

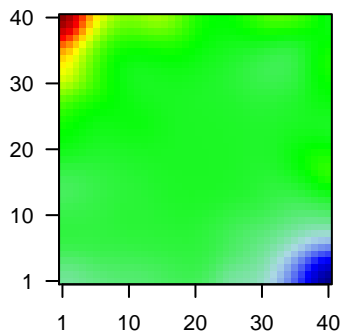
# 02.4920.001\_cH

## Global Summary

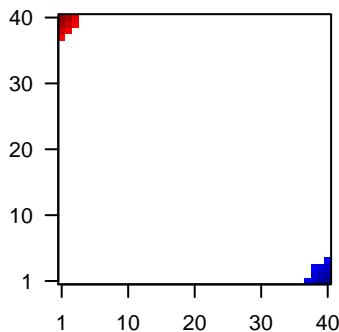
%DE = 0.26  
 # genes with fdr < 0.2 = 4881 ( 2380 + / 2501 - )  
 # genes with fdr < 0.1 = 4534 ( 2224 + / 2310 - )  
 # genes with fdr < 0.05 = 4142 ( 2059 + / 2083 - )  
 # genes with fdr < 0.01 = 3507 ( 1766 + / 1741 - )  
  
 # genes in genesets = 18990

<FC> = 0  
 <t-score> = 0  
 <p-value> = 0  
 <fdr> = 0.74

Profile



Regulated Spots



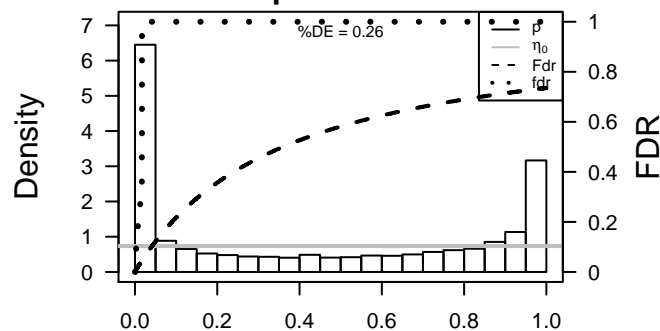
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000001	0.22	2e-16	3e-15	36 x 4 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:HGNC:10345]
2	ENSG00000001	0.22	2e-16	3e-15	1 x 33 matrix-remodelling associated 8 [Source:HGNC Symbol;Acc:HGNC:10345]
3	ENSG00000001	0.18	2e-16	3e-15	14 x 40 von Willebrand factor A domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10345]
4	ENSG00000001	0.14	2e-16	3e-15	32 x 40 parkinson protein 7 [Source:HGNC Symbol;Acc:HGNC:16366]
5	ENSG00000000	0.21	2e-16	3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
6	ENSG00000001	-0.17	2e-16	3e-15	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;Acc:HGNC:10345]
7	ENSG00000001	0.62	2e-16	3e-15	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [Source:HGNC Symbol;Acc:HGNC:10345]
8	ENSG00000001	-0.28	2e-16	3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:10345]
9	ENSG00000001	-0.16	2e-16	3e-15	25 x 1 aldo-keto reductase family 7, member A3 (afatoxin aldehyde dehydrogenase) [Source:HGNC Symbol;Acc:HGNC:10345]
10	ENSG00000001	-0.18	2e-16	3e-15	25 x 1 ring finger protein 186 [Source:HGNC Symbol;Acc:HGNC:25122]
11	ENSG00000001	0.57	2e-16	3e-15	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:10345]
12	ENSG00000001	-0.21	2e-16	3e-15	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:10345]
13	ENSG00000001	-0.24	2e-16	3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
14	ENSG00000001	0.26	2e-16	3e-15	1 x 33 low density lipoprotein receptor class A domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10345]
15	ENSG00000001	0.41	2e-16	3e-15	1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:HGNC:10345]
16	ENSG00000001	0.23	2e-16	3e-15	1 x 4 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:HGNC:10345]
17	ENSG00000001	0.3	2e-16	3e-15	5 x 5 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:HGNC:10345]
18	ENSG00000001	-0.13	2e-16	3e-15	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:HGNC:10345]
19	ENSG00000001	-0.31	2e-16	3e-15	38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:HGNC:10345]
20	ENSG00000001	-0.14	2e-16	3e-15	9 x 1 proline-rich nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:HGNC:10345]

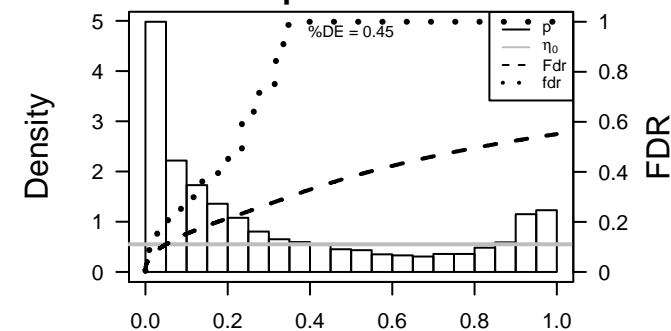
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.57	0e+00	132	Colon Cancer, Liou, Prostate Cancer, Cluster-b
2	22.19	1e-03	16	Cancer, Liou, Prostate Cancer, DN
3	21.5	9e-06	196	GSEA, C2, PCCALUGA, ANGIOIMMUNOBLASTIC LYMPHOMA_UP
4	21.5	9e-06	18	GSEA, C2, NIELSEN, LEIOMYOSARCOMA, CNN1_UP
5	20.98	1e-05	22	GSEA, C2, REACTOME, SMOOTH MUSCLE CONTRACTION
6	20.74	1e-05	478	GSEA, C2, LIM, MAMMARY STEM CELL_UP
7	20.37	1e-05	368	GSEA, C2, INDGREN, BLADDER CANCER_CLUSTER_2B
8	19.34	2e-05	535	GSEA, C2, CHICAS, RB1_TARGETS_CONFLUENT
9	19.16	2e-05	198	HM, HALLMARK, EPITHELIAL_MESENCHYMAL_TRANSITION
10	18.84	2e-05	314	Lymphoma, Lipp, June14, MMML937 tumors+controls_group.overexpression
11	18.54	2e-05	315	Lymphoma, WIRTH, lymphoma937_spot E
12	18.34	2e-05	44	GSEA, C2, REACTOME, MUSCLE CONTRACTION
13	18.23	2e-05	326	GSEA, C2, SCHUETZ, BREAST CANCER_DUCTAL_INVASIVE_UP
14	17.64	2e-05	303	GSEA, C2, PASINI, SUZ12_TARGETS_DN
15	16.43	2e-05	40	GSEA, C2, TOMLINS, PROSTATE CANCER_DN
16	16.04	2e-05	294	GSEA, C2, ACEVEDO, FGFR1_TARGETS_IN_PROSTATE CANCER_MODEL
17	15.89	3e-05	105	BP, muscle contraction
18	15.63	3e-05	160	GSEA, C2, BERTUCCI, MEDULLARY_VS_DUCTAL_BREAST CANCER_DN
19	15.54	3e-05	261	Lymphoma, WIRTH, Stromal signature 1
20	14.81	3e-05	10	GSEA, C2, MAINA, VHL_TARGETS_UP
<i>Underexpressed</i>				
1	-20.2	1e-05	110	Colon Cancer, Liou, Prostate Cancer, Cluster-b
2	-17.16	2e-05	104	Colon Cancer, Liou, Prostate Cancer, TCGA_group.over_A_normal_UP
3	-15.78	3e-05	429	GSEA, C2, CHARAFE, BREAST CANCER_LUMINAL_VS_MESENCHYMAL
4	-15.2	3e-05	616	Colon Cancer, Liou, Prostate Cancer, TCGA-expr_kmeans_M_CIMP_H_DN
5	-14.7	3e-05	507	Colon Cancer, Liou, Prostate Cancer, TCGA_corr_C_normal_UP
6	-14.57	3e-05	688	Colon Cancer, Liou, Prostate Cancer, TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN
7	-14.25	4e-05	126	GSEA, C2, ECCHI, GASTRIC CANCER_ADVANCED_VS_EARLY_DN
8	-14.01	4e-05	222	GSEA, C2, COLDREN, GEFITINIB_RESISTANCE_DN
9	-13.65	4e-05	455	GSEA, C2, ZONDER, CDH1_TARGETS_2_DN
10	-13.63	4e-05	412	GSEA, C2, LIM, MAMMARY STEM CELL_DN
11	-13.37	4e-05	643	Colon Cancer, Liou, Prostate Cancer, TCGA_meth_kmeans_L_CIMP_H_DN
12	-13.1	4e-05	682	GSEA, C2, CREIGHTON, ENDOCRINE_THERAPY_RESISTANCE_3
13	-12.66	6e-05	251	GSEA, C2, WAMUNYOKOLI, OVARIAN CANCER_LMP_UP
14	-12.5	6e-05	144	Lymphoma, WIRTH, lymphoma937_spot G
15	-12.2	7e-05	132	GSEA, C2, WAMUNYOKOLI, OVARIAN CANCER_GRADES_1_2_UP
16	-11.88	8e-05	142	Lymphoma, Lipp, June14, MMML937 tumors+controls_group.overexpression
17	-10.94	1e-04	1624	GSEA, C2, DODD, NASOPHARYNGEAL CARCINOMA_UP
18	-9.75	2e-04	115	GSEA, C2, CHARAFE, BREAST CANCER_BASAL_VS_MESENCHYMAL_UP
19	-9.58	3e-04	19	BP, cellular glucuronidation
20	-9.45	3e-04	17	GSEA, C2, REACTOME, GLUCURONIDATION

p-values



p-values



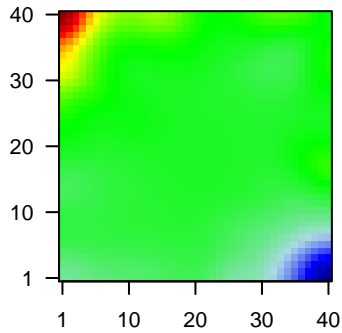
# 02.4920.001\_cH

## Local Summary

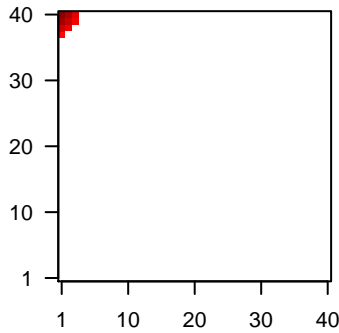
%DE = 0.98  
 # metagenes = 9  
 # genes = 206  
 # genes in genesets = 205  
  
 # genes with  $fdr < 0.1$  = 199 ( 195 + / 4 -)  
 # genes with  $fdr < 0.05$  = 199 ( 195 + / 4 -)  
 # genes with  $fdr < 0.01$  = 199 ( 195 + / 4 -)

<r> metagenes = 1  
 <r> genes = 0.81  
  
 <FC> = 0.37  
 <t-score> = 7.58  
 <p-value> = 0  
 <fdr> = 0.03

Profile



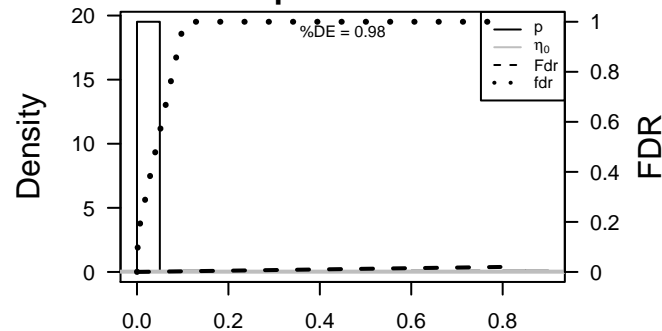
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.62	2e-16	6e-18	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [
2	ENSG0000001	0.36	2e-16	6e-18	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
3	ENSG0000001	0.3	2e-16	6e-18	1 x 40 nexilin (F actin binding protein) [Source:HGNC Symbol;Acc:H
4	ENSG0000001	0.52	2e-16	6e-18	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
5	ENSG0000001	0.29	2e-16	6e-18	2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f
6	ENSG0000000	0.16	2e-16	6e-18	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
7	ENSG0000001	0.16	2e-16	6e-18	1 x 40 tetraspanin 2 [Source:HGNC Symbol;Acc:HGNC:20659]
8	ENSG0000001	0.3	2e-16	6e-18	1 x 40 calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
9	ENSG0000000	0.52	2e-16	6e-18	1 x 39 pleckstrin homology domain containing, family O member 1 [f
10	ENSG0000001	0.27	2e-16	6e-18	1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:
11	ENSG0000001	0.34	2e-16	6e-18	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
12	ENSG0000001	0.26	2e-16	6e-18	2 x 40 discoidin domain receptor tyrosine kinase 2 [Source:HGNC S
13	ENSG0000001	0.41	2e-16	6e-18	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc:
14	ENSG0000001	0.48	2e-16	6e-18	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
15	ENSG0000001	0.16	2e-16	6e-18	1 x 37 laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;A
16	ENSG0000001	0.56	2e-16	6e-18	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc:
17	ENSG0000001	0.86	2e-16	6e-18	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
18	ENSG0000001	0.68	2e-16	6e-18	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
19	ENSG0000000	0.32	2e-16	6e-18	1 x 40 protein phosphatase 1, regulatory subunit 12B [Source:HGNC
20	ENSG0000001	0.4	2e-16	6e-18	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11

p-values



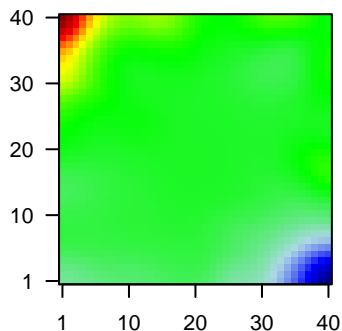
# 02.4920.001\_cH

## Local Summary

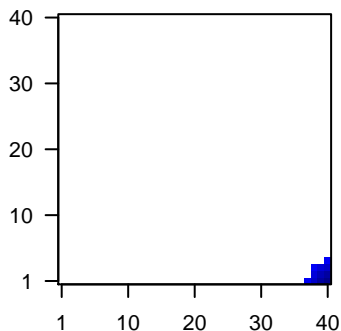
%DE = 0.98  
 # metagenes = 11  
 # genes = 227  
 # genes in genesets = 223  
  
 # genes with  $fdr < 0.1$  = 222 ( 3 + / 219 -)  
 # genes with  $fdr < 0.05$  = 222 ( 3 + / 219 -)  
 # genes with  $fdr < 0.01$  = 222 ( 3 + / 219 -)

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.67  
  
 $\langle FC \rangle$  = -0.31  
 $\langle t\text{-score} \rangle$  = -6.34  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.02

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.28	2e-16	5e-18	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:1712]
2	ENSG0000001	-0.21	2e-16	5e-18	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1712]
3	ENSG0000001	-0.24	2e-16	5e-18	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
4	ENSG0000001	-0.31	2e-16	5e-18	38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:HGNC:1712]
5	ENSG0000001	-0.14	2e-16	5e-18	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC Symbol;Acc:HGNC:1712]
6	ENSG0000001	-0.35	2e-16	5e-18	40 x 1 serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:232]
7	ENSG0000001	-0.3	2e-16	5e-18	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:232]
8	ENSG0000000	-0.51	2e-16	5e-18	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:232]
9	ENSG0000001	-0.92	2e-16	5e-18	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:232]
10	ENSG0000002	-0.25	2e-16	5e-18	38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symbol;Acc:HGNC:20657]
11	ENSG0000001	-0.72	2e-16	5e-18	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
12	ENSG0000000	-0.59	2e-16	5e-18	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:20657]
13	ENSG0000001	-0.31	2e-16	5e-18	40 x 3 EPS8-like 3 [Source:HGNC Symbol;Acc:HGNC:21297]
14	ENSG0000001	-0.26	2e-16	5e-18	40 x 4 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:21297]
15	ENSG0000001	-0.49	2e-16	5e-18	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:2545]
16	ENSG0000001	-0.26	2e-16	5e-18	38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
17	ENSG0000001	-0.42	2e-16	5e-18	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:17429]
18	ENSG0000001	-0.28	2e-16	5e-18	38 x 1 cingulin [Source:HGNC Symbol;Acc:HGNC:17429]
19	ENSG0000001	-0.19	2e-16	5e-18	S100 calcium binding protein A14 [Source:HGNC Symbol;Acc:HGNC:14685]
20	ENSG0000001	-0.27	2e-16	5e-18	40 x 4 F11 receptor [Source:HGNC Symbol;Acc:HGNC:14685]

p-values

