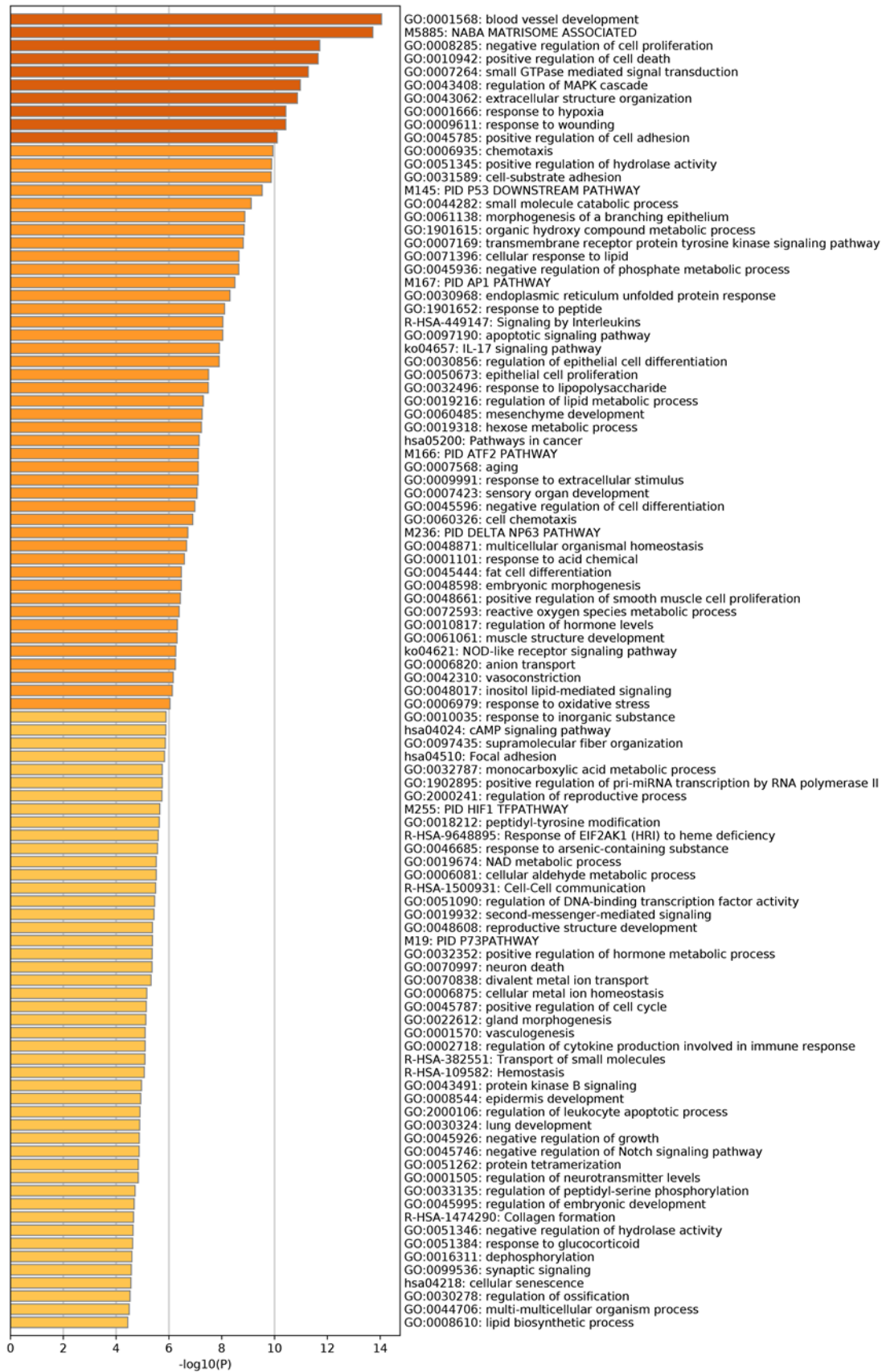


Supplementary Figure 1. The structure of the vector



Supplementary Figure 2. Enrichment Heatmap Selection of Top 100 GO terms

Supplementary Table 1. Synthesize oligo information

NO.	5'	STEM	Loop	STEM	3'
AFAP1- AS1- RNAi(918 25-1)-a	Ccgg	TGGCAAACCAGTTCTGG GCTT	CTCGA G	AAGCCCAGAACTGGTTT GCCA	TTTT Tg
AFAP1- AS1- RNAi(918 25-1)-b	aattcaaa aa	TGGCAAACCAGTTCTGG GCTT	CTCGA G	AAGCCCAGAACTGGTTT GCCA	
AFAP1- AS1- RNAi(918 26-1)-a	Ccgg	CACCTTCTTTCTCTGGGA AAT	CTCGA G	ATTCCCAGAGAAAGAA GGTG	TTTT Tg
AFAP1- AS1- RNAi(918 26-1)-b	aattcaaa aa	CACCTTCTTTCTCTGGGA AAT	CTCGA G	ATTCCCAGAGAAAGAA GGTG	
AFAP1- AS1- RNAi(918 27-1)-a	Ccgg	AGGCACACGGCTTATAAT TAA	CTCGA G	TTAATTATAAGCCGTGTG CCT	TTTT Tg
AFAP1- AS1- RNAi(918 27-1)-b	aattcaaa aa	AGGCACACGGCTTATAAT TAA	CTCGA G	TTAATTATAAGCCGTGTG CCT	

Supplementary Table 2. KEGG enrichment

ID	Description	GeneRa	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04657	IL-17 signaling pathway	20/546	94/8076	3.38E-06	0.001055	0.000876	10758/574	20
hsa04668	TNF signaling pathway	20/546	112/8076	5.18E-05	0.008083	0.006709	84699/574	20
hsa04024	cAMP signaling pathway	29/546	216/8076	0.000278	0.028929	0.024009	1387/8469	29
hsa05323	Rheumatoid arthritis	16/546	93/8076	0.000444	0.029351	0.02436	2920/7042	16
hsa04621	NOD-like receptor signaling pathway	25/546	181/8076	0.00047	0.029351	0.02436	2920/7188	25
hsa04060	Cytokine-cytokine receptor interaction	35/546	295/8076	0.000742	0.03858	0.03202	51330/360	35
hsa04510	Focal adhesion	26/546	201/8076	0.001001	0.044608	0.037022	9564/5063	26
hsa04064	NF-kappa B signaling pathway	16/546	104/8076	0.001552	0.054718	0.045414	5743/2920	16
hsa04151	PI3K-Akt signaling pathway	39/546	354/8076	0.001578	0.054718	0.045414	84699/226	39
hsa04218	Cellular senescence	21/546	156/8076	0.001813	0.056562	0.046944	1870/1075	21
hsa01521	EGFR tyrosine kinase inhibitor resistance	13/546	79/8076	0.002264	0.064223	0.053303	2261/7422	13
hsa05164	Influenza A	22/546	171/8076	0.002556	0.066468	0.055165	1387/5646	22
hsa05222	Small cell lung cancer	14/546	92/8076	0.003311	0.070108	0.058187	1870/5743	14
hsa05142	Chagas disease	15/546	102/8076	0.003371	0.070108	0.058187	7042/4792	15
hsa05146	Amoebiasis	15/546	102/8076	0.003371	0.070108	0.058187	6317/2920	15
hsa04974	Protein digestion and absorption	15/546	103/8076	0.003707	0.071701	0.059509	5646/5764	15
hsa04015	Rep1 signaling pathway	25/546	210/8076	0.003907	0.071701	0.059509	9564/2261	25
hsa05134	Legionellosis	10/546	57/8076	0.004417	0.073762	0.06122	2920/4792	10
hsa04010	MAPK signaling pathway	32/546	294/8076	0.00486	0.073762	0.06122	2261/7042	32
hsa05165	Human papillomavirus infection	35/546	331/8076	0.005252	0.073762	0.06122	1387/8469	35
hsa05215	Prostate cancer	14/546	97/8076	0.00539	0.073762	0.06122	1387/1870	14
hsa05219	Bladder cancer	8/546	41/8076	0.005429	0.073762	0.06122	1870/1118	8
hsa00051	Fructose and mannose metabolism	7/546	33/8076	0.005668	0.073762	0.06122	57103/231	7
hsa04978	Mineral absorption	10/546	59/8076	0.005693	0.073762	0.06122	490/79901	10
hsa05231	Choline metabolism in cancer	14/546	98/8076	0.00591	0.073762	0.06122	8611/5337	14
hsa04061	Viral protein interaction with cytokine and cytokine receptor	14/546	100/8076	0.007073	0.081507	0.067648	2920/6347	14
hsa04933	AGE-RAGE signaling pathway in diabetic complications	14/546	100/8076	0.007073	0.081507	0.067648	1906/7042	14
hsa04014	Ras signaling pathway	26/546	232/8076	0.007315	0.081507	0.067648	11186/226	26
hsa05169	Epstein-Barr virus infection	23/546	202/8076	0.009375	0.09796	0.081303	1870/5704	23
hsa04115	p53 signaling pathway	11/546	73/8076	0.009419	0.09796	0.081303	7161/896/	11
hsa05202	Transcriptional misregulation in cancer	22/546	192/8076	0.010167	0.102327	0.084928	5327/604/	22
hsa05135	Yersinia infection	17/546	137/8076	0.01069	0.10423	0.086506	9564/2533	17
hsa04380	Osteoclast differentiation	16/546	128/8076	0.012202	0.104728	0.08692	7042/2976	16
hsa05418	Fluid shear stress and atherosclerosis	17/546	139/8076	0.012263	0.104728	0.08692	1906/5327	17
hsa05133	Pertussis	11/546	76/8076	0.012635	0.104728	0.08692	2770/3569	11
hsa05212	Pancreatic cancer	11/546	76/8076	0.012635	0.104728	0.08692	1870/5337	11
hsa05166	Human T-cell leukemia virus 1 infection	24/546	219/8076	0.01265	0.104728	0.08692	1387/1870	24
hsa05161	Hepatitis B	19/546	162/8076	0.012879	0.104728	0.08692	1387/1870	19
hsa04926	Relaxin signaling pathway	16/546	129/8076	0.013091	0.104728	0.08692	84699/190	16
hsa00830	Retinol metabolism	10/546	67/8076	0.013866	0.105579	0.087626	56603/612	10
hsa05140	Leishmaniasis	11/546	77/8076	0.013874	0.105579	0.087626	5743/7042	11
hsa04727	GABAergic synapse	12/546	89/8076	0.016134	0.119852	0.099472	6540/778/	12
hsa05230	Central carbon metabolism in cancer	10/546	70/8076	0.018522	0.134393	0.111541	2261/5710	10
hsa05167	Kaposi sarcoma-associated herpesvirus infection	21/546	193/8076	0.020314	0.141787	0.117678	1387/1870	21
hsa05224	Breast cancer	17/546	147/8076	0.02045	0.141787	0.117678	1870/2246	17
hsa05218	Melanoma	10/546	72/8076	0.022207	0.148899	0.12358	1870/2246	10
hsa04310	Wnt signaling pathway	18/546	160/8076	0.02243	0.148899	0.12358	1387/2580	18
hsa05162	Measles	16/546	139/8076	0.02502	0.159736	0.132574	7161/4792	16
hsa04630	JAK-STAT signaling pathway	18/546	162/8076	0.025087	0.159736	0.132574	1387/2273	18
hsa04071	Sphingolipid signaling pathway	14/546	119/8076	0.029397	0.175462	0.145627	56848/552	14

Supplementary Table 3. GSEA report for TCGA OSCC tumor

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT LEADING EDGE
HALLMARK DNA_REPAIR	150	0.6452855	1.7792888	0.00199601	0.045302	0.024	13989 tags=70%, list=25%, signal=93%
HALLMARK UNFOLDED_PROTEIN_RESPONSE	110	0.64524287	1.7792441	0	0.022651	0.024	13844 tags=66%, list=25%, signal=92%
HALLMARK MTORC1_SIGNALING	198	0.62546444	1.694007	0.00594059	0.054536	0.067	12964 tags=66%, list=23%, signal=86%
HALLMARK E2F_TARGETS	198	0.7860378	1.6799289	0	0.049193	0.075	7413 tags=78%, list=13%, signal=89%
HALLMARK MITOTIC_SPINDLE	199	0.69071716	1.658022	0	0.052791	0.091	9707 tags=60%, list=17%, signal=73%
HALLMARK G2M_CHECKPOINT	196	0.7427995	1.6519508	0.00198413	0.04783	0.101	9934 tags=77%, list=18%, signal=93%
HALLMARK MYC_TARGETS_V1	196	0.6441084	1.6504803	0.01670146	0.041395	0.101	14479 tags=70%, list=26%, signal=94%
HALLMARK GLYCOLYSIS	199	0.56166184	1.650255	0.01277372	0.036331	0.101	10784 tags=50%, list=19%, signal=62%
HALLMARK MYC_TARGETS_V2	58	0.70326555	1.6338797	0.02057613	0.038027	0.119	11584 tags=78%, list=21%, signal=98%
HALLMARK INTERFERON_GAMMA_RESPONSE	198	0.709834	1.5793331	0.04190476	0.063259	0.183	9267 tags=65%, list=17%, signal=78%
HALLMARK INTERFERON_ALPHA_RESPONSE	96	0.7730088	1.5704821	0.02298851	0.063374	0.197	8875 tags=79%, list=16%, signal=94%
HALLMARK UV_RESPONSE_UP	156	0.51772034	1.5698351	0.02197802	0.058437	0.199	12758 tags=52%, list=23%, signal=67%
HALLMARK ANGIOGENESIS	36	0.68420625	1.5498921	0.03971119	0.068648	0.228	8409 tags=56%, list=15%, signal=65%
HALLMARK EPITHELIAL_MESENCHYMAL_TRANSITION	200	0.7029892	1.5337912	0.04008016	0.074093	0.251	6956 tags=55%, list=13%, signal=63%
HALLMARK APICAL_JUNCTION	200	0.5530708	1.5296863	0.03985507	0.071494	0.254	11221 tags=52%, list=20%, signal=65%
HALLMARK P53_PATHWAY	196	0.5023445	1.5158978	0.05065666	0.077295	0.288	10587 tags=41%, list=19%, signal=50%
HALLMARK APOPTOSIS	160	0.5324266	1.4930605	0.06805293	0.089311	0.325	15325 tags=61%, list=28%, signal=84%
HALLMARK PI3K_AKT_MTOR_SIGNALING	105	0.53066754	1.488598	0.07962963	0.087294	0.331	15169 tags=67%, list=27%, signal=92%
HALLMARK COMPLEMENT	200	0.5550699	1.4812552	0.07001796	0.087729	0.343	11757 tags=52%, list=21%, signal=66%
HALLMARK TGF_BETA_SIGNALING	54	0.6184321	1.4585011	0.08971962	0.099442	0.379	14031 tags=61%, list=25%, signal=82%
HALLMARK WNT_BETA_CATENIN_SIGNALING	42	0.58167046	1.4228483	0.08348135	0.120932	0.431	10090 tags=50%, list=18%, signal=61%
HALLMARK HYPOXIA	200	0.49026576	1.3932887	0.12007169	0.141581	0.5	10683 tags=45%, list=19%, signal=55%
HALLMARK INFLAMMATORY_RESPONSE	200	0.57047635	1.3857462	0.13148148	0.142605	0.514	13027 tags=57%, list=23%, signal=74%
HALLMARK NOTCH_SIGNALING	32	0.5778528	1.3584872	0.12648222	0.161393	0.549	15056 tags=56%, list=27%, signal=77%
HALLMARK PROTEIN_SECRETION	96	0.5558608	1.3560865	0.16893204	0.156997	0.551	16616 tags=72%, list=30%, signal=102%
HALLMARK IL2_STAT5_SIGNALING	199	0.5090145	1.355567	0.12987013	0.151239	0.551	9105 tags=43%, list=16%, signal=52%
HALLMARK TNFA_SIGNALING_VIA_NFKB	200	0.5372671	1.3348306	0.18026565	0.161971	0.569	9637 tags=42%, list=17%, signal=50%
HALLMARK IL6_JAK_STAT3_SIGNALING	87	0.54992425	1.3204484	0.18333334	0.167075	0.583	13895 tags=55%, list=25%, signal=73%
HALLMARK HEDGEHOG_SIGNALING	36	0.5418442	1.2652144	0.20545454	0.210571	0.638	12087 tags=58%, list=22%, signal=75%
HALLMARK COAGULATION	138	0.45254573	1.2362733	0.23022847	0.231492	0.671	10815 tags=38%, list=19%, signal=47%
HALLMARK SPERMATOGENESIS	134	0.4327849	1.2311333	0.16535433	0.228416	0.676	9014 tags=29%, list=16%, signal=35%
HALLMARK ALLOGRAFT_REJECTION	196	0.5328977	1.2234296	0.267658	0.228407	0.686	16999 tags=63%, list=31%, signal=90%
HALLMARK CHOLESTEROL_HOMEOSTASIS	74	0.4271246	1.2000593	0.26145038	0.242447	0.709	15876 tags=54%, list=29%, signal=76%
HALLMARK KRAS_SIGNALING_UP	199	0.4572746	1.1915507	0.27041742	0.242547	0.714	10378 tags=41%, list=19%, signal=50%
HALLMARK ESTROGEN_RESPONSE_LATE	200	0.38959563	1.1783155	0.23707666	0.245623	0.718	7618 tags=31%, list=14%, signal=35%
HALLMARK APICAL_SURFACE	44	0.44719255	1.1678874	0.2647059	0.247767	0.727	5038 tags=32%, list=9%, signal=35%
HALLMARK HEME_METABOLISM	196	0.39394072	1.1603714	0.2834507	0.248747	0.738	13751 tags=43%, list=25%, signal=57%
HALLMARK UV_RESPONSE_DN	144	0.45386428	1.0587609	0.42913386	0.340273	0.814	11590 tags=43%, list=21%, signal=54%
HALLMARK PANCREAS_BETA_CELLS	40	0.36517042	0.97355086	0.5082873	0.426566	0.859	13876 tags=40%, list=25%, signal=53%
HALLMARK REACTIVE_OXYGEN_SPECIES_PATHWAY	49	0.33396947	0.9717423	0.5	0.418198	0.861	16080 tags=47%, list=29%, signal=66%
HALLMARK PEROXISOME	104	0.31409073	0.929327	0.5434028	0.451302	0.877	10597 tags=30%, list=19%, signal=37%
HALLMARK ANDROGEN_RESPONSE	99	0.34342694	0.9011799	0.576779	0.474947	0.89	8751 tags=28%, list=16%, signal=34%

Supplementary Table 4. GSEA report for TCGA OSCC AFAP1-AS1 positive

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT N LEADING EDGE
HALLMARK_G2M_CHECKPOINT	196	0.74629456	2.2247572	0	0	0	10223 tags=82%, list=18%, signal=100%
HALLMARK_E2F_TARGETS	198	0.7425431	2.2139285	0	0	0	8752 tags=74%, list=16%, signal=88%
HALLMARK_MTORC1_SIGNALING	198	0.7037224	2.0952759	0	0	0	12462 tags=77%, list=22%, signal=99%
HALLMARK_MYC_TARGETS_V1	196	0.70252603	2.0938375	0	0	0	9294 tags=67%, list=17%, signal=80%
HALLMARK_MYC_TARGETS_V2	58	0.7320118	2.0835984	0	0	0	9141 tags=71%, list=16%, signal=85%
HALLMARK_MITOTIC_SPINDLE	199	0.6912418	2.078484	0	0	0	12904 tags=76%, list=23%, signal=99%
HALLMARK_PROTEIN_SECRETION	96	0.6688995	1.9558089	0	0	0	13179 tags=73%, list=24%, signal=95%
HALLMARK_ANDROGEN_RESPONSE	99	0.6438273	1.8835975	0	0	0	10413 tags=56%, list=19%, signal=68%
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	110	0.6318518	1.8524572	0	0	0	11568 tags=65%, list=21%, signal=83%
HALLMARK_TGF_BETA_SIGNALING	54	0.64472616	1.8228045	0	1.00E-04	0.001	13351 tags=70%, list=24%, signal=93%
HALLMARK_NOTCH_SIGNALING	32	0.673875	1.8190925	0	9.09E-05	0.001	12294 tags=66%, list=22%, signal=84%
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	0.6178622	1.8033425	0	8.33E-05	0.001	13230 tags=67%, list=24%, signal=87%
HALLMARK_GLYCOLYSIS	199	0.59878564	1.7820572	0	7.69E-05	0.001	13160 tags=59%, list=24%, signal=77%
HALLMARK_ESTROGEN_RESPONSE_EARLY	200	0.58781683	1.763922	0	7.14E-05	0.001	13593 tags=58%, list=24%, signal=76%
HALLMARK_UV_RESPONSE_UP	156	0.5981204	1.761776	0	1.33E-04	0.002	11577 tags=56%, list=21%, signal=71%
HALLMARK_UV_RESPONSE_DN	144	0.59347975	1.7463686	0	1.25E-04	0.002	17636 tags=71%, list=23%, signal=104%
HALLMARK_ADIPOGENESIS	199	0.5835229	1.7388382	0	1.18E-04	0.002	11765 tags=54%, list=21%, signal=69%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	0.5794751	1.72985	0	1.11E-04	0.002	16857 tags=68%, list=20%, signal=97%
HALLMARK_INFLAMMATORY_RESPONSE	200	0.57002664	1.7077427	0	2.11E-04	0.004	17020 tags=65%, list=31%, signal=93%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	0.5714853	1.7063427	0	2.50E-04	0.005	9253 tags=46%, list=17%, signal=55%
HALLMARK_DNA_REPAIR	150	0.57484376	1.7026342	0	2.38E-04	0.005	11158 tags=49%, list=20%, signal=62%
HALLMARK_HEME_METABOLISM	196	0.5655724	1.6980306	0	2.27E-04	0.005	13696 tags=54%, list=25%, signal=71%
HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	0.6079776	1.6923085	0	2.17E-04	0.005	11263 tags=55%, list=20%, signal=69%
HALLMARK_FATTY_ACID_METABOLISM	157	0.56730145	1.6884434	0	2.08E-04	0.005	9694 tags=48%, list=17%, signal=58%
HALLMARK_ESTROGEN_RESPONSE_LATE	200	0.5618763	1.6859959	0	2.00E-04	0.005	13593 tags=54%, list=24%, signal=71%
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	49	0.59288985	1.6656048	0	2.31E-04	0.006	12166 tags=51%, list=22%, signal=65%
HALLMARK_SPERMATOGENESIS	134	0.5626934	1.6576073	0	2.59E-04	0.007	13587 tags=53%, list=24%, signal=70%
HALLMARK_HEDGEHOG_SIGNALING	36	0.60384	1.655545	0.00102354	2.50E-04	0.007	11335 tags=58%, list=20%, signal=73%
HALLMARK_APOPTOSIS	160	0.55448776	1.6488194	0	2.76E-04	0.008	13403 tags=51%, list=24%, signal=67%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	200	0.5495397	1.6431664	0	2.67E-04	0.008	17289 tags=63%, list=31%, signal=91%
HALLMARK_IL6_JAK_STAT3_SIGNALING	87	0.55679315	1.6230671	0	2.58E-04	0.008	16694 tags=62%, list=30%, signal=89%
HALLMARK_BILE_ACID_METABOLISM	112	0.5522266	1.6209872	0	2.50E-04	0.008	11435 tags=50%, list=21%, signal=63%
HALLMARK_PEROXISOME	104	0.55287796	1.6092043	0	3.94E-04	0.013	9357 tags=50%, list=17%, signal=60%
HALLMARK_ANGIOGENESIS	36	0.5849081	1.6015522	0.00306122	4.12E-04	0.014	12195 tags=58%, list=22%, signal=75%
HALLMARK_XENOBIOTIC_METABOLISM	198	0.5360463	1.5992119	0	4.86E-04	0.017	13276 tags=53%, list=24%, signal=69%
HALLMARK_HYPOXIA	200	0.52903754	1.5952027	0	6.12E-04	0.022	14416 tags=52%, list=26%, signal=70%
HALLMARK_APICAL_SURFACE	44	0.5692939	1.5948368	0.00201207	5.96E-04	0.022	15020 tags=64%, list=27%, signal=87%
HALLMARK_IL2_STATS_SIGNALING	199	0.5256712	1.5649533	0	8.69E-04	0.033	16111 tags=56%, list=29%, signal=78%
HALLMARK_KRAS_SIGNALING_UP	199	0.5290634	1.5636257	0	8.47E-04	0.033	15915 tags=57%, list=29%, signal=79%
HALLMARK_APICAL_JUNCTION	200	0.5223029	1.5559175	0	9.51E-04	0.037	18118 tags=62%, list=33%, signal=91%
HALLMARK_COMPLEMENT	200	0.5155343	1.5361603	0	0.001343454	0.054	15978 tags=56%, list=29%, signal=78%
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	0.53234845	1.51958	0.001	0.001789601	0.073	14338 tags=51%, list=26%, signal=69%
HALLMARK_KRAS_SIGNALING_DN	199	0.4872019	1.4594383	0	0.004126737	0.163	19857 tags=59%, list=36%, signal=92%
HALLMARK_P53_PATHWAY	196	0.48443833	1.4437654	0	0.005081184	0.203	16943 tags=57%, list=31%, signal=81%
HALLMARK_ALLOGRAFT_REJECTION	196	0.46986198	1.4027046	0.001	0.008244476	0.305	14227 tags=39%, list=26%, signal=53%
HALLMARK_COAGULATION	138	0.45511463	1.3521607	0.004	0.015797907	0.531	16805 tags=49%, list=30%, signal=70%
HALLMARK_MYOGENESIS	199	0.4516461	1.3418391	0.001	0.017657226	0.586	17643 tags=45%, list=32%, signal=66%
HALLMARK_INTERFERON_GAMMA_RESPONSE	198	0.44586277	1.3273268	0.002	0.02085915	0.657	17148 tags=49%, list=31%, signal=71%
HALLMARK_PANCREAS_BETA_CELLS	40	0.44553512	1.2221217	0.17741935	0.07274013	0.982	13574 tags=38%, list=24%, signal=50%
HALLMARK_INTERFERON_ALPHA_RESPONSE	96	0.39566496	1.150148	0.1981982	0.15883394	1	21213 tags=60%, list=38%, signal=98%

Supplementary Table 5. GSEA report for sh-nc

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT N LEADING EDGE
HALLMARK_MYC_TARGETS_V2	58	0.4503603	1.8610045	0	0.00342539	0.004	4934 tags=36%, list=15%, signal=42%
HALLMARK_FATTY_ACID_METABOLISM	150	0.3196943	1.5751292	0	0.04358355	0.091	4746 tags=27%, list=14%, signal=32%
HALLMARK_MYC_TARGETS_V1	196	0.3056746	1.5570745	0.003267974	0.03556569	0.107	10765 tags=44%, list=32%, signal=65%
HALLMARK_HYPOXIA	194	0.2888853	1.4860667	0	0.04642299	0.176	5070 tags=32%, list=15%, signal=38%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	184	0.2689977	1.3726331	0.013245033	0.10008589	0.413	7329 tags=32%, list=22%, signal=40%
HALLMARK_ADIPOGENESIS	194	0.2487298	1.2725424	0.020761246	0.18870343	0.703	4904 tags=23%, list=15%, signal=27%
HALLMARK_E2F_TARGETS	198	0.2468181	1.2647983	0.055555556	0.17410497	0.727	4934 tags=22%, list=15%, signal=26%
HALLMARK_PEROXISOME	100	0.2629742	1.2091644	0.14763232	0.23101008	0.862	5076 tags=25%, list=15%, signal=29%
HALLMARK_GLYCOLYSIS	196	0.2357699	1.2041322	0.077380955	0.2129317	0.871	5178 tags=24%, list=16%, signal=29%
HALLMARK_INTERFERON_GAMMA_RESPONSE	196	0.2231481	1.1322472	0.173333333	0.31897497	0.971	4746 tags=23%, list=14%, signal=27%
HALLMARK_ESTROGEN_RESPONSE_LATE	190	0.2223513	1.125871	0.1826923	0.30336136	0.975	5096 tags=24%, list=15%, signal=28%
HALLMARK_INTERFERON_ALPHA_RESPONSE	95	0.2350829	1.0760702	0.25872093	0.38991925	0.995	4746 tags=20%, list=14%, signal=23%
HALLMARK_G2M_CHECKPOINT	194	0.2036195	1.0465093	0.3097643	0.43397725	1	5069 tags=20%, list=15%, signal=24%
HALLMARK_NOTCH_SIGNALING	32	0.2672567	0.97626424	0.5060827	0.59255594	1	4924 tags=22%, list=15%, signal=26%
HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	0.2519513	0.96540415	0.52870816	0.5828644	1	5027 tags=24%, list=15%, signal=28%
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	49	0.1944221	0.78409606	0.824147	0.915005	1	6885 tags=27%, list=21%, signal=33%

Supplementary Table 6. myc-target genes

HSPD1	PPIA	RPS5	MCM2	UTP20
CDK4	G3BP1	SRPK1	EIF4H	SUPV3L1
GNL3	PSMD1	RFC4	HNRNPA2	BYSL
MCM5	RPL34	PSMC4	RPS10	DCTPP1
PHB	NHP2	CCNA2	SNRPD3	WDR43
NPM1	KPNB1	EIF3D	SF3B3	SLC29A2
CBX3	CCT2	SNRPA	KPNA2	GRWD1
DDX18	CDC20	PSMA7	PPM1G	DUSP2
MYC	SSB	PSMB2	SNRPA1	MAP3K6
NOLC1	PSMD3	PTGES3	DHX15	MRTO4
HSPE1	PABPC4	SNRPD1	ORC2	SLC19A1
AIMP2	VBP1	RUVBL2	DUT	HK2
NOP56	GLO1	NCBP1	CCT5	NIP7
RRP9	PRDX3	PSMD8	RANBP1	IMP4
SRM	SRSF1	CDC45	FBL	NOP2
MCM4	CLNS1A	SRSF7	TARDBP	NDUF4F4
NOP16	XPOT	HDAC2	USP1	FARSA
PA2G4	U2AF1	HNRNPU	TRIM28	RCL1
PRPF31	PHB2	SET	STARD7	PLK4
HDGF	IARS	MRPL9	DDX21	NOC4L
POLE3	XRCC6	NME1	AP3S1	EXOSC5
TOMM70A	TXNL4A	PCNA	PSMD7	TFB2M
PSMA2	ERH	ABCE1	SF3A1	SORD
UBA2	EEF1B2	COPS5	KARS	MPHOSPH
MRPL23	C1QBP	HNRNPA3	RAN	TMEM97
SRSF2	PRPS2	CSTF2	PWP1	MYBBP1A
PSMA4	RSL1D1	ILF2	EIF2S2	TCOF1
GOT2	RPLP0	HSP90AB1	PSMD14	PUS1
TYMS	HNRNPD	PRDX4	TRA2B	UNG
DEK	NCBP2	RPS6	RAD23B	TBRG4
PSMA6	EIF4E	FAM120A	ETF1	PLK1
POLD2	PCBP1	CCT3	TFDP1	LAS1L
HDDC2	UBE2E1	RPL18	CDK2	PES1
CNBP	EIF3J	CANX	HNRNPC	PPAN
RPS2	SYNCRIP	RPL22	PSMC6	PPRC1
YWHAQ	SMARCC1	CYC1	EIF4A1	RRP12
RNPS1	APEX1	LDHA	MAD2L1	PRMT3
CCT4	ACP1	EIF2S1	EXOSC7	WDR74
SNRPG	TUFM	SRSF3	LSM7	RABEPK
XPO1	RPL6	EPRS	RRM1	IPO4
EIF4G2	TCP1	PSMA1	ODC1	
BUB3	SSBP1	GSPT1	SNRPB2	
HNRNPR	NDUFAB1	MRPS18B	NAP1L1	
COX5A	GNB2L1	RPL14	CUL1	
SLC25A3	SERBP1	MCM6	PGK1	
EIF1AX	UBE2L3	HNRNPA1	YWHAE	
CAD	RPS3	IFRD1	MCM7	
CTPS	HPRT1	LSM2	CCT7	
VDAC3	H2AFZ	PABPC1	SNRPD2	
VDAC1	EIF3B	IMPDH2	PSMB3	