



**Table S1.** List of processes based on the GSEA analysis of MSigDB gene sets enriched in HNSCC patients with lower and higher levels of *miR-154-5p* in all localization as well as depending on the localization in oral cavity, larynx or pharynx. Only gene sets with nominal  $p < 0.05$  were presented; SIZE - number of enriched genes in specified process, ES - enrichment score, NES - normalized enrichment score, FDR q-val - false discovery rate.

	NAME	SIZE	ES	NES	p-val	FDR q-val
Localization	<b>patients with low expression of miR-154-5p</b>					
	SINGH_KRAS_DEPENDENT_SIGNATURE	20	-0.700524	-1.5727571	0.08045977	0.663567
	TBK1.DF_DN	258	-0.4619756	-1.56569	0.054054055	0.34981143
All localizations	<b>patients with high expression of miR-154-5p</b>					
	AKT_UP.V1_DN	179	0.5298579	2.0809271	0.0	0.010224129
	AKT_UP_MTOR_DN.V1_DN	177	0.42670274	1.8757594	0.0	0.093307704
	MTOR_UP.V1_DN	170	0.44283426	1.8146863	0.0	0.0974028
	ESC_J1_UP_EARLY.V1_DN	158	0.35960007	1.6201601	0.0019607844	0.18996853
	CRX_DN.V1_DN	127	0.44080538	1.7359952	0.003992016	0.13988577
	GCNP_SHH_UP_LATE.V1_DN	168	0.36878064	1.6192702	0.004008016	0.17715292
	ESC_V6.5_UP_EARLY.V1_DN	153	0.50741667	1.8727603	0.0040650405	0.06392599
	JNK_DN.V1_DN	174	0.4444347	1.7508625	0.00407332	0.14491369
	CYCLIN_D1_UP.V1_UP	178	0.38466176	1.6065778	0.0058708414	0.16989867
	GLI1_UP.V1_UP	21	0.51938635	1.6415216	0.009578544	0.23385362
	CAHOY_ASTROGLIAL	91	0.47678348	1.7227652	0.009652509	0.13629018
	CAHOY_OLIGODENDROCYTIC	85	0.38774285	1.5628906	0.01775148	0.16555104
	LEF1_UP.V1_UP	186	0.43609655	1.6494541	0.018832391	0.24566129
	KRAS.600.LUNG.BREAST_UP.V1_UP	267	0.3913184	1.6114745	0.019723866	0.17489475
	NRL_DN.V1_DN	121	0.35250053	1.5266105	0.021611001	0.17696068
	EIF4E_UP	88	0.4670218	1.6271266	0.021782178	0.1955343

BMI1_DN_MEL18_DN.V1_DN	137	0.4354125	1.6353568	0.024809161	0.2210591
CTIP_DN.V1_UP	120	0.42776752	1.5839401	0.026119404	0.15453193
PKCA_DN.V1_DN	146	0.34221587	1.4658694	0.029239766	0.20648196
KRAS.50_UP.V1_UP	47	0.49730524	1.6009626	0.031311154	0.16576183
CRX_NRL_DN.V1_DN	111	0.35360312	1.4673762	0.03206413	0.2162339
KRAS.AMP.LUNG_UP.V1_UP	130	0.40797198	1.5366397	0.03265306	0.17746533
WNT_UP.V1_UP	169	0.3281619	1.4002154	0.033203125	0.23158869
RB_P130_DN.V1_UP	116	0.41796416	1.5319397	0.033797216	0.17631269
CYCLIN_D1_KE_.V1_UP	182	0.32691562	1.4527216	0.034274194	0.20706365
KRAS.KIDNEY_UP.V1_UP	136	0.4982055	1.6296653	0.036821704	0.20976704
ATM_DN.V1_UP	140	0.36542484	1.4805324	0.03777336	0.21914394
ATF2_S_UP.V1_DN	176	0.42690405	1.5966355	0.038022812	0.15418139
P53_DN.V2_DN	141	0.3371459	1.415629	0.038383838	0.23218915
KRAS.600_UP.V1_UP	261	0.4146874	1.600918	0.03846154	0.15655284
CRX_NRL_DN.V1_UP	129	0.32568383	1.3895055	0.039447732	0.23613079
CAHOY_NEURONAL	94	0.433898	1.5554782	0.04016064	0.16692613
KRAS.300_UP.V1_UP	136	0.42623508	1.5853728	0.040229887	0.16072713
KRAS.PROSTATE_UP.V1_UP	126	0.3875258	1.4564825	0.046184737	0.21344519
BMI1_DN.V1_DN	128	0.37935737	1.4708267	0.048732944	0.21842751
ESC_V6.5_UP_LATE.V1_UP	170	0.3962382	1.5070236	0.04950495	0.19469327
HALLMARK_ANGIOGENESIS	36	0.7268911	1.9551228	0.0	0.028812956
HALLMARK_MYOGENESIS	198	0.70394534	2.0488024	0.0020449897	0.019075861
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	0.7119223	1.9293958	0.003984064	0.027211443

	HALLMARK_COAGULATION	136	0.5151289	1.8114622	0.0075901328	0.06288996
	HALLMARK_PANCREAS_BETA_CELLS	40	0.47945312	1.6128231	0.02	0.22418033
	<b>patients with low expression of miR-154-5p</b>					
	HALLMARK_ESTROGEN_RESPONSE_EARLY	192	-0.3684512	-1.508271	0.032989692	1.0
	<b>patients with high expression of miR-154-5p</b>					
Larynx	AKT_UP_MTOR_DN.V1_DN	177	0.34209406	1.4716623	0.03269231	1.0
	AKT_UP.V1_DN	179	0.40278888	1.5882095	0.03992016	1.0
	HALLMARK_ANGIOGENESIS	36	0.59281003	1.6746945	0.03164557	0.36380783
	HALLMARK_MYOGENESIS	198	0.54568565	1.7289077	0.037109375	0.49452442
	<b>patients with low expression of miR-154-5p</b>					
	DCA_UP.V1_DN	162	-0.32457164	-1.4496114	0.01934236	1.0
	ESC_J1_UP_EARLY.V1_UP	151	-0.32092696	-1.4028095	0.040935673	1.0
	HALLMARK_ALLOGRAFT_REJECTION	195	-0.63805974	-1.8395994	0.030927835	0.17024265
	<b>patients with high expression of miR-154-5p</b>					
Pharynx	CRX_DN.V1_DN	127	0.42043114	1.6781394	0.010204081	0.3680043
	CRX_NRL_DN.V1_DN	111	0.3611626	1.5442594	0.010330578	0.5486713
	AKT_UP.V1_DN	179	0.43504387	1.6993006	0.016	0.6178347
	AKT_UP_MTOR_DN.V1_DN	177	0.3354621	1.4691406	0.031847134	0.5388127

Oral cavity	ESC_V6.5_UP_EARLY.V1_DN	153	0.45361865	1.6186346	0.03469388	0.42191383
	CAHOY_OLIGODENDRO CUTIC	85	0.35082164	1.4489464	0.03526971	0.53511864
	ESC_J1_UP_LATE.V1_UP	176	0.37258855	1.4947804	0.035789475	0.5297214
	HALLMARK_MYOGENESIS	198	0.67982894	2.0338547	0.0041753654	0.006919477
	HALLMARK_EPITHELIAL _MESENCHYMAL_TRANS ITION	194	0.6718212	1.7521929	0.02745098	0.11570975
	<b>patients with low expression of miR-154-5p</b>					
	RB_P130_DN.V1_DN	120	-0.48940206	-1.7510496	0.009345794	0.10240098
	TBK1.DF_DN	258	-0.5196189	-1.7025776	0.01622718	0.10524474
	SINGH_KRAS_DEPENDENT NCY_SIGNATURE	20	-0.76683635	-1.7550769	0.028397566	0.20084381
	<b>patients with high expression of miR-154-5p</b>					
	GCNP_SHH_UP_LATE.V1 _DN	168	0.3742599	1.6583126	0.002020202	0.59006065
	RB_P130_DN.V1_UP	116	0.47475716	1.7137499	0.0020833334	1.0
	AKT_UP_MTOR_DN.V1_D N	177	0.36592835	1.6096988	0.0061728396	0.51515704
	CRX_DN.V1_UP	124	0.35605535	1.5382963	0.008350731	0.42748865
	SRC_UP.V1_UP	148	0.41562843	1.5529585	0.0139442235	0.5566733
	AKT_UP.V1_DN	179	0.43954867	1.7097505	0.018789144	0.5878324
	MTOR_UP.V1_DN	170	0.40486565	1.651626	0.0256917	0.46497825
	JNK_DN.V1_DN	174	0.4018756	1.5947857	0.02736842	0.48263174
	CRX_NRL_DN.V1_UP	129	0.3468031	1.4924229	0.035416666	0.5221901
	CYCLIN_D1_UP.V1_UP	178	0.34826428	1.4817967	0.035490606	0.47595248
	ESC_J1_UP_LATE.V1_DN	160	0.31664708	1.3999306	0.040983606	0.4827413

ESC_V6.5_UP_LATE.V1_D N	162	0.31629592	1.4213246	0.04233871	0.52835584
KRAS.AMP.LUNG_UP.V1_ UP	130	0.40842712	1.5475217	0.047916666	0.5047504

**Table S2.** List of processes based on the GSEA analysis of MSigDB gene sets enriched in HNSCC patients with lower and higher levels of *miR-154-3p* in all localization as well as depending on the localization in oral cavity, larynx or pharynx. Only gene sets with nominal  $p < 0.05$  were presented; SIZE - number of enriched genes in specified process, ES - enrichment score, NES - normalized enrichment score, FDR q-val - false discovery rate.

	NAME	SIZE	ES	NES	NOM p-val	FDR q-val
Lokalization	patients with low expression of miR-154-3p	No enrichment				
	patients with high expression of miR-154-3p					
All localizations	AKT_UP.V1_DN	186	0.56028676	2.1796565	0.0	0.0017931035
	ESC_V6.5_UP_LATE.V1_UP	187	0.4912813	1.9530286	0.0	0.024408296
	AKT_UP_MTOR_DN.V1_D N	183	0.44236442	1.9442787	0.0	0.01993367
	MTOR_UP.V1_DN	179	0.46488515	1.8907892	0.0	0.029356206
	ESC_V6.5_UP_EARLY.V1_ DN	170	0.5393009	2.0287793	0.0018761726	0.015598844
	CRX_DN.V1_DN	133	0.43369287	1.7313417	0.0019569471	0.064509705
	CYCLIN_D1_UP.V1_UP	185	0.41847295	1.766866	0.0020120724	0.05659865
	CYCLIN_D1_KE_.V1_UP	187	0.36532766	1.6089052	0.0020120724	0.10600192
	GCNP_SHH_UP_LATE.V1_ DN	175	0.38807258	1.6995656	0.0057142857	0.07046442
	LEF1_UP.V1_UP	193	0.48920476	1.8454154	0.005791506	0.039553046
	KRAS.600_UP.V1_UP	273	0.45381328	1.7537911	0.005859375	0.059982512
	CAHOY_ASTROGLIAL	100	0.50143784	1.8302763	0.0058708414	0.03419879
	NRL_DN.V1_DN	129	0.37102777	1.633271	0.0059405942	0.100295834
	BMI1_DN.V1_UP	144	0.56438947	1.8351312	0.007736944	0.038197946
	KRAS.300_UP.V1_UP	143	0.47411144	1.7534115	0.007874016	0.055062752
	KRAS.PROSTATE_UP.V1_ UP	133	0.4167321	1.6173216	0.007874016	0.108538985
	PKCA_DN.V1_DN	160	0.36382353	1.5571125	0.008	0.120997645

P53_DN.V2_DN	143	0.36883068	1.563393	0.008281574	0.11919013
ATF2_S_UP.V1_DN	183	0.47763944	1.7724284	0.009578544	0.06050411
CRX_NRL_DN.V1_DN	126	0.36530733	1.5539541	0.009823183	0.11645774
ESC_J1_UP_LATE.V1_UP	190	0.43791965	1.7128996	0.0114722755	0.07128647
JNK_DN.V1_DN	183	0.40268537	1.6128576	0.013618677	0.107554965
SNF5_DN.V1_DN	161	0.397052	1.6032484	0.015384615	0.10261076
KRAS.AMP.LUNG_UP.V1_UP	139	0.39752188	1.5398251	0.015968064	0.12231667
ATM_DN.V1_UP	144	0.3898237	1.6068971	0.01622718	0.103437915
CORDENONSI_YAP_CONSERVED_SIGNATURE	57	0.5127401	1.7085344	0.017274473	0.069210045
CAHOY_OLIGODENDROCTIC	97	0.382373	1.5325611	0.017964073	0.1257437
ESC_J1_UP_EARLY.V1_DN	174	0.31309244	1.4448574	0.01908397	0.1757776
WNT_UP.V1_UP	177	0.34359294	1.4747274	0.01984127	0.15992926
PTEN_DN.V1_UP	185	0.41450268	1.5927682	0.022	0.10579497
KRAS.KIDNEY_UP.V1_UP	142	0.49838185	1.647517	0.024242423	0.0982057
CSR_LATE_UP.V1_DN	161	0.38936192	1.5541435	0.026768642	0.12012326
BCAT.100_UP.V1_DN	38	0.44301105	1.5733078	0.026804123	0.11801403
PTEN_DN.V2_DN	137	0.33657074	1.4035423	0.03422053	0.18592863
MEL18_DN.V1_UP	140	0.5115615	1.6619292	0.036053132	0.093064725
KRAS.50_UP.V1_UP	48	0.50891614	1.6336975	0.03646833	0.10493443
RB_P130_DN.V1_UP	128	0.4099905	1.5316194	0.036734693	0.12316106
PRC2_SUZ12_UP.V1_DN	182	0.34558478	1.4611349	0.03875969	0.16666754
BCAT_BILD_ET_AL_UP	45	0.438524	1.5237733	0.03952569	0.12706403
BCAT.100_UP.V1_UP	47	0.44722173	1.5408704	0.040152963	0.12528561
BCAT_GDS748_DN	43	0.4005337	1.4635793	0.043010753	0.16798286
HALLMARK_MYOGENESIS	198	0.5857865	1.8978672	0.010683761	0.12087148

	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	0.6463002	1.8134077	0.027542373	0.14074229
Larynx	patients with low expression of miR-154-3p	No enrichment				
	patients with high expression of miR-154-3p					
	CSR_LATE_UP.V1_UP	170	0.5095815	1.8798832	0.004132231	0.08499931
	AKT_UP_MTOR_DN.V1_DN	183	0.3547783	1.5097848	0.015717093	0.4540008
	ESC_V6.5_UP_LATE.V1_UP	187	0.41751322	1.6434906	0.017509727	0.70383555
	BCAT_GDS748_UP	48	0.44833022	1.5904704	0.019305019	0.7317408
	SNF5_DN.V1_DN	161	0.36164638	1.5084386	0.024291499	0.41381618
	CRX_NRL_DN.V1_DN	126	0.3428042	1.4622862	0.04048583	0.41364855
	KRAS.600_UP.V1_UP	273	0.4309471	1.5710124	0.041257367	0.6375813
	KRAS.300_UP.V1_UP	143	0.43796596	1.5487969	0.046783626	0.60819215
	HALLMARK_MYOGENESIS	198	0.5857865	1.8978672	0.010683761	0.12087148
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	0.6463002	1.8134077	0.027542373	0.14074229	
Pharynx	patients with low expression of miR-154-3p					
	HALLMARK_E2F_TARGETS	187	-0.6802637	-1.8862922	0.014112903	0.11118078
	HALLMARK_G2M_CHECKPOINT	184	-0.6064035	-1.8568065	0.018595042	0.07270152
	patients with high expression of miR-154-3p					
	ESC_J1_UP_LATE.V1_UP	190	0.48204732	1.929881	0.0	0.041719574
	BCAT.100_UP.V1_UP	47	0.5718491	1.8956203	0.0	0.035667643

CRX_NRL_DN.V1_DN	126	0.42834833	1.86238	0.0	0.02767766
CRX_DN.V1_DN	133	0.4646415	1.8566265	0.0	0.024174072
NRL_DN.V1_DN	129	0.41368577	1.8391927	0.0	0.025369184
AKT_UP_MTOR_DN.V1_DN	183	0.38696566	1.6563246	0.0	0.0771485
AKT_UP.V1_DN	186	0.50033617	1.8796655	0.0018248175	0.023064781
CAHOY_OLIGODENDRO CUTIC	97	0.4253644	1.7329963	0.0018691589	0.048996754
ESC_V6.5_UP_LATE.V1_UP	187	0.47258893	1.8950207	0.0019047619	0.023778427
SNF5_DN.V1_DN	161	0.44967312	1.7536162	0.0019267823	0.04548479
MTOR_UP.V1_DN	179	0.4247355	1.7566849	0.0036630037	0.048450958
ESC_V6.5_UP_EARLY.V1_DN	170	0.5127685	1.8070983	0.0056179776	0.032437876
LEF1_UP.V1_UP	193	0.46868858	1.7509977	0.0057803467	0.043366257
YAP1_UP	46	0.46993658	1.6788923	0.0058365758	0.06923028
WNT_UP.V1_UP	177	0.3788462	1.6375798	0.0058708414	0.07936641
KRAS.KIDNEY_UP.V1_UP	142	0.5444543	1.7869693	0.0060362173	0.036202777
CAHOY_ASTROGLIAL	100	0.47663546	1.7024447	0.015267176	0.059626777
KRAS.300_UP.V1_UP	143	0.4651405	1.7122635	0.015748031	0.057191994
CORDENONSI_YAP_CON SERVED_SIGNATURE	57	0.5108649	1.6654265	0.015936255	0.07502026
KRAS.600_UP.V1_UP	273	0.42238936	1.6462033	0.018036073	0.08146983
JNK_DN.V1_DN	183	0.3808899	1.5554901	0.018181818	0.14036986
MEL18_DN.V1_DN	148	0.44720942	1.6443839	0.019723866	0.07875094
GCNP_SHH_UP_LATE.V1_DN	175	0.32447812	1.4128036	0.02079395	0.22958317
ATM_DN.V1_UP	144	0.36395836	1.5410647	0.022540983	0.14352724
NOTCH_DN.V1_UP	185	0.34537467	1.4807234	0.023904383	0.1763045
ATF2_S_UP.V1_DN	183	0.4366	1.6162044	0.0251938	0.0882855
GLI1_UP.V1_UP	27	0.46683082	1.559212	0.027777778	0.14257443



	KRAS.50_UP.V1_UP	48	0.52359563	1.6350644	0.030947777	0.07757031
	BMI1_DN_MEL18_DN.V1_DN	146	0.4059437	1.542301	0.03187251	0.14784521
	KRAS.600.LUNG.BREAST_UP.V1_UP	274	0.36797923	1.4930128	0.038229376	0.18165754
	CTIP_DN.V1_UP	126	0.39599085	1.4975284	0.04477612	0.18251292
	PTEN_DN.V1_UP	185	0.3815244	1.4915613	0.046277665	0.1784513
	BCAT_BILD_ET_AL_UP	45	0.44675708	1.5034374	0.04681648	0.18095581
	CYCLIN_D1_KE_.V1_UP	187	0.33151716	1.4300984	0.04887218	0.22248046
	HALLMARK_MYOGENESIS	198	0.7145784	2.117106	0.0	0.0010399999
	HALLMARK_ANGIOGENESIS	36	0.69430226	1.8271418	0.001980198	0.03932752
	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	0.72035646	1.8964407	0.0039138943	0.04117608
	HALLMARK_COAGULATION	136	0.52564484	1.8423983	0.006085193	0.04639429
	HALLMARK_APICAL_JUNCTION	194	0.4655951	1.6966884	0.013861386	0.074379586
	HALLMARK_UV_RESPONSE_DN	137	0.5291569	1.7341154	0.02434457	0.069298126
Oral cavity	<b>patients with low expression of miR-154-3p</b>					
	AKT_UP.V1_UP	166	-0.36235863	-1.5241708	0.020449897	0.53579515
	RB_P130_DN.V1_DN	136	-0.462385	-1.6441884	0.024	0.65249217
	AKT_UP_MTOR_DN.V1_UP	180	-0.32997704	-1.440209	0.032719836	0.552364
	SINGH_KRAS_DEPENDENCY_SIGNATURE_	20	-0.7355437	-1.6171035	0.037037037	0.40179473
	HALLMARK_ESTROGEN_RESPONSE_LATE	195	-0.3557498	-1.507586	0.021696253	1.0
	HALLMARK_HEME_METABOLISM	190	-0.30163595	-1.3503901	0.046692606	0.61580694

patients with high expression of miR-154-3p					
AKT_UP.V1_DN	186	0.50241196	1.9108553	0.0020618557	0.091749
AKT_UP_MTOR_DN.V1_D N	183	0.37051854	1.5987741	0.006355932	0.80869895
P53_DN.V2_DN	143	0.35756117	1.5130025	0.012765957	0.57937676
MTOR_UP.V1_DN	179	0.41138262	1.6778622	0.014344262	0.6059425
PTEN_DN.V2_DN	137	0.34919706	1.4653875	0.022680413	0.423244
CYCLIN_D1_UP.V1_UP	185	0.34569985	1.4742062	0.027027028	0.42829973
RB_P130_DN.V1_UP	128	0.43527794	1.553512	0.036437247	0.5809809
VEGF_A_UP.V1_UP	193	0.40866178	1.5551827	0.036659878	0.68731534
SNF5_DN.V1_UP	174	0.42084318	1.5565385	0.047325104	0.8492638
HALLMARK_MYOGENESI S	198	0.6216926	1.8754559	0.018789144	0.10435163
HALLMARK_ANGIOGEN ESIS	36	0.5797845	1.6619582	0.04008016	0.24042602
HALLMARK_EPITHELIAL _MESENCHYMAL_TRANS ITION	194	0.5964984	1.7075882	0.047131147	0.2522565

**Supplementary Table S2.** [Correlation between miR-154-5p and 24 genes selected based on miRNA targets with score, function and interactions between targets using the GeneMANIA tool.](#)

Correlation miR-154-5p and its target					
Analyzed pair	Spearman/Pearson R	R-coefficient	95% confidence interval	P value	Number of XY Pairs
miR-154-5p vs. ABI1	Spearman r	-0.1954	-0.2853 to -0.1020	<0.0001	449
miR-154-5p vs. CPEB3	Spearman r	-0.1873	-0.2777 to -0.09376	<0.0001	449

<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">DMXL1</a>	<a href="#">Spearman r</a>	<a href="#">-0.2121</a>	<a href="#">-0.3012 to -0.1192</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">NPEPPS</a>	<a href="#">Pearson r</a>	<a href="#">-0.1895</a>	<a href="#">-0.2772 to -0.09866</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">PLAGL2</a>	<a href="#">Pearson r</a>	<a href="#">-0.1601</a>	<a href="#">-0.2489 to -0.06854</a>	<a href="#">0.0007</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">CNOT4</a>	<a href="#">Spearman r</a>	<a href="#">-0.1821</a>	<a href="#">-0.2727 to -0.08842</a>	<a href="#">0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">LIN9</a>	<a href="#">Spearman r</a>	<a href="#">-0.1223</a>	<a href="#">-0.2150 to -0.02733</a>	<a href="#">0.0095</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">VPS4B</a>	<a href="#">Spearman r</a>	<a href="#">-0.3055</a>	<a href="#">-0.3894 to -0.2165</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">WAC</a>	<a href="#">Spearman r</a>	<a href="#">-0.1242</a>	<a href="#">-0.2169 to -0.02925</a>	<a href="#">0.0084</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">CEACAM7</a>	<a href="#">Spearman r</a>	<a href="#">-0.2039</a>	<a href="#">-0.2934 to -0.1108</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">LRRC1</a>	<a href="#">Spearman r</a>	<a href="#">-0.2211</a>	<a href="#">-0.3099 to -0.1286</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">MYO6</a>	<a href="#">Spearman r</a>	<a href="#">-0.2353</a>	<a href="#">-0.3233 to -0.1432</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">PTBP3</a>	<a href="#">Spearman r</a>	<a href="#">-0.1404</a>	<a href="#">-0.2326 to -0.04575</a>	<a href="#">0.0029</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">RNF138</a>	<a href="#">Spearman r</a>	<a href="#">-0.1013</a>	<a href="#">-0.1947 to -0.006130</a>	<a href="#">0.0318</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a>	<a href="#">Spearman r</a>	<a href="#">-0.1458</a>	<a href="#">-0.2378 to -0.05126</a>	<a href="#">0.002</a>	<a href="#">449</a>

<a href="#">C12ORF29</a>					
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">CDKN2B</a>	<a href="#">Spearman r</a>	<a href="#">-0.1923</a>	<a href="#">-0.2824 to -0.09886</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">DCAF16</a>	<a href="#">Pearson r</a>	<a href="#">-0.09533</a>	<a href="#">-0.1862 to -0.002809</a>	<a href="#">0.0435</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">ESRP1</a>	<a href="#">Spearman r</a>	<a href="#">-0.1884</a>	<a href="#">-0.2786 to -0.09482</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">GNAI3</a>	<a href="#">Spearman r</a>	<a href="#">-0.1007</a>	<a href="#">-0.1941 to -0.005451</a>	<a href="#">0.033</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">LIN54</a>	<a href="#">Pearson r</a>	<a href="#">-0.1847</a>	<a href="#">-0.2726 to -0.09381</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">NSD2</a>	<a href="#">Pearson r</a>	<a href="#">-0.09532</a>	<a href="#">-0.1862 to -0.002806</a>	<a href="#">0.0435</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">OVOL1</a>	<a href="#">Spearman r</a>	<a href="#">-0.1977</a>	<a href="#">-0.2875 to -0.1044</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">TMPRSS11D</a>	<a href="#">Spearman r</a>	<a href="#">-0.1379</a>	<a href="#">-0.2301 to -0.04320</a>	<a href="#">0.0034</a>	<a href="#">449</a>
<a href="#">miR-154-5p</a> <a href="#">vs.</a> <a href="#">XPO7</a>	<a href="#">Spearman r</a>	<a href="#">-0.1862</a>	<a href="#">-0.2766 to -0.09260</a>	<a href="#">&lt;0.0001</a>	<a href="#">449</a>
<b><a href="#">Functions of miR-154-5p targets</a></b>					
<a href="#">Function</a>			<a href="#">FDR</a>	<a href="#">Genes in network</a>	<a href="#">Genes in genome</a>
<a href="#">ESCRT complex disassembly</a>			<a href="#">0.0242999293293435</a> <a href="#">7</a>	<a href="#">3</a>	<a href="#">10</a>
<a href="#">cell cycle checkpoint</a>			<a href="#">0.0526712161109135</a> <a href="#">6</a>	<a href="#">6</a>	<a href="#">201</a>
<a href="#">negative regulation of mitotic cell cycle</a>			<a href="#">0.0855856859725957</a> <a href="#">1</a>	<a href="#">6</a>	<a href="#">263</a>

	<a href="#">0.0855856859725957</a>		
<a href="#">positive regulation of viral life cycle</a>	<a href="#">1</a>	<a href="#">3</a>	<a href="#">25</a>
	<a href="#">0.0855856859725957</a>		
<a href="#">regulation of viral release from host cell</a>	<a href="#">1</a>	<a href="#">3</a>	<a href="#">26</a>
	<a href="#">0.0855856859725957</a>		
<a href="#">midbody</a>	<a href="#">1</a>	<a href="#">3</a>	<a href="#">21</a>
	<a href="#">0.0885427763281852</a>		
<a href="#">virion assembly</a>	<a href="#">7</a>	<a href="#">3</a>	<a href="#">29</a>
	<a href="#">0.0885427763281852</a>		
<a href="#">viral release from host cell</a>	<a href="#">7</a>	<a href="#">3</a>	<a href="#">29</a>
	<a href="#">0.0885427763281852</a>		
<a href="#">multivesicular body organization</a>	<a href="#">7</a>	<a href="#">3</a>	<a href="#">30</a>
	<a href="#">0.0897192220870177</a>		
<a href="#">negative regulation of cell cycle G1/S phase transition</a>	<a href="#">3</a>	<a href="#">4</a>	<a href="#">93</a>
	<a href="#">0.0897192220870177</a>		
<a href="#">exit from host</a>	<a href="#">3</a>	<a href="#">3</a>	<a href="#">33</a>
	<a href="#">0.0897192220870177</a>		
<a href="#">exit from host cell</a>	<a href="#">3</a>	<a href="#">3</a>	<a href="#">33</a>
<b>Score and function</b>			
<a href="#">Gene</a>	<a href="#">Score</a>	<a href="#">Functions</a>	
<a href="#">LIN9</a>	<a href="#">0.8147884106262913</a>		
<a href="#">LRRC1</a>	<a href="#">0.7570225744326464</a>		
<a href="#">WAC</a>	<a href="#">0.7514653433623196</a>	<a href="#">cell cycle checkpoint</a>	
<a href="#">DCAF16</a>	<a href="#">0.7357887790082105</a>		
<a href="#">C12orf29</a>	<a href="#">0.7309620162356512</a>		
<a href="#">CPEB3</a>	<a href="#">0.7247154071581097</a>		
<a href="#">OVOL1</a>	<a href="#">0.7159273552468898</a>		
<a href="#">CDKN2B</a>	<a href="#">0.7057027545919609</a>	<a href="#">cell cycle checkpoint, negative regulation of cell cycle G1/S phase transition, negative regulation of mitotic cell cycle</a>	
<a href="#">CNOT4</a>	<a href="#">0.6856385674944434</a>	<a href="#">cell cycle checkpoint, negative regulation of cell cycle G1/S phase transition, negative regulation of mitotic cell cycle</a>	
<a href="#">PLAGL2</a>	<a href="#">0.6817377390752662</a>		

<a href="#">NSD2</a>	<a href="#">0.68137600097079</a>				
<a href="#">PTBP3</a>	<a href="#">0.6803369404968923</a>				
<a href="#">NPEPPS</a>	<a href="#">0.6738095573295986</a>				
<a href="#">CEACAM7</a>	<a href="#">0.6716646125926766</a>				
<a href="#">XPO7</a>	<a href="#">0.6671771642456521</a>				
<a href="#">TMPRSS11D</a>	<a href="#">0.6521309249840034</a>				
<a href="#">DMXL1</a>	<a href="#">0.6408571244012663</a>				
<a href="#">ABI1</a>	<a href="#">0.6360087013917106</a>				
<a href="#">RNF138</a>	<a href="#">0.633831587103936</a>				
<a href="#">MYO6</a>	<a href="#">0.6255285691983021</a>				
<a href="#">ESRP1</a>	<a href="#">0.6186632993783615</a>				
<a href="#">LIN54</a>	<a href="#">0.6093346904694159</a>				
<a href="#">VPS4B</a>	<a href="#">0.6017001241319717</a>	<a href="#">ESCRT complex disassembly, exit from host, exit from host cell, midbody, multivesicular body organization, positive regulation of viral life cycle, regulation of viral release from host cell, viral release from host cell, virion assembly</a>			
<a href="#">GNAI3</a>	<a href="#">0.5644190534521365</a>				
<a href="#">LIN52</a>	<a href="#">0.0484538980046133</a> 6				
<a href="#">LIN37</a>	<a href="#">0.0400031120649518</a> 3				
<a href="#">MYBL1</a>	<a href="#">0.0378457639368982</a>				
<a href="#">L3MBTL2</a>	<a href="#">0.0373369325970173</a> 7				
<a href="#">RBBP4</a>	<a href="#">0.0335285503978775</a>				
<a href="#">MYBL2</a>	<a href="#">0.0295998425093396</a> 7				
<a href="#">DYRK1A</a>	<a href="#">0.0134234082728587</a> 61				

<a href="#">DDB1</a>	<a href="#">0.0123566510799688</a> <a href="#">06</a>	<a href="#">exit from host, exit from host cell, positive regulation of viral life cycle, regulation of viral release from host cell, viral release from host cell</a>			
<a href="#">MICAL3</a>	<a href="#">0.0112805958213961</a> <a href="#">78</a>	<a href="#">midbody</a>			
<a href="#">MAU2</a>	<a href="#">0.0086454208869554</a> <a href="#">13</a>				
<a href="#">RECQL4</a>	<a href="#">0.0086072686457085</a> <a href="#">99</a>				
<a href="#">VTA1</a>	<a href="#">0.0080022755727215</a> <a href="#">96</a>	<a href="#">ESCRT complex disassembly, multivesicular body organization, virion assembly</a>			
<a href="#">TOP2A</a>	<a href="#">0.0071598108723617</a> <a href="#">27</a>	<a href="#">cell cycle checkpoint, negative regulation of mitotic cell cycle</a>			
<a href="#">RBL1</a>	<a href="#">0.0070209074887812</a> <a href="#">58</a>	<a href="#">negative regulation of cell cycle G1/S phase transition, negative regulation of mitotic cell cycle</a>			
<a href="#">RELCH</a>	<a href="#">0.0067657263361064</a> <a href="#">48</a>				
<a href="#">RNF111</a>	<a href="#">0.0064105577743465</a> <a href="#">15</a>				
<a href="#">RALB</a>	<a href="#">0.0063929211645848</a> <a href="#">97</a>				
<a href="#">CDC25A</a>	<a href="#">0.0059972536066349</a> <a href="#">45</a>				
<a href="#">E2F1</a>	<a href="#">0.0059877956437482</a> <a href="#">95</a>	<a href="#">cell cycle checkpoint, negative regulation of cell cycle G1/S phase transition, negative regulation of mitotic cell cycle</a>			
<a href="#">VPS4A</a>	<a href="#">0.0057962397856759</a> <a href="#">496</a>	<a href="#">cell cycle checkpoint, ESCRT complex disassembly, exit from host, exit from host cell, midbody, multivesicular body organization, negative regulation of mitotic cell cycle, positive regulation of viral life cycle, regulation of viral release from host cell, viral release from host cell, virion assembly</a>			
<a href="#">Interactions between targets</a>					
<a href="#">Gene 1</a>	<a href="#">Gene 2</a>	<a href="#">Weight</a>	<a href="#">Network group</a>	<a href="#">Network</a>	
<a href="#">NPEPPS</a>	<a href="#">C12orf29</a>	<a href="#">0.022279615</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">TMPRSS11D</a>	<a href="#">CDKN2B</a>	<a href="#">0.015407225</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">TMPRSS11D</a>	<a href="#">CEACAM7</a>	<a href="#">0.017072676</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">ABI1</a>	<a href="#">C12orf29</a>	<a href="#">0.028698482</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">ESRP1</a>	<a href="#">LRRC1</a>	<a href="#">0.008100562</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">ESRP1</a>	<a href="#">PTBP3</a>	<a href="#">0.010739899</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	

<a href="#">VPS4B</a>	<a href="#">LRRC1</a>	<a href="#">0.01042017</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">VPS4B</a>	<a href="#">ABI1</a>	<a href="#">0.010710415</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">GNAI3</a>	<a href="#">PTBP3</a>	<a href="#">0.012533406</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">GNAI3</a>	<a href="#">VPS4B</a>	<a href="#">0.0058445884</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">MYBL2</a>	<a href="#">MYBL1</a>	<a href="#">0.012533161</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">VTA1</a>	<a href="#">NPEPPS</a>	<a href="#">0.023306785</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RBL1</a>	<a href="#">MYBL2</a>	<a href="#">0.01107938</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RELCH</a>	<a href="#">C12orf29</a>	<a href="#">0.022101806</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RELCH</a>	<a href="#">NPEPPS</a>	<a href="#">0.018847946</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RELCH</a>	<a href="#">ABI1</a>	<a href="#">0.022219187</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RELCH</a>	<a href="#">VPS4B</a>	<a href="#">0.009669509</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RNF111</a>	<a href="#">WAC</a>	<a href="#">0.008207716</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RNF111</a>	<a href="#">C12orf29</a>	<a href="#">0.007489541</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RNF111</a>	<a href="#">NPEPPS</a>	<a href="#">0.0069940635</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RNF111</a>	<a href="#">ABI1</a>	<a href="#">0.007820658</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RALB</a>	<a href="#">NPEPPS</a>	<a href="#">0.021908162</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RALB</a>	<a href="#">ABI1</a>	<a href="#">0.029890688</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RALB</a>	<a href="#">VPS4B</a>	<a href="#">0.0103175</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">RALB</a>	<a href="#">RELCH</a>	<a href="#">0.020367647</a>	<a href="#">Co-expression</a>	<a href="#">Zlotnik-2019</a>	
<a href="#">DCAF16</a>	<a href="#">WAC</a>	<a href="#">0.01693839</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">PLAGL2</a>	<a href="#">DCAF16</a>	<a href="#">0.0098297475</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">NSD2</a>	<a href="#">DCAF16</a>	<a href="#">0.013989579</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">NSD2</a>	<a href="#">PLAGL2</a>	<a href="#">0.0083880285</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">PTBP3</a>	<a href="#">CDKN2B</a>	<a href="#">0.009976122</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">DYRK1A</a>	<a href="#">RNF138</a>	<a href="#">0.011046242</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">RECQL4</a>	<a href="#">NSD2</a>	<a href="#">0.009081764</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">RECQL4</a>	<a href="#">MYBL2</a>	<a href="#">0.006867876</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">VTA1</a>	<a href="#">ABI1</a>	<a href="#">0.008112838</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">TOP2A</a>	<a href="#">NSD2</a>	<a href="#">0.006955337</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">TOP2A</a>	<a href="#">MYBL2</a>	<a href="#">0.0056763375</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">TOP2A</a>	<a href="#">RECQL4</a>	<a href="#">0.0066834856</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">RNF111</a>	<a href="#">DMXL1</a>	<a href="#">0.006378078</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	
<a href="#">RNF111</a>	<a href="#">DYRK1A</a>	<a href="#">0.014407489</a>	<a href="#">Co-expression</a>	<a href="#">Brown-2019</a>	



<a href="#">RALB</a>	<a href="#">CEACAM7</a>	<a href="#">0.0168126</a>	<a href="#">Co-expression</a>	<a href="#">hen-Brown-20</a>	
<a href="#">CDC25A</a>	<a href="#">PLAGL2</a>	<a href="#">0.0077637723</a>	<a href="#">Co-expression</a>	<a href="#">hen-Brown-20</a>	
<a href="#">CDC25A</a>	<a href="#">NSD2</a>	<a href="#">0.008300521</a>	<a href="#">Co-expression</a>	<a href="#">hen-Brown-20</a>	
<a href="#">CDC25A</a>	<a href="#">TOP2A</a>	<a href="#">0.0070079416</a>	<a href="#">Co-expression</a>	<a href="#">hen-Brown-20</a>	
<a href="#">E2F1</a>	<a href="#">MYBL2</a>	<a href="#">0.009568628</a>	<a href="#">Co-expression</a>	<a href="#">hen-Brown-20</a>	
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