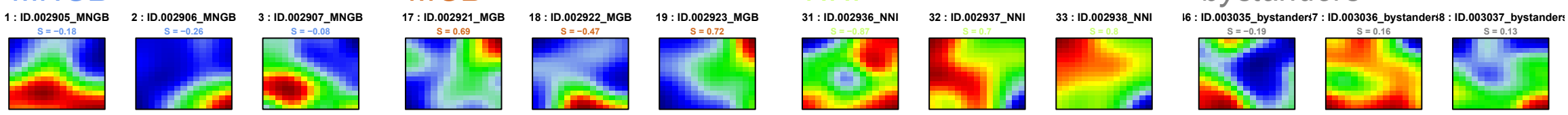
(a)



(b)

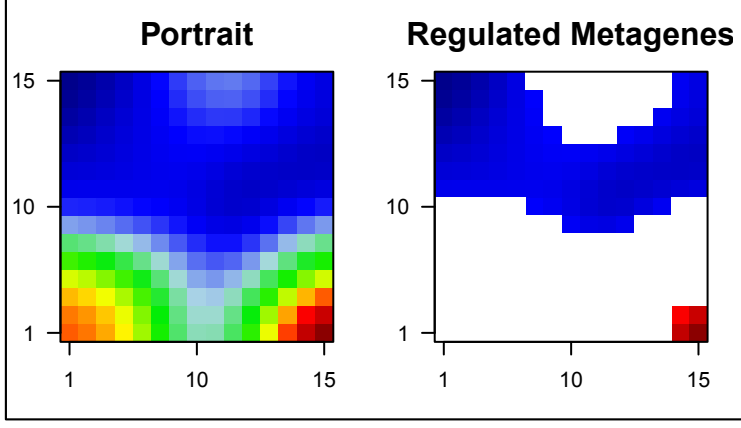
MNGB

Global Summary

%DE = 0.01
genes with fdr < 0.2 = 100 (0 + / 100 −)
genes with fdr < 0.1 = 100 (0 + / 100 −)
genes with fdr < 0.05 = 100 (0 + / 100 −)
genes with fdr < 0.01 = 100 (0 + / 100 −)

genes in genesets = 9964

<FC> = 0.05
<t−score> = −0.36
<p−value> = 0
<fdr> = 0.99



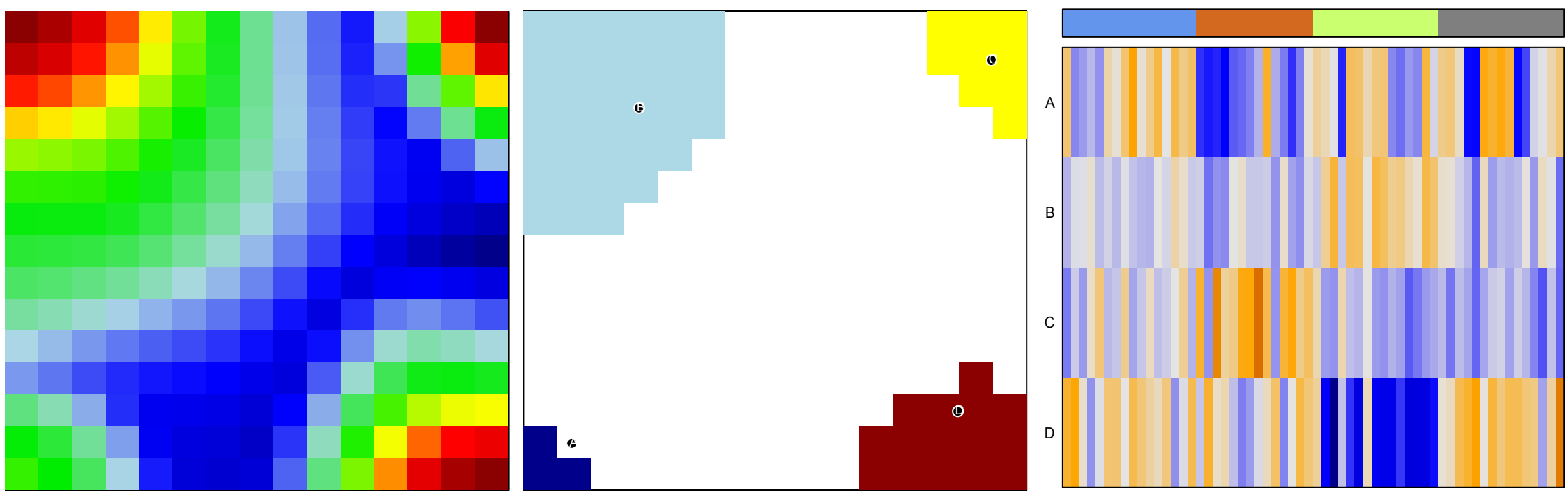
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSMUSG00	−0.57	0	1e−12	13 x 13	target of myb1−like 2 (chicken) [Source:MGI Symbol;Acc:MGI
2	ENSMUSG00	−0.4	0	1e−12	12 x 14	family with sequence similarity 193, member B [Source:MGI S
3	ENSMUSG00	−0.31	0	1e−12	8 x 15	sorbin and SH3 domain containing 3 [Source:MGI Symbol;Ac
4	ENSMUSG00	−0.19	0	1e−12	8 x 15	junctophilin 3 [Source:MGI Symbol;Acc:MGI:1891497]
5	ENSMUSG00	−0.5	0	1e−12	1 x 8	harbinger transposase derived 1 [Source:MGI Symbol;Acc:M
6	ENSMUSG00	−0.31	0	1e−12	13 x 14	IQ motif containing GTPase activating protein 3 [Source:MGI
7	ENSMUSG00	−0.15	0	1e−12	5 x 2	growth differentiation factor 3 [Source:MGI Symbol;Acc:MGI:9
8	ENSMUSG00	−0.18	0	1e−12	5 x 1	RIKEN cDNA 3830403N18 gene [Source:MGI Symbol;Acc:M
9	ENSMUSG00	−0.37	0	1e−12	4 x 3	Mab−21 domain containing 1 [Source:MGI Symbol;Acc:MGI:2
10	ENSMUSG00	−0.28	0	1e−12	11 x 9	kinesin family member 9 [Source:MGI Symbol;Acc:MGI:1098
11	ENSMUSG00	−1.08	0	1e−12	9 x 14	LysM, putative peptidoglycan−binding, domain containing 3 [S
12	ENSMUSG00	−0.6	0	1e−12	2 x 14	collectin sub−family member 12 [Source:MGI Symbol;Acc:MG
13	ENSMUSG00	−0.35	0	1e−12	9 x 9	Trp53 induced glycolysis repulatory phosphatase [Source:MG
14	ENSMUSG00	−0.1	0	1e−12	7 x 6	homeobox A7 [Source:MGI Symbol;Acc:MGI:96179]
15	ENSMUSG00	−0.97	0	1e−12	15 x 11	angiopoietin−like 6 [Source:MGI Symbol;Acc:MGI:1917976]
16	ENSMUSG00	−0.21	0	1e−12	13 x 13	kynurenine 3−monooxygenase (kynurenine 3−hydroxylase) [S
17	ENSMUSG00	−0.83	0	1e−12	10 x 1	ST8 alpha−N−acetyl−neuraminide alpha−2,8−sialyltransferas
18	ENSMUSG00	−0.21	0	1e−12	10 x 6	integrin alpha 1 [Source:MGI Symbol;Acc:MGI:96599]
19	ENSMUSG00	−0.24	0	1e−12	5 x 6	ALS2 C−terminal like [Source:MGI Symbol;Acc:MGI:2447532
20	ENSMUSG00	−0.69	0	1e−12	7 x 10	calcium release activated channel regulator 2B [Source:MGI S

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	3.25	NULL	773	MF	poly(A) RNA binding
2	2.52	NULL	1217	CC	membrane
3	2.18	NULL	52	BP	response to virus
4	2.06	NULL	4248	MF	protein binding
5	2.01	NULL	498	CC	nucleolus
6	2.01	NULL	644	Chr	Chr 5
7	1.97	NULL	108	MF	GTPase activity
8	1.93	NULL	21	BP	negative regulation of viral genome replication
9	1.92	NULL	1125	CC	nucleoplasm
10	1.9	NULL	2310	CC	nucleus
11	1.84	NULL	48	MF	double−stranded RNA binding
12	1.81	NULL	16	CC	mitochondrial ribosome
13	1.75	NULL	56	BP	positive regulation of NF−kappaB transcription factor activity
14	1.65	NULL	85	BP	response to lipopolysaccharide
15	1.56	NULL	128	BP	translation
16	1.56	NULL	249	MF	RNA binding
17	1.51	NULL	632	Chr	Chr 4
18	1.5	NULL	90	CC	cytoplasmic vesicle
19	1.49	NULL	365	Chr	Chr 19
20	1.46	NULL	20	BP	regulation of blood pressure
Underexpressed					
1	−10.85	NULL	10	BP	oligosaccharide metabolic process
2	−9.06	NULL	13	BP	learning
3	−8.42	NULL	18	BP	memory
4	−7.84	NULL	10	BP	N−glycan processing
5	−7.53	NULL	17	BP	release of sequestered calcium ion into cytosol
6	−6.96	NULL	19	BP	neuromuscular process controlling balance
7	−6.7	NULL	27	CC	integral component of Golgi membrane
8	−6	NULL	12	CC	collagen trimer
9	−5.56	NULL	10	MF	clathrin binding
10	−5.33	NULL	10	BP	negative regulation of BMP signaling pathway
11	−5.3	NULL	29	CC	perikaryon
12	−5.26	NULL	14	BP	negative regulation of reactive oxygen species metabolic process
13	−5.24	NULL	18	BP	positive regulation of DNA repair
14	−4.97	NULL	17	CC	podosome
15	−4.79	NULL	18	BP	response to ischemia
16	−4.77	NULL	50	BP	protein glycosylation
17	−4.46	NULL	18	BP	negative regulation of neuron death
18	−4.3	NULL	15	MF	collagen binding
19	−4.25	NULL	28	BP	activation of MAPK activity
20	−4.21	NULL	21	BP	response to gamma radiation

(c)



(d)

Module Report

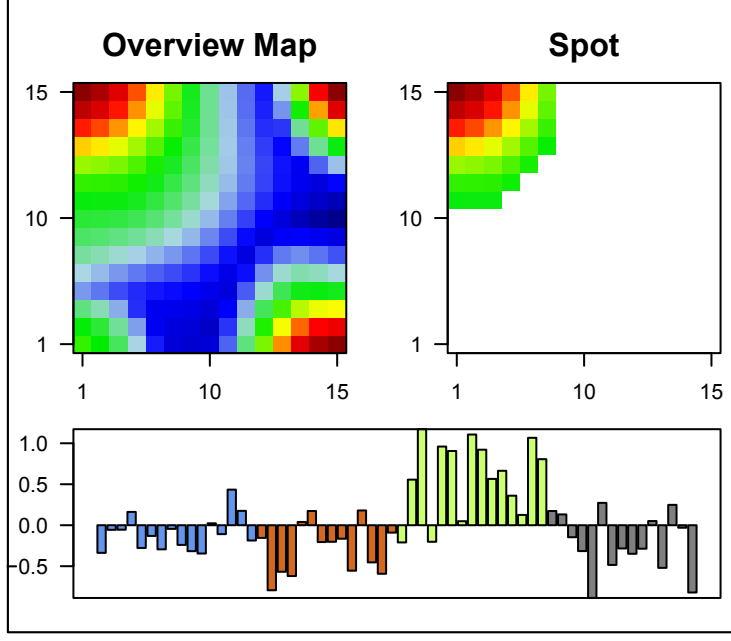
Spot Summary: B

metagenes = 36
genes = 1930

<r> metagenes = 0.75

beta: r2= 16.47 / log p= −Inf

samples with spot = 6 (10 %)
NNI : 6 (40 %)



Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSMUSG00	8.94	−4.49	0.38	Apoe	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]
2	ENSMUSG00	8.18	−2.21	0.39	Apoc2	apolipoprotein C−II [Source:MGI Symbol;Acc:MGI:88054]
3	ENSMUSG00	8	−1.52	0.42	F13a1	coagulation factor XIII, A1 subunit [Source:MGI Symbol;Acc:M
4	ENSMUSG00	7.62	−4.21	0.4	Cx3cr1	chemokine (C−X3−C motif) receptor 1 [Source:MGI Symbol;A
5	ENSMUSG00	7.33	−2.86	0.35	Mfge8	milk fat globule−EGF factor 8 protein [Source:MGI Symbol;Ac
6	ENSMUSG00	7.31	−0.85	0.3	Arhgap19	Rho GTPase activating protein 19 [Source:MGI Symbol;Acc:M
7	ENSMUSG00	7.12	−1.98	0.38	Hibch	3−hydroxyisobutyryl−Coenzyme A hydrolase [Source:MGI Sy
8	ENSMUSG00	6.94	−2.63	0.84	Gas6	growth arrest specific 6 [Source:MGI Symbol;Acc:MGI:95660]
9	ENSMUSG00	6.88	−1.36	0.23	Cdc42bpb	CDC42 binding protein kinase beta [Source:MGI Symbol;Acc
10	ENSMUSG00	6.86	−4.89	0.28	Fabp5	fatty acid binding protein 5, epidermal [Source:MGI Symbol;A
11	ENSMUSG00	6.84	−3.67	0.48	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ sys
12	ENSMUSG00	6.72	−2.33	0.22	Slc24a5	solute carrier family 24, member 5 [Source:MGI Symbol;Acc:M
13	ENSMUSG00	6.68	−1.81	0.23	Cadm1	cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1889
14	ENSMUSG00	6.68	−3.82	0.47	Angptl2	angiopoietin−like 2 [Source:MGI Symbol;Acc:MGI:1347002]
15	ENSMUSG00	6.63	−0.52	0.06	Ccr2	chemokine (C−C motif) receptor 2 [Source:MGI Symbol;Acc:M
16	ENSMUSG00	6.57	−1.63	0.43	Gdf15	growth differentiation factor 15 [Source:MGI Symbol;Acc:MGI
17	ENSMUSG00	6.57	−0.53	0.26	Helq	helicase, POLQ−like [Source:MGI Symbol;Acc:MGI:2176740]
18	ENSMUSG00	6.55	−4.72	0.56	Plau	plasminogen activator, urokinase [Source:MGI Symbol;Acc:M
19	ENSMUSG00	6.54	−1.06	0.12	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11 [Source:M
20	ENSMUSG00	6.53	−3.31	0.46	Hist1h1c	histone cluster 1, H1c [Source:MGI Symbol;Acc:MGI:193152

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	10 / 13	BP	DNA replication initiation
2	8e−05	10 / 15	MF	ATP−dependent DNA helicase activity
3	1e−04	9 / 13	BP	skin development
4	1e−04	15 / 30	BP	DNA duplex unwinding
5	2e−04	24 / 61	CC	nuclear chromosome, telomeric region
6	8e−04	43 / 140	CC	lysosome
7	1e−03	13 / 28	BP	cellular oxidant detoxification
8	1e−03	22 / 60	CC	chromatin
9	2e−03	36 / 116	CC	extracellular region
10	2e−03	78 / 296	CC	extracellular space
11	2e−03	8 / 14	BP	cholesterol biosynthetic process
12	2e−03	9 / 17	BP	neural tube development
13	2e−03	33 / 106	MF	magnesium ion binding
14	3e−03	72 / 274	BP	oxidation−reduction process
15	3e−03	14 / 34	CC	filopodium
16	3e−03	7 / 12	CC	nucleosome
17	3e−03	26 / 80	BP	regulation of gene expression
18	4e−03	38 / 130	BP	DNA repair
19	4e−03	18 / 50	BP	protein glycosylation
20	5e−03	6 / 10	BP	tissue homeostasis
21	6e−03	8 / 16	CC	neuronal postsynaptic density
22	6e−03	22 / 67	CC	microtubule cytoskeleton
23	6e−03	166 / 723	MF	ATP binding
24	7e−03	10 / 23	MF	pyridoxal phosphate binding
25	8e−03	16 / 45	BP	cellular response to insulin stimulus
26	8e−03	9 / 20	BP	DNA damage checkpoint
27	8e−03	11 / 27	MF	4 iron, 4 sulfur cluster binding
28	9e−03	7 / 14	BP	cognition
29	1e−02	50 / 189	CC	integral component of plasma membrane
30	1e−02	6 / 11	BP	brown fat cell differentiation
31	1e−02	6 / 11	BP	centrosome duplication
32	1e−02	6 / 11	BP	humoral immune response
33	1e−02	6 / 11	BP	negative regulation of DNA replication
34	1e−02	6 / 11	BP	positive regulation of glucose import
35	1e−02	6 / 11	BP	positive regulation of protein localization to nucleus
36	1e−02	6 / 11	BP	response to iron ion
37	1e−02	10 / 24	BP	cellular response to glucose stimulus
38	1e−02	10 / 24	BP	positive regulation of fibroblast proliferation
39	1e−02	39 / 142	MF	protein kinase activity
40	1e−02	124 / 533	MF	DNA binding