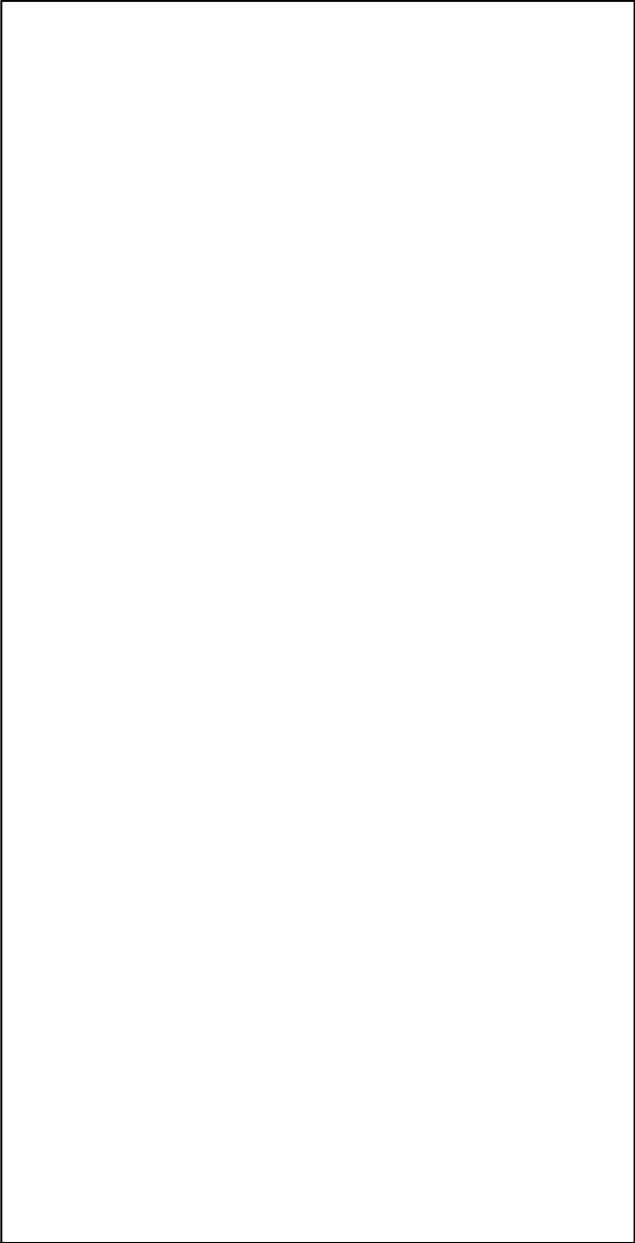
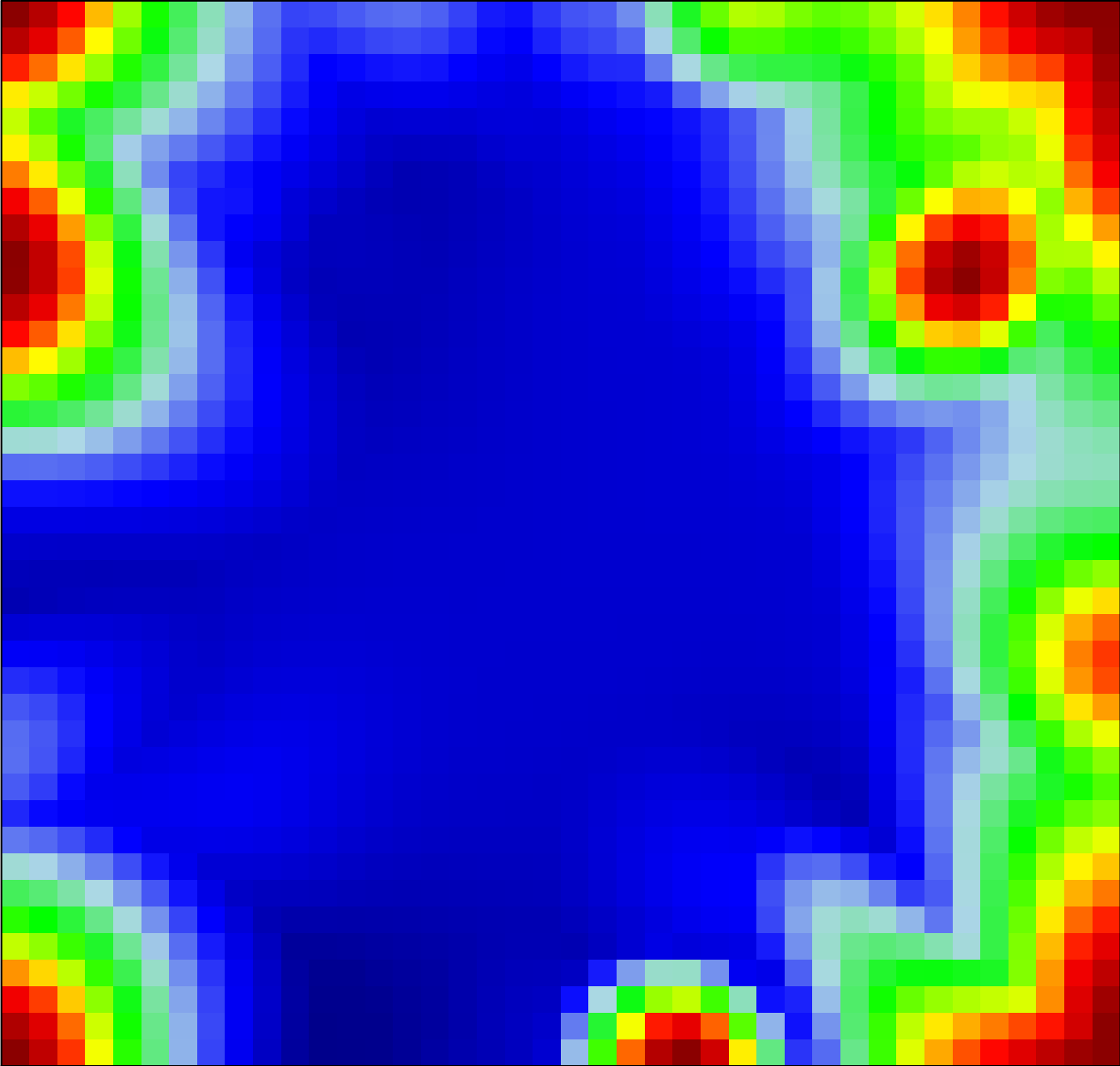


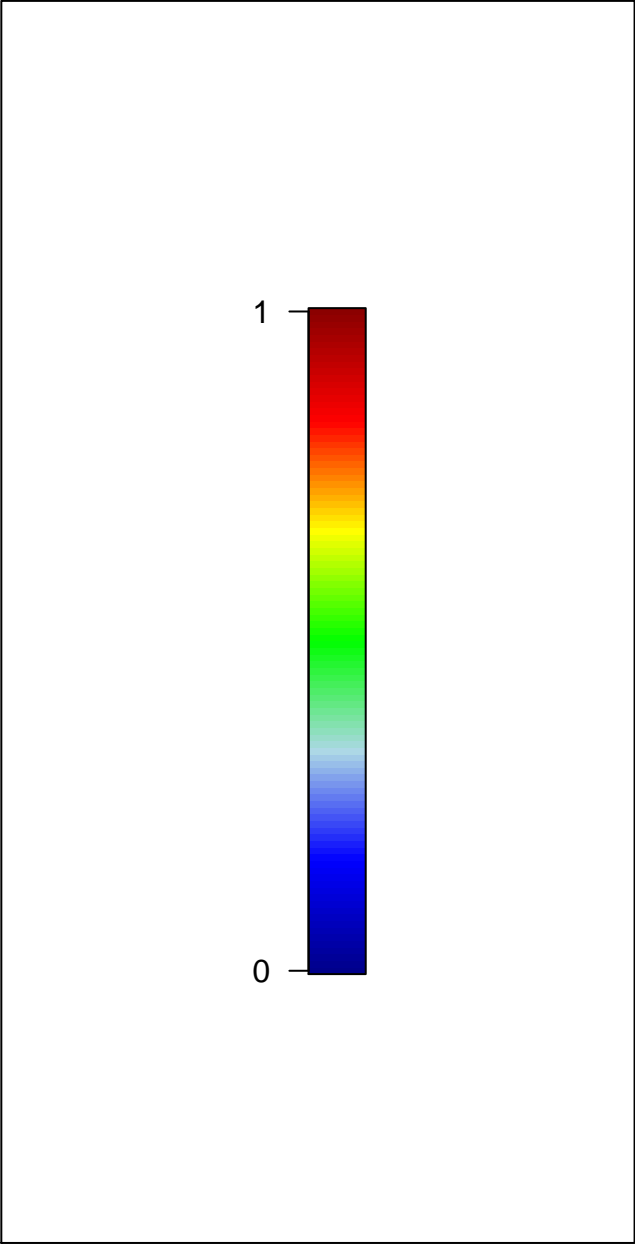
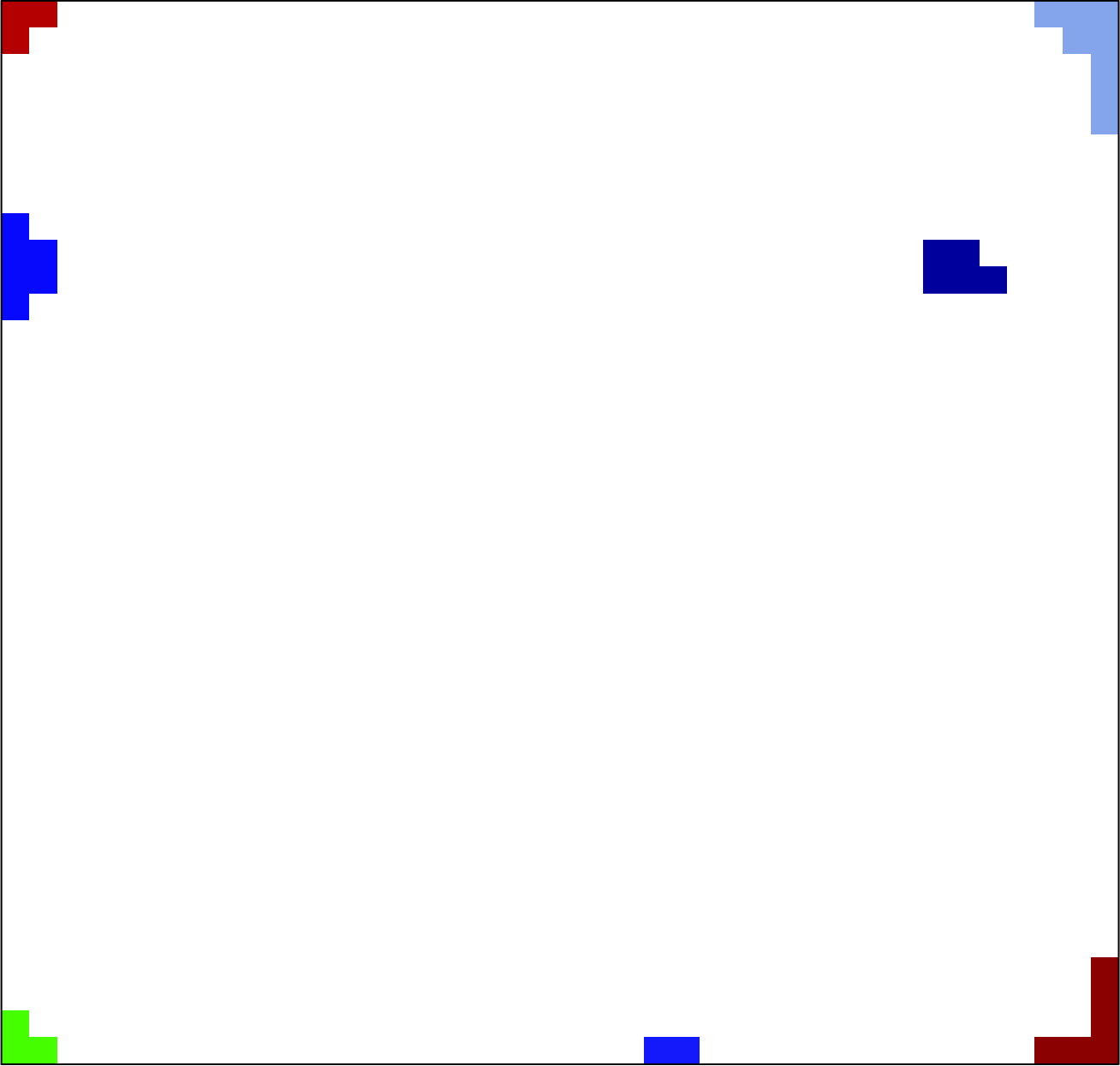
# Overexpression Spots

landscape



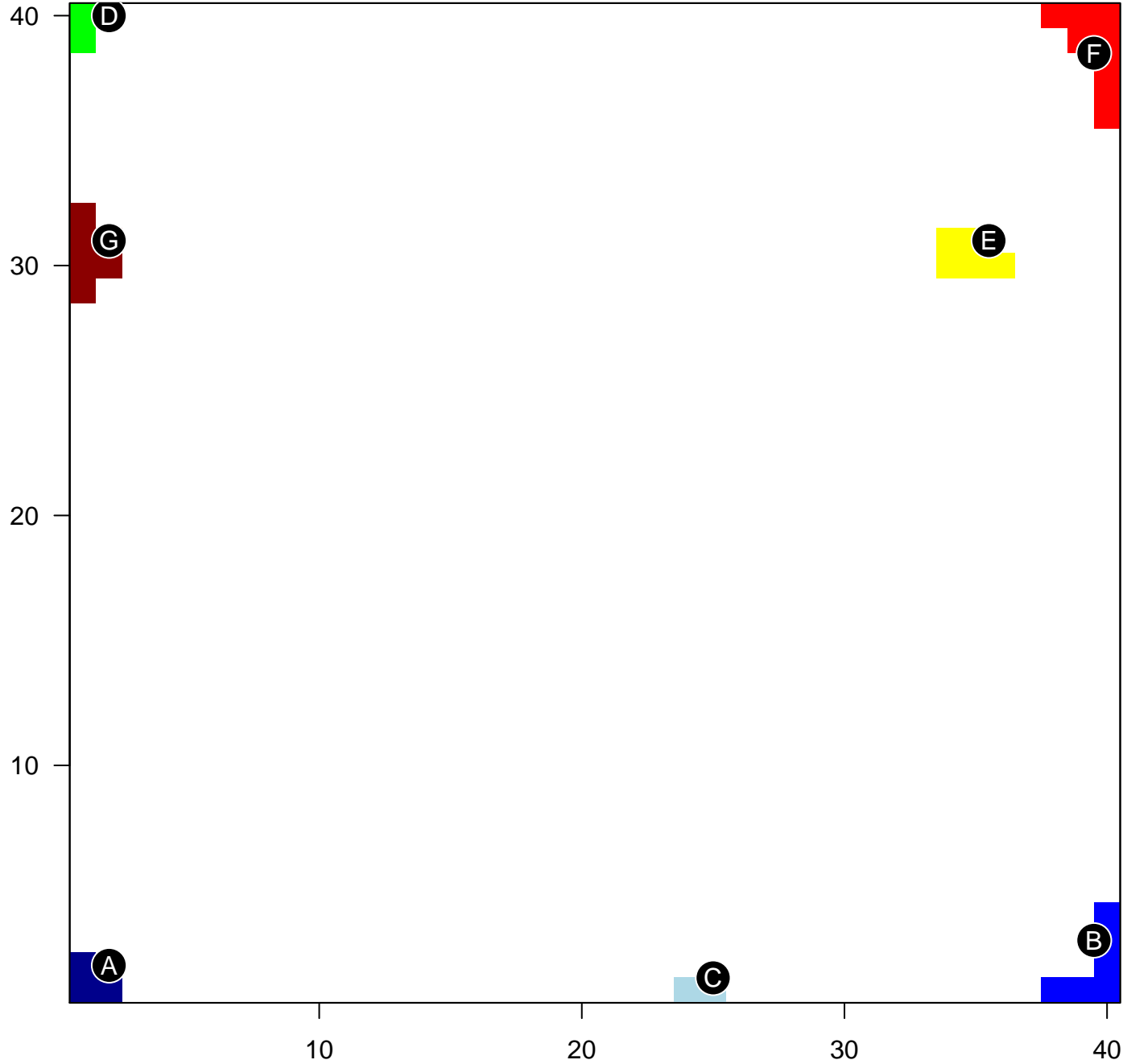
# Overexpression Spots

beta-scores

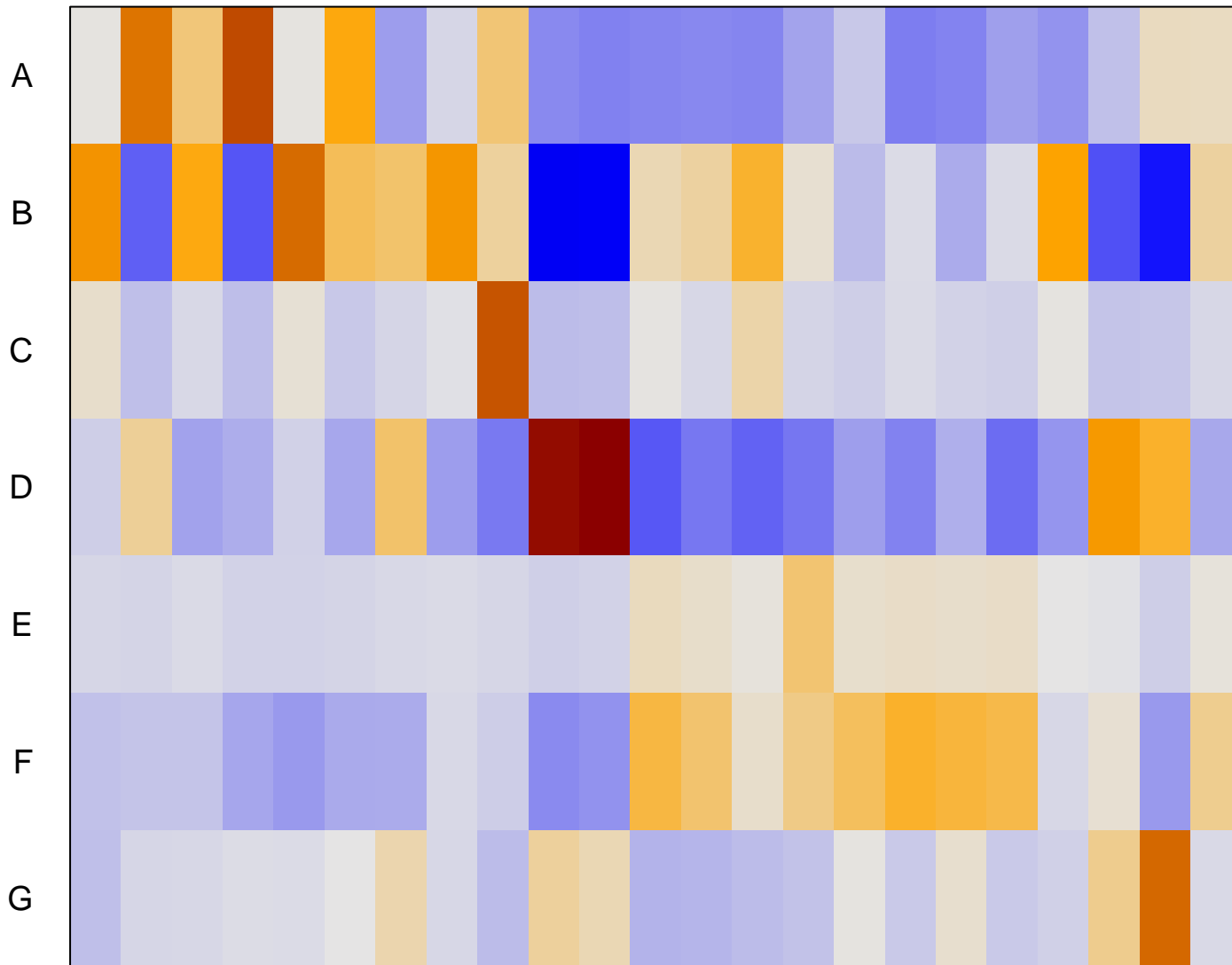


# Overexpression Spots

annotation

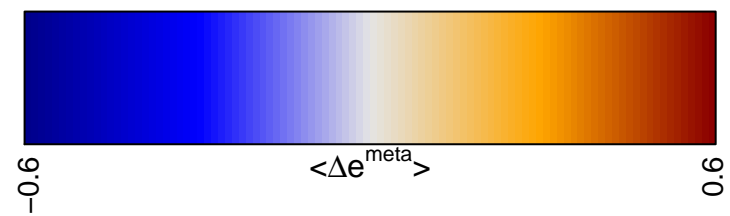


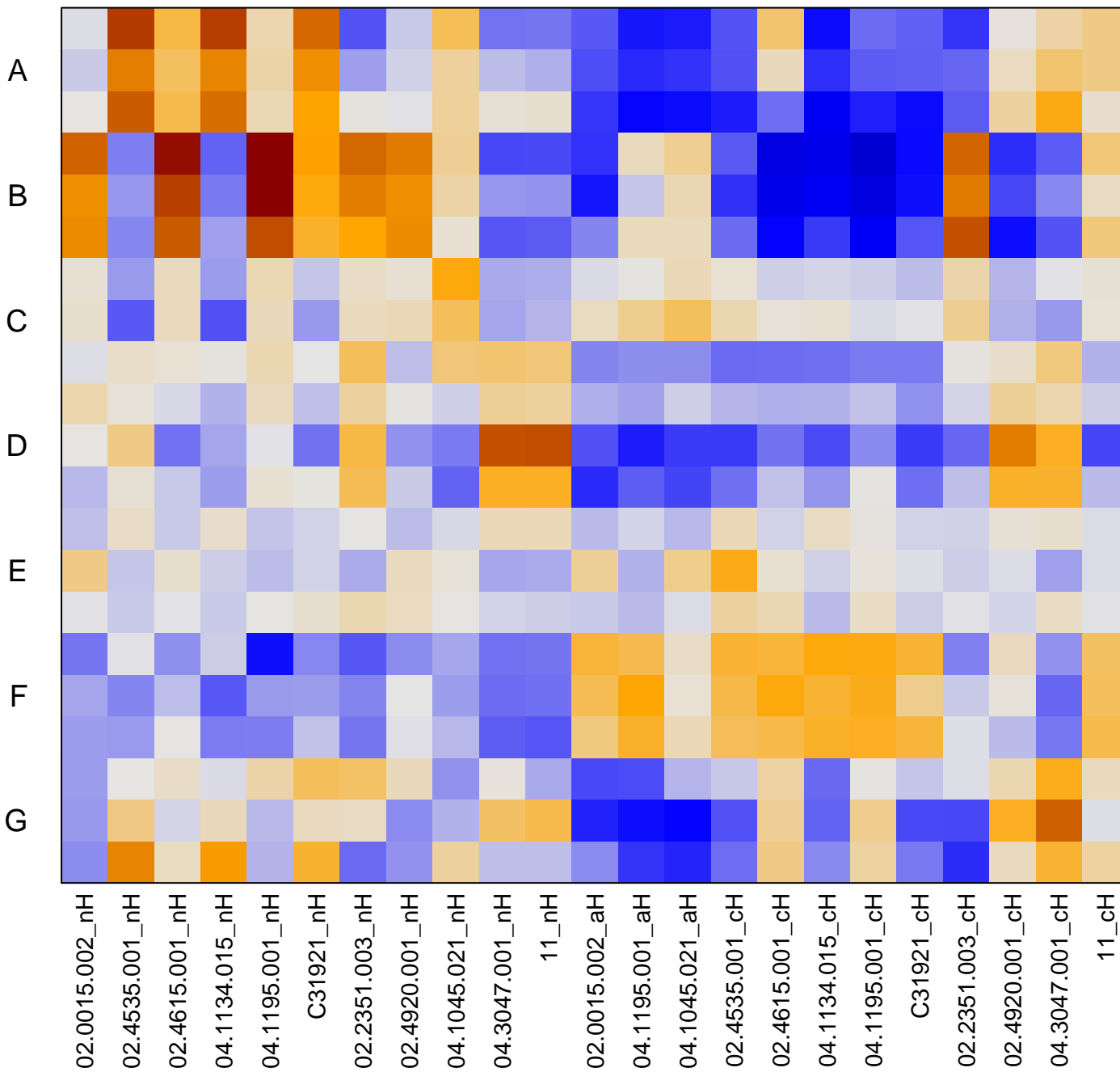
- A ■ Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_0  
WALLACE\_PROSTATE\_CANCER\_RACE\_UP  
SMID\_BREAST\_CANCER\_NORMAL\_LIKE\_UP
- B ■ Pentrack\_CRC\_TCGA\_group.over\_A\_normal\_UP  
Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP  
Marisa\_CRC-cluster-h
- C ■ HSIAO\_LIVER\_SPECIFIC\_GENES  
small molecule metabolic process  
VECCHI\_GASTRIC\_CANCER\_EARLY\_DN
- D ■ LIU\_PROSTATE\_CANCER\_DN  
Marisa\_CRC-cluster-b  
PASINI\_SUZ12\_TARGETS\_DN
- E ■ Chr X  
Chr 19  
SATO\_SILENCED\_BY\_DEACETYLATION\_IN\_PANCREATI
- F ■ GRADE\_COLON\_CANCER\_UP  
VECCHI\_GASTRIC\_CANCER\_EARLY\_UP  
LI\_AMPLIFIED\_IN\_LUNG\_CANCER
- G ■ HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB  
SCHUETZ\_BREAST\_CANCER\_DUCTAL\_INVASIVE\_UP  
Lembcke\_Colonc Inflammation



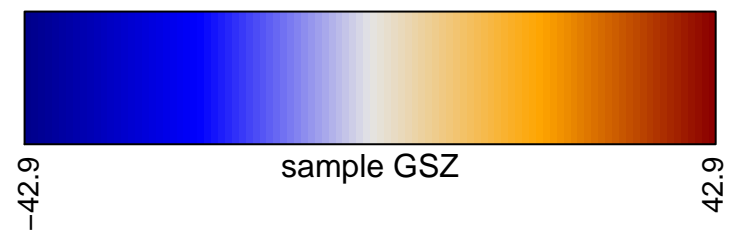
- Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_DN
- WALLACE\_PROSTATE\_CANCER\_RACE\_UP
- SMID\_BREAST\_CANCER\_NORMAL\_LIKE\_UP
  
- Pentrack\_CRC\_TCGA\_group.over\_A\_normal\_UP
- Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP
- Marisa\_CRC-cluster-h
  
- HSIAO\_LIVER\_SPECIFIC\_GENES
- small molecule metabolic process
- VECCHI\_GASTRIC\_CANCER\_EARLY\_DN
  
- LIU\_PROSTATE\_CANCER\_DN
- Marisa\_CRC-cluster-b
- PASINI\_SUZ12\_TARGETS\_DN
  
- Chr X
- Chr 19
- SATO\_SILENCED\_BY\_DEACETYLATION\_IN\_PANCREATIC\_CANCER
  
- GRADE\_COLON\_CANCER\_UP
- VECCHI\_GASTRIC\_CANCER\_EARLY\_UP
- LI\_AMPLIFIED\_IN\_LUNG\_CANCER
  
- HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB
- SCHUETZ\_BREAST\_CANCER\_DUCTAL\_INVASIVE\_UP
- Lembcke\_Colonic Inflammation

02.0015.002\_nH  
 02.4535.001\_nH  
 02.4615.001\_nH  
 04.1134.015\_nH  
 04.1195.001\_nH  
 C31921\_nH  
 02.2351.003\_nH  
 02.4920.001\_nH  
 04.1045.021\_nH  
 04.3047.001\_nH  
 11\_nH  
 02.0015.002\_aH  
 04.1195.001\_aH  
 04.1045.021\_aH  
 02.4535.001\_cH  
 02.4615.001\_cH  
 04.1134.015\_cH  
 04.1195.001\_cH  
 C31921\_cH  
 02.2351.003\_cH  
 02.4920.001\_cH  
 04.3047.001\_cH  
 11\_cH





- Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_DN
- WALLACE\_PROSTATE\_CANCER\_RACE\_UP
- SMID\_BREAST\_CANCER\_NORMAL\_LIKE\_UP
- Pentrack\_CRC\_TCGA\_group.over\_A\_normal\_UP
- Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP
- Marisa\_CRC-cluster-h
- HSIAO\_LIVER\_SPECIFIC\_GENES
- small molecule metabolic process
- VECCHI\_GASTRIC\_CANCER\_EARLY\_DN
- LIU\_PROSTATE\_CANCER\_DN
- Marisa\_CRC-cluster-b
- PASINI\_SUZ12\_TARGETS\_DN
- Chr X
- Chr 19
- SATO\_SILENCED\_BY\_DEACETYLATION\_IN\_PANCREATIC\_CANCER
- GRADE\_COLON\_CANCER\_UP
- VECCHI\_GASTRIC\_CANCER\_EARLY\_UP
- LI\_AMPLIFIED\_IN\_LUNG\_CANCER
- HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB
- SCHUETZ\_BREAST\_CANCER\_DUCTAL\_INVASIVE\_UP
- Lembcke\_Colonic Inflammation



# Overexpression Spots

## Spot Summary: A

# metagenes = 3  
# genes = 126

<r> metagenes = 1

<r> genes = 0.81

beta: r2= 0.56 / log p= -4.45

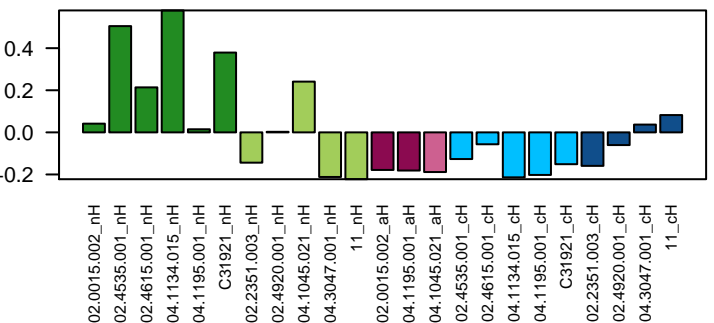
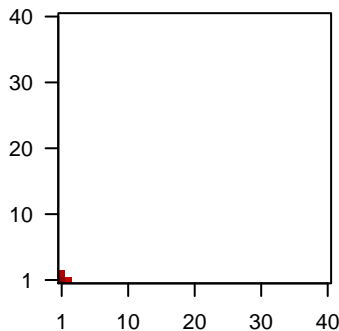
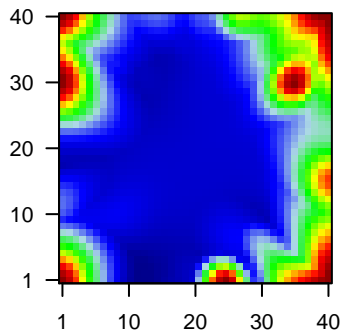
# samples with spot = 5 ( 21.7 %)

MLH1\_normHNPCC : 4 ( 66.7 %)

other\_normHNPCC : 1 ( 20 %)

### Overview Map

### Spot

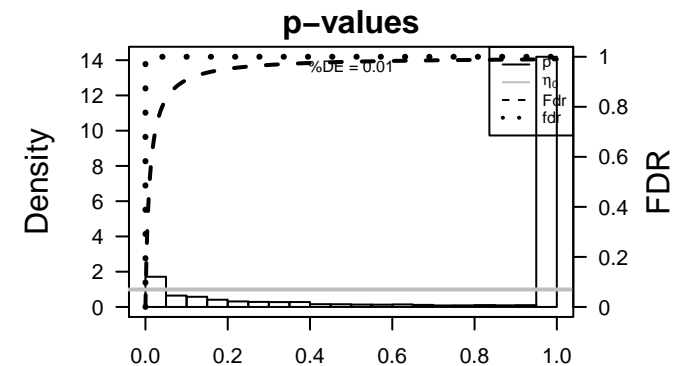


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSG0000001	1.4	-0.53	0.86	FDCSP follicular dendritic cell secreted protein [Source:HGNC Symbc
2	ENSG0000001	1.34	-0.7	0.92	CCL21 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
3	ENSG0000001	1.14	-0.59	0.94	CCL19 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
4	ENSG0000001	1.14	-0.52	0.94	CXCL13 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
5	ENSG0000002	1.11	-0.68	0.48	UBD ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
6	ENSG0000001	1.01	-0.54	0.96	CD52 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
7	ENSG0000001	0.95	-0.25	0.94	CR2 complement component (3d/Epstein Barr virus) receptor 2 [Si
8	ENSG0000002	0.95	-0.72	0.5	MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
9	ENSG0000001	0.93	-0.22	0.98	CCR7 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
10	ENSG0000001	0.89	-0.51	0.95	CXCR4 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
11	ENSG0000001	0.85	-0.35	0.97	LCP1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Syr
12	ENSG0000002	0.85	-0.8	0.45	MT-RNR2-like 9 [Source:HGNC Symbol;Acc:HGNC:37166]
13	ENSG0000001	0.85	-0.2	0.9	IL7R interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
14	ENSG0000001	0.84	-0.29	0.97	MS4A1 membrane-spanning 4-domains, subfamily A, member 1 [So
15	ENSG0000001	0.83	-0.25	0.93	GIMAP7 GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:
16	ENSG0000001	0.82	-0.25	0.91	ETS1 v-ets avian erythroblastosis virus E26 oncogene homolog 1 [
17	ENSG0000001	0.82	-0.39	0.95	CD79A CD79a molecule, immunoglobulin-associated alpha [Source:
18	ENSG0000001	0.81	-0.24	0.98	FCMR Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGf
19	ENSG0000000	0.8	-0.2	0.96	PTPRC protein tyrosine phosphatase, receptor type, C [Source:HGNC
20	ENSG0000001	0.79	-0.35	0.99	CD53 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-75	78 / 844	Colon Lembcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	2e-54	46 / 263	GSE/ WALLACE_PROSTATE_CANCER_RACE_UP
3	7e-53	52 / 436	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	8e-52	51 / 427	Tissu/ WIRTH_Immune system
5	1e-44	40 / 259	GSE/ POOLA_INVASIVE_BREAST_CANCER_UP
6	2e-44	38 / 220	GSE/ MCLACHLAN_DENTAL_CARIES_UP
7	2e-42	49 / 574	Canci/ Lembcke_Colonc Inflammation
8	2e-38	34 / 210	GSE/ MCLACHLAN_DENTAL_CARIES_DN
9	4e-38	39 / 343	BP/ immune response
10	4e-33	29 / 175	GSE/ LEE_DIFFERENTIATING_T_LYMPHOCYTE
11	3e-32	40 / 522	GSE/ SMID_BREAST_CANCER_LUMINAL_B_DN
12	1e-29	14 / 16	CC/ MHC class II protein complex
13	5e-27	20 / 79	GSE/ FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
14	2e-24	27 / 279	Glio/ WILLSCHER_GBM_Verhaak-CL & MES_up
15	4e-23	25 / 246	GSE/ QI_PLASMACYTOMA_UP
16	4e-22	22 / 181	HM/ HALLMARK_ALLOGRAFT_REJECTION
17	5e-22	16 / 61	BP/ antigen processing and presentation
18	1e-21	21 / 163	GSE/ PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
19	4e-21	27 / 368	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2B
20	4e-21	22 / 201	CC/ external side of plasma membrane
21	2e-20	22 / 218	GSE/ HOSHIDA_LIVER_CANCER_SUBCLASS_S1
22	2e-19	16 / 86	GSE/ WIELAND_UP_BY_HBV_INFECTION
23	8e-19	9 / 11	BP/ antigen processing and presentation of peptide or polysaccharide antigen v
24	3e-18	14 / 64	BP/ T cell costimulation
25	6e-18	13 / 51	GSE/ MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
26	7e-17	94 / 7592	Lymp/ HOPP_Strong_enhancer
27	5e-16	24 / 435	GSE/ RODWELL_AGING_KIDNEY_UP
28	5e-16	22 / 346	GSE/ SANSOM_APC_TARGETS_DN
29	6e-16	12 / 53	GSE/ KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
30	1e-15	18 / 208	Tissu/ PALMER_B-Cell signature up
31	6e-15	13 / 83	GSE/ KEGG_HEMATOPOIETIC_CELL_LINEAGE
32	2e-14	13 / 92	BP/ T cell receptor signaling pathway
33	3e-14	8 / 16	MF/ MHC class II protein complex binding
34	2e-13	12 / 82	GSE/ MORI_MATURE_B_LYMPHOCYTE_UP
35	2e-13	9 / 31	GSE/ KEGG_PRIMARY_IMMUNODEFICIENCY
36	3e-13	19 / 324	Canci/ SPANG_BCL6-index2
37	3e-13	10 / 46	GSE/ WINTER_HYPOXIA_DN
38	4e-13	35 / 1340	GSE/ PUJANA_ATM_PCC_NETWORK
39	5e-13	12 / 90	BP/ antigen processing and presentation of exogenous peptide antigen via MHC
40	5e-13	13 / 116	GSE/ LENAOUR_DENDRITIC_CELL_MATURATION_DN





# Overexpression Spots

## Spot Summary: B

# metagenes = 6  
# genes = 181

<r> metagenes = 0.99

<r> genes = 0.67

beta: r2= 1.03 / log p= -Inf

# samples with spot = 7 ( 30.4 %)

MLH1\_normHNPCC : 4 ( 66.7 %)

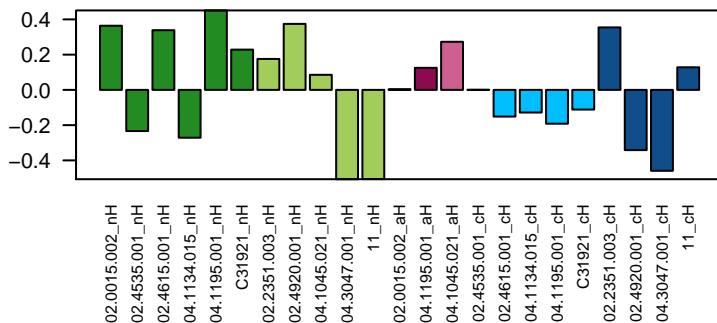
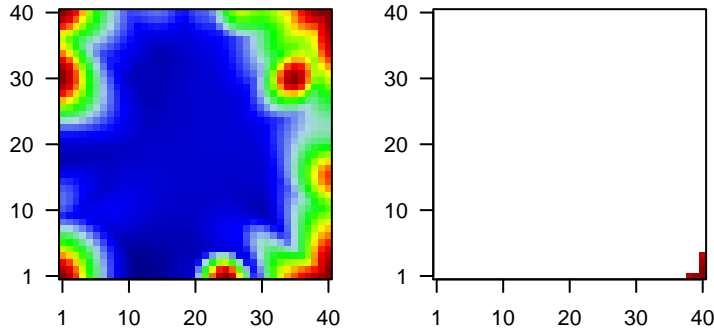
other\_normHNPCC : 1 ( 20 %)

other\_adenomaHNPCC : 1 ( 100 %)

other\_cancerHNPCC : 1 ( 25 %)

Overview Map

Spot

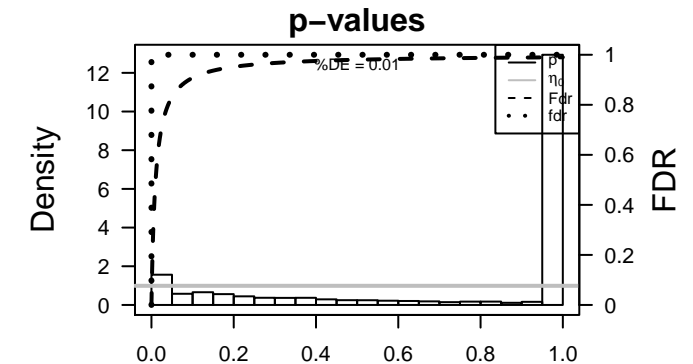


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSG000002	1.55	-0.86	0.89	PHGR1 proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:HGNC:11755]
2	ENSG000001	1.42	-0.99	0.88	GUCA2Aguanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:11755]
3	ENSG000001	1.33	-0.38	0.49	PP7080 uncharacterized LOC25845 [Source:EntrezGene;Acc:25845]
4	ENSG000001	1.3	-0.63	0.74	AQP8 aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG000001	1.28	-0.52	0.65	ANPEP alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:HGNC:11755]
6	ENSG000000	1.26	-0.59	0.72	CLCA4 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:11755]
7	ENSG000000	1.24	-0.81	0.86	SLC26A3solute carrier family 26 (anion exchanger), member 3 [Source:HGNC Symbol;Acc:HGNC:11755]
8	ENSG000000	1.24	-0.99	0.82	CEACAM7carcinoembryonic antigen-related cell adhesion molecule 7 [Source:HGNC Symbol;Acc:HGNC:11755]
9	ENSG000001	1.24	-0.49	0.76	ZG16 zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGNC:11755]
10	ENSG000000	1.22	-0.52	0.8	GUCA2Bguanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:11755]
11	ENSG000001	1.21	-0.51	0.64	TFF1 trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	-0.44	0.69	PRAP1 proline-rich acidic protein 1 [Source:HGNC Symbol;Acc:HGNC:11755]
13	ENSG000002	1.15	-0.61	0.84	PHGR1 proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:HGNC:11755]
14	ENSG000001	1.13	-1.09	0.9	FABP1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:11755]
15	ENSG000001	1.12	-0.37	0.74	AKR1B1aldol-keto reductase family 1, member B10 (aldose reductase) [Source:HGNC Symbol;Acc:HGNC:11755]
16	ENSG000001	1.1	-0.7	0.58	PI3 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Acc:HGNC:11755]
17	ENSG000001	1.06	-1.31	0.68	PIGR polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:HGNC:11755]
18	ENSG000001	1.02	-1.15	0.73	CEACAM5carcinoembryonic antigen-related cell adhesion molecule 5 [Source:HGNC Symbol;Acc:HGNC:11755]
19	ENSG000001	1	-0.96	0.91	KRT20 keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
20	ENSG000001	1	-0.35	0.77	C11orf86chromosome 11 open reading frame 86 [Source:HGNC Symt

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-65	45 / 104	Colon Pentrack_CRC_TCGA_group.over_A_normal_UP
2	2e-49	60 / 507	Colon Pentrack_CRC_TCGA_corr_C_normal_UP
3	3e-34	29 / 110	Colon Marisa_CRC-cluster-h
4	1e-26	45 / 643	Colon Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	2e-26	44 / 616	Colon Lembcke_TCGA-expr_kmeans_M_CIMP.H_DN
6	4e-25	82 / 2638	CC extracellular exosome
7	7e-22	34 / 429	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
8	3e-19	21 / 144	Lymph WIRTH_lymphoma937_spot G
9	5e-19	32 / 455	GSE/ ONDER_CDH1_TARGETS_2_DN
10	9e-19	24 / 222	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
11	2e-18	30 / 412	GSE/ LIM_MAMMARY_STEM_CELL_DN
12	4e-18	20 / 142	Lymph Hopp_June14_MMML937_tumors+controls_group.overexpression_G_tonsil
13	1e-17	24 / 248	GSE/ JAEGER_METASTASIS_DN
14	6e-17	54 / 1624	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	2e-16	18 / 126	GSE/ VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
16	5e-16	23 / 262	GSE/ SABATES_COLORECTAL_ADENOMA_DN
17	6e-16	20 / 181	GSE/ WU_CELL_MIGRATION
18	6e-16	74 / 3064	Glio Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
19	3e-14	33 / 711	GSE/ LEE_BMP2_TARGETS_UP
20	8e-14	71 / 3122	Color TxEnhG1_Colon
21	1e-13	15 / 109	GSE/ LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
22	3e-13	35 / 877	Color TxEnhG2_Colon
23	8e-13	11 / 49	Color Marisa_CRC-cluster-f
24	2e-12	15 / 132	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
25	2e-12	20 / 280	GSE/ ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
26	4e-12	28 / 608	Disea GUDJ_psooriasis up
27	4e-12	14 / 115	GSE/ CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
28	6e-12	19 / 261	GSE/ MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
29	1e-11	29 / 682	GSE/ CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
30	1e-11	24 / 465	GSE/ SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
31	1e-11	24 / 467	GSE/ SWEET_LUNG_CANCER_KRAS_UP
32	7e-11	10 / 54	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_DN
33	8e-11	19 / 303	GSE/ LEI_MYB_TARGETS
34	1e-10	15 / 174	GSE/ LI_AMPLIFIED_IN_LUNG_CANCER
35	2e-10	12 / 102	GSE/ LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
36	5e-10	149 / 11791	Color Enh_Colon
37	5e-10	8 / 32	GSE/ AIGNER_ZEB1_TARGETS
38	5e-10	15 / 195	HM HALLMARK_ESTROGEN_RESPONSE_LATE
39	6e-10	13 / 137	Tissu WIRTH_Mucosa
40	6e-10	9 / 48	GSE/ KEGG_DRUG_METABOLISM_OTHER_ENZYMES







# Overexpression Spots

## Spot Summary: C

# metagenes = 2  
# genes = 100

<r> metagenes = 1  
<r> genes = 0.85  
beta: r2= 0.19 / log p= -1.44

# samples with spot = 1 ( 4.3 %)  
other\_normHNPCC : 1 ( 20 %)

## Spot Genelist

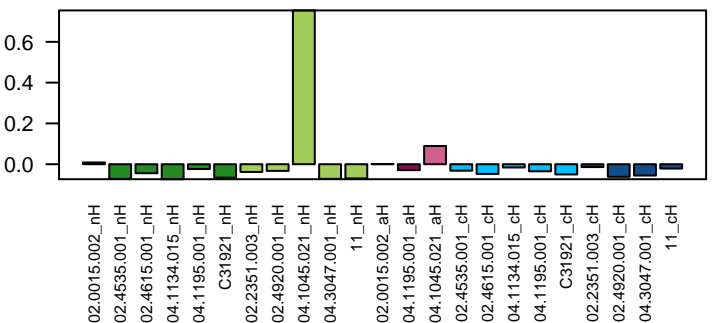
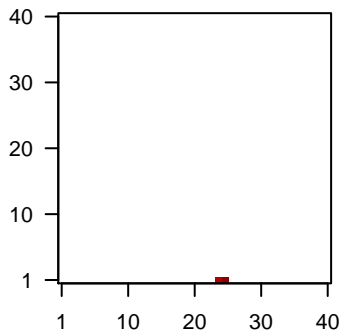
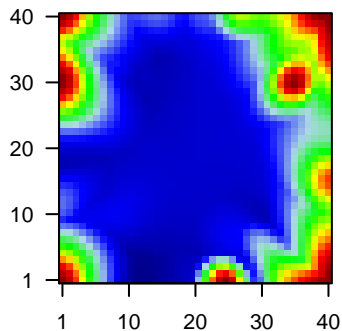
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG0000001	2.14	-0.26	0.98	ALDOB aldolase B, fructose-bisphosphate [Source:HGNC Symbol;Acc:HGNC:602]
2	ENSG0000001	2	-0.1	0.98	APOA4 apolipoprotein A-IV [Source:HGNC Symbol;Acc:HGNC:602]
3	ENSG0000001	1.85	-0.15	0.99	RBP2 retinol binding protein 2, cellular [Source:HGNC Symbol;Acc:HGNC:610]
4	ENSG0000001	1.46	-0.07	0.98	APOC3 apolipoprotein C-III [Source:HGNC Symbol;Acc:HGNC:610]
5	ENSG0000001	1.38	-0.08	0.98	CYP3A4 cytochrome P450, family 3, subfamily A, polypeptide 4 [Source:HGNC Symbol;Acc:HGNC:610]
6	ENSG0000001	1.36	-0.06	0.98	S100G S100 calcium binding protein G [Source:HGNC Symbol;Acc:HGNC:610]
7	ENSG0000000	1.3	-0.29	0.86	SMIM24 small integral membrane protein 24 [Source:HGNC Symbol;Acc:HGNC:610]
8	ENSG0000001	1.24	-0.06	0.98	APOA1 apolipoprotein A-I [Source:HGNC Symbol;Acc:HGNC:600]
9	ENSG0000000	1.18	-0.06	0.98	APOB apolipoprotein B [Source:HGNC Symbol;Acc:HGNC:603]
10	ENSG0000001	1.13	-0.18	0.96	SLC5A1 solute carrier family 5 (sodium/glucose cotransporter), member 1 [Source:HGNC Symbol;Acc:HGNC:600]
11	ENSG0000002	1.12	-0.08	0.97	GSTA1 glutathione S-transferase alpha 1 [Source:HGNC Symbol;Acc:HGNC:600]
12	ENSG0000001	1.11	-0.06	0.98	CCL25 chemokine (C-C motif) ligand 25 [Source:HGNC Symbol;Acc:HGNC:600]
13	ENSG0000001	1.09	-0.34	0.68	SERPINA5 serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 5 [Source:HGNC Symbol;Acc:HGNC:600]
14	ENSG0000001	1.07	-0.23	0.94	FBP1 fructose-1,6-bisphosphatase 1 [Source:HGNC Symbol;Acc:HGNC:600]
15	ENSG0000000	1.06	-0.08	0.98	CREB3L3 cAMP responsive element binding protein 3-like 3 [Source:HGNC Symbol;Acc:HGNC:600]
16	ENSG0000001	1.04	-0.09	0.87	DEFA5 defensin, alpha 5, Paneth cell-specific [Source:HGNC Symbol;Acc:HGNC:600]
17	ENSG0000000	0.98	-0.05	0.98	FOLH1B folate hydrolase (prostate-specific membrane antigen) 1 [Source:HGNC Symbol;Acc:HGNC:600]
18	ENSG0000000	0.98	-0.1	0.96	SI sucrase-isomaltase (alpha-glucosidase) [Source:HGNC Symbol;Acc:HGNC:600]
19	ENSG0000001	0.97	-0.21	0.94	CBR1 carbonyl reductase 1 [Source:HGNC Symbol;Acc:HGNC:154]
20	ENSG0000001	0.94	-0.05	0.98	CYP1A1 cytochrome P450, family 1, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:600]

## Geneset Overrepresentation

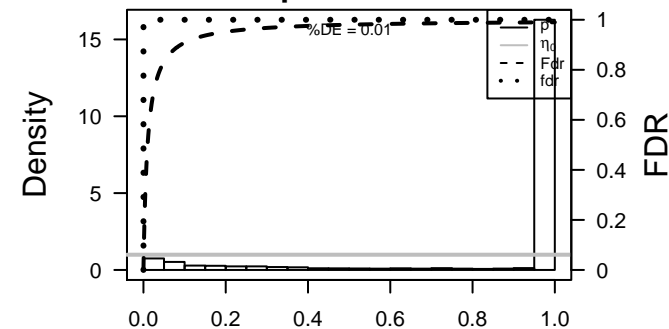
Rank	p-value	#in/all	Geneset
1	2e-23	23 / 229	GSE/ HSHAO_LIVER_SPECIFIC_GENES
2	5e-20	40 / 1418	BP small molecule metabolic process
3	6e-16	20 / 336	GSE/ VECCHI_GASTRIC_CANCER_EARLY_DN
4	3e-13	47 / 3064	Glio Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
5	1e-12	13 / 154	BP xenobiotic metabolic process
6	2e-12	10 / 67	GSE/ KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
7	9e-12	15 / 268	CC apical plasma membrane
8	2e-11	8 / 38	BP lipoprotein metabolic process
9	3e-11	16 / 346	GSE/ SANSOM_APC_TARGETS_DN
10	4e-11	9 / 64	BP cholesterol homeostasis
11	5e-11	6 / 14	CC chylomicron
12	7e-11	7 / 27	BP cholesterol efflux
13	9e-11	11 / 132	GSE/ REACTOME_BIOLOGICAL_OXIDATIONS
14	3e-10	39 / 2638	CC extracellular exosome
15	5e-10	8 / 56	BP retinoid metabolic process
16	6e-10	6 / 20	CC very-low-density lipoprotein particle
17	7e-10	19 / 641	GSE/ FEVR_CTNNB1_TARGETS_UP
18	1e-09	8 / 62	GSE/ KEGG_RETINOL_METABOLISM
19	2e-09	6 / 24	BP triglyceride homeostasis
20	2e-09	19 / 688	Color Lembecke_TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN
21	2e-09	7 / 43	GSE/ REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT
22	2e-09	8 / 68	GSE/ KEGG_DRUG_METABOLISM_CYTOCHROME_P450
23	3e-09	18 / 616	Color Lembecke_TCGA-expr_kmeans_M_CIMP_H_DN
24	3e-09	10 / 141	GSE/ OHGUCHI_LIVER_HNF4A_TARGETS_DN
25	7e-09	5 / 14	GSE/ REACTOME_XENOBIOTICS
26	7e-09	6 / 29	BP drug metabolic process
27	8e-09	7 / 51	MF monooxygenase activity
28	1e-08	12 / 257	GSE/ HOSHIDA_LIVER_CANCER_SUBCLASS_S3
29	1e-08	8 / 83	BP lipid transport
30	1e-08	7 / 54	BP arachidonic acid metabolic process
31	1e-08	5 / 16	GSE/ REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT
32	2e-08	8 / 87	GSE/ CADWELL_ATG16L1_TARGETS_UP
33	2e-08	16 / 541	GSE/ FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
34	2e-08	10 / 170	GSE/ CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
35	3e-08	5 / 18	MF cholesterol transporter activity
36	3e-08	7 / 62	GSE/ LEE_LIVER_CANCER_ACOX1_DN
37	4e-08	5 / 19	BP epoxygenase P450 pathway
38	5e-08	7 / 65	GSE/ REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS
39	5e-08	23 / 1213	GSE/ YOSHIMURA_MAPK8_TARGETS_UP
40	6e-08	10 / 191	BP lipid metabolic process

### Overview Map

### Spot



### p-values





# Overexpression Spots

## Spot Summary: D

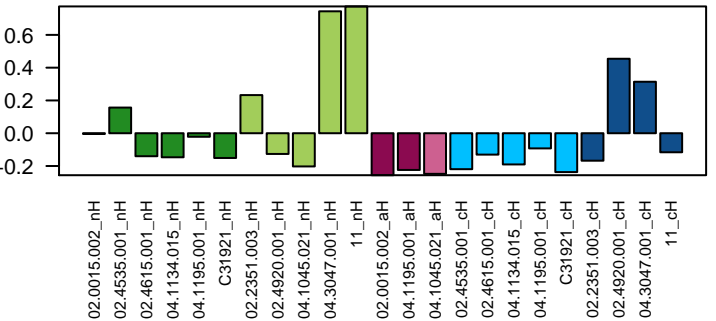
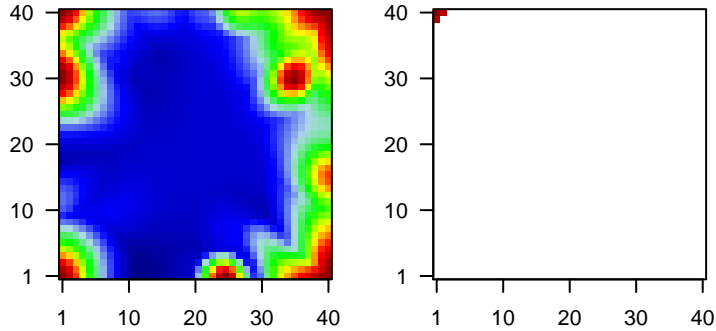
# metagenes = 3  
# genes = 134

<r> metagenes = 1  
<r> genes = 0.86  
beta: r2= 0.97 / log p= -Inf

# samples with spot = 5 ( 21.7 %)  
other\_normHNPCC : 3 ( 60 %)  
other\_cancerHNPCC : 2 ( 50 %)

### Overview Map

### Spot

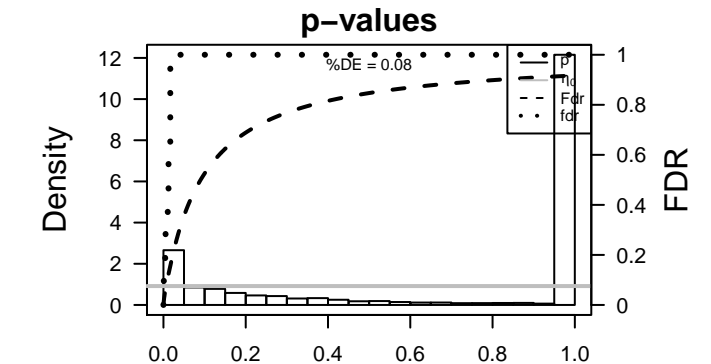


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG0000001	1.59	-0.8	0.89	DES desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	ENSG0000001	1.46	-0.53	0.96	MYH11 myosin, heavy chain 11, smooth muscle [Source:HGNC Syml
3	ENSG0000001	1.44	-0.52	0.95	CNN1 calponin 1, basic, smooth muscle [Source:HGNC Symbol;Acc
4	ENSG0000001	1.42	-0.68	0.94	ACTG2 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
5	ENSG0000001	1.35	-0.91	0.93	MYL9 myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:1
6	ENSG0000001	1.32	-0.37	0.97	SYNM synemin, intermediate filament protein [Source:HGNC Symbc
7	ENSG0000001	1.3	-0.58	0.97	FLNA filamin A, alpha [Source:HGNC Symbol;Acc:HGNC:3754]
8	ENSG0000001	1.29	-0.49	0.96	TPM2 tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
9	ENSG0000001	1.24	-0.52	0.74	IGFBP7 insulin-like growth factor binding protein 7 [Source:HGNC Sy
10	ENSG0000001	1.21	-0.38	0.99	CSRP1 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
11	ENSG0000001	1.2	-0.74	0.94	TAGLN transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
12	ENSG0000000	1.17	-0.45	0.96	HSPB6 heat shock protein, alpha-crystallin-related, B6 [Source:HG
13	ENSG0000000	1.17	-0.25	0.95	NDE1 nudE neurodevelopment protein 1 [Source:HGNC Symbol;Ac
14	ENSG0000001	1.17	-0.39	0.99	CALD1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
15	ENSG0000000	1.17	-0.4	0.97	FHL1 four and a half LIM domains 1 [Source:HGNC Symbol;Acc:HC
16	ENSG0000001	1.17	-0.36	0.99	LMOD1 leiomodrin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
17	ENSG0000001	1.14	-0.57	0.96	ACTA2 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
18	ENSG0000000	1.14	-0.3	0.98	MYLK myosin light chain kinase [Source:HGNC Symbol;Acc:HGNC:
19	ENSG0000001	1.12	-0.31	0.98	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
20	ENSG0000001	1.1	-0.27	0.98	SYNPO2synaptopodin 2 [Source:HGNC Symbol;Acc:HGNC:17732]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-61	3 / 16	Cancer LIU_PROSTATE_CANCER_DN
2	5e-50	37 / 132	Colon Marisa_CRC-cluster-b
3	5e-37	38 / 303	GSE/ PASINI_SUZ12_TARGETS_DN
4	5e-33	29 / 160	GSE/ BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
5	2e-32	42 / 535	GSE/ CHICAS_RB1_TARGETS_CONFLUENT
6	2e-32	37 / 368	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2B
7	2e-29	38 / 478	GSE/ LIM_MAMMARY_STEM_CELL_UP
8	7e-29	28 / 196	GSE/ PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
9	8e-26	26 / 198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	4e-25	29 / 294	GSE/ ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
11	3e-23	30 / 378	CC focal adhesion
12	4e-23	31 / 418	GSE/ SWEET_LUNG_CANCER_KRAS_DN
13	1e-22	37 / 692	GSE/ WONG_ADULT_TISSUE_STEM_MODULE
14	4e-21	30 / 445	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
15	6e-21	12 / 22	GSE/ REACTOME_SMOOTH_MUSCLE_CONTRACTION
16	8e-21	14 / 40	GSE/ TOMLINS_PROSTATE_CANCER_DN
17	4e-20	11 / 18	GSE/ NIELSEN_LEIOMYOSARCOMA_CNN1_UP
18	4e-19	21 / 195	HM HALLMARK_MYOGENESIS
19	4e-19	27 / 399	Disea GUDJ_psooriasis down
20	5e-19	25 / 326	GSE/ SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
21	9e-19	17 / 105	BP muscle contraction
22	3e-18	13 / 44	GSE/ REACTOME_MUSCLE_CONTRACTION
23	3e-18	24 / 314	Lymph Hopp_June14_MMML937_tumors+controls_group.overexpression_E_GC-
24	3e-18	24 / 315	Lymph WIRTH_lymphoma937_spot E
25	3e-17	15 / 86	GSE/ SASSON_RESPONSE_TO_GONADOTROPHINS_DN
26	1e-16	19 / 195	GSE/ KEGG_FOCAL_ADHESION
27	4e-16	27 / 525	GSE/ WEST_ADRENOCORITICAL_TUMOR_DN
28	8e-16	20 / 248	GSE/ ONDER_CDH1_TARGETS_2_UP
29	8e-16	19 / 215	GSE/ SENESE_HDAC1_AND_HDAC2_TARGETS_DN
30	1e-15	14 / 87	GSE/ SASSON_RESPONSE_TO_FORSKOLIN_DN
31	2e-15	20 / 261	Lymph LENZ_Stromal signature 1
32	1e-14	13 / 81	GSE/ SWEET_KRAS_TARGETS_UP
33	3e-14	14 / 109	CC Z disc
34	5e-14	23 / 436	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
35	1e-13	15 / 148	Colon Marisa_CRC-cluster-a
36	2e-13	10 / 40	GSE/ PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
37	2e-13	53 / 2638	CC extracellular exosome
38	4e-13	20 / 341	GSE/ GRUETZMANN_PANCREATIC_CANCER_UP
39	6e-13	18 / 267	GSE/ WANG_SMARCE1_TARGETS_UP
40	6e-13	11 / 63	GSE/ TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL



Rank	p-value	#in/all
1	0.000000	124
2	0.000000	124
3	0.000000	124
4	0.000000	124
5	0.000000	124
6	0.000000	124
7	0.000000	124
8	0.000000	124
9	0.000000	124
10	0.000000	124
11	0.000000	124
12	0.000000	124
13	0.000000	124
14	0.000000	124
15	0.000000	124
16	0.000000	124
17	0.000000	124
18	0.000000	124
19	0.000000	124
20	0.000000	124
21	0.000000	124
22	0.000000	124
23	0.000000	124
24	0.000000	124
25	0.000000	124
26	0.000000	124
27	0.000000	124
28	0.000000	124
29	0.000000	124
30	0.000000	124
31	0.000000	124
32	0.000000	124
33	0.000000	124
34	0.000000	124
35	0.000000	124
36	0.000000	124
37	0.000000	124
38	0.000000	124
39	0.000000	124
40	0.000000	124
41	0.000000	124
42	0.000000	124
43	0.000000	124
44	0.000000	124
45	0.000000	124
46	0.000000	124
47	0.000000	124
48	0.000000	124
49	0.000000	124
50	0.000000	124
51	0.000000	124
52	0.000000	124
53	0.000000	124
54	0.000000	124
55	0.000000	124
56	0.000000	124
57	0.000000	124
58	0.000000	124
59	0.000000	124
60	0.000000	124
61	0.000000	124
62	0.000000	124
63	0.000000	124
64	0.000000	124
65	0.000000	124
66	0.000000	124
67	0.000000	124
68	0.000000	124
69	0.000000	124
70	0.000000	124
71	0.000000	124
72	0.000000	124
73	0.000000	124
74	0.000000	124
75	0.000000	124
76	0.000000	124
77	0.000000	124
78	0.000000	124
79	0.000000	124
80	0.000000	124
81	0.000000	124
82	0.000000	124
83	0.000000	124
84	0.000000	124
85	0.000000	124
86	0.000000	124
87	0.000000	124
88	0.000000	124
89	0.000000	124
90	0.000000	124
91	0.000000	124
92	0.000000	124
93	0.000000	124
94	0.000000	124
95	0.000000	124
96	0.000000	124
97	0.000000	124
98	0.000000	124
99	0.000000	124
100	0.000000	124

Geneset	#in/all
downregulating_genes_meth_UP	124
HORVATH_age_genes_meth_UP	124
TESCHENDORFF_age_hypermethylated	124

Rank	p-value	#in/all
1	0.000000	306
2	0.000000	306
3	0.000000	306
4	0.000000	306
5	0.000000	306
6	0.000000	306
7	0.000000	306
8	0.000000	306
9	0.000000	306
10	0.000000	306
11	0.000000	306
12	0.000000	306
13	0.000000	306
14	0.000000	306
15	0.000000	306
16	0.000000	306
17	0.000000	306
18	0.000000	306
19	0.000000	306
20	0.000000	306
21	0.000000	306
22	0.000000	306
23	0.000000	306
24	0.000000	306
25	0.000000	306
26	0.000000	306
27	0.000000	306
28	0.000000	306
29	0.000000	306
30	0.000000	306
31	0.000000	306
32	0.000000	306
33	0.000000	306
34	0.000000	306
35	0.000000	306
36	0.000000	306
37	0.000000	306
38	0.000000	306
39	0.000000	306
40	0.000000	306
41	0.000000	306
42	0.000000	306
43	0.000000	306
44	0.000000	306
45	0.000000	306
46	0.000000	306
47	0.000000	306
48	0.000000	306
49	0.000000	306
50	0.000000	306
51	0.000000	306
52	0.000000	306
53	0.000000	306
54	0.000000	306
55	0.000000	306
56	0.000000	306
57	0.000000	306
58	0.000000	306
59	0.000000	306
60	0.000000	306
61	0.000000	306
62	0.000000	306
63	0.000000	306
64	0.000000	306
65	0.000000	306
66	0.000000	306
67	0.000000	306
68	0.000000	306
69	0.000000	306
70	0.000000	306
71	0.000000	306
72	0.000000	306
73	0.000000	306
74	0.000000	306
75	0.000000	306
76	0.000000	306
77	0.000000	306
78	0.000000	306
79	0.000000	306
80	0.000000	306
81	0.000000	306
82	0.000000	306
83	0.000000	306
84	0.000000	306
85	0.000000	306
86	0.000000	306
87	0.000000	306
88	0.000000	306
89	0.000000	306
90	0.000000	306
91	0.000000	306
92	0.000000	306
93	0.000000	306
94	0.000000	306
95	0.000000	306
96	0.000000	306
97	0.000000	306
98	0.000000	306
99	0.000000	306
100	0.000000	306

Geneset	#in/all
muscle contraction	306
extracellular matrix organization	306
platelet aggregation	306
cell-matrix adhesion	306
axon guidance	306
cell adhesion	306
extracellular matrix disassembly	306
endothelial cell differentiation	306
negative regulation of arthritis	306
angiogenesis	306
muscle filament sliding	306
regulation of muscle contraction	306
actin filament organization	306
cell junction assembly	306
blood coagulation	306
integrin-mediated signaling pathway	306
sarcomere organization	306
extracellular fibrin organization	306
response to mechanical stimulus	306
collagen catabolic process	306

Rank	p-value	#in/all
1	0.000000	109
2	0.000000	109
3	0.000000	109
4	0.000000	109
5	0.000000	109
6	0.000000	109
7	0.000000	109
8	0.000000	109
9	0.000000	109
10	0.000000	109
11	0.000000	109
12	0.000000	109
13	0.000000	109
14	0.000000	109
15	0.000000	109
16	0.000000	109
17	0.000000	109
18	0.000000	109
19	0.000000	109
20	0.000000	109
21	0.000000	109
22	0.000000	109
23	0.000000	109
24	0.000000	109
25	0.000000	109
26	0.000000	109
27	0.000000	109
28	0.000000	109
29	0.000000	109
30	0.000000	109
31	0.000000	109
32	0.000000	109
33	0.000000	109
34	0.000000	109
35	0.000000	109
36	0.000000	109
37	0.000000	109
38	0.000000	109
39	0.000000	109
40	0.000000	109
41	0.000000	109
42	0.000000	109
43	0.000000	109
44	0.000000	109
45	0.000000	109
46	0.000000	109
47	0.000000	109
48	0.000000	109
49	0.000000	109
50	0.000000	109
51	0.000000	109
52	0.000000	109
53	0.000000	109
54	0.000000	109
55	0.000000	109
56	0.000000	109
57	0.000000	109
58	0.000000	109
59	0.000000	109
60	0.000000	109
61	0.000000	109
62	0.000000	109
63	0.000000	109
64	0.000000	109
65	0.000000	109
66	0.000000	109
67	0.000000	109
68	0.000000	109
69	0.000000	109
70	0.000000	109
71	0.000000	109
72	0.000000	109
73	0.000000	109
74	0.000000	109
75	0.000000	109
76	0.000000	109
77	0.000000	109
78	0.000000	109
79	0.000000	109
80	0.000000	109
81	0.000000	109
82	0.000000	109
83	0.000000	109
84	0.000000	109
85	0.000000	109
86	0.000000	109
87	0.000000	109
88	0.000000	109
89	0.000000	109
90	0.000000	109
91	0.000000	109
92	0.000000	109
93	0.000000	109
94	0.000000	109
95	0.000000	109
96	0.000000	109
97	0.000000	109
98	0.000000	109
99	0.000000	109
100	0.000000	109

Geneset	#in/all
z disc	109
extracellular exosome	109
stress fiber	109
extracellular matrix	109
cytoskeleton	109
costamere	109
sarcolemma	109
cytoskeleton	109
extracellular space	109
membrane raft	109
basement membrane	109
proteinaceous extracellular matrix	109
ruffle	109
cell surface	109
plasma membrane	109
cytosol	109
lamellipodium	109
protein complex	109
cleavage furrow	109

Rank	p-value	#in/all
1	0.000000	1920
2	0.000000	1920
3	0.000000	1920
4	0.000000	1920
5	0.000000	1920
6	0.000000	1920
7	0.000000	1920
8	0.000000	1920
9	0.000000	1920
10	0.000000	1920
11	0.000000	1920
12	0.000000	1920
13	0.000000	1920
14	0.000000	1920
15	0.000000	1920
16	0.000000	1920
17	0.000000	1920
18	0.000000	1920
19	0.000000	1920
20	0.000000	1920
21	0.000000	1920
22	0.000000	1920
23	0.000000	1920
24	0.000000	1920
25	0.000000	1920
26	0.000000	1920
27	0.000000	1920
28	0.000000	1920
29	0.000000	1920
30	0.000000	1920
31	0.000000	19

# Overexpression Spots

## Spot Summary: E

# metagenes = 5  
# genes = 81

<r> metagenes = 0.99

<r> genes = 0.71

beta: r2= 0.03 / log p= -0.36

# samples with spot = 1 ( 4.3 %)

MLH1\_cancerHNPCC : 1 ( 20 %)

## Spot Genelist

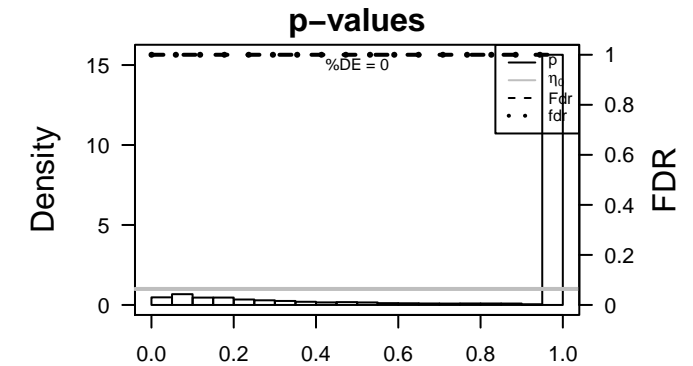
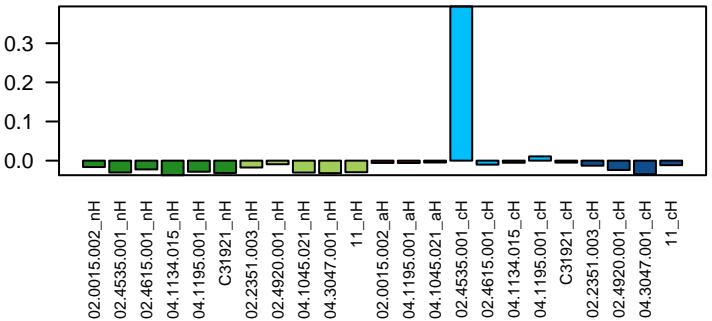
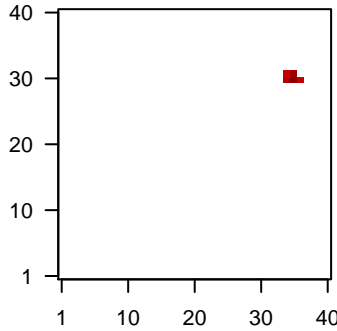
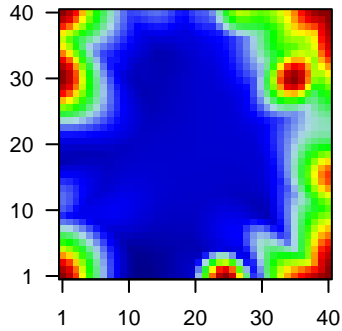
Rank	ID	max e	r	min e	Description
1	ENSG000000	1.19	-0.05	0.99	PAGE1 P antigen family, member 1 (prostate associated) [Source:HGNC]
2	ENSG000000	0.98	-0.05	0.99	
3	ENSG000000	0.93	-0.04	0.99	GAGE12G antigen 12G [Source:HGNC Symbol;Acc:HGNC:31907]
4	ENSG000000	0.93	-0.04	0.99	GAGE2DG antigen 12F [Source:HGNC Symbol;Acc:HGNC:31906]
5	ENSG000000	0.86	-0.04	0.99	
6	ENSG000000	0.79	-0.04	0.99	GAGE12J antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	ENSG000000	0.79	-0.13	0.8	RBP4 retinol binding protein 4, plasma [Source:HGNC Symbol;Acc:HGNC:31905]
8	ENSG000000	0.79	-0.04	0.99	
9	ENSG000000	0.78	-0.04	0.99	
10	ENSG000000	0.74	-0.03	0.99	GAGE12E antigen 12E [Source:HGNC Symbol;Acc:HGNC:31905]
11	ENSG000000	0.73	-0.17	0.76	EXOC3 exocyst complex component 3 [Source:HGNC Symbol;Acc:HGNC:31905]
12	ENSG000000	0.72	-0.07	0.95	GPC3 glypican 3 [Source:HGNC Symbol;Acc:HGNC:4451]
13	ENSG000000	0.72	-0.03	0.99	MAGEA6melanoma antigen family A6 [Source:HGNC Symbol;Acc:HGNC:31905]
14	ENSG000000	0.71	-0.03	0.99	GAGE12C antigen 12C [Source:HGNC Symbol;Acc:HGNC:28402]
15	ENSG000000	0.71	-0.03	0.99	GAGE12D antigen 12D [Source:HGNC Symbol;Acc:HGNC:31904]
16	ENSG000000	0.7	-0.03	0.99	
17	ENSG000000	0.66	-0.03	0.99	MAGEA3melanoma antigen family A3 [Source:HGNC Symbol;Acc:HGNC:31905]
18	ENSG000000	0.64	-0.03	0.99	GAGE12H antigen 12H [Source:HGNC Symbol;Acc:HGNC:31908]
19	ENSG000000	0.63	-0.09	0.86	CYP2B6 cytochrome P450, family 2, subfamily B, polypeptide 6 [Source:HGNC Symbol;Acc:HGNC:4099]
20	ENSG000000	0.63	-0.03	0.99	GAGE8 G antigen 2A [Source:HGNC Symbol;Acc:HGNC:4099]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-11	19 / 746	Chr Chr X
2	4e-08	21 / 1425	Chr Chr 19
3	1e-06	5 / 48	GSE/ SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER
4	5e-06	4 / 30	Glio Gorovets_LGG_NB_subclass
5	8e-06	7 / 193	GSE/ WANG_CISPLATIN_RESPONSE_AND_XPC_UP
6	2e-05	3 / 15	GSE/ MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
7	3e-05	3 / 16	GSE/ LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
8	8e-05	3 / 22	GSE/ HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP
9	8e-05	5 / 117	GSE/ YEGNASUBRAMANIAN_PROSTATE_CANCER
10	1e-04	3 / 24	GSE/ DALESSIO_TSA_RESPONSE
11	1e-04	3 / 26	GSE/ HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
12	2e-04	7 / 316	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
13	5e-04	9 / 616	Color Lembecke_TCGA-expr_kmeans_M_CIMP_H_DN
14	6e-04	3 / 43	GSE/ JAEGER_METASTASIS_UP
15	6e-04	4 / 103	GSE/ SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
16	7e-04	9 / 640	BP oxidation-reduction process
17	7e-04	6 / 284	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
18	8e-04	3 / 49	GSE/ GERHOLD_ADIPOGENESIS_UP
19	9e-04	4 / 112	Lymp Hopp_June14_MMML937_tumors+controls_group.overexpression_MM_MM
20	1e-03	4 / 116	Lymp WIRTH_lymphoma937_spot MM
21	1e-03	3 / 56	BP retinoid metabolic process
22	1e-03	4 / 126	BP anatomical structure morphogenesis
23	2e-03	3 / 63	GSE/ RAMASWAMY_METASTASIS_UP
24	2e-03	2 / 17	GSE/ RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
25	2e-03	2 / 18	CC dendrite membrane
26	2e-03	2 / 18	GSE/ SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP
27	2e-03	2 / 19	BP positive regulation of innate immune response
28	3e-03	2 / 20	CC inclusion body
29	3e-03	2 / 20	GSE/ WENG_POR_TARGETS_GLOBAL_UP
30	3e-03	23 / 3406	Color ReprPC_Colon
31	3e-03	2 / 23	GSE/ HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP
32	4e-03	2 / 25	BP positive regulation of smoothened signaling pathway
33	4e-03	5 / 282	GSE/ AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
34	5e-03	21 / 3109	Color TssP_Colon
35	5e-03	3 / 89	BP phototransduction, visible light
36	5e-03	2 / 28	BP embryonic hindlimb morphogenesis
37	5e-03	2 / 28	GSE/ COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOMASTOMA_DN
38	5e-03	6 / 419	GSE/ HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
39	5e-03	4 / 185	GSE/ REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES
40	5e-03	2 / 29	MF SH2 domain binding

## Overview Map

## Spot







# Overexpression Spots

## Spot Summary: F

# metagenes = 8  
# genes = 258

<r> metagenes = 0.99

<r> genes = 0.63

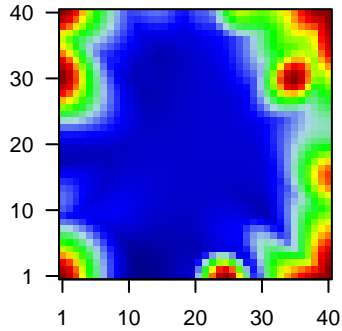
beta: r2= 0.3 / log p= -2.2

# samples with spot = 3 ( 13 %)

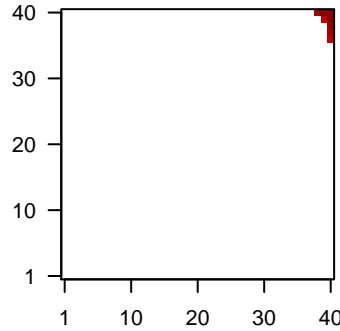
MLH1\_adenomaHNPCC : 1 ( 50 %)

MLH1\_cancerHNPCC : 2 ( 40 %)

### Overview Map



### Spot

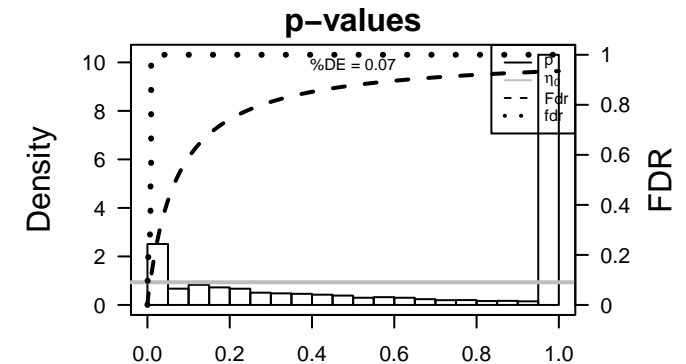
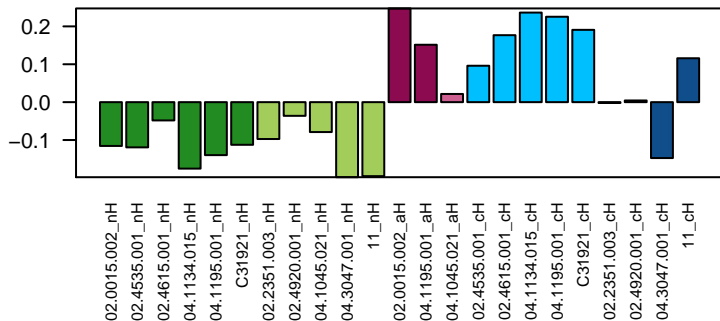


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSG0000001	1.84	-0.57	0.58	REG1A regenerating islet-derived 1 alpha [Source:HGNC Symbol;Acc:HGNC:17190]
2	ENSG0000001	1.71	-0.34	0.53	ITLN1 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;Acc:HGNC:17190]
3	ENSG0000001	1.65	-0.75	0.62	OLFM4 olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
4	ENSG0000001	1.57	-0.24	0.59	REG3A regenerating islet-derived 3 alpha [Source:HGNC Symbol;Acc:HGNC:17190]
5	ENSG0000001	1.47	-0.28	0.6	MMP1 matrix metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:17190]
6	ENSG0000001	1.33	-0.75	0.44	PLA2G2A phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:17190]
7	ENSG0000001	1.31	-0.29	0.38	CXCL8 chemokine (C-X-C motif) ligand 8 [Source:HGNC Symbol;Acc:HGNC:17190]
8	ENSG0000001	1.27	-0.21	0.53	REG1B regenerating islet-derived 1 beta [Source:HGNC Symbol;Acc:HGNC:17190]
9	ENSG0000001	1.25	-0.21	0.61	DMBT1 deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:HGNC:17190]
10	ENSG0000001	1.17	-0.36	0.53	REG4 regenerating islet-derived family, member 4 [Source:HGNC Symbol;Acc:HGNC:17190]
11	ENSG0000001	1.16	-0.2	0.58	MMP3 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC:17190]
12	ENSG0000001	1.15	-0.44	0.76	SPINK1 serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symbol;Acc:HGNC:17190]
13	ENSG0000000	1.15	-0.35	0.5	CLCA1 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HGNC:17190]
14	ENSG0000002	1.1	-0.18	0.56	TNFRSF6B tumor necrosis factor receptor superfamily, member 6b, decoy [Source:HGNC Symbol;Acc:HGNC:17190]
15	ENSG0000001	1.05	-0.66	0.87	LCN2 lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
16	ENSG0000001	1.05	-0.87	0.82	AGR2 anterior gradient 2, protein disulphide isomerase family member 2 [Source:HGNC Symbol;Acc:HGNC:17190]
17	ENSG0000001	0.97	-0.41	0.68	SPINK4 serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symbol;Acc:HGNC:17190]
18	ENSG0000001	0.91	-1	0.79	GPX2 glutathione peroxidase 2 [Source:HGNC Symbol;Acc:HGNC:17190]
19	ENSG0000001	0.87	-0.25	0.49	CYP2S1 cytochrome P450, family 2, subfamily S, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:17190]
20	ENSG0000001	0.84	-0.29	0.58	S100A9 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:HGNC:17190]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-34	67 / 813	GSE/ GRADE_COLON_CANCER_UP
2	2e-27	44 / 400	GSE/ VECCHI_GASTRIC_CANCER_EARLY_UP
3	1e-24	30 / 174	GSE/ LI_AMPLIFIED_IN_LUNG_CANCER
4	6e-24	52 / 713	Colon Pentrack_CRC_TCGA_group.over_C_normal_DN
5	2e-23	26 / 128	GSE/ SABATES_COLORECTAL_ADENOMA_UP
6	6e-23	58 / 944	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	1e-19	51 / 850	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
8	8e-19	23 / 138	GSE/ ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	8e-19	47 / 754	GSE/ MARTENS_TRETINOIN_RESPONSE_DN
10	1e-17	42 / 645	GSE/ CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
11	3e-17	47 / 830	Colon Pentrack_CRC_TCGA_corr_R_normal_DN
12	4e-17	20 / 113	GSE/ WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	7e-17	30 / 323	GSE/ PENG_Glutamine_Deprivation_DN
14	8e-17	31 / 350	GSE/ RHEIN_ALL_GLUCCORTICOID_THERAPY_DN
15	9e-17	38 / 550	Cancr Lembecke_Normal vs Adenoma
16	9e-17	39 / 582	GSE/ CAIRO_HEPATOBLASTOMA_CLASSES_UP
17	4e-16	173 / 8123	Colon TssF_Colon
18	5e-16	36 / 519	GSE/ BERENJENO_TRANSFORMED_BY_RHOA_UP
19	2e-15	25 / 239	GSE/ PENG_RAPAMYCIN_RESPONSE_DN
20	3e-15	20 / 138	GSE/ DANG_MYC_TARGETS_UP
21	5e-15	84 / 2638	CC extracellular exosome
22	9e-15	3 / 16	Cancr SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
23	3e-14	26 / 292	GSE/ MUELLER_PLURINET
24	4e-14	21 / 179	GSE/ GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
25	6e-14	3 / 16	Cancr RHODES_CANCER_META_SIGNATURE
26	7e-14	36 / 608	Disea GUDJ_psooriasis_up
27	9e-14	19 / 145	Glio WILLSCHER_GBM_Verhaak-CL_up ( C)
28	1e-13	24 / 259	BP translation
29	2e-13	26 / 317	Lymp TARTE_Plasmablast signature
30	2e-13	41 / 807	Lymp Hopp_June14_MMML937_tumors+controls_group.overexpression_D_cell
31	9e-13	40 / 811	Lymp WIRTH_lymphoma937_spot D
32	1e-12	14 / 74	GSE/ TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
33	1e-12	2 / 14	Cancr LIU_PROSTATE_CANCER_UP
34	2e-12	14 / 77	GSE/ MORI_PRE_BI_LYMPHOCYTE_UP
35	2e-12	14 / 78	Lymp TARTE_Plasma cell signature
36	2e-12	15 / 95	GSE/ CROONQUIST_IL6_DEPRIVATION_DN
37	2e-12	25 / 327	GSE/ WONG_EMBRYONIC_STEM_CELL_CORE
38	3e-12	5 / 16	Cancr RHODES_UNDIFFERENTIATED_CANCER
39	3e-12	12 / 52	GSE/ ISHIDA_E2F_TARGETS
40	4e-12	18 / 158	GSE/ HOFFMANN_LARGE_TO_SMALL_PRE_BI_LYMPHOCYTE_UP







# Overexpression Spots

## Spot Summary: G

# metagenes = 6  
# genes = 151

<r> metagenes = 0.99  
<r> genes = 0.68  
beta: r2= 0.18 / log p= -1.37

# samples with spot = 1 ( 4.3 %)  
other\_cancerHNPCC : 1 ( 25 %)

## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG0000001	1.82	-0.23	0.9	FABP4 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
2	ENSG0000002	1.31	-0.26	0.92	GPX3 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:10513]
3	ENSG0000002	1.17	-0.14	0.36	HBB hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
4	ENSG0000001	1.11	-0.22	0.93	SFRP2 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:HGNC:10513]
5	ENSG0000001	1.02	-0.41	0.88	CTGF connective tissue growth factor [Source:HGNC Symbol;Acc:HGNC:10513]
6	ENSG0000001	1.01	-0.27	0.78	BGN biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
7	ENSG0000001	1	-0.16	0.92	ADAMTS1 ADAM metalloproteinase with thrombospondin type 1 motif, 1 [Source:HGNC Symbol;Acc:HGNC:10513]
8	ENSG0000001	0.98	-0.25	0.66	SAA1 serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]
9	ENSG0000001	0.95	-0.62	0.76	DUSP1 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:10513]
10	ENSG0000001	0.9	-0.24	0.83	FOSB FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:HGNC:10513]
11	ENSG0000001	0.89	-0.09	0.86	ADIPOQ adiponectin, C1Q and collagen domain containing [Source:HGNC Symbol;Acc:HGNC:10513]
12	ENSG0000001	0.87	-0.18	0.97	C11orf96 chromosome 11 open reading frame 96 [Source:HGNC Symt]
13	ENSG0000001	0.86	-0.22	0.82	C10orf10 chromosome 10 open reading frame 10 [Source:HGNC Symt]
14	ENSG0000001	0.86	-0.19	0.85	G0S2 G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]
15	ENSG0000001	0.84	-0.09	0.94	RBP7 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:HGNC:10513]
16	ENSG0000001	0.83	-0.15	0.91	SERPINC1 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) [Source:HGNC Symbol;Acc:HGNC:10513]
17	ENSG0000002	0.82	-0.11	0.91	MUSTN1 musculoskeletal, embryonic nuclear protein 1 [Source:HGNC Symbol;Acc:HGNC:10513]
18	ENSG0000002	0.81	-0.2	0.83	ACKR1 atypical chemokine receptor 1 (Duffy blood group) [Source:HGNC Symbol;Acc:HGNC:10513]
19	ENSG0000001	0.81	-0.07	0.91	PLIN1 perilipin 1 [Source:HGNC Symbol;Acc:HGNC:9076]
20	ENSG0000001	0.78	-0.09	0.91	ID4 inhibitor of DNA binding 4, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:HGNC:10513]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-25	26 / 192	HM HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	9e-25	31 / 326	GSE/ SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	1e-24	38 / 574	Cancer_Lembcke_Colonc_Inflammation
4	1e-23	40 / 692	GSE/ WONG_ADULT_TISSUE_STEM_MODULE
5	6e-23	49 / 1176	CC extracellular space
6	8e-23	32 / 413	GSE/ BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
7	5e-22	30 / 368	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2B
8	1e-21	34 / 525	GSE/ WEST_ADRENOCORTICAL_TUMOR_DN
9	1e-21	28 / 314	Lymp Hopp_June14_MMML937_tumors+controls_group.overexpression_E_GC-TC
10	1e-21	28 / 315	Lymp WIRTH_lymphoma937_spot E
11	1e-21	24 / 202	CC extracellular matrix
12	2e-21	24 / 204	GSE/ BOQUEST_STEM_CELL_DN
13	1e-20	42 / 945	GSE/ NABA_MATRISOME
14	3e-19	48 / 1374	CC extracellular region
15	3e-19	22 / 198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	3e-18	22 / 220	GSE/ MCLACHLAN_DENTAL_CARIES_UP
17	3e-18	17 / 101	GSE/ CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
18	1e-17	30 / 522	GSE/ SMID_BREAST_CANCER_LUMINAL_B_DN
19	2e-17	14 / 59	Lymp LENZ_Stromal signature 2
20	3e-17	27 / 418	GSE/ SWEET_LUNG_CANCER_KRAS_DN
21	8e-17	13 / 50	GSE/ BURTON_ADIPOGENESIS_PEAK_AT_2HR
22	3e-16	13 / 55	GSE/ CROONQUIST_STROMAL_STIMULATION_UP
23	1e-15	20 / 224	BP angiogenesis
24	1e-15	14 / 78	GSE/ NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
25	2e-15	13 / 62	GSE/ ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
26	4e-15	11 / 37	GSE/ UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
27	2e-14	14 / 95	GSE/ CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
28	3e-14	10 / 31	GSE/ AMIT_SERUM_RESPONSE_40_MCF10A
29	7e-14	18 / 210	GSE/ MCLACHLAN_DENTAL_CARIES_DN
30	7e-14	24 / 436	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
31	7e-14	15 / 126	GSE/ ZHU_CMV_ALL_DN
32	7e-14	17 / 181	GSE/ WU_CELL_MIGRATION
33	9e-14	14 / 104	GSE/ WESTON_VEGFA_TARGETS
34	1e-13	19 / 248	GSE/ ONDER_CDH1_TARGETS_2_UP
35	2e-13	19 / 261	Lymp LENZ_Stromal signature 1
36	2e-13	19 / 261	GSE/ NABA_CORE_MATRISOME
37	3e-13	13 / 90	GSE/ ZHU_CMV_24_HR_DN
38	3e-13	16 / 166	GSE/ CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN
39	3e-13	18 / 230	GSE/ WINTER_HYPOXIA_METAGENE
40	3e-13	16 / 168	GSE/ NAGASHIMA_NRG1_SIGNALING_UP

### Overview Map

### Spot

