Lrf suppresses prostate cancer through repression of a Sox9dependent pathway for cellular senescence bypass and tumor invasion

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Suppl. Figure 1. Lrf transgenic mice show no signs of prostate neoplasia. (a) IHC and Western Blot analysis for Lrf expression in the three prostate lobes of 12 week-old WT mice. (b) Schematic representation of ARR2PB-Lrf construct.
(c) IHC and Western Blot analysis for Flag-Lrf expression in the three prostate lobes of 16-18 month-old transgenic mice.
(d) H&E of Anterior, Ventral, and Dorso-Lateral prostate lobes of WT and Lrf transgenic 16-18 month-old mice.
(e) Incidence of prostate hyperplasia and PIN in WT and Lrf transgenic 16-18 month-old mice.

a



Suppl. Figure 2. Loss of Lrf does not affect p53 functions. (a-b) qPCR analysis of p21 and Mdm2 expression in *WT* (black bars), *Lrflox/flox;Pb-Cre4* (green bars), *Ptenflox/flox;Pb-Cre4* (red bars), and *Ptenflox/flox;Lrfflox/flox;Pb-Cre4* (blue bars) prostates of n=3/genotype 12 week-old mice. Data are presented as mean \pm standard deviation. (c) WB analysis for Lrf and p19Arf in *Lrfflox/flox* mouse embryonic fibroblasts (MEFs) infected by Cre-recombinase or control vector.

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Suppl. Figure 3. Loss of Lrf dictates Sox9 transcriptional hyper-activity. (a) Heat-map of three different Sox9 transcriptional target genes (Mia, Dmbt1, and H19) in *WT*, *Lrfflox/flox;Pb-Cre4*, *Ptenflox/flox;Pb-Cre4*, and *Ptenflox/flox;Lrfflox/flox;Pb-Cre4* prostates of n=3/genotype 12 week-old mice. (b) WB analysis of SOX9 and LRF over-expression for the luciferase assay in PC3. (c) Dual-luciferase assay with a Sox9-reporter in DU145 cells shows that LRF suppresses the transcriptional activity of SOX9 in a dose-dependent manner.



Suppl. Figure 4. microRNA profiling. Nanostring nCounter® Mouse miRNA Expression Assay Kit technology was used to analyze the miRNAs differentially expressed (p<0.05) in *Ptenflox/flox;Lrfflox/flox;Pb-Cre4* versus *Ptenflox/flox;Pb-Cre4* prostates of n=3/genotype 12 week-old mice.



Suppl. Figure 5. LRF mRNA is significantly down-regulated in a subset of primary human prostate cancers (Oncomine).



Suppl. Figure 6. LRF downregulation by the oncogenic miR106b~25 cluster. (a) aCGH analysis showing genetic loss of LRF in 18% of advanced human prostate cancer. **(b)** Schematic representation of miR-106b~25 cluster inside the Intron 13 of the MCM7 gene. **(c)** miR-106b and miR-93 sequences. **(d)** Schematic representation of ZBTB7a RNA with the miR-106b/93 target sites highlighted (red triangles) in the 3'UTR. **(e)** Western blot analysis showing reduction in the levels of LRF in DU145 prostate cell lines transfected by miR-106b, miR-93, and miR-25.



Suppl. Figure 7. Immunohistochemical staining for LRF and SOX9 in high Gleason score (8-10) prostate tumors. (a) Representative image of immunohistochemical staining of LRF and SOX9 in human prostate tumors. (b) Percentage of SOX9hi/LRFnorm and SOX9hi/LRFneg in high Gleason score (8-10) prostate cancer (n=38).

Suppl. Table 2: oPOSSUM analysis

a

TF	Background gene hits	Background gene	Target gene hits	Target gene s non-hits	Background TFBS hits	I Background TFBS rate	Target TFBS	Target TFBS	Z score	Fisher score	Fisher
		non-hits					hits	rate			
HNF1A	2552	12598	93	287	3659	0.0022	146	0.003	13.43	1.199e-04	1.20E-04
Foxa2	8526	6624	242	138	29104	0.0152	908	0.0159	5.253	2.231e-03	2.23E-03
HLF	5181	9969	168	212	9448	0.0049	305	0.0054	5.095	4.129e-05	4.13E-05
ELF5	12185	2965	329	51	73478	0.0287	2250	0.0296	4.518	1.177e-03	1.18E-03
SRY	10985	4165	298	82	68971	0.0269	2111	0.0278	4.306	5.456e-03	5.46E-03
sox9*	8854	6296	250	130	29087	0.0114	904	0.0119	4.181	2.225e-03	2.23E-03
Ar	585	14565	19	361	619	0.0006	22	0.0007	3.948	1.582e-01	1.58E-01
REL	7798	7352	232	148	18677	0.0081	583	0.0085	3.866	1.281e-04	1.28E-04
SRF	713	14437	23	357	793	0.0004	28	0.0005	3.16	1.372e-01	1.37E-01
Foxql	5673	9477	166	214	12614	0.006	392	0.0063	3.027	8.009e-03	8.01E-03

b

TF Backg gene l	round hits	Backgr gene non-hit	ound s	Target gene hit	Targ s non	jet gene -hits	Background TFBS hits	I Background TFBS rate	Target TFBS hits	Target TFBS rate	Z score	Fisher score	Fisher
		1.0	1 4 4 7			0.1.0	F 0 0	0 0004	1.6	0 0 0 1	00.10	R 000 05	
SRF	/	13	1443	3/ 2	.9	248	193	0.0004	46	0.001	20.17	/.083e-05	/.08E-05
TAL1-TCF3	5	459	9691	L 1	.32	145	10058	0.0052	293	0.0061	8.706	5.608e-05	5.61E-05
Roaz	4	281	1086	59 1	10	167	7214	0.0047	205	0.0053	6.756	3.172e-05	3.17E-05
Sox5	1	1256	3894	1 2	26	51	73449	0.0223	1954	0.0236	6.584	2.827e-03	2.83E-03
Ar	5	85	1456	55 2	20	257	619	0.0006	21	0.0008	6.422	6.531e-03	6.53E-03
TLX1-NFIC	8	11	1433	39 2	26	251	879	0.0005	29	0.0007	5.449	4.646e-03	4.65E-03
Pax6	1	024	1412	26 2	24	253	1165	0.0007	36	0.0009	4.597	1.310e-01	1.31E-01
Hand1-Tcfe2a	a 1	0659	4491	L 2	25	52	44947	0.0195	1179	0.0203	4.556	2.877e-05	2.88E-05
Foxql	5	673	9477	7 1	20	157	12614	0.006	341	0.0065	4.399	2.701e-02	2.70E-02
NHLH1	4	534	1061	L6 1	17	160	7563	0.0039	207	0.0043	4.191	1.125e-05	1.13E-05

Suppl. Table 3: Ingenuity pathway analysis

Top Canonical Pathways		
Name	p-value	Ratio
Virus Entry via Endocytic Pathways ILK Signaling LPS/IL-1 Mediated Inhibition of RXR Function Tight Junction Signaling Integrin Signaling	5.53E-07 2E-06 1.1E-05 1.56E-05 1.75E-05	16/99 (0.162) 23/192 (0.12) 24/239 (0.1) 19/161 (0.118) 22/207 (0.106)

h	Тор	Networks									
	ID	Associated Network Functions		Score							
	1	Cancer, Cellular Development, Tumor Morphology		43							
	2	2 Post-Translational Modification, Cellular Function and Maintenance, Skeletal and Muscular System Development and Function									
	3	3 Drug Metabolism, Protein Synthesis, Glutathione Depletion In Liver									
	4	Neurological Disease, Psychological Disorders, Carbohydrate Metabolism									
	5	5 Cellular Movement, Tissue Development, Nervous System Development and Function									
С	Тор	o Bio Functions									
	Dise	eases and Disorders	p-value # Me	olecule							
	Car	ncer	1.40E-21 - 6.71E-03	311							
	Rep	productive System Disease	5.16E-20 - 4.87E-03	173							
	Gas	strointestinal Disease	4.44E-12 - 6.57E-03	155							
	Org	anismal Injury and Abnormalities	4.54E-05 - 6.05E-03	63							
	Her	reditary Disorder	6.80E-05 - 5.36E-03	40							
	Mol	ecular and Cellular Functions	p-value # Mo	olecule							
	Cel	Iular Movement	5.16E-10 - 6.70E-03	151							
	Cel	I Death and Survival	6.82E-09 - 6.19E-03	222							
	Cel	lular Growth and Proliferation	6.13E-08 - 6.25E-03	235							
	Cel	lular Assembly and Organization	3.30E-07 - 6.57E-03	146							
	Cel	Iular Function and Maintenance	3.30E-07 - 6.32E-03	144							
	Phy	siological System Development and Function	p-value # Mo	olecule							
	Org	janismal Development	5.43E-07 - 6.82E-03	151							
	Car	diovascular System Development and Function	8.69E-07 - 6.05E-03	133							
	Org	jan Morphology	2.11E-06 - 6.82E-03	124							
	Ske	eletal and Muscular System Development and Function	2.11E-06 - 6.82E-03	113							
	Tiss	sue Morphology	2.39E-06 - 6.58E-03	165							

d Top Molecules

а

Log Ratio up-regulated		Log Ratio down	-regulated
Molecules	Exp. Value	Molecules	Exp. Value
SPINK1	† 6.009	XAF1*	↓ -6.066
REG3A*	† 5.483	TNNC2	↓ -3.197
REG1A	† 4.769	PRR9	↓ -3.185
MIA	† 4.340	CPA3	↓ -2.781
Muc2 (includes EG:17831)	† 4.334	MYH11	↓ -2.479
CLCA1	† 4.333	INMT	↓ -2.459
H19	† 4.246	PCP4	↓ -2.431
ONECUT2*	† 4.087	SYNPO2*	↓ -2.431
CXCL6	† 4.071	Defb1*	↓ -2.408
KRT20	↑ 3.954	ACTA2*	↓ -2.303

Suppl. Table 4: GSEA analysis

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	*	·			NOM	EDR	FWER	RANK	
	C2 Gene Signature	SIZE	ES	NES	p-val	g-val	p-val	AT MAX	LEADING EDGE
1	HSA03022 BASAL TRANSCRIPTION	15	0.71	2.08	0.000	0.074	0.064	860	tags=40% list=13% signal=46%
	FACTORS	10	0.7 1	2.00	0.000	0.014	0.004	000	
2	UVB NHEK3 C2	30	0.57	1.98	0.000	0.152	0.234	1913	tags=63%, list=28%, signal=88%
3	LAL KO 3MO UP	22	0.58	1.83	0.004	0.501	0.746	960	tags=41%, list=14%, signal=47%
4	HYPOXIA REVIEW	53	0.46	1.81	0.002	0.465	0.812	1051	tags=34%, list=15%, signal=40%
5	HYPOXIA REG UP	22	0.56	1.79	0.005	0.462	0.870	978	tags=41%, list=14%, signal=48%
6	AS3 FIBRO DN	19	0.59	1.79	0.006	0.388	0.872	1547	tags=53%, list=23%, signal=68%
7	LEE DENA UP	41	0.47	1.78	0.004	0.359	0.896	915	tags=29%, list=13%, signal=34%
8	LAL KO 6MO UP	28	0.52	1.77	0.002	0.354	0.928	960	tags=39%, list=14%, signal=46%
9	CHEN HOXA5 TARGETS UP	112	0.39	1.77	0.000	0.318	0.929	2096	tags=46%, list=31%, signal=66%
10	DEATHPATHWAY	16	0.59	1.77	0.009	0.286	0.929	1710	tags=56%, list=25%, signal=75%
11	UVB NHEK3 ALL	284	0.34	1.76	0.000	0.279	0.939	1631	tags=36%, list=24%, signal=45%
12	ZHAN MULTIPLE MYELOMA	20	0.56	1.73	0.008	0.337	0.972	84	tags=15%, list=1%, signal=15%
	_VS_NORMAL_DN								
13	HSA03050_PROTEASOME	16	0.57	1.72	0.006	0.331	0.979	2683	tags=88%, list=39%, signal=144%
14	UVB_SCC_DN	69	0.41	1.72	0.004	0.325	0.985	1636	tags=41%, list=24%, signal=53%
15	ET743_SARCOMA_DN	171	0.36	1.71	0.000	0.311	0.986	1887	tags=41%, list=28%, signal=55%
16	UVB_SCC_UP	67	0.41	1.71	0.000	0.301	0.987	1576	tags=40%, list=23%, signal=52%
17	HINATA NFKB UP	59	0.42	1.71	0.000	0.287	0.988	1561	tags=39%, list=23%, signal=50%
18	FLECHNER KIDNEY	25	0.51	1.69	0.015	0.315	0.990	1226	tags=48%, list=18%, signal=58%
	TRANSPLANT WELL PBL DN								
19	LINDSTEDT DEND 8H VS 48H UP	30	0.50	1.69	0.009	0.308	0.990	408	tags=27%, list=6%, signal=28%
20	CELL_MOTILITY	57	0.42	1.67	0.002	0.334	0.997	1759	tags=47%, list=26%, signal=63%
		0175	50		NOM	FDR	FWER	RANK	
	C4 Gene Signature	SIZE	ES	NES	p-val	q-val	p-val	AT MAX	LEADING EDGE
1	GCM CBEB	53	0.52	2 04	0.000	0 049	0.048	2063	tags=58% list=30% signal=83%
2	MODULE 239	85	0.46	2.02	0.000	0.032	0.062	2085	tags=52% list=31% signal=74%
3	GNE2 TDG	23	0.10	1 99	0.002	0.002	0.084	2027	tags=74% list=30% signal=105%
4	GNF2_KPNB1	53	0.50	1.00	0.002	0.020	0.004	2060	tags=62% list=30% signal=89%
5	GNE2_UBE2I	18	0.60	1.07	0.000	0.020	0.236	1834	tags=72% list=27% signal=99%
6	GNE2_XBCC5	58	0.02	1.90	0.000	0.051	0.258	2159	tags=57% list=32% signal=83%
7	MODULE 233	17	0.40	1.89	0.000	0.001	0.282	2062	tags=71% list=30% signal=101%
8	MODULE 342	115	0.04	1.83	0.000	0.040	0.202	1474	tags=43% list=22% signal=55%
g	MODULE 295	15	0.40	1.00	0.000	0.077	0.407	647	tags 40% , list 22% , signal 40%
10	MODULE 91	30	0.51	1.70	0.006	0.100	0.661	2713	tags = 87% list=40% signal=143%
10	GNE2 BNIP2	23	0.51	1.76	0.006	0.107	0.698	1675	tags=65% list=25% signal=86%
12	MODULE 357	30	0.00	1.76	0.000	0.100	0.000	1520	tags=51% list=22% signal=66%
13	GNE2 APEX1	65	0.40	1.76	0.000	0.100	0.701	2027	tags=48% list=30% signal=67%
14	MODULE 139	48	0.40	1.76	0.000	0.004	0.704	1121	tags= 40% list= 16% signal= 47%
15	MODULE 297	38	0.48	1 75	0.008	0.090	0 736	1520	tags 10% , list 10% , signal 11%
16	GCM RAD21	27	0.52	1 74	0.008	0.089	0 752	1913	tags=56% list=28% signal=77%
17	GCM_ZNE198	64	0.42	1 73	0.000	0.090	0.776	2592	tags=70% list=38% signal=112%
18	MORE PPP2R5E	53	0.43	1 71	0.008	0 102	0.825	1603	tags=47% list=24% signal=61%
19			00	1 71	0.002	0.099	0.830	1010	tags=30% list=15% signal=35%
		69	0 4 1		0.002	0.000	0.833	4500	tago 0070, not 1070, olginar 0070
20	MODULE_181 MODULE_154	69 35	0.41 0.48	1.71	0.008	0.095	0.000	1520	tags=51%, list=22%, signal=66%
20	MODULE_181 MODULE_154	69 35	0.41 0.48	1.71	0.008	0.095 FDR	FWER	RANK	tags=51%, list=22%, signal=66%
20	MODULE_181 MODULE_154 C5 Gene Signature	69 35 SIZE	0.41 0.48 ES	1.71 NES	0.008 NOM p-val	0.095 FDR q-val	FWER p-val	RANK AT MAX	tags=51%, list=22%, signal=66% LEADING EDGE
20 1	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN	69 35 SIZE 20	0.41 0.48 ES 0.61	1.71 NES 1.93	0.008 NOM p-val 0.000	0.095 FDR q-val 0.295	FWER p-val 0.214	RANK AT MAX 721	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33%
10 20 1 2	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY	69 35 SIZE 20 28	0.41 0.48 ES 0.61 0.52	1.71 NES 1.93 1.81	0.008 NOM p-val 0.000 0.008	0.095 FDR q-val 0.295 0.473	6.035 FWER p-val 0.214 0.547	1520 RANK AT MAX 721 2522	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124%
20 1 2 TRANS	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS	69 35 SIZE 20 28	0.41 0.48 ES 0.61 0.52	1.71 NES 1.93 1.81	0.008 NOM p-val 0.000 0.008	0.095 FDR q-val 0.295 0.473	6.653 FWER p-val 0.214 0.547	RANK AT MAX 721 2522	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124%
1 20 1 2 TRANS	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN	69 35 SIZE 20 28 16	0.41 0.48 ES 0.61 0.52 0.60	1.71 NES 1.93 1.81 1.81	0.008 NOM p-val 0.000 0.008	0.095 FDR q-val 0.295 0.473 0.330	0.003 FWER p-val 0.214 0.547 0.561	1520 RANK AT MAX 721 2522 647	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48%
1 2 TRANS 3 LYASE	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY	69 35 SIZE 20 28 16	0.41 0.48 ES 0.61 0.52 0.60	1.71 NES 1.93 1.81 1.81	0.008 NOM p-val 0.000 0.008	0.095 FDR q-val 0.295 0.473 0.330	0.555 FWER 0.214 0.547 0.561	The second sec	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48%
1 20 1 2 TRANS 3 LYASE_ 4	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL GTPASE	69 35 SIZE 20 28 16 30	0.41 0.48 ES 0.61 0.52 0.60 0.51	1.71 NES 1.93 1.81 1.81 1.78	0.008 NOM p-val 0.000 0.008 0.008	0.095 FDR q-val 0.295 0.473 0.330 0.335	0.535 FWER 0.214 0.547 0.561 0.659	1520 RANK AT MAX 721 2522 647 1763	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67%
1 20 1 2 TRANS 3 _LYASE_ 4 REGUL	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR ACTIVITY	69 35 SIZE 20 28 16 30	0.41 0.48 ES 0.61 0.52 0.60 0.51	1.71 NES 1.93 1.81 1.81 1.78	0.008 NOM p-val 0.000 0.008 0.008 0.008	0.095 FDR q-val 0.295 0.473 0.330 0.335	6.053 FWER p-val 0.214 0.547 0.561 0.659	RANK AT MAX 721 2522 647 1763	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67%
1 20 1 2 TRANS 3 LYASE_ 4 REGUL 5	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE ACTIVITY	69 35 SIZE 20 28 16 30 22	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55	1.71 NES 1.93 1.81 1.81 1.78 1.77	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281	FWER p-val 0.214 0.547 0.561 0.659 0.679	1520 RANK AT MAX 721 2522 647 1763 2522	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129%
1 2 TRANS 3 _LYASE_ 4 _REGUL 5 TRANS	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING GROUPS OTHER THAN AMINO	69 35 SIZE 20 28 16 30 22 ACYL GF	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS	1.71 NES 1.93 1.81 1.81 1.78 1.77	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281	FWER p-val 0.214 0.547 0.561 0.659 0.679	RANK AT MAX 721 2522 647 1763 2522	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129%
1 2 TRANS 3 _LYASE_ 4 REGUL 5 TRANS 6	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINC CYTOPLASMIC MEMBRANE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS 0.42	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832	RANK AT MAX 721 2522 647 1763 2522 1028	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34%
1 2 TRANS 3 _LYASE_ 4 _REGUL 5 _TRANS 6 BOUND	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS 0.42	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832	RANK AT MAX 721 2522 647 1763 2522 1028	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34%
1 2 TRANS 3 LYASE 4 REGUL 5 TRANS 6 BOUND 7	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINC CYTOPLASMIC_MEMBRANE _VESICLE CYTOPLASMIC VESICLE MEMBRANE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS 0.42 0.55	1.71 NES 1.93 1.81 1.81 1.77 1.72 1.71	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%=
10 1 2 TRANS 3 LYASE_4 REGUL 5 BOUND 7 8	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINOC CYTOPLASMIC_MEMBRANE _VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE BOUND VESICLE	69 35 20 28 16 30 22 0_ACYL_GF 66 18 67	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS 0.42 0.55 0.41	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=26%, signal=67% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33%
1 20 1 2 TRANS 3 _LYASE_ 4 REGUL 5 TRANS 6 BOUND 7 8 9	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE CYTOPLASMIC_VESICLE	69 35 20 28 16 30 22 0_ACYL_GF 66 18 67 67	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=26%, signal=67% tags=82%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33%
1 20 1 2 TRANS 3 LYASE_4 4 REGUL 5 TRANS 6 BOUND 7 8 9 10	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID METABOLIC PROCESS	69 35 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 ROUPS 0.42 0.55 0.41 0.36	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028 1112	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=67% tags=28%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33%
1 20 1 2 TRANS 3 LYASE_4 REGUL 5 REGUL 5 TRANS 6 BOUND 7 8 9 10 11	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE _VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 148 69	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.36 0.40	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.376 0.325 0.293 0.293	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1112 1028	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32%
1 20 1 2 TRANS 3 LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPL ASMIC_VESICLE PART	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.36 0.40 0.55	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.293	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.925 0.963	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 0 1028 0	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=15%, signal=32% tags=28%, list=15%, signal=32% tags=6% list=15%, signal=6%
1 20 1 2 TRANS 3 _LYASE_ 4 _REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.293 0.325	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.925 0.963 0.972	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 112 1028 0 1028 0 1028 0 1096	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=32% tags=25%, list=16%, signal=29%
1 20 1 2 TRANS 3 _LYASE_ 4 REGUL 5 TRANS 6 TRANS 6 BOUND 7 8 9 10 11 12 13 14	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38 0.50	1.71 NES 1.93 1.81 1.81 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.293 0.319 0.325 0.305	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.905 0.963 0.972 0.972	Ib20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1112 1028 1028 1028 1028 1028 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=6% tags=28%, list=16%, signal=6% tags=28%, list=16%, signal=6% tags=28%, list=16%, signal=6% tags=28%, list=16%, signal=6% tags=28%, list=16%, signal=6%
1 20 1 2 TRANS 3 _LYASE_ 4 _REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO MO	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE _VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYCOUPLED VEMENT_OF_SUBSTANCES	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38 0.50	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.293 0.319 0.325 0.305	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907 0.925 0.963 0.972 0.972	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 0 1028 1028 112 1028 0 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=26%, list=0%, signal=6% tags=25%, list=16%, signal=29% tags=28%, list=27%, signal=65%
1 20 1 2 TRANS 3 _LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_ACTING	69 35 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38 0.50	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.0011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.319 0.325 0.305	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.925 0.963 0.972 0.972	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1112 1028 0 1028 1012 1028 0 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=15%, signal=32% tags=6%, list=0%, signal=6% tags=25%, list=16%, signal=29% tags=48%, list=27%, signal=65%
1 20 1 2 TRANS 3 _LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 ON_AC	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYCOUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITYACTING ID_ANHYDRIDESCATALYZING	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.41 0.36 0.40 0.55 0.38 0.50	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013 0.002 0.013 0.002 0.010	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.319 0.325 0.305 0.298	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.925 0.963 0.972 0.972	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1112 1028 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=0%, signal=6% tags=25%, list=0%, signal=6% tags=25%, list=0%, signal=6% tags=25%, list=27%, signal=68%
1 20 1 2 TRANS 3 _LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 12 13 14 TO_MO 15 ON_AC TRANS	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38 0.50 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013 0.002 0.010	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.298	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.925 0.963 0.972 0.972	1520 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1028 1028 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=26%, list=0%, signal=6% tags=25%, list=0%, signal=6% tags=48%, list=27%, signal=68%
1 20 1 2 TRANS 3 LYASE 4 - REGUL 5 _ TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 _ ON_AC _ TRANS SUBSTI	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE P_VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYCOUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITYACTING ID_ANHYDRIDESCATALYZING MEMBRANE_MOVEMENT_OF ANCES	69 35 SIZE 20 28 16 30 22 0-ACYL_GF 66 18 67 67 148 69 18 81 23 22	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.36 0.40 0.55 0.38 0.50 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013 0.002 0.010	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.340 0.325 0.293 0.293 0.305 0.298	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.905 0.963 0.972 0.972	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1112 1028 1096 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=6% tags=25%, list=27%, signal=65% tags=50%, list=27%, signal=68%
1 20 1 2 TRANS 3 _LYASE_4 _REGUL 5 _TRANS 6 _BOUND 7 8 9 10 11 12 13 14 _TO_MO 15 _ON_AC _TRANS _SUBST/ 16	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYCOUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDESCATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE MEMBRANE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22 22	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.41 0.41 0.41 0.55 0.38 0.50 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.013 0.010 0.010	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.298	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.925 0.963 0.972 0.972 0.977 0.977	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1096 1820 0 0 0 1820 0 0 0 1820 0 0 0 1820 0 0 0 1820 0 0 1820 0 0 1820 0 0 0 0 1820 0 1820 1820	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=6%= tags=28%, list=15%, signal=6%= tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=32% tags=25%, list=16%, signal=29% tags=48%, list=27%, signal=65% tags=50%, list=0%, signal=68%
1 20 1 2 TRANS 3 LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 ON_AC TRANS SUBST/ 16 17	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22 19 152	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.41 0.41 0.55 0.42 0.55 0.41 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.010 0.019 0.000	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.298 0.376 0.371	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907 0.972 0.972 0.972	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1096 1820 0 1120	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=29% tags=25%, list=16%, signal=6% tags=50%, list=27%, signal=68% tags=5%, list=0%, signal=5% tags=5%, list=0%, signal=5% tags=26%, list=16%, signal=30%
1 20 1 2 TRANS 3 LYASE 4 _REGUL 5 _TRANS 6 _BOUND 7 8 9 10 11 12 13 14 _TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 MORPH	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE MEMBRANE ANATOMICAL_STRUCTURE IOGENESIS	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22 22 19 152	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.36 0.40 0.55 0.38 0.50 0.51 0.51 0.52 0.34	1.71 NES 1.93 1.81 1.81 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.69 1.65 1.65 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.010 0.019 0.000	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.298 0.376 0.376	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907 0.907 0.972 0.972 0.972 0.977	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1028 1028 0 1028 0 1028 0 1028 0 1820 0 1120	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=6%, list=0%, signal=6% tags=25%, list=27%, signal=68% tags=5%, list=0%, signal=5% tags=26%, list=16%, signal=30%
1 20 1 2 TRANS 3 LYASE_4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 _MORPH 18	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINC CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYACTING ID_ANHYDRIDESCATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE IOGENESIS GUANYL_NUCCEOTIDE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 148 69 18 81 23 22 19 152 10	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.41 0.36 0.40 0.55 0.38 0.50 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66 1.65 1.65 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.010 0.019 0.000 0.031	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.298 0.376 0.371 0.528	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907 0.907 0.972 0.972 0.972 0.977 0.992 0.994 1.000	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 0 1096 1820 0 1120 848	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=6%, list=0%, signal=6% tags=25%, list=0%, signal=65% tags=50%, list=27%, signal=68% tags=5%, list=0%, signal=5% tags=26%, list=16%, signal=30% tags=32%, list=12%, signal=30%
1 20 1 2 TRANS 3 LYASE 4 REGUL 5 TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 _MORPH 18 FXCHA	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE IOGE FACTOR_ACTIVITY_	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22 19 152 19	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.36 0.40 0.55 0.38 0.50 0.51 0.52 0.34 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.68 1.66 1.65 1.65 1.65 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.010 0.010 0.019 0.0031	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.319 0.325 0.305 0.298 0.376 0.371 0.528	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.925 0.963 0.972 0.972 0.977 0.992 0.994 1.000	RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 1028 0 1096 1820 0 1120 848	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=6%, list=0%, signal=6% tags=25%, list=0%, signal=6% tags=50%, list=27%, signal=68% tags=5%, list=0%, signal=5% tags=26%, list=16%, signal=30% tags=32%, list=12%, signal=36%
1 20 1 2 TRANS 3 LYASE 4 -REGUL 5 _TRANS 6 BOUND 7 8 9 10 11 12 13 14 _TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 _MORPH 18 _EXCHA 19	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE IOGENESIS GUANYL_NUCLEOTIDE NGE_FACTOR_ACTIVITY GTPASE	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 67 148 69 18 81 23 22 19 152 19 65	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.41 0.41 0.55 0.41 0.55 0.41 0.55 0.41 0.55 0.41 0.55 0.41 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.41 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.55 0.55 0.55 0.55 0.55 0.55 0.5	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.69 1.65 1.65 1.65 1.65 1.65 1.65 1.65	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.010 0.010 0.019 0.0031 0.011	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.293 0.293 0.319 0.325 0.305 0.298 0.376 0.371 0.528 0.509	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.925 0.963 0.972 0.972 0.977 0.992 0.994 1.000 1.000	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028 1028 1029 1028 1029 1096 1820 0 1120 848 925	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=32% tags=26%, list=27%, signal=68% tags=50%, list=0%, signal=5% tags=26%, list=12%, signal=30% tags=32%, list=12%, signal=36% tags=32%, list=12%, signal=36%
1 20 1 2 TRANS 3 LYASE 4 7 8 9 10 11 12 13 14 TO_MO 15 0 7 8 9 10 11 12 13 14 TO_MO 15 ON_AC TRANS SUBST/ 16 17 _MORPH 18 _ECCH	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE HOGENESIS GUANYL_NUCLEOTIDE NGE_FACTOR_ACTIVITY GTPASE ATOR_ACTIVITY	69 35 SIZE 20 28 16 30 22 0-ACYL_GF 66 18 67 148 69 18 81 23 22 19 152 19 65	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.55 0.38 0.50 0.51 0.51 0.51 0.52 0.34 0.51 0.51 0.52	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65 1.65 1.65 1.65 1.65 1.64 1.54	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.011 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.010 0.010 0.011 0.0011	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.393 0.293 0.305 0.293 0.305 0.298 0.305 0.298 0.376 0.371 0.528 0.509	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.925 0.963 0.972 0.972 0.977 0.992 0.977 0.992 0.994 1.000 1.000	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028 1112 1028 0 1096 1820 0 1120 848 925	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=28%, list=0%, signal=6% tags=25%, list=0%, signal=6% tags=50%, list=27%, signal=68% tags=50%, list=0%, signal=5% tags=26%, list=12%, signal=30% tags=32%, list=12%, signal=30% tags=26%, list=14%, signal=30%
1 20 1 2 TRANS 3 LYASE 4 REGUL 5 _TRANS 6 BOUND 7 8 9 10 11 12 13 14 TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 _MORPH- 18 _REGUL 20	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITYCOUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITYACTING ID_ANHYDRIDESCATALYZING MEMBRANE_MOVEMENT_OF ANATOMICAL_STRUCTURE IOGENESIS GUANYL_NUCLEOTIDE NGE_FACTOR_ACTIVITY TRANSMEMBRANE_RECEPTOP	69 35 SIZE 20 28 16 30 22 0-ACYL_GF 66 18 67 148 69 18 81 23 22 19 152 19 65 47	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.41 0.41 0.55 0.38 0.50 0.51 0.51 0.51 0.52 0.34 0.51 0.37 0.40	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.68 1.66 1.65 1.65 1.65 1.65 1.65 1.65 1.64 1.54 1.54	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.010 0.002 0.010 0.010 0.010 0.011 0.0011 0.024	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.305 0.293 0.305 0.298 0.376 0.371 0.528 0.509 0.520	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.925 0.963 0.972 0.972 0.977 0.992 0.977 0.992 0.994 1.000 1.000	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028 1028 1028 1096 1820 1820 0 1120 848 925 1381	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=28%, list=15%, signal=34% tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=33% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=32% tags=28%, list=16%, signal=29% tags=48%, list=27%, signal=65% tags=50%, list=0%, signal=5% tags=50%, list=16%, signal=30% tags=32%, list=12%, signal=30% tags=26%, list=14%, signal=30% tags=26%, list=14%, signal=30% tags=38%, list=20%, signal=30%
1 2 1 2 TRANS 3 LYASE 4 REGUL 5 _TRANS 6 _BOUND 7 8 9 10 11 12 13 14 _TO_MO 15 _ON_AC _TRANS _SUBST/ 16 17 _MORPH 18 _ECUL 20 PROTE	MODULE_181 MODULE_154 C5 Gene Signature CHROMATIN TRANSFERASE_ACTIVITY SFERRING_ACYL_GROUPS CARBON_OXYGEN ACTIVITY SMALL_GTPASE ATOR_ACTIVITY TRANSFERASE_ACTIVITY SFERRING_GROUPS_OTHER_THAN_AMINO CYTOPLASMIC_MEMBRANE VESICLE CYTOPLASMIC_VESICLE_MEMBRANE MEMBRANE_BOUND_VESICLE CYTOPLASMIC_VESICLE LIPID_METABOLIC_PROCESS VESICLE CYTOPLASMIC_VESICLE_PART DEFENSE_RESPONSE ATPASE_ACTIVITY_COUPLED VEMENT_OF_SUBSTANCES HYDROLASE_ACTIVITY_ACTING ID_ANHYDRIDES_CATALYZING MEMBRANE_MOVEMENT_OF ANCES VESICLE_MEMBRANE ANATOMICAL_STRUCTURE IOGENESIS GUANYL_NUCLEOTIDE NGE_FACTOR_ACTIVITY TRANSMEMBRANE_RECEPTOR IN TYROSINE KINASE_SIGNALING_PATHIMA	69 35 SIZE 20 28 16 30 22 0_ACYL_GF 66 18 67 148 69 18 81 23 22 19 152 19 65 47	0.41 0.48 ES 0.61 0.52 0.60 0.51 0.55 0.42 0.55 0.42 0.55 0.42 0.55 0.41 0.41 0.41 0.41 0.41 0.41 0.41 0.55 0.38 0.50 0.51 0.51 0.51 0.51 0.52 0.34 0.51 0.52 0.34 0.51	1.71 NES 1.93 1.81 1.81 1.78 1.77 1.72 1.71 1.70 1.69 1.69 1.69 1.69 1.65 1.65 1.65 1.65 1.65 1.65 1.64 1.54 1.54 1.53	0.008 NOM p-val 0.000 0.008 0.008 0.008 0.001 0.005 0.013 0.002 0.006 0.000 0.007 0.002 0.010 0.002 0.010 0.010 0.011 0.0011 0.024	0.095 FDR q-val 0.295 0.473 0.330 0.335 0.281 0.382 0.376 0.340 0.325 0.293 0.319 0.325 0.305 0.293 0.305 0.298 0.305 0.298 0.376 0.371 0.528 0.509 0.529	FWER p-val 0.214 0.547 0.561 0.659 0.679 0.832 0.877 0.890 0.907 0.907 0.907 0.907 0.972 0.972 0.977 0.992 0.994 1.000 1.000	B20 RANK AT MAX 721 2522 647 1763 2522 1028 0 1028 0 1028 1028 1028 1028 1096 1820 1820 0 1120 848 925 1381	tags=51%, list=22%, signal=66% LEADING EDGE tags=30%, list=11%, signal=33% tags=79%, list=37%, signal=124% tags=44%, list=9%, signal=48% tags=50%, list=26%, signal=67% tags=82%, list=37%, signal=129% tags=29%, list=15%, signal=34% tags=6%, list=0%, signal=6%= tags=28%, list=15%, signal=33% tags=28%, list=15%, signal=32% tags=28%, list=16%, signal=32% tags=6%, list=0%, signal=6% tags=25%, list=16%, signal=29% tags=50%, list=27%, signal=68% tags=50%, list=16%, signal=30% tags=26%, list=12%, signal=30% tags=26%, list=14%, signal=30% tags=26%, list=20%, signal=30% tags=32%, list=20%, signal=30%

GENE SYMBOL	REFERENCES
H19	Berteaux N, <i>et al</i> , The J Biol Chem, 2006
MMP7	Johnson J.L. <i>et al.</i> , Canc Res, 2011
MMP14	Johnson J.L. <i>et al.</i> , Canc Res, 2011
MMP23	Johnson J.L. <i>et al.</i> , Canc Res, 2011
WASF1	Iwanaga R. <i>et al.,</i> Oncogene, 2006
BNIP3	Gang H. <i>et al.,</i> Pediatr Cardiol, 2011
BSG	Tarin C. <i>et al.,</i> Free Rad Biol & Med, 2011
CDT1	Yoshida K. <i>et al.</i> , Oncogene, 2004
CcnD1	Lee R.J. <i>et al.,</i> Mol Cell Biol, 2000
APAF1	Furukawa Y. <i>et al</i> ., The J Biol Chem, 2002
BIN1	Cassimere E.K. <i>et al.</i> , Cell Death Diff, 2009
Casp3	Nahle Z. <i>et al.,</i> Nat Cell Biol, 2002
H2Ax	Yagi H. <i>et al.,</i> The J Biol Chem, 1995
Kpnβ1	Van der Watt P.J. <i>et al.,</i> PLoS ONE, 2011
ASK1	Kherrouche Z. <i>et al.,</i> Biochem J, 2006
MCM7	Bruemmer D. et al., Bioch Biophys Res Com, 2003
MYB	Sahin F., Sladek T.L., Int J Biol Sci, 2010
PTTG1	Zhou C. <i>et al.,</i> Mol Endocrinol, 2009
SLC44A1	Yuan Z. <i>et al</i> ., Physiol Genomics, 2006
SOX2	O'Connor M.D. <i>et al.</i> , Exp Hematol, 2011
SP3	Tapias A. <i>et al</i> ., Bioch Biophys Acta, 2008
WNT4	Devgan V. <i>et al.,</i> Genes Dev, 2005
YAP1	Cheng L. <i>et al.</i> , Oncogene, 2010

Suppl. Table 5: E2F transcriptional target genes

Suppl. Table 6: Expression profile datasets analysis

Sheet1

Study	Platform	Data source	Probesets ID	Probeset sequence analysis ¹ (when applicable)	Signal quality control ² applicable)	(when Use	Behavior ³	Reference
		050 4-4-						Tomlins et al.
Tomiins	spotted CDNA	GEO data	HS6-32-3-7		not present	no		Nat. Genet (2007)
	spotted cDNA	GEO data	Hs6-8-13-3		present	yes	DOWN *	
								Vancia et al Cancer
Vanaja	U133A	Oncomine	213299_at	ZTBT7A ^a		yes	NO CHANGE	Res (2003)
	U133A	Oncomine	213303 x at	ZBTB7A		yes	UP *	
	U133A	Oncomine	222082_at	intronic		no		
	U133B	Oncomine	230709_x_at	ZBTB7A		yes	DOWN *	
	U133B	Oncomine	226554_at	ZBTB7A		yes	NO CHANGE	
								Lanointe et al PNAS
Lapointe	spotted cDNA	Oncomine	Hs6-32-3-7			yes	NO CHANGE	(2004)
	spotted cDNA	Oncomine	Hs6-8-13-3			yes	NO CHANGE	()
	•							
								Stephenson et al.
Stephenson	U133A	GEO data	213299_at	ZTBT7A*	not present	no		Cancer (2005)
	U133A	GEO data	213303_X_at	ZBIB/A	present	yes	DOWN *	
	U 133A	GEO data	222082_al	intergonic	not present	no		
L	0133A	OLO data	213100_41	intergenie	present	110		
1	11122.4		212200 ot		not propont			Liu P. et al. Cancer
Liu	0133A	Allay Expless	215299_at	ZTBT7A*	not present	10		Res (2006)
	U133A	Array Express	213303_x_at	ZBTB7A	not present	no		
	U133A	Array Express	222082_at	intronic	not present	no		
	U133A	Array Express	219186_at	Intergenic	present	no		
	U 133B	Array Express	230709_X_at		not present	no		
L	01338	Array Express	220004_at	ZBTB/A	not present	10		
								Luo JH et al.
Luo	U95A_V2	Oncomine	39540_at	ZTBT7A ^a		yes	NO CHANGE	Mol Carcinog (2002)
	Hu35kSub_A	Oncomine	AF000561_at	ZTBT7A ^a		yes	DOWN *	
	Hu35kSub_A	Oncomine	H14210_s_at	ZBTB7A		yes	NO CHANGE	
L	Hu35kSub_D	Oncomine	RC_F04371_at	intergenic		no		
								Taular at al. Canaar
Taylor	Human Exon 1.0 ST Array	GEO data	13564	ZBTB7A		yes	DOWN *	Cell (2010)
L								
LaTulinno	1954 \/2	Oncomino	30540 at	770774				LaTulippe et al.
La runppe	033A_V2	Oncomme	39340_at	ZIBI/A°		yes	DOWN	Cancer Res (2002)
Arrodouani	11133 Plue?	Oncomino	213200 at	ZTBT7A ^a		yes		Arredouani et al. Clin
Arreuouani	UI33 Plus2	Oncomine	213299_dl	707070		VOS		Calicel Res (2009)
	11133 Plus2	Oncomine	222082 at	intronic		yes no		
	U133 Plus2	Oncomine	230709 x at	ZBTB7A		ves	UP *	
	U133 Plus2	Oncomine	226554_at	ZBTB7A		yes	DOWN *	
		0					DOI:	Grasso et al.
Grasso	Agilent Human Genome 44K	Oncomine	A_23_P16423			yes	DOWN *	Nature (2012)
L	Aglient Human Genome 44K	Uncomine	A_23_P27827			yes	DOWN -	
								Wallace et al. Cancer
Wallace	U133A 2.0	Oncomine	213299_at	ZTBT7A ^a		yes	NO CHANGE	Res (2008)
	U133A 2.0	Oncomine	213303 x at	ZBTB7A		ves	NO CHANGE	
	U133A 2.0	Oncomine	222082_at	intronic		no		
·					² Present: dotoctable sign	nal in		

Genome Browser) and BLAST ¹ Based on BLAT (UCSC present: detectable signal in less than 60% of samples

³ significance (*) when p <= 0.05; NO_CHANGE => FoldChange ~ 1

with other ZBTB family genes

⁽NCBÍ)

^a possibility of cross-hybridization

Suppl. Table 7: Clinical information from human specimens collected on TMAs

Number	٨σ٥	Organ	Dignosis	Grade	Gleason	Type
Number		O Prostate	Adenocarcinoma	Grade		Malignant
		O Prostate	Adenocarcinoma		2 1 1 1	Malignant
		6 Prostate	Adenocarcinoma		5 4T4 7 1 7	Malignant
		C Prostate	Adenocarcinoma		2 1+2	Malignant
	+ /	A Prostate	Adenocarcinoma		5 Z+Z	Malignant
	ס כ	Prostate	Adenocarcinoma		2 2+2	Malignant
	י כ ר ר	2 Prostate	Adenocarcinoma		1 1+2	Malignant
		1 Prostate	Adenocarcinoma		2 2+4	Malignant
	5 C	2 Prostate	Adenocarcinoma		2 3+4	Malignant
1	9 / D F	2 Prostate	Adenocarcinoma		3 4+5	Malignant
1	J 5	A Prostate	Adenocarcinoma		2 3+4	Malignant
1.		os Prostate	Adenocarcinoma		3 4+5	Malignant
1.	2 7	O Prostate	Adenocarcinoma		2 3+5	Malignant
1.		os Prostate	Adenocarcinoma		2 3+5	Malignant
14	+ a	SO Prostate	Adenocarcinoma		2 5+3	Malignant
1:		S Prostate	Adenocarcinoma		2 4+5	Malignant
1.		S Prostate	Adenocarcinoma		3 4+5	Malignant
1		9 Prostate	Adenocarcinoma		2 3+4	Malignant
10	5 5	67 Prostate	Adenocarcinoma		3 4+5	Malignant
1	9 / D 7	4 Prostate	Adenocarcinoma		2 3+4	Malignant
20	J 7	6 Prostate	Adenocarcinoma		2 2+5	Malignant
2.		5 Prostate	Adenocarcinoma		2 2+4	Malignant
2.	2 5	7 Prostate	Adenocarcinoma		3 4+5	Malignant
2:	3 /	7 Prostate	Adenocarcinoma		3 4+5	Malignant
24	4 / - 7	3 Prostate	Adenocarcinoma		3 4+5	Malignant
2:	5 / C	6 Prostate	Adenocarcinoma		3 5+4	Malignant
20	s s	2 Prostate	Adenocarcinoma		3 5+4	Malignant
2		8 Prostate	Adenocarcinoma		3 5+4	Malignant
20		3 Prostate	Adenocarcinoma		3 5+5	Malignant
2:		9 Prostate	Adenocarcinoma		3 3+5	Malignant
30	J /	3 Prostate	Adenocarcinoma		3 5+5	Malignant
3.		5 Prostate	Adenocarcinoma		3 5+5	Malignant
3.	28	3 Prostate	Adenocarcinoma		3 4+5	Malignant
3:	5 t	4 Prostate	Adenocarcinoma		2 3+4	Malignant
34	4 6 F	64 Prostate	Adenocarcinoma		3 4+5	Malignant
5:		9 Prostate	Adenocarcinoma		5 5+5	Malignant
21	o /	1 Prostate	Adenocarcinoma		2 3+5	Malignant
3.	כ / ד מ	1 Prostate	Adenocarcinoma		2 3+4	Malignant
20	s /		Adenocarcinoma			Malignant
3:	9 D D 7	O Prostate	Adenocarcinoma		5 5+4 2 4 5	Malignant
40	J 7 1 6	O Prostate	Adenocarcinoma		2 4+5	Malignant
4.		O Prostate	Adenocarcinoma		5 5+5 2 5 5	Malignant
4.	2 7	7 Prostate	Adenocarcinoma		5 5+5 5 E+4	Malignant
4:	כ כ	2 Prostate	Adenocarcinoma			Malignant
44	+ /	2 Prostate	Adenocarcinoma		2 5+4	Malignant
4.		O Prostate	Adenocarcinoma		2 5+4	Malignant
4	5 0 7 7	2 Prostate	Adenocarcinoma		2 5+4	Malignant
4		2 Prostate	Adenocarcinoma		2 5+4	Malignant
40		7 Prostate	Adenocarcinoma		2 1+5	Malignant
43) [5 Prostate	Adenocarcinoma		3 4+5	Malignant
5	כ כ ד	O Prostate	Normal prostate tissue	-	-	Manghallt
5.	- /) 6	5 Prostate	Normal prostate tissue	_	_	
5.	- 0 2 7	2 Prostate	Normal prostate tissue	-	-	
5.	י כ ד 1	1 Prostate	Normal prostate tissue	-	-	
5	- / 5 6	3 Prostate	Normal prostate tissue		-	
5.	- 0 5 7	7 Prostate	Normal prostate tissue		-	
5	2 קרק	5 Prostate	Normal prostate tissue		-	
5	, 2 R 7	1 Prostate	Normal prostate tissue		-	
50		8 Prostate	Normal prostate tissue	-	-	
5.			in a prostate tissue			

Suppl. Table 8: Primers sequence

PtenLoxP_Fwd 5'-AAAAGTTCCCCTGCTGATGATTTGT-3' PtenLoxP_Rev 5'-TGTTTTTGACCAATTAAAGTAGGCTGTG-3'

PCFW1 5'-TCTGAGGCCCGGTGCAT-3' PCFW2 5'-AGGGTGGTGCTCCCTCTAGAC-3' PCFW3 5'-ACCGCGGTCTAGGGATCC-3' PCRV 5'-GCTTGGGCTCCCCATGTAG-3' PCNeo 5'-GGATGTGGAATGTGTGCGAG-3'

MIA1_Fwd 5'-CTGGGCAACAGAGCAAGACT-3' MIA1_Rev 5'- ACTGCAGCCTCAACCTCCTA-3'

H19_Fwd 5'-GTGTCCCCATTCTTTGGATG-3' H19_Rev 5'- TGGTGAGACAGAAGGGGAAG-3'

DMBT1_Fwd 5'- GAACAGTGCATGGCAAAGAA-3' DMBT1_Rev 5'-GACAGCTTTCCAGGACTTGC-3'