

Supplemental Material to:

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Armin Pscherer, Martina Seiffert and Peter Lichter**

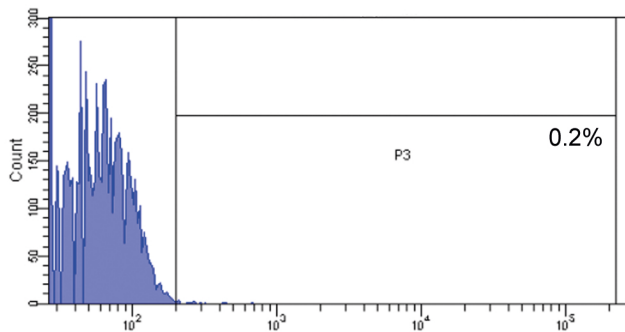
**Genome-wide identification of translationally
inhibited and degraded miR-155 targets
using RNA-interacting protein-IP**

2013; 10(6)

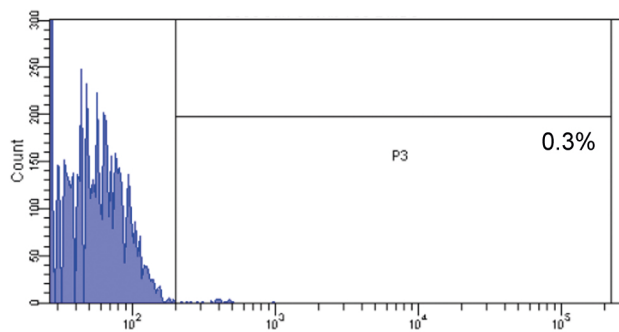
<http://dx.doi.org/10.4161/rna.24553>

www.landesbioscience.com/journals/rnabiology/article/24553/

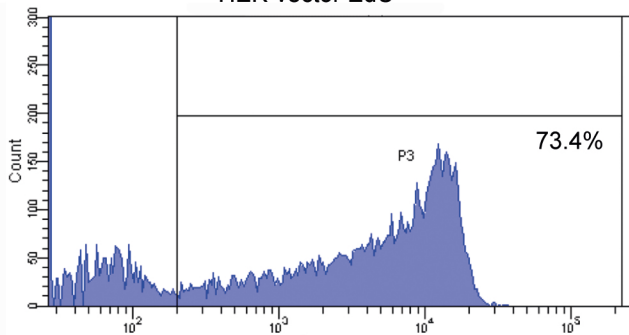
HEK-vector Control



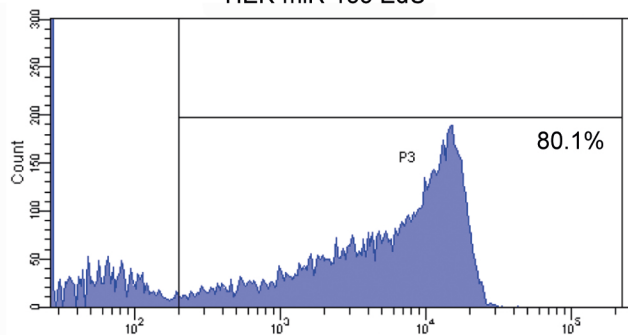
HEK-miR-155 Control



HEK-vector EdU



HEK-miR-155 EdU



MEC-1 RIPA

MEC-1 PLB

IgG1 SN

IgG1 IP

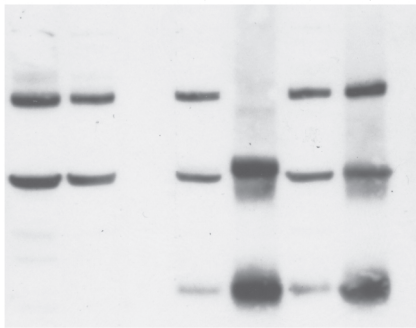
Ago2 SN

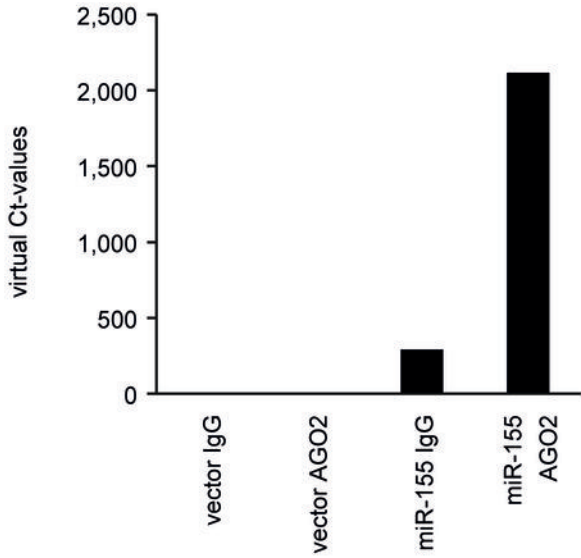
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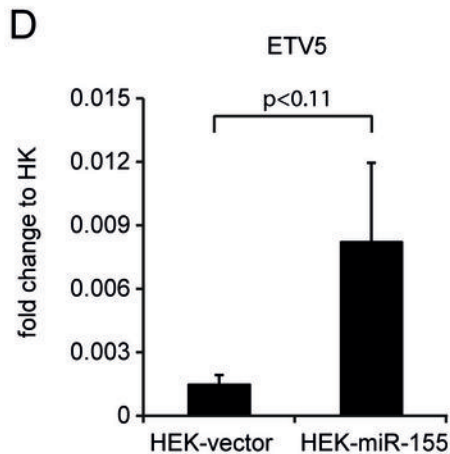
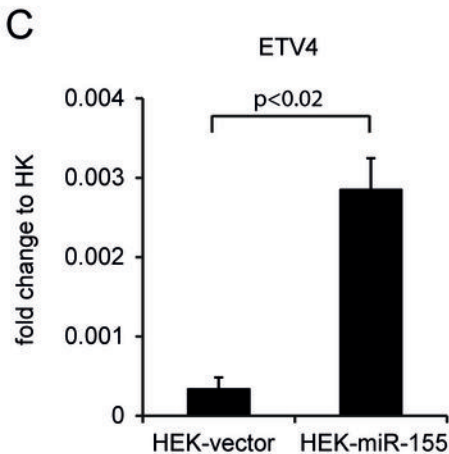
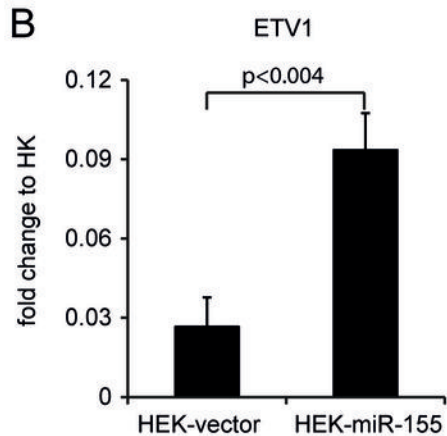
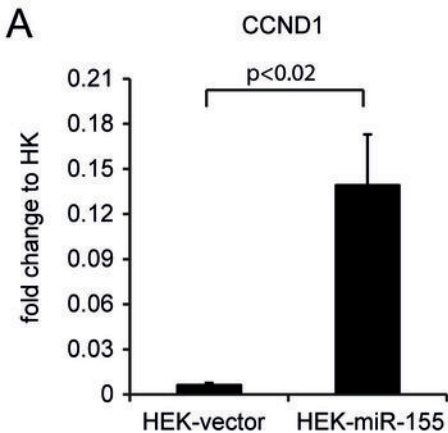
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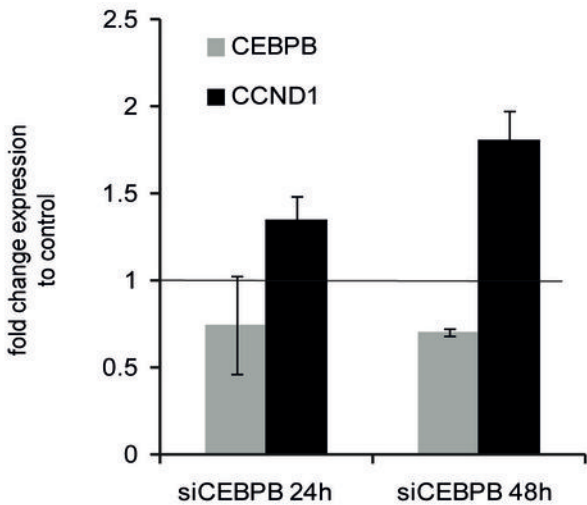
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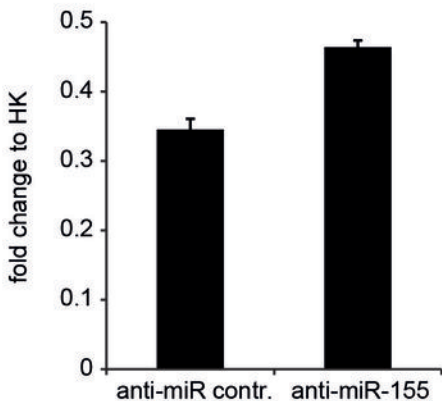




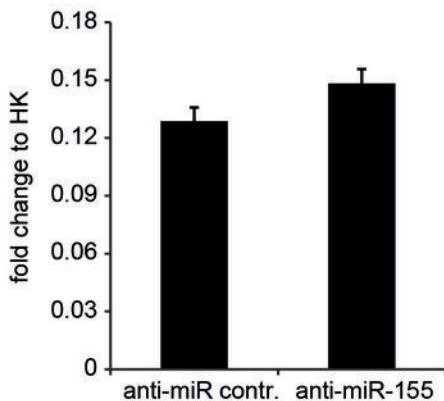




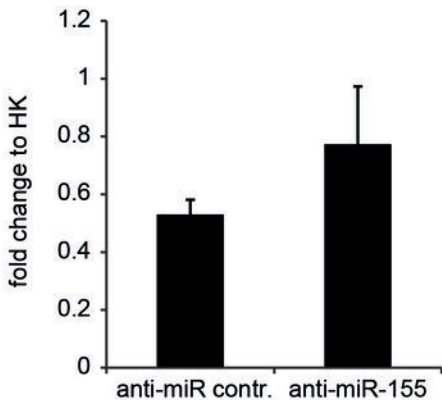
ZFP36 mRNA



JARID2 mRNA



BACH1 mRNA

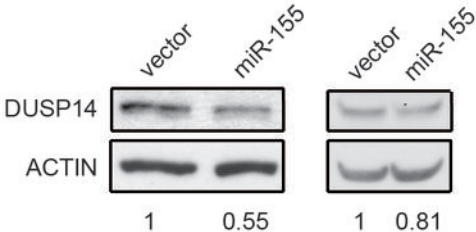


P-values (student's t-test):

ZFP36: $p < 0.002$

JARID2: $p < 0.15$

BACH1: $p < 0.11$



S1 mRNAs differentially expressed in HEKmiR-155 TL

down in HEK-miR-155 TL			up in HEK-miR-155 TL		
	log2 FC	n=339 adjusted p- value		log2 FC	n=121 adjusted p- value
SPARC	-7.06E+00	7.43E-52	FAM78A	2.13E+00	1.38E-23
DOK6	-4.46E+00	2.05E-46	TNFRSF11B	5.53E+00	1.36E-19
GALNT13	-3.38E+00	1.16E-43	DPYSL3	1.98E+00	1.94E-19
RHBDD2	-7.30E-01	1.81E-02	CCND1	4.19E+00	1.96E-12
CDO1	-5.51E+00	4.50E-32	ZNF813	2.02E+00	4.35E-12
COL2A1	-2.56E+00	1.69E-29	KCNQ2	1.32E+00	1.88E-10
PLA2G4A	-4.57E+00	5.43E-25	ALDH1A2	1.24E+00	1.71E-09
TKTL1	-1.63E+00	1.15E-02	FAM84B	1.09E+00	1.04E-07
BAIAP3	-9.28E-01	3.91E-02	CA12	1.14E+00	6.92E-07
OAS3	-4.97E+00	9.60E-24	NDRG1	1.19E+00	1.95E-06
EPAS1	-2.17E+00	1.09E-23	ZNF85	2.18E+00	3.35E-06
CALCOCO1	-6.93E-01	1.00E-02	PROCR	1.04E+00	1.09E-05
PGCP	-4.30E+00	1.47E-22	EDA2R	3.78E+00	1.46E-05
UBE2QL1	-2.74E+00	1.49E-22	ADCYAP1R1	9.74E-01	1.62E-05
ULK2	-1.98E+00	4.64E-20	POLR3G	1.14E+00	2.24E-05
IKZF2	-9.76E-01	4.25E-02	BMP2	1.83E+00	2.51E-05
DSG2	-6.17E-01	2.00E-02	C19orf51	9.74E-01	4.40E-05
FGF13	-3.05E+00	6.31E-18	ATP1A3	9.36E-01	5.23E-05
ZFP106	-1.68E+00	4.16E-17	HMOX1	1.05E+00	6.45E-05
ATP9A	-6.35E-01	1.56E-02	LY6E	8.72E-01	9.48E-05
PCDH10	-1.65E+00	2.50E-16	BEND4	9.23E-01	1.10E-04
CYP26B1	-1.94E+00	3.86E-14	BOP1	9.07E-01	1.38E-04
MAMLD1	-1.77E+00	4.35E-14	TRMT12	8.56E-01	3.61E-04
FAT3	-2.08E+00	2.23E-13	COTL1	8.24E-01	5.14E-04
PRKCB	-1.61E+00	1.70E-12	ZNF256	1.25E+00	5.54E-04
SNCAIP	-1.09E+00	2.37E-02	MRPL13	8.04E-01	6.32E-04
OPTN	-1.36E+00	2.79E-11	EXT1	8.09E-01	7.92E-04
PLCB2	-2.78E+00	2.87E-11	SPRY1	8.28E-01	8.33E-04
MGAT4A	-5.78E-01	4.88E-02	KLRG2	8.24E-01	1.22E-03
CYBRD1	-7.80E-01	2.37E-02	ETV1	1.25E+00	1.57E-03
CLCN4	-1.81E+00	3.68E-02	DHRS2	1.13E+00	1.61E-03
PTGS2	-3.46E+00	1.87E-02	C8orf33	7.39E-01	2.20E-03
SAMD12	-1.69E+00	8.51E-11	ALPL	8.46E-01	2.88E-03
FOSL2	-7.67E-01	2.04E-02	ARSJ	9.01E-01	3.05E-03
PLD1	-9.16E-01	4.03E-02	ELOVL6	7.35E-01	3.53E-03
B3GALT1	-2.23E+00	1.30E-10	ABCE1	6.83E-01	3.58E-03
NES	-2.77E+00	2.48E-10	C12orf35	7.26E-01	3.62E-03
EDIL3	-4.31E+00	2.49E-10	FAM150A	1.93E+00	3.67E-03
ST8SIA4	-3.77E+00	3.70E-10	COL14A1	1.28E+00	3.80E-03
FAM20C	-1.46E+00	2.15E-09	DNMT3B	7.34E-01	3.93E-03
PPP1R15A	-7.31E-01	1.42E-02	SULT1A1	1.04E+00	3.93E-03
CDH2	-1.74E+00	2.18E-09	TATDN1	7.31E-01	4.06E-03
STXBP5L	-2.22E+00	2.51E-09	GPATCH4	7.12E-01	4.29E-03
EBF4	-7.17E-01	2.98E-02	SPRED2	7.40E-01	4.96E-03
YPEL3	-9.37E-01	2.48E-02	TERT	1.30E+00	4.98E-03
EHBP1L1	-1.46E+00	7.13E-09	RNF125	7.19E-01	5.25E-03

MYO3A	-9.71E-01	3.09E-02	GPRIN3	7.53E-01	5.34E-03
MMP11	-6.53E-01	5.00E-02	PYCR1	7.81E-01	5.43E-03
MYO5B	-1.60E+00	1.15E-08	RASGEF1A	7.31E-01	5.83E-03
CELF2	-1.97E+00	1.17E-08	THEM4	6.95E-01	6.45E-03
RYR2	-2.72E+00	1.27E-08	FBXO32	7.56E-01	6.97E-03
SLC8A3	-2.21E+00	1.77E-02	PDZRN3	7.76E-01	7.48E-03
RPS6KA5	-6.65E-01	3.52E-02	RAB39	9.65E-01	7.58E-03
KCNQ1	-1.72E+00	1.82E-08	POP1	6.83E-01	7.91E-03
ESRRG	-2.56E+00	2.00E-08	KHDRBS3	7.12E-01	8.54E-03
PRKG2	-2.88E+00	2.20E-08	SLC11A1	1.49E+00	8.66E-03
SNPH	-6.92E-01	2.49E-02	ETV5	1.85E+00	8.71E-03
JAG1	-8.79E-01	2.65E-02	HSPE1	6.82E-01	8.99E-03
APH1B	-1.24E+00	2.20E-08	ETV4	2.16E+00	9.60E-03
CHRD1	-1.32E+00	1.63E-02	FAM49B	6.55E-01	9.91E-03
SYTL4	-6.71E-01	3.17E-02	TMEM145	8.37E-01	1.02E-02
TTBK2	-1.23E+00	2.20E-08	PALM2	1.01E+00	1.02E-02
GALC	-1.55E+00	5.19E-08	GABRD	9.54E-01	1.10E-02
AIFM2	-2.15E+00	5.20E-08	FAM91A1	6.37E-01	1.16E-02
FOXF1	-6.61E-01	2.74E-02	EFR3A	6.42E-01	1.17E-02
STARD9	-1.19E+00	6.24E-08	CAMKV	7.14E-01	1.26E-02
SERPING1	-3.40E+00	8.57E-08	WDR67	6.47E-01	1.30E-02
BMF	-1.44E+00	2.05E-02	UTP23	6.45E-01	1.33E-02
SPINT2	-1.72E+00	8.66E-08	ZNF44	8.38E-01	1.38E-02
CCNDBP1	-1.20E+00	1.09E-07	TEX15	6.45E-01	1.54E-02
WNT9A	-1.61E+00	1.40E-07	SEH1L	6.25E-01	1.56E-02
DMRT3	-2.91E+00	2.34E-07	PCDH19	8.58E-01	1.62E-02
DDIT4L	-1.62E+00	2.93E-07	PPID	6.26E-01	1.74E-02
SNAP91	-1.88E+00	3.71E-07	CACYBP	6.22E-01	1.78E-02
CACNA1G	-1.58E+00	5.05E-07	TNFRSF10D	6.87E-01	1.87E-02
C1orf172	-4.00E+00	5.24E-07	C4orf43	6.09E-01	1.96E-02
DNAH11	-7.99E-01	5.00E-02	ADA	6.85E-01	2.00E-02
LGALS1	-1.18E+00	5.54E-07	ZNF586	8.54E-01	2.00E-02
SLIT2	-1.04E+00	6.92E-07	DSCC1	5.93E-01	2.00E-02
UBR1	-1.09E+00	8.39E-07	MT1X	7.22E-01	2.04E-02
EPHB6	-1.61E+00	4.37E-02	TRIB1	1.20E+00	2.04E-02
HSPB1	-6.79E-01	1.24E-02	CYC1	7.01E-01	2.14E-02
NACAD	-1.33E+00	8.42E-07	EGLN3	6.74E-01	2.24E-02
RGP1	-5.63E-01	4.88E-02	TAP2	6.40E-01	2.32E-02
ATRNL1	-6.82E-01	3.07E-02	CHRAC1	6.24E-01	2.32E-02
EFNB3	-6.17E-01	3.00E-02	MMP2	9.21E-01	2.35E-02
NMU	-6.88E-01	2.26E-02	CHRNA4	1.34E+00	2.35E-02
LCMT2	-1.08E+00	1.95E-06	C3orf14	6.10E-01	2.43E-02
PRRX1	-2.33E+00	2.60E-06	BCL6B	6.20E-01	2.85E-02
HOXA5	-1.15E+00	2.60E-06	NRG2	9.31E-01	2.95E-02
SOX6	-7.06E-01	2.61E-02	WT1	6.78E-01	2.97E-02
RAI2	-1.51E+00	3.01E-06	NIP7	5.97E-01	2.99E-02
VPS39	-1.01E+00	3.23E-06	NEIL2	6.46E-01	2.99E-02
ODZ1	-4.93E+00	3.35E-06	TRIM71	7.61E-01	2.99E-02
SMOC2	-4.05E+00	3.27E-02	IL12RB2	8.68E-01	3.08E-02
CUL9	-6.73E-01	1.31E-02	TESC	7.78E-01	3.09E-02

OSBPL7	-1.39E+00	3.80E-06	SQLE	5.86E-01	3.15E-02
TTC9	-1.34E+00	4.62E-06	SLC24A4	8.73E-01	3.23E-02
SLC27A6	-1.14E+00	1.83E-02	LYAR	5.91E-01	3.23E-02
GPRC5C	-1.55E+00	4.91E-06	HRSP12	6.01E-01	3.24E-02
TRIM23	-6.78E-01	1.42E-02	FBXO41	6.51E-01	3.24E-02
CDAN1	-1.06E+00	5.06E-06	TOP1MT	5.97E-01	3.24E-02
PLCL1	-1.71E+00	5.08E-06	TRPS1	5.95E-01	3.27E-02
MBP	-1.54E+00	5.08E-06	CCT6A	5.69E-01	3.39E-02
GCA	-6.57E-01	3.10E-02	ZNF528	1.63E+00	3.52E-02
BEX2	-9.82E-01	5.95E-06	NFASC	8.08E-01	3.55E-02
PDE10A	-1.34E+00	6.34E-06	ZC3H15	5.74E-01	3.55E-02
TMEM62	-1.08E+00	6.90E-06	PRPS2	5.66E-01	3.69E-02
CXCL16	-1.04E+00	6.90E-06	NCS1	5.89E-01	3.74E-02
TMEM87A	-9.99E-01	6.90E-06	PLCD3	5.85E-01	3.94E-02
PARD3B	-6.86E-01	3.85E-02	PRR5L	8.79E-01	4.07E-02
SPTAN1	-9.51E-01	1.04E-05	ANKRD34A	6.69E-01	4.20E-02
ADAL	-1.00E+00	1.21E-05	ASAP1	5.68E-01	4.23E-02
ANKRD1	-1.48E+00	1.22E-05	ADAT2	5.88E-01	4.28E-02
MNS1	-1.42E+00	1.22E-05	ZNF121	6.05E-01	4.48E-02
CLVS2	-2.37E+00	1.27E-05	GCLM	5.55E-01	4.50E-02
YPEL5	-6.88E-01	4.16E-02	RBFOX3	1.16E+00	4.50E-02
NME5	-2.31E+00	1.49E-05	OR2V2	4.11E+00	4.77E-02
LPL	-2.24E+00	1.57E-05	FAM196A	1.31E+00	4.78E-02
PTGFR	-1.26E+00	1.28E-02	C1QBP	5.48E-01	4.86E-02
AS3MT	-1.03E+00	1.57E-05	EPHA8	1.00E+00	5.00E-02
LRP1	-5.99E-01	3.92E-02			
GOS2	-1.86E+00	2.14E-05			
BEND5	-2.59E+00	2.24E-05			
LSR	-9.72E-01	2.31E-05			
POR	-6.02E-01	3.14E-02			
AC010336.1	-1.47E+00	2.63E-05			
TMSB4X	-1.40E+00	3.06E-05			
ZSCAN29	-9.39E-01	3.23E-05			
EPSTI1	-1.61E+00	3.63E-05			
STARD8	-7.44E-01	3.39E-02			
BASP1	-2.88E+00	3.80E-05			
PGPEP1	-6.14E-01	3.65E-02			
PLXNA3	-6.54E-01	1.52E-02			
GANC	-1.04E+00	3.80E-05			
TP53INP1	-9.90E-01	4.09E-05			
LGALS3	-8.44E-01	1.48E-02			
LRRTM4	-1.73E+00	4.57E-05			
ITGB4	-9.06E-01	1.80E-02			
LYPD6	-9.44E-01	4.62E-05			
INADL	-6.00E-01	4.51E-02			
MTMR11	-1.30E+00	5.23E-05			
APOBEC3B	-1.69E+00	5.41E-05			
SORT1	-5.46E-01	4.57E-02			
FBXO27	-1.03E+00	5.90E-05			
AHRR	-9.02E-01	5.96E-05			

EDNRB	-4.91E+00	4.40E-02
MIXL1	-1.78E+00	5.96E-05
LRRC57	-9.43E-01	8.24E-05
SLC22A23	-6.19E-01	3.00E-02
SPTB	-1.16E+00	9.61E-05
PLD5	-3.79E+00	1.09E-04
TCP11L2	-1.09E+00	1.12E-04
KCTD12	-9.23E-01	1.22E-04
SLC44A5	-6.15E-01	3.26E-02
CYP1B1	-2.21E+00	2.18E-02
PVALB	-1.98E+00	1.22E-04
HOXA6	-1.69E+00	1.28E-04
DKK3	-1.38E+00	1.59E-04
FRAS1	-6.65E-01	1.50E-02
SLC38A4	-1.64E+00	1.12E-02
IFI27L2	-9.44E-01	1.59E-04
SNAP23	-8.66E-01	1.59E-04
FAM105A	-8.49E-01	2.48E-04
OTX2	-1.28E+00	2.58E-04
CACNA2D3	-1.04E+00	2.63E-04
FREM2	-9.02E-01	2.78E-04
IQGAP1	-6.55E-01	1.39E-02
SECTM1	-1.68E+00	1.11E-02
FAM71E1	-1.13E+00	1.24E-02
ATP6V1G1	-8.16E-01	3.25E-04
BRWD3	-8.60E-01	3.40E-04
HMCN1	-1.38E+00	1.26E-02
SLITRK5	-8.45E-01	3.40E-04
LYST	-5.97E-01	4.72E-02
ABHD1	-1.12E+00	3.52E-02
RAPGEF2	-8.49E-01	3.67E-04
ZNF652	-8.50E-01	3.91E-04
IGSF11	-3.03E+00	4.00E-04
GAB3	-1.64E+00	4.62E-04
EFEMP2	-1.62E+00	4.77E-04
DTX1	-3.42E+00	4.78E-04
TSLP	-9.32E-01	4.57E-02
GPR126	-1.05E+00	4.78E-04
NR3C2	-8.98E-01	4.97E-04
GSN	-6.77E-01	2.97E-02
CDHR1	-9.69E-01	1.89E-02
TRIM36	-9.26E-01	5.09E-04
FGF9	-1.78E+00	5.77E-04
HES1	-8.33E-01	5.82E-04
KCNA6	-2.64E+00	1.07E-02
TMTC2	-1.29E+00	5.83E-04
TMEM86A	-8.82E-01	1.61E-02
COL4A4	-2.14E+00	6.36E-04
MFSD6	-9.51E-01	2.36E-02
LAMB2	-8.18E-01	6.53E-04

HSPB8	-1.48E+00	4.50E-02
KCNK13	-1.21E+00	3.10E-02
GUCY1A2	-1.66E+00	1.28E-02
IGFBPL1	-5.66E+00	7.70E-04
AHR	-9.12E-01	8.04E-04
GPX3	-7.78E-01	8.04E-04
SLC16A5	-3.42E+00	8.98E-04
BACH1	-6.31E-01	2.32E-02
PCDH1	-1.20E+00	2.93E-02
LRRN2	-1.32E+00	8.98E-04
NMNAT2	-1.22E+00	1.00E-02
MAP6	-1.24E+00	8.98E-04
JARID2	-7.99E-01	9.35E-04
CAMK4	-1.04E+00	9.66E-04
PPP1R9A	-9.75E-01	3.63E-02
PINK1	-6.42E-01	2.04E-02
L3MBTL4	-1.26E+00	1.00E-03
CA8	-2.48E+00	1.04E-03
C19orf57	-9.75E-01	1.08E-03
ISM1	-1.02E+00	1.13E-03
TM7SF2	-7.81E-01	1.17E-03
SCN1B	-1.23E+00	1.18E-03
NPY1R	-2.92E+00	1.24E-03
ITGA8	-8.05E-01	1.30E-03
SLAIN1	-9.36E-01	1.32E-03
TUBGCP4	-7.73E-01	1.39E-03
GFI1	-7.99E-01	2.00E-02
LONRF2	-8.08E-01	1.43E-03
ANTXR2	-7.41E-01	2.38E-02
FSTL1	-6.61E-01	1.03E-02
LMOD1	-8.31E-01	2.49E-02
ZNF513	-6.37E-01	1.96E-02
QPCT	-1.19E+00	1.47E-03
KLHL32	-1.75E+00	1.57E-03
SLC46A3	-8.47E-01	1.65E-03
SYT1	-8.51E-01	1.67E-03
CXCL12	-6.09E+00	1.79E-03
FOXQ1	-1.58E+00	4.74E-02
SLC13A4	-9.15E-01	2.51E-02
PLAT	-1.28E+00	1.82E-03
MCOLN3	-8.39E-01	1.88E-03
HDX	-7.55E-01	2.26E-02
MAP7	-7.79E-01	1.99E-03
KIF1A	-2.26E+00	2.02E-03
CXCR4	-1.73E+00	2.29E-03
PROX1	-9.50E-01	2.38E-03
MAN1C1	-9.90E-01	2.39E-03
ADAMTS15	-8.46E-01	3.39E-02
C10orf26	-5.69E-01	3.27E-02
KRBA2	-2.32E+00	2.43E-03

TMEM132E	-2.30E+00	2.68E-03
PLEKHA7	-6.73E-01	3.56E-02
SLFN5	-9.40E-01	3.28E-02
PIK3CD	-8.07E-01	2.77E-03
DCHS1	-9.49E-01	2.97E-03
MIDN	-9.07E-01	5.00E-02
CLSTN2	-2.73E+00	2.97E-03
NPFFR2	-3.34E+00	2.99E-03
ABCA3	-1.09E+00	1.40E-02
TAP1	-5.99E-01	4.03E-02
NPR1	-1.99E+00	3.05E-03
C18orf1	-6.81E-01	3.44E-02
ANG	-1.42E+00	3.24E-03
MOB3C	-9.98E-01	3.36E-03
TAPT1	-6.41E-01	2.32E-02
VGLL2	-9.36E-01	3.57E-02
MXD1	-7.58E-01	3.36E-03
OCLN	-7.49E-01	3.36E-03
MYO7A	-3.43E+00	3.36E-03
S1PR1	-1.03E+00	3.36E-03
THRB	-7.70E-01	3.59E-03
KCNS3	-1.09E+00	2.86E-02
DLK2	-7.06E-01	3.55E-02
BRSK1	-8.58E-01	3.93E-03
TTLL7	-7.59E-01	4.06E-03
DPY19L1	-6.11E-01	3.04E-02
IQGAP3	-7.44E-01	4.22E-03
FAM131A	-7.00E-01	2.04E-02
MCTP1	-1.24E+00	1.91E-02
PRDM8	-1.41E+00	4.40E-03
KDM5B	-7.20E-01	4.41E-03
CFHR3	-1.94E+00	4.96E-03
BOK	-8.75E-01	3.86E-02
RPRM	-2.93E+00	3.39E-02
ZFP36	-8.59E-01	4.98E-03
DMRTA2	-1.63E+00	5.04E-03
ACVR1C	-1.54E+00	5.04E-03
APOLD1	-7.64E-01	1.27E-02
GPM6A	-9.38E-01	5.19E-03
WSCD1	-9.60E-01	1.78E-02
C8orf42	-1.21E+00	2.97E-02
SLC2A10	-7.82E-01	5.45E-03
FCGRT	-7.50E-01	5.46E-03
RPH3AL	-8.94E-01	1.23E-02
TMSB15A	-7.33E-01	5.59E-03
RFX6	-1.86E+00	5.82E-03
PLXNA4	-3.00E+00	5.83E-03
ARHGEF17	-7.69E-01	5.83E-03
ABAT	-6.44E-01	4.01E-02
DSCR6	-7.45E-01	1.81E-02

HAUS2	-7.12E-01	5.85E-03
NUDT14	-6.64E-01	3.52E-02
RIMS1	-2.71E+00	6.11E-03
LSAMP	-4.01E+00	6.19E-03
FGF12	-2.50E+00	6.59E-03
ZNF467	-1.30E+00	6.88E-03
TCN2	-2.76E+00	2.35E-02
HS6ST3	-1.72E+00	1.00E-02
METTL7A	-7.81E-01	4.32E-02
HOXA4	-1.02E+00	7.00E-03
RAB9B	-8.09E-01	7.00E-03
PAK3	-1.42E+00	7.34E-03
CAV1	-9.22E-01	7.39E-03
SPOCK3	-1.44E+00	7.44E-03
ALG1L	-9.00E-01	4.33E-02
SLC35F1	-6.26E-01	2.54E-02
PARD6A	-1.06E+00	7.91E-03
ARHGAP33	-7.68E-01	8.02E-03
GALNT3	-3.05E+00	8.19E-03
GMCL1	-7.08E-01	8.21E-03
LGR5	-8.71E-01	8.42E-03
DTX3L	-7.66E-01	8.46E-03
CHSY3	-7.78E-01	4.03E-02
KIAA1539	-8.79E-01	8.66E-03
MT1F	-1.20E+00	1.43E-02
PTPRO	-1.65E+00	8.72E-03
LHX9	-1.15E+00	8.86E-03
C2orf72	-7.59E-01	1.80E-02
MICB	-7.71E-01	4.01E-02
RET	-9.22E-01	8.86E-03
GFRA1	-1.14E+00	8.91E-03
TMEM200C	-1.58E+00	1.02E-02
DDAH2	-7.29E-01	1.78E-02
HOXA3	-9.18E-01	9.12E-03
PRKCH	-7.96E-01	9.13E-03
TP73	-6.94E-01	9.41E-03
KIAA0913	-5.64E-01	4.75E-02
RP11-428C6.1	-9.18E-01	2.47E-02
KCNT2	-2.07E+00	9.69E-03
ATXN1L	-5.93E-01	2.39E-02
EPPK1	-2.12E+00	3.39E-02
PCDHGC4	-1.51E+00	2.24E-02
PRR16	-1.11E+00	9.98E-03

S2 mRNAs differentially enriched in IP fractions

enriched in HEK-vector			enriched in HEK-miR-155		
		n=409			n=213
	log2 FC	adjusted p-value		log2 FC	adjusted p-value
SPARC	-4.70E+00	3.71E-27	TNFRSF11B	6.10E+00	7.99E-17
GALNT13	-2.84E+00	6.11E-26	FAM78A	1.78E+00	4.29E-16
EPAS1	-2.26E+00	1.28E-22	KCNQ2	1.59E+00	2.20E-15
DOK6	-3.79E+00	1.47E-22	C21orf37	5.59E+00	7.51E-11
COL2A1	-2.47E+00	6.07E-20	CCND1	3.88E+00	1.03E-10
ULK2	-2.06E+00	2.41E-19	DPYSL3	1.55E+00	5.27E-10
UBE2QL1	-2.71E+00	2.56E-18	TCF4	1.32E+00	5.38E-10
CDO1	-4.58E+00	8.50E-17	ALDH1A2	1.23E+00	2.65E-09
CYP26B1	-2.26E+00	1.06E-16	ZNF483	1.92E+00	2.65E-09
PCDH10	-1.68E+00	3.30E-15	CA12	1.36E+00	4.84E-09
ZFP106	-1.54E+00	1.99E-13	AGTRAP	1.20E+00	7.32E-09
PGCP	-3.57E+00	2.24E-12	COL27A1	1.20E+00	2.67E-08
FAM20C	-1.62E+00	9.82E-12	LY6E	1.04E+00	9.23E-07
OAS3	-4.48E+00	1.95E-11	C12orf39	1.33E+00	1.53E-06
EHBP1L1	-1.84E+00	7.74E-11	FAM84B	1.02E+00	1.62E-06
STARD9	-1.50E+00	7.74E-11	BMP2	2.18E+00	3.28E-06
TTBK2	-1.61E+00	1.35E-10	PROCR	1.08E+00	3.88E-06
MAMLD1	-1.74E+00	1.60E-10	NDRG1	1.15E+00	3.96E-06
CDH2	-1.95E+00	6.45E-10	OR2V2	5.02E+00	5.36E-06
OPTN	-1.30E+00	1.78E-09	C19orf51	1.06E+00	1.19E-05
MYO5B	-1.97E+00	1.78E-09	PNPT1	8.90E-01	8.07E-05
PLA2G4A	-3.32E+00	2.65E-09	COTL1	8.89E-01	9.17E-05
APH1B	-1.36E+00	2.65E-09	EDA2R	3.64E+00	9.25E-05
SLIT2	-1.19E+00	4.11E-09	USPL1	9.02E-01	9.25E-05
FGF13	-2.68E+00	7.32E-09	PPA2	8.75E-01	9.25E-05
DMRT3	-3.94E+00	1.17E-08	FCRLB	1.46E+00	9.25E-05
VPS39	-1.18E+00	2.67E-08	HMOX1	1.01E+00	1.50E-04
OSBPL7	-1.88E+00	8.23E-08	SOD1	8.45E-01	1.66E-04
DDIT4L	-1.92E+00	1.61E-07	TRMT12	8.80E-01	2.39E-04
GANC	-1.37E+00	1.87E-07	ZNF813	1.59E+00	2.71E-04
LRP1	-1.19E+00	2.38E-07	BBS7	8.74E-01	2.79E-04
CDAN1	-1.21E+00	2.62E-07	PHC2	1.50E+00	3.21E-04
PVALB	-2.88E+00	4.56E-07	CHST15	8.55E-01	3.25E-04
PRKCB	-1.34E+00	4.67E-07	FAM150A	2.24E+00	3.26E-04
TP53INP1	-1.23E+00	4.73E-07	ALPL	9.46E-01	3.88E-04
FBXO27	-1.20E+00	5.58E-07	C3orf18	8.89E-01	4.24E-04
ZSCAN29	-1.12E+00	5.77E-07	ADCYAP1R1	8.63E-01	6.47E-04
UBR1	-1.13E+00	6.99E-07	POLR3G	1.02E+00	7.08E-04
CCNDBP1	-1.17E+00	8.57E-07	FAM49B	7.94E-01	7.91E-04
WNT9A	-1.59E+00	8.57E-07	TESC	9.80E-01	8.36E-04
AIFM2	-2.02E+00	9.38E-07	MECR	7.88E-01	8.53E-04
SAMD12	-1.56E+00	1.53E-06	THEM4	7.73E-01	9.61E-04
NACAD	-1.50E+00	2.22E-06	INTS10	7.84E-01	1.01E-03
TMSB4X	-1.57E+00	4.63E-06	C8orf33	7.66E-01	1.20E-03
PLCB2	-2.20E+00	5.84E-06	VAMP3	7.53E-01	1.30E-03
KCNQ1	-1.42E+00	6.93E-06	SPRED1	8.30E-01	1.37E-03

TMEM62	-1.13E+00	6.93E-06	TBC1D14	7.60E-01	1.49E-03
TMEM87A	-1.04E+00	6.93E-06	ARSJ	1.01E+00	1.52E-03
CELF2	-1.68E+00	1.09E-05	ADA	8.15E-01	1.82E-03
RYR2	-2.66E+00	1.09E-05	MRPL13	7.48E-01	1.96E-03
LCMT2	-1.04E+00	1.25E-05	ETV1	1.38E+00	1.98E-03
CLVS2	-3.75E+00	1.25E-05	BCL6B	7.82E-01	2.02E-03
HOXA5	-1.06E+00	1.28E-05	EIF2C2	9.18E-01	2.24E-03
ODZ1	-5.34E+00	1.34E-05	KHDRBS3	7.73E-01	2.25E-03
PDE10A	-1.41E+00	1.34E-05	METTL21A	7.54E-01	2.26E-03
CACNA1G	-1.68E+00	1.37E-05	ZNF586	1.09E+00	2.51E-03
LMO7	-1.07E+00	1.77E-05	DET1	1.48E+00	2.61E-03
GOS2	-1.84E+00	2.22E-05	LIPT1	7.88E-01	2.61E-03
OTX2	-1.59E+00	2.44E-05	COPS2	6.98E-01	2.66E-03
STXBP5L	-2.18E+00	3.24E-05	SPRY1	7.84E-01	2.82E-03
IQGAP3	-9.85E-01	3.25E-05	EPHA8	1.32E+00	3.25E-03
KCTD12	-9.82E-01	3.75E-05	TRIM32	7.40E-01	3.38E-03
MAP7	-9.87E-01	4.98E-05	FBXO32	8.60E-01	3.56E-03
ST8SIA4	-3.65E+00	5.99E-05	DSCC1	7.02E-01	3.86E-03
EFEMP2	-1.83E+00	6.79E-05	ARRDC2	7.77E-01	3.89E-03
SNAP91	-1.74E+00	6.80E-05	TSTA3	7.19E-01	3.93E-03
SLC16A5	-4.61E+00	6.85E-05	IER5	7.41E-01	3.95E-03
SLC35F3	-2.71E+00	6.91E-05	C20orf27	7.05E-01	4.03E-03
GPRC5C	-1.47E+00	8.07E-05	TATDN3	7.07E-01	4.05E-03
TUBGCP4	-9.67E-01	8.08E-05	PYCRL	7.96E-01	4.19E-03
ADAL	-9.79E-01	8.57E-05	TATDN1	7.12E-01	4.37E-03
ACO10336.1	-1.78E+00	8.57E-05	HOMEZ	7.35E-01	4.51E-03
OCLN	-1.01E+00	8.57E-05	C12orf24	6.99E-01	4.58E-03
SNAP23	-9.04E-01	8.67E-05	CHRA1	6.92E-01	4.64E-03
FREM2	-1.23E+00	9.17E-05	UAP1	6.91E-01	4.69E-03
B3GALT1	-1.92E+00	9.43E-05	SLIRP	6.95E-01	4.69E-03
LONRF2	-1.08E+00	9.54E-05	DCK	7.09E-01	4.69E-03
APOBEC3B	-1.86E+00	9.86E-05	SLC11A1	1.59E+00	4.71E-03
LAMB2	-9.14E-01	1.03E-04	ATP1A3	7.31E-01	4.89E-03
THRB	-1.01E+00	1.09E-04	EID2	7.31E-01	5.03E-03
DCHS1	-1.40E+00	1.10E-04	STAP2	1.36E+00	5.24E-03
BEX2	-8.93E-01	1.10E-04	CYC1	7.69E-01	5.47E-03
SLITRK5	-9.34E-01	1.10E-04	GLRX5	6.92E-01	5.55E-03
SPINT2	-1.34E+00	1.48E-04	PLCD3	6.88E-01	5.98E-03
TTL7	-1.02E+00	1.48E-04	MT1X	7.72E-01	6.08E-03
MBP	-1.58E+00	1.50E-04	CACYBP	6.90E-01	6.15E-03
NKAIN2	-2.57E+00	1.50E-04	ETV4	2.26E+00	6.51E-03
PRRX1	-2.19E+00	1.58E-04	PFN2	6.65E-01	6.87E-03
GPR126	-1.56E+00	1.59E-04	EXT1	6.82E-01	7.23E-03
RAB9B	-1.11E+00	2.42E-04	EEF1E1	6.76E-01	7.42E-03
NPY1R	-5.47E+00	2.45E-04	TADA2B	6.78E-01	7.79E-03
CALCOCO1	-9.32E-01	2.66E-04	HSPE1	6.82E-01	7.81E-03
HIP1	-8.63E-01	2.88E-04	MYCL1	6.89E-01	8.27E-03
SPEN	-8.13E-01	3.00E-04	NCS1	6.71E-01	8.68E-03
MCOLN3	-1.04E+00	3.05E-04	TRIP13	6.63E-01	8.90E-03
FSTL1	-8.40E-01	3.26E-04	DHRS2	1.12E+00	9.69E-03

RAI2	-1.24E+00	3.69E-04	FXN	6.64E-01	9.89E-03
PRKG2	-3.28E+00	3.77E-04	C3orf14	6.48E-01	1.00E-02
DNAH11	-1.50E+00	4.01E-04	C1orf124	6.61E-01	1.01E-02
SYT1	-1.02E+00	4.42E-04	PANK1	6.69E-01	1.01E-02
MNS1	-1.50E+00	4.48E-04	SRD5A3	6.59E-01	1.02E-02
NES	-2.08E+00	4.63E-04	CEBPB	1.44E+00	1.02E-02
FRAS1	-9.05E-01	4.71E-04	ZFP36	7.78E-01	1.02E-02
PARP9	-1.22E+00	4.84E-04	UBE2V2	7.77E-01	1.03E-02
LGR5	-1.24E+00	5.36E-04	ATP6V1E2	7.22E-01	1.03E-02
HSBP1L1	-1.62E+00	5.49E-04	GAL	6.68E-01	1.10E-02
TMSB15A	-8.47E-01	5.61E-04	PSMB10	6.80E-01	1.15E-02
LRRN2	-1.50E+00	5.76E-04	NDUFAF2	6.54E-01	1.16E-02
CA8	-2.74E+00	7.65E-04	MRPS18C	6.69E-01	1.19E-02
FOSL2	-1.07E+00	7.71E-04	ELOVL6	6.59E-01	1.21E-02
LPL	-2.67E+00	7.71E-04	RGS3	7.58E-01	1.26E-02
DUSP10	-9.25E-01	7.73E-04	SYNPO	9.38E-01	1.28E-02
CUL9	-8.66E-01	7.82E-04	EFNA3	7.07E-01	1.29E-02
ANKRD1	-1.43E+00	7.91E-04	FBXO9	6.38E-01	1.38E-02
LGALS1	-9.18E-01	8.20E-04	NDUFC1	6.33E-01	1.48E-02
BRSK1	-9.49E-01	8.33E-04	TCF7L2	6.52E-01	1.48E-02
LYPD6	-8.21E-01	8.39E-04	MMP2	1.15E+00	1.51E-02
FAT3	-1.21E+00	8.46E-04	ANAPC5	6.41E-01	1.53E-02
CAMK4	-1.12E+00	8.51E-04	CHCHD7	6.44E-01	1.53E-02
ADAMTSL3	-2.54E+00	8.53E-04	UROS	6.20E-01	1.54E-02
ODZ4	-1.75E+00	9.14E-04	IMPDH1	6.23E-01	1.59E-02
AHR	-1.04E+00	9.14E-04	C17orf96	6.43E-01	1.64E-02
DGKA	-9.66E-01	9.57E-04	EXOSC4	8.37E-01	1.65E-02
HOXA4	-1.17E+00	9.60E-04	ABCE1	6.23E-01	1.67E-02
CXCL12	-6.49E+00	9.72E-04	KLRG2	6.96E-01	1.70E-02
ATP9A	-7.89E-01	9.76E-04	NRARP	6.23E-01	1.78E-02
MFSD6	-1.36E+00	9.80E-04	APRT	6.01E-01	1.81E-02
C8orf4	-4.56E+00	1.00E-03	NELL1	4.33E+00	1.84E-02
HOXA6	-1.53E+00	1.01E-03	PDZRN3	7.83E-01	1.86E-02
CXCL16	-8.57E-01	1.03E-03	CHRNA4	1.54E+00	1.89E-02
SRRM2	-7.65E-01	1.04E-03	GNG4	6.04E-01	1.91E-02
FAM5C	-5.47E+00	1.12E-03	CHAC2	6.48E-01	1.93E-02
ARHGEF17	-8.73E-01	1.19E-03	CKMT1A	9.27E-01	1.93E-02
MOB3C	-1.10E+00	1.34E-03	NDUFA8	6.28E-01	1.99E-02
CREBBP	-7.67E-01	1.36E-03	UQCRFS1	6.23E-01	2.01E-02
IRS4	-7.63E-01	1.49E-03	CDC42EP4	6.41E-01	2.01E-02
MCTP1	-1.94E+00	1.52E-03	PRPS2	6.12E-01	2.01E-02
FAM134B	-1.01E+00	1.58E-03	AL050321.1	9.73E-01	2.01E-02
PLEKHB1	-9.16E-01	1.67E-03	MARS2	6.33E-01	2.01E-02
PLD5	-4.92E+00	1.71E-03	GABRD	9.27E-01	2.07E-02
EPHB6	-2.62E+00	1.82E-03	DUSP14	6.46E-01	2.21E-02
CDHR1	-1.22E+00	1.88E-03	TPRKB	6.04E-01	2.25E-02
PTH1R	-1.66E+00	1.94E-03	GPRIN3	7.97E-01	2.31E-02
NR3C2	-8.99E-01	1.96E-03	FAM179A	1.44E+00	2.34E-02
HOXA3	-1.01E+00	1.96E-03	MRPS12	6.27E-01	2.36E-02
KCNT2	-2.55E+00	1.98E-03	HRSP12	6.17E-01	2.36E-02

PLEKHA7	-9.72E-01	2.10E-03	SEH1L	6.14E-01	2.37E-02
SLIT3	-1.32E+00	2.11E-03	ISM2	8.18E-01	2.37E-02
CTTNBP2	-9.26E-01	2.16E-03	BOP1	6.51E-01	2.38E-02
ANK1	-2.69E+00	2.23E-03	LRIF1	6.14E-01	2.38E-02
SLC12A6	-9.55E-01	2.33E-03	ETV5	1.92E+00	2.38E-02
MED12	-7.72E-01	2.41E-03	DCTD	5.95E-01	2.40E-02
ITGA6	-8.36E-01	2.58E-03	EGLN3	6.66E-01	2.50E-02
MXD1	-8.09E-01	2.67E-03	TSKU	6.28E-01	2.51E-02
SPTB	-1.09E+00	2.84E-03	CTSC	6.00E-01	2.52E-02
PPP1R15A	-8.63E-01	2.84E-03	PRR5L	8.74E-01	2.61E-02
SPTAN1	-7.31E-01	2.91E-03	LSM4	5.89E-01	2.67E-02
ITGA8	-8.03E-01	2.94E-03	HSPD1	5.79E-01	2.68E-02
QPCT	-1.20E+00	2.96E-03	EYA2	7.07E-01	2.69E-02
CXCR4	-1.87E+00	3.02E-03	ZNF85	1.49E+00	2.69E-02
BASP1	-2.46E+00	3.10E-03	PPID	6.10E-01	2.69E-02
DOCK9	-7.75E-01	3.12E-03	WDR77	6.01E-01	2.81E-02
PKIB	-1.09E+00	3.12E-03	MAP2K6	6.31E-01	2.95E-02
DYSF	-2.20E+00	3.12E-03	LSM12	5.77E-01	2.95E-02
FLT3	-2.17E+00	3.12E-03	GTF2E2	6.07E-01	2.96E-02
CLSTN2	-3.42E+00	3.15E-03	OR7D2	1.93E+00	2.96E-02
AS3MT	-8.31E-01	3.21E-03	TNFRSF10D	7.19E-01	2.99E-02
CACNA2D3	-9.55E-01	3.21E-03	SLC25A33	6.02E-01	2.99E-02
L3MBTL4	-1.36E+00	3.21E-03	RPL17	9.59E-01	2.99E-02
MTMR11	-1.12E+00	3.25E-03	OAF	5.93E-01	3.06E-02
KIF13B	-9.17E-01	3.38E-03	PVRL4	1.55E+00	3.18E-02
KIF1A	-2.18E+00	3.75E-03	TMEM177	5.84E-01	3.21E-02
SEMA6A	-7.97E-01	3.84E-03	WDYHV1	6.33E-01	3.21E-02
TANC2	-7.80E-01	3.84E-03	TMEM14B	5.86E-01	3.30E-02
TTC9	-9.66E-01	3.86E-03	SLC25A32	6.13E-01	3.32E-02
NMNAT2	-1.42E+00	3.89E-03	SLC25A4	6.06E-01	3.35E-02
TMEM132E	-2.65E+00	4.15E-03	NEIL2	6.21E-01	3.40E-02
KIAA1370	-9.78E-01	4.22E-03	QPRT	8.78E-01	3.40E-02
ADRB2	-1.00E+00	4.22E-03	ACN9	5.95E-01	3.42E-02
DLK2	-8.59E-01	4.36E-03	RASGEF1A	6.08E-01	3.56E-02
PLAT	-1.25E+00	4.69E-03	ZNF44	8.05E-01	3.56E-02
EP300	-7.02E-01	4.88E-03	MRPS18A	5.93E-01	3.57E-02
GPM6A	-1.09E+00	5.10E-03	CHEK2	5.83E-01	3.57E-02
BCOR	-6.76E-01	5.37E-03	RRP7A	5.78E-01	3.57E-02
SIPA1L2	-7.48E-01	5.38E-03	LSM6	5.95E-01	3.64E-02
KIAA1731	-7.25E-01	5.55E-03	SRXN1	5.81E-01	3.66E-02
ISM1	-1.01E+00	6.08E-03	SNCB	1.02E+00	3.68E-02
TP73	-7.25E-01	6.08E-03	RNF139	6.69E-01	3.68E-02
NUP210	-8.03E-01	6.12E-03	WNT10B	6.49E-01	3.68E-02
HAUS2	-7.21E-01	6.12E-03	FRAT2	5.71E-01	3.98E-02
SMARCA1	-7.18E-01	6.36E-03	MLF1IP	5.54E-01	4.02E-02
POU4F1	-7.26E-01	6.36E-03	TMEM145	6.91E-01	4.08E-02
HES1	-7.06E-01	6.68E-03	SH2D5	6.86E-01	4.08E-02
STAG3	-1.75E+00	6.70E-03	RIMS4	5.89E-01	4.13E-02
KIAA1407	-1.33E+00	6.73E-03	FGFR4	6.04E-01	4.23E-02
KIAA0355	-7.34E-01	7.17E-03	RABEPK	5.84E-01	4.24E-02

CGNL1	-1.12E+00	7.44E-03	BEND4	6.20E-01	4.33E-02
SLAIN1	-8.50E-01	7.44E-03	FAM155B	5.81E-01	4.33E-02
CHSY3	-1.09E+00	7.44E-03	METT5	5.66E-01	4.33E-02
BEND5	-1.96E+00	7.61E-03	CENPV	5.58E-01	4.33E-02
TM6SF2	-2.03E+00	7.61E-03	IKBKE	7.65E-01	4.35E-02
DOPEY1	-7.61E-01	7.64E-03	PRDX4	5.54E-01	4.41E-02
DTX1	-3.93E+00	7.90E-03	SPRED2	5.82E-01	4.63E-02
TSLP	-1.30E+00	8.04E-03	ISCA1	5.49E-01	4.68E-02
ITGA7	-1.16E+00	8.18E-03	COL14A1	1.05E+00	4.73E-02
NMI	-1.10E+00	8.68E-03	TSHZ3	5.54E-01	4.77E-02
ZNF536	-1.03E+00	8.68E-03	POP1	5.98E-01	4.87E-02
OPHN1	-8.33E-01	8.90E-03	DFFA	5.39E-01	4.87E-02
ABCA3	-1.15E+00	8.90E-03	TOP1MT	5.55E-01	4.87E-02
SLC13A4	-1.03E+00	9.21E-03	NOP16	5.71E-01	4.92E-02
HEATR5B	-7.11E-01	9.25E-03	PNO1	5.60E-01	4.92E-02
HOXB3	-6.99E-01	9.25E-03	GPATCH4	5.56E-01	4.92E-02
SLFN5	-1.46E+00	9.25E-03	WDR67	5.57E-01	4.92E-02
NME5	-1.82E+00	9.32E-03			
CBLB	-8.34E-01	9.43E-03			
FZD10	-1.32E+00	9.69E-03			
DMRTA2	-1.78E+00	9.69E-03			
CAV1	-9.52E-01	1.00E-02			
TTC28	-6.87E-01	1.03E-02			
GOLGA2	-7.04E-01	1.03E-02			
LRRC57	-7.03E-01	1.05E-02			
PLXNA4	-3.18E+00	1.06E-02			
RALGAPA2	-6.94E-01	1.09E-02			
IFI27L2	-7.54E-01	1.10E-02			
NEK11	-1.12E+00	1.10E-02			
SCAPER	-7.45E-01	1.11E-02			
CADPS2	-1.32E+00	1.13E-02			
GAP43	-1.71E+00	1.14E-02			
SCN8A	-1.02E+00	1.14E-02			
HERC1	-7.10E-01	1.15E-02			
KIAA0889	-6.92E-01	1.15E-02			
SLC2A10	-7.85E-01	1.17E-02			
STAT3	-6.51E-01	1.18E-02			
PLCL1	-1.46E+00	1.19E-02			
ANG	-1.56E+00	1.19E-02			
CBX5	-6.50E-01	1.21E-02			
MAP6	-1.10E+00	1.21E-02			
IGF2R	-6.49E-01	1.22E-02			
PAK3	-1.95E+00	1.26E-02			
FBN2	-6.84E-01	1.27E-02			
CXorf58	-2.17E+00	1.33E-02			
C8orf42	-1.11E+00	1.37E-02			
SBNO1	-6.58E-01	1.39E-02			
ABCB4	-1.98E+00	1.39E-02			
C19orf57	-8.36E-01	1.48E-02			
CELSR2	-6.73E-01	1.50E-02			

RNF175	-2.16E+00	1.52E-02
PLD1	-1.07E+00	1.52E-02
HERC3	-7.09E-01	1.53E-02
MLL2	-6.23E-01	1.53E-02
KIAA0913	-6.42E-01	1.53E-02
EPST1	-1.28E+00	1.56E-02
SORT1	-6.14E-01	1.56E-02
EFTUD1	-6.88E-01	1.64E-02
ABCA5	-7.47E-01	1.64E-02
C12orf51	-6.39E-01	1.64E-02
KNTC1	-6.50E-01	1.64E-02
PPP1R12B	-7.63E-01	1.65E-02
ATF7IP	-6.93E-01	1.65E-02
LMLN	-7.46E-01	1.65E-02
PRKCH	-8.24E-01	1.66E-02
LRRC33	-1.12E+00	1.78E-02
KANK1	-6.96E-01	1.79E-02
SYTL4	-8.30E-01	1.81E-02
PGPEP1	-6.89E-01	1.81E-02
INSR	-7.89E-01	1.83E-02
NMU	-7.22E-01	1.86E-02
DDAH2	-7.19E-01	1.86E-02
SAMD5	-9.60E-01	1.87E-02
MYO3A	-1.11E+00	1.93E-02
APBA1	-1.39E+00	1.93E-02
NTNG1	-3.13E+00	1.93E-02
RASGRP1	-1.03E+00	1.93E-02
LTK	-9.18E-01	1.94E-02
SLC17A5	-6.47E-01	1.94E-02
SZT2	-7.14E-01	2.01E-02
ANTXR2	-8.25E-01	2.06E-02
SLC46A3	-7.09E-01	2.06E-02
ALG1L	-1.05E+00	2.07E-02
DOCK8	-9.09E-01	2.09E-02
PHIP	-6.87E-01	2.11E-02
SRCAP	-5.99E-01	2.14E-02
PARD3B	-8.67E-01	2.14E-02
YPEL5	-7.61E-01	2.14E-02
PTPN14	-7.53E-01	2.14E-02
ZNF396	-9.41E-01	2.14E-02
C2orf72	-7.30E-01	2.18E-02
DKK3	-9.09E-01	2.21E-02
GOLGB1	-8.13E-01	2.22E-02
AFF3	-6.75E-01	2.24E-02
MAP1A	-1.48E+00	2.24E-02
GPX3	-5.99E-01	2.25E-02
MAP2	-1.81E+00	2.27E-02
EGR2	-1.42E+00	2.31E-02
SERPING1	-2.19E+00	2.34E-02
DIAPH3	-6.52E-01	2.37E-02

VGLL2	-1.03E+00	2.37E-02
TRIB2	-7.27E-01	2.38E-02
LIG4	-6.51E-01	2.38E-02
SYNJ1	-6.30E-01	2.40E-02
EXOC6B	-6.33E-01	2.47E-02
SDK1	-7.43E-01	2.51E-02
RIMBP3	-2.38E+00	2.51E-02
AMOTL2	-7.17E-01	2.51E-02
IQGAP1	-6.16E-01	2.51E-02
ARL10	-5.98E-01	2.51E-02
GALC	-8.94E-01	2.52E-02
SMC4	-6.18E-01	2.55E-02
DAPK1	-6.17E-01	2.57E-02
TAP1	-6.30E-01	2.58E-02
CYBRD1	-7.84E-01	2.61E-02
MYO7A	-3.57E+00	2.64E-02
LBH	-9.74E-01	2.66E-02
BAI3	-8.79E-01	2.67E-02
BCL6	-7.79E-01	2.68E-02
C7orf46	-8.59E-01	2.68E-02
SLC44A5	-6.37E-01	2.69E-02
BICC1	-6.35E-01	2.83E-02
ARHGAP33	-6.85E-01	2.85E-02
SLC22A23	-6.30E-01	2.89E-02
ARHGAP31	-7.40E-01	2.95E-02
FAM65B	-1.66E+00	2.95E-02
ARHGAP27	-7.90E-01	2.95E-02
HDX	-8.43E-01	2.96E-02
ARMCX4	-7.74E-01	2.96E-02
RGS7	-1.15E+00	3.01E-02
DST	-6.06E-01	3.02E-02
TKTL1	-1.65E+00	3.13E-02
GPC5	-1.44E+00	3.13E-02
RAPGEF5	-7.89E-01	3.17E-02
RFX6	-1.93E+00	3.28E-02
NCKAP5L	-6.12E-01	3.29E-02
MDGA1	-6.45E-01	3.32E-02
COL24A1	-1.32E+00	3.40E-02
COLEC12	-7.55E-01	3.43E-02
TOP2A	-5.69E-01	3.44E-02
SPOCK3	-1.58E+00	3.53E-02
CHD7	-5.95E-01	3.56E-02
CLSPN	-6.03E-01	3.57E-02
TBC1D5	-6.61E-01	3.57E-02
RNASEL	-8.67E-01	3.57E-02
AGTR1	-1.10E+00	3.57E-02
IFITM1	-1.18E+00	3.58E-02
FRMPD3	-8.42E-01	3.59E-02
KDM5A	-5.78E-01	3.61E-02
CLSTN3	-6.39E-01	3.64E-02

RIPK1	-5.84E-01	3.64E-02
SYNGAP1	-6.82E-01	3.65E-02
CD109	-7.73E-01	3.66E-02
MYO5C	-7.17E-01	3.67E-02
RNF144B	-9.65E-01	3.67E-02
ACVR1C	-1.67E+00	3.68E-02
FGF12	-2.56E+00	3.68E-02
TCN2	-2.64E+00	3.69E-02
FBN1	-6.99E-01	3.73E-02
MBD5	-6.31E-01	3.74E-02
PRKCSH	-5.82E-01	3.78E-02
EFNB3	-5.96E-01	3.84E-02
DNAJC6	-6.44E-01	3.84E-02
LHX8	-8.29E-01	3.85E-02
CDKL5	-9.56E-01	3.85E-02
PROX1	-1.02E+00	3.91E-02
HIF1A	-5.81E-01	4.04E-02
ASH1L	-5.75E-01	4.07E-02
KIAA1539	-7.25E-01	4.15E-02
PLXNA3	-5.98E-01	4.17E-02
PNPLA8	-8.55E-01	4.17E-02
TFAP2A	-6.24E-01	4.20E-02
C7orf13	-1.18E+00	4.24E-02
EBF4	-6.90E-01	4.25E-02
C5orf42	-6.20E-01	4.29E-02
MAN1C1	-8.29E-01	4.31E-02
MAGI1	-7.91E-01	4.32E-02
KAT6B	-5.87E-01	4.33E-02
RAD54L2	-5.87E-01	4.33E-02
KIF14	-6.03E-01	4.34E-02
DNMBP	-6.14E-01	4.35E-02
TP53BP1	-5.83E-01	4.36E-02
FAM71E1	-1.02E+00	4.41E-02
TP53INP2	-6.16E-01	4.41E-02
SH3D21	-9.24E-01	4.42E-02
CCDC15	-8.52E-01	4.46E-02
PCDH17	-7.70E-01	4.48E-02
MON2	-5.96E-01	4.56E-02
BMF	-1.31E+00	4.61E-02
SCD5	-6.03E-01	4.61E-02
FRY	-8.12E-01	4.62E-02
CYP1B1	-1.99E+00	4.62E-02
YWHAG	-5.30E-01	4.62E-02
NOTCH2	-5.47E-01	4.63E-02
KAT6A	-5.59E-01	4.73E-02
INPP1	-6.93E-01	4.73E-02
TAOK1	-6.24E-01	4.73E-02
ZZEF1	-5.65E-01	4.77E-02
C15orf42	-5.55E-01	4.77E-02
ATP1B2	-7.67E-01	4.77E-02

GAS2L3	-6.41E-01	4.77E-02
NFAT5	-5.90E-01	4.82E-02
AMOTL1	-5.54E-01	4.82E-02
PTPN21	-6.11E-01	4.84E-02
NNT	-5.69E-01	4.84E-02
ERC1	-5.93E-01	4.87E-02
VPS13C	-6.20E-01	4.87E-02
MYH10	-5.54E-01	4.87E-02
GFRA1	-1.13E+00	4.91E-02
NRP1	-5.95E-01	4.92E-02
GCA	-6.25E-01	4.92E-02
ASAP2	-6.37E-01	4.93E-02
HSPA2	-1.24E+00	4.97E-02

S3 mRNAs enriched in HEK-miR-155 compensated IP

n=100

ENSMBL ID	Gene ID	difference log2 FC	p.value	FDR 10%
ENSG00000006062	MAP3K14	6.32E-01	9.67E-04	
ENSG00000008083	JARID2	1.03E+00	2.59E-04	
ENSG00000010072	C1orf124	6.68E-01	2.99E-04	
ENSG00000038382	TRIO	5.75E-01	8.37E-04	
ENSG00000039319	ZFYVE16	7.21E-01	4.39E-04	
ENSG00000046604	DSG2	6.99E-01	1.40E-04	
ENSG00000049245	VAMP3	8.93E-01	2.49E-04	
ENSG00000063245	EPN1	6.62E-01	8.17E-04	
ENSG00000063438	AHRR	3.90E-01	1.10E-03	
ENSG00000064655	EYA2	7.11E-01	5.18E-04	
ENSG00000071539	TRIP13	5.78E-01	9.07E-04	
ENSG00000072415	MPP5	4.21E-01	1.83E-03	
ENSG00000072518	MARK2	6.07E-01	5.08E-04	
ENSG00000087338	GMCL1	7.61E-01	3.29E-04	
ENSG00000088543	C3orf18	8.17E-01	7.48E-04	
ENSG00000099889	ARVCF	6.79E-01	1.13E-03	
ENSG00000100065	CARD10	6.13E-01	4.09E-04	
ENSG00000104613	INTS10	5.33E-01	4.19E-04	
ENSG00000105643	ARRDC2	7.70E-01	5.28E-04	
ENSG00000108219	TSPAN14	4.69E-01	1.18E-03	
ENSG00000108406	DHX40	9.32E-01	1.20E-04	
ENSG00000109113	RAB34	5.04E-01	9.37E-04	
ENSG00000109756	RAPGEF2	1.01E+00	1.69E-04	
ENSG00000112079	STK38	4.17E-01	1.50E-03	
ENSG00000112146	FBXO9	5.82E-01	3.59E-04	
ENSG00000113658	SMAD5	4.17E-01	1.53E-03	
ENSG00000117139	KDM5B	4.66E-01	8.07E-04	
ENSG00000117906	RCN2	5.05E-01	1.96E-03	
ENSG00000119401	TRIM32	1.01E+00	1.30E-04	
ENSG00000119946	CNNM1	8.40E-01	1.89E-04	
ENSG00000120539	MASTL	5.60E-01	5.68E-04	
ENSG00000121297	TSHZ3	8.34E-01	4.78E-04	
ENSG00000121931	LRIF1	7.20E-01	2.69E-04	
ENSG00000128016	ZFP36	1.42E+00	1.50E-04	
ENSG00000130758	MAP3K10	1.20E+00	1.59E-04	
ENSG00000132405	TBC1D14	6.70E-01	1.09E-03	
ENSG00000132952	USPL1	1.11E+00	5.98E-05	
ENSG00000133275	CSNK1G2	1.11E+00	3.19E-04	
ENSG00000134686	PHC2	1.58E+00	9.97E-06	
ENSG00000136888	ATP6V1G1	8.85E-01	2.09E-04	
ENSG00000138035	PNPT1	6.14E-01	1.20E-03	
ENSG00000138686	BBS7	7.19E-01	5.98E-04	
ENSG00000138777	PPA2	4.79E-01	1.34E-03	
ENSG00000140543	DET1	1.73E+00	2.99E-05	
ENSG00000140807	NKD1	1.11E+00	2.29E-04	
ENSG00000142168	SOD1	5.21E-01	1.85E-03	
ENSG00000143344	RGL1	6.21E-01	1.26E-03	

ENSG00000144401	METTL21A	6.39E-01	6.98E-04
ENSG00000147650	LRP12	4.10E-01	1.60E-03
ENSG00000147862	NFIB	6.21E-01	6.18E-04
ENSG00000148737	TCF7L2	1.11E+00	1.99E-05
ENSG00000152256	PDK1	3.65E-01	1.54E-03
ENSG00000154511	FAM69A	6.85E-01	4.29E-04
ENSG00000155097	ATP6V1C1	6.73E-01	3.49E-04
ENSG00000156136	DCK	7.92E-01	1.79E-04
ENSG00000156273	BACH1	6.18E-01	1.44E-03
ENSG00000157978	LDLRAP1	5.79E-01	7.58E-04
ENSG00000158717	RNF166	5.93E-01	1.38E-03
ENSG00000159792	PSKH1	8.89E-01	6.98E-05
ENSG00000159921	GNE	3.90E-01	1.97E-03
ENSG00000161326	DUSP14	6.17E-01	6.88E-04
ENSG00000162783	IER5	8.73E-01	4.49E-04
ENSG00000163577	EIF5A2	4.25E-01	1.81E-03
ENSG00000164144	ARFIP1	5.35E-01	9.27E-04
ENSG00000164778	EN2	8.11E-01	2.19E-04
ENSG00000165288	BRWD3	6.91E-01	3.39E-04
ENSG00000165323	FAT3	1.12E+00	9.97E-05
ENSG00000166200	COPS2	6.11E-01	1.49E-03
ENSG00000167670	CHAF1A	4.36E-01	1.28E-03
ENSG00000169139	UBE2V2	5.57E-01	1.21E-03
ENSG00000169762	TAPT1	5.33E-01	1.72E-03
ENSG00000170345	FOS	5.50E-01	1.27E-03
ENSG00000172216	CEBPB	1.91E+00	4.98E-05
ENSG00000173011	TADA2B	7.01E-01	4.88E-04
ENSG00000173852	DPY19L1	6.46E-01	5.78E-04
ENSG00000176396	EID2	6.11E-01	9.17E-04
ENSG00000177674	AGTRAP	1.41E+00	3.99E-05
ENSG00000178177	LCORL	7.71E-01	3.69E-04
ENSG00000179104	TMTC2	5.51E-01	1.63E-03
ENSG00000179604	CDC42EP4	5.57E-01	8.27E-04
ENSG00000180370	PAK2	6.20E-01	3.89E-04
ENSG00000182022	CHST15	1.06E+00	7.97E-05
ENSG00000182986	ZNF320	9.29E-01	2.39E-04
ENSG00000185658	BRWD1	5.40E-01	8.47E-04
ENSG00000185722	ANKFY1	4.22E-01	1.52E-03
ENSG00000196628	TCF4	1.57E+00	8.97E-05
ENSG00000196705	ZNF431	6.75E-01	4.98E-04
ENSG00000196739	COL27A1	9.22E-01	2.89E-04
ENSG00000197694	SPTAN1	4.47E-01	1.01E-03
ENSG00000198561	CTNND1	6.80E-01	5.38E-04
ENSG00000198680	TUSC1	5.12E-01	6.38E-04
ENSG00000198740	ZNF652	7.35E-01	3.09E-04
ENSG00000204516	MICB	8.65E-01	3.79E-04
ENSG00000204604	ZNF468	6.99E-01	9.77E-04
ENSG00000213699	C2orf18	4.47E-01	1.70E-03
ENSG00000213799	ZNF845	1.21E+00	1.99E-04
ENSG00000213930	GALT	6.70E-01	1.19E-03

ENSG00000215271	HOMEZ	7.32E-01	1.10E-04
ENSG00000215472	RPL17	9.19E-01	2.79E-04
ENSG00000232040	SCAND3	7.26E-01	5.58E-04

S4 differentially expressed miRNA in TL fractions

ct-values normalized to median ct-value

Median 0.990661094
STDEV 0.030789855

	ratio		ratio		
miRNAs lower in HEK-miR-155	HEK-empty TL/ HEK-miR-155 TL	miRNAs lower in HEK-vector	HEK-empty TL/ HEK-miR-155 TL	miRNAs only detectable in TL of HEK-vector	miRNAs only detectable in TL of HEK-miR-155
hsa-miR-224	0.860880328	hsa-miR-331-5p	1.021600629	hsa-miR-1	hsa-miR-150
hsa-miR-576-3p	0.893519262	hsa-miR-629	1.02198609	hsa-miR-135b	hsa-miR-198
hsa-miR-98	0.904465719	hsa-miR-199a-3p	1.022326835	hsa-miR-142-5p	hsa-miR-155
hsa-miR-181c	0.909513572	hsa-let-7a	1.023287961	hsa-miR-302c	hsa-miR-483-5p
hsa-miR-204	0.915365851	hsa-miR-221	1.02417777	hsa-miR-411	hsa-miR-501-3p
hsa-miR-589	0.922662438	hsa-miR-142-3p	1.025954272	hsa-miR-561	
hsa-miR-215	0.928533196	hsa-miR-130a	1.026863186	hsa-miR-570	
hsa-miR-628-5p	0.934547317	hsa-miR-449b	1.029846497	hsa-miR-888	
hsa-miR-138	0.937462837	hsa-miR-758	1.031704911	hsa-miR-891a	
hsa-miR-223	0.938687796	hsa-miR-375	1.031955639	hsa-miR-147	
hsa-miR-181a	0.941081492	hsa-miR-106a	1.039823675	hsa-miR-219-1-3p	
hsa-miR-338-3p	0.942393271	hsa-miR-548d-5p	1.041274195		
hsa-miR-202	0.943413652	hsa-miR-20a	1.048135149		
hsa-miR-218	0.94883009	hsa-miR-296-3p	1.049855797		
hsa-miR-545	0.948942201	hsa-miR-199b	1.07511416		
hsa-miR-203	0.953586802	hsa-miR-501	1.083228002		
hsa-miR-15a	0.955358821	hsa-miR-34a	1.134814351		
hsa-miR-148a	0.9571446				
hsa-miR-95	0.957434249				
n=19		n=17		n=11	n=5

S5 primer sequences

Name	Sequence (5'>3')
miR-155_f	TTTAAGCTTCTATATGCTGTCACTCCAGCTTT
miR-155_r	TTTCTCGAGTGGCAGATAGCTTCTGGAAT
qRT_CCND1_f	ACGAAGGTCTGCGCGTGTT
qRT_CCND1_r	CCGCTGGCCATGAACTACCT
qRT_CEBPB_f1	ctctctgcttctccctctgc
qRT_CEBPB_r1	gattgcatcaacttcgaaacc
qRT_PHC2_f	caccaagtggaatgtagaagacg
qRT_PHC2_r	ggaattcctctgctatctcctg
qRT_GAPDH_f	gctctctgctcctcctgttc
qRT_GAPDH_r	acgaccaaatccgttgactc
qRT_DCTN2_f	actagcgacctacctgagga
qRT_DCTN2_r	tcataggcagcattaggattgac
ZFP36_qRT_f	ccaagtgtgcaagctcag
ZFP36_qRT_r	ccccaagaacctcggaag
qRT_ZNF652_f	aagcagtacttcgacgaacaca
qRT_ZNF652_r	agctttgccacagatttcac
qRT_BACH1_f	tgcatcacttcctcaaac
qRT_BACH1_r	ctttcaagacgctgccaaa
qRT_FBXO9_f	tggtgtgcagaggattctacat
qRT_FBXO9_r	ctccaggacgtgtacggaac
ETV1_qRT_f	cccagaaaaattcgatggag
ETV1_qRT_r	tatgtgggtcctcccgata
ETV4_qRT_f	gcagttgttcttgattcca
ETV4_qRT_r	actctggggctcctcttg
ETV5_qRT_f	catcctacatgagaggggggta
ETV5_qRT_r	aagtataatcggggatcttttca
qRT_DUSP14_f1	gcacactggactcttgaggaa
qRT_DUSP14_r1	cggcaagaccagagtgttt
JARID2_qRT_f	aaggtggacaccaacactcac
JARID2_qRT_r	gaggacggtgaggttccat
AGTRAP_qRT_f	atcgacgccataagcatgt
AGTRAP_qRT_r	atgctgatgtgcacgatgtc

S6 NGS read counts

Cell line	Fraction	Replicate	Total read count	Useable read count	% of total count
HEK-vector	IP	1	38847512	26697792	68.72
HEK-vector	IP	2	35200455	24681908	70.12
HEK-vector	IP	3	34633980	24064313	69.48
HEK-vector	TL	1	77647039	56479074	72.74
HEK-vector	TL	2	51827659	38276456	73.85
HEK-vector	TL	3	66831196	48956322	73.25
HEK-miR-155	IP	1	33679129	23334445	69.28
HEK-miR-155	IP	2	34442706	24432299	70.94
HEK-miR-155	IP	3	35082010	24734154	70.5
HEK-miR-155	TL	1	69955916	50830568	72.66
HEK-miR-155	TL	2	71385945	53103311	74.39
HEK-miR-155	TL	3	72132189	53445065	74.09

Raw data were sorted and analyzed according to barcoded library adaptors allowing one basepair mismatch within the barcode sequence