretation.

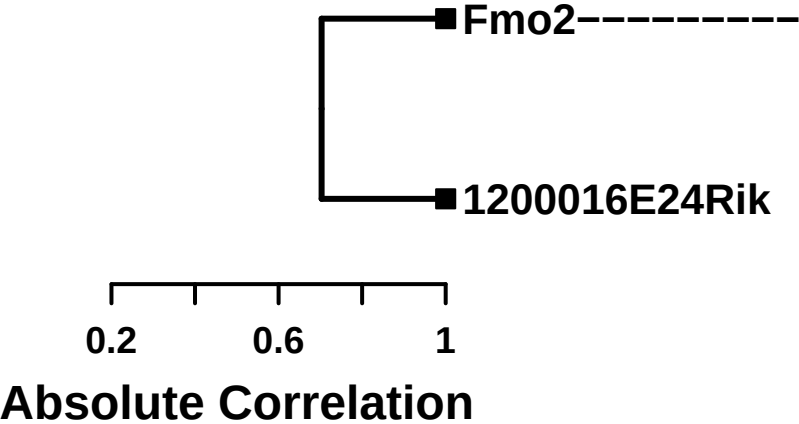
- Gene is significantly up regulated by CR ($P_u < 0.05$)
- Gene is significantly down regulated by CR ($P_d < 0.05$)
- Gene is marginally up regulated by CR ($0.05 < P_u < 0.10$)
- Gene is marginally down regulated by CR ($0.05 < P_d < 0.10$)
- Non-significant CR effect ($P_u > 0.10$ and $P_d > 0.10$)
- × No data (gene not represented for a given tissue or array annotation was limiting)
- * Evidence conflicts, but favors up regulation by CR
- * Evidence conflicts, but favors down regulation by CR

The last two categories (* and *) indicate significant effects with conflicting evidence. This can arise if there is significant up regulation by CR in one experiment, and significant down regulation by CR in another experiment that has examined the same tissue. Alternatively, a conflict may arise if $P_u < 0.05$ and also $P_d < 0.05$ for a given tissue type. Symbols shown in charts are based upon a comparison-wise type I error rate of 0.05.

Contact: William R. Swindell, wswindel@umich.edu

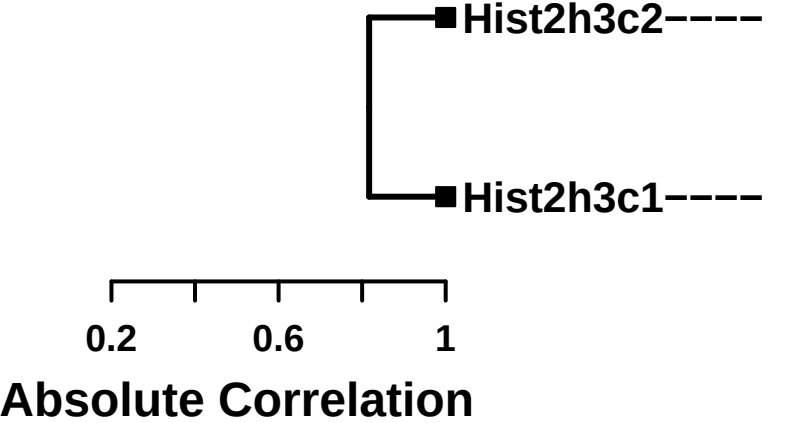
CR-Regulated Modules (2 Genes)

M = 10.7, P = 0.0625



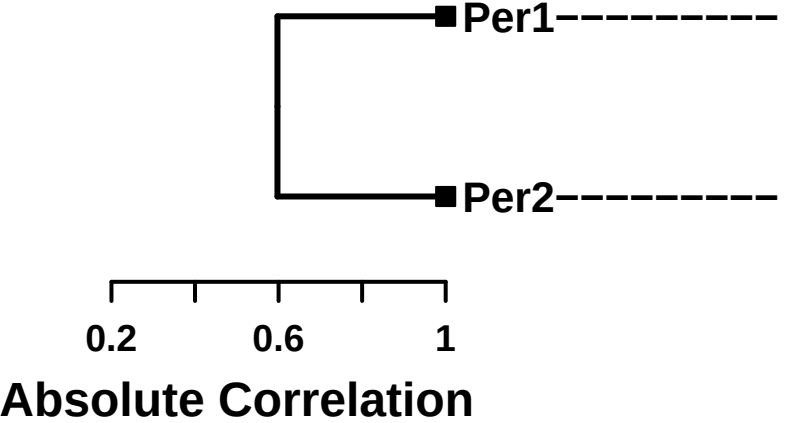
	msl	lvr	hrt	ctx	mmy	coc	cln	wat	hip	thm	str	spc	lng	kid	gon	cbm	hyp
Fmo2	●	●	●	●	●	●	●	×	-	×	×	×	×	×	×	×	●
1200016E24Rik	●	●	●	●	●	●	■	×	×	×	×	×	×	×	×	×	■

M = 10.5, P = 0.136



	hip	mmy	thm	str	spc	lng	kid	cbm	wat	gon	coc	msl	lvr	hyp	hrt	ctx	cln
Hist2h3c2	×	-	×	×	×	×	×	×	×	×	-	●	●	●	●	●	●
Hist2h3c1	●	●	×	×	×	-	×	×	●	●	●	●	●	●	●	●	●

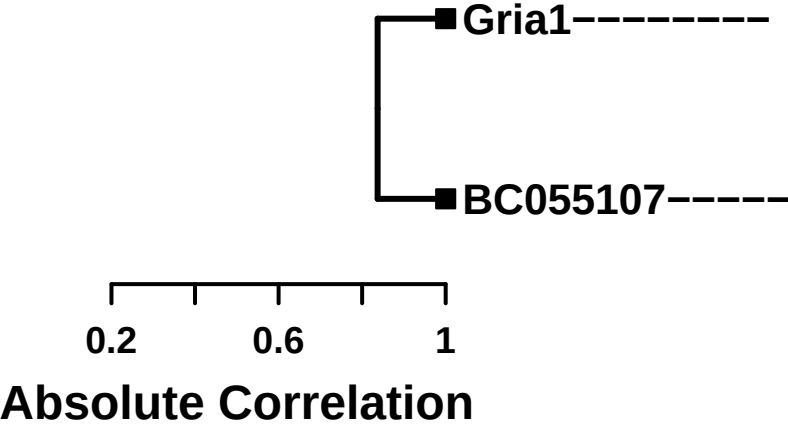
M = 10.1, P = 0.393



	wat	msl	lvr	hrt	coc	cln	hyp	lng	gon	thm	str	spc	kid	cbm	mmy	hip	ctx
Per1	●	●	●	●	●	●	■	●	●	×	×	×	×	×	●	-	●
Per2	●	●	●	●	●	●	●	-	-	×	×	×	×	×	■	●	●

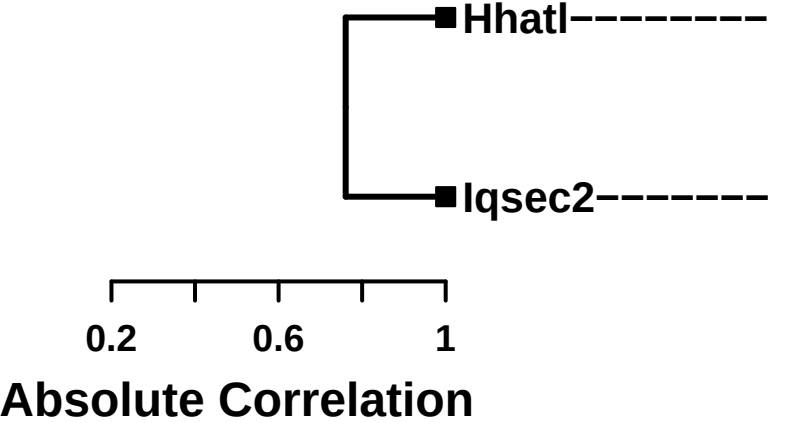
CR-Regulated Modules (2 Genes)

M = 10, P = 0.551



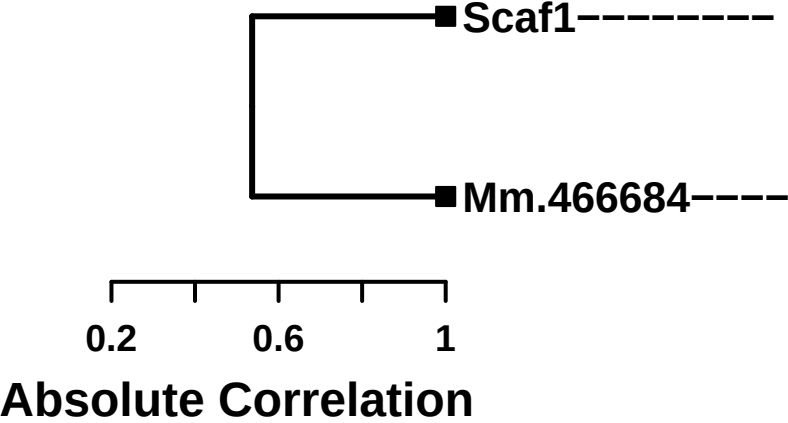
	hyp	hrt	coc	msl	lvr	lng	cln	wat	hip	ctx	thm	str	spc	kid	gon	cbm	mmy
Gria1	●	●	●	-	-	●	-	-	-	●	×	×	×	×	×	×	—
BC055107	●	●	●	●	●	×	●	-	×	●	×	×	×	×	×	×	×

M = 9.82, P = 0.751



	cln	wat	lvr	hip	thm	str	spc	mmy	lng	kid	gon	coc	cbm	msl	hyp	hrt	ctx
Hhatl	●	-	●	-	×	×	×	-	×	×	×	●	×	—	-	●	●
Iqsec2	●	×	●	×	×	×	×	×	×	×	×	●	×	*	●	●	●

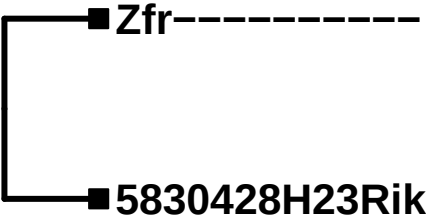
M = 9.71, P = 0.859



	hyp	coc	hip	thm	str	spc	mmy	lng	kid	gon	cbm	wat	cln	msl	lvr	hrt	ctx
Scaf1	●	●	×	×	×	×	×	×	×	×	×	●	-	—	●	●	●
Mm.466684	—	-	×	×	×	×	-	×	×	×	×	×	●	●	●	●	●

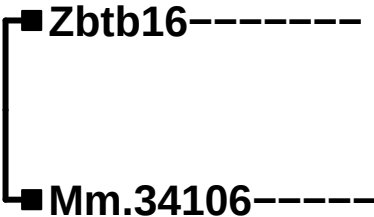
CR-Regulated Modules (2 Genes)

M = 9.55, P = 0.952



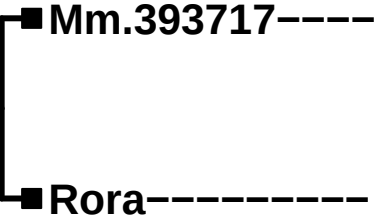
	coc	lng	msh	wat	hyp	hrt	hip	str	kid	cln	cbm	thm	spc	gon	lvr	ctx	mmy
Zfr	●	●	●	—	●	●	●	—	×	—	—	—	●	●	●	●	●
5830428H23Rik	●	×	—	×	●	●	●	×	×	—	×	×	×	×	●	●	●

M = 9.53, P = 0.965



	msh	lvr	hrt	ctx	coc	cln	wat	lng	hyp	hip	thm	str	spc	mmy	kid	gon	cbm
Zbtb16	●	●	●	●	●	●	●	●	—	—	×	×	×	—	×	—	×
Mm.34106	●	●	●	●	●	●	×	×	—	—	×	×	×	—	×	×	×

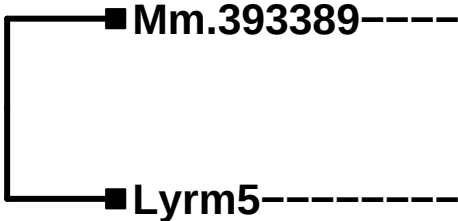
M = 9.51, P = 0.972



	lvr	hyp	hrt	coc	wat	ctx	lng	cln	hip	thm	str	spc	mmy	kid	gon	cbm	msh
Mm.393717	●	●	●	●	×	—	×	●	×	×	×	×	×	×	×	×	●
Rora	●	●	●	●	●	●	●	—	—	×	×	×	—	—	—	×	×

CR-Regulated Modules (2 Genes)

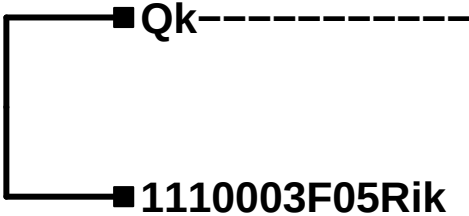
M = 9.47, P = 0.99



Mm.393389	msl	hyp	cln	ctx	coc	wat	hrt	hip	thm	str	spc	mmy	lng	kid	gon	cbm	lvr
Lyrm5	msl	hyp	cln	ctx	coc	wat	hrt	hip	thm	str	spc	mmy	lng	kid	gon	cbm	lvr

Absolute Correlation

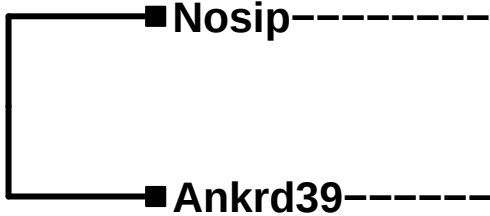
M = 9.43, P = 0.994



Qk	lvr	hyp	coc	lng	mmy	wat	hip	ctx	thm	str	spc	kid	cln	cbm	hrt	gon	msl
1110003F05Rik	lvr	hyp	coc	lng	mmy	wat	hip	ctx	thm	str	spc	kid	cln	cbm	hrt	gon	msl

Absolute Correlation

M = 9.38, P = 0.997

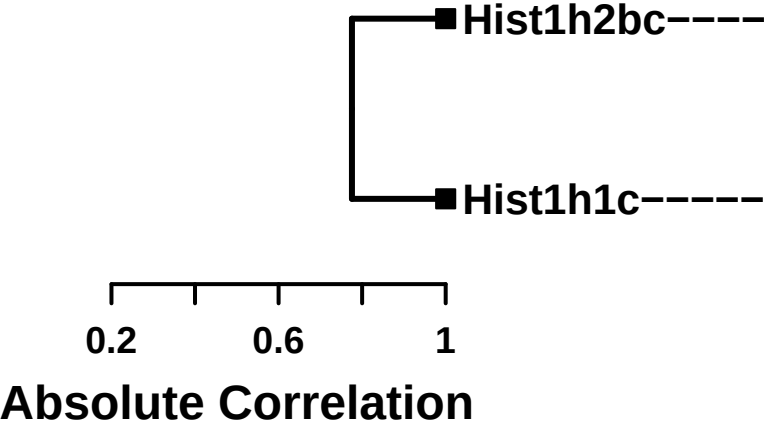


Nosip	hyp	coc	cln	hip	wat	msl	ctx	thm	str	spc	lng	kid	gon	cbm	mmy	lvr	hrt
Ankrd39	hyp	coc	cln	hip	wat	msl	ctx	thm	str	spc	lng	kid	gon	cbm	mmy	lvr	hrt

Absolute Correlation

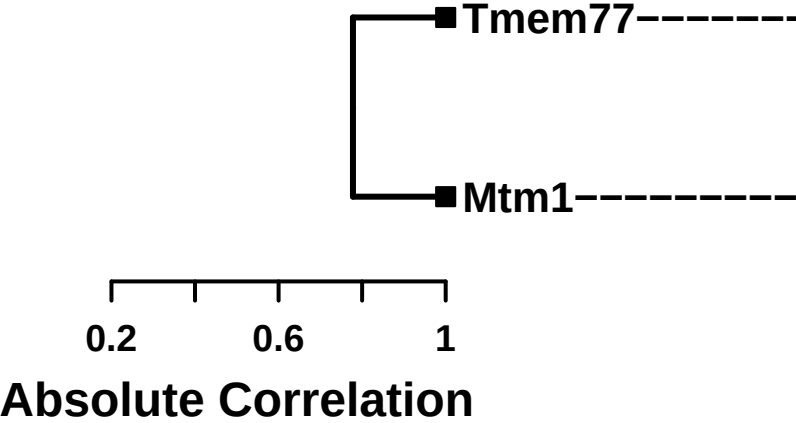
CR-Regulated Modules (2 Genes)

M = 9.37, P = 0.998



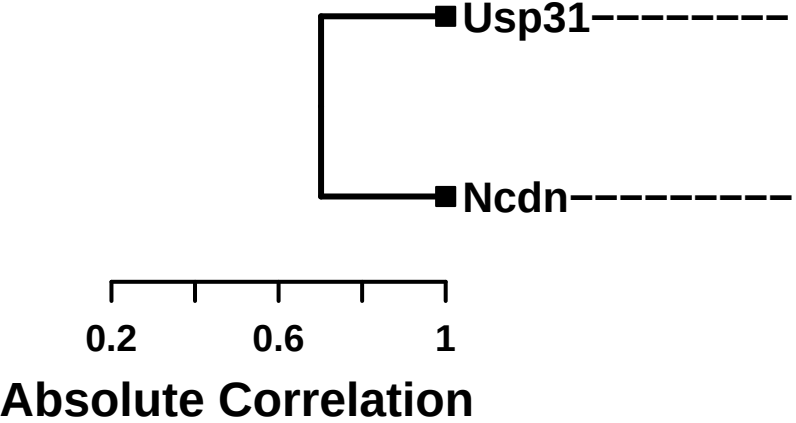
	Ing	thm	str	spc	kid	coc	cbm	hip	ctx	wat	msl	lvr	hrt	mmy	gon	hyp	cln
Hist1h2bc	●	×	×	×	×	●	×	—	●	●	*	●	●	—	●	●	●
Hist1h1c	×	×	×	×	×	●	×	—	—	×	●	*	—	●	×	●	●

M = 9.32, P = 0.999



	hrt	ctx	mmy	Ing	wat	msl	lvr	hyp	hip	thm	str	spc	gon	coc	cln	cbm	kid
Tmem77	●	●	●	×	×	*	●	—	—	×	×	×	×	●	●	×	×
Mtm1	●	—	—	●	—	●	●	—	—	×	×	×	×	●	●	×	●

M = 9.32, P = 0.999



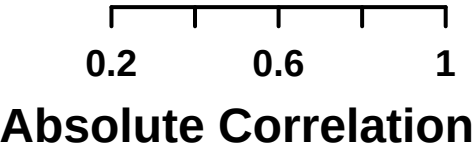
	hyp	lvr	Ing	hip	thm	str	spc	kid	coc	cln	cbm	wat	mmy	gon	msl	hrt	ctx
Usp31	●	●	×	×	×	×	×	×	●	—	×	×	×	●	●	●	●
Ncdn	—	—	●	—	×	×	×	×	●	—	×	●	●	×	●	●	●

CR-Regulated Modules (2 Genes)

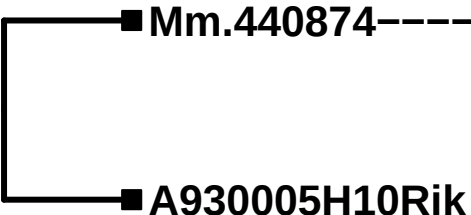
M = 9.31, P = 0.999



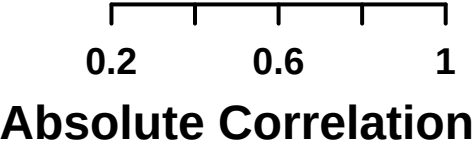
	hyp	coc	cln	wat	cbm	msl	thm	str	spc	lng	kid	gon	lvr	hip	mmy	hrt	ctx
Sfrs18	●	●	●	●	×	*	×	×	×	×	×	×	●	●	×	●	●
Rbm5	●	●	●	×	●	*	—	—	—	×	×	×	*	—	●	●	●



M = 9.31, P = 1

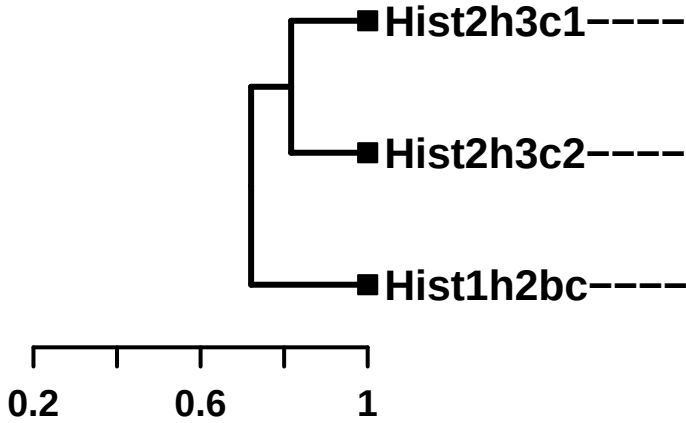


	ctx	cln	wat	msl	hip	thm	str	spc	mmy	lng	kid	gon	cbm	hrt	hyp	lvr	coc
Mm.440874	—	—	×	●	×	×	×	×	×	×	×	×	×	—	—	●	●
A930005H10Rik	●	●	×	*	×	×	×	×	×	×	×	×	×	●	●	●	●



CR-Regulated Modules (3 Genes)

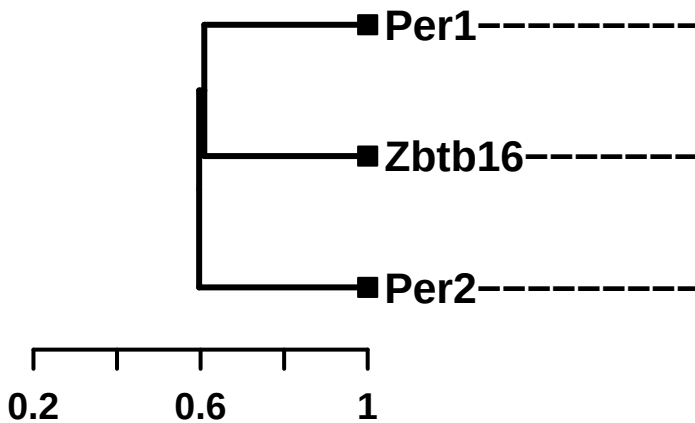
M = 10.2, P = 0.0045



Absolute Correlation

	1	2	3
mmmy	—	—	●
lng	●	×	—
hip	—	×	●
thm	×	×	×
str	×	×	×
spc	×	×	×
kid	×	×	×
coc	●	—	●
cbm	×	×	×
wat	●	×	●
msl	*	●	●
gon	●	×	●
lvr	●	●	●
hyp	●	●	●
hrt	●	●	●
ctx	●	●	●
cln	●	●	●

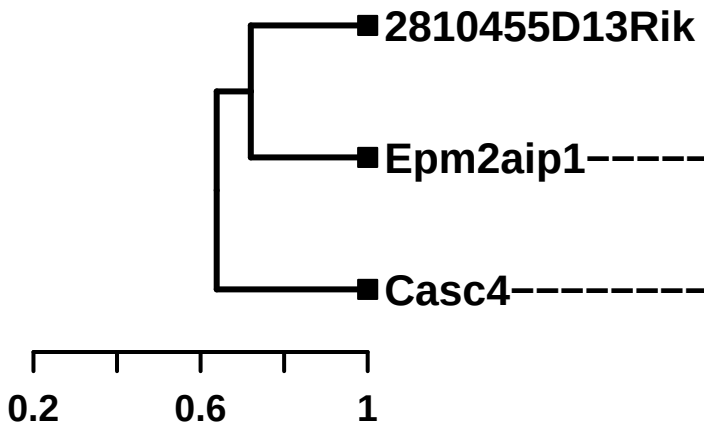
M = 10, P = 0.008



Absolute Correlation

wat	●	●	●
msl	●	●	
lvr	●	●	
hrt	●	●	
coc	●	●	
cln	●	●	
hyp	●	—	
lng	—	●	
gon	—	—	
thm	×	×	
str	×	×	
spc	×	×	
kid	×	×	
cbm	×	×	
mmmy	—	—	
hip	●	—	
ctx	●	●	

M = 9.73, P = 0.033

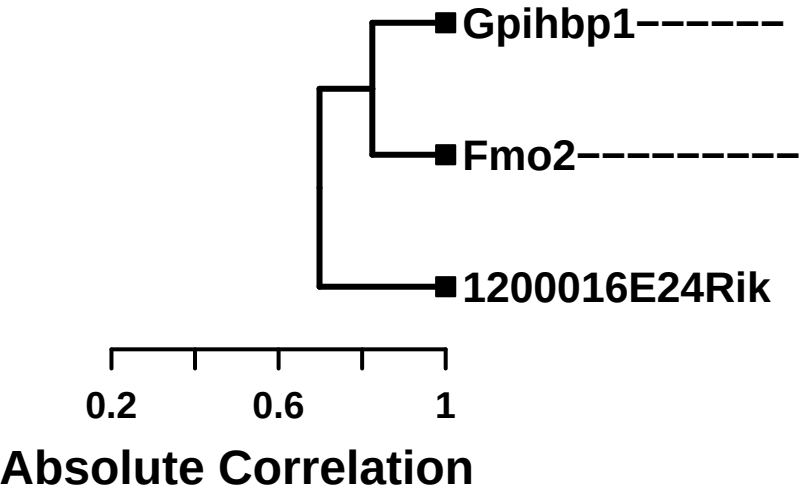


Absolute Correlation

	coc	hyp	cln	wat	thm	str	spc	lng	kid	gon	cbm	ctx	mst	hrt	hip	mmv	lvr
(0)	●	-	-	x	x	x	x	x	x	x	x	-	●	●	x	x	-
(1)	●	●	-	-	x	x	x	x	x	x	x	●	●	●	●	●	●
(2)	●	●	●	x	x	x	x	x	x	x	x	●	●	●	x	x	●

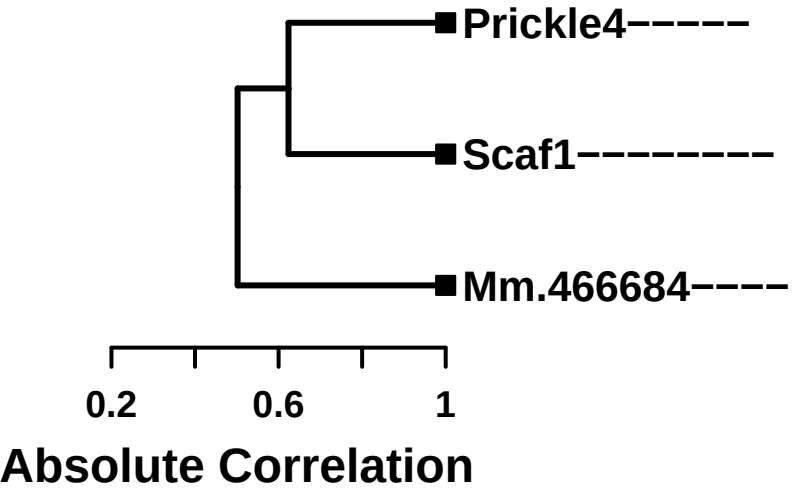
CR-Regulated Modules (3 Genes)

M = 9.48, P = 0.102



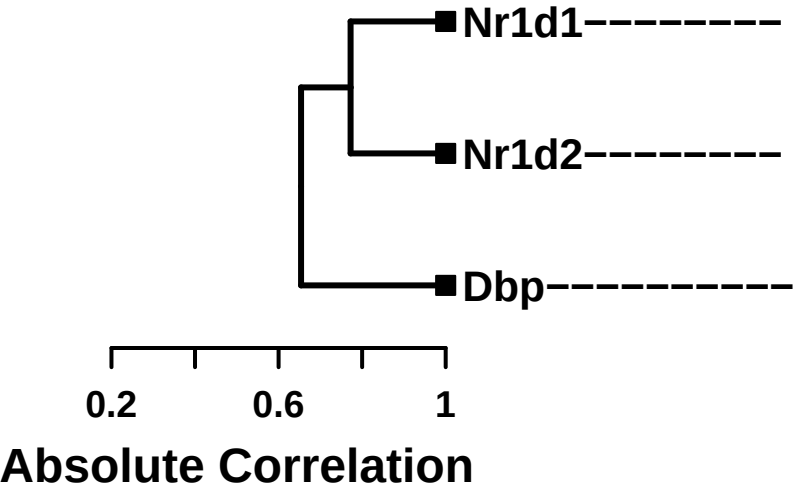
	msl	lvr	hrt	coc	ctx	mmy	cln	cbm	wat	thm	spc	lng	kid	gon	hip	str	hyp
Gpihbp1	●	●	●	—	—	×	●	—	×	—	—	×	×	—	—	●	●
Fmo2	●	●	●	●	●	●	●	×	×	×	×	×	×	×	—	×	●
1200016E24Rik	●	●	●	●	●	●	—	×	×	×	×	×	×	×	×	×	—

M = 9.47, P = 0.105



	hyp	coc	mmy	hip	thm	str	spc	lng	kid	gon	cbm	wat	cln	msl	lvr	hrt	ctx
Prickle4	●	●	●	—	×	×	×	×	×	×	×	×	—	●	●	●	●
Scaf1	●	●	×	×	×	×	×	×	×	×	×	●	—	—	●	●	●
Mm.466684	—	—	—	×	×	×	×	×	×	×	×	×	●	●	●	●	●

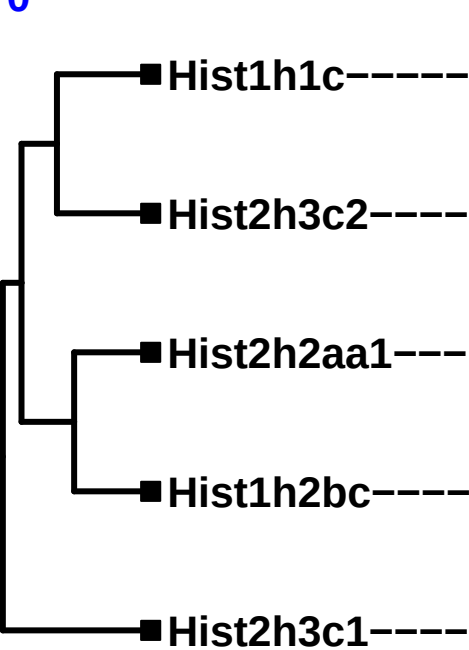
M = 9.4, P = 0.14



	coc	hip	cln	hyp	wat	lvr	thm	str	spc	kid	gon	cbm	hrt	lng	msl	ctx	mmy
Nr1d1	●	●	—	—	×	●	×	×	×	×	×	×	●	×	●	●	●
Nr1d2	●	—	●	—	×	●	—	—	—	×	×	—	●	×	*	—	●
Dbp	●	●	●	—	—	*	×	×	×	×	×	×	*	●	●	●	●

CR-Regulated Modules (5 Genes)

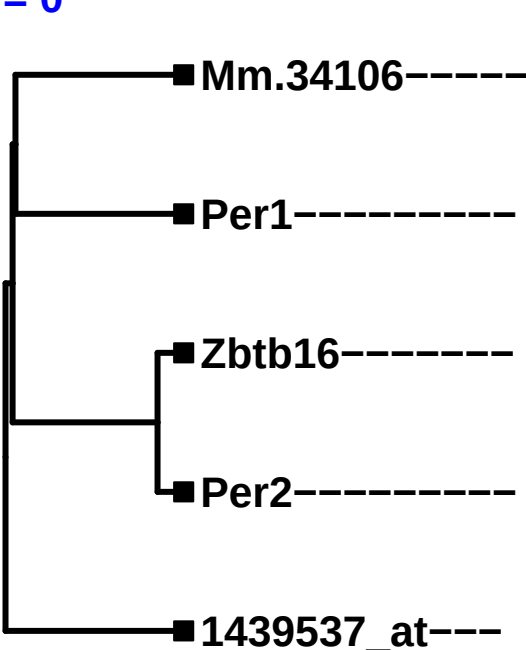
M = 9.79, P = 0



Ing	hip	thm	str	spc	mmy	kid	coc	cbm	gon	ctx	wat	msl	cln	lvr	hrt	hyp
×	—	×	×	×	●	×	●	×	×	—	×	●	●	*	—	●
×	×	×	×	×	—	×	—	×	×	●	×	●	●	●	●	●
—	×	×	×	×	—	×	●	×	●	●	—	●	●	●	*	●
●	—	×	×	×	—	×	●	×	●	●	●	*	●	●	●	●
—	●	×	×	×	●	×	●	×	●	●	●	●	●	●	●	●

Absolute Correlation

M = 9.29, P = 0

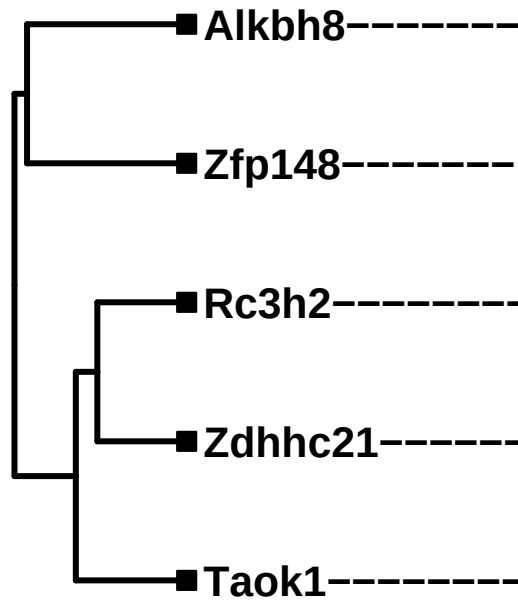


msl	coc	hrt	cln	wat	lvr	Ing	hyp	ctx	gon	thm	str	spc	kid	cbm	mmy	hip
●	●	●	●	×	●	×	—	●	×	×	×	×	×	×	—	—
●	●	●	●	●	●	●	—	●	●	×	×	×	×	×	●	—
●	●	●	●	●	●	●	—	●	—	×	×	×	×	×	—	—
●	●	●	●	●	●	—	●	●	—	×	×	×	×	×	—	●
●	●	—	—	×	●	×	●	●	×	×	×	×	×	×	×	×

Absolute Correlation

CR-Regulated Modules (5 Genes)

M = 8.91, P = 0.0065

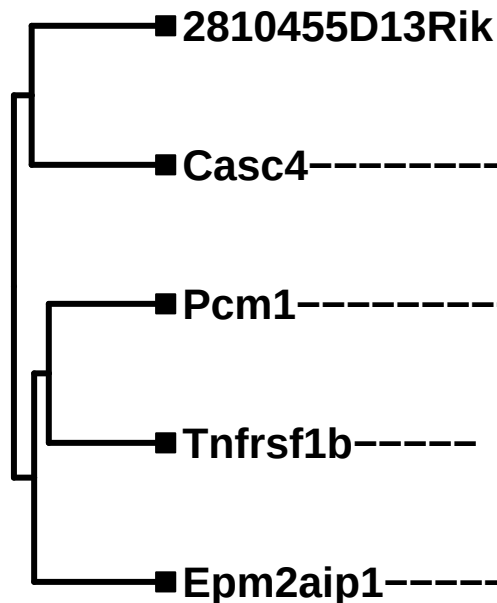


A horizontal number line with tick marks at 0.2, 0.6, and 1. The line starts at 0 on the left and ends at 1 on the right. There are four equal intervals between 0 and 1, with tick marks at 0.2, 0.6, and 1.

Absolute Correlation

hyp	●	●	—	×	×
coc	●	●	—	×	×
ctx	●	—	×	×	×
cln	●	—	×	×	×
lng	×	×	×	×	×
hip	—	×	×	×	×
wat	×	×	×	×	×
str	—	×	×	×	×
spc	—	×	×	×	×
kid	×	×	×	×	×
gon	—	×	×	×	×
cbm	—	×	×	×	×
thm	●	×	×	×	×
lvr	●	×	×	×	×
mmy	●	×	×	×	×
msl	●	×	×	×	×
hrt	●	×	×	×	×

M = 8.76, P = 0.019



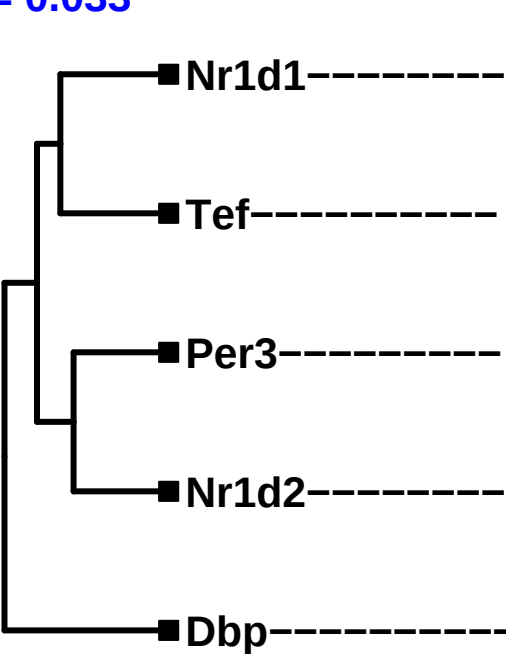
A horizontal number line with tick marks at 0.2, 0.6, and 1. The line starts at 0 on the left and ends at 1 on the right. There are four equal intervals between the tick marks.

Absolute Correlation

coc	●	-	●	●	●
hyp	●	■	●	■	●
str	x	x	●	x	x
cln	-	-	-	-	-
thm	x	x	-	x	x
spc	x	x	-	x	x
kid	x	x	x	x	x
gon	x	x	x	-	x
cbm	x	x	-	x	x
wat	-	●	x	●	-
hip	●	-	-	-	●
lng	x	●	x	●	x
ctx	●	-	●	-	●
lvr	●	●	●	●	●
mmy	●	x	●	-	●
msl	●	●	●	●	●
hrt	●	●	●	●	●

CR-Regulated Modules (5 Genes)

M = 8.68, P = 0.033

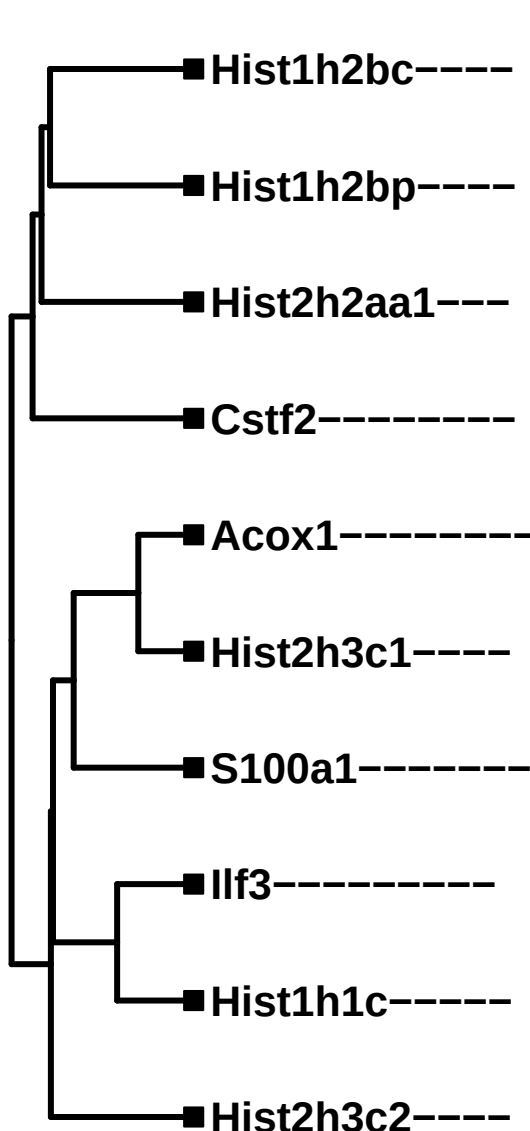


-	×	-	●	●	●	●	×	×	×	×	×	×	●	●	×	●
●	●	●	-	●	●	●	-	-	×	-	-	-	●	●	-	●
●	-	-	-	*	●	●	-	-	×	×	-	-	*	●	-	●
●	×	-	-	●	●	-	-	-	×	×	-	-	*	●	×	●
●	-	-	●	*	●	●	×	×	×	×	×	×	●	*	●	●
cln	wat	hyp	hip	lvr	coc	ctx	thm	spc	kid	gon	str	cbm	msl	hrt	lng	mmy

0.2 0.6 1
Absolute Correlation

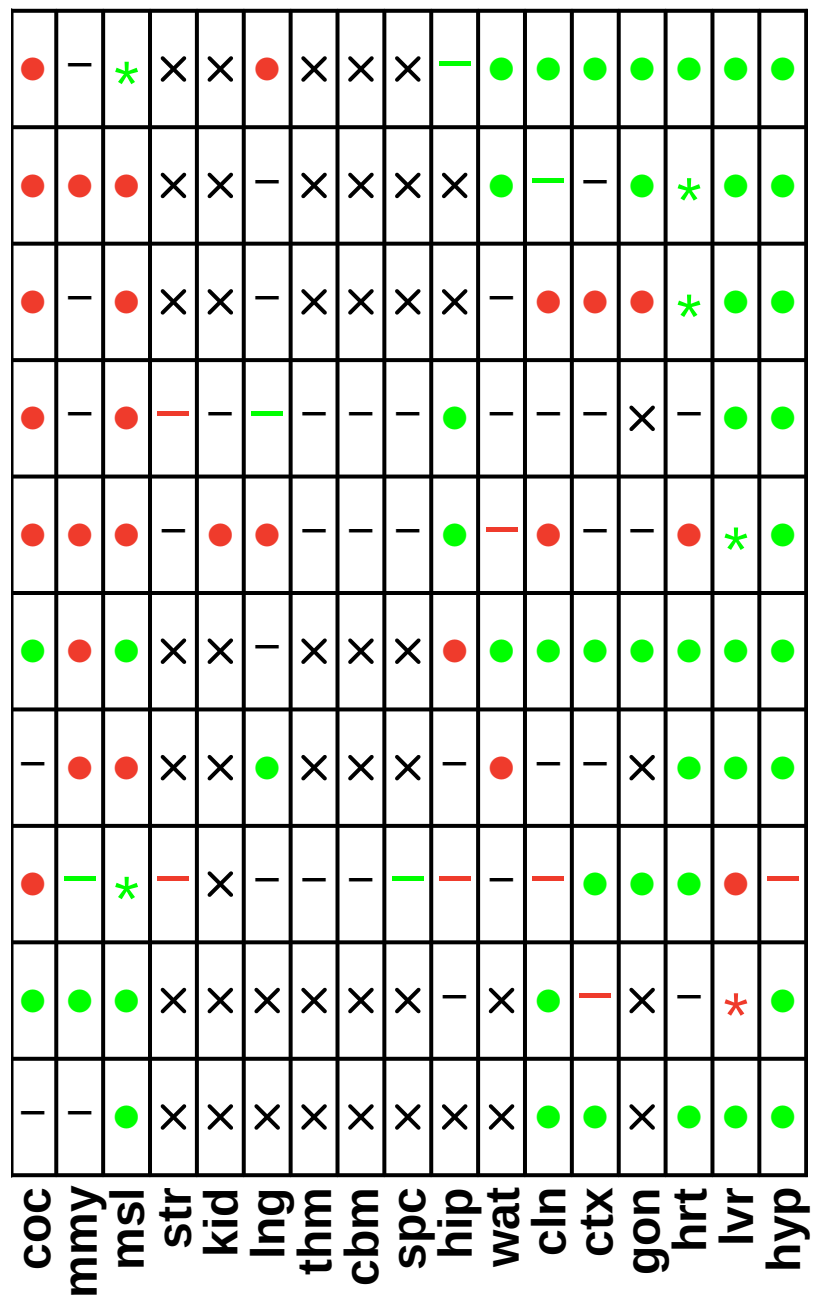
CR-Regulated Modules (10 Genes)

M = 8.55, P = 0



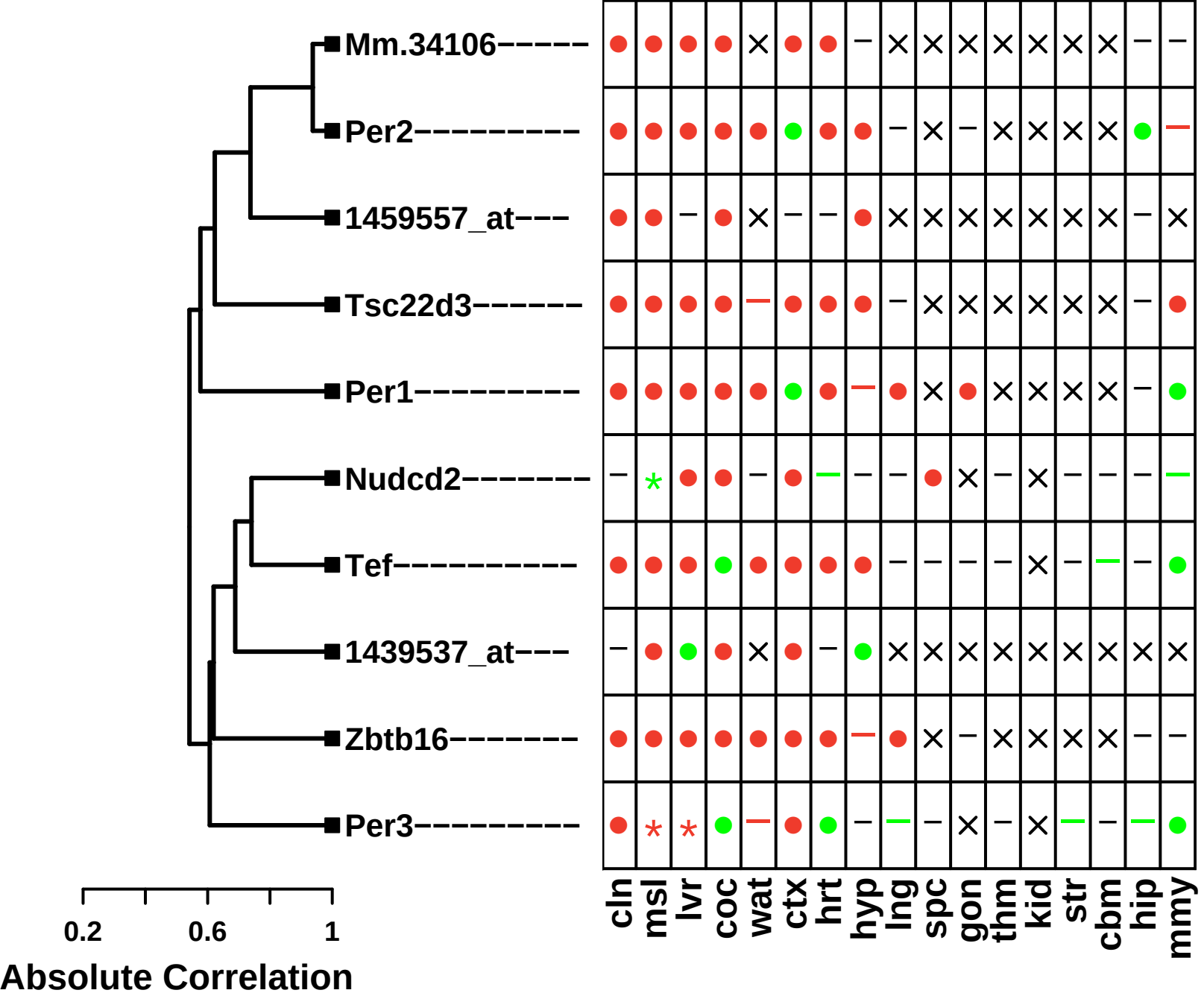
A horizontal number line with tick marks at 0.2, 0.6, and 1. The line is labeled with these values below the tick marks.

Absolute Correlation



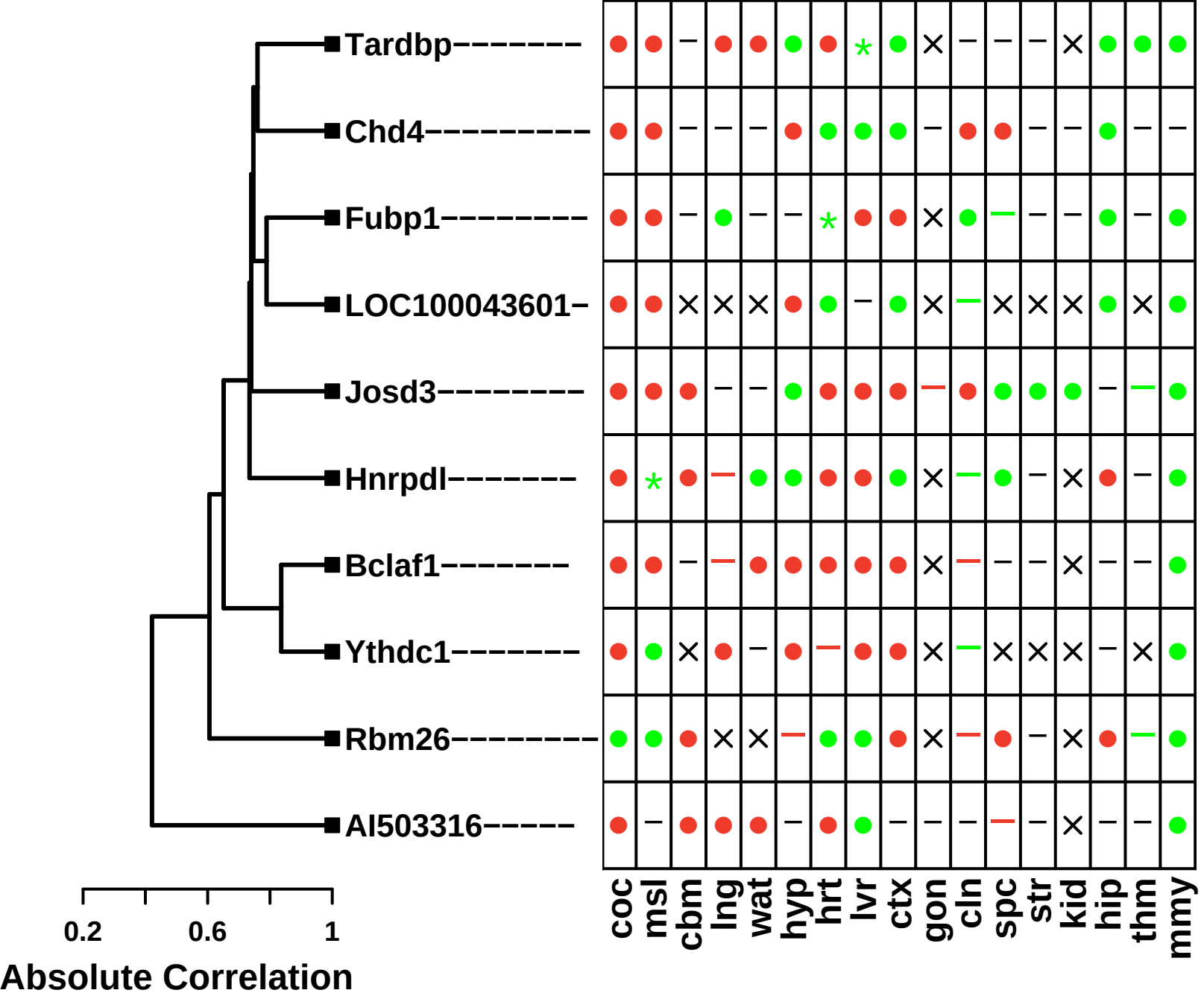
CR-Regulated Modules (10 Genes)

M = 8.4, P = 0



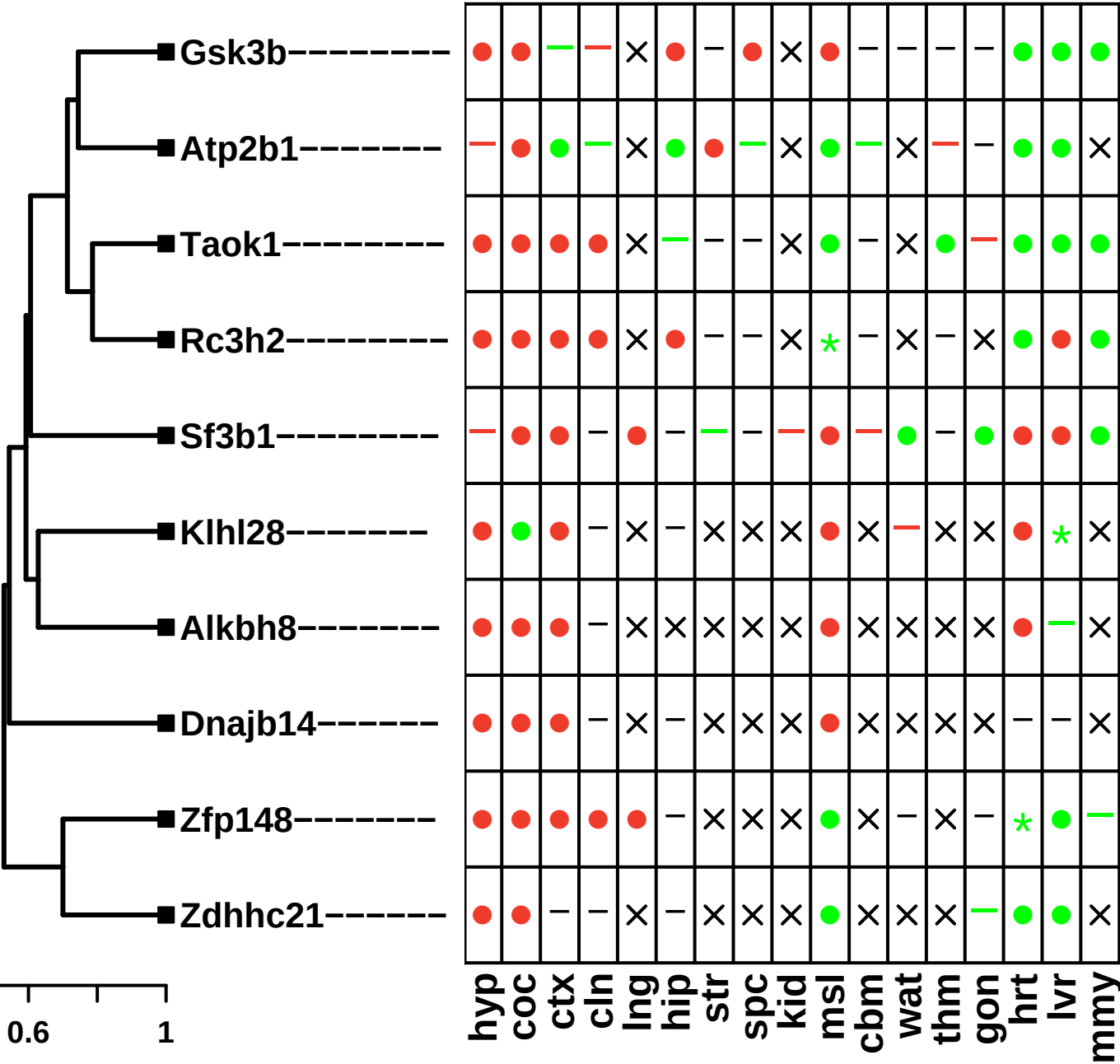
CR-Regulated Modules (10 Genes)

M = 8.22, P = 0



CR-Regulated Modules (10 Genes)

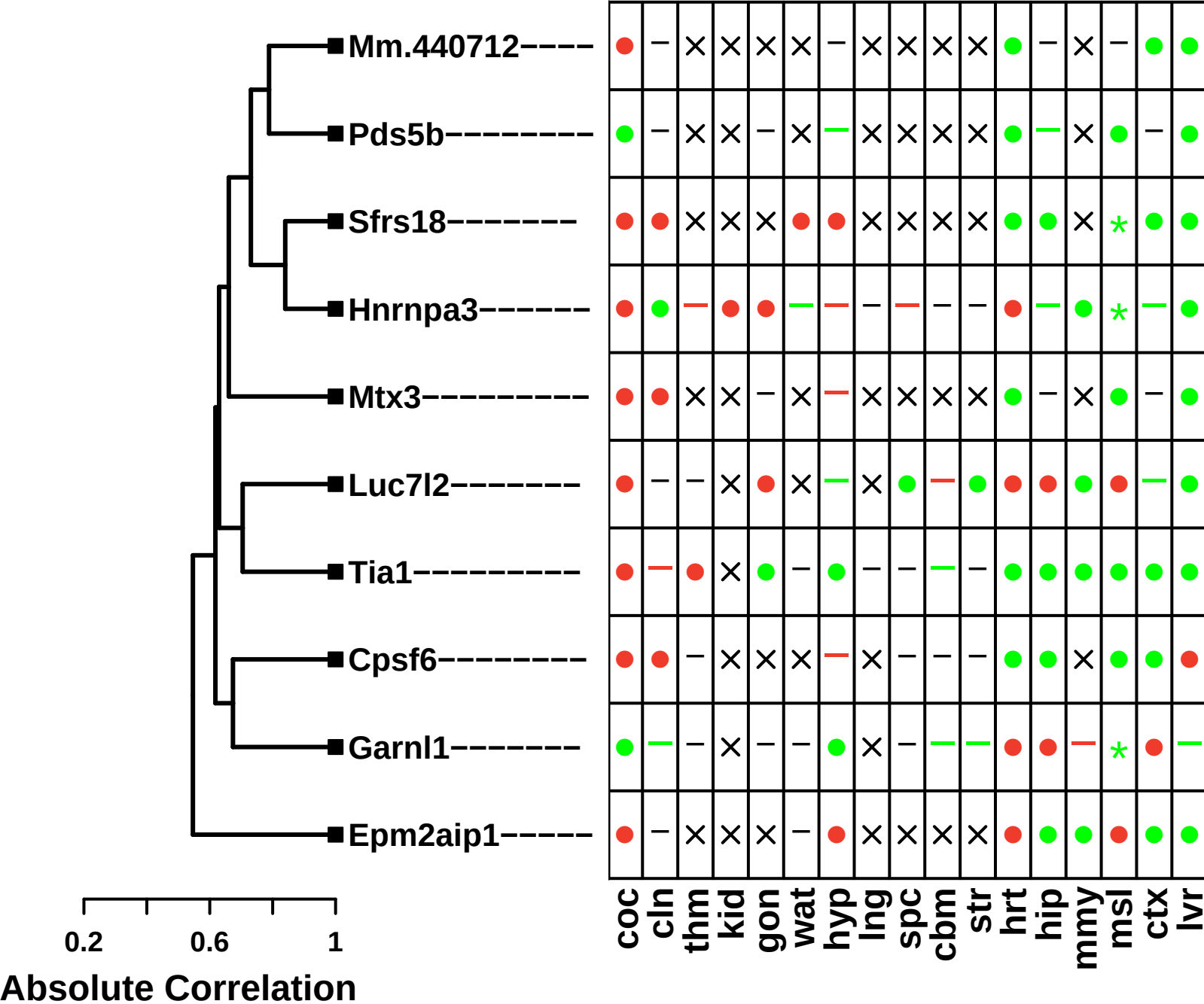
M = 8.22, P = 0



Absolute Correlation

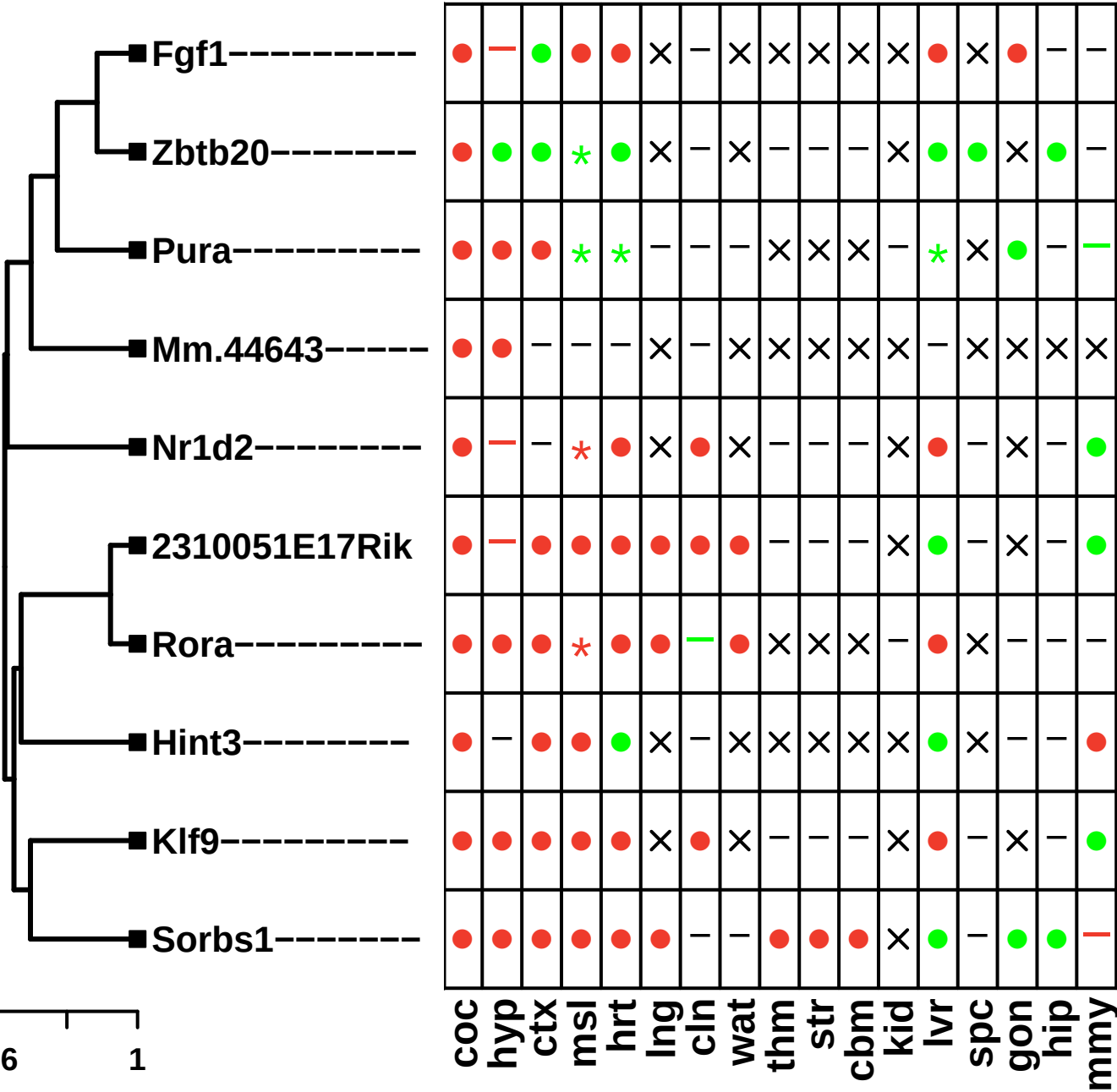
CR-Regulated Modules (10 Genes)

M = 8.08, P = 0.0015



CR-Regulated Modules (10 Genes)

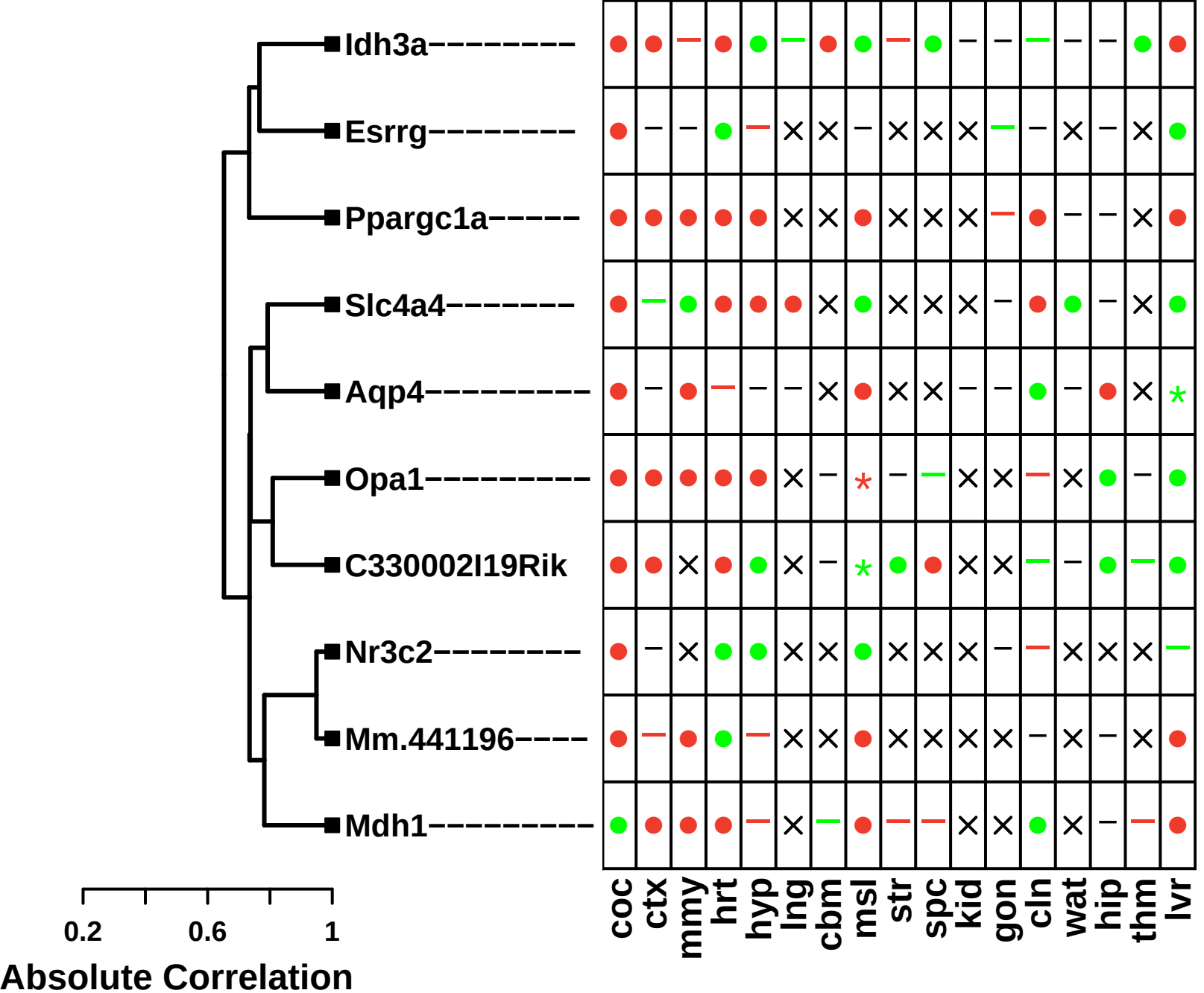
M = 7.96, P = 0.003



Absolute Correlation

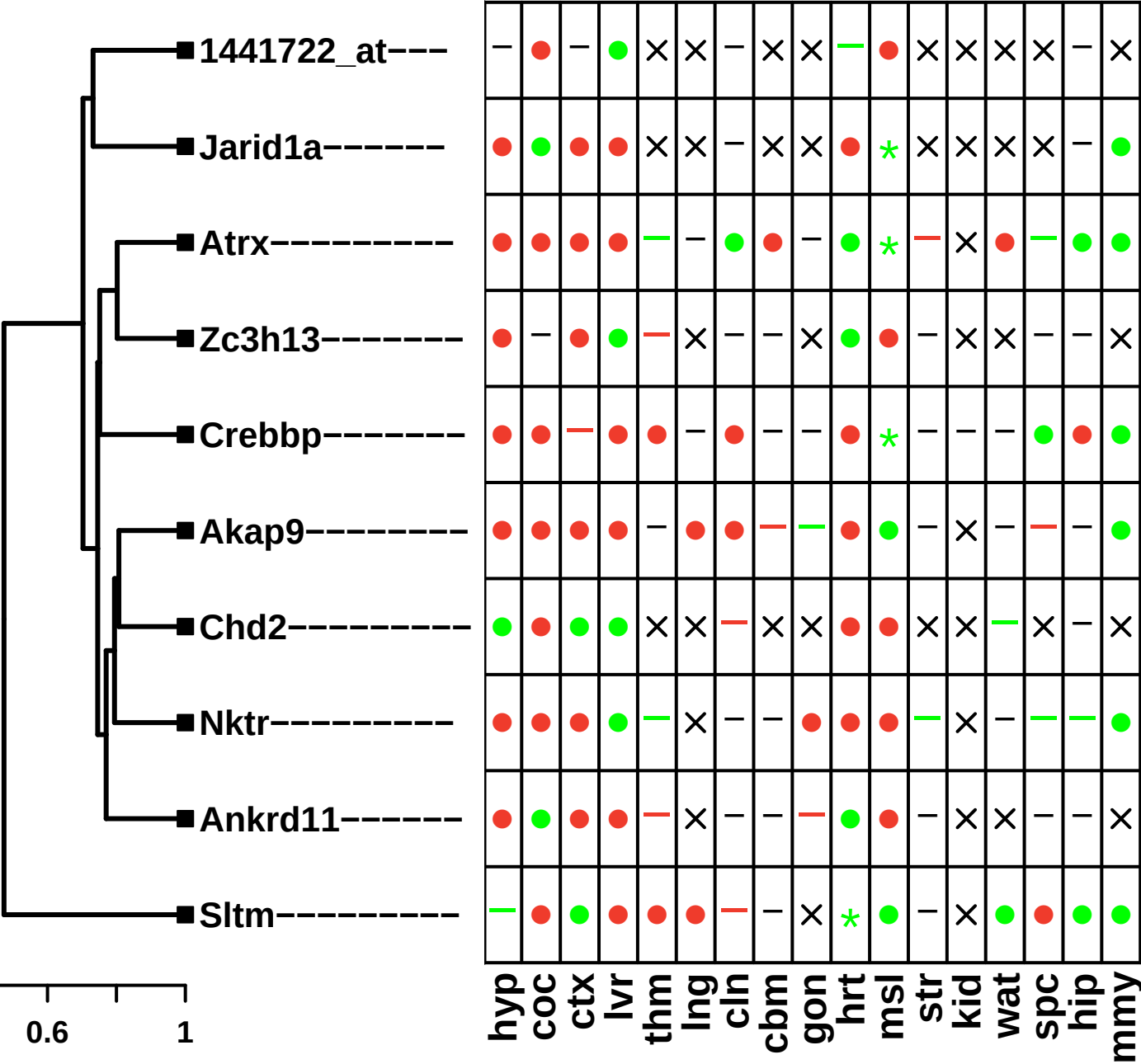
CR-Regulated Modules (10 Genes)

M = 7.95, P = 0.003



CR-Regulated Modules (10 Genes)

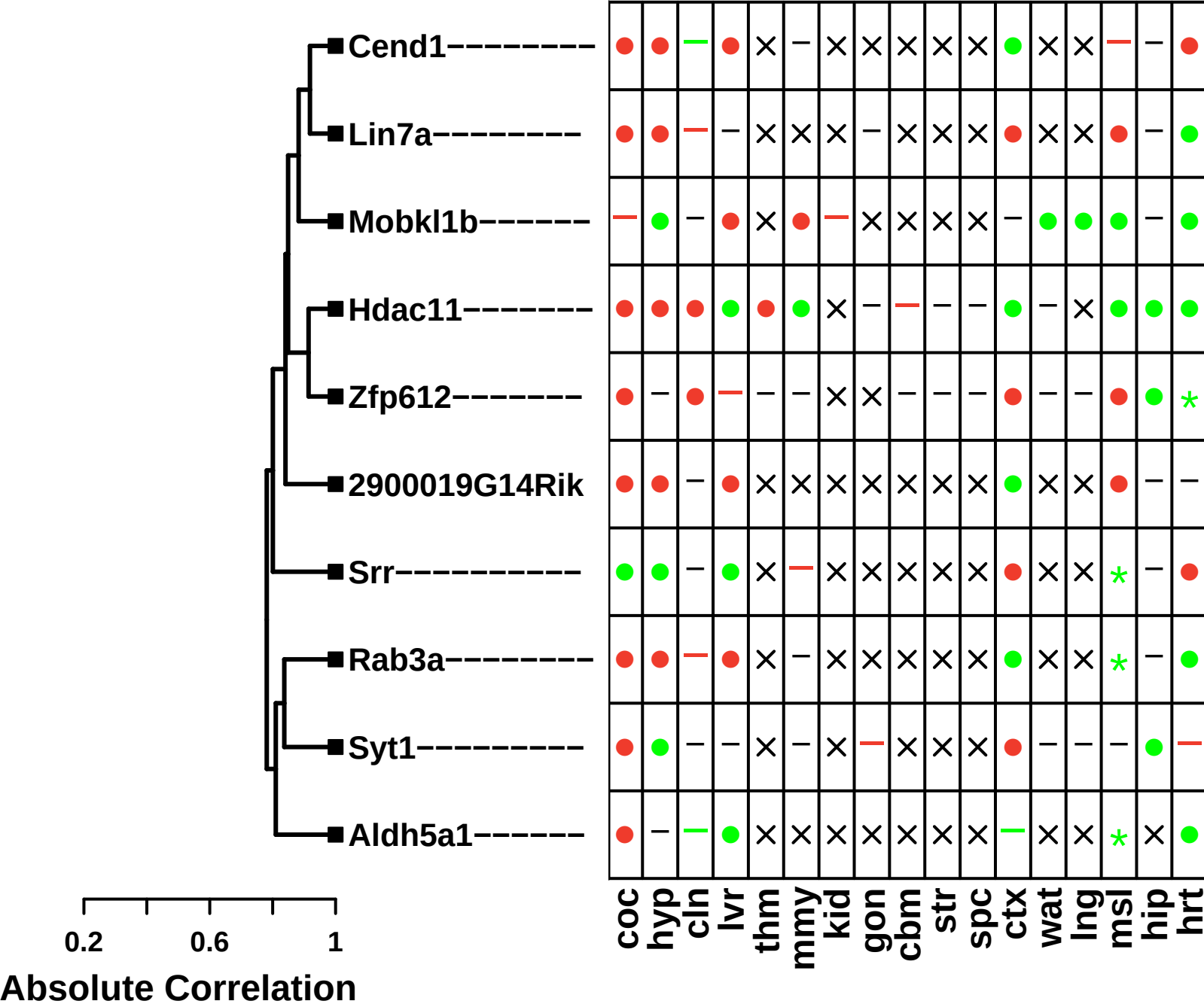
M = 7.93, P = 0.004



Absolute Correlation

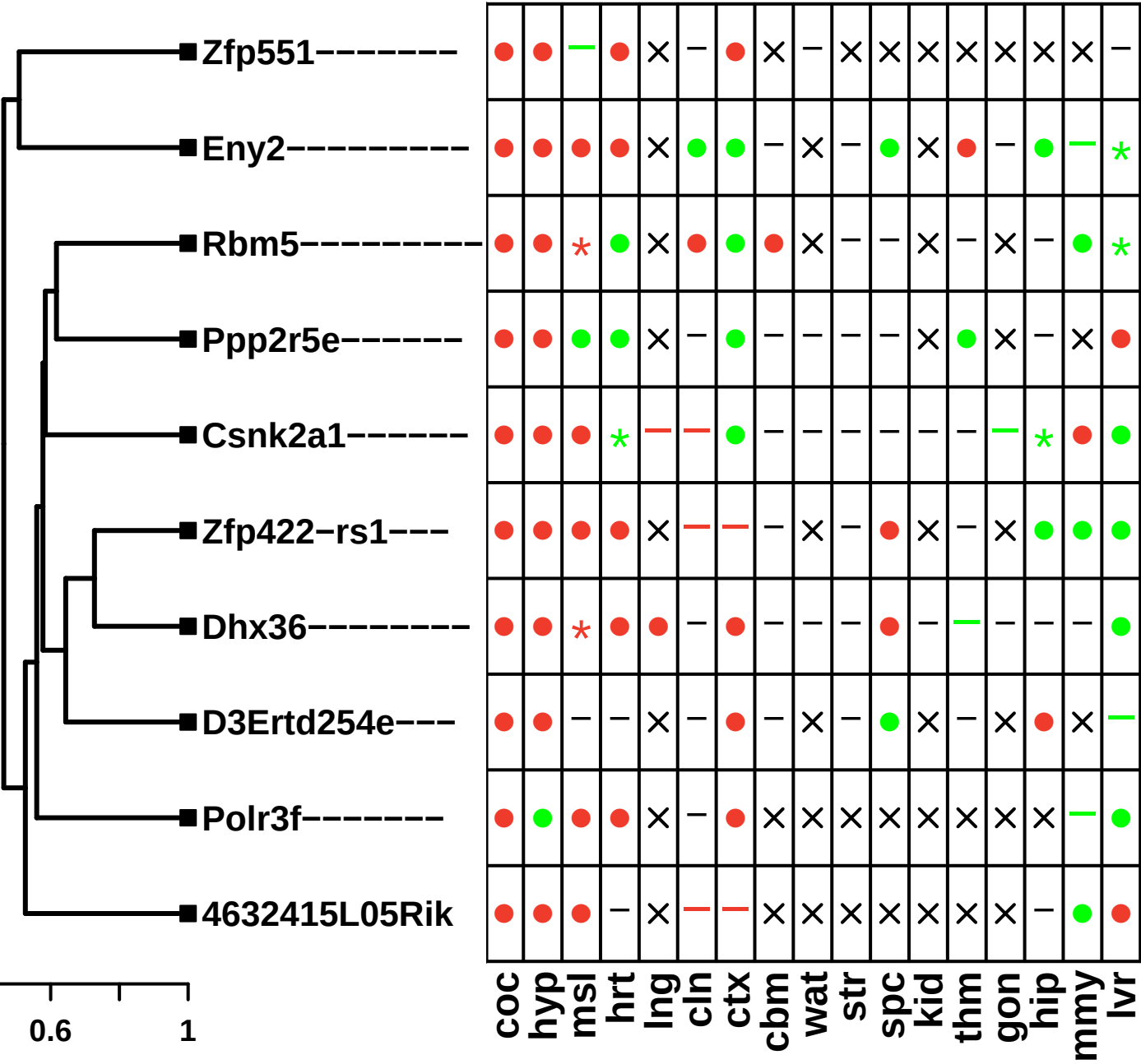
CR-Regulated Modules (10 Genes)

M = 7.92, P = 0.004



CR-Regulated Modules (10 Genes)

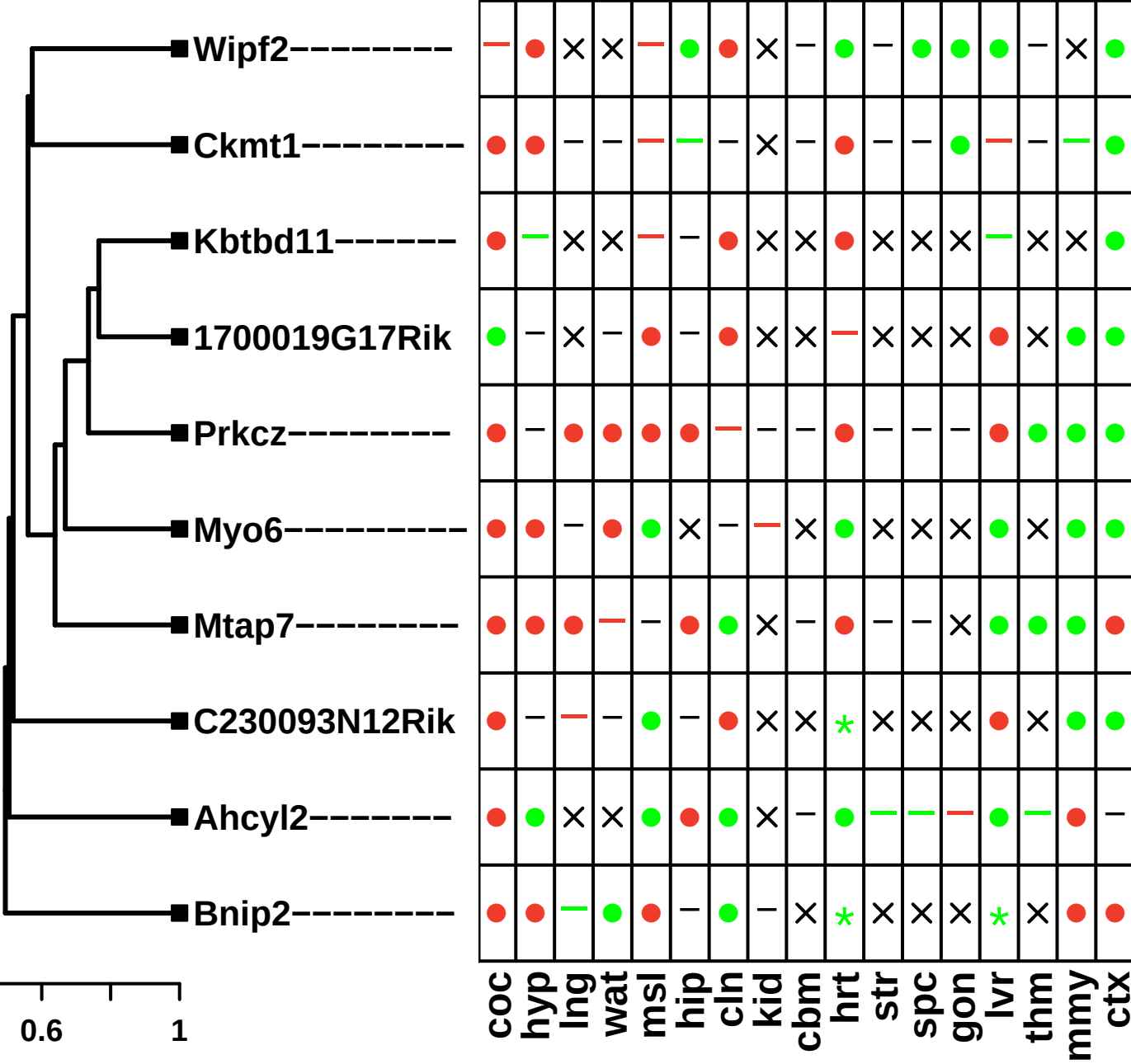
M = 7.88, P = 0.004



Absolute Correlation

CR-Regulated Modules (10 Genes)

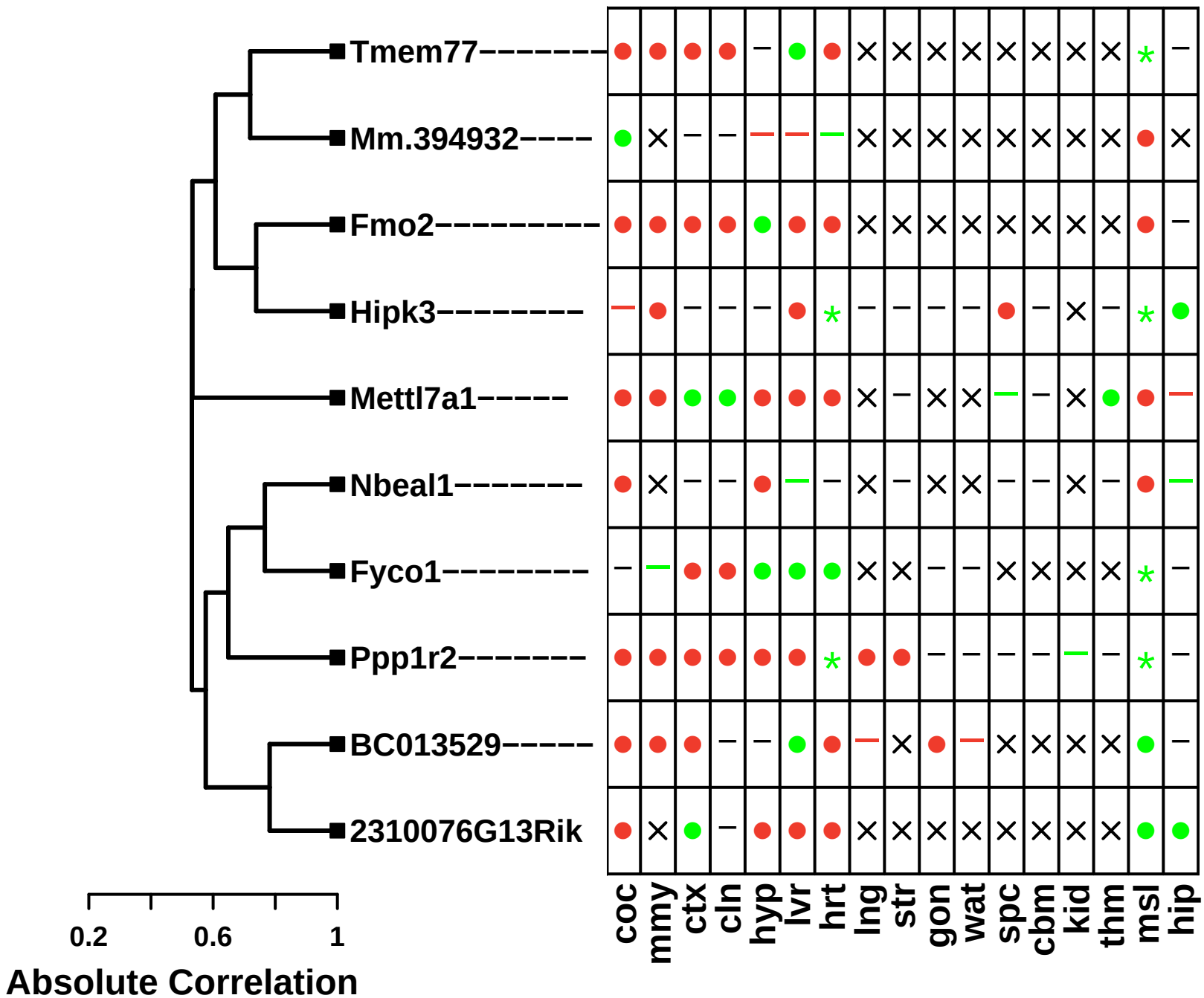
M = 7.87, P = 0.004



Absolute Correlation

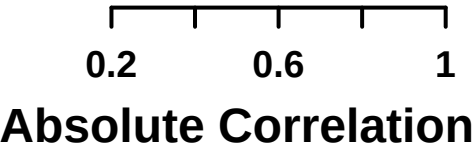
CR-Regulated Modules (10 Genes)

M = 7.85, P = 0.004



CR-Regulated Modules (10 Genes)

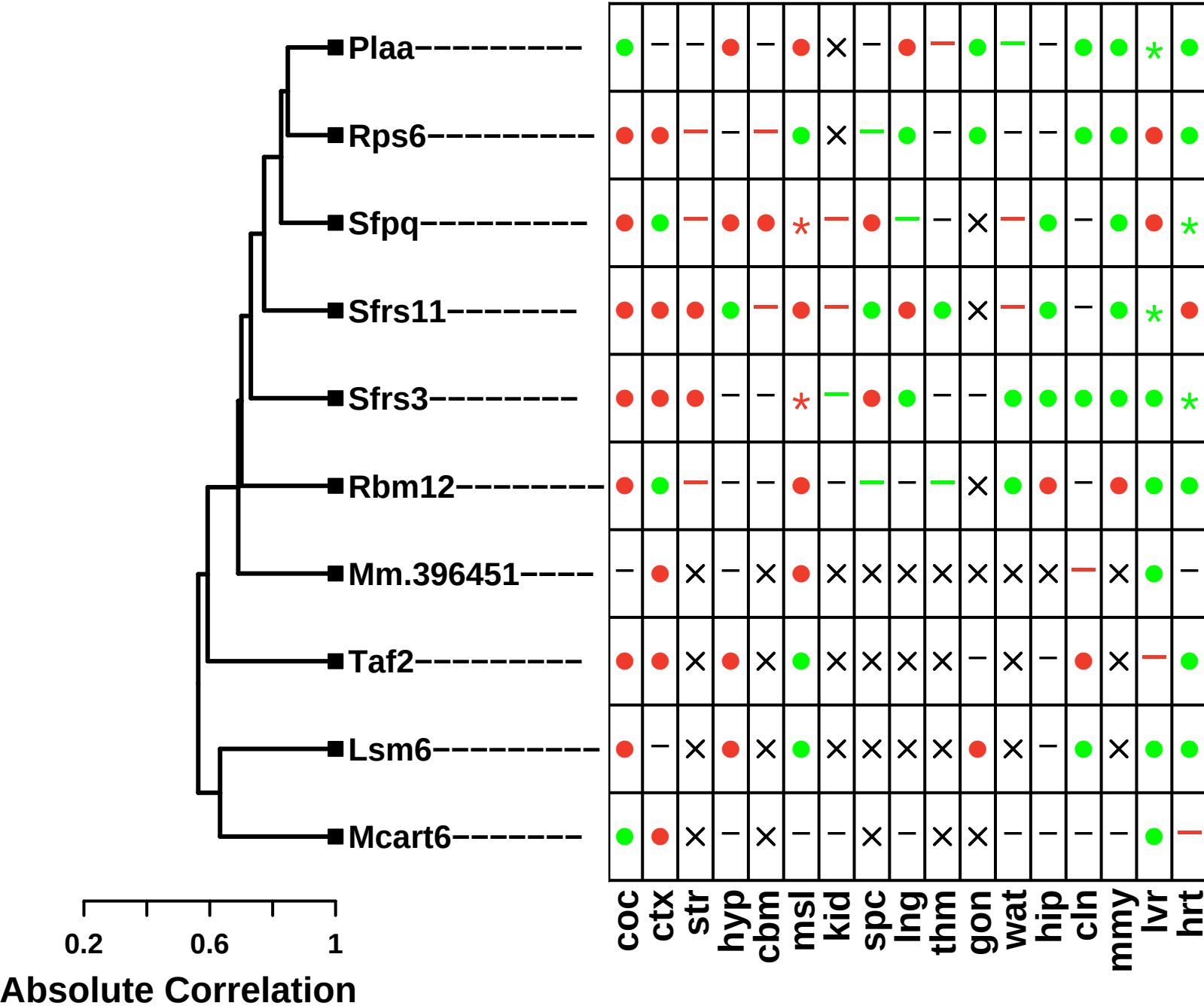
M = 7.79, P = 0.005



	coc	hrt	lng	msl	wat	hyp	spc	kid	cln	thm	cbm	str	ctx	gon	hip	mmy	lvr
Arid4b	●	●	×	✱	×	●	×	×	●	×	×	×	●	—	×	●	●
Clk1	●	●	●	●	●	—	—	●	—	—	—	—	●	—	—	—	●
Mm.404103	●	—	×	●	×	●	×	×	—	×	×	×	●	×	×	×	●
Ccnt2	●	●	×	●	×	●	—	×	●	—	—	—	—	×	—	—	●
Prpf39	●	●	—	●	—	—	×	×	●	×	×	×	—	●	×	●	✱
Clk4	●	●	●	✱	—	—	—	—	—	—	—	—	—	×	—	—	—
Rbm39	●	●	●	●	●	—	●	—	—	—	—	—	●	—	—	●	●
Crebzf	●	●	×	✱	×	●	×	×	—	×	×	×	●	×	●	●	●
Prpf4b	●	●	—	✱	—	●	—	×	—	—	—	—	—	—	●	—	✱
Akap8	●	●	●	✱	—	●	—	×	—	—	—	—	●	—	—	●	●

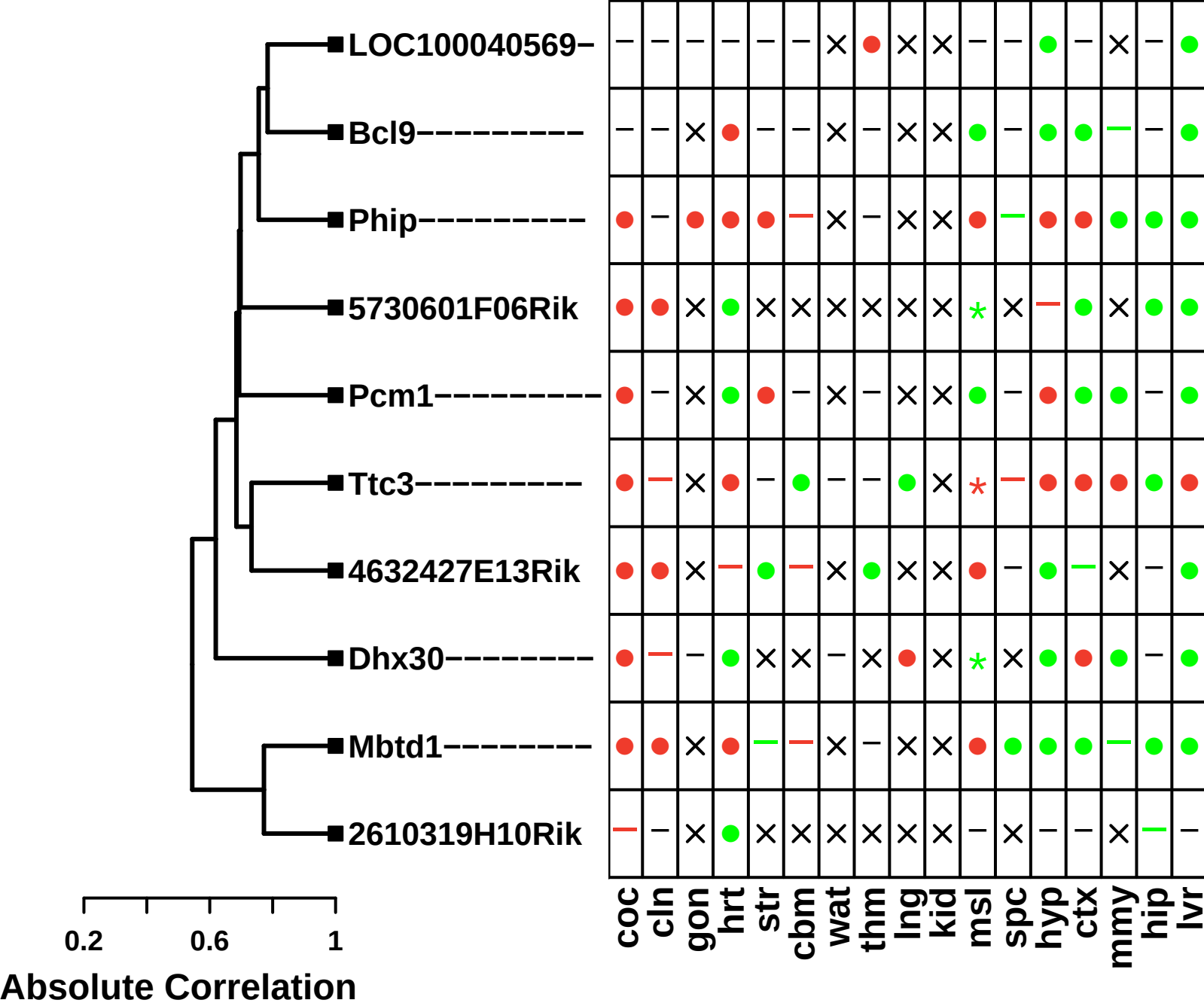
CR-Regulated Modules (10 Genes)

M = 7.78, P = 0.0055



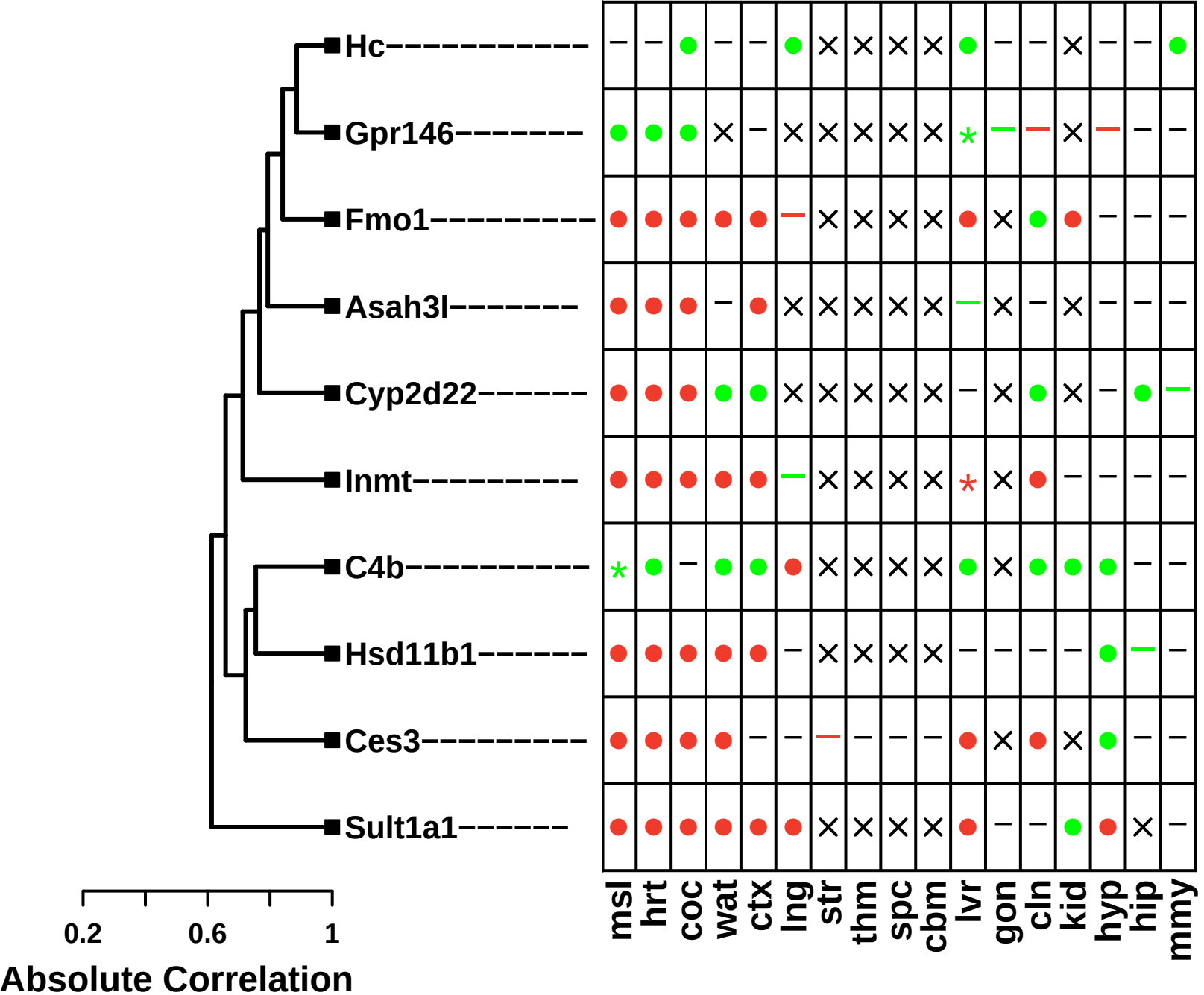
CR-Regulated Modules (10 Genes)

M = 7.76, P = 0.009



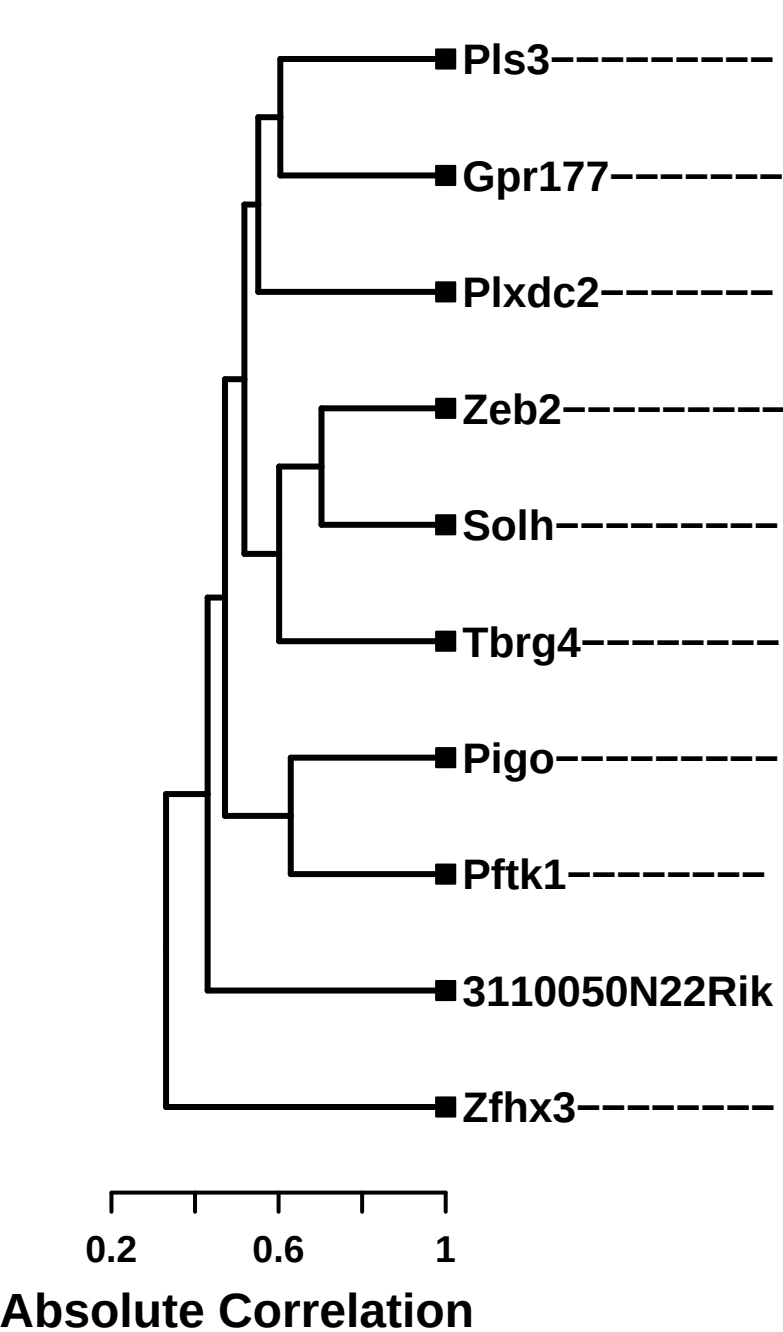
CR-Regulated Modules (10 Genes)

M = 7.72, P = 0.0115



CR-Regulated Modules (10 Genes)

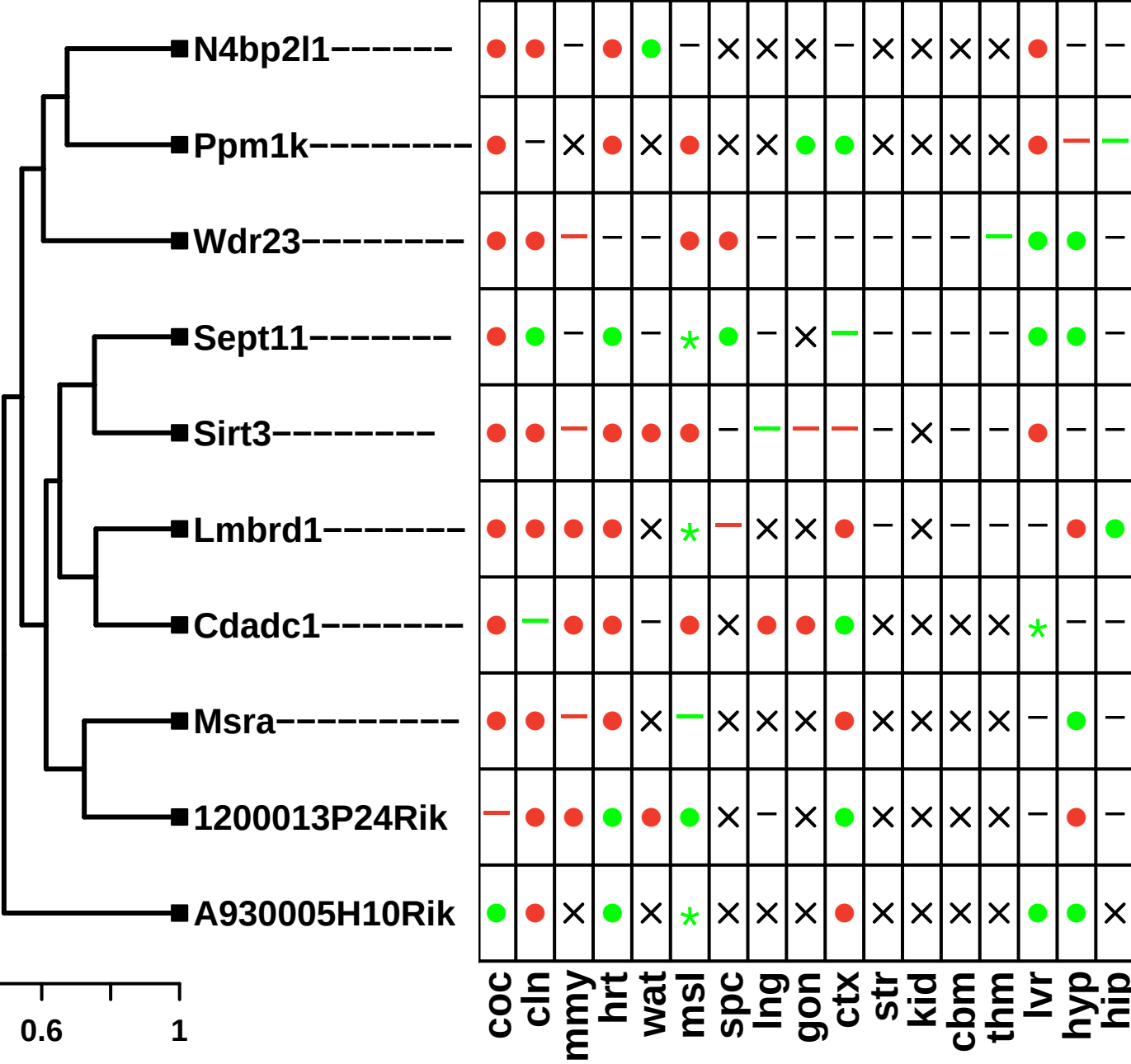
M = 7.72, P = 0.013



	●	—	—	●	—	—	—	—	—	—	×	—	●	—	—	—
	●	—	—	●	—	×	×	×	●	×	—	×	●	●	—	●
	●	●	●	×	—	—	—	—	●	×	—	—	●	●	●	—
	●	×	●	×	—	×	×	×	—	×	×	×	●	●	●	—
	●	×	●	×	—	×	×	×	—	×	×	×	●	●	●	●
	●	×	●	×	●	—	—	×	—	—	×	—	●	●	●	—
	●	×	●	×	—	×	×	×	—	×	×	×	●	●	●	●
	●	—	●	—	—	×	×	—	●	×	×	×	*	●	●	—
	●	×	●	×	—	—	—	×	—	—	×	—	—	●	●	×
	●	—	●	●	—	×	×	×	—	×	●	×	—	—	●	●
coc	●	—	—	●	—	—	—	—	—	—	×	—	●	—	—	—
wat	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
hyp	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
lng	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
hip	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
str	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
spc	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
gon	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
cln	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
thm	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
kid	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
cbm	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
msl	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
hrt	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
ctx	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
mmy	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—
lvr	—	—	—	—	—	×	×	×	—	×	×	×	—	—	—	—

CR-Regulated Modules (10 Genes)

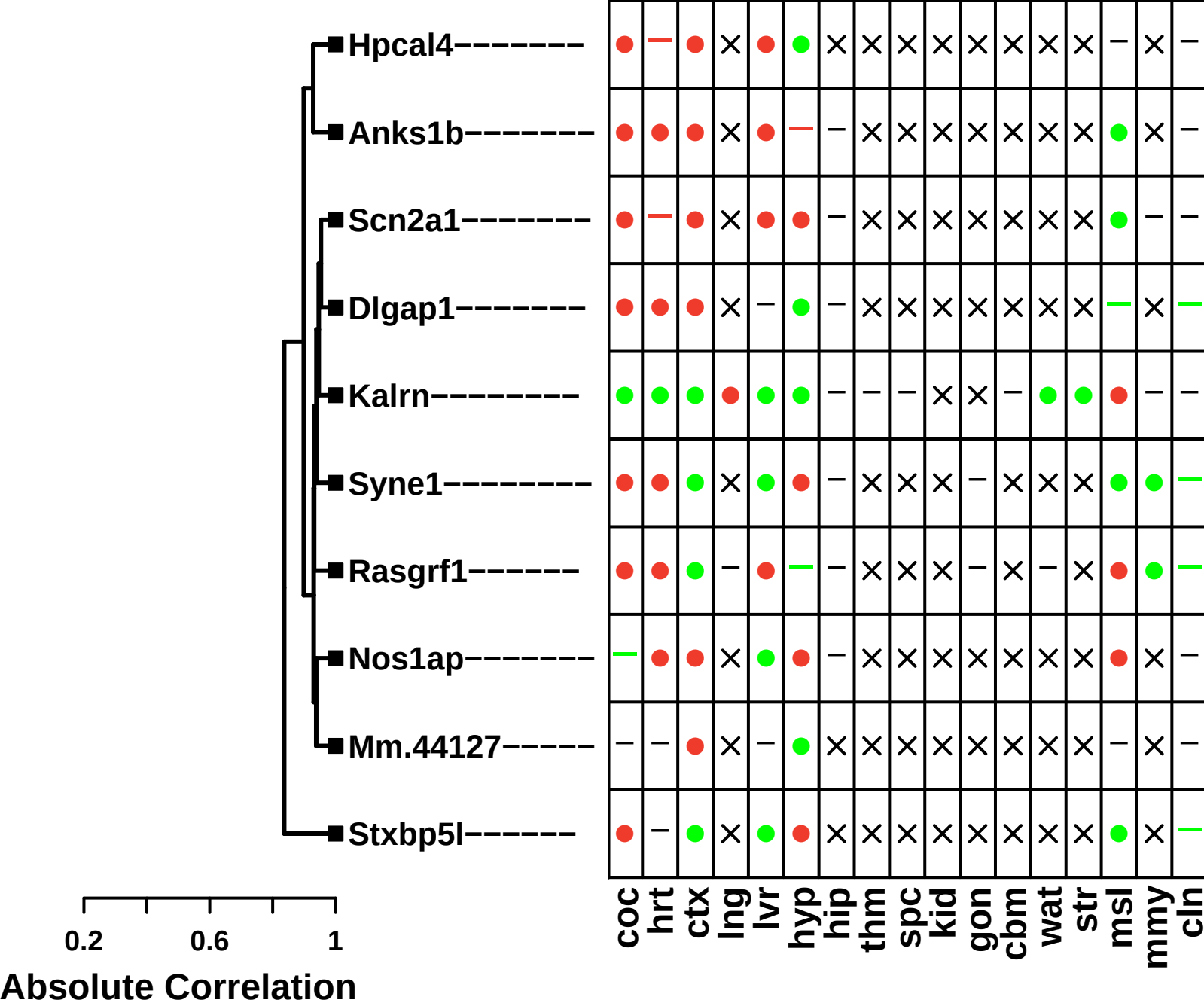
M = 7.68, P = 0.023



Absolute Correlation

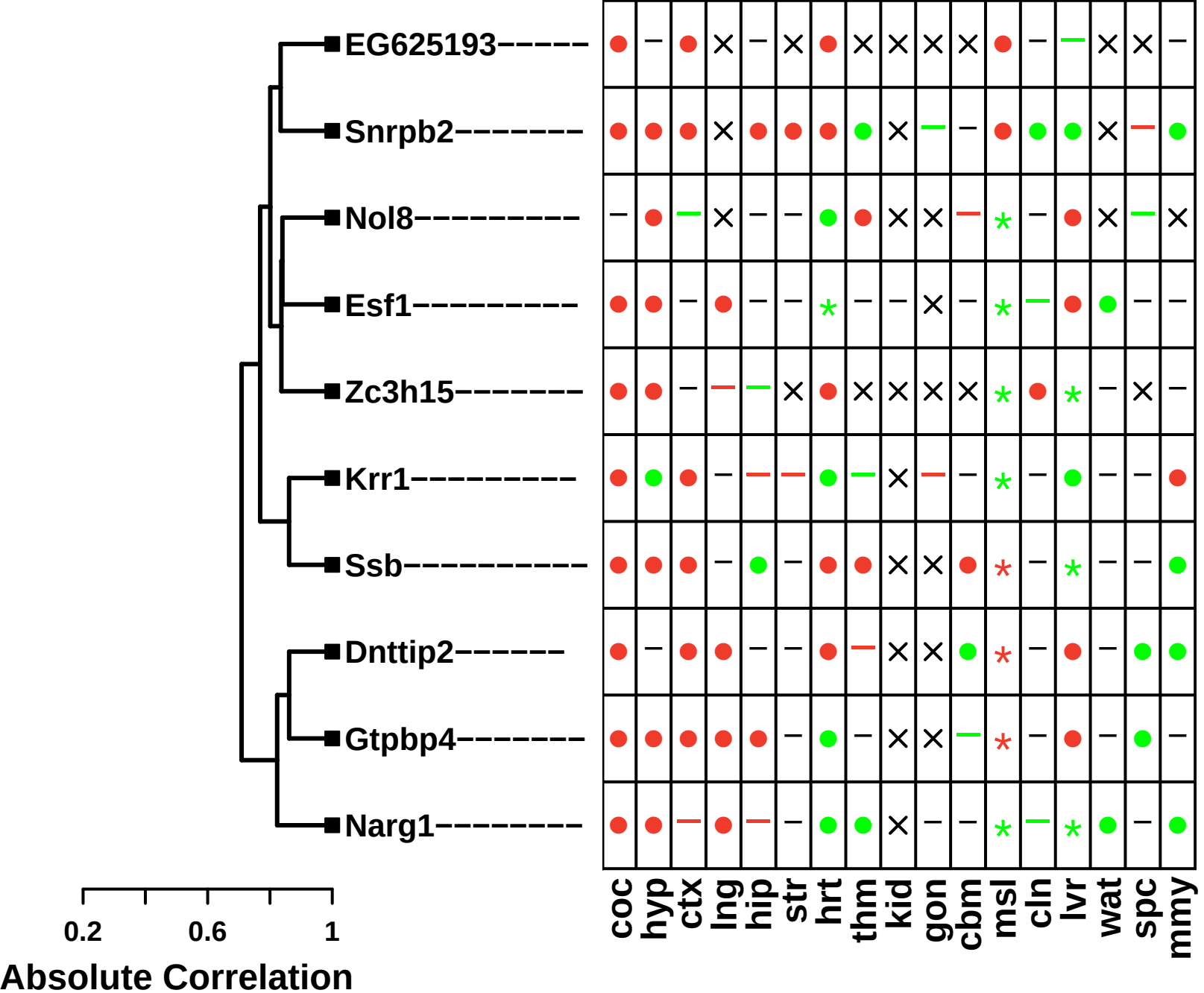
CR-Regulated Modules (10 Genes)

M = 7.65, P = 0.029



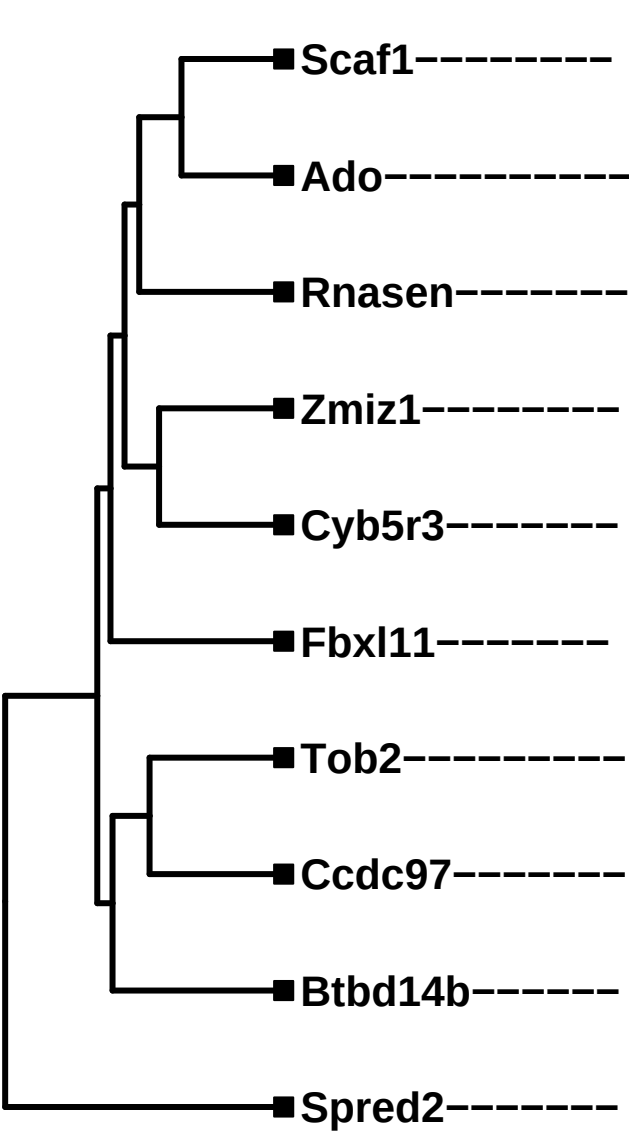
CR-Regulated Modules (10 Genes)

M = 7.62, P = 0.039



CR-Regulated Modules (10 Genes)

M = 7.62, P = 0.042

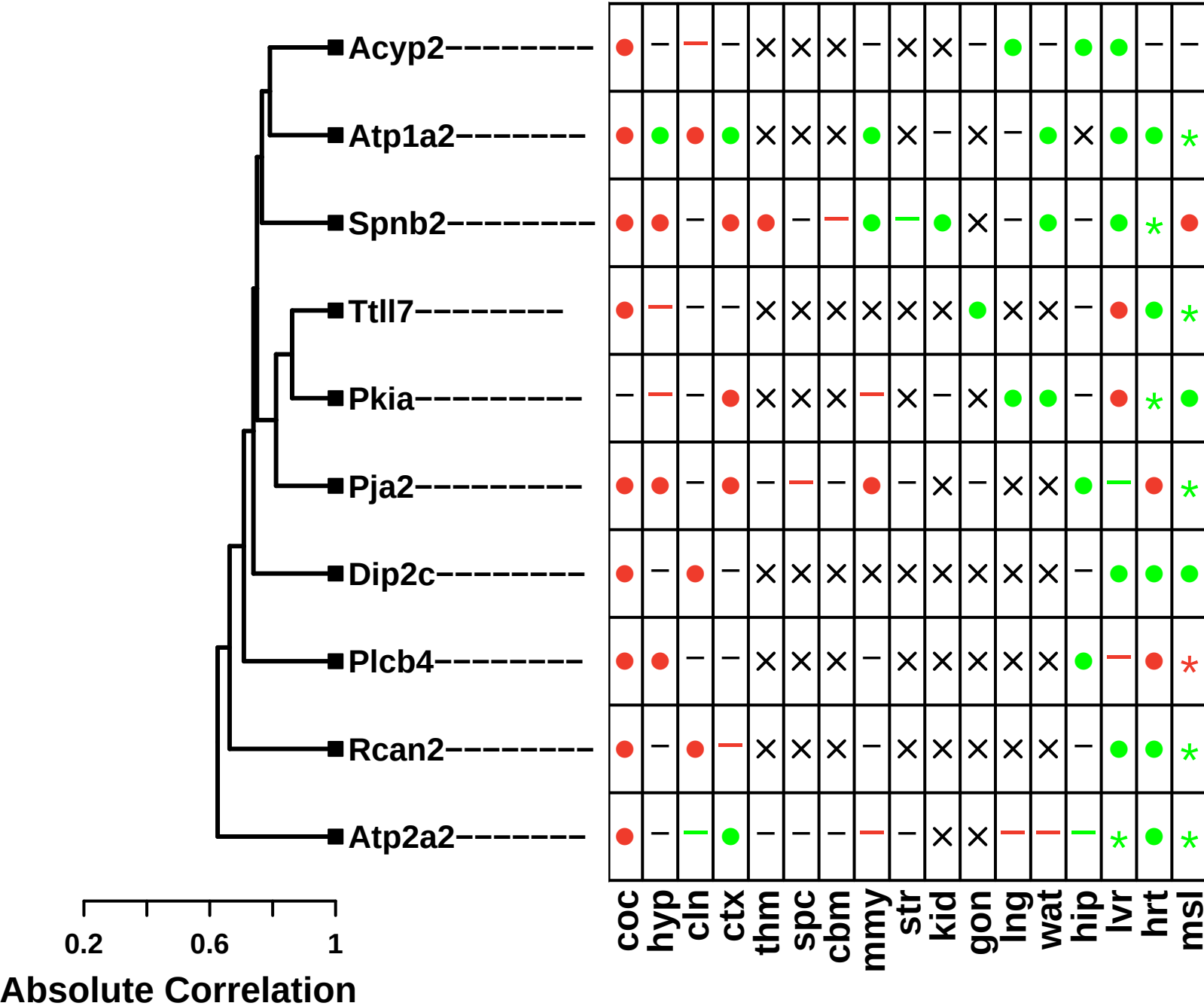


	●	●	×	×	×	●	×	×	×	●	×	×	×	—	—	●	●
	—	●	—	—	×	●	—	×	—	×	×	—	—	●	●	—	●
	●	●	—	—	×	●	●	×	—	×	×	×	—	●	●	●	●
	●	●	●	—	×	●	—	×	—	—	—	×	●	—	●	—	●
	●	●	—	●	●	●	—	×	—	—	●	●	—	●	●	—	●
	●	●	●	●	×	●	●	×	—	×	×	—	—	●	●	●	●
	●	●	●	—	×	●	—	×	—	—	●	—	—	●	●	—	●
	●	—	—	—	×	●	—	×	—	—	—	—	—	●	●	●	●
	—	●	×	×	×	—	×	×	×	×	—	●	—	●	*	●	●
	●	●	—	—	●	●	—	×	—	—	—	—	—	—	●	●	*
hyp																	
coc																	
spc																	
str																	
lng																	
lvr																	
thm																	
kid																	
cbm																	
wat																	
mmy																	
gon																	
hip																	
cln																	
msl																	
ctx																	
hrt																	

0.2 0.6 1
Absolute Correlation

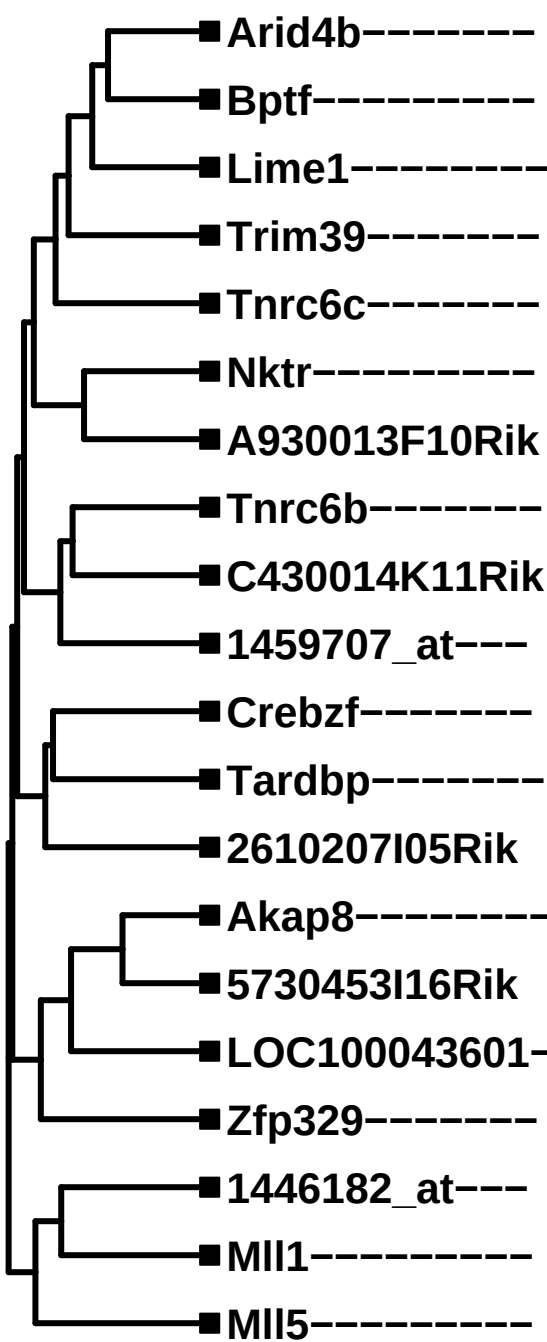
CR-Regulated Modules (10 Genes)

M = 7.61, P = 0.0455



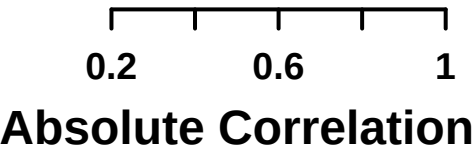
CR-Regulated Modules (20 Genes)

M = 8.08, P = 0



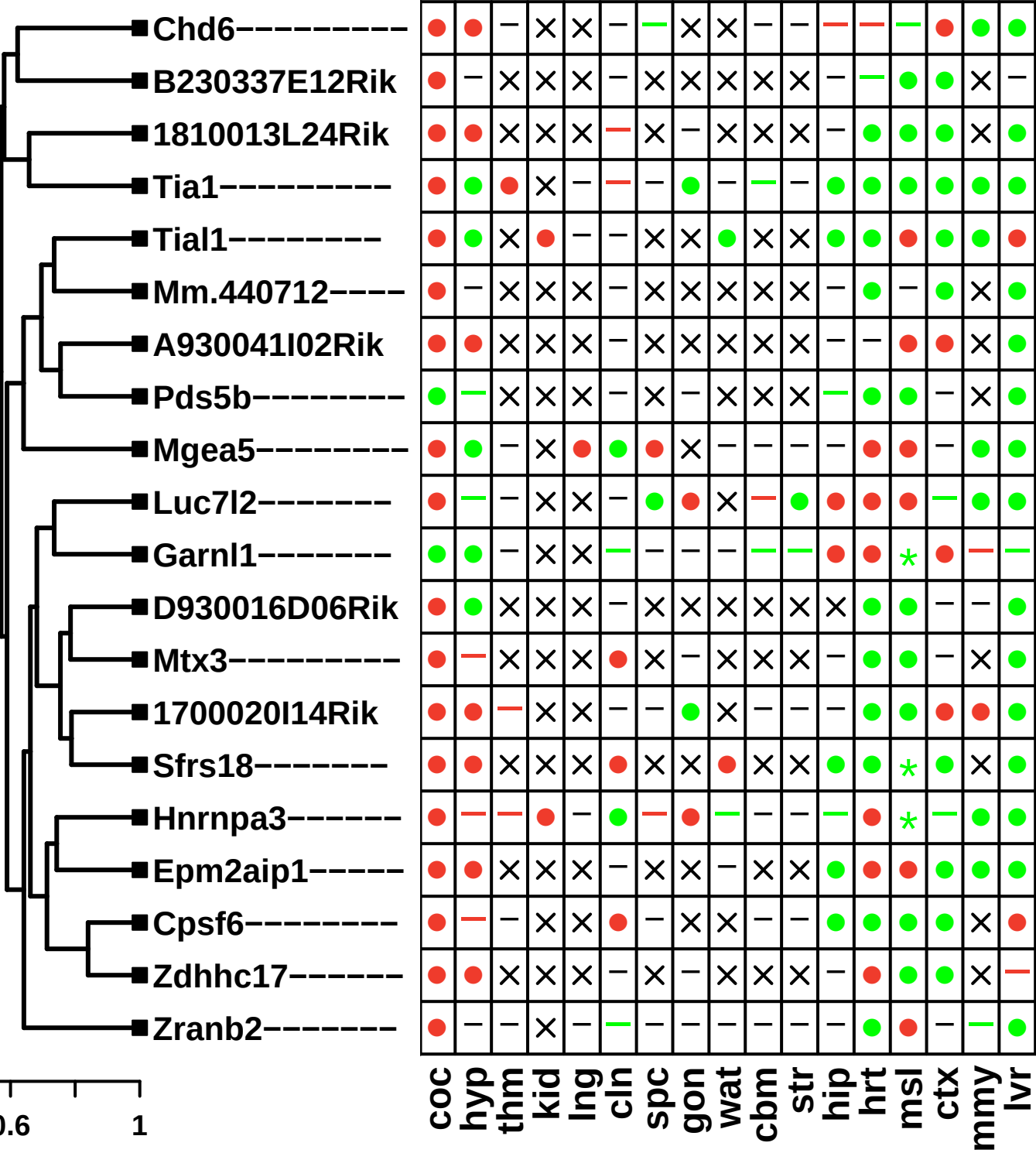
●	●	×	●	*	×	×	×	×	×	×	×	—	●	●	×	●	●
●	—	×	●	●	●	×	—	×	●	—	●	●	●	●	●	●	●
—	—	×	—	●	×	—	×	×	×	×	×	●	●	●	—	●	●
●	—	×	—	●	×	—	×	×	×	×	×	●	—	×	●	●	●
●	—	×	●	*	×	×	×	×	×	×	●	●	—	—	●	—	●
●	—	×	●	●	—	—	—	×	—	—	●	●	●	—	●	●	●
—	—	×	●	●	×	×	×	×	×	×	×	—	—	×	×	●	●
●	—	×	●	*	—	×	—	×	—	—	×	●	●	●	●	●	●
—	—	×	—	—	×	×	×	×	×	×	×	●	●	×	×	●	●
—	—	×	●	—	×	×	×	×	×	×	×	—	—	—	×	●	●
●	—	×	●	*	×	×	×	×	×	×	×	●	●	●	●	●	●
●	—	●	●	●	—	●	—	×	●	—	×	●	●	●	●	●	*
●	—	×	—	●	—	×	—	×	●	—	×	●	●	●	×	●	●
●	—	●	—	●	×	—	×	—	×	×	—	●	●	×	●	—	—
●	—	×	●	●	×	×	×	×	×	×	×	●	●	●	●	—	—
●	—	×	●	●	×	×	×	×	×	×	—	●	●	—	●	●	●
●	●	×	—	●	×	×	×	×	×	×	×	—	—	×	×	●	●
●	—	●	●	●	×	—	×	●	×	×	●	*	●	×	—	●	●
●	●	●	●	●	—	—	●	—	●	—	×	●	●	—	●	*	*

coc
cln
lng
hyp
msl
cbm
wat
str
kid
thm
spc
gon
hrt
ctx
hip
mmy
lvr



CR-Regulated Modules (20 Genes)

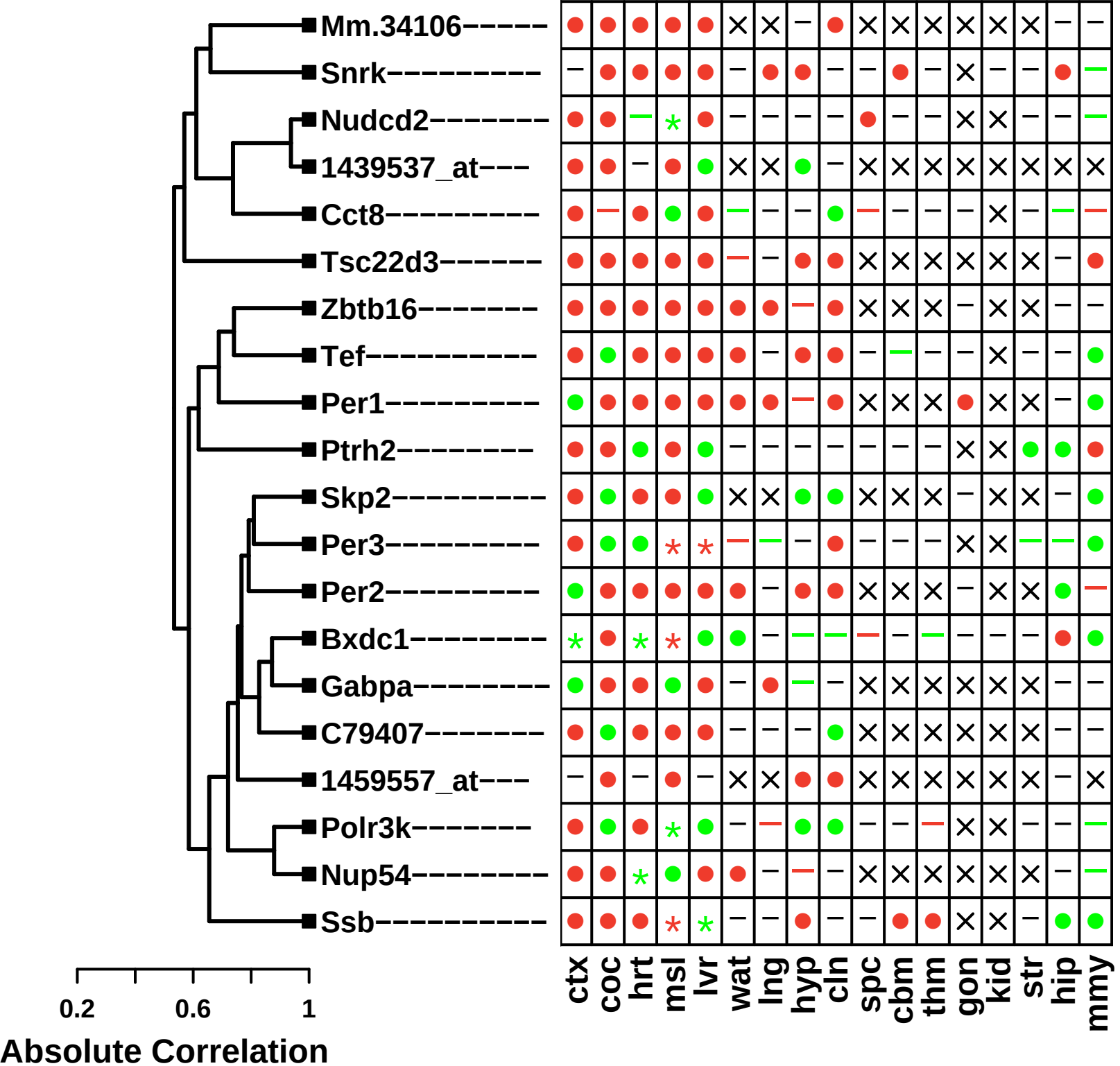
M = 7.8, P = 0



Absolute Correlation

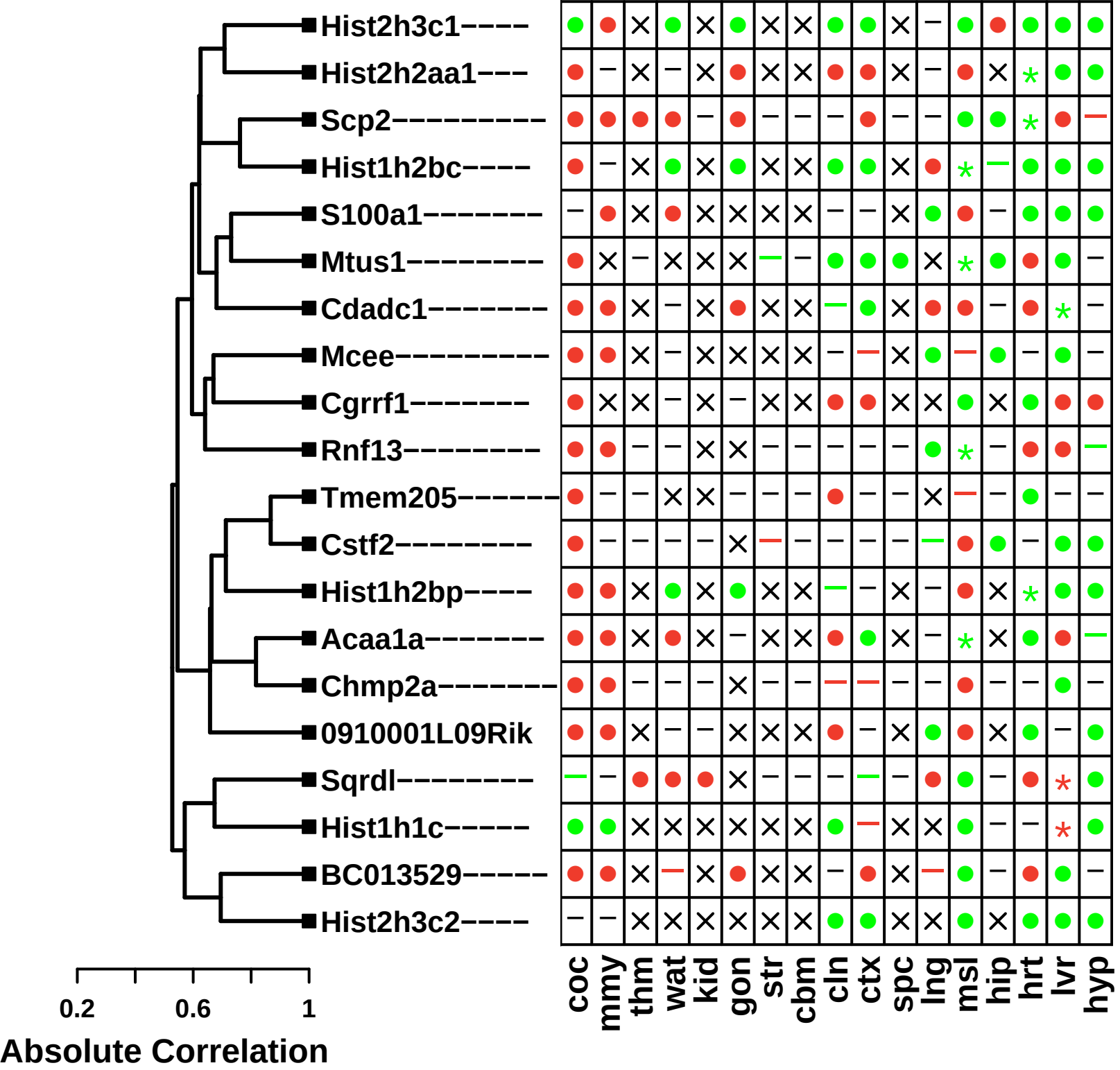
CR-Regulated Modules (20 Genes)

M = 7.79, P = 0



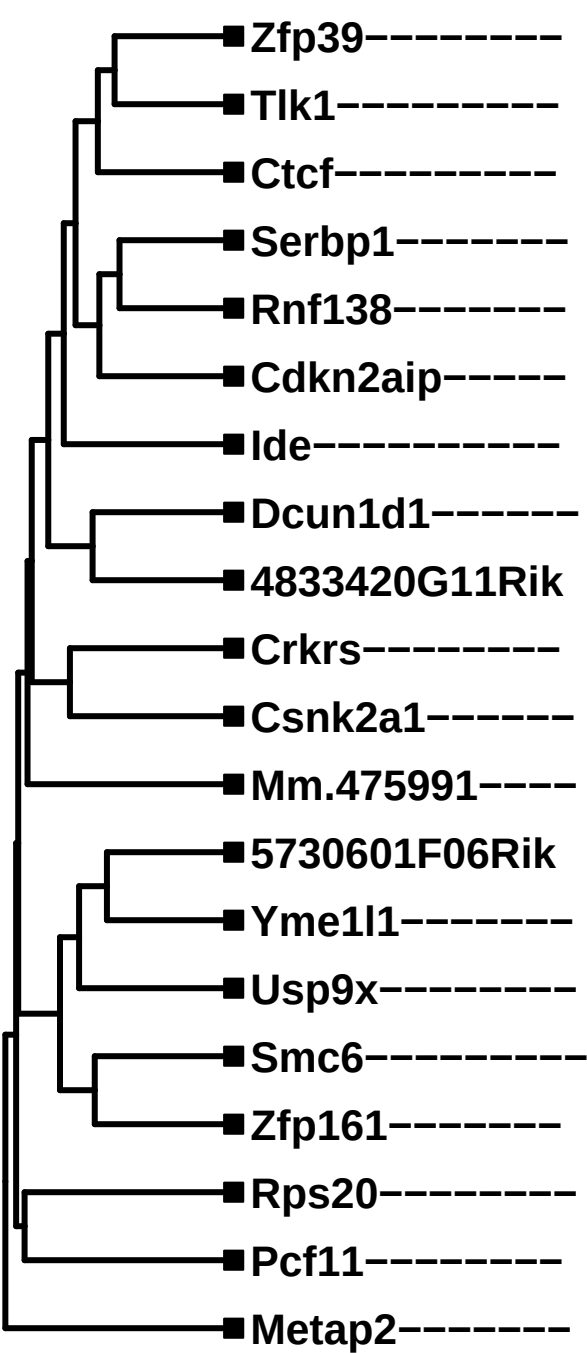
CR-Regulated Modules (20 Genes)

M = 7.76, P = 0



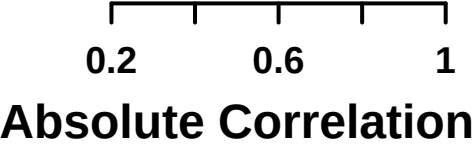
CR-Regulated Modules (20 Genes)

M = 7.58, P = 0



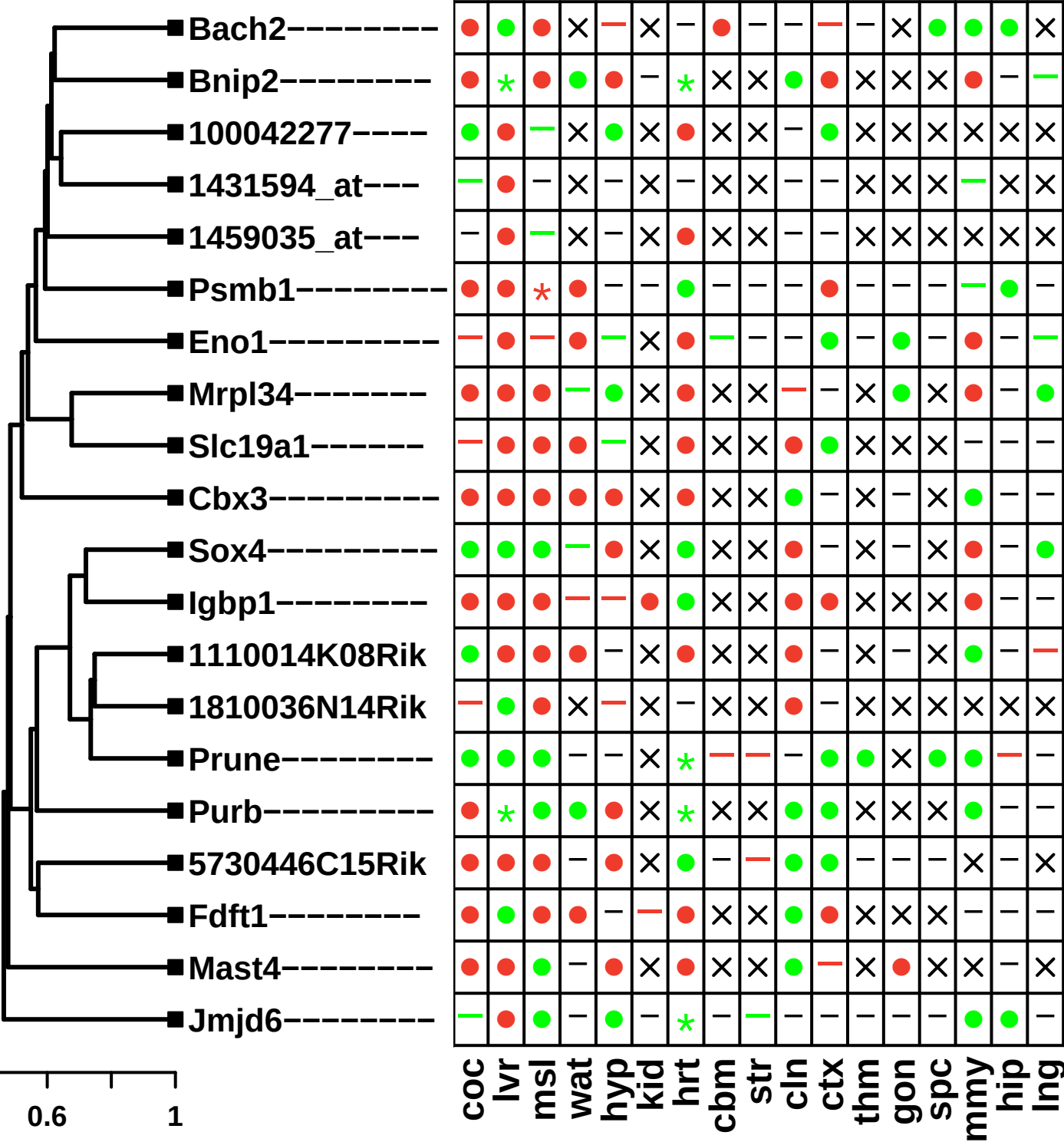
●	●	-	-	×	-	●	×	×	-	-	-	×	×	-	×	●
●	-	●	●	×	×	●	×	×	×	×	-	×	×	*	×	●
●	-	●	-	-	-	●	×	-	-	×	-	-	-	*	-	●
●	●	●	●	-	-	*	×	-	-	-	-	-	●	●	-	*
-	●	●	●	-	-	-	-	×	-	×	-	×	×	-	×	*
-	●	●	-	×	-	-	×	×	×	×	-	×	×	*	×	-
●	●	●	●	-	●	●	-	×	●	-	-	×	×	●	×	*
●	●	●	-	×	×	●	×	-	●	×	-	-	-	*	●	●
●	-	-	-	×	×	●	×	×	●	×	×	×	×	●	×	-
●	●	●	●	×	×	●	×	×	-	●	-	×	×	*	×	●
●	●	●	-	-	-	*	-	-	●	-	*	-	-	●	-	●
-	●	●	-	×	×	●	×	×	×	×	×	×	×	●	×	-
-	●	●	●	×	×	●	×	×	×	×	●	×	×	*	×	●
●	●	●	●	●	-	●	×	×	-	×	●	×	×	●	×	●
●	-	●	-	●	-	●	-	-	-	×	●	●	-	*	●	●
●	●	●	-	×	-	●	×	-	●	●	●	●	-	*	-	●
●	●	●	●	-	●	●	-	-	●	-	-	-	-	●	●	-
●	●	●	-	×	×	-	×	-	-	×	-	-	-	●	-	●
●	●	●	-	×	×	●	-	-	●	●	-	-	-	*	-	*
●	●	●	-	-	-	●	●	-	●	×	●	●	-	●	-	●

hyp
ctx
coc
cln
lng
wat
hrt
kid
cbm
mmy
gon
hip
str
spc
msl
thm
lvr



CR-Regulated Modules (20 Genes)

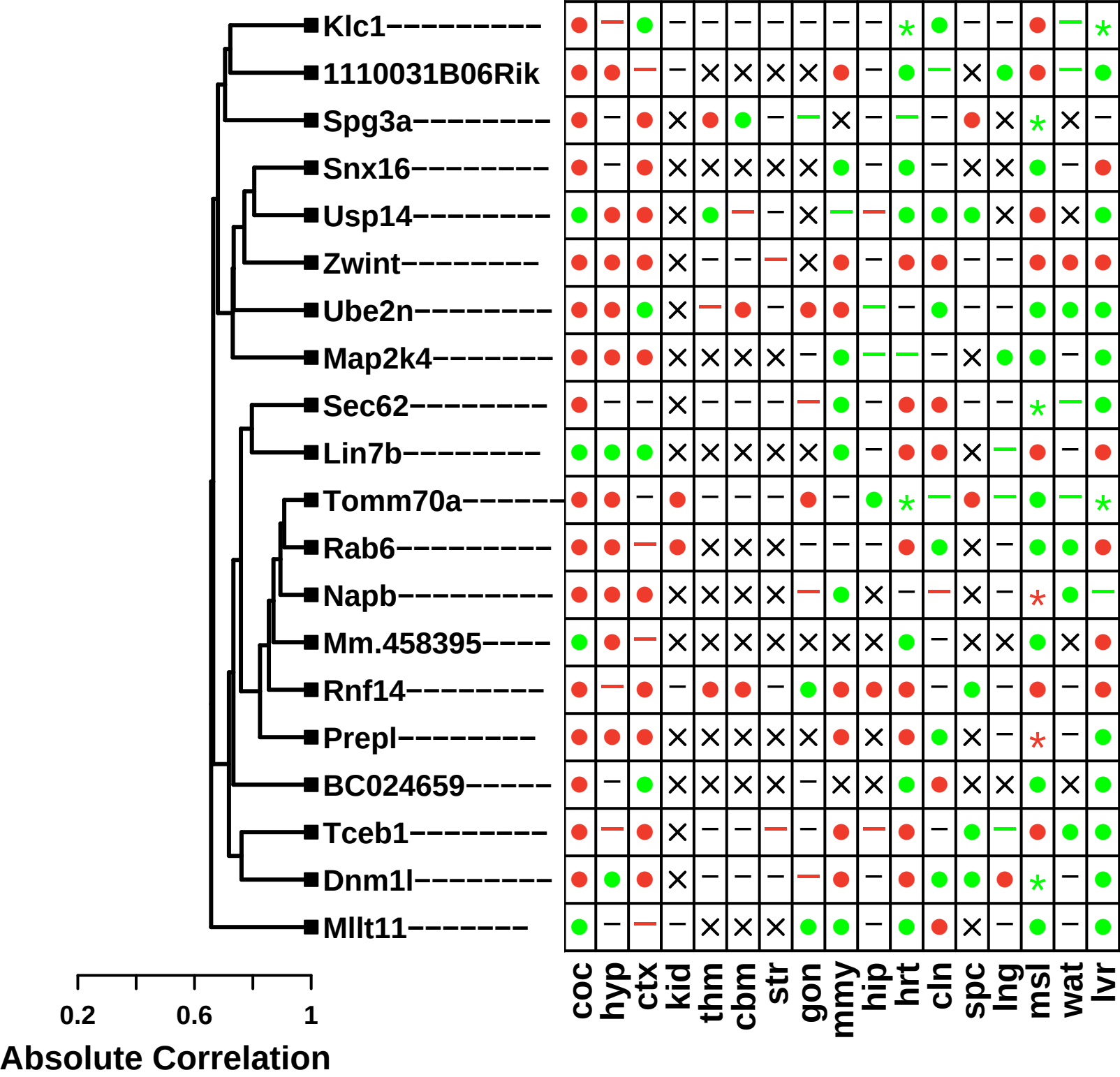
M = 7.58, P = 0



Absolute Correlation

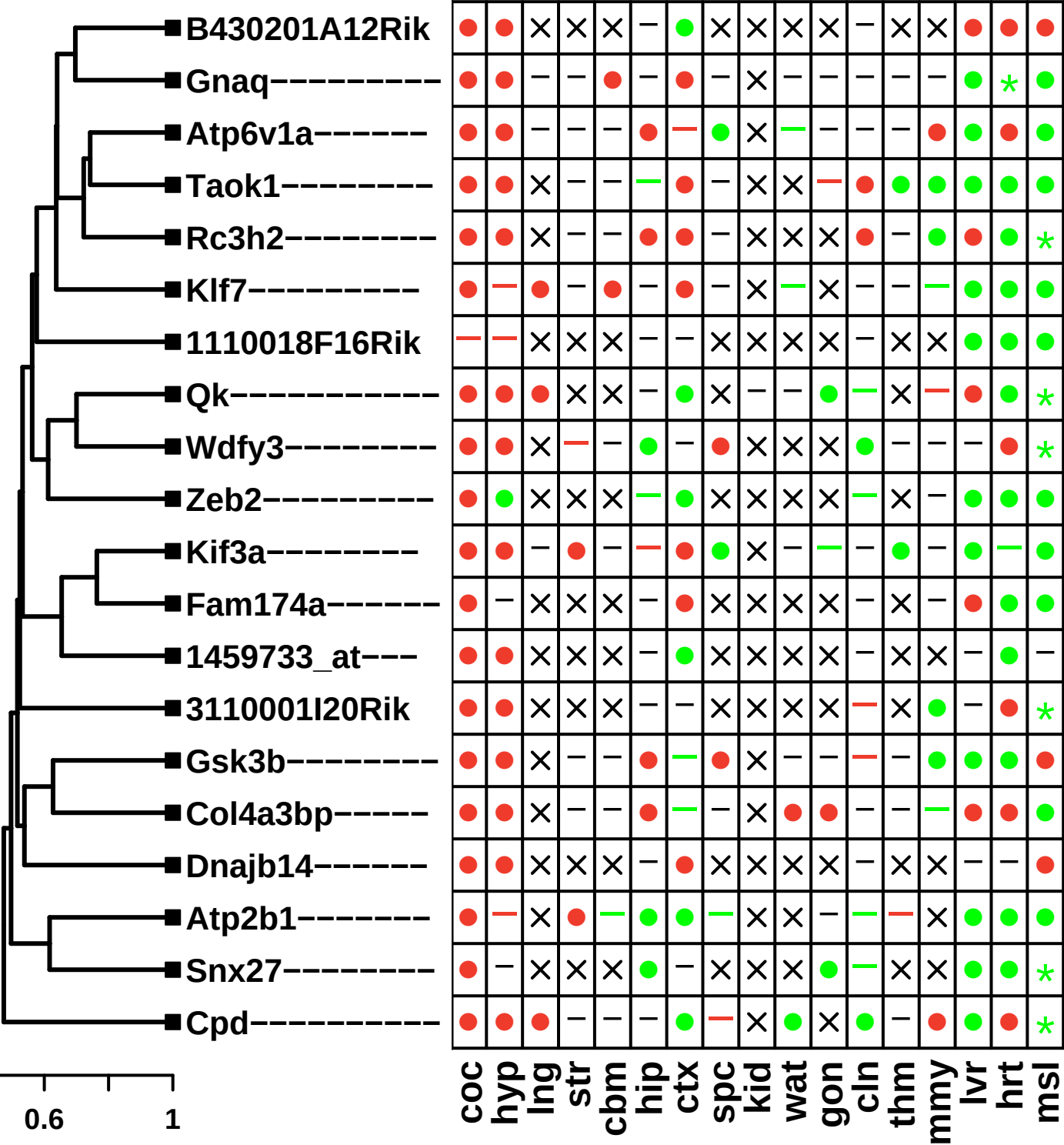
CR-Regulated Modules (20 Genes)

M = 7.56, P = 0



CR-Regulated Modules (20 Genes)

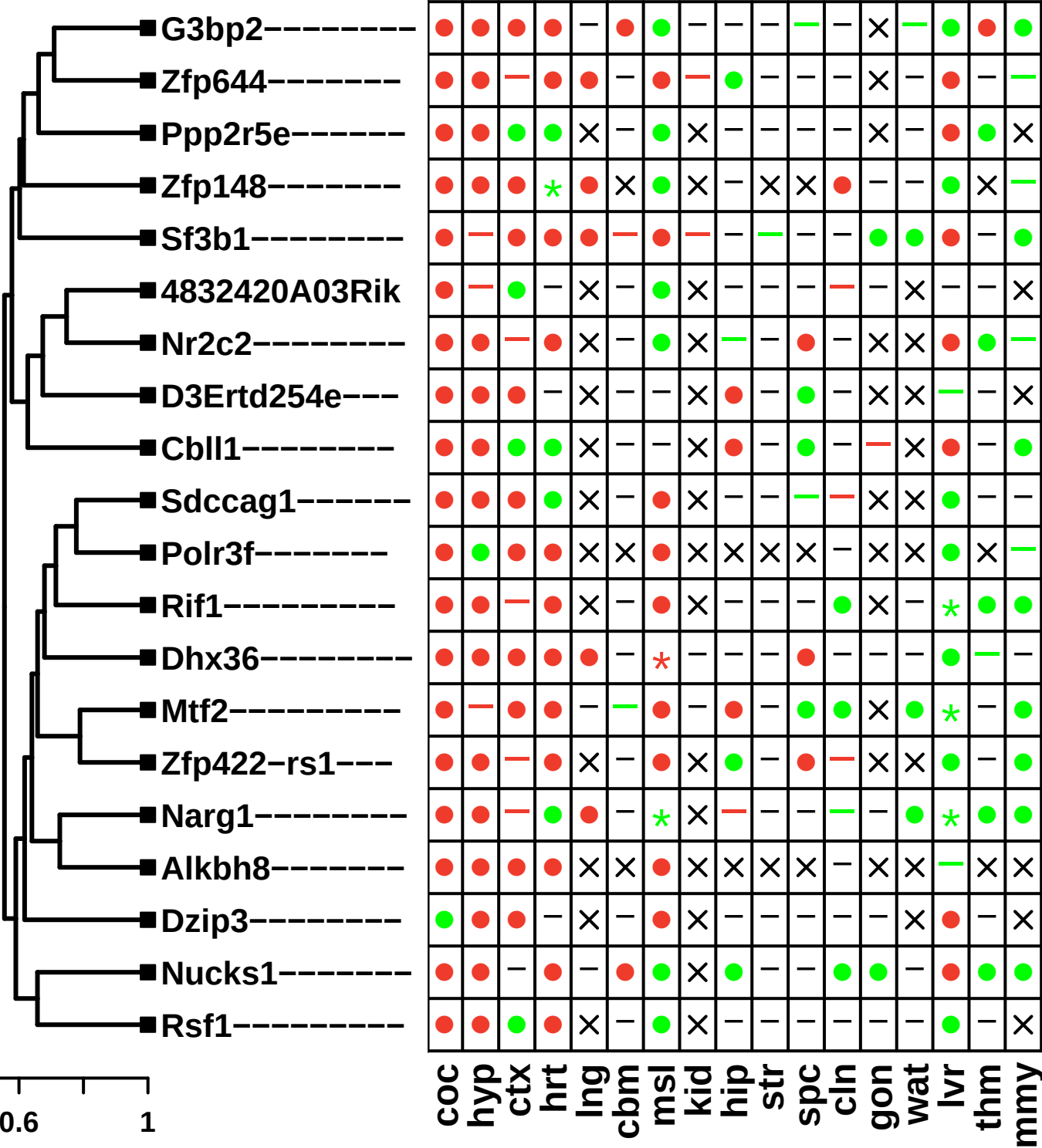
M = 7.5, P = 0



Absolute Correlation

CR-Regulated Modules (20 Genes)

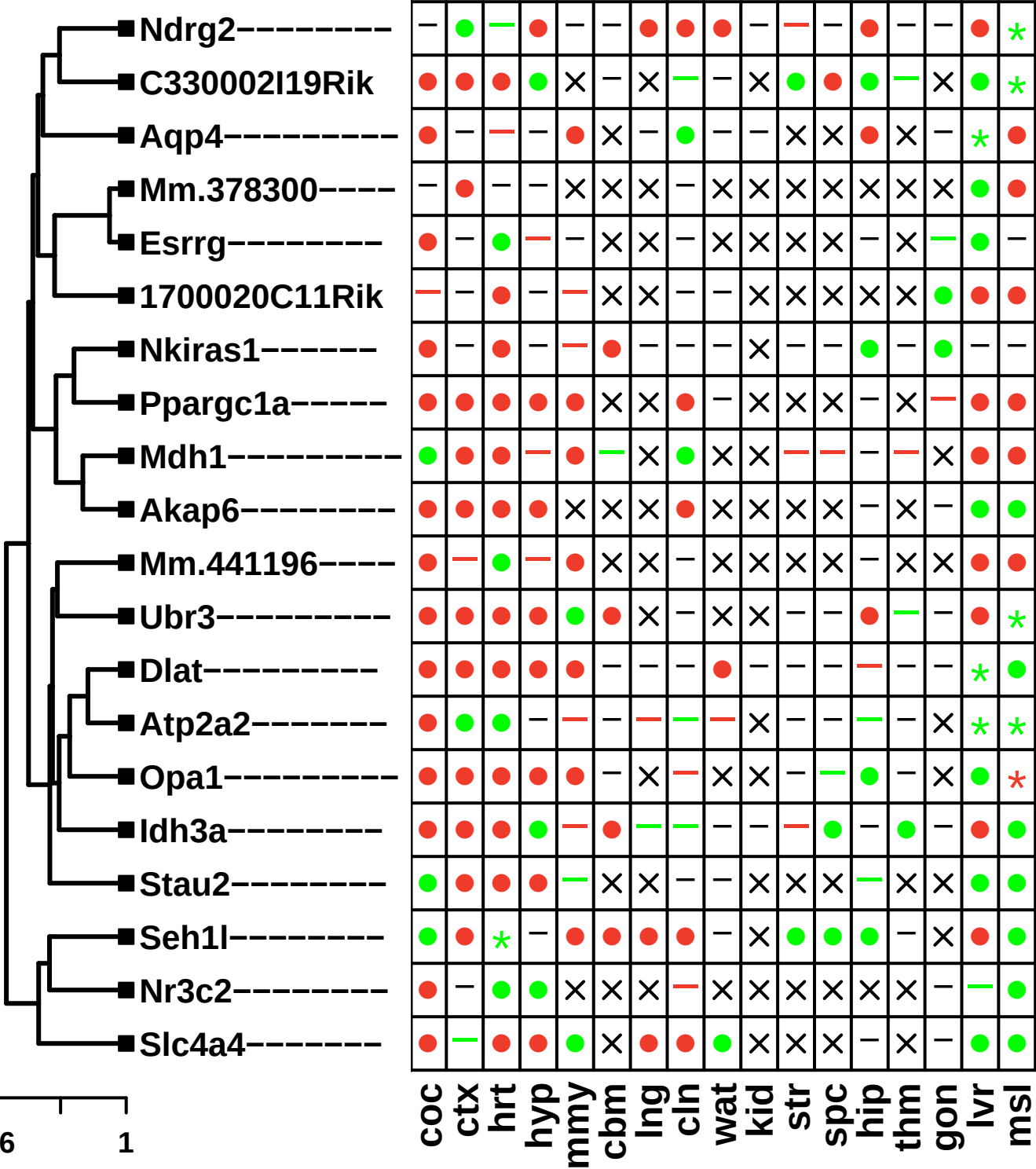
M = 7.5, P = 0



Absolute Correlation

CR-Regulated Modules (20 Genes)

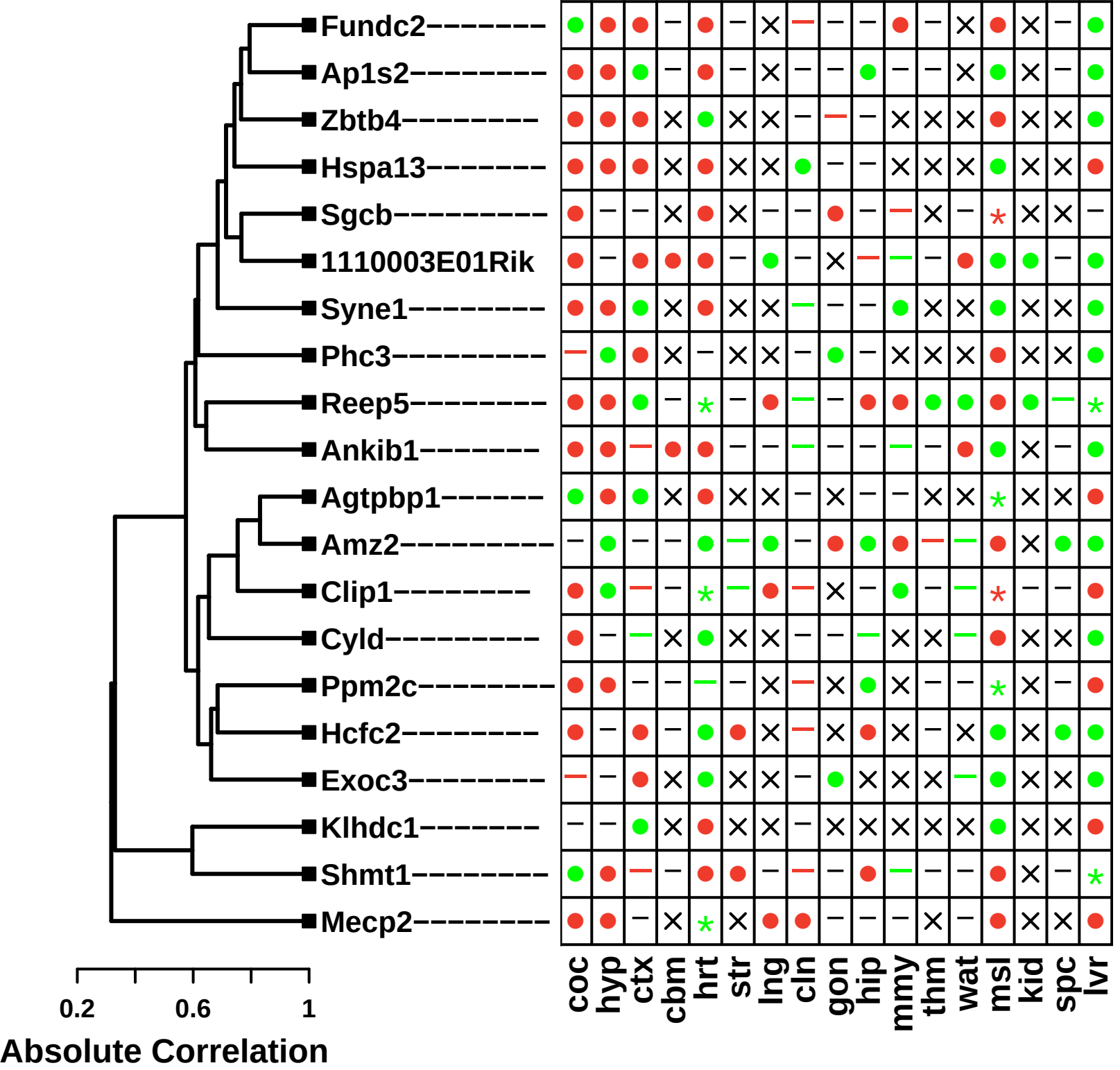
M = 7.46, P = 0



Absolute Correlation

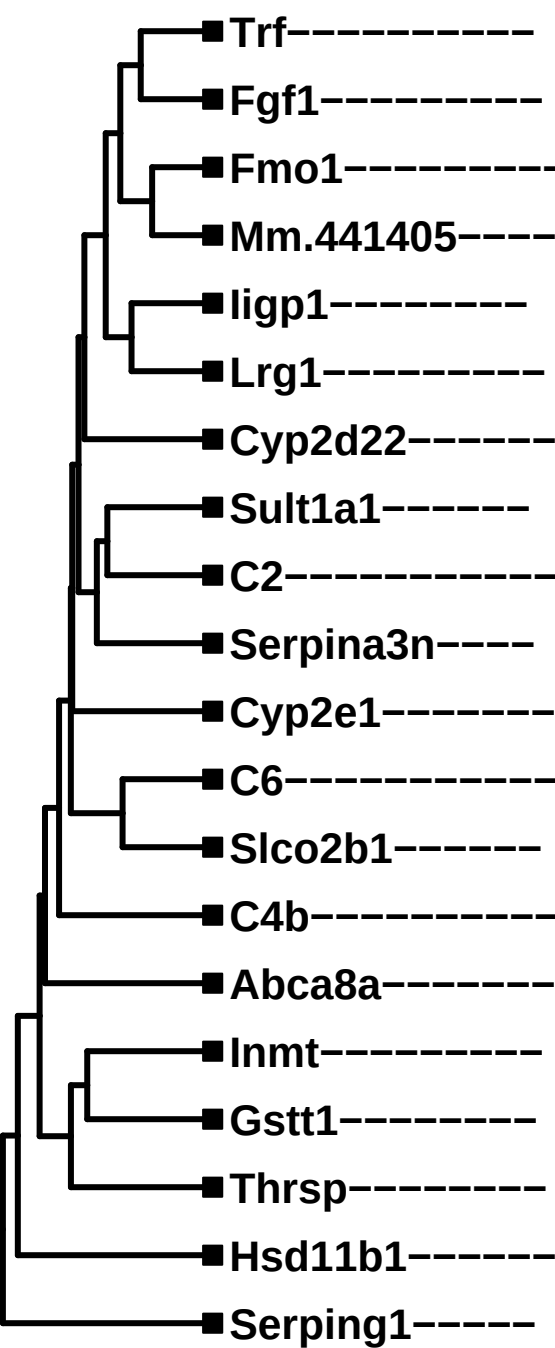
CR-Regulated Modules (20 Genes)

M = 7.41, P = 0



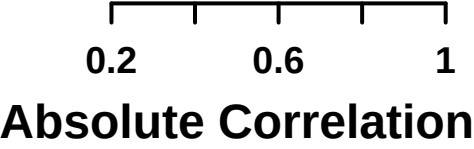
CR-Regulated Modules (20 Genes)

M = 7.36, P = 0



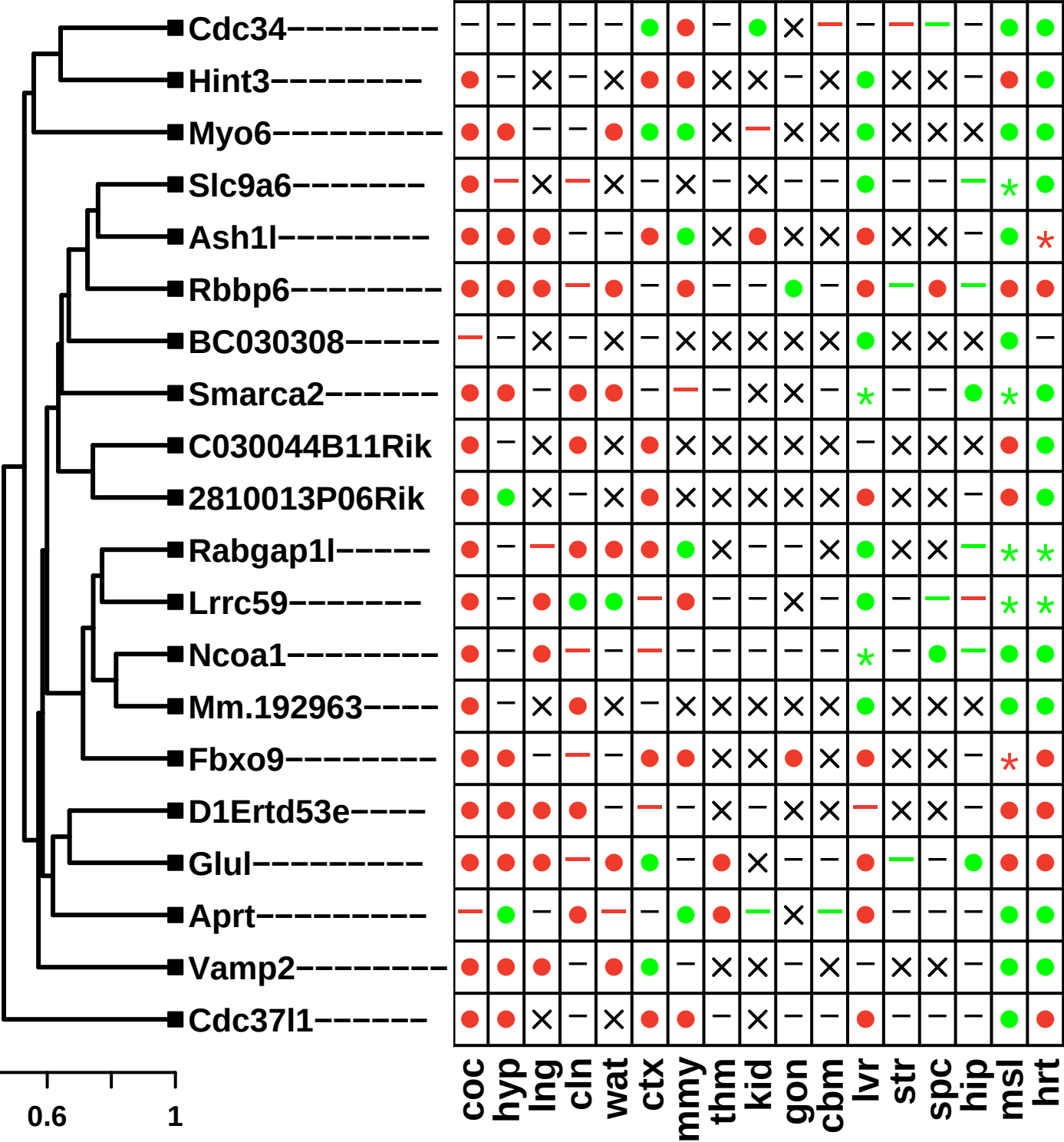
	●	—	●	●	—	×	—	—	×	×	×	×	×	●	—	●	—
	●	●	●	●	—	×	●	—	×	×	×	×	×	—	×	●	—
	●	●	●	●	—	—	×	—	×	×	×	×	●	●	●	●	—
	●	—	—	—	×	×	×	—	×	×	×	×	×	—	×	—	●
	●	●	●	—	—	●	—	—	×	×	×	×	×	—	●	●	—
	—	●	—	●	—	●	—	—	×	×	×	×	—	—	●	—	—
	●	●	●	●	—	×	×	●	×	×	×	×	×	●	●	—	—
	●	●	●	●	—	●	—	×	×	×	×	×	●	—	●	●	●
	●	—	●	—	●	—	●	—	×	×	×	×	—	—	●	●	—
	—	—	●	—	—	●	×	—	×	×	×	×	×	—	●	—	—
	●	●	●	—	—	—	×	—	×	×	×	×	—	●	●	●	—
	●	—	●	—	—	×	×	—	×	×	×	×	×	—	×	●	—
	●	●	●	—	×	×	—	●	—	—	—	●	×	●	●	●	●
	—	*	●	●	—	●	×	—	×	×	×	×	●	●	●	●	●
	—	—	●	—	●	×	×	—	×	×	×	×	×	—	—	—	●
	●	●	●	●	—	—	×	—	×	×	×	×	—	●	●	*	—
	—	●	●	●	●	●	×	—	×	×	×	×	●	—	—	●	—
	●	●	●	—	●	●	—	—	×	×	×	×	×	●	●	*	●
	●	●	●	●	—	—	—	—	×	×	×	×	—	—	●	—	●
	●	—	—	●	●	—	×	—	—	—	—	—	●	—	●	●	●

coc
msl
hrt
ctx
mmy
lng
gon
hip
thm
cbm
str
spc
kid
cln
wat
lvr
hyp



CR-Regulated Modules (20 Genes)

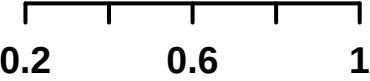
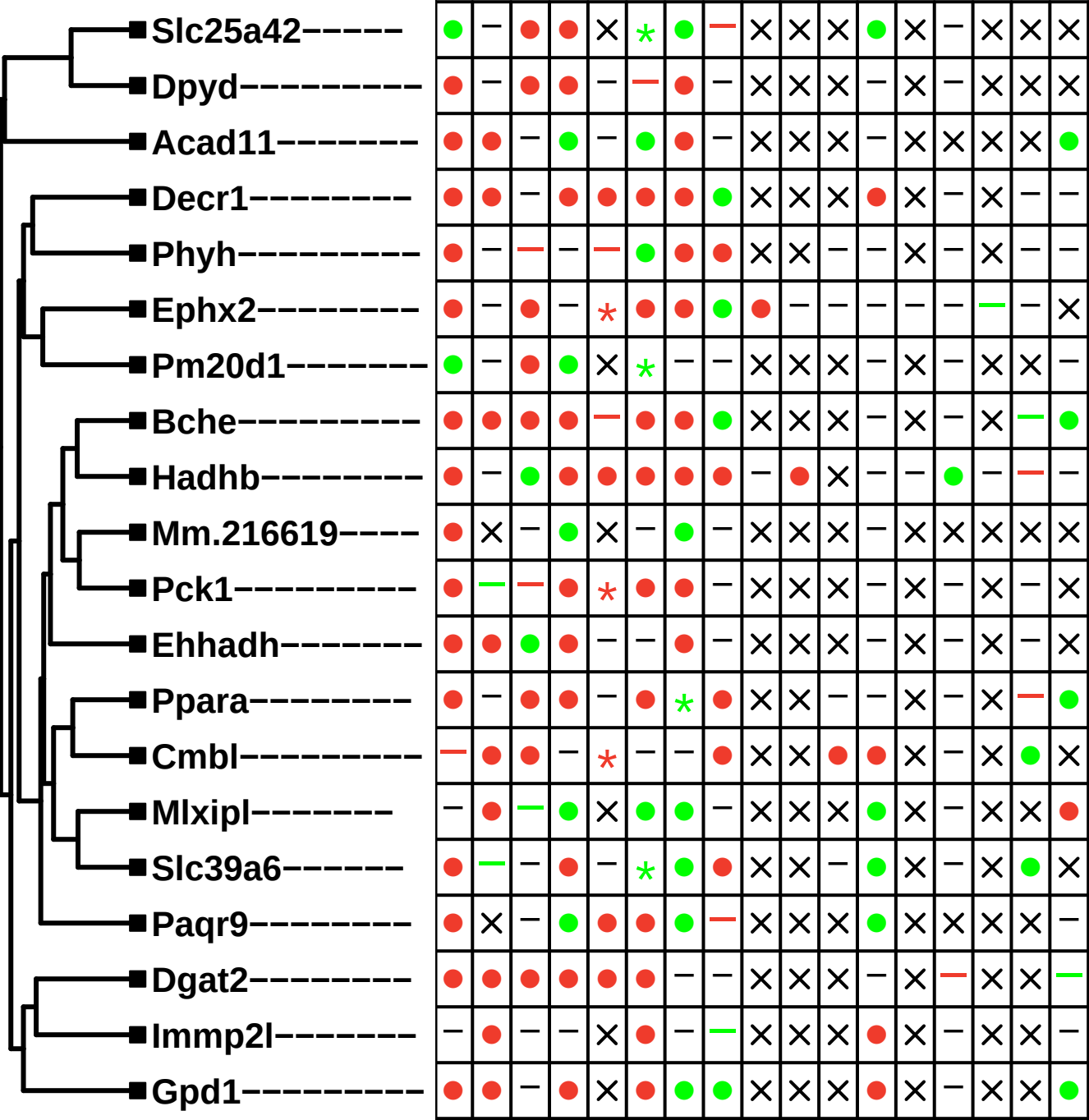
M = 7.36, P = 0



Absolute Correlation

CR-Regulated Modules (20 Genes)

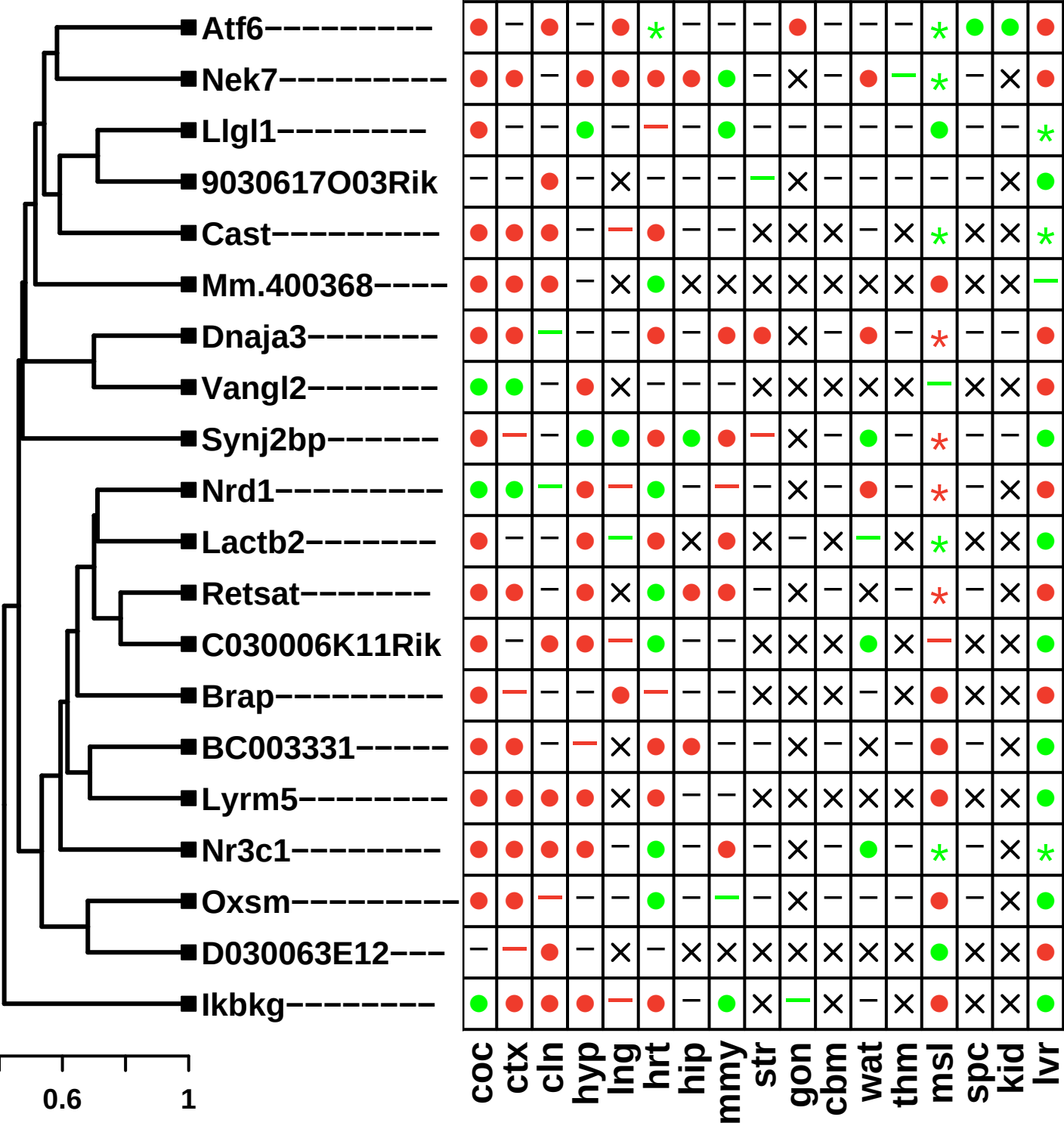
M = 7.34, P = 0



Absolute Correlation

CR-Regulated Modules (20 Genes)

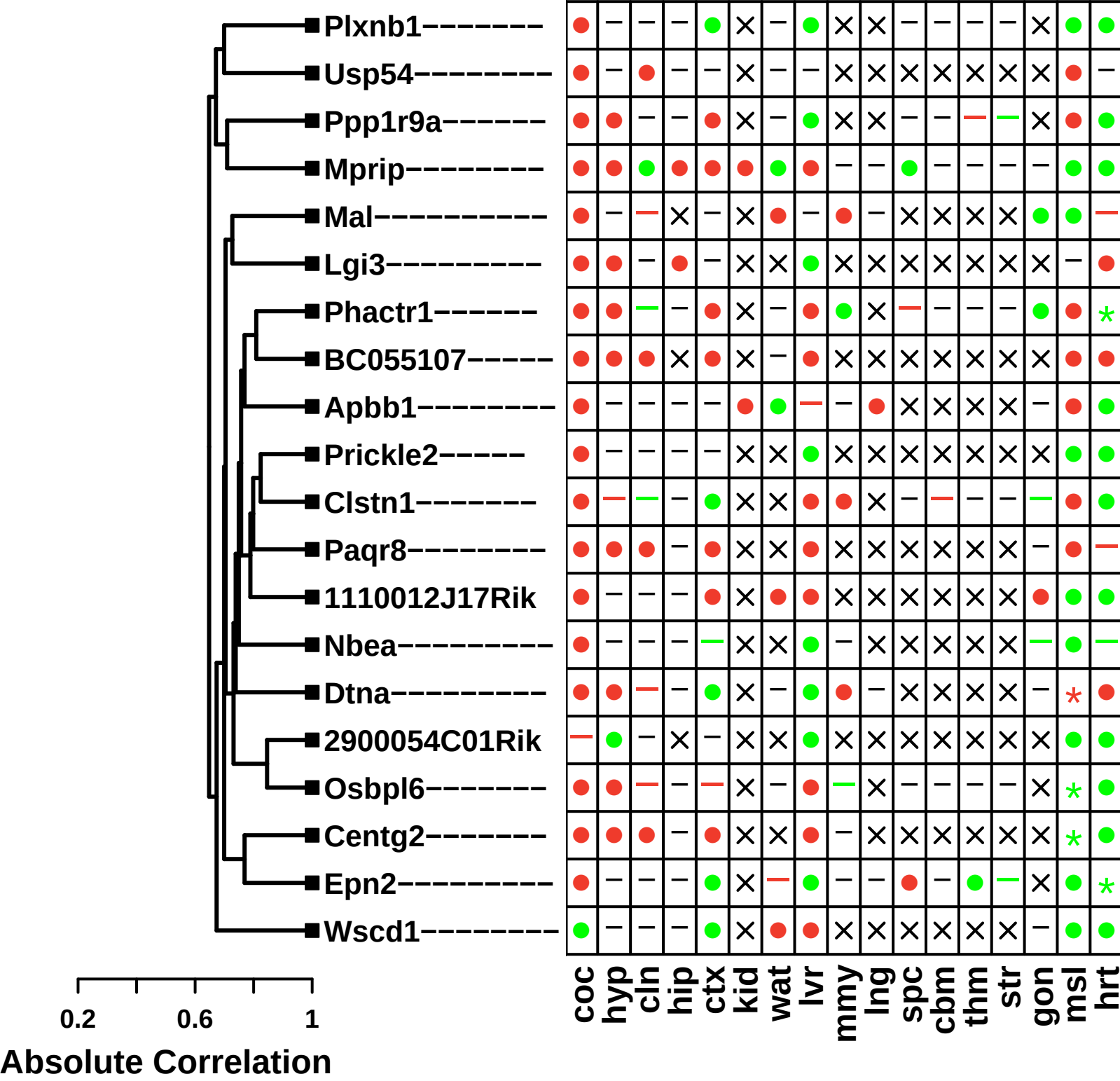
M = 7.28, P = 0



Absolute Correlation

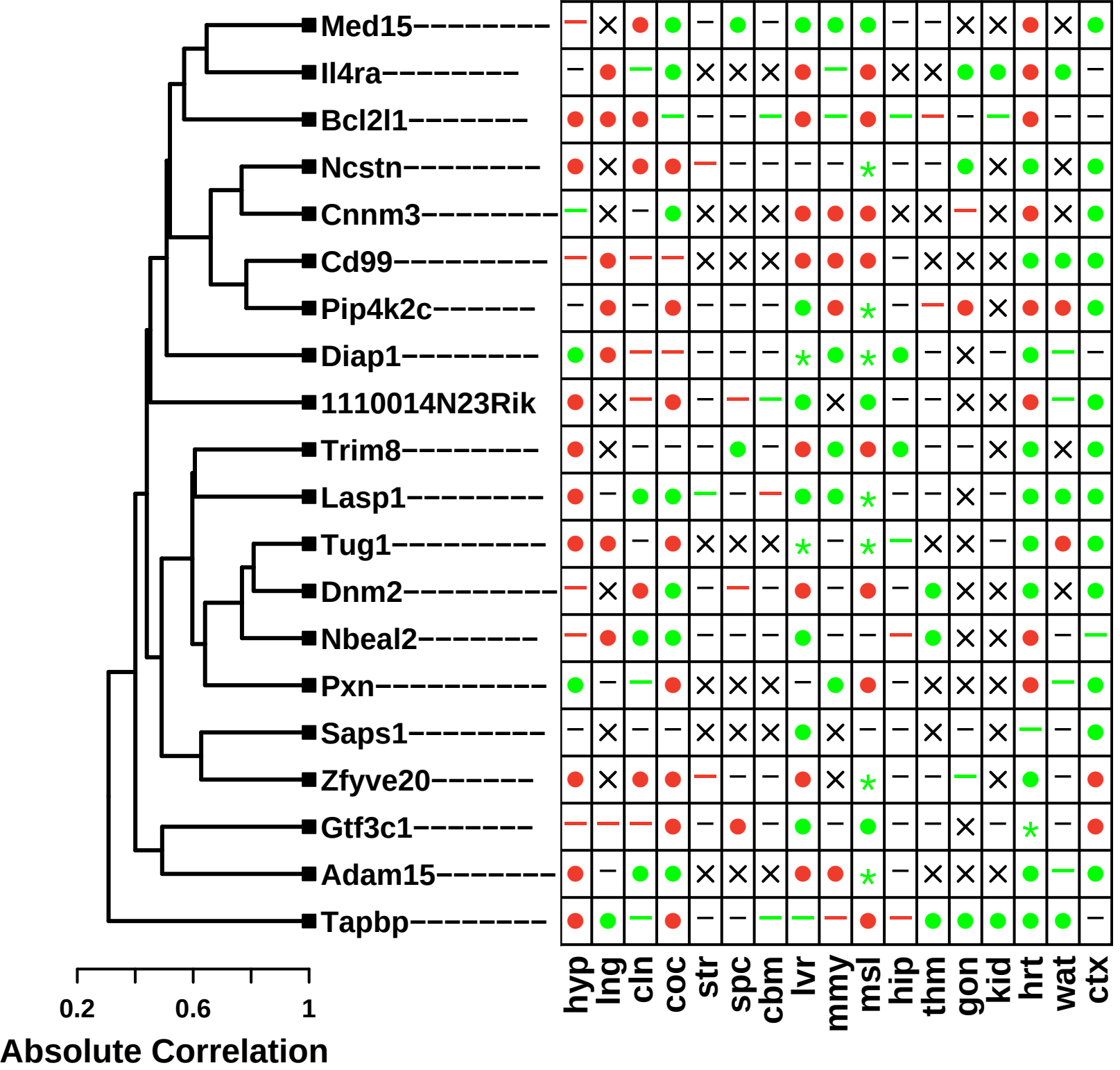
CR-Regulated Modules (20 Genes)

M = 7.25, P = 0



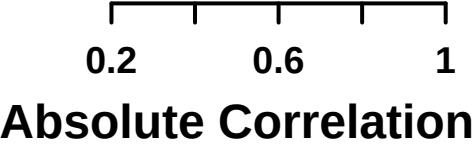
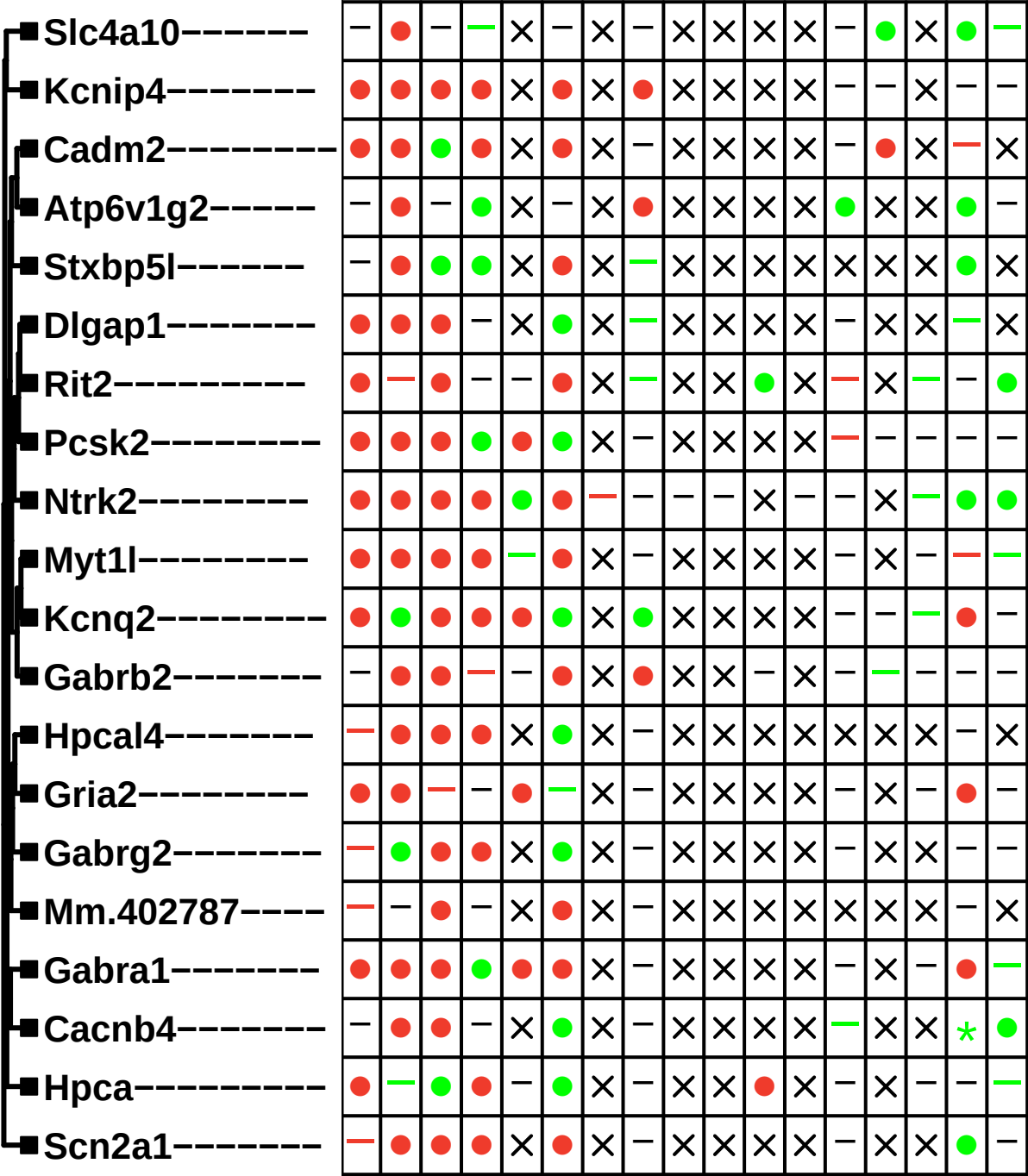
CR-Regulated Modules (20 Genes)

M = 7.25, P = 0



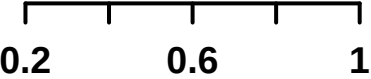
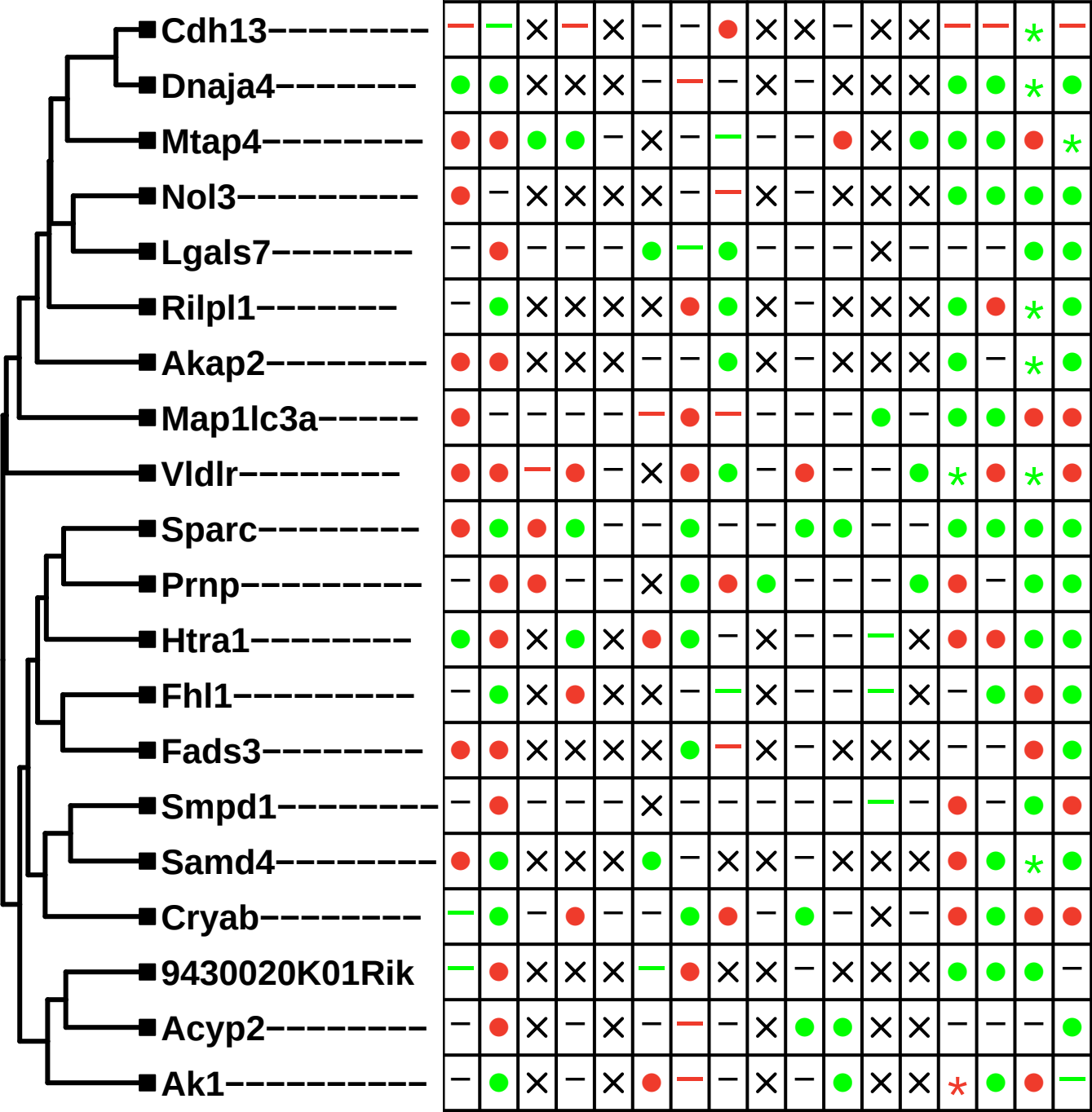
CR-Regulated Modules (20 Genes)

M = 7.24, P = 5e-04



CR-Regulated Modules (20 Genes)

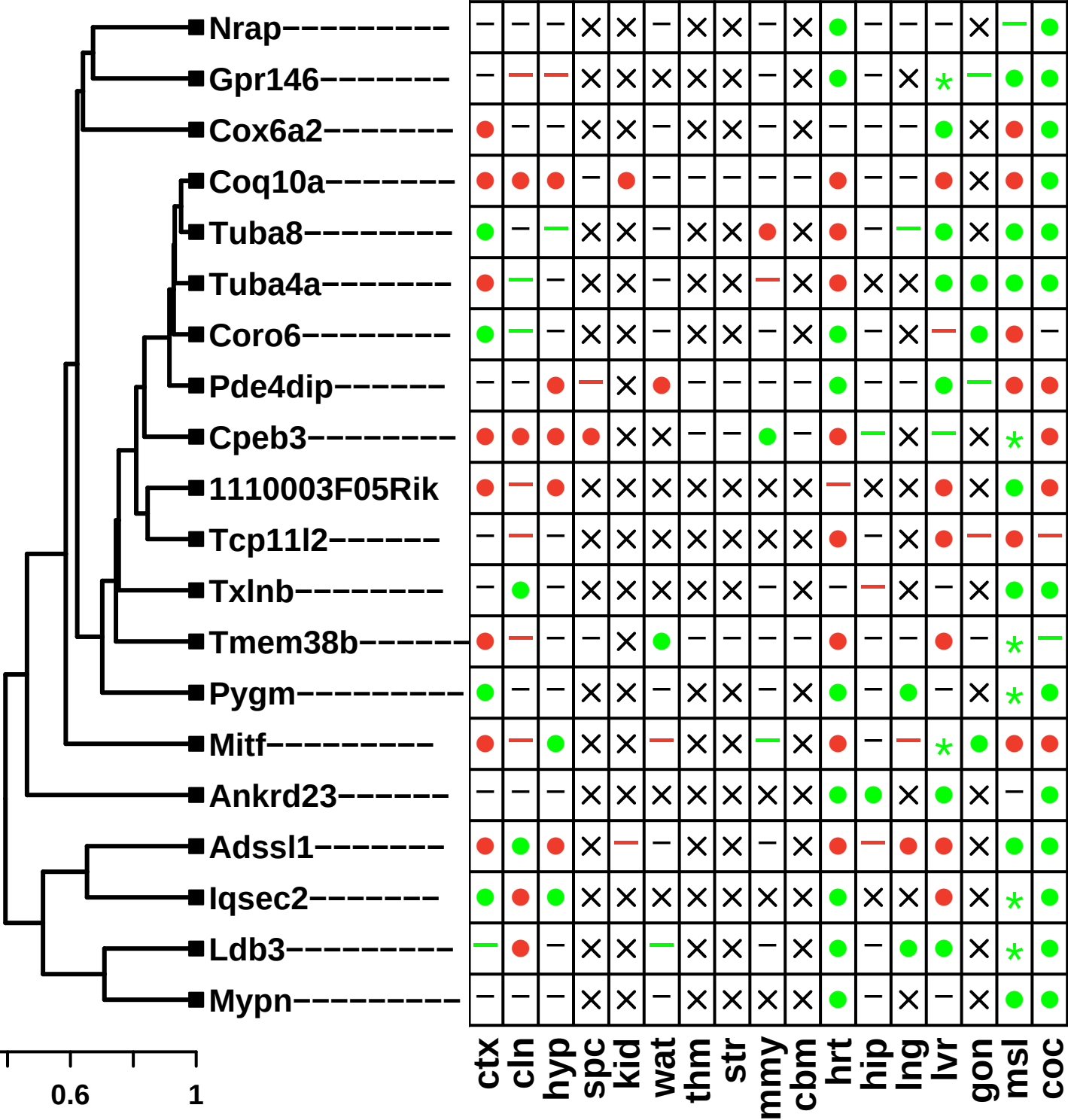
M = 7.18, P = 0.0015



Absolute Correlation

CR-Regulated Modules (20 Genes)

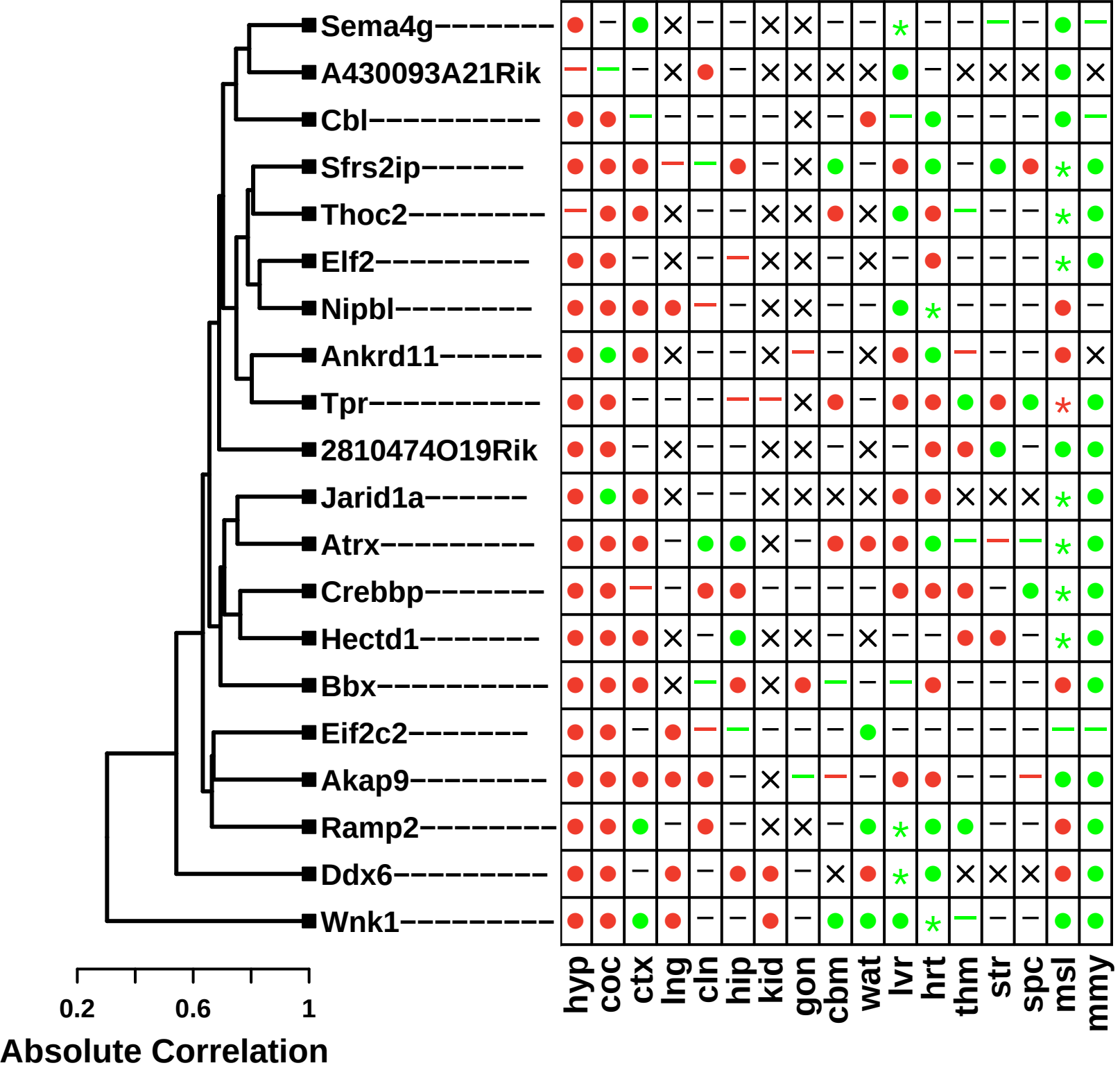
M = 7.16, P = 0.002



Absolute Correlation

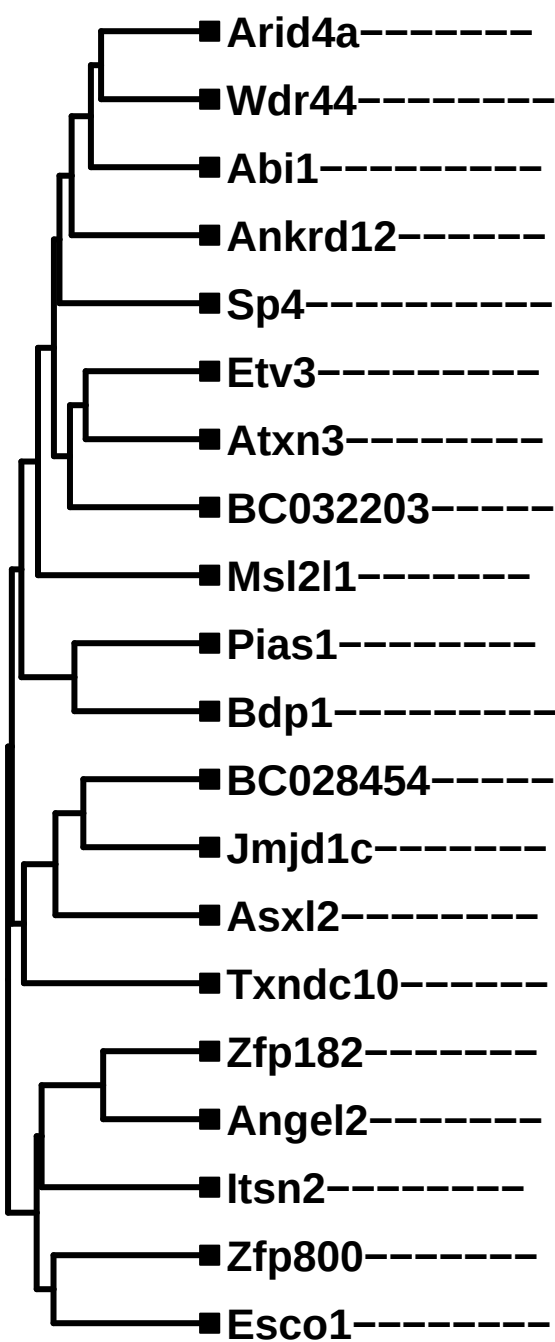
CR-Regulated Modules (20 Genes)

M = 7.16, P = 0.002



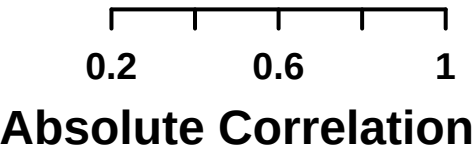
CR-Regulated Modules (20 Genes)

M = 7.15, P = 0.002



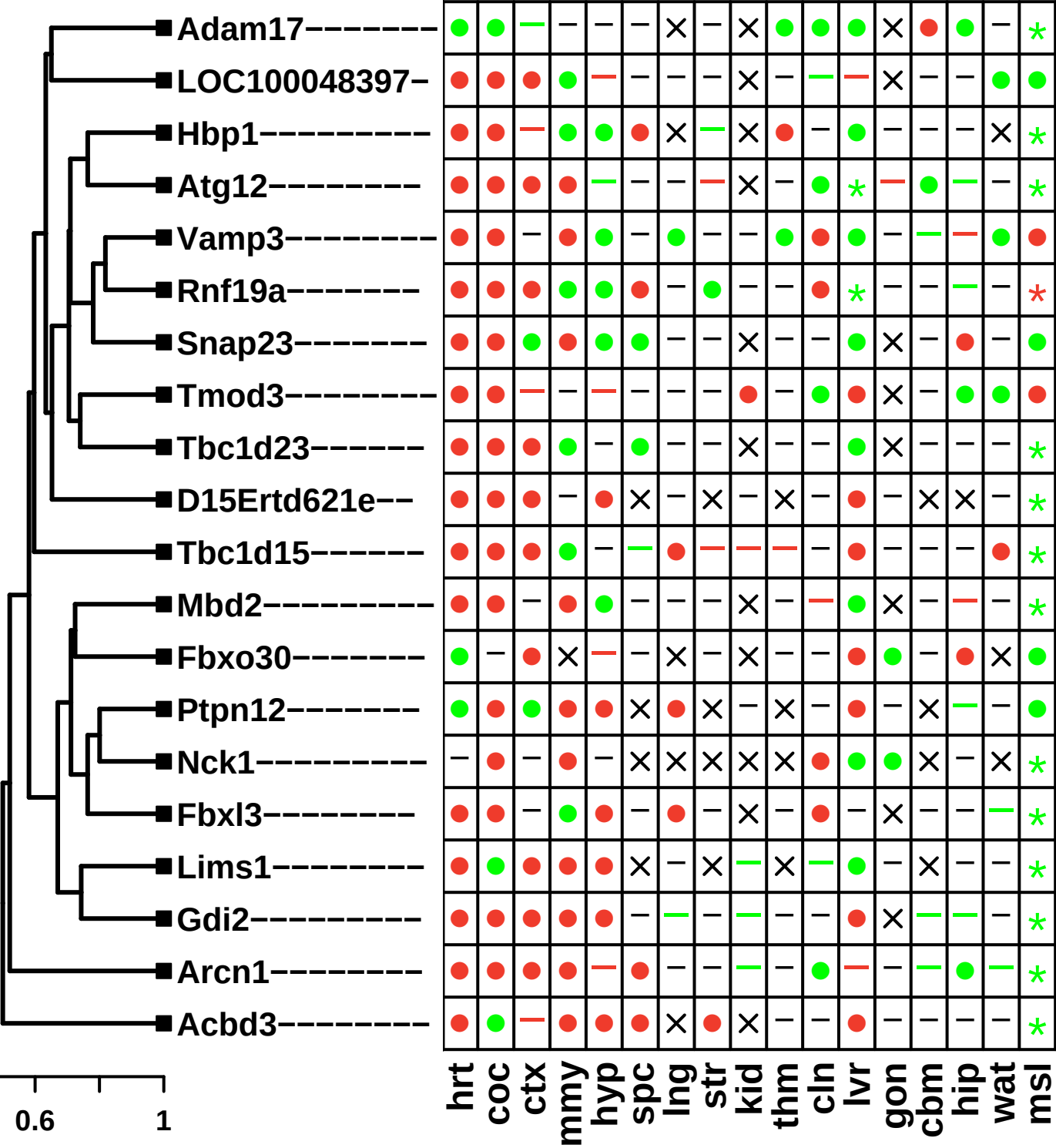
---	-	●	●	×	×	-	×	●	●	×	-	-	-	---	×	●
-	-	●	-	×	×	×	×	-	---	×	×	×	×	●	×	-
●	-	●	-	×	---	×	●	---	●	×	×	×	×	-	---	●
●	●	●	●	×	×	●	-	*	●	×	-	-	-	●	---	●
●	-	●	-	●	---	×	---	---	●	●	×	×	×	×	---	●
●	-	●	●	×	×	×	×	●	●	×	×	×	×	-	●	-
-	-	●	-	×	×	×	×	●	---	×	×	×	×	-	×	●
●	-	●	-	×	-	×	-	●	●	×	×	×	×	-	×	●
●	-	●	-	---	-	×	×	*	*	×	×	×	×	×	●	●
●	●	●	-	●	-	×	×	●	●	×	×	×	×	-	●	●
-	●	●	●	×	×	×	×	---	●	×	×	×	×	-	×	●
●	●	●	-	×	×	×	×	-	●	×	×	×	×	×	×	-
●	●	●	-	×	×	×	×	●	●	×	×	×	×	---	●	●
●	●	●	---	×	×	-	×	●	●	×	-	-	●	●	×	---
---	-	---	●	×	×	-	×	●	●	×	-	---	-	-	×	●
-	●	-	---	×	×	×	×	-	-	×	×	×	×	-	×	●
●	●	●	●	●	●	-	×	*	●	-	-	-	-	-	●	●
●	●	---	●	×	-	-	-	●	●	×	---	---	-	-	●	●
●	●	●	●	×	-	-	●	●	●	×	●	-	-	---	×	●
●	-	-	●	×	×	×	×	●	●	×	×	×	×	---	●	-

ctx
cln
coc
hyp
lng
wat
thm
gon
msl
hrt
kid
spc
str
cbm
hip
mmy
lvr



CR-Regulated Modules (20 Genes)

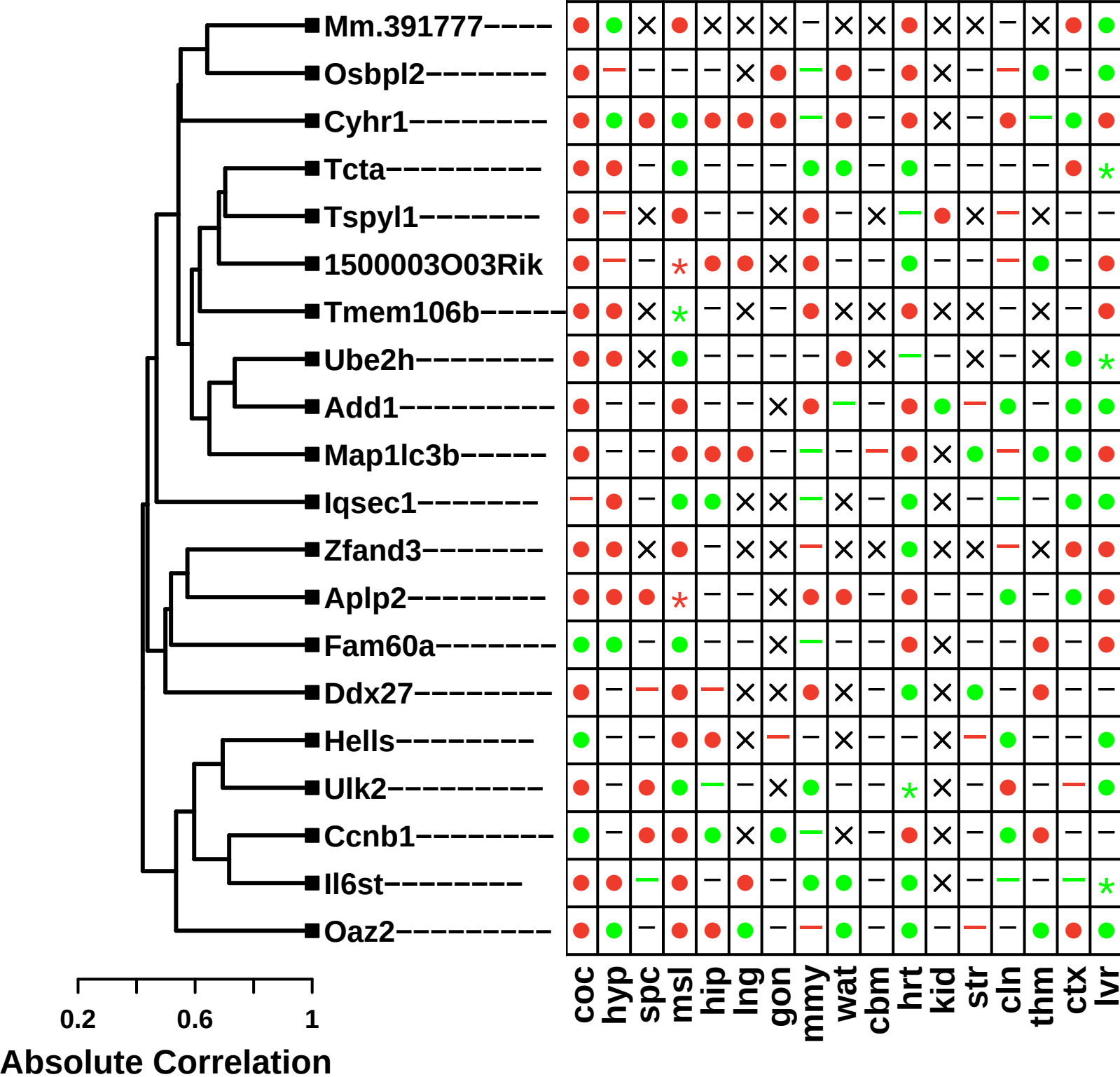
M = 7.15, P = 0.002



Absolute Correlation

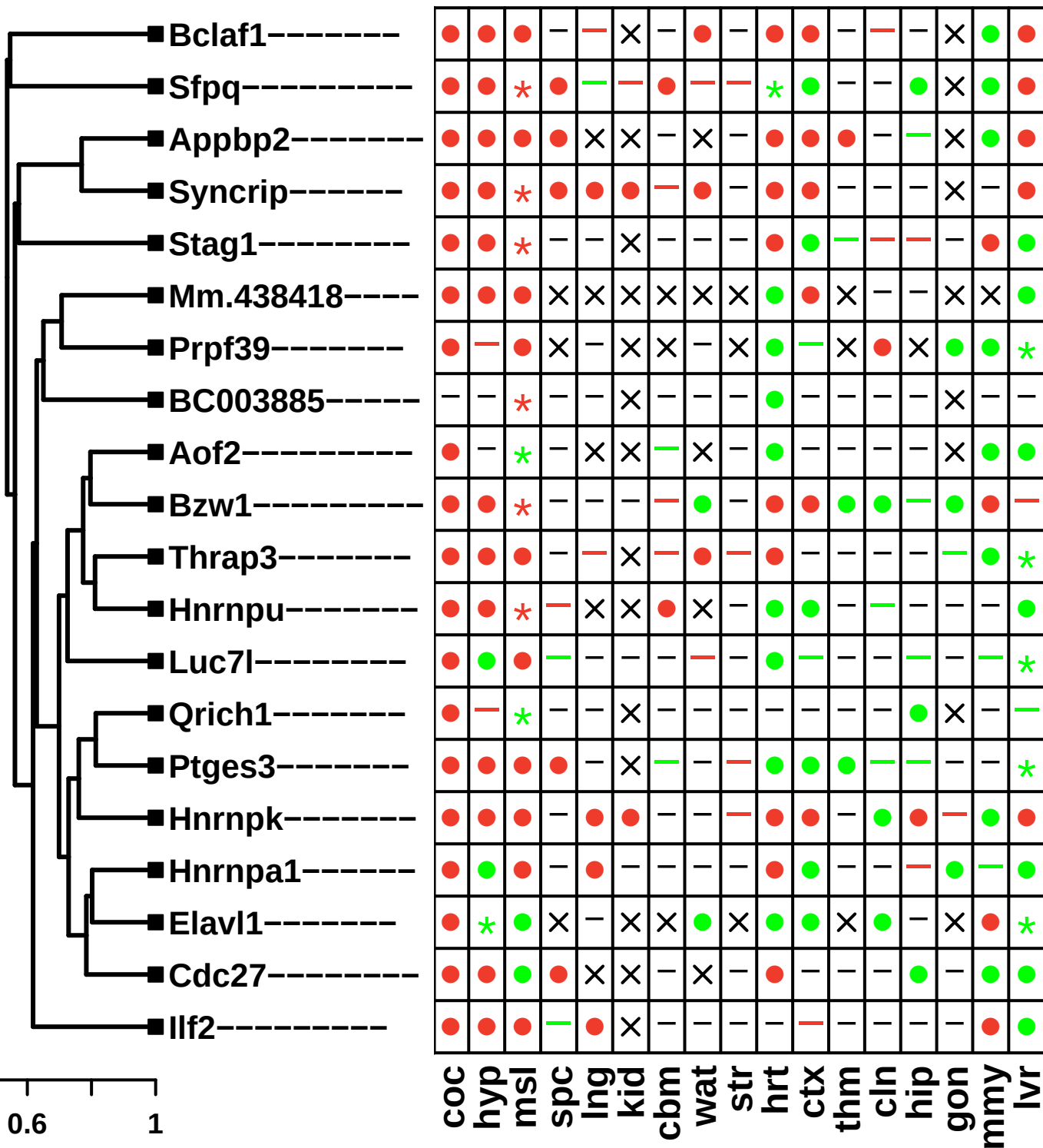
CR-Regulated Modules (20 Genes)

M = 7.14, P = 0.002



CR-Regulated Modules (20 Genes)

M = 7.11, P = 0.0025

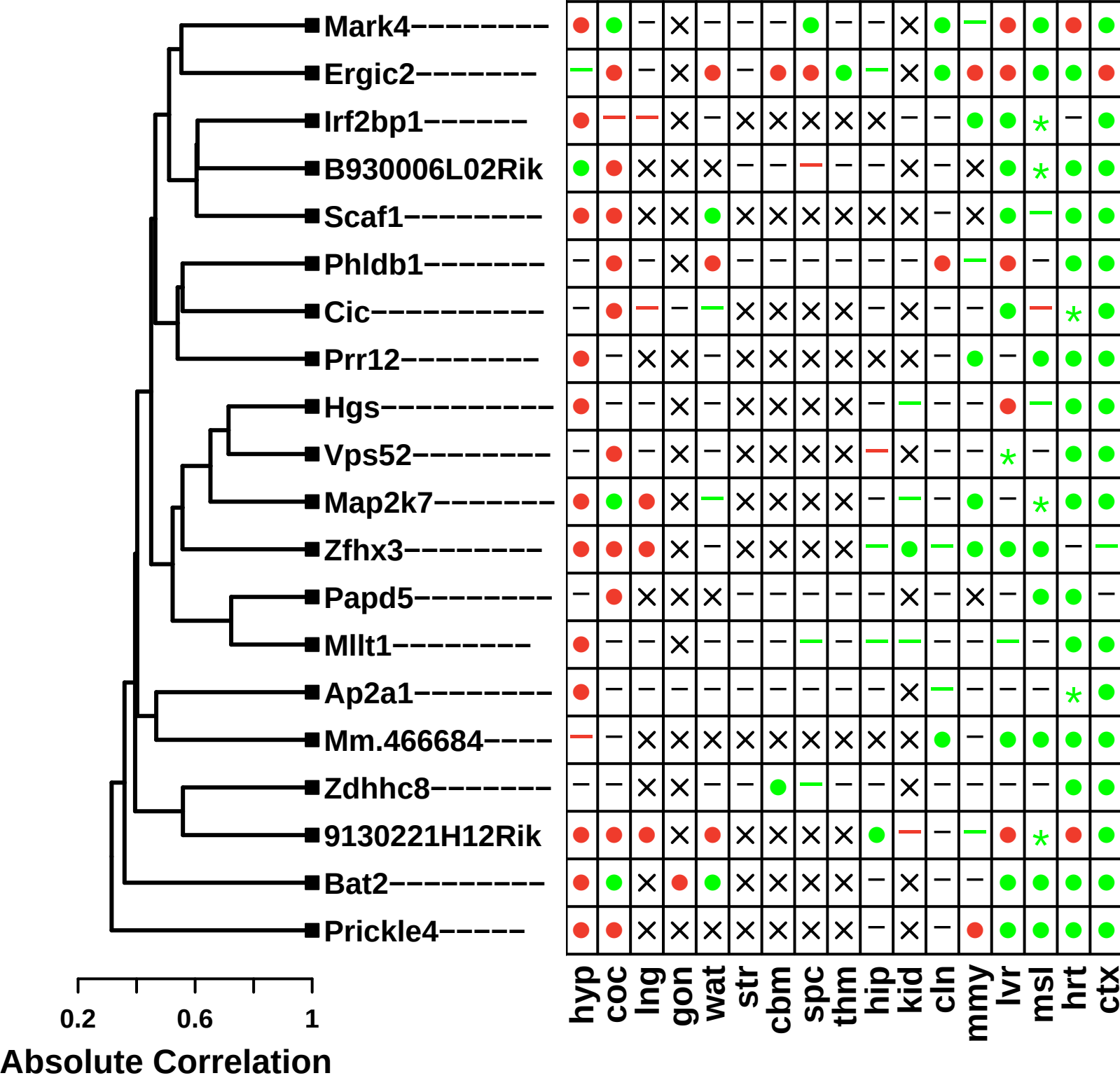


A horizontal number line with a vertical tick mark at the left end and another at the right end. There are three additional vertical tick marks between them. Below the line, the first tick mark is labeled '0.2', the third is labeled '0.6', and the rightmost is labeled '1'.

Absolute Correlation

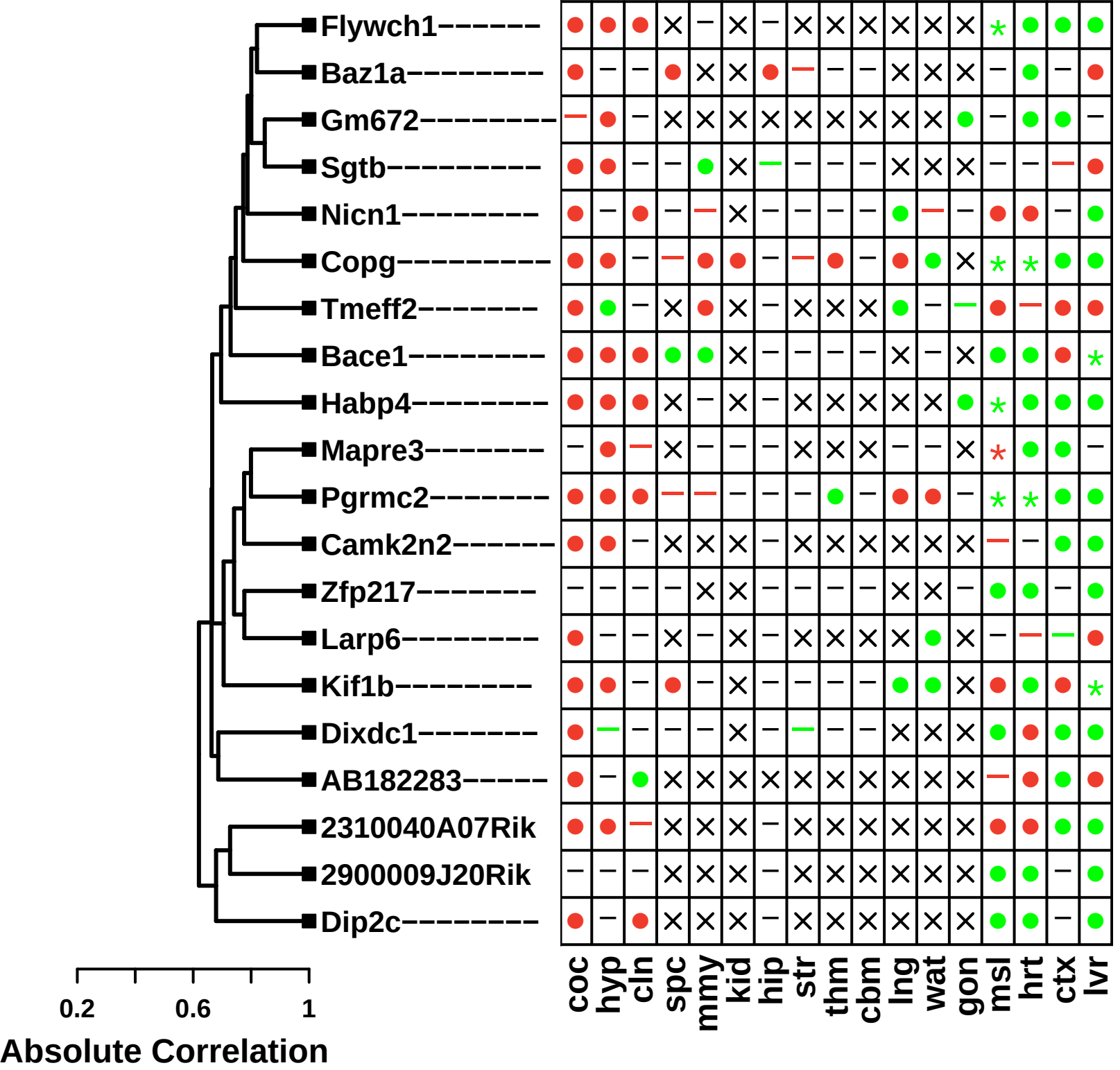
CR-Regulated Modules (20 Genes)

M = 7.09, P = 0.0035



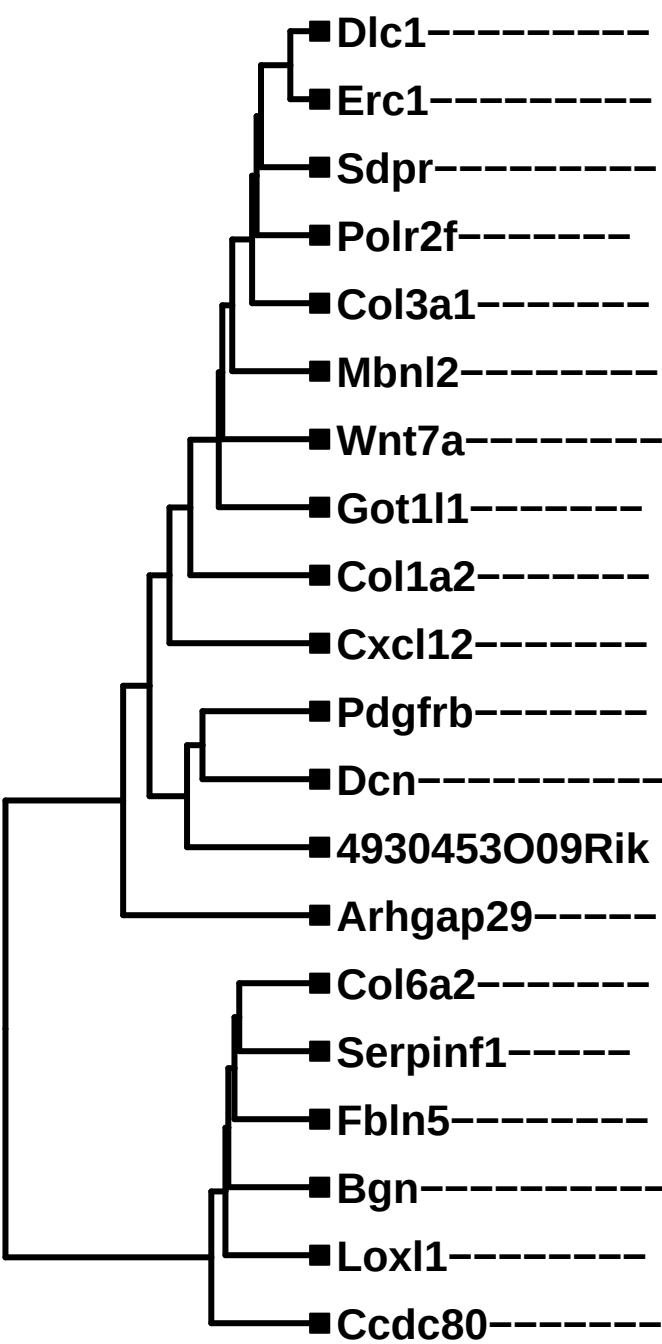
CR-Regulated Modules (20 Genes)

M = 7.09, P = 0.0035



CR-Regulated Modules (20 Genes)

M = 7.08, P = 0.0035

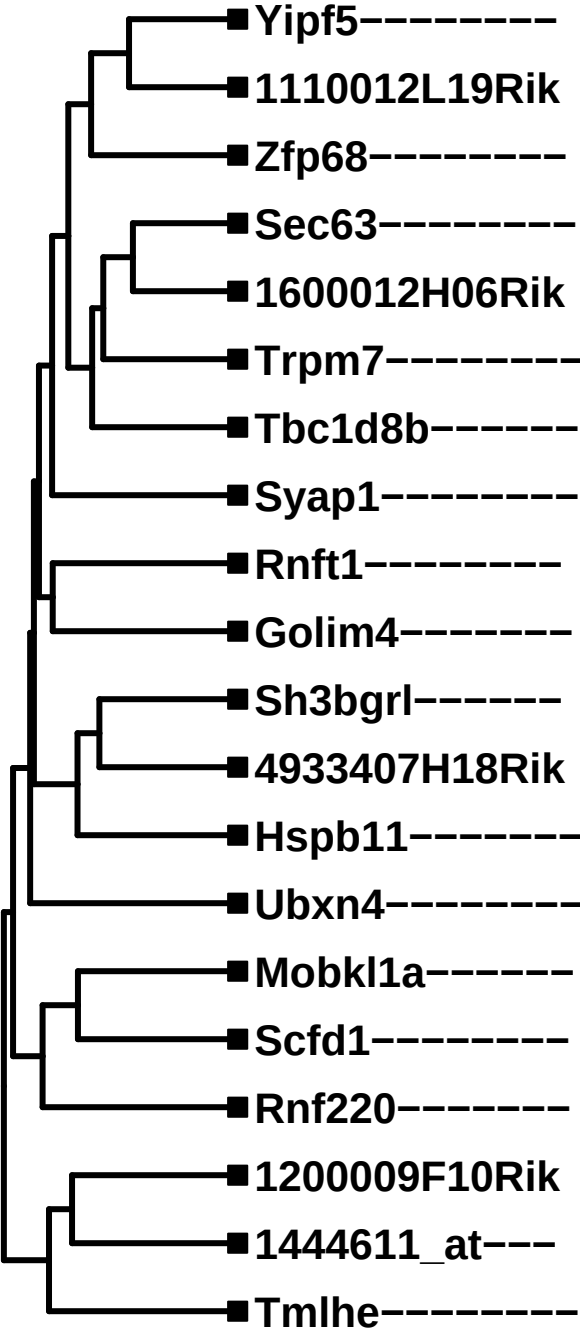


mmy																			
spc																			
thm																			
cbm																			
ctx																			
gon																			
kid																			
str																			
hrt																			
coc																			
lvr																			
hip																			
lng																			
hyp																			
cln																			
msl																			
wat																			

Absolute Correlation

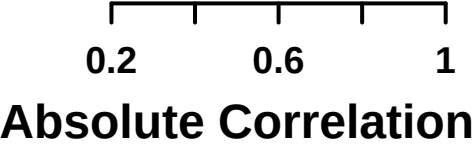
CR-Regulated Modules (20 Genes)

M = 7.05, P = 0.007



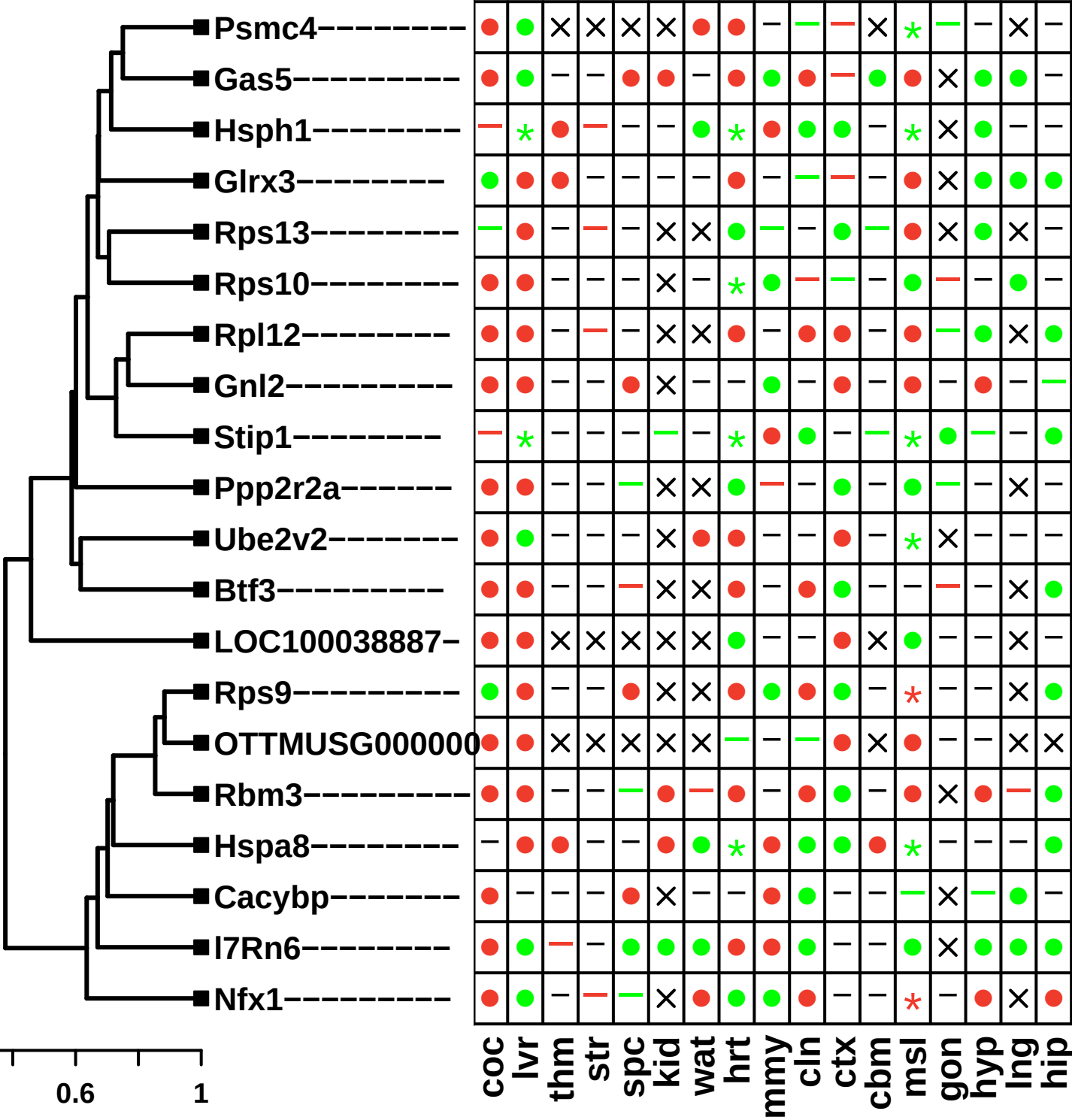
	●	●	—	—	●	●	—	●	—	*	×	—	×	—	●	—	●
	●	●	●	—	●	×	×	×	×	—	×	—	×	●	×	×	—
	●	●	●	—	●	—	—	—	●	●	×	●	—	●	●	—	●
	●	—	●	●	●	—	—	—	—	*	—	—	—	—	—	—	●
	●	●	—	●	●	×	×	—	×	●	×	×	×	●	—	×	●
	●	●	●	—	●	●	—	×	—	●	×	●	●	—	×	●	●
	●	—	●	—	●	×	×	×	×	●	×	×	×	—	×	×	—
	●	●	—	—	—	×	×	×	×	*	×	—	×	●	×	×	●
	●	—	—	—	—	×	×	●	×	●	×	—	×	—	—	×	*
	●	—	●	—	—	—	—	●	●	—	—	●	—	●	—	—	●
	●	●	●	●	—	—	—	—	—	●	×	—	×	●	—	—	●
	●	●	●	×	—	×	×	×	×	●	×	×	×	●	×	×	●
	●	—	●	—	—	×	×	—	×	●	×	—	×	—	—	×	●
	●	—	●	●	●	—	●	●	—	●	×	●	×	—	●	—	*
	●	●	●	—	●	—	—	—	—	—	×	—	×	—	—	—	●
	●	●	●	—	●	—	—	×	—	●	×	—	—	—	×	●	●
	●	●	●	●	●	—	—	—	—	●	×	—	—	—	—	—	—
	●	—	●	—	—	×	×	×	×	*	×	×	×	—	●	×	*
	●	●	—	×	—	×	×	×	×	—	×	×	×	—	×	×	—
	●	—	●	●	●	×	×	×	×	●	×	×	—	●	×	×	*

coc
ctx
hrt
mmy
hyp
str
spc
lng
cbm
msl
kid
hip
gon
cln
wat
thm
lvr



CR-Regulated Modules (20 Genes)

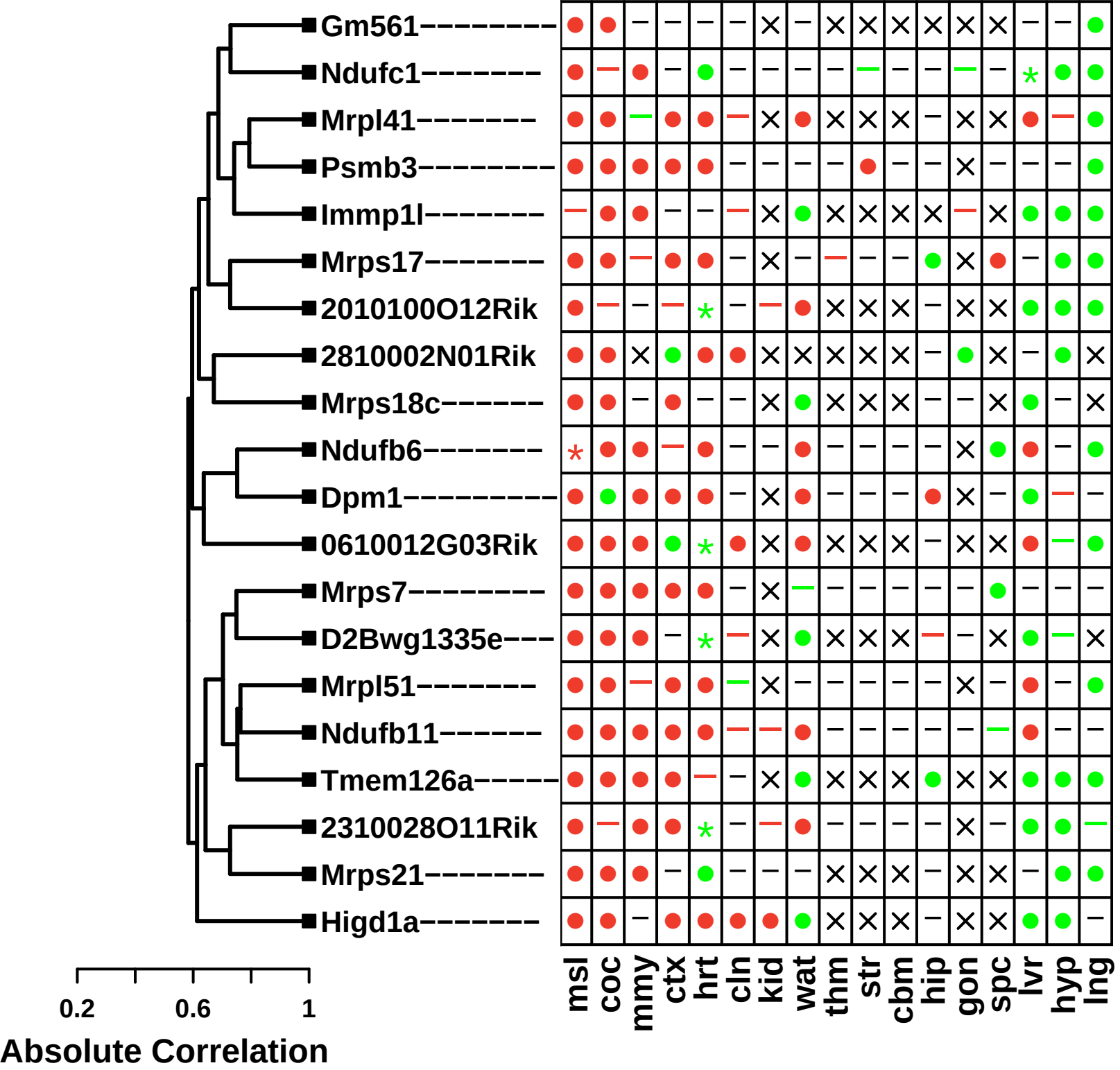
M = 7.04, P = 0.0075



Absolute Correlation

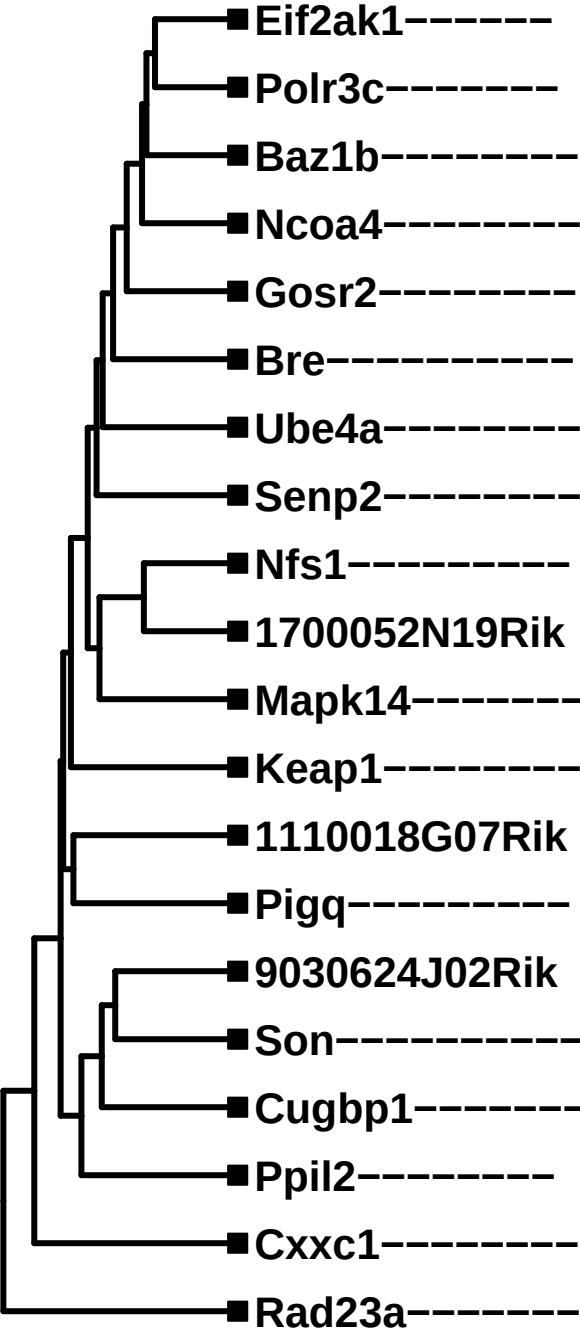
CR-Regulated Modules (20 Genes)

M = 7.04, P = 0.0075



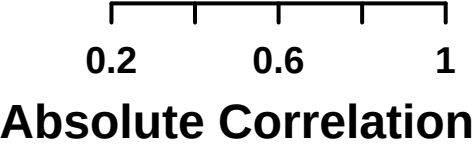
CR-Regulated Modules (20 Genes)

M = 7, P = 0.0115



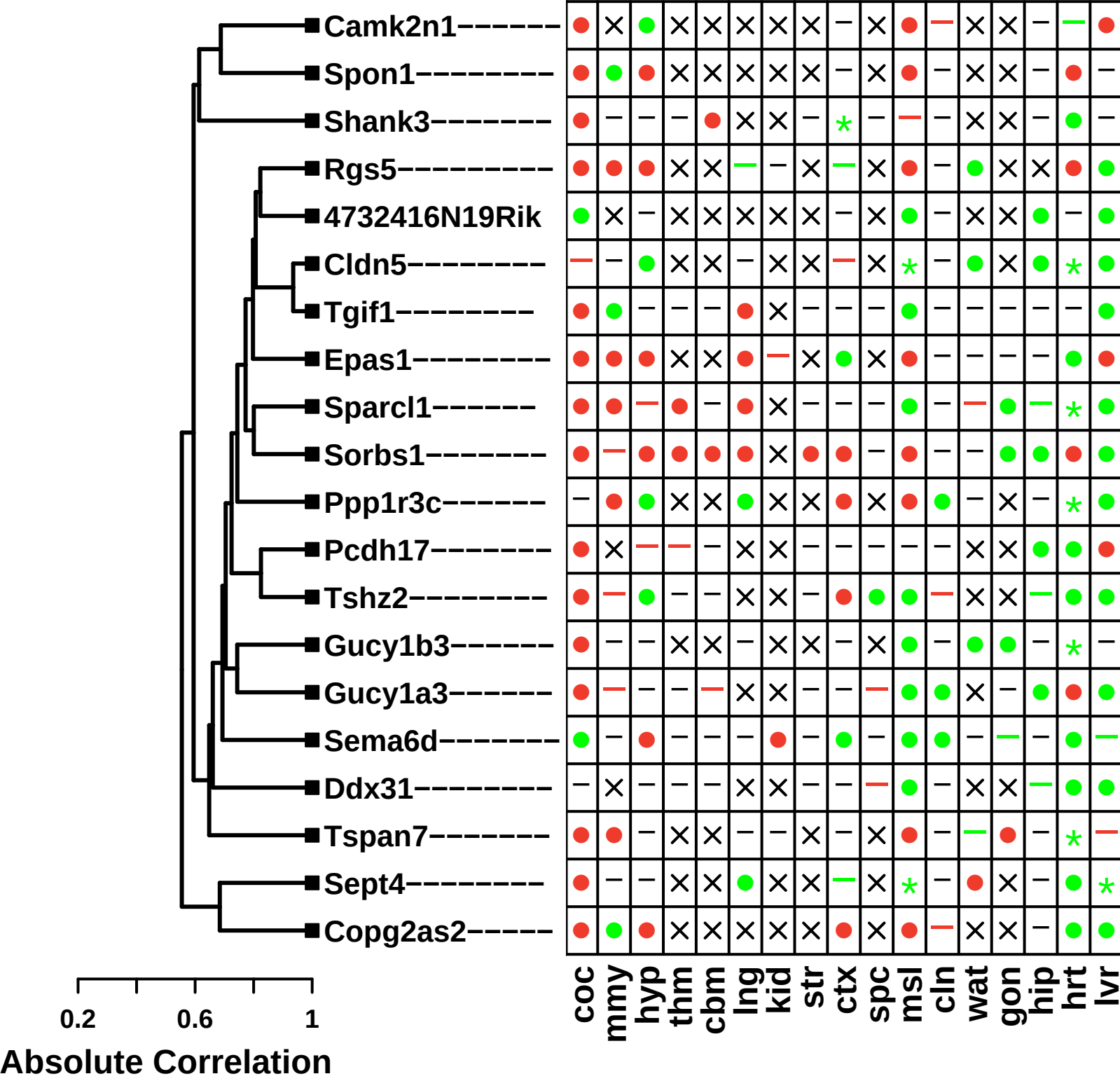
	●	—	●	●	●	●	●	×	×	×	×	×	×	—	●	*	●
	●	—	—	●	×	●	●	×	×	×	●	×	×	—	●	●	—
	●	●	—	●	—	—	●	×	×	—	—	×	×	—	●	*	●
	●	—	●	●	●	—	●	—	—	—	—	—	—	—	—	*	●
	●	—	●	●	—	●	●	—	—	×	●	—	●	●	—	●	*
	●	●	—	●	●	—	●	—	—	×	×	—	●	—	●	*	●
	—	—	—	●	×	●	●	×	×	×	—	×	×	—	●	*	*
	●	●	—	●	×	—	●	—	—	×	×	—	—	—	—	*	—
	●	—	—	●	—	—	●	×	×	×	×	×	×	—	—	●	—
	●	●	×	●	×	—	—	—	—	×	×	—	—	●	—	●	●
	●	—	—	●	—	—	●	—	—	—	×	—	—	—	—	*	*
	●	●	—	—	—	●	●	×	×	×	—	×	×	●	—	●	●
	×	—	—	●	×	—	●	—	—	×	×	—	—	—	●	*	●
	●	●	●	●	—	●	●	—	—	●	×	—	—	●	—	*	●
	—	—	×	●	×	—	●	—	—	×	—	—	—	—	—	*	●
	●	●	—	●	●	●	●	—	—	—	—	—	—	—	—	*	●
	●	●	—	*	—	●	●	—	—	—	×	●	—	●	●	●	●
	—	—	—	●	—	—	●	●	—	×	×	—	●	●	—	*	●
	—	—	×	●	×	●	—	—	—	×	×	—	—	●	—	●	*
	—	●	●	●	●	●	●	×	×	×	×	×	×	—	●	●	—

mmy
hyp
wat
hrt
lng
ctx
coc
cbm
str
kid
gon
spc
thm
hip
cln
msl
lvr



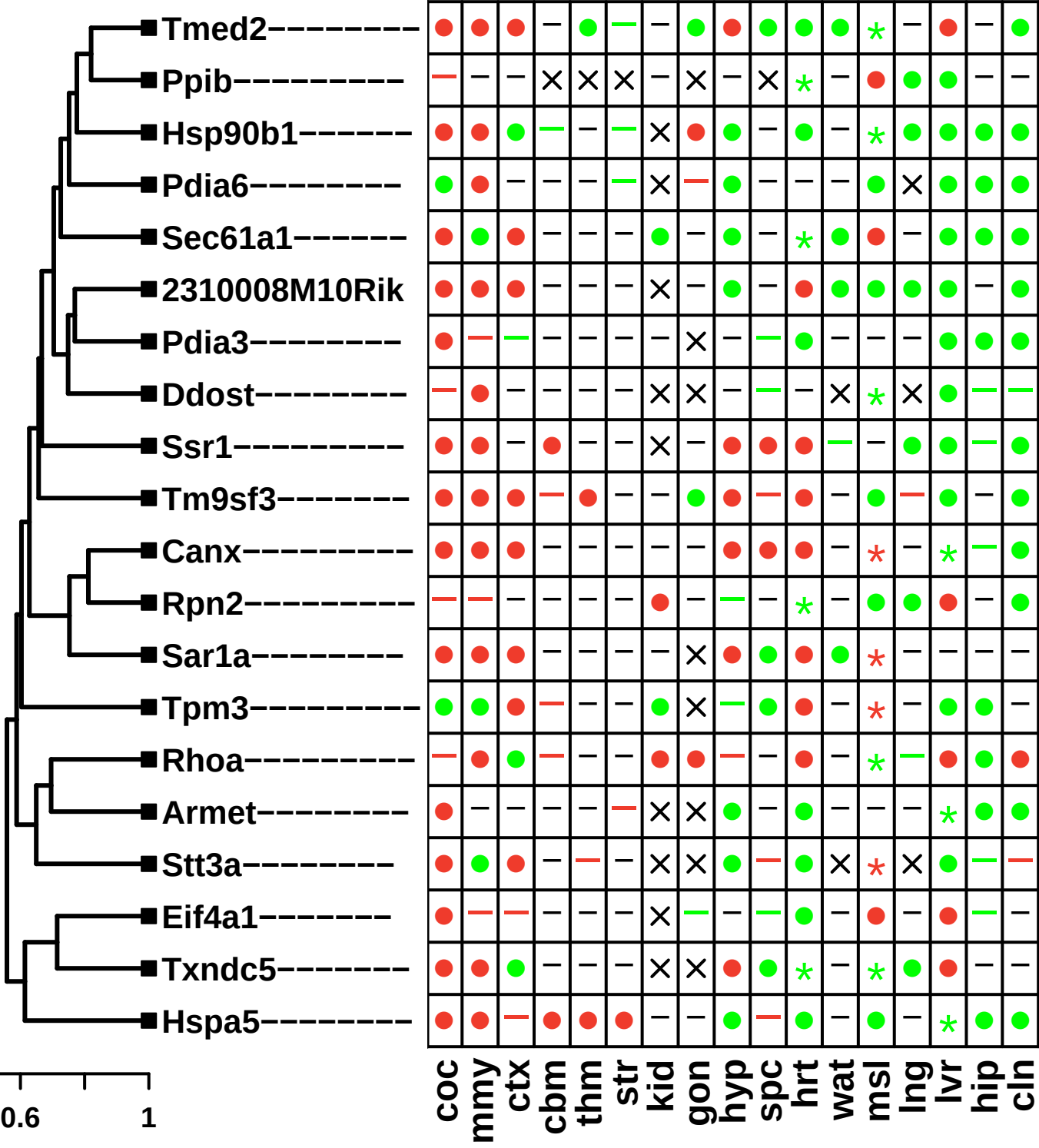
CR-Regulated Modules (20 Genes)

M = 6.99, P = 0.0125



CR-Regulated Modules (20 Genes)

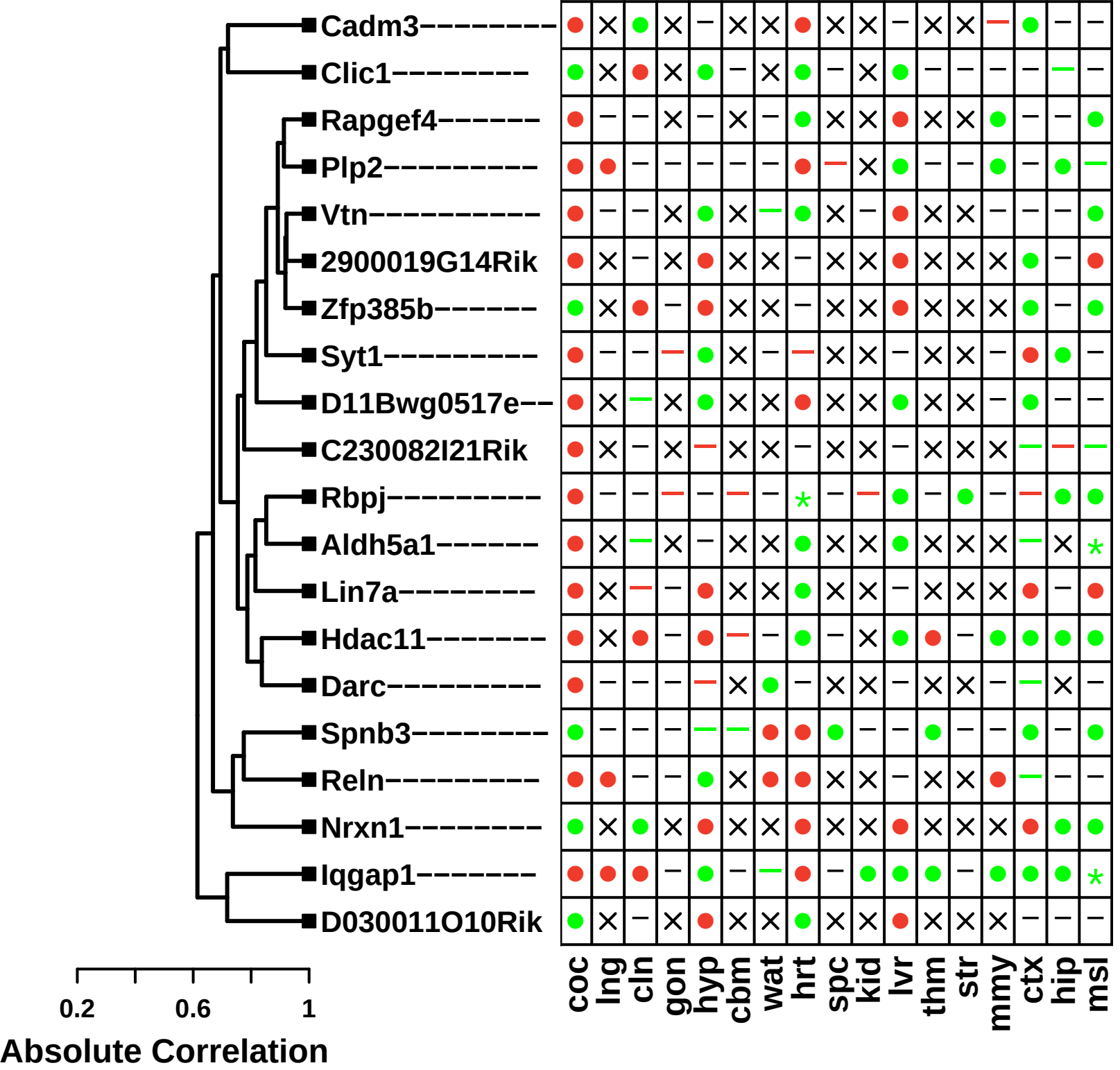
M = 6.98, P = 0.0155



Absolute Correlation

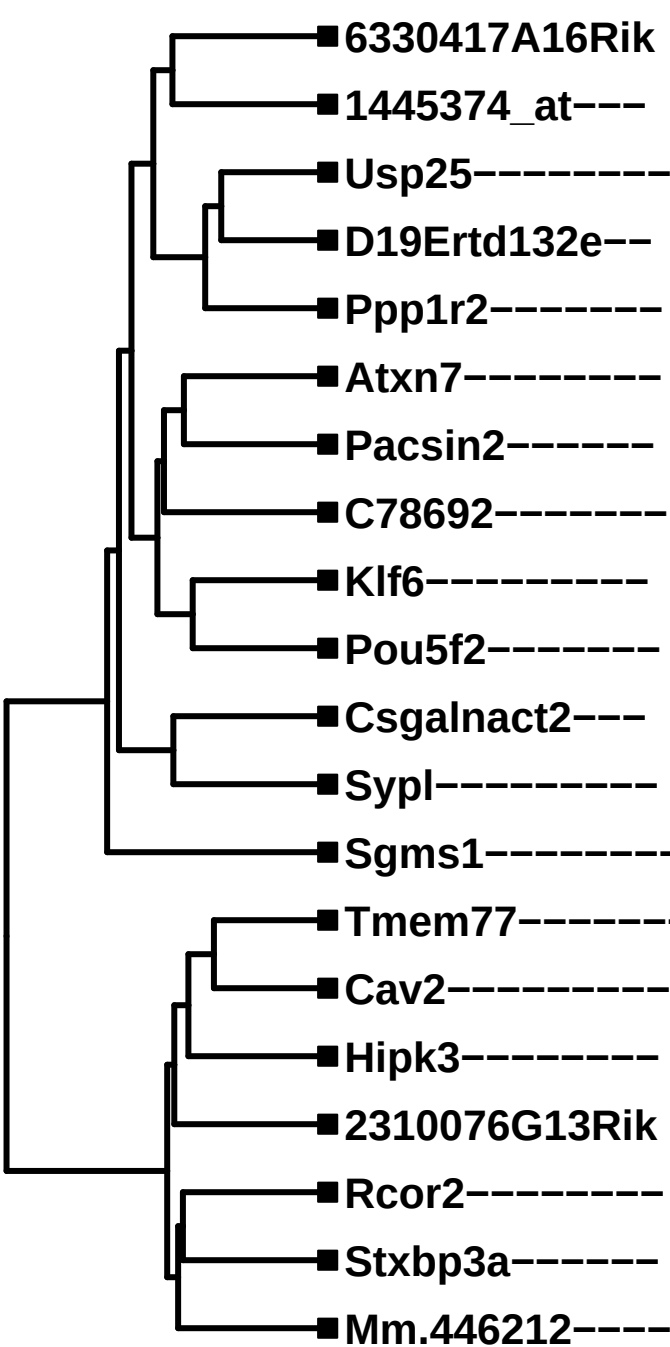
CR-Regulated Modules (20 Genes)

M = 6.98, P = 0.017



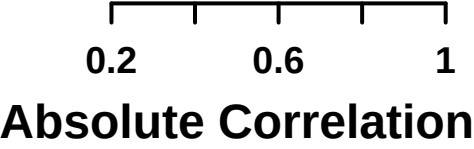
CR-Regulated Modules (20 Genes)

M = 6.97, P = 0.0215



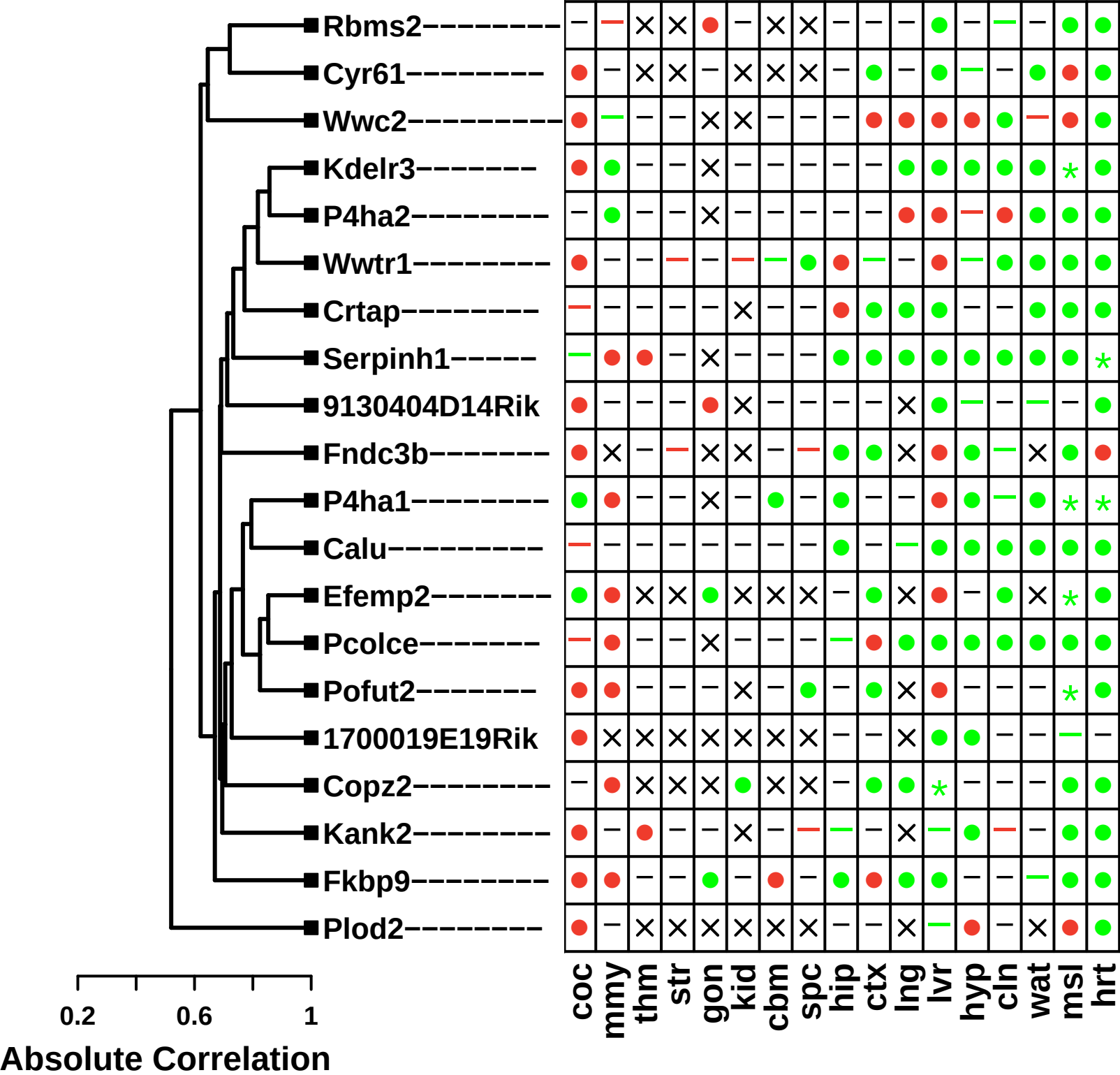
	●	-	×	×	×	●	×	-	×	×	●	×	-	×	×	×	-
	●	-	×	×	×	-	×	-	×	×	-	×	-	×	×	-	-
	●	●	-	×	●	●	-	●	-	-	●	×	●	-	×	●	●
	-	-	×	×	×	●	×	-	×	×	●	×	-	×	×	-	●
	●	●	●	●	-	●	-	●	●	-	●	-	*	-	-	-	*
	●	●	●	×	×	●	×	-	×	×	●	×	●	×	×	-	●
	●	●	●	×	-	●	×	-	-	-	-	×	●	-	×	-	-
	●	-	×	×	×	●	×	●	×	×	-	×	●	×	×	×	●
	●	●	●	●	-	●	●	●	-	-	●	×	●	-	●	●	●
	●	-	×	×	×	-	×	-	×	×	●	×	-	×	×	-	●
	●	●	-	×	×	-	×	-	×	×	-	×	●	×	-	-	●
	●	-	●	-	●	●	●	-	-	-	-	-	●	-	-	●	●
	●	●	●	×	●	●	×	●	-	-	●	×	●	●	×	●	*
	●	●	-	×	×	●	×	●	×	×	-	×	●	×	×	-	●
	-	-	●	-	●	●	-	-	-	-	-	×	*	-	-	●	*
	●	●	×	×	×	●	×	-	×	×	●	×	●	×	×	●	●
	●	●	-	×	×	●	●	-	×	×	-	×	-	×	×	-	-
	●	-	●	●	×	●	-	-	×	×	-	-	-	×	-	-	*
	●	-	×	×	×	-	×	●	×	×	-	×	-	×	×	×	●

coc
ctx
mmy
lng
spc
lvr
wat
cln
str
cbm
hyp
kid
hrt
thm
gon
hip
msl



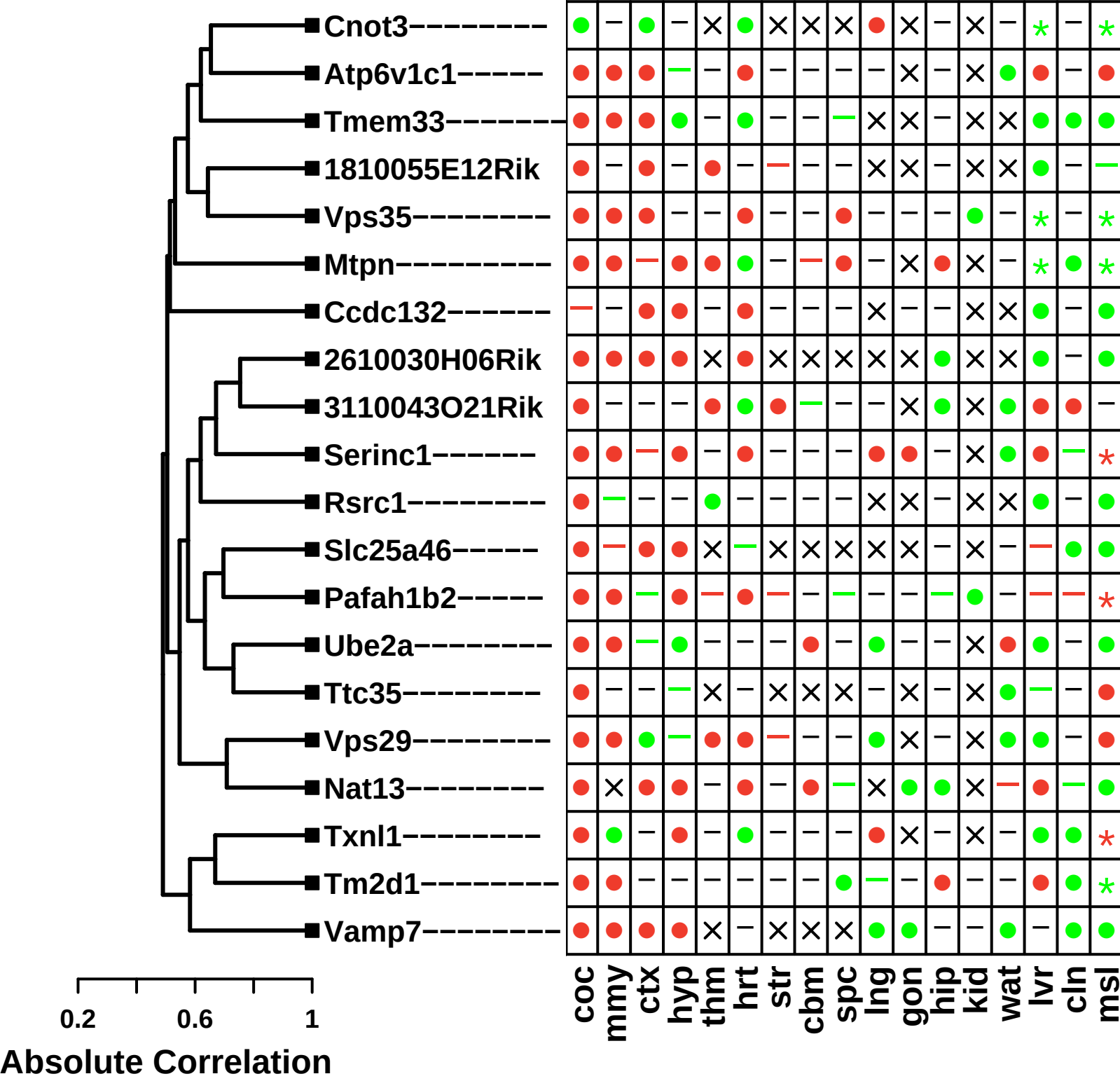
CR-Regulated Modules (20 Genes)

M = 6.96, P = 0.022



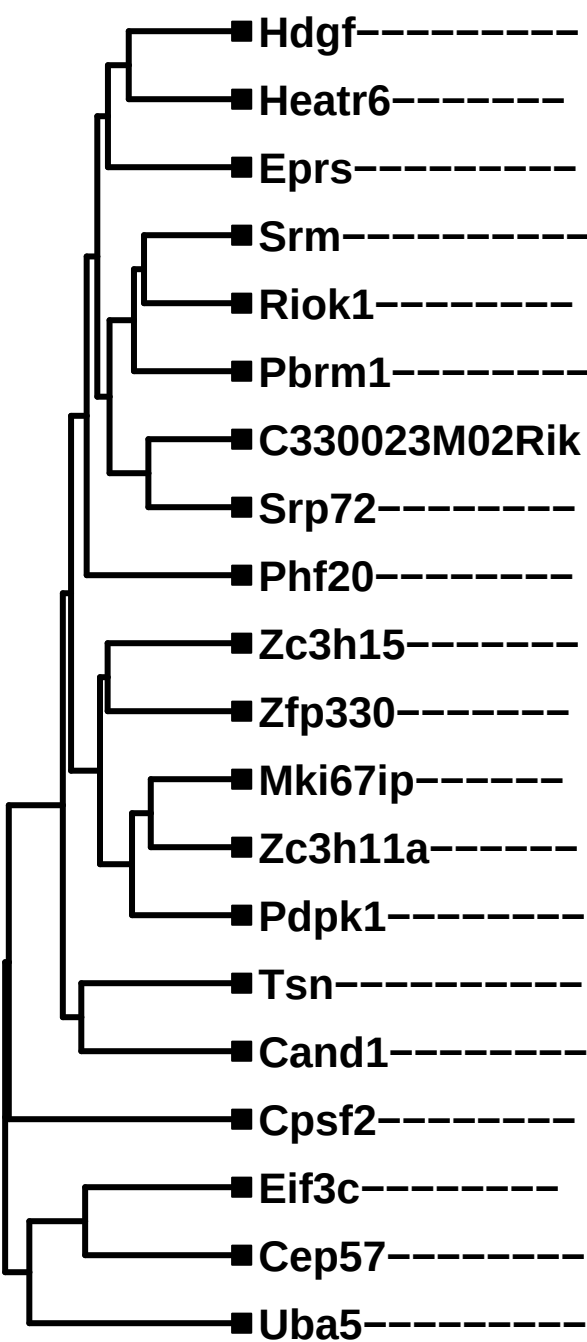
CR-Regulated Modules (20 Genes)

M = 6.96, P = 0.0245

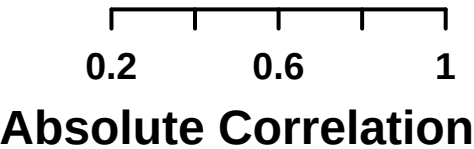


CR-Regulated Modules (20 Genes)

M = 6.94, P = 0.037

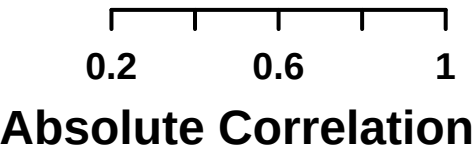
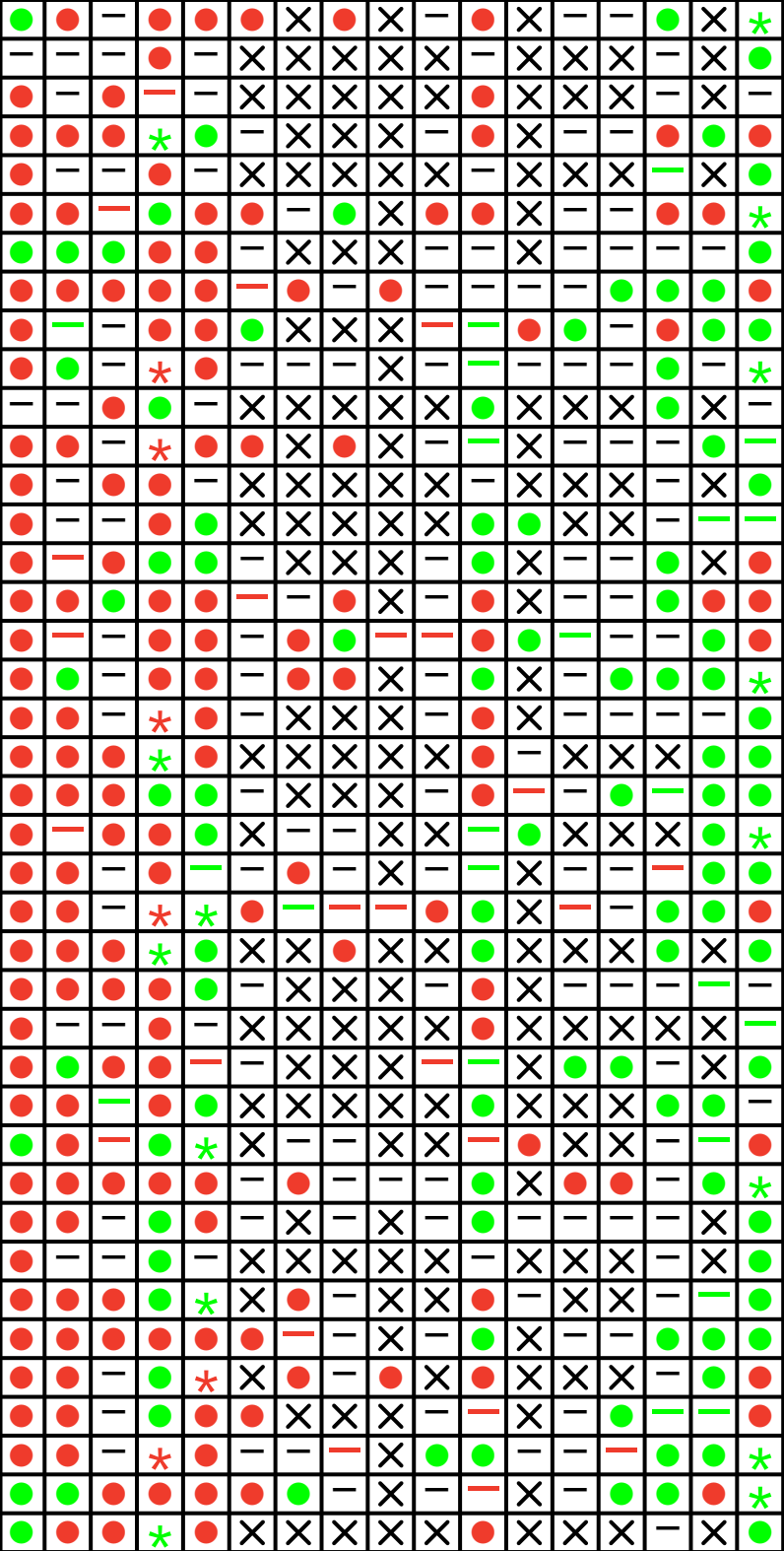
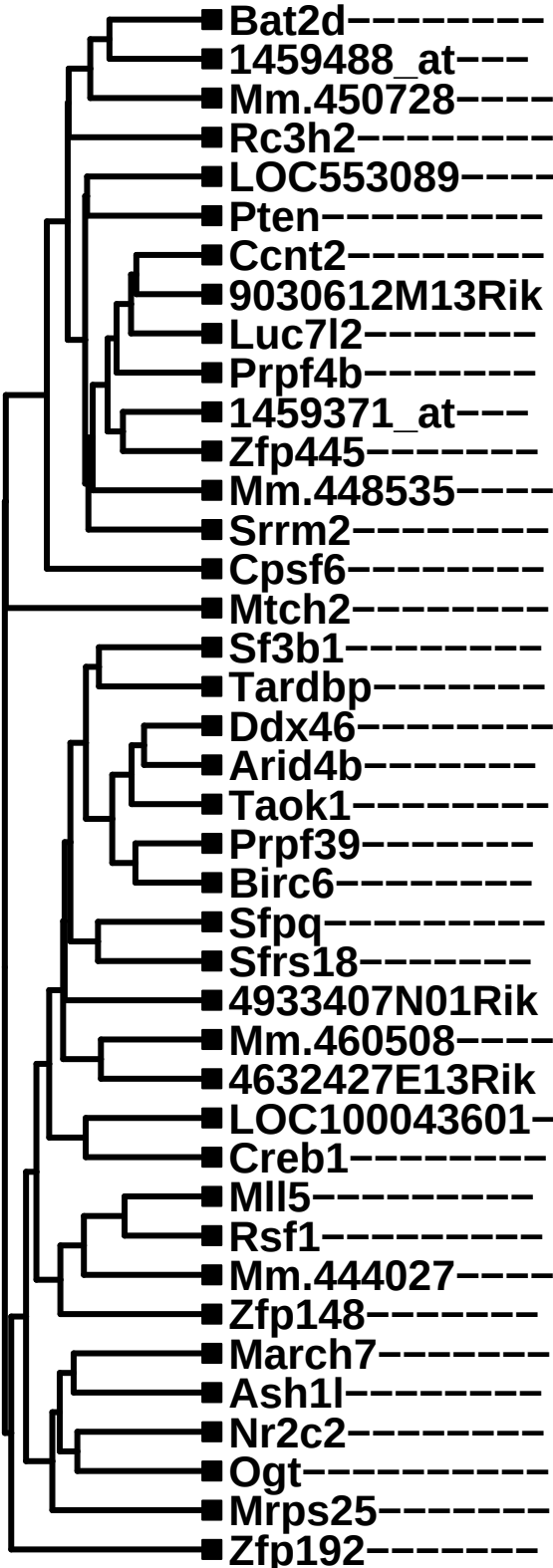


	coc	ctx	hyp	lng	gon	cbm	kid	str	spc	msl	thm	cln	wat	lvr	hip	hrt	mmy
Hdgf	●	●	●	●	-	-	-	-	-	●	-	-	-	●	-	*	-
Heatr6	●	●	●	×	×	×	×	×	×	*	×	●	×	●	-	●	-
Eprs	●	-	●	●	×	-	×	-	-	*	●	-	●	●	-	*	●
Srm	-	●	-	●	×	-	●	-	-	●	-	-	●	-	●	●	●
Riok1	●	●	-	-	-	-	×	-	-	*	●	-	-	●	●	●	●
Pbrm1	●	●	-	-	×	-	-	-	-	*	-	●	-	●	●	*	●
C330023M02Rik	-	-	●	×	×	-	×	-	-	●	-	-	×	●	-	●	×
Srp72	●	●	●	×	●	-	×	-	●	●	-	-	-	-	●	-	×
Phf20	●	●	●	×	×	-	×	-	-	●	-	-	-	●	●	●	●
Zc3h15	●	-	●	-	×	×	×	×	×	*	×	●	-	*	-	●	-
Zfp330	●	●	-	×	×	-	×	-	-	-	-	-	×	-	-	-	●
Mki67ip	-	●	-	×	-	-	×	-	-	●	-	-	-	-	-	●	-
Zc3h11a	●	●	●	●	×	-	×	●	-	●	-	-	-	●	-	●	●
Pdpk1	●	●	-	●	●	-	×	-	-	●	●	-	-	*	-	-	●
Tsn	●	●	●	×	-	-	×	-	-	*	-	-	×	●	●	●	-
Cand1	●	-	●	×	-	-	×	-	-	●	●	-	×	●	-	●	-
Cpsf2	●	-	●	-	×	-	×	-	-	●	-	-	●	●	●	*	●
Eif3c	●	-	●	●	-	-	-	-	-	●	-	-	-	●	-	●	-
Cep57	●	●	●	×	-	●	×	-	-	●	-	-	-	-	-	●	×
Uba5	●	●	●	●	×	×	×	×	×	●	×	●	*	●	-	*	●



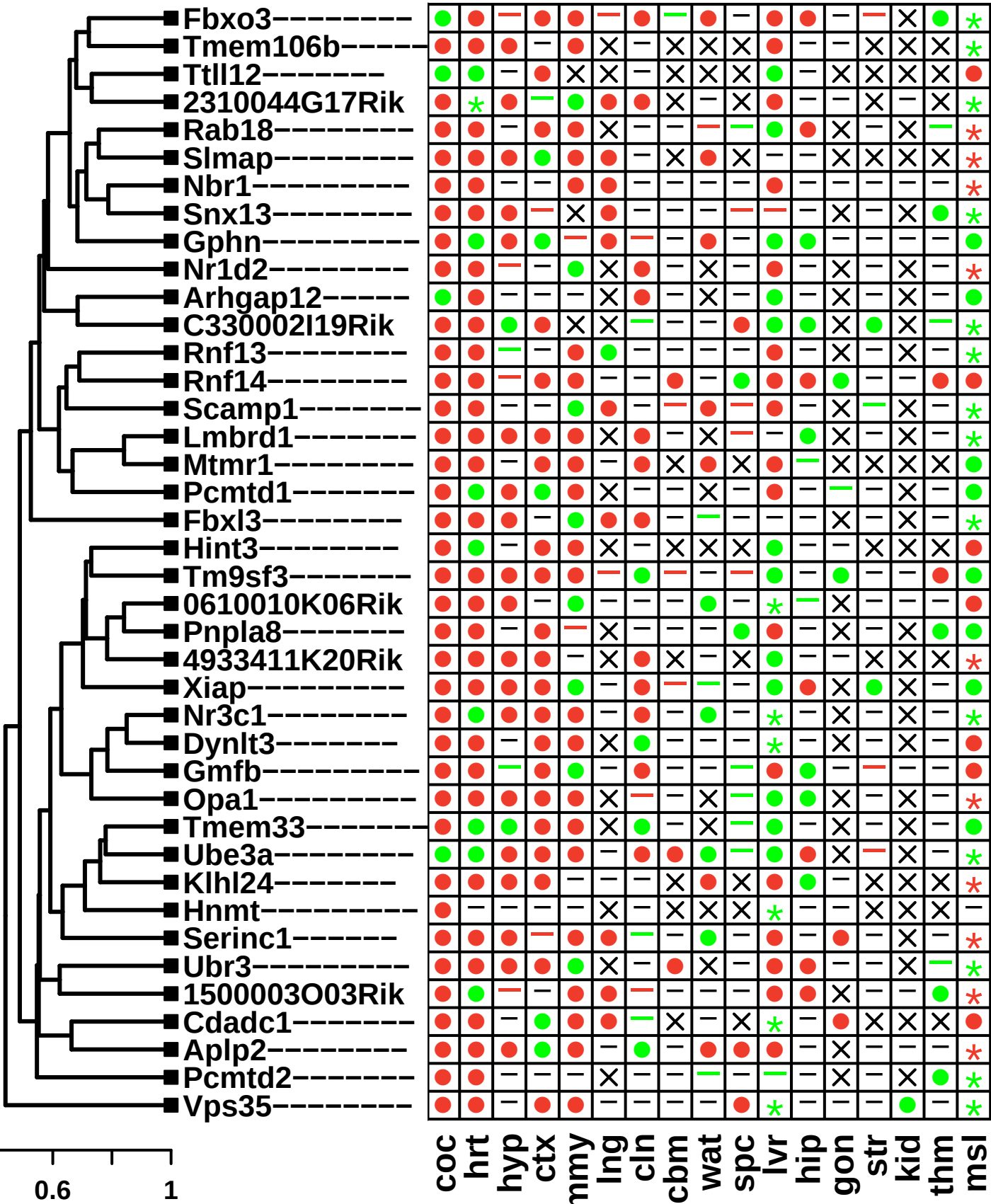
CR-Regulated Modules (40 Genes)

M = 7.61, P = 0



CR-Regulated Modules (40 Genes)

M = 7.37, P = 0

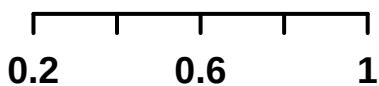


Absolute Correlation

M = 7.3, P = 0

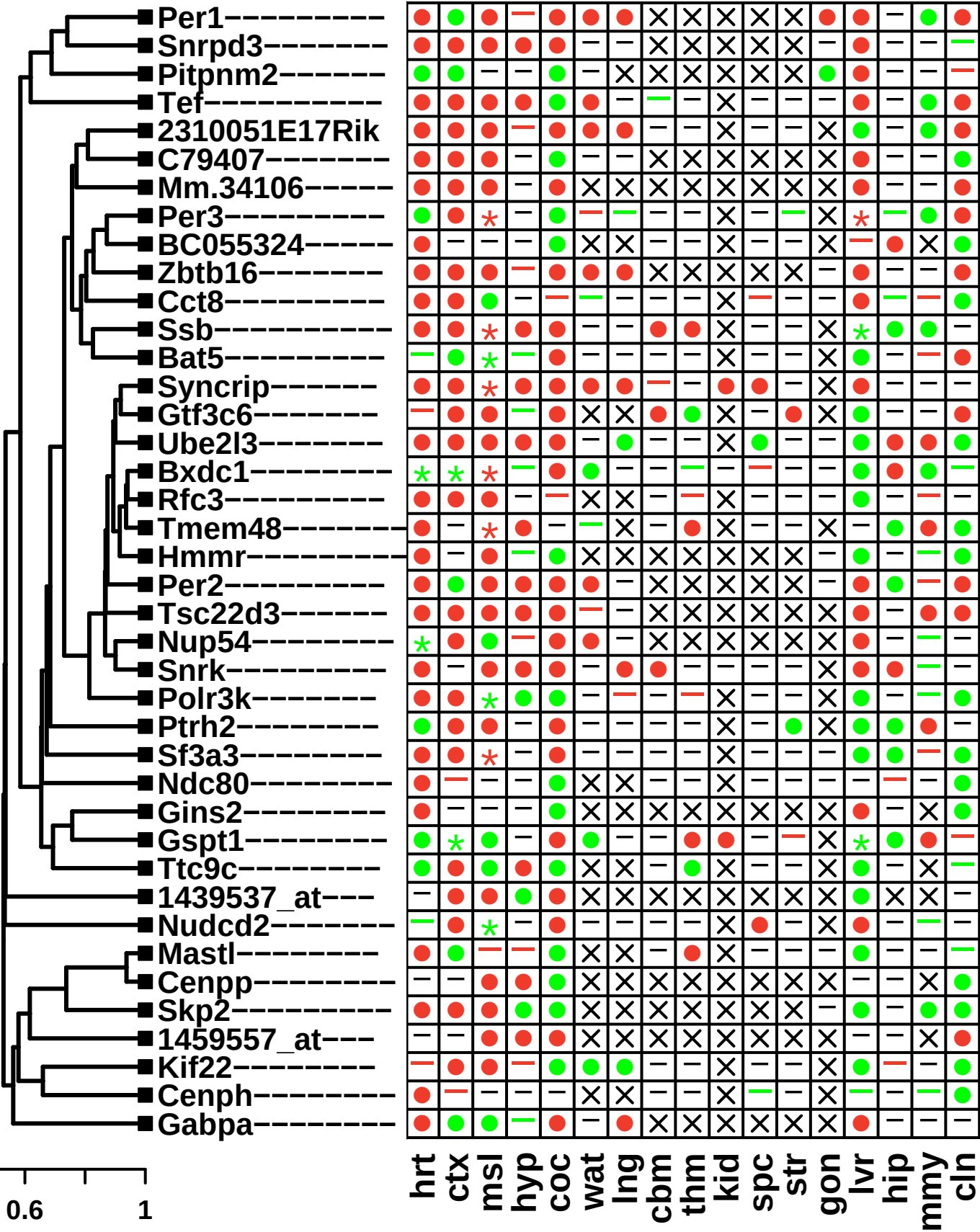


M = 7.21, P = 0

[illegible]

CR-Regulated Modules (40 Genes)

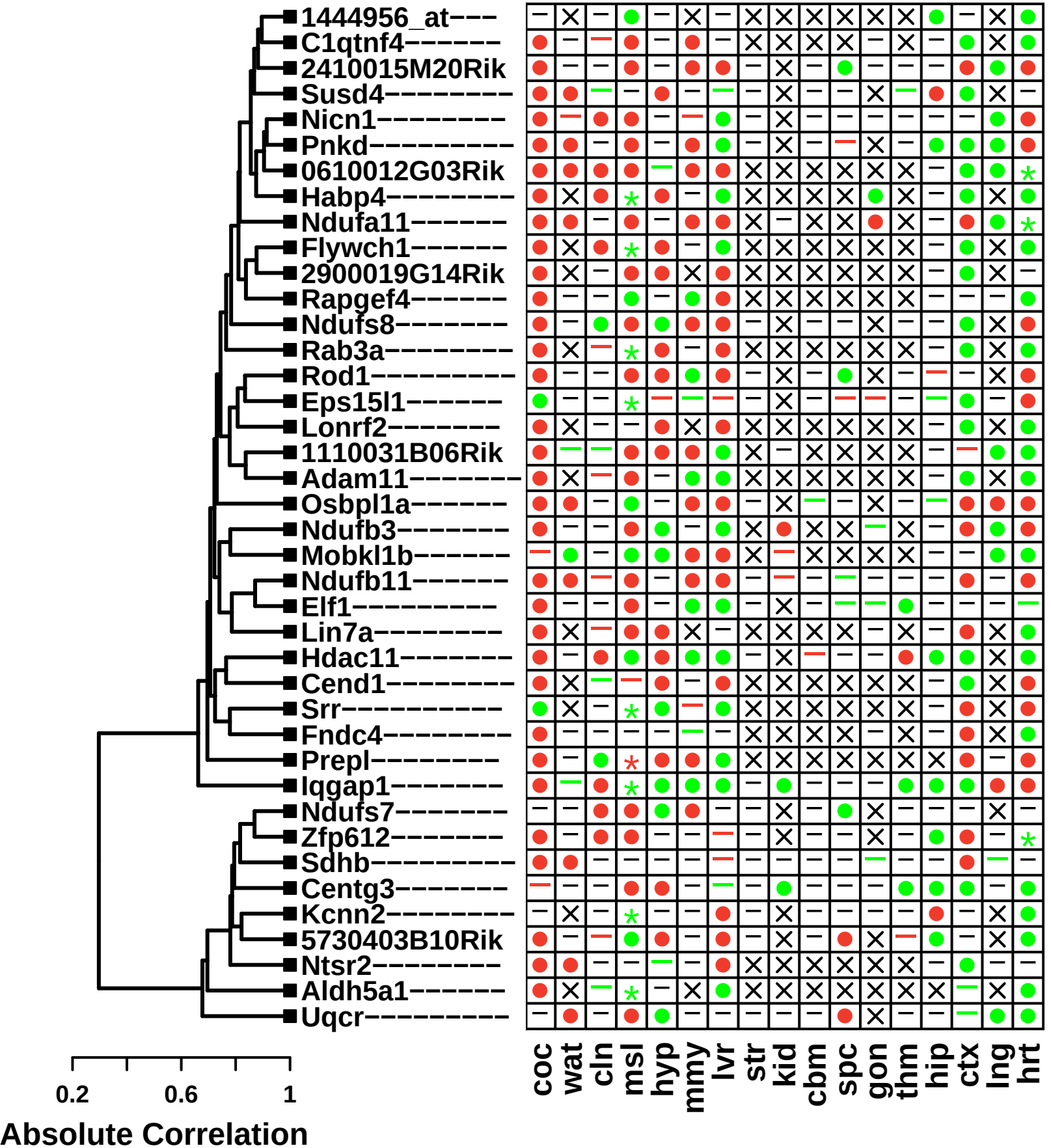
M = 7.19, P = 0



Absolute Correlation

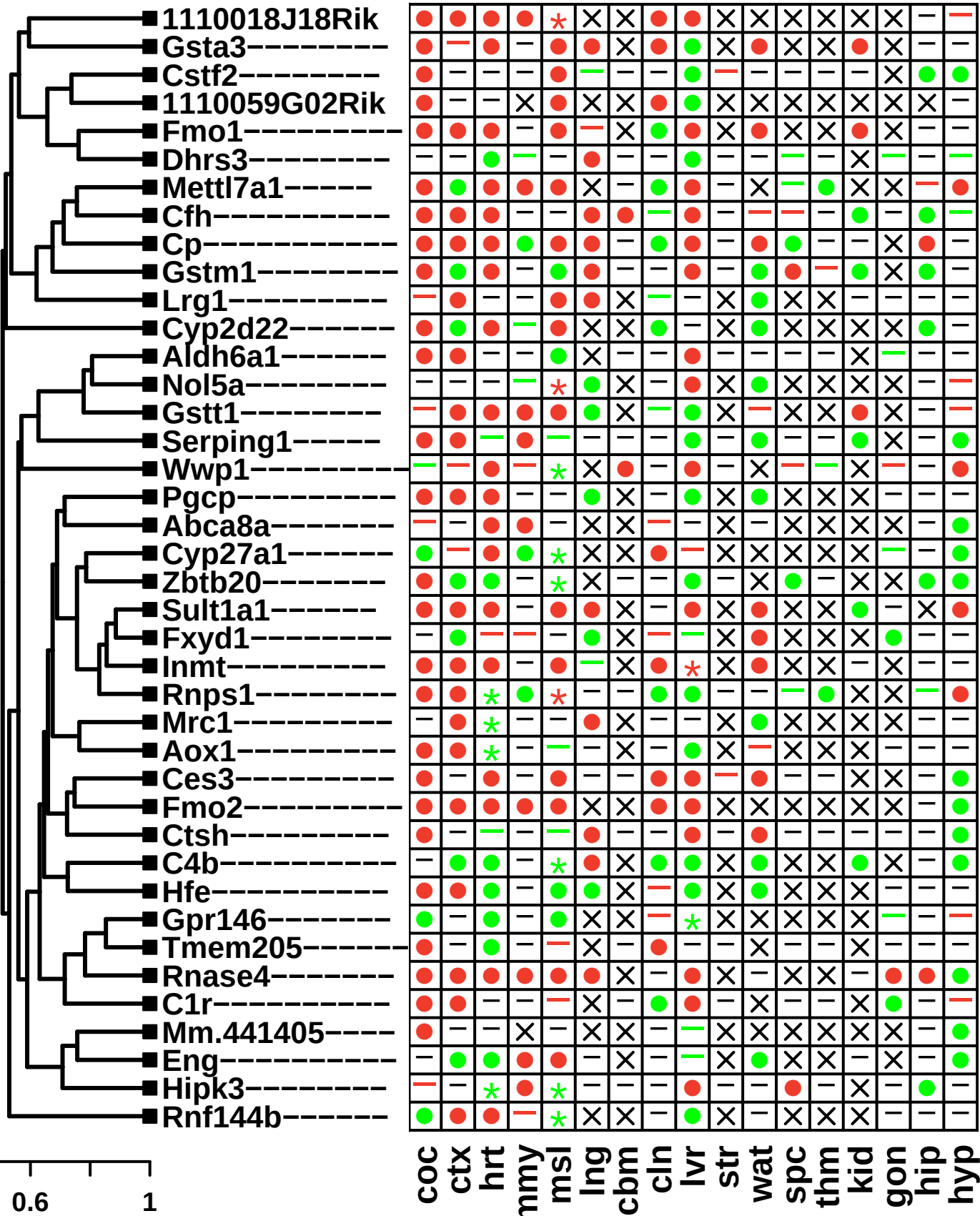
CR-Regulated Modules (40 Genes)

M = 7.14, P = 0



CR-Regulated Modules (40 Genes)

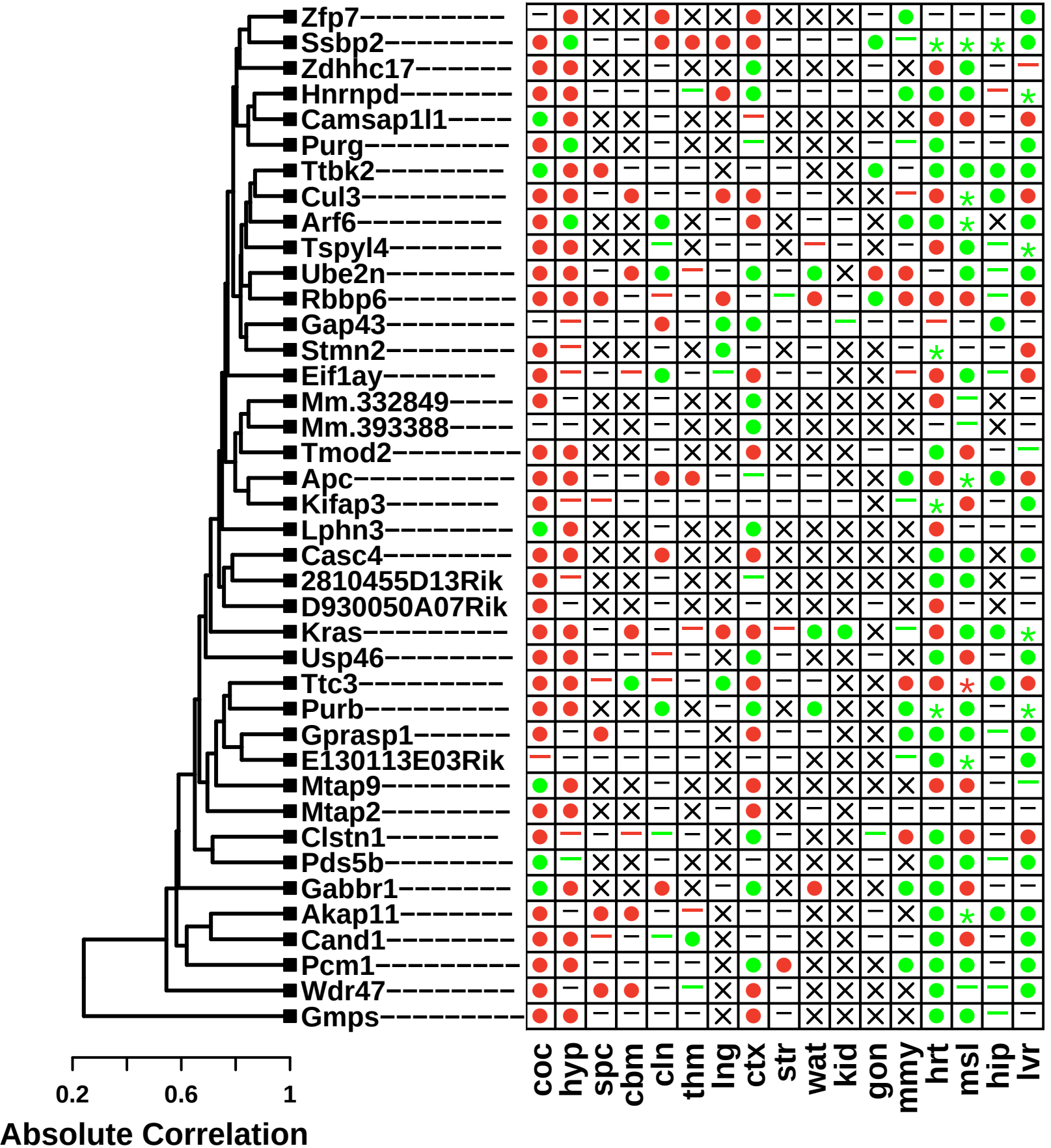
M = 7.14, P = 0



Absolute Correlation

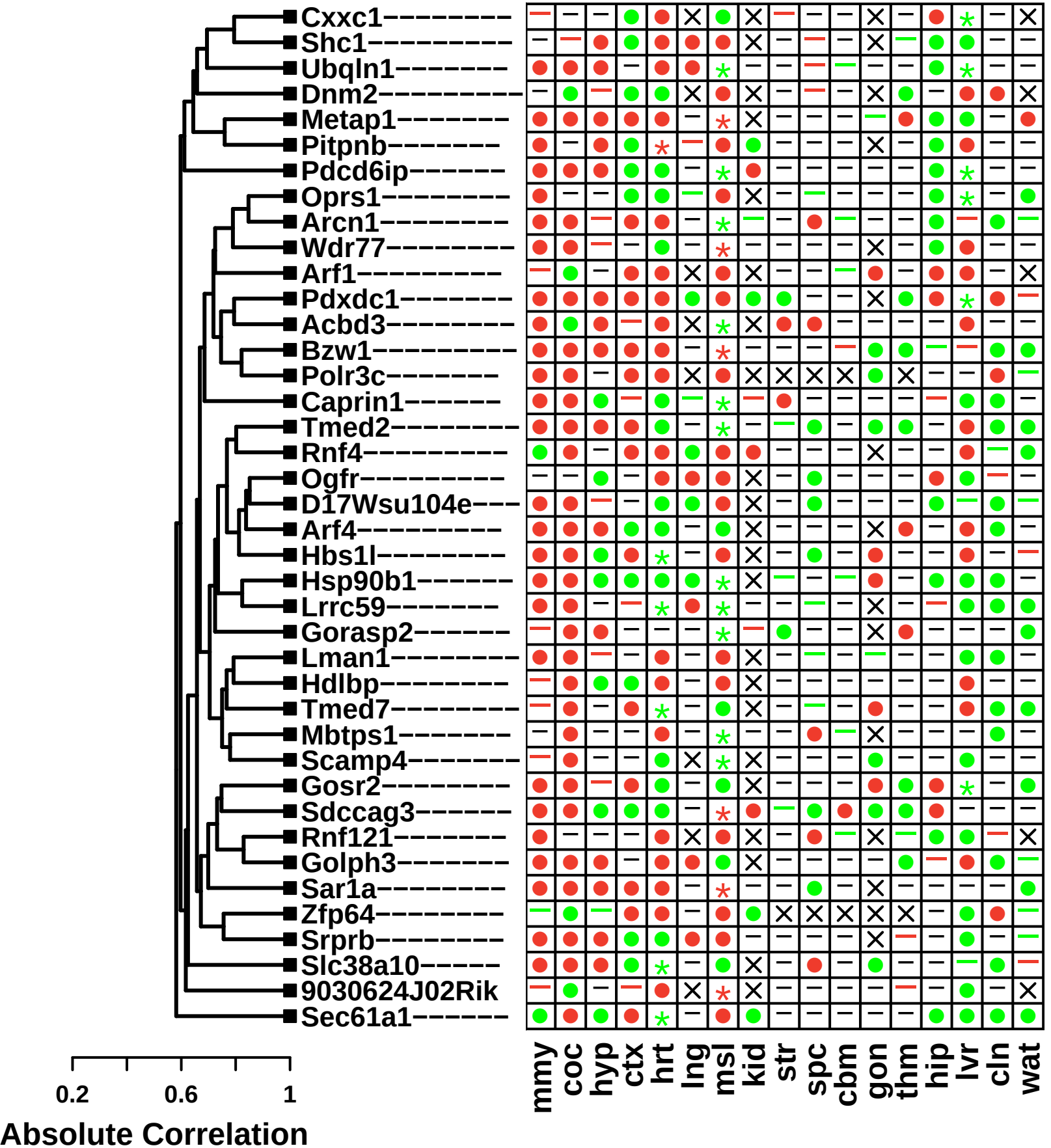
CR-Regulated Modules (40 Genes)

M = 7.01, P = 0



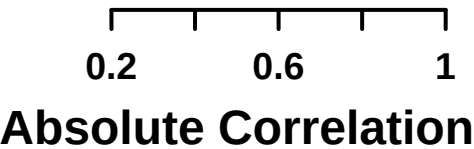
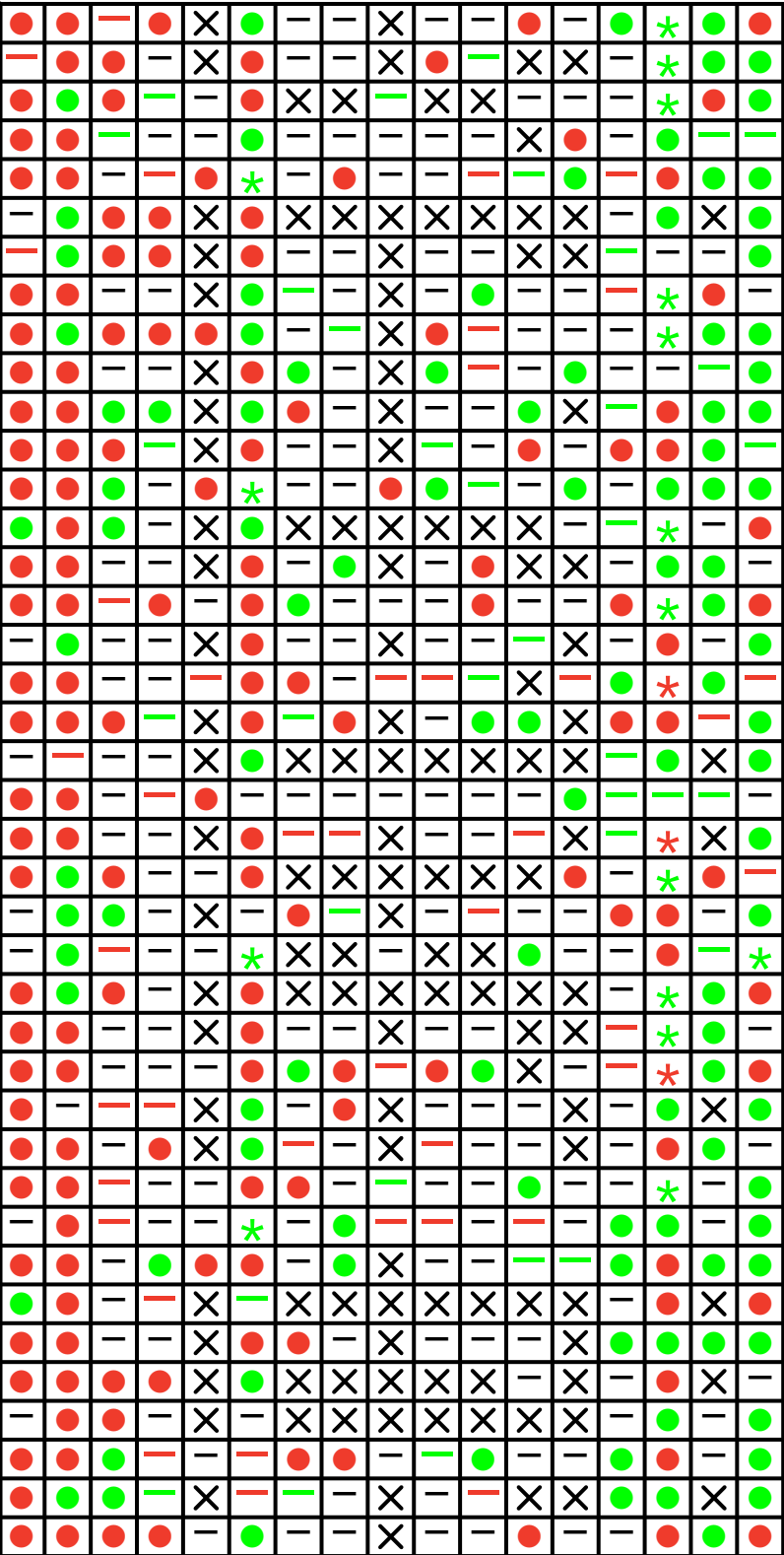
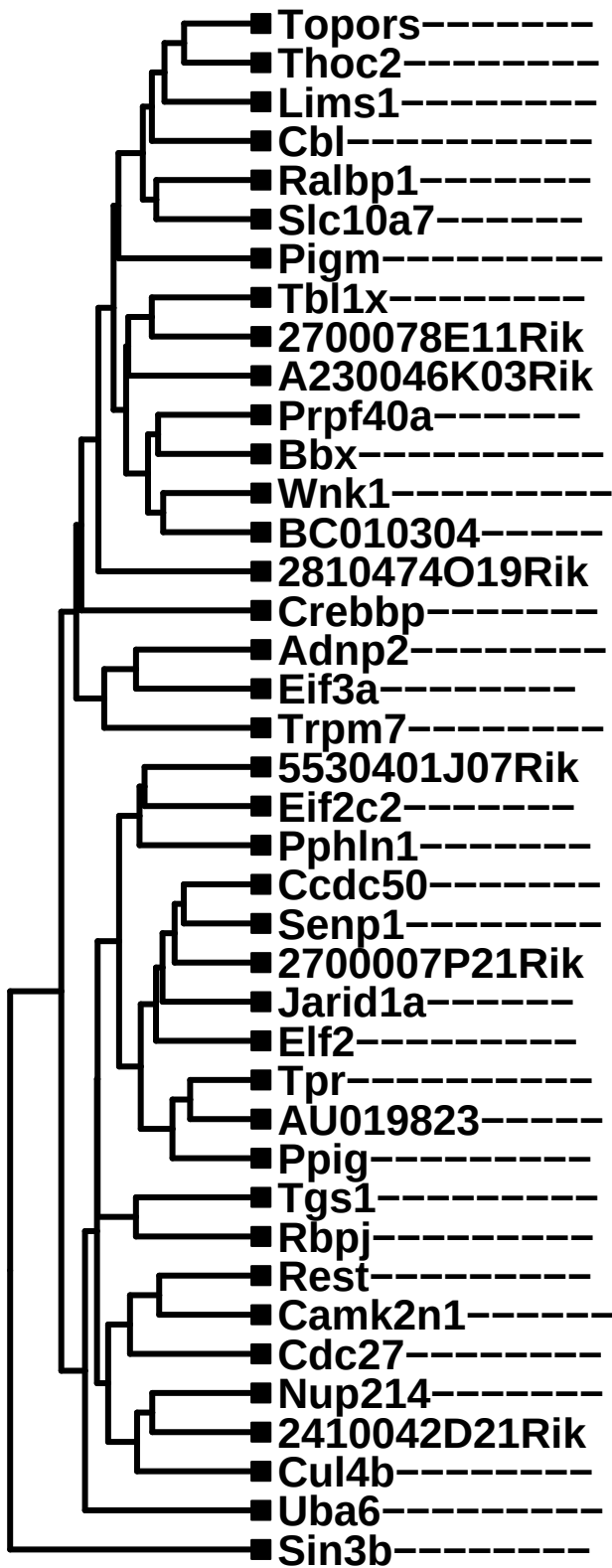
CR-Regulated Modules (40 Genes)

M = 6.96, P = 0



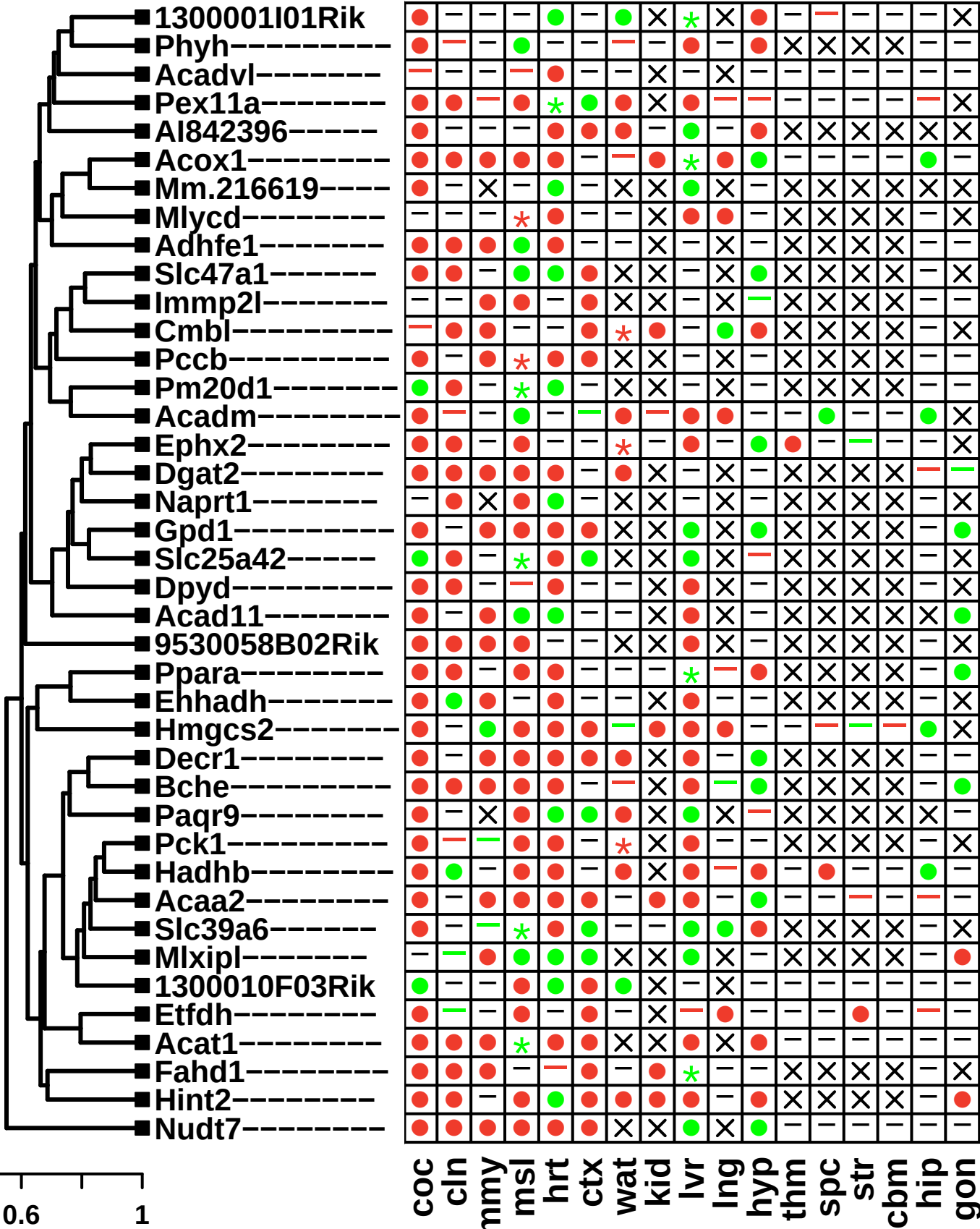
CR-Regulated Modules (40 Genes)

M = 6.96, P = 0



CR-Regulated Modules (40 Genes)

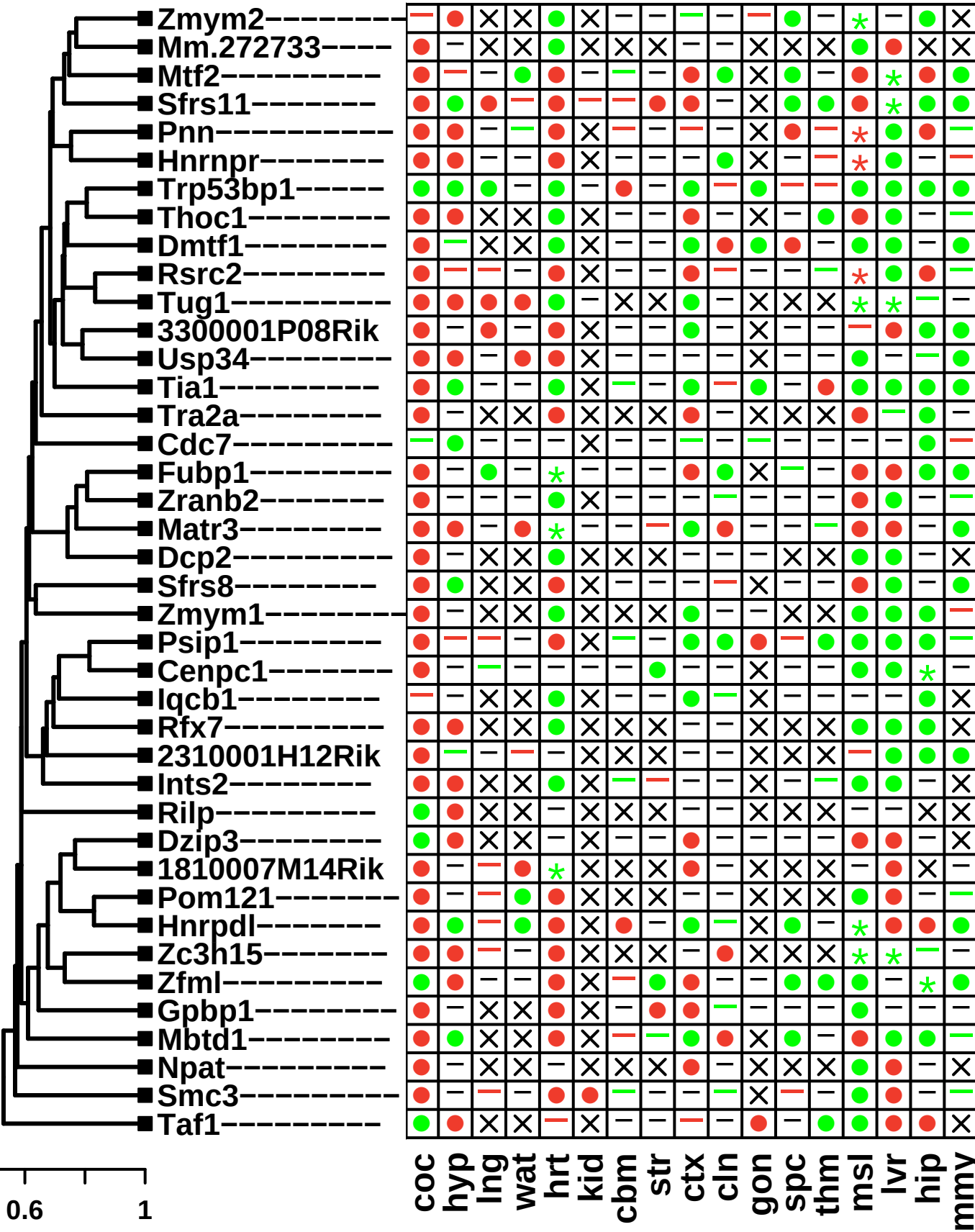
M = 6.94, P = 0



Absolute Correlation

CR-Regulated Modules (40 Genes)

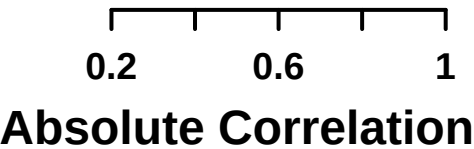
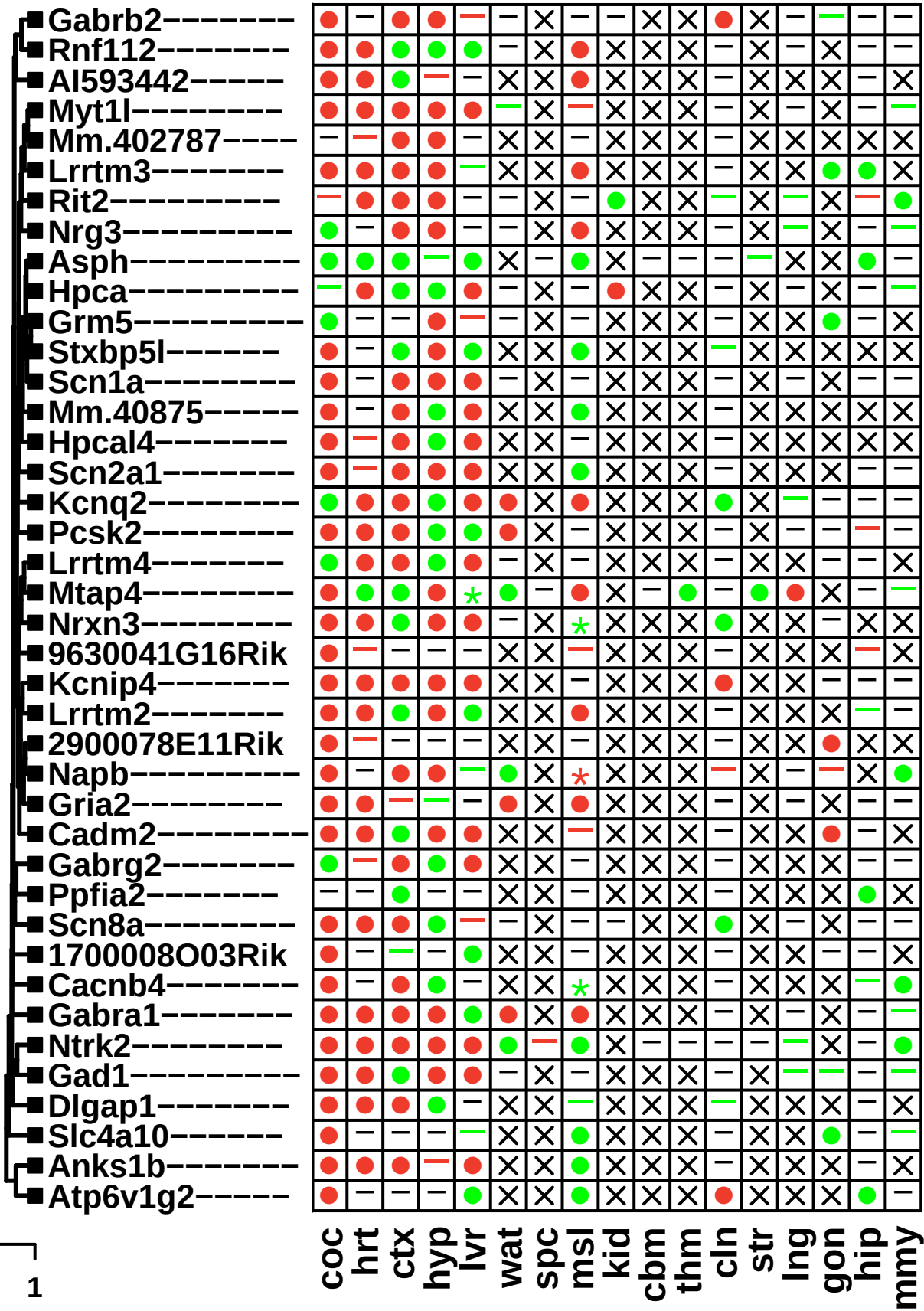
M = 6.91, P = 0



Absolute Correlation

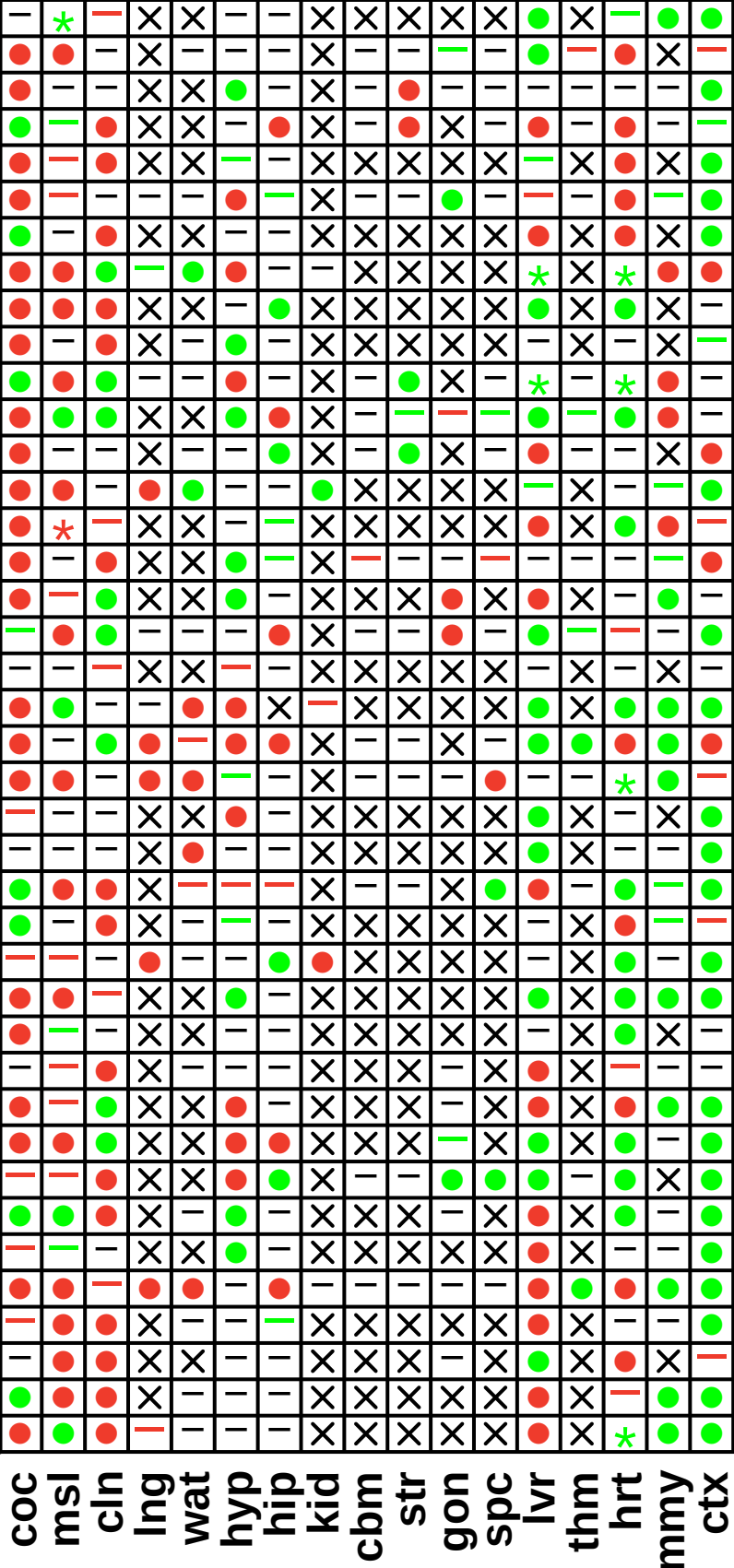
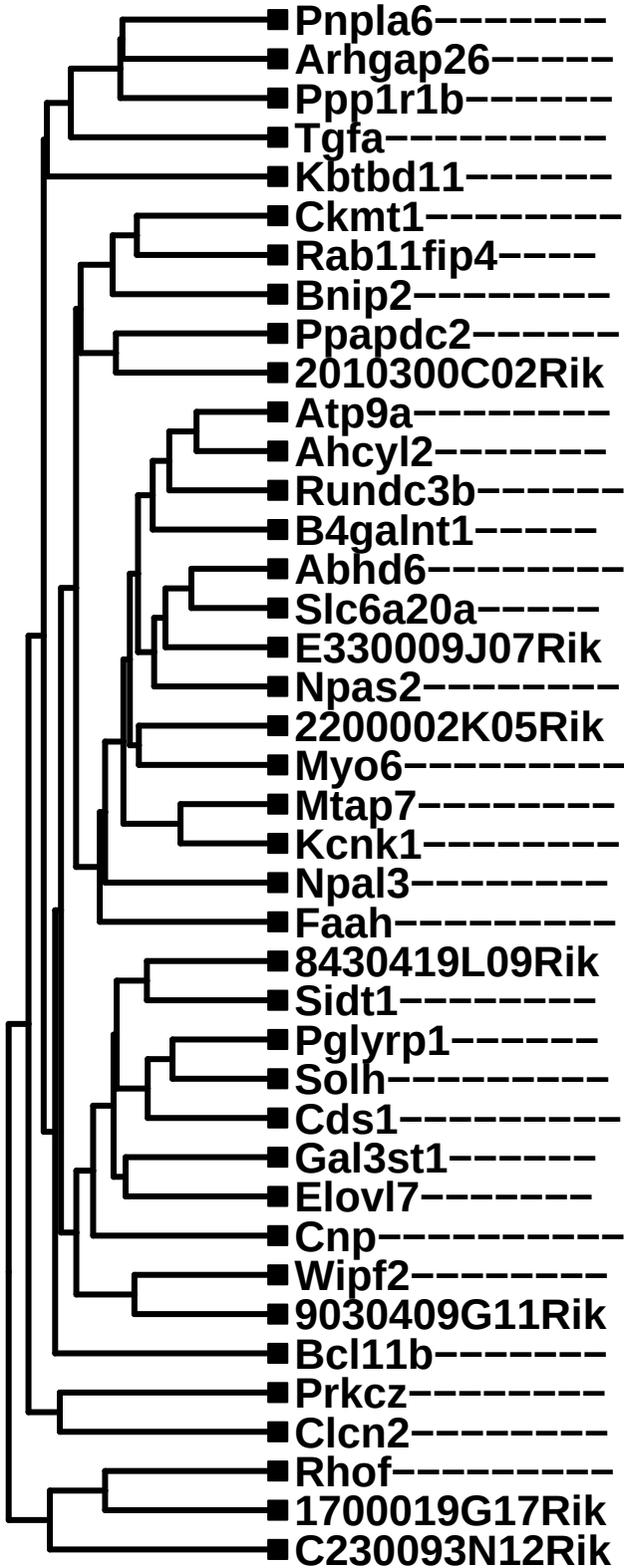
CR-Regulated Modules (40 Genes)

M = 6.9, P = 0



CR-Regulated Modules (40 Genes)

M = 6.86, P = 0

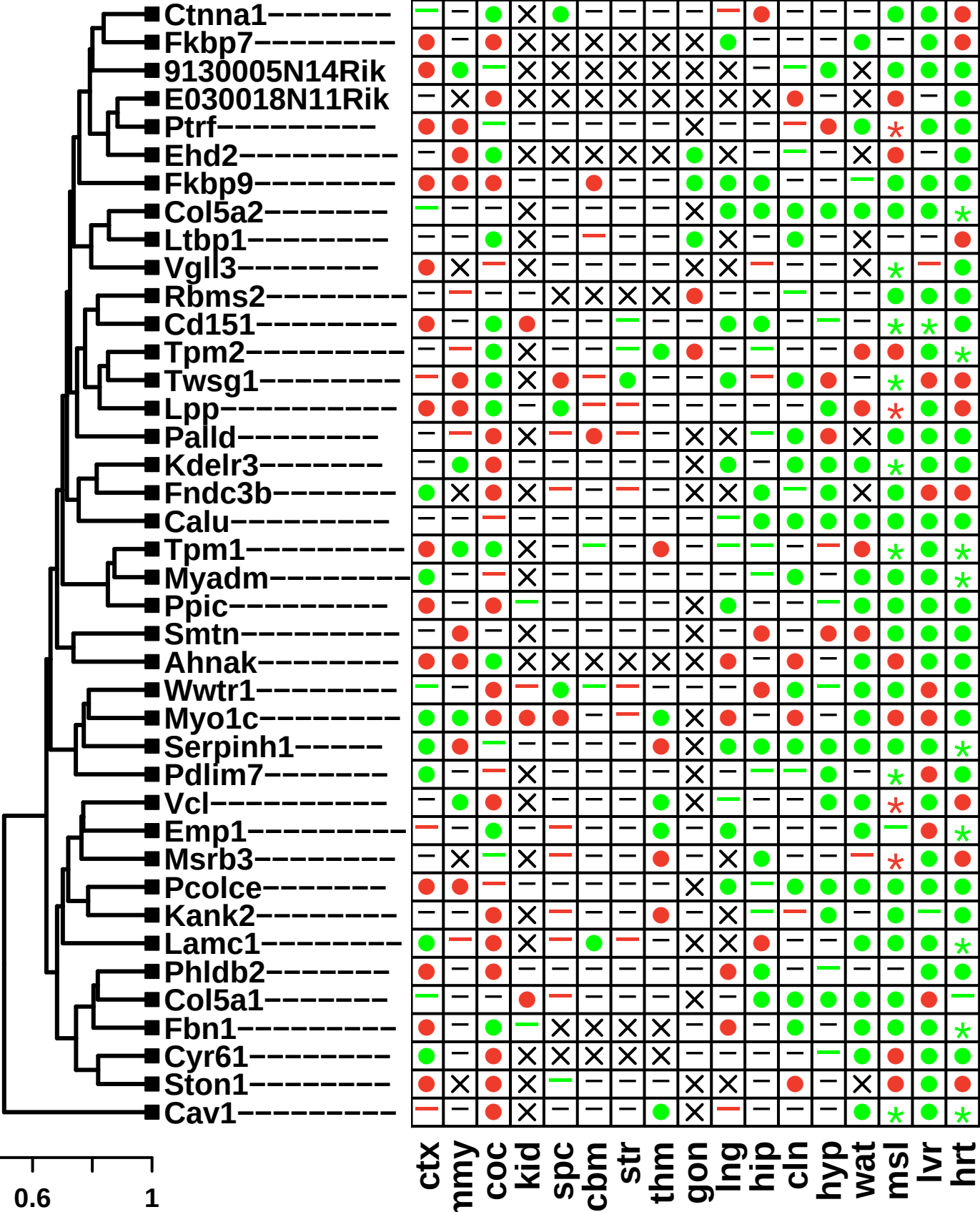


0.2 0.6 1

Absolute Correlation

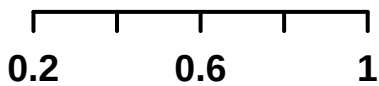
CR-Regulated Modules (40 Genes)

M = 6.83, P = 0



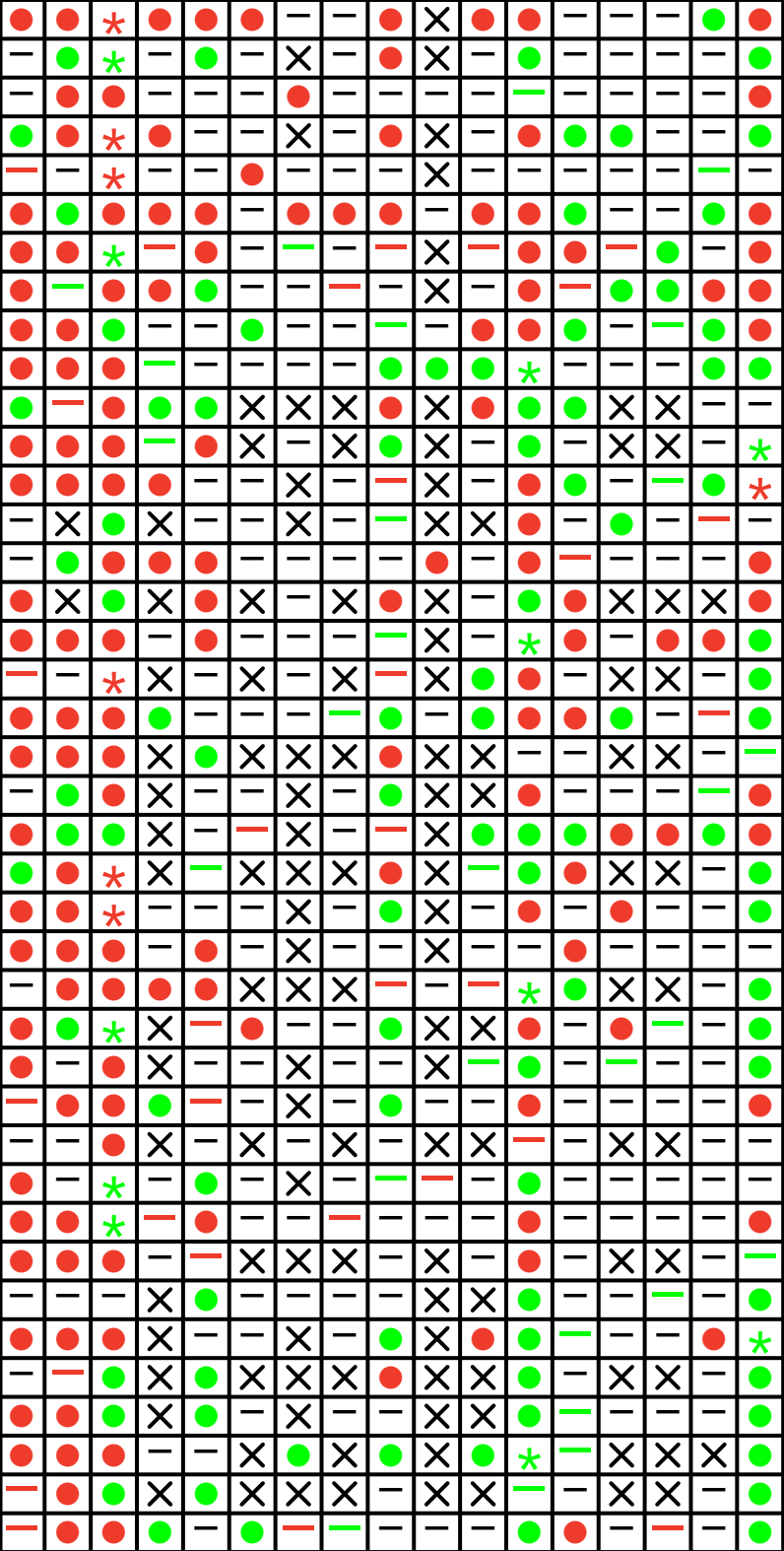
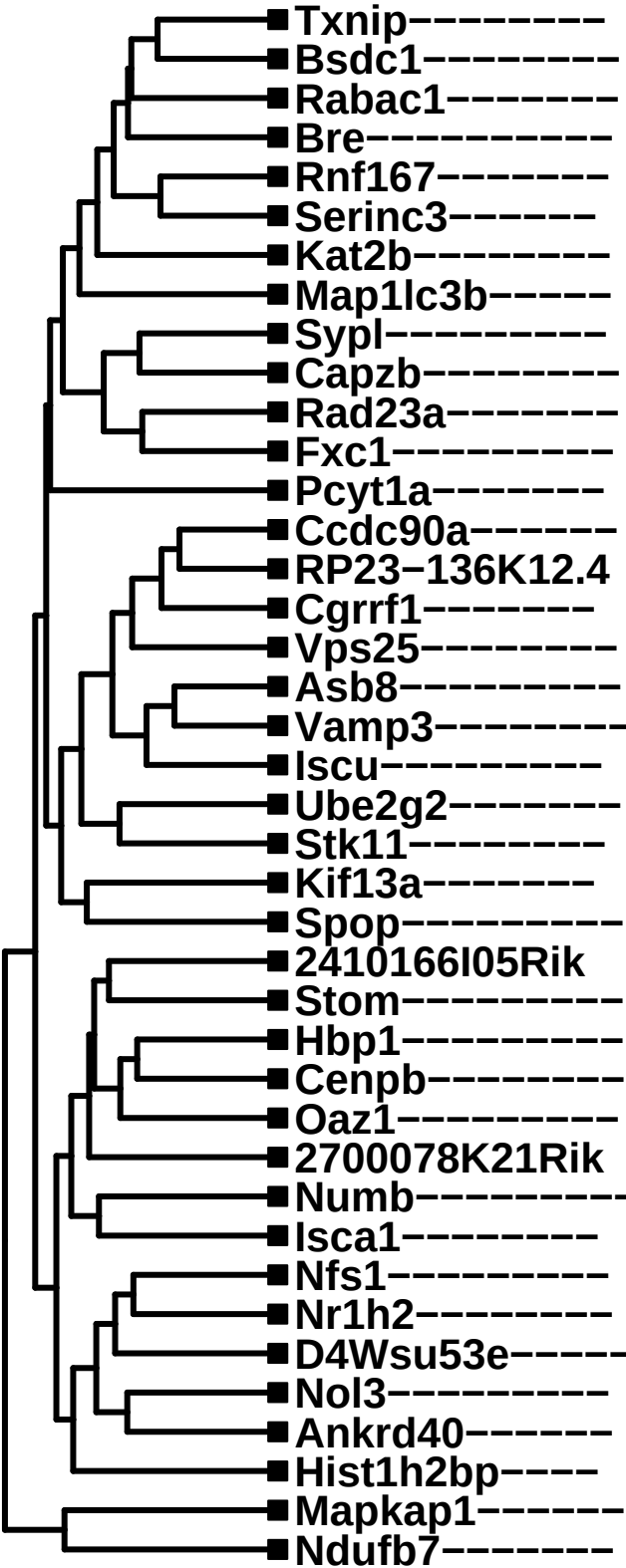
Absolute Correlation

M = 6.78, P = 0

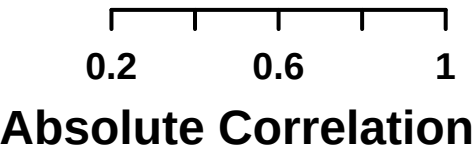
[illegible]

CR-Regulated Modules (40 Genes)

M = 6.76, P = 0

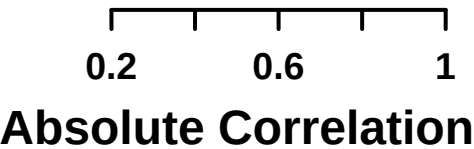
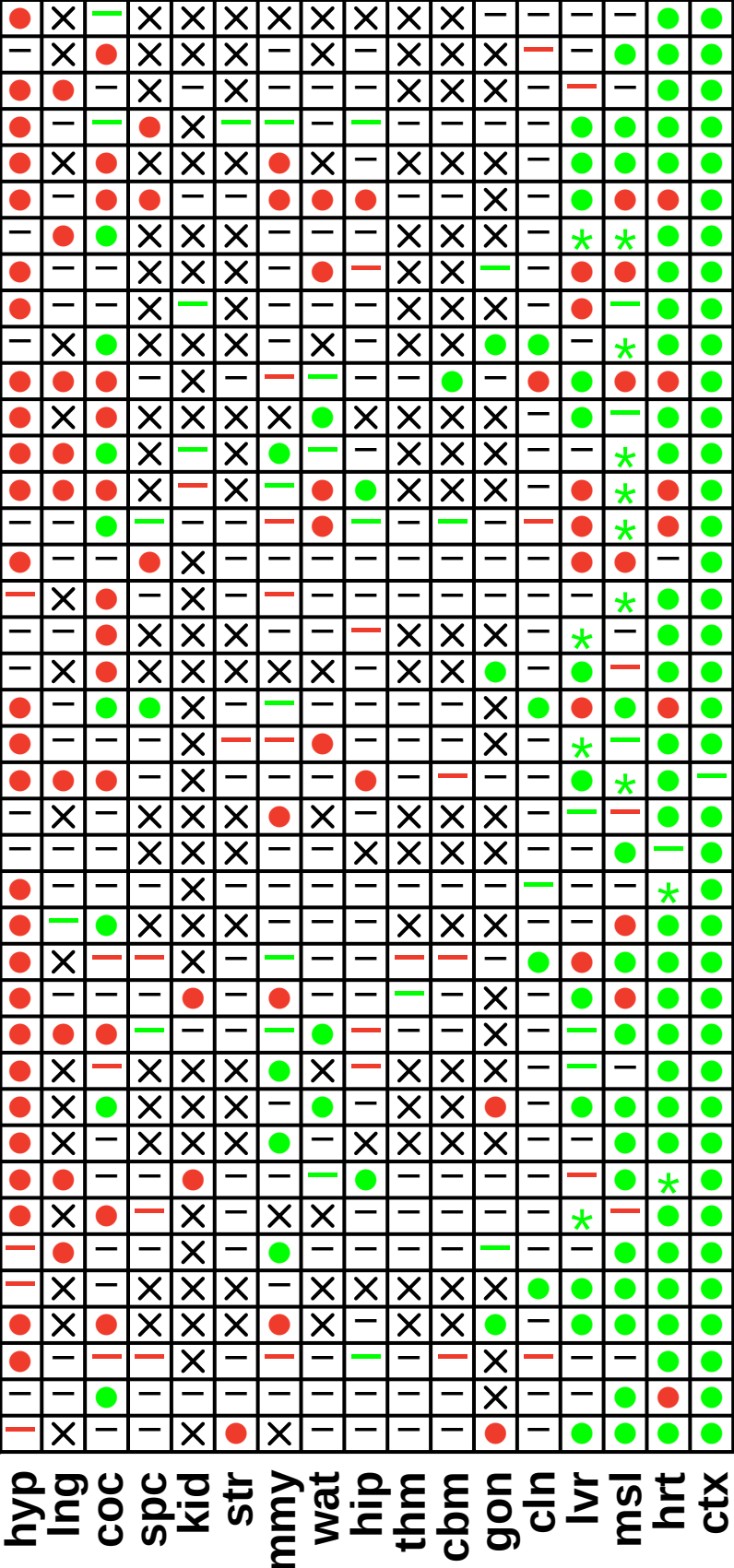
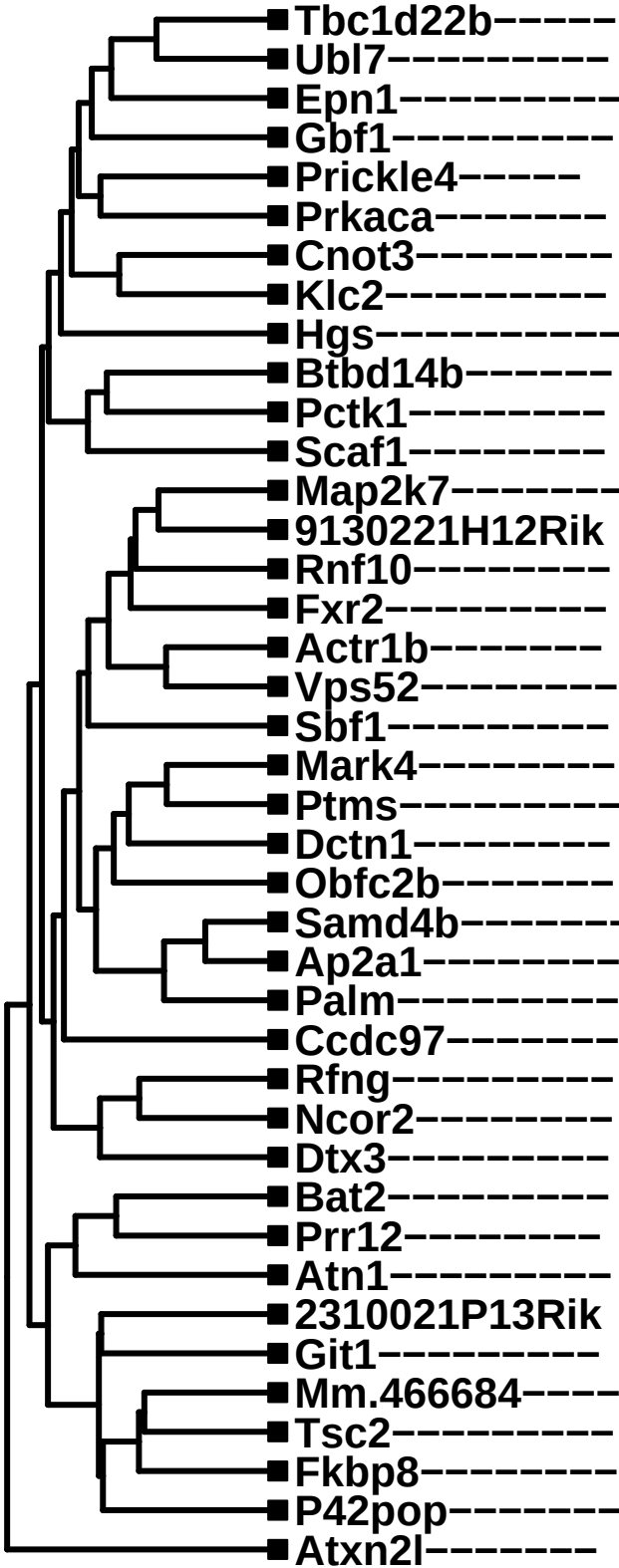


coc
mmy
msl
lng
ctx
spc
gon
cbm
hyp
kid
wat
hrt
cln
thm
str
hip
lvr



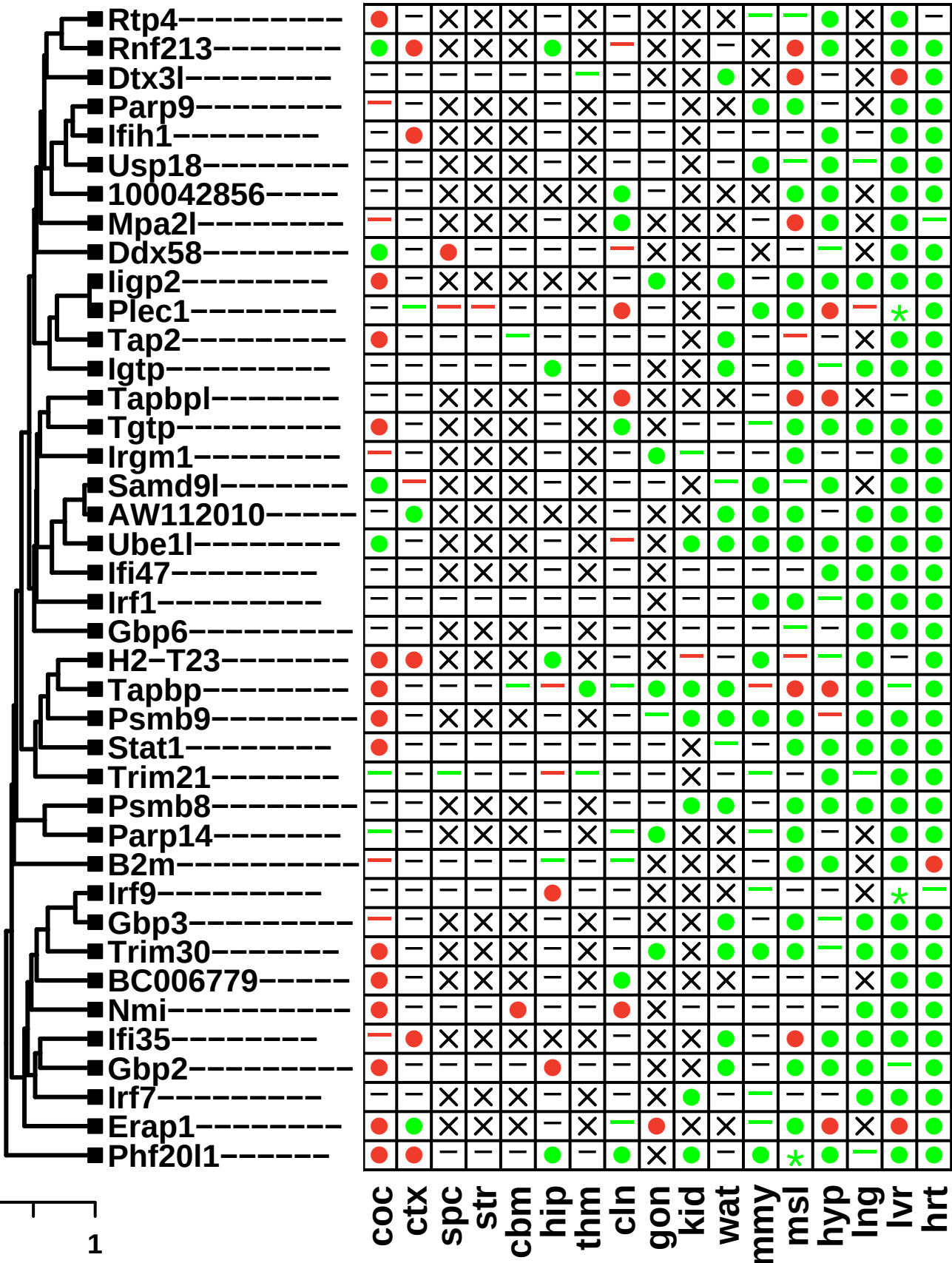
CR-Regulated Modules (40 Genes)

M = 6.65, P = 5e-04



CR-Regulated Modules (40 Genes)

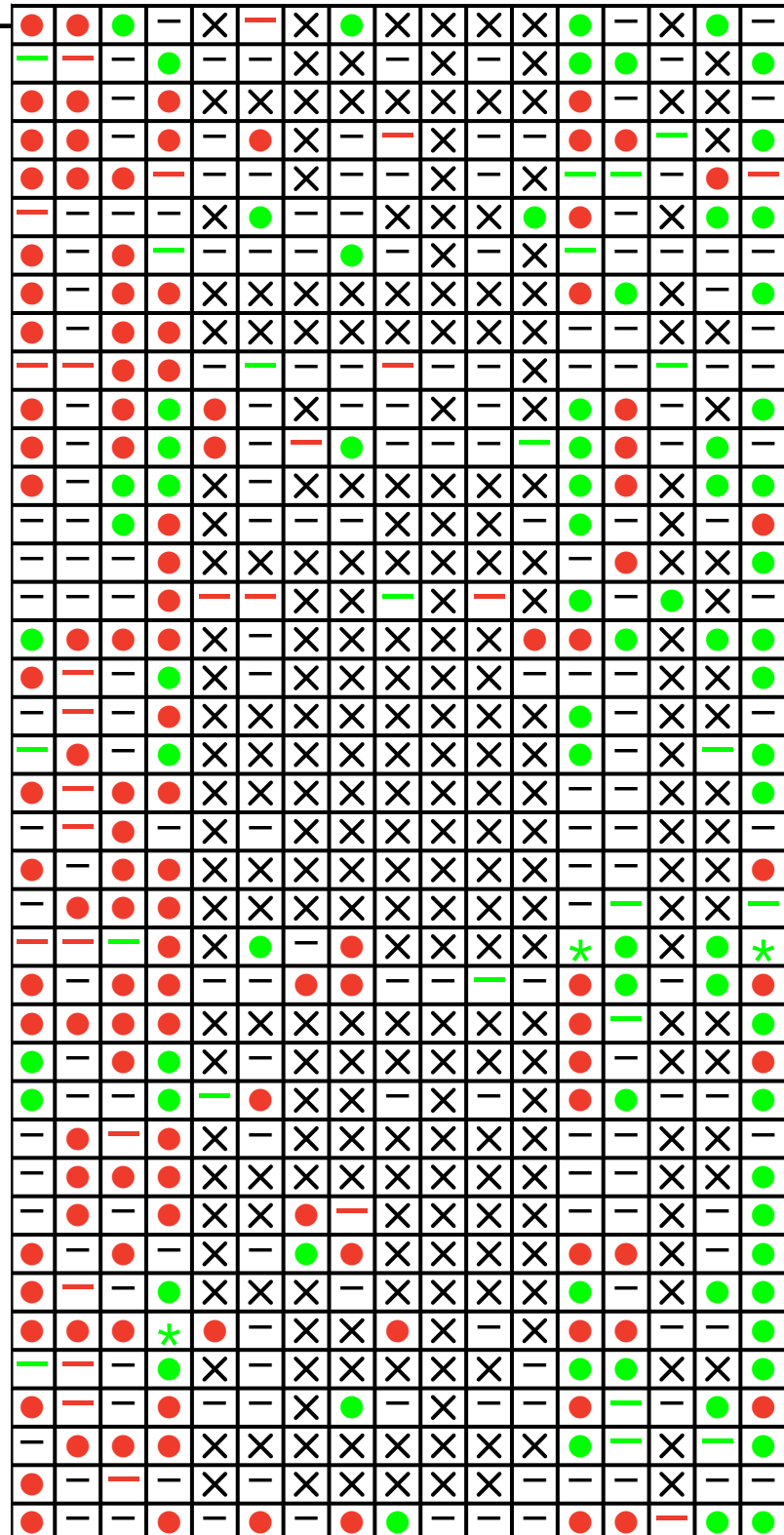
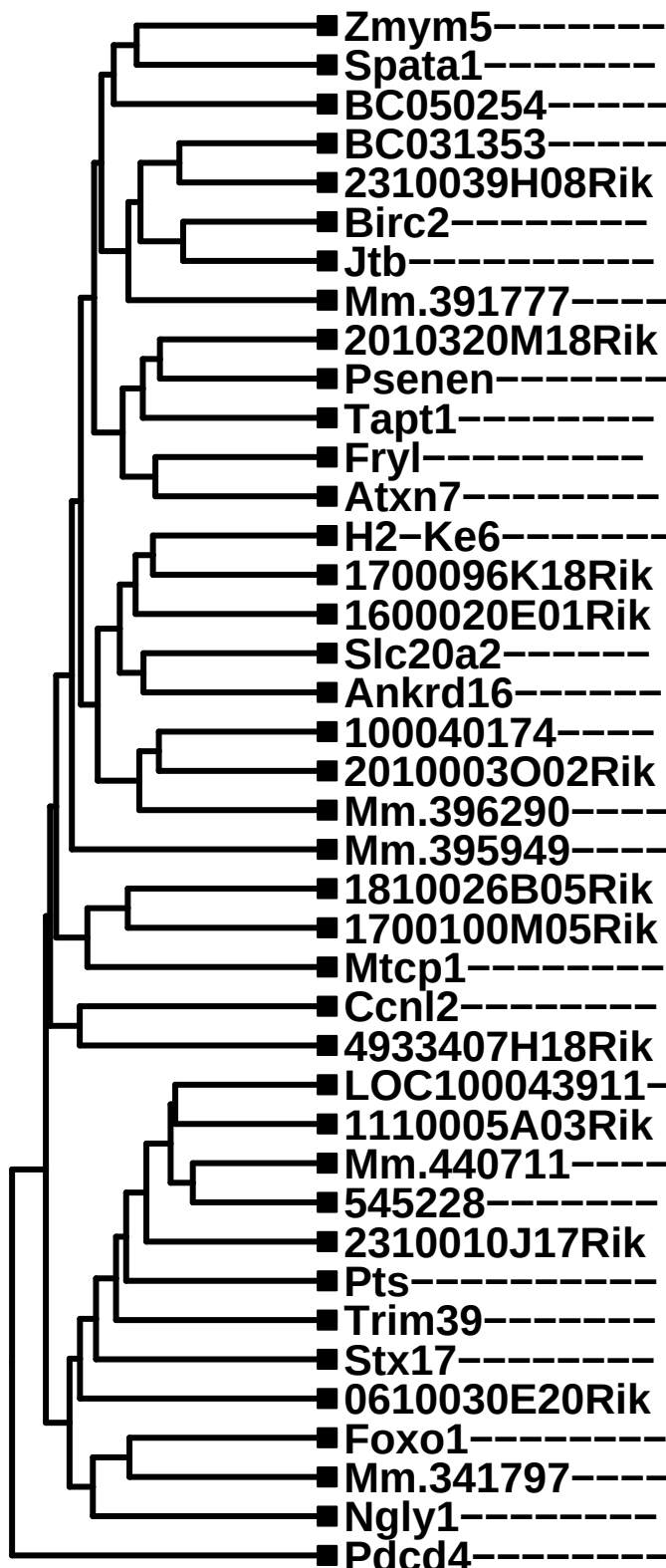
M = 6.62, P = 0.001



Absolute Correlation

CR-Regulated Modules (40 Genes)

M = 6.57, P = 0.003

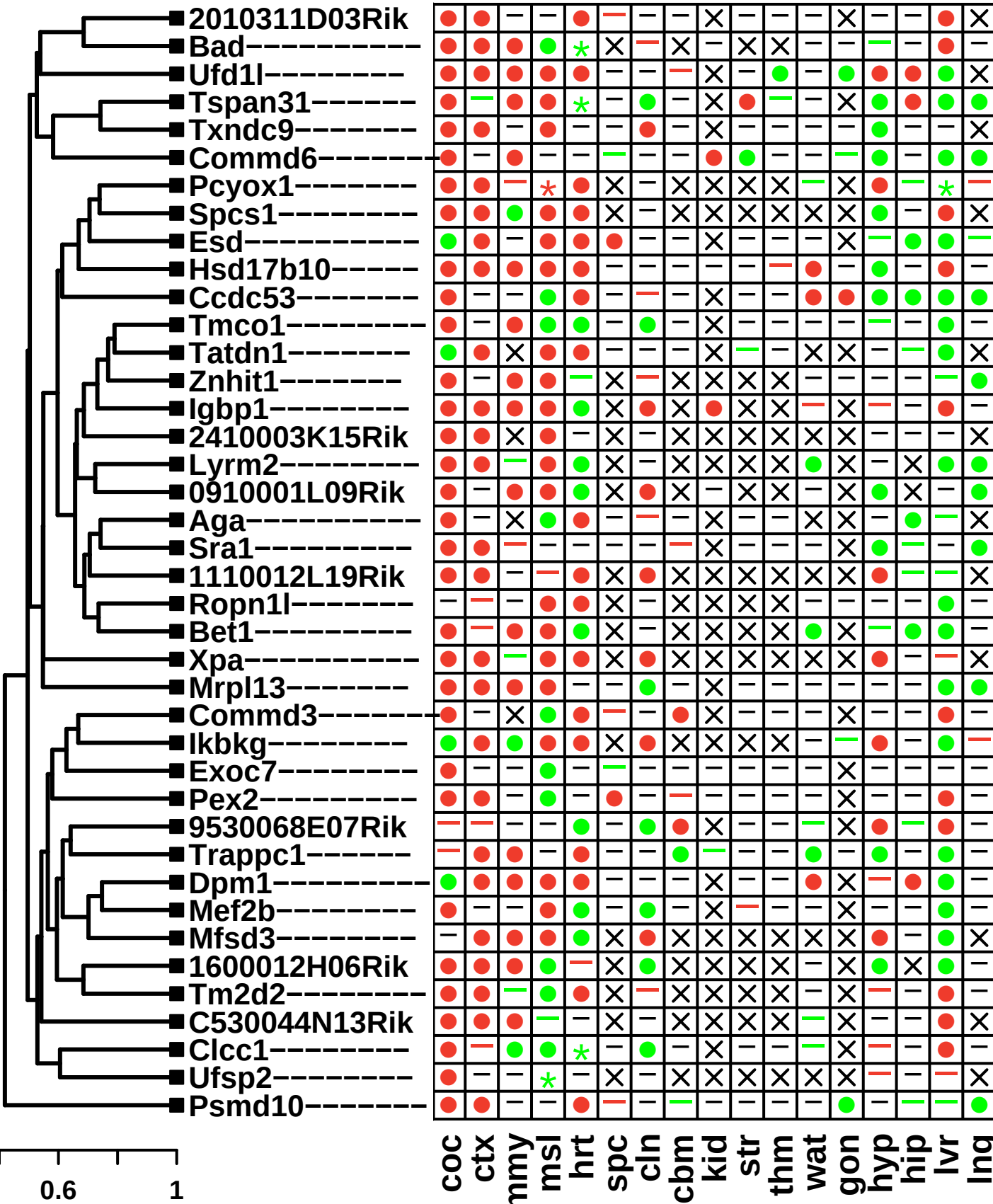


0.2 0.6 1

Absolute Correlation

CR-Regulated Modules (40 Genes)

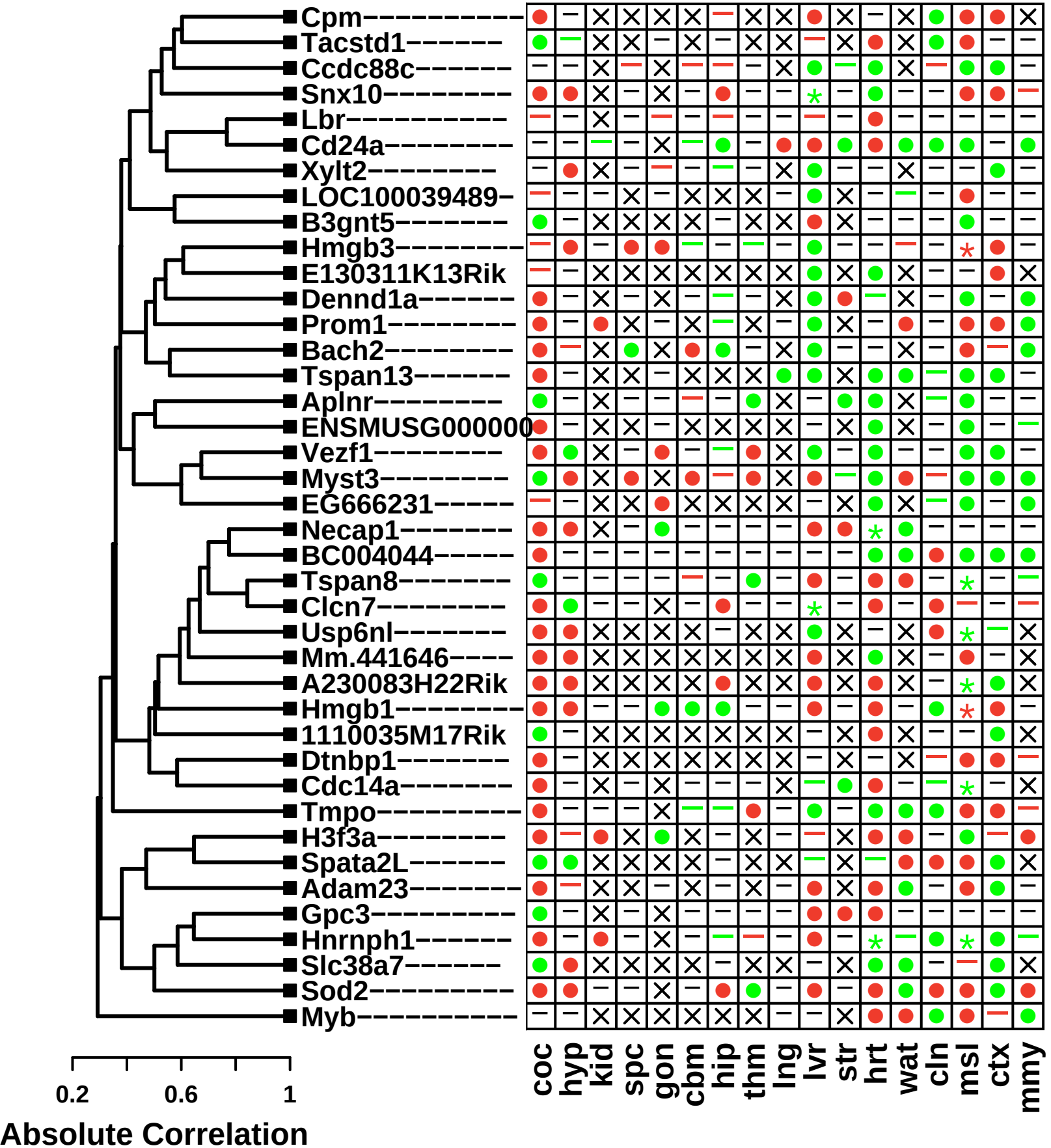
M = 6.54, P = 0.0055



Absolute Correlation

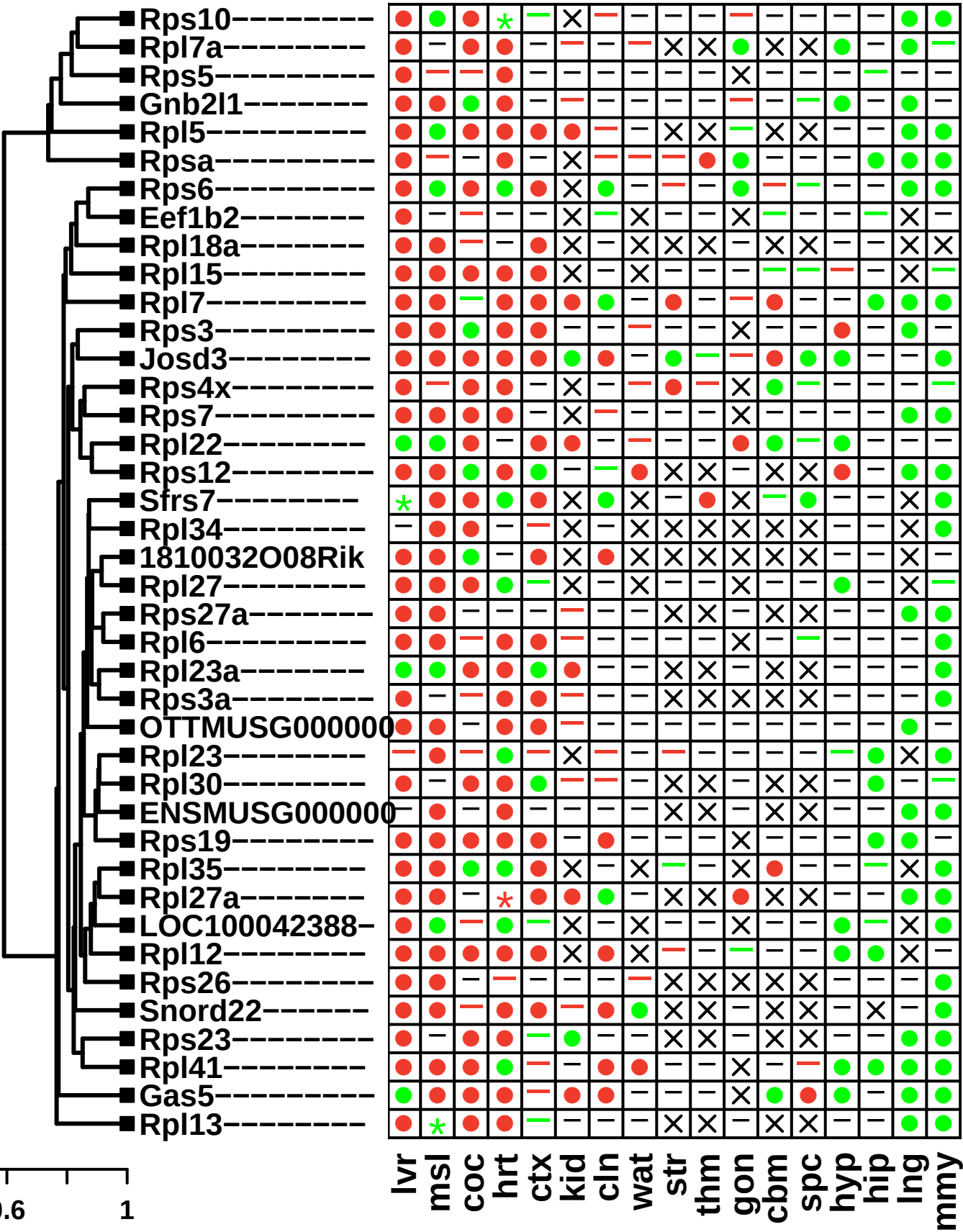
CR-Regulated Modules (40 Genes)

M = 6.53, P = 0.007



CR-Regulated Modules (40 Genes)

M = 6.53, P = 0.007



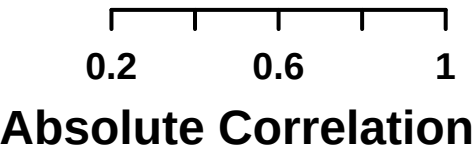
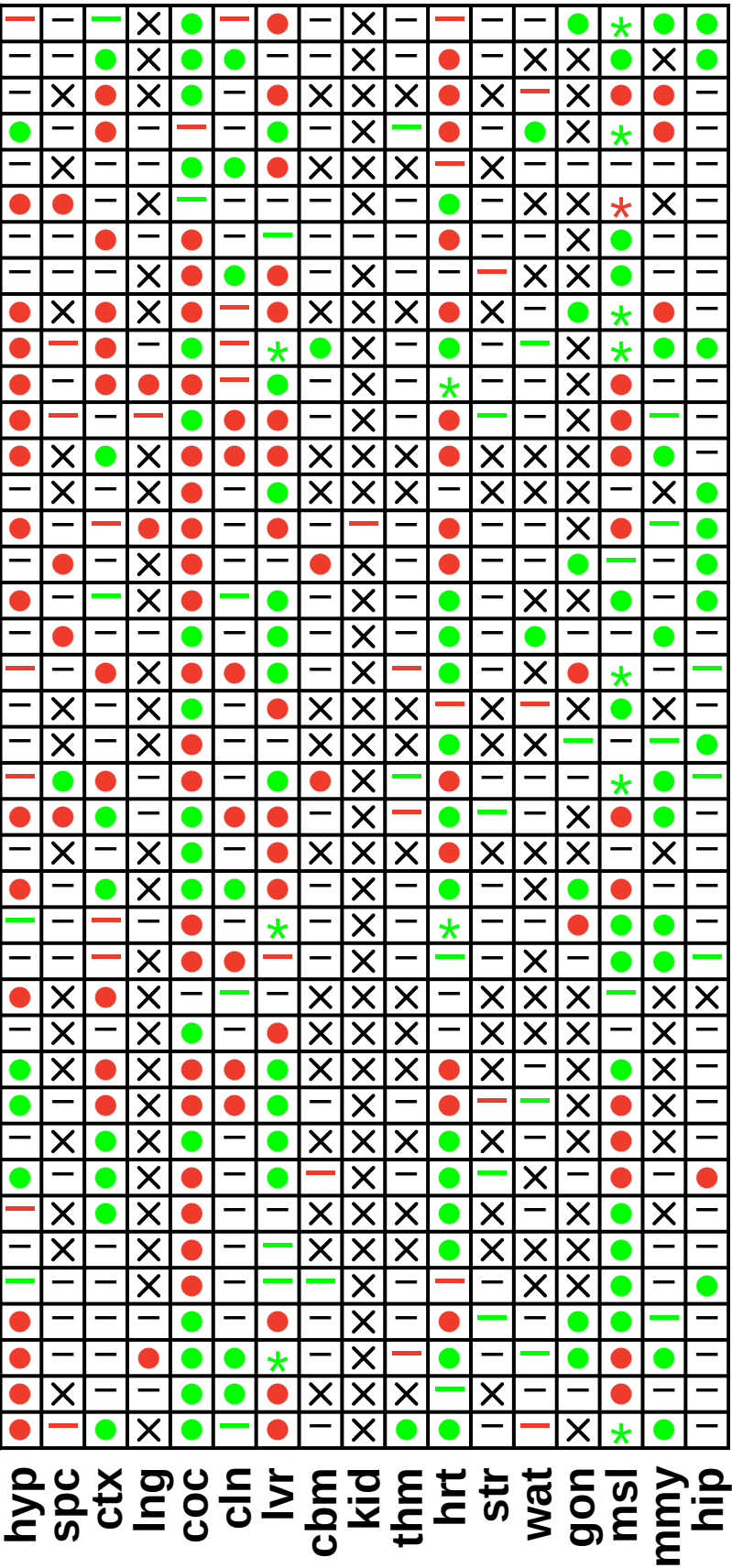
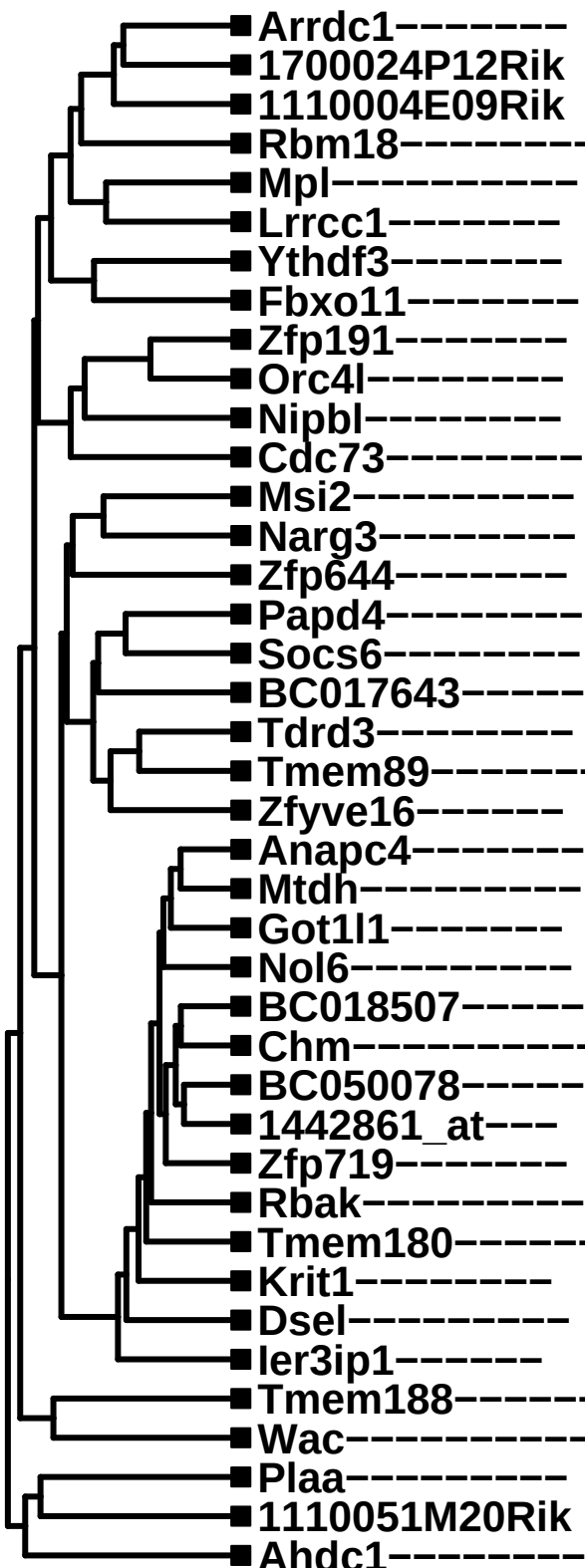
Absolute Correlation

M = 6.5, P = 0.014



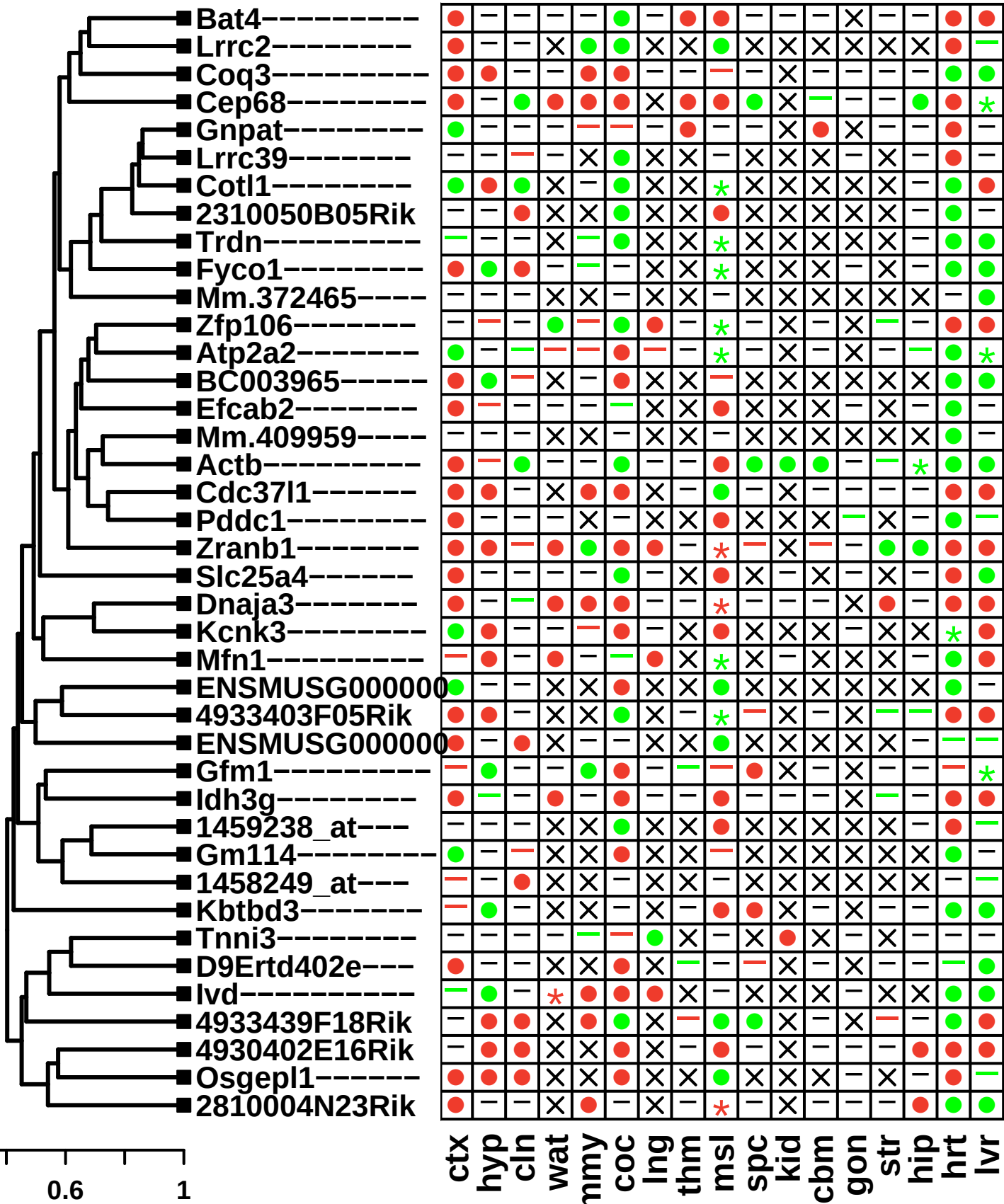
CR-Regulated Modules (40 Genes)

M = 6.48, P = 0.021



CR-Regulated Modules (40 Genes)

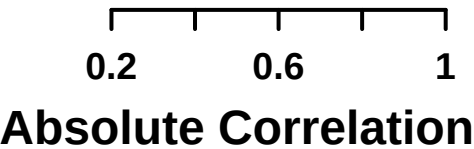
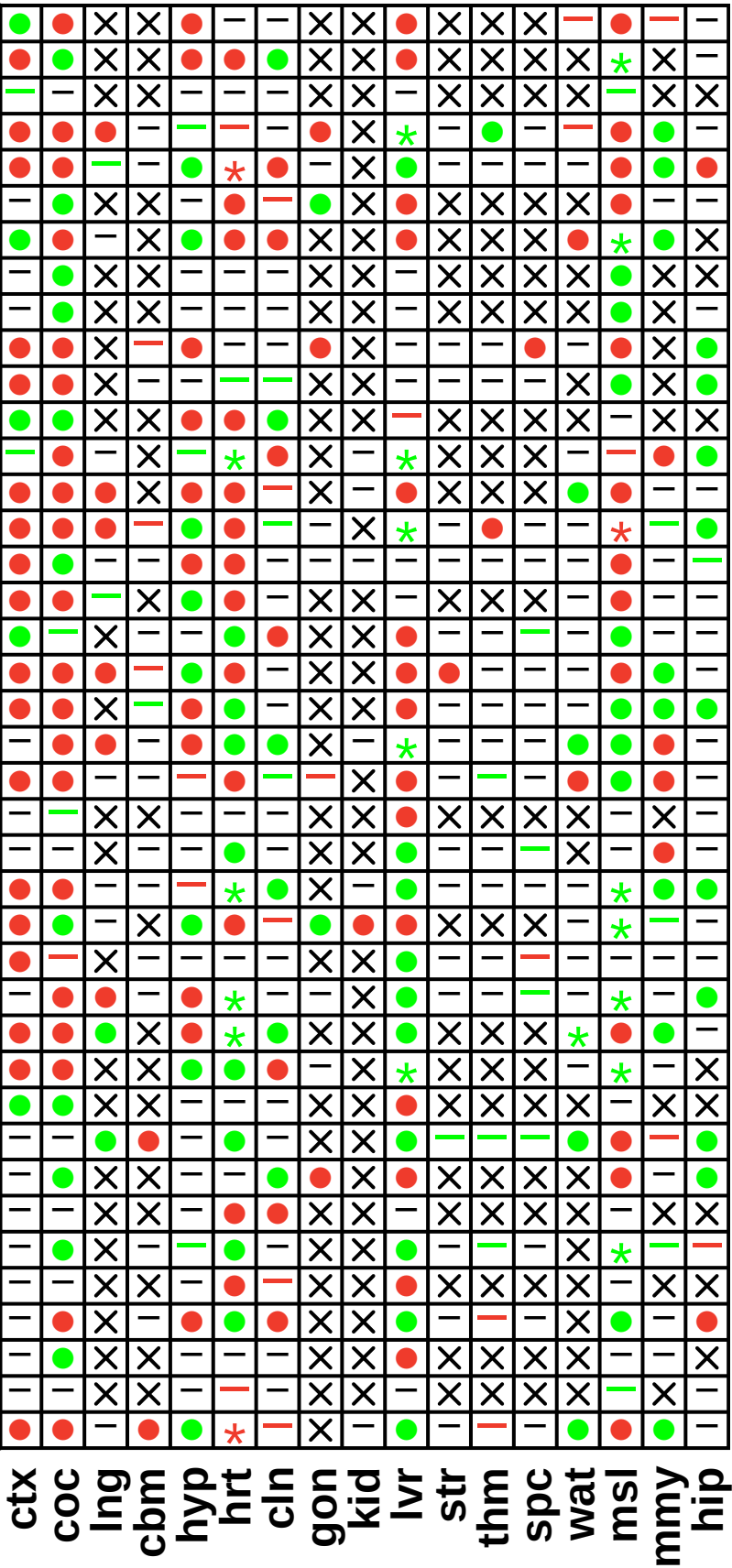
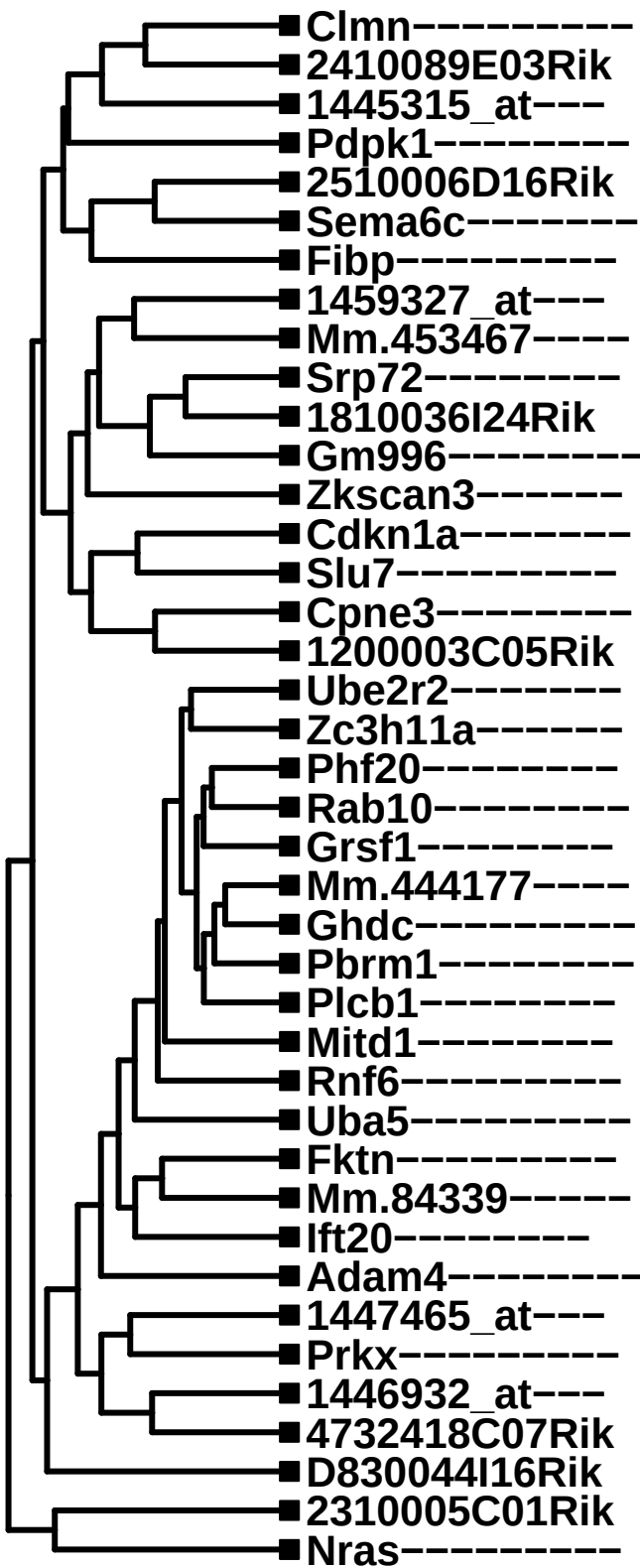
M = 6.47, P = 0.022



Absolute Correlation

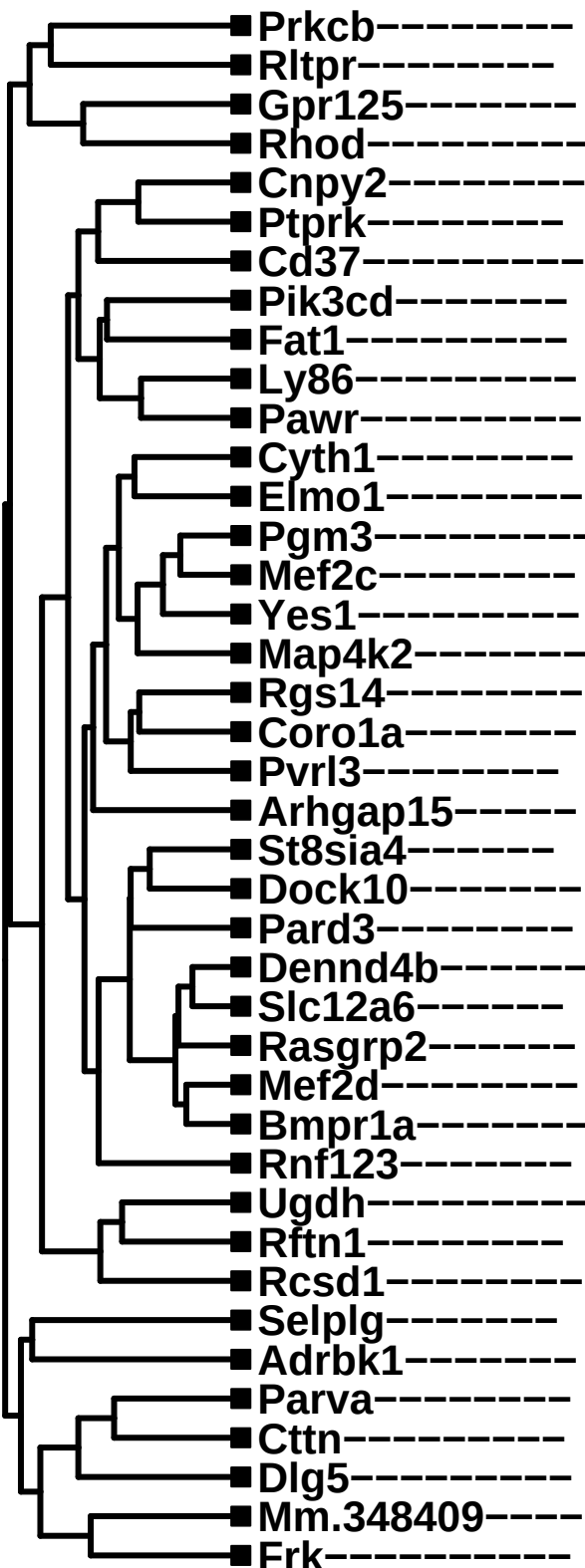
CR-Regulated Modules (40 Genes)

M = 6.47, P = 0.024



CR-Regulated Modules (40 Genes)

M = 6.47, P = 0.0255



Prkcb	●	●	-	-	X	X	-	-	-	-	●	●	●	-	-	●	-
Rltpr	●	●	X	X	X	X	●	X	X	X	●	●	●	-	X	X	X
Gpr125	●	-	●	-	X	X	●	-	-	-	●	-	*	●	-	●	-
Rhod	●	-	-	-	X	X	-	-	-	-	●	-	-	●	-	-	●
Cnpy2	●	●	-	-	X	X	●	●	●	-	●	●	●	-	-	●	●
Ptpkr	●	●	-	-	X	X	●	●	-	-	●	●	●	●	●	X	X
Cd37	-	-	X	X	X	●	-	-	X	X	-	-	●	●	-	●	-
Pik3cd	●	●	-	-	X	X	●	-	-	-	●	●	-	●	●	-	-
Fat1	●	-	-	-	X	X	-	●	-	-	●	●	●	-	X	X	X
Ly86	-	●	X	X	-	●	-	●	X	X	●	●	●	-	-	●	●
Pawr	●	●	-	-	X	X	●	●	-	-	-	●	●	-	-	X	X
Cyth1	●	-	X	X	X	X	●	-	X	X	●	-	●	●	-	-	-
Elmo1	●	●	X	X	-	X	-	-	X	X	●	●	-	-	-	X	X
Pgm3	●	●	X	X	-	X	*	-	X	X	●	●	-	-	X	X	-
Mef2c	●	●	X	X	●	X	*	-	X	X	●	●	●	●	●	●	●
Yes1	●	-	-	-	X	X	*	-	-	-	●	-	●	-	-	-	-
Map4k2	-	●	X	X	-	X	●	-	X	X	-	●	-	●	●	-	-
Rgs14	●	●	X	X	-	-	●	-	X	X	-	●	-	-	-	●	-
Coro1a	-	-	X	X	●	X	●	-	X	X	●	-	-	-	-	●	●
Pvrl3	●	-	-	-	X	-	●	●	-	-	●	-	●	-	-	●	-
Arhgap15	●	●	X	X	-	X	●	-	X	X	●	●	-	-	X	X	X
St8sia4	●	-	X	X	●	X	-	●	X	X	●	-	-	-	-	●	●
Dock10	-	●	X	X	X	X	-	-	X	X	●	-	●	-	X	X	X
Pard3	●	-	●	-	X	X	*	●	-	●	●	●	●	-	-	●	-
Dennd4b	-	-	X	X	X	X	●	-	X	X	●	-	-	-	-	X	X
Slc12a6	●	-	-	-	X	X	●	●	-	-	●	●	-	-	●	X	X
Rasgrp2	●	-	X	X	X	X	●	-	X	X	●	●	●	-	-	-	-
Mef2d	●	●	-	-	X	●	●	-	-	-	*	●	●	-	●	●	-
Bmpr1a	●	●	-	-	●	●	*	-	-	-	*	●	●	●	-	-	●
Rnf123	-	-	X	X	X	X	●	-	X	X	-	-	●	-	-	X	X
Ugdh	-	●	-	-	X	X	●	-	-	-	●	-	-	-	-	-	-
Rftn1	-	-	X	X	X	X	●	-	X	X	●	-	-	●	X	X	●
Rcsd1	●	●	X	X	-	X	*	-	X	X	●	●	●	-	-	X	-
Selplg	-	-	-	-	●	-	-	-	-	-	●	●	●	-	-	●	●
Adrbk1	-	●	-	-	X	X	●	-	-	-	●	●	●	-	-	-	●
Parva	-	●	-	-	X	X	-	●	-	-	●	-	●	-	●	X	-
Ctnn	●	●	-	-	-	-	*	-	-	-	●	●	●	-	●	-	-
Dlg5	-	●	X	X	-	X	●	-	X	X	●	-	●	-	-	X	●
Mm.348409	-	●	X	X	X	X	-	X	X	X	●	●	●	-	X	X	X
Frk	●	-	-	-	X	X	●	-	-	-	-	-	-	●	●	-	●

coc hyp spc cbm gon kid msl hip str thm hrt ctx lvr cln mmy lng wat

