SUPPLEMENTAL MATERIAL

dsRNA expression in the mouse elicits RNAi in oocytes and low adenosine deamination in somatic cells

Running title: dsRNA in mammals

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SUPPLEMENTARY FIGURES

Figure S1 Expression constructs

(A) A schematic overview of *Mos* transcribed sequences used for vector cloning, dsRNA expression and experimental analysis. *Mos* gene is intronless. The blue arrow depicts the coding sequence. The length of the dsRNA region is about 0.5 kb. Drawn approximately to the scale. (B) A schematic organization of MosIR, MosP, Mos3 trangenes. *Mos* sequence present in MosP and Mos3 vectors correspond to the sequence fragment shown in the panel A. The last two schemes depict expression cassettes of RL-Mos3 and FF reporter plasmids used in cell culture experiments. (C) EGFP fluorescence in MosP, Mos3 and MosIR transgenic lines used in the project. The fresh tail biopsies were photographed together.

Figure S2 Analysis of MosIR expression

(A) Relative MosIR levels in transgenic organs. The graph shows the MosIR expression displayed as $\log_2$ relative to *Hprt*, a routinely used internal standard in qPCR. MosIR expression was monitored with CagI primers (Table SIII). (B) Comparison of expression of MosIR and pCAGEGFP (parental plasmid into which was inserted the Mos inverted repeat) transcripts in cultured cells suggests similar mRNA expression from both plasmids. 293 cells grown in a 24-well plate were transfected with indicated amounts of MosIR and pCAGEGFP and the level of CAG-driven mRNA was determined 48 hours after transfection by qPCR using CagI qPCR primers. (C) MosIR produces significantly reduced levels of EGFP. 293 cells grown in a 24-well plate were transfected with indicated amounts of MosIR and pCAGEGFP and the amount of EGFP was determined 48 hours after transfection by flow cytometry. The X-axis shows green fluorescence intensity (FL1-H), the Y axis indicates the frequency of cells with a given intensity ($5\text{x}10^4$ cells were counted).

Figure S3 SOLiD analysis of transgenic organs and transfected 293 cells.

(A) Column graphs show absolute numbers of reads in three SOLiD small RNA libraries and counts of reads of different sequence lengths. Pie graphs show representation of several different classes of small RNAs in analyzed samples. (B) Distribution of 21-23 nt long reads along the MosIR transgene. Graph depicts cumulative counts of 5’ ends of 21-23 nt long small RNAs. Sense and antisense RNAs are shown above and below the line, respectively. Note small RNAs generated from the plasmid backbone and antisense small RNAs from intronic and EGFP coding sequences, which indicate that the transfected MosIR plasmid is transcribed in a rather complex manner. (C) Length distribution of small RNAs from EGFP and Mos inverted repeat (MosIR) regions of the MosIR transgene in the transgenic brain and in 293 cells transiently transfected with the MosIR transgene.

Figure S4 Methylation status of different *Mos* sequences in different genetic backgrounds

Mos DNA bisulfite sequencing was performed as described previously (1). Each row of circles represents one clone from bisulfite sequencing. White circles represent unmethylated cytosines, black circles represent methylated cytosines. Shaded area denotes a region of the *Mos* sequence that is complementary to the MosIR hairpin. Unframed data are derived from the endogenous *Mos* gene sequence while clones in red frames are derived from transgenic *Mos* sequences, which carry a mutation of one KpnI site (highlighted in the Supplementary Figure S1) allowing for distinguishing between endogenous and transgenic clones. The upper two datasets show methylation of endogenous *Mos* gene sequences in tail DNA from two independent MosIR transgenic lines. Tail EGFP fluorescence shows that the MosIR transgene is active in these tissues. In contrast to the endogenous *Mos* sequence, the *Mos* sequence inserted in the Mos3 transgene is hypermethylated in the genome. DNA methylation is not unusual for exonic sequences. *Mos* sequence in an active MosP transgene is hypomethylated. The last panel shows analysis of tail DNA from an animal showing signs of spontaneous silencing of the MosP transgene, which identified a hypermethylated clone derived from the MosP sequence.

Figure S5 Adenosine deamination in nuclear, cytoplasmic and polysomal fractions

(A) Analysis of adenosine deamination of MosIR RNA in nuclear and cytoplasmic fractions from MEFs derived from transgenic embryos. Adenosine deamination was analyzed by cloning RT-PCR products from the MosIR region indicated on the top. Lower panels show results of editing analysis of MosIR transcripts from nuclear and cytoplasmic fractions, which were prepared from MosIR MEFs as described previously (2). Each row of squares represents one sequenced clone. Each square represents an individual adenosine in the analyzed sequence. A part of the PCR product is derived from the stem (dsRNA) sequence (white squares) and a part from single stranded sequence (grey squares). A/G conversions are indicated by black squares. (B) Polysome profiling of MosIR-positive MEFs. Profiling was performed as described previously (3). Material sampling for qPCR is indicated by vertical lines. (C) qPCR analysis of relative abundance of *Hprt* and MosIR RNAs in the three fractions indicated in the panel A. Relative RNA content in the monosomal fraction was arbitrarily set to one. (D) Edited MosIR RNA is present in the polysomal fraction in transgenic MEFs. qPCR product obtained from the polysomal fraction was cloned and 23 individual clones were sequenced. Since the qPCR product localizes into the inverted repeat, two regions from both arms were apparently amplified (grey areas), which can be distinguished by a single nucleotide mutation in one of the arms. Sequenced clones were first sorted out according to their origin from sense or antisense arm and their editing (apparent as A/G conversion) was determined. The bottom panel shows five clones, in which we identified RNA editing (highlighted as black squares among white squares; each row of squares represents all adenosines in an individual sequenced clone). Origin of edited clones from the sense or antisense arms of the MosIR is indicated.

SUPPLEMENTARY TABLES

Table SI -.Probe sets differentially expressed upon dsRNA expression in 293 and HeLa cells

Table SII - Differentially expressed probe sets (>2-fold) in 293 and HeLa cells transfected with the MosIR plasmid.

Table SIII - Sequences of primes used in this study

REFERENCES

1. Svoboda, P., Stein, P., Filipowicz, W. and Schultz, R.M. (2004) Lack of homologous sequence-specific DNA methylation in response to stable dsRNA expression in mouse oocytes. *Nucleic Acids Res*, **32**, 3601-3606.
2. Djouder, N., Metzler, S.C., Schmidt, A., Wirbelauer, C., Gstaiger, M., Aebersold, R., Hess, D. and Krek, W. (2007) S6K1-mediated disassembly of mitochondrial URI/PP1gamma complexes activates a negative feedback program that counters S6K1 survival signaling. *Mol Cell*, **28**, 28-40.
3. Chiu, W.L., Wagner, S., Herrmannova, A., Burela, L., Zhang, F., Saini, A.K., Valasek, L. and Hinnebusch, A.G. (2010) The C-terminal region of eukaryotic translation initiation factor 3a (eIF3a) promotes mRNA recruitment, scanning, and, together with eIF3j and the eIF3b RNA recognition motif, selection of AUG start codons. *Mol Cell Biol*, **30**, 4415-4434.

Figure S1

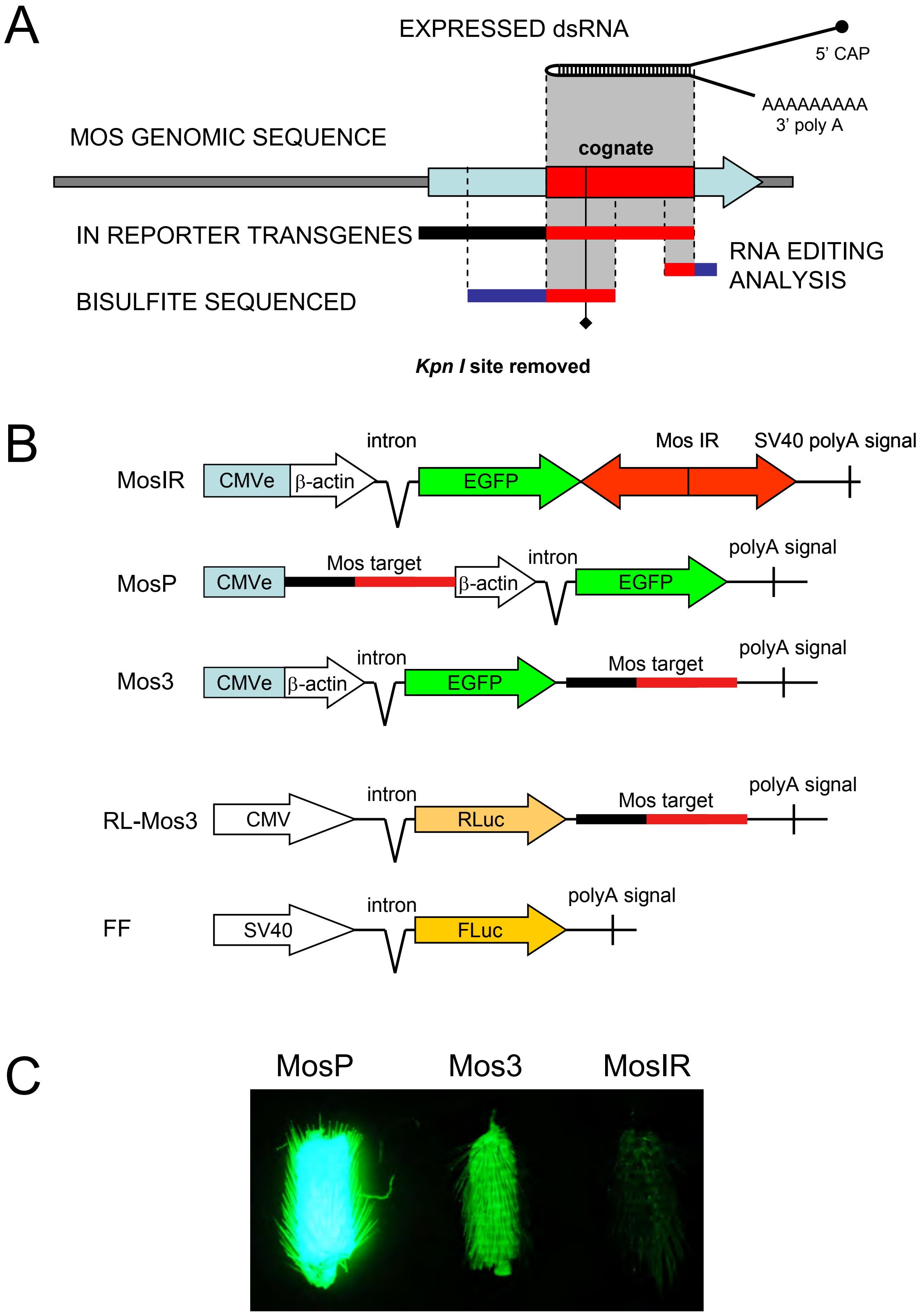
A
EXPRESSED dsRNA
5' CAP
AAAAAAAAA
3' poly A
MOS GENOMIC SEQUENCE
cognate
IN REPORTER TRANSGENES
RNA EDITING
ANALYSIS
BISULFITE SEQUENCED
Kpn I site removed
B
MosIR
CMVe
β-actin
intron
EGFP
Mos IR
SV40 polyA signal
MosP
CMVe
Mos target
β-actin
intron
EGFP
polyA signal
Mos3
CMVe
β-actin
intron
EGFP
Mos target
polyA signal
RL-Mos3
CMV
intron
RLuc
Mos target
polyA signal
FF
SV40
intron
FLuc
polyA signal
C
MosP
Mos3
MosIR

Figure S2

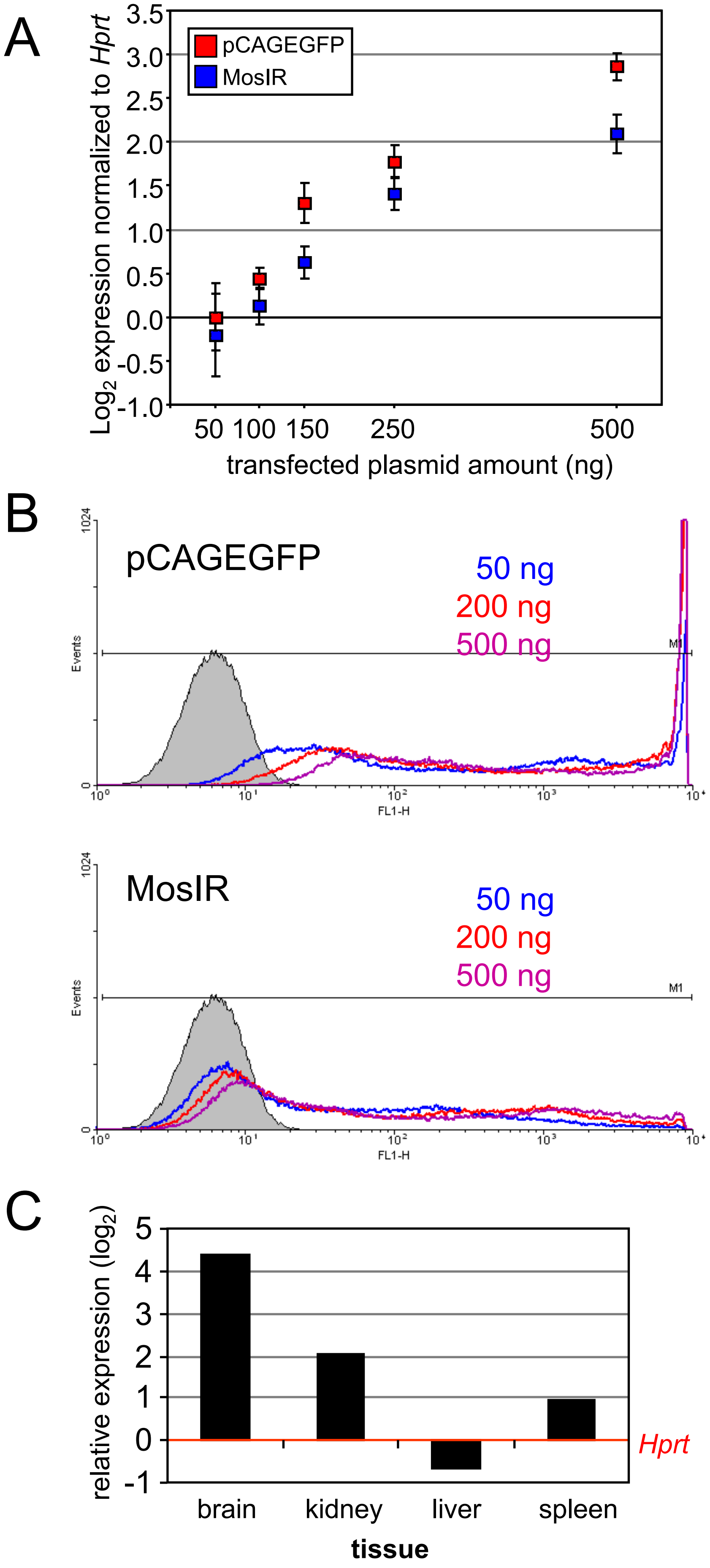
A
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
-1.0
Log2 expression normalized to Hprt
🟥 pCAGEGFP
🟦 MosIR
50 100 150 250 500
transfected plasmid amount (ng)
B
pCAGEGFP
50 ng
200 ng
500 ng
M1
1024
Events
0
10⁰ 10¹ 10² 10³ 10⁴
FL1-H
MosIR
50 ng
200 ng
500 ng
M1
1024
Events
0
10⁰ 10¹ 10² 10³ 10⁴
FL1-H
C
5
4
3
2
1
0
-1
relative expression (log2)
Hprt
brain
kidney
liver
spleen
tissue

Figure S3

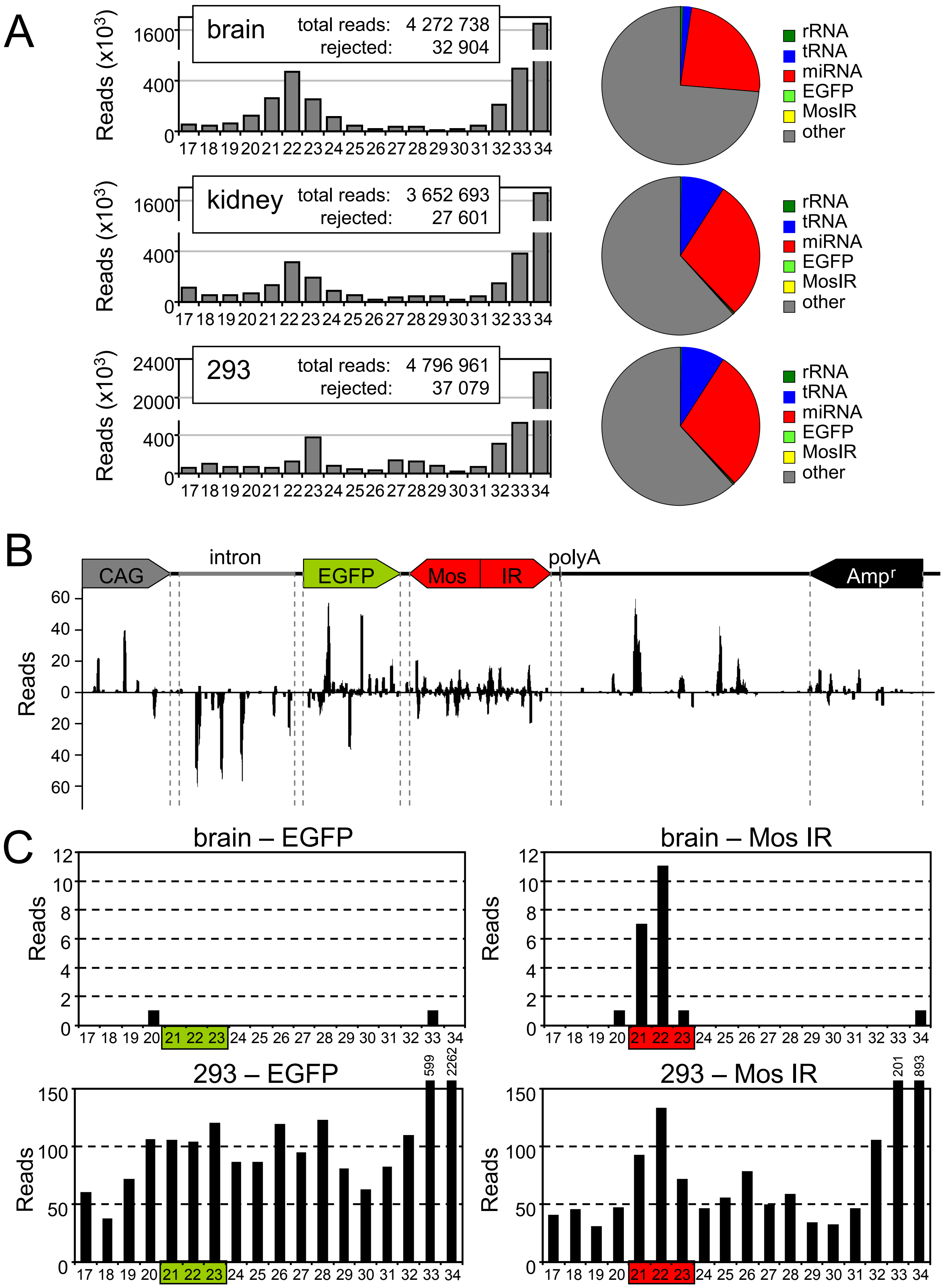
A
brain
total reads: 4 272 738
rejected: 32 904
Reads (x10^3)
1600
400
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
rRNA
tRNA
miRNA
EGFP
MosIR
other
kidney
total reads: 3 652 693
rejected: 27 601
Reads (x10^3)
1600
400
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
rRNA
tRNA
miRNA
EGFP
MosIR
other
293
total reads: 4 796 961
rejected: 37 079
Reads (x10^3)
2400
2000
400
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
rRNA
tRNA
miRNA
EGFP
MosIR
other
B
CAG
intron
EGFP
Mos
IR
polyA
Amp^r
Reads
60
40
20
0
20
40
60
C
brain – EGFP
Reads
12
10
8
6
4
2
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
brain – Mos IR
Reads
12
10
8
6
4
2
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
293 – EGFP
599
2262
Reads
150
100
50
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
293 – Mos IR
201
893
Reads
150
100
50
0
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34

Figure S4

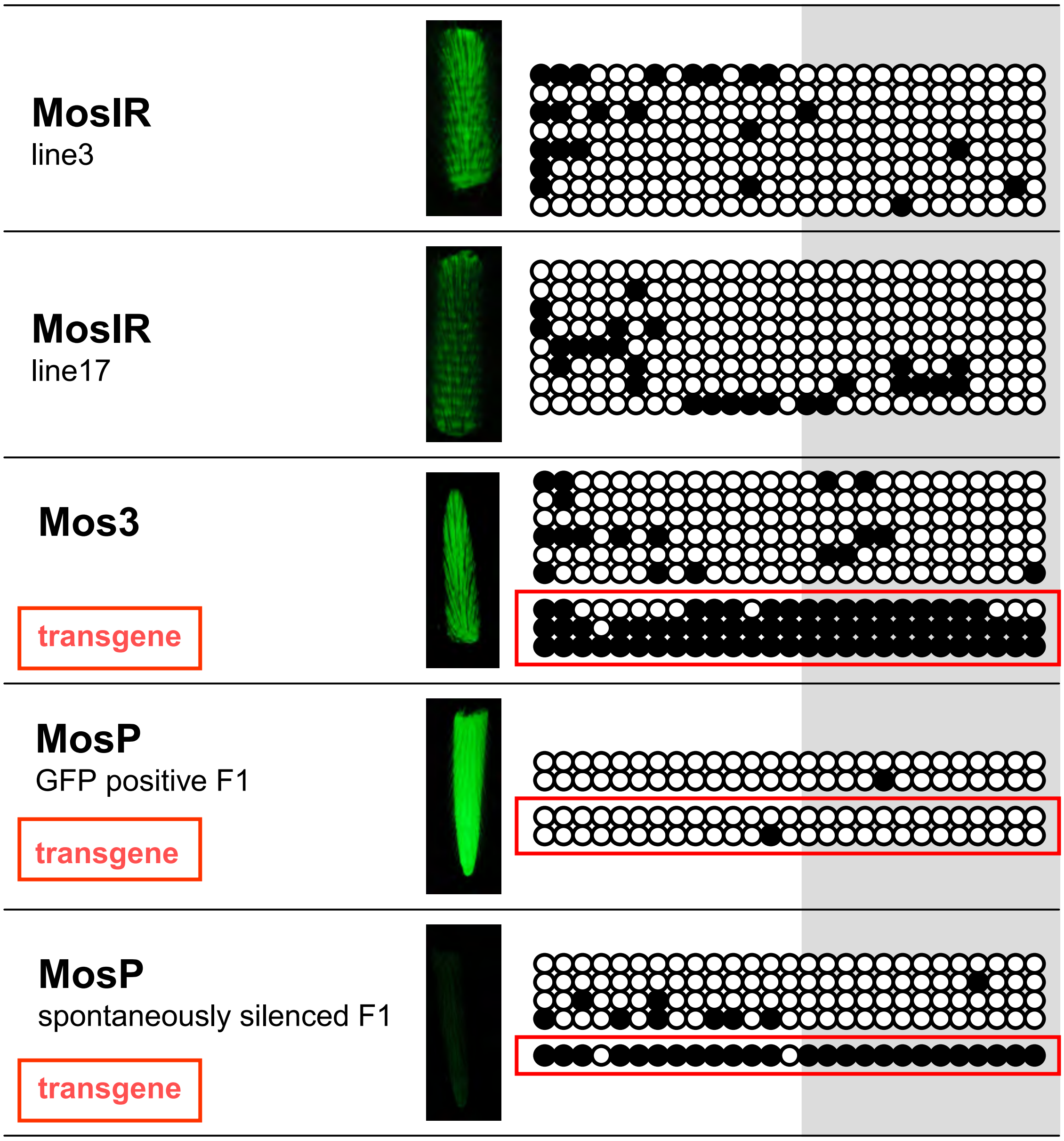
MosIR
line3
MosIR
line17
Mos3
transgene
MosP
GFP positive F1
transgene
MosP
spontaneously silenced F1
transgene

Figure S5

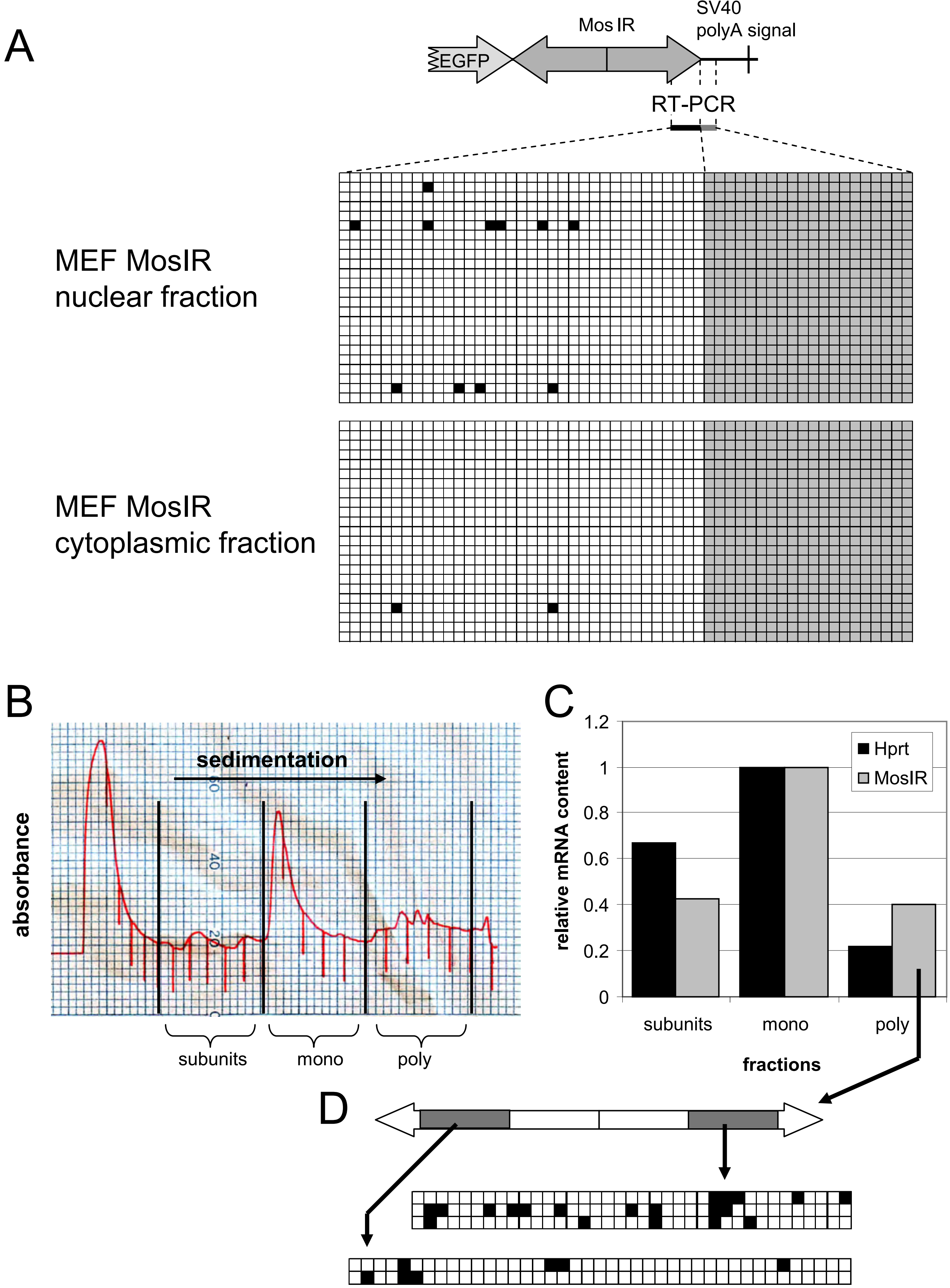
A
EGFP
Mos IR
SV40
polyA signal
RT-PCR
MEF MosIR
nuclear fraction
MEF MosIR
cytoplasmic fraction
B
absorbance
sedimentation
60
40
20
0
subunits
mono
poly
C
relative mRNA content
1.2
1
0.8
0.6
0.4
0.2
0
■ Hprt
□ MosIR
subunits
mono
poly
fractions
D

Table SI

Gene	Description	RefSeq	fold change HeLa	 293
C1orf79	chromosome 1 open reading frame 79	XM_378848	5.51	4.61
CIP29	cytokine induced protein 29 kDa	NM_033082	2.53	3.35
DKFZp686L1418	hypothetical gene supported by BX538329	XM_499121	10.47	3.86
FAM24B	family with sequence similarity 24, member B	NM_152644	2.96	2.72
FAM80B	family with sequence similarity 80, member B	NM_020734	3.44	2.74
FLJ37953	hypothetical protein FLJ37953	NM_152382	2.28	2.21
HIST1H4H	histone 1, H4h	NM_003543	3.02	2.23
HIST2H4	histone 2, H4	NM_003548	2.06	5.73
INHBE	inhibin, beta E	NM_031479	2.83	3.32
KHDRBS1	KH domain containing, RNA binding, signal transduction associated	NM_006559	3.57	5.69
LOC441241	chaperonin containing TCP1, subunit 6A (zeta 1)-like	XM_496886	2.33	3.33
LOC441378	Pvt1 oncogene homolog, MYC activator (mouse), LOC441378	XM_372058	2.21	2.78
P8	p8 protein (candidate of metastasis 1)	NM_012385	2	2.61
SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	NM_0010316	3.51	2.38
ST7L	suppression of tumorigenicity 7 like	NM_017744	2.02	2.37
TARS	Threonyl-tRNA synthetase	NM_152295	10.24	2.85
WDFY3	WD repeat and FYVE domain containing 3	NM_014991	2.4	2.53

Table SII

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
210118_s_at	IL1A	NM_000575	Hs.1722	34.11	0.82
205476_at	CCL20	NM_004591	Hs.75498	20.72	0.97
207850_at	CXCL3	NM_002090	Hs.89690	11.91	1.11
204760_s_at	NR1D1, THRA	NM_003250	Hs.724	11.56	1.75
231412_at	DKFZp686L14188	XM_499121	Hs.150298	10.43	3.86
240206_at	TARS	NM_152295	Hs.481860	10.22	2.94
211506_s_at	IL8	NM_000584	Hs.624	9.43	1.07
205205_at	RELB	NM_006509	Hs.307905	9.38	1.76
204470_at	CXCL1	NM_001511	Hs.789	8.20	0.81
205599_at	TRAF1	NM_005658	Hs.531251	8.16	0.95
244070_at	SYNE1	NM_015293	Hs.12967	7.93	1.06
206157_at	PTX3	NM_002852	Hs.567326	7.74	1.18
209305_s_at	GADD45B	NM_015675	Hs.110571	7.63	0.81
31637_s_at	NR1D1, THRA	NM_003250	Hs.724	7.46	1.55
1569020_at	NEDD9	NM_006403	Hs.37982	7.27	0.91
239669_at	HIST1H3D	NM_003530	Hs.532144	7.09	1.56
1554980_a_at	ATF3	NM_001030287	Hs.460	7.04	1.23
227099_s_at	LOC387763	XM_373497	Hs.530443	6.87	1.04
206814_at	NGFB	NM_002506	Hs.2561	6.84	0.94
242329_at	LOC401317	XM_379479	Hs.585228	6.77	1.70
218066_at	SLC12A7	NM_006598	Hs.172613	6.68	0.96
209774_x_at	CXCL2	NM_002089	Hs.75765	6.49	1.00
1562153_a_at	PVT1	XM_372058	Hs.584794	6.48	1.25
209304_x_at	GADD45B	NM_015675	Hs.110571	6.36	1.10
223484_at	NMES1	NM_032413	Hs.112242	6.23	0.99
229518_at	FAM46B	NM_052943	Hs.59771	6.08	0.82
219270_at	MGC4504	NM_024111	Hs.155569	5.97	2.07
205409_at	FOSL2	NM_005253	Hs.568265	5.88	1.21
202859_x_at	IL8	NM_000584	Hs.624	5.83	0.74
206085_s_at	CTH	NM_001902	Hs.19904	5.76	1.87
202531_at	IRF1	NM_002198	Hs.436061	5.68	1.26
205193_at	MAFF	NM_012323	Hs.517617	5.67	1.03
224588_at	XIST	NR_001564	Hs.529901	5.66	1.00
207574_s_at	GADD45B	NM_015675	Hs.110571	5.66	1.06
223774_at	C1orf79	XM_378848	Hs.528699	5.48	4.61
202672_s_at	ATF3	NM_001030287	Hs.460	5.48	1.43
220987_s_at	C11orf17, NUAK2	NM_020642	Hs.131180	5.47	1.06
215495_s_at	SAMD4	NM_015589	Hs.98259	5.42	0.96
211414_at	GLS	NM_014905	Hs.116448	5.17	1.02
238725_at	IRF1	NM_002198	Hs.436061	5.10	1.18
202014_at	PPP1R15A	NM_014330	Hs.76556	5.09	1.31
202643_s_at	TNFAIP3	NM_006290	Hs.211600	5.06	1.07
230542_at	ZNF597	NM_152457	Hs.88630	4.85	0.86
236898_at	transcribed locus		Hs.550924	4.79	0.95
37028_at	PPP1R15A	NM_014330	Hs.76556	4.56	1.55
209636_at	NFKB2	NM_002502	Hs.73090	4.56	1.15
202638_s_at	ICAM1	NM_000201	Hs.515126	4.39	0.85
207113_s_at	TNF	NM_000594	Hs.241570	4.33	0.89
202023_at	EFNA1	NM_004428	Hs.516664	4.32	1.31
209457_at	DUSP5	NM_004419	Hs.2128	4.26	0.89
236987_at	IMAGE:2365727			4.14	1.13
221530_s_at	BHLHB3	NM_030762	Hs.177841	4.06	1.32
234799_at	ADARB1	NM_001033049	Hs.474018	3.98	0.88
214472_at	HIST1H3D	NM_003530	Hs.532144	3.92	1.76
221728_x_at	XIST	NR_001564	Hs.529901	3.87	1.06
36711_at	MAFF	NM_012323	Hs.517617	3.87	1.43
222802_at	EDN1			3.81	1.06
218880_at	FOSL2	NM_005253	Hs.220971	3.79	1.04
203725_at	GADD45A	NM_001924	Hs.80409	3.77	1.30
202644_s_at	TNFAIP3	NM_006290	Hs.211600	3.70	1.12

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
223196_s_at	SESN2	NM_031459	Hs.469543	3.66	1.25
225142_at	KIAA1718	XM_376680	Hs.308710	3.57	1.79
219826_at	ZNF419	NM_024691	Hs.98593	3.57	1.42
36829_at	PER1	NM_002616	Hs.445534	3.53	0.71
213146_at	KIAA0346			3.52	1.13
213649_at	SFRS7	NM_001031684	Hs.309090	3.47	2.38
227458_at	CD274	NM_014143	Hs.521989	3.45	1.06
229520_s_at	C14orf118	NM_017926	Hs.410231	3.43	1.76
229344_x_at	FAM80B	NM_020734	Hs.504670	3.43	2.74
218995_s_at	EDN1	NM_001955	Hs.511899	3.40	0.87
214185_at	KHDRBS1	NM_006559	Hs.445893	3.38	5.69
1558305_at	TNRC15	NM_015575	Hs.435841	3.38	0.96
235857_at	KCTD11	NM_001002914	Hs.585037	3.35	0.77
209383_at	DDIT3	NM_004083	Hs.505777	3.33	1.34
210538_s_at	BIRC3	NM_001165	Hs.127799	3.33	0.94
225557_at	AXUD1	NM_033027	Hs.370950	3.33	1.64
204907_s_at	BCL3	NM_005178	Hs.31210	3.31	0.99
221805_at	NEFL	NM_006158	Hs.521461	3.26	0.94
203927_at	NFKBIE	NM_004556	Hs.458276	3.23	1.28
214447_at	ETS1	NM_005238	Hs.369438	3.20	1.10
1554283_at	CCRN4L	NM_012118	Hs.548091	3.19	1.21
212471_at	KIAA0241	NM_015060	Hs.128056	3.13	1.25
215243_s_at	GJB3	NM_001005752	Hs.522561	3.13	1.09
221602_s_at	FAIM3	NM_005449	Hs.58831	3.09	1.37
202637_s_at	ICAM1	NM_000201	Hs.515126	3.09	1.01
1559064_at	NUP153	NM_005124	Hs.121088	3.08	1.33
218280_x_at	HIST2H2AA	NM_003516	Hs.530461	3.07	1.59
233245_at	C6orf107	NM_017754	Hs.555954	3.04	1.18
235128_at	SYNPO	NM_007286	Hs.435228	3.04	0.91
238422_at	LOC151534		Hs.516124	3.03	1.13
1559060_a_at	KIAA1961	NM_001008738	Hs.483329	3.03	0.95
210069_at	CHKB, CPT1B	NM_004377	Hs.439777	3.02	1.51
202861_at	PER1	NM_002616	Hs.445534	3.00	0.87
208180_s_at	HIST1H4H	NM_003543	Hs.421737	3.00	2.23
202150_s_at	NEDD9	NM_006403	Hs.37982	2.99	1.05
214502_at	HIST1H2BJ	NM_021058	Hs.132550	2.99	1.22
AFFX-M27830_5	28S rRNA			2.98	1.25
201694_s_at	EGR1	NM_001964	Hs.326035	2.98	1.12
240982_at	CARS	NM_001014437	Hs.274873	2.98	1.12
223780_s_at	THRAP1	NM_005121	Hs.282678	2.98	1.72
218881_s_at	FOSL2	NM_005253	Hs.568265	2.96	1.00
223217_s_at	NFKBIZ	NM_001005474	Hs.319171	2.95	0.87
230283_at	NEURL2	NM_080749	Hs.517094	2.95	1.28
238476_at	LOC153222	NM_153607	Hs.484195	2.95	1.32
231146_at	FAM24B	NM_152644		2.94	2.76
206144_at	MAGI1	NM_001033057	Hs.567389	2.94	1.29
214522_x_at	HIST1H3D	NM_003530	Hs.532144	2.92	1.11
207535_s_at	NFKB2	NM_002502	Hs.73090	2.91	1.05
228153_at	IBRDC2	NM_182757	Hs.148741	2.90	1.10
204035_at	SCG2	NM_003469	Hs.516726	2.90	1.28
202821_s_at	LPP	NM_005578	Hs.444362	2.90	0.96
214455_at	HIST1H2BC	NM_003526	Hs.546314	2.89	0.92
209010_s_at	TRIO	NM_007118	Hs.130031	2.88	0.99
236947_at	SEMA3C	NM_006379	Hs.269109	2.88	1.15
1554420_at	ATF3	NM_001030287	Hs.460	2.87	1.15
58367_s_at	ZNF419	NM_024691	Hs.98593	2.87	1.30
223773_s_at	C1orf79	XM_378848	Hs.528699	2.85	3.01
205113_at	NEF3	NM_005382	Hs.458657	2.84	1.05
231468_at	IMAGE:3134456			2.84	1.15
210587_at	INHBE	NM_031479	Hs.279497	2.83	3.33

Table SII

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
225015_s_at	STK40	NM_032017	Hs.471768	2.81	0.93
230973_at	SH2D5	XM_375698	Hs.166270	2.80	0.96
206374_at	DUSP8	NM_004420	Hs.41688	2.78	1.37
235737_at	TSLP	NM_033035	Hs.389874	2.76	1.30
211286_x_at	CSF2RA	NM_006140	Hs.520937	2.74	1.15
227180_at	ELOVL7	NM_024930	Hs.274256	2.72	0.91
210070_s_at	CHKB, CPT1B	NM_004377	Hs.439777	2.70	1.39
230104_s_at	TPPP	NM_007030	Hs.584860	2.69	0.81
1554997_a_at	PTGS2	NM_000963	Hs.196384	2.68	0.95
209912_s_at	KIAA0415	XM_166527	Hs.558440	2.66	1.36
203372_s_at	SOCS2	NM_003877	Hs.485572	2.66	1.43
209908_s_at	TGFB2	NM_003238	Hs.133379	2.63	1.06
206411_s_at	ABL2	NM_005158	Hs.159472	2.63	0.67
214290_s_at	HIST2H2AA	NM_003516	Hs.530461	2.63	1.62
223195_s_at	SESN2	NM_031459	Hs.469543	2.62	1.40
228946_at	PDZK6	NM_015693	Hs.391481	2.60	1.77
1555614_at	IMAGE:3538202			2.59	1.11
217127_at	CTH	NM_001902	Hs.19904	2.59	1.90
220324_at	C6orf155	NM_024882	Hs.368337	2.59	1.11
206359_at	SOCS3	NM_003955	Hs.527973	2.58	0.77
215501_s_at	DUSP10	NM_007207	Hs.497822	2.58	1.50
213900_at	C9orf61	NM_004816	Hs.118003	2.56	0.74
1555355_a_at	ETS1	NM_005238	Hs.369438	2.55	0.55
226612_at	FLJ25076	XM_059689	Hs.126856	2.54	1.70
243894_at	SLC41A2	NM_032148	Hs.238996	2.54	1.28
205749_at	CYP1A1	NM_000499	Hs.72912	2.54	1.32
225840_at	TEF	NM_003216	Hs.181159	2.54	0.95
223878_at	INPP4B	NM_003866	Hs.480837	2.54	1.07
240454_at	TTC7A	NM_020458	Hs.370603	2.54	0.87
209401_s_at	SLC12A4	NM_005072	Hs.10094	2.53	1.25
236402_at	IMAGE:2664543			2.53	1.34
229069_at	CIP29	NM_033082	Hs.505676	2.53	3.30
215078_at	SOD2	NM_000636	Hs.487046	2.52	1.05
1555441_at	FLJ10808	NM_018227	Hs.212774	2.51	0.95
214138_at	ZNF79	NM_007135	Hs.522399	2.50	1.89
220994_s_at	STXBP6	NM_014178	Hs.508958	2.49	0.99
205816_at	ITGB8	NM_002214	Hs.285724	2.48	0.91
219256_s_at	SH3TC1	NM_018986	Hs.479116	2.48	0.99
201009_s_at	TXNIP	NM_006472	Hs.533977	2.47	1.07
244852_at	C18orf4	NM_032160	Hs.124673	2.47	1.19
220046_s_at	CCNL1	NM_020307	Hs.4859	2.46	1.47
202708_s_at	HIST2H2BE	NM_003528	Hs.2178	2.45	1.50
203373_at	SOCS2	NM_003877	Hs.485572	2.45	1.35
1559257_a_at	MAGI1	NM_001033057	Hs.567389	2.44	1.09
206864_s_at	HRK	NM_003806	Hs.87247	2.44	1.37
1552314_a_at	EYA3	NM_001990	Hs.185774	2.44	1.48
234902_s_at	ZNF416	NM_017879	Hs.247711	2.44	1.53
227599_at	LOC151963	NM_178496	Hs.151443	2.43	0.90
243861_at	KIAA1961	NM_001008738	Hs.483329	2.43	1.33
214482_at	ZBTB25	NM_006977	Hs.164347	2.43	1.17
216549_s_at	TBC1D22B	NM_017772	Hs.485270	2.42	0.81
1554229_at	LOC153222	NM_153607	Hs.484195	2.42	0.94
242316_at	transcribed locus		Hs.511399	2.42	1.12
226847_at	FST	NM_006350	Hs.9914	2.41	1.24
220671_at	CCRN4L	NM_012118	Hs.548091	2.40	0.98
201531_at	ZFP36	NM_003407	Hs.534052	2.40	1.05
238660_at	WDFY3	NM_014991	Hs.480116	2.39	2.57
204200_s_at	PDGFB	NM_002608	Hs.1976	2.39	0.94
203010_at	STAT5A	NM_003152	Hs.437058	2.39	1.15
207510_at	BDKRB1	NM_000710	Hs.553486	2.39	1.12

Table SII

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
241529_at	FLJ20397	NM_017802	Hs.521328	2.38	1.10
207085_x_at	CSF2RA	NM_006140	Hs.520937	2.38	1.17
227404_s_at	EGR1	NM_001964	Hs.326035	2.38	1.11
1559826_a_at	LOC401074	XM_376247	Hs.528540	2.36	1.23
227392_at	NISCH	NM_007184	Hs.435290	2.36	1.37
241396_at	IMAGE:4693718			2.36	0.82
204472_at	GEM	NM_005261	Hs.345139	2.36	1.01
222142_at	CYLD	NM_015247	Hs.432993	2.35	1.28
38037_at	HBEGF	NM_001945	Hs.799	2.35	0.73
204549_at	IKBKE	NM_014002	Hs.321045	2.34	1.11
1559051_s_at	C6orf150	NM_138441	Hs.344080	2.33	1.09
216200_at	PLEKHM1	NM_014798	Hs.514242	2.33	1.16
227301_at	LOC441241, LOC441244	XM_496886	Hs.488399	2.33	3.33
203249_at	EZH1	NM_001991	Hs.194669	2.33	0.87
204958_at	PLK3	NM_004073	Hs.153640	2.32	1.16
1555411_a_at	CCNL1	NM_020307	Hs.4859	2.32	1.43
203691_at	PI3	NM_002638	Hs.112341	2.31	1.13
233112_at	C9orf150	NM_203403	Hs.445356	2.30	1.00
208094_s_at	MGC10471	NM_030818	Hs.24998	2.30	1.69
206566_at	SLC7A1	NM_003045	Hs.14846	2.29	0.94
218000_s_at	PHLDA1	NM_007350	Hs.484885	2.29	1.01
213353_at	ABCA5	NM_018672	Hs.421474	2.28	1.16
221603_at	PEX16	NM_004813	Hs.100915	2.27	0.95
206926_s_at	IL11	NM_000641	Hs.467304	2.27	1.05
218847_at	IMP-2	NM_001007225	Hs.35354	2.27	1.02
206175_x_at	ZNF222	NM_013360	Hs.279840	2.27	1.82
224978_s_at	USP36	NM_025090	Hs.464243	2.27	1.04
1554986_a_at	SNX19	NM_014758	Hs.444024	2.27	1.12
210004_at	OLR1	NM_002543	Hs.412484	2.26	0.87
220606_s_at	NBLA03831	NM_020233	Hs.47668	2.25	1.29
237439_at	USP43	XM_371015	Hs.23935	2.25	0.99
232035_at	HIST1H4H	NM_003543	Hs.421737	2.25	2.10
235686_at	FLJ37953	NM_152382	Hs.204619	2.25	2.20
211038_s_at	MGC12760	XM_496351	Hs.522876	2.24	1.71
1568695_s_at	DDX26	NM_012141	Hs.439440	2.23	0.87
236117_at	transcribed locus		Hs.42747	2.23	1.12
209832_s_at	CDT1	NM_030928	Hs.122908	2.22	1.25
207219_at	ZNF643	NM_023070	Hs.133034	2.22	1.64
1558290_a_at	LOC441378, PVT1	XM_372058	Hs.133107	2.21	2.78
202500_at	DNAJB2	NM_006736	Hs.77768	2.21	1.42
203439_s_at	STC2	NM_003714	Hs.233160	2.21	1.59
209850_s_at	CDC42EP2	NM_006779	Hs.343380	2.21	0.81
227486_at	NT5E	NM_002526	Hs.153952	2.21	0.89
232832_at	DKFZp434J0226	XM_375629	Hs.466975	2.20	1.06
241433_at	RCOR3	NM_018254	Hs.356399	2.20	0.65
229264_at	PARP8	NM_024615	Hs.369581	2.20	1.65
235914_at	SYNPO	NM_007286	Hs.435228	2.20	0.97
209959_at	NR4A3	NM_006981	Hs.279522	2.20	1.09
205181_at	ZNF193	NM_006299	Hs.100921	2.20	1.52
214520_at	FOXC2	NM_005251	Hs.558329	2.19	1.04
1565579_at	TATDN2	NM_014760	Hs.475401	2.19	0.99
238910_at	MGC3020	NM_024048	Hs.460642	2.18	1.16
206673_at	GPR	NM_007223	Hs.37196	2.18	0.77
213139_at	SNAI2	NM_003068	Hs.360174	2.18	1.04
244441_at	USP31	NM_020718	Hs.183817	2.18	0.97
203602_s_at	ZBTB17	NM_003443	Hs.433764	2.18	1.13
231963_at	IMAGE:3869276		Hs.26039	2.18	0.66
201010_s_at	TXNIP	NM_006472	Hs.533977	2.17	1.08
202847_at	PCK2	NM_001018073	Hs.75812	2.17	1.31
225979_at	PLEKHG2	NM_022835	Hs.111217	2.17	0.80

Table SII

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
205228_at	RBMS2	NM_002898	Hs.505729	2.17	1.04
1555007_s_at	WDR66	NM_144668	Hs.507125	2.16	1.08
203828_s_at	IL32	NM_001012631	Hs.943	2.16	1.23
205207_at	IL6	NM_000600	Hs.512234	2.16	0.75
213323_s_at	ZC3H7B	NM_017590	Hs.474970	2.16	0.91
226206_at	MAFK	NM_002360	Hs.584824	2.16	0.85
216271_x_at	SYDE1	NM_033025	Hs.528701	2.15	0.84
206744_s_at	ZMYM5	NM_014242	Hs.530988	2.15	1.81
208436_s_at	IRF7	NM_001572	Hs.166120	2.15	1.74
232076_at	ZNF707	NM_173831	Hs.521922	2.15	0.91
214443_at	PVR	NM_006505	Hs.171844	2.15	0.78
206523_at	PSCD3	NM_004227	Hs.487479	2.15	0.86
220121_at	LINS1	NM_018148	Hs.105633	2.15	1.39
243560_at	transcribed locus		Hs.553158	2.15	0.97
227140_at	INHBA	NM_002192	Hs.28792	2.14	1.04
237367_x_at	CFLAR	NM_003879	Hs.390736	2.14	0.88
221563_at	DUSP10	NM_007207	Hs.497822	2.14	1.41
210387_at	HIST1H2BG	NM_003518	Hs.240135	2.14	1.20
205490_x_at	GJB3	NM_001005752	Hs.522561	2.14	1.18
1554291_at	KIAA0701	NM_001006947	Hs.387336	2.14	0.88
219492_at	CHIC2	NM_012110	Hs.335393	2.13	1.35
209193_at	PIM1	NM_002648	Hs.81170	2.13	1.03
1560485_at	HIVEP1	NM_002114	Hs.567284	2.13	1.00
230013_s_at	ARHGAP23	XM_290799	Hs.374446	2.12	1.05
230450_at	IMAGE:2357664			2.12	1.10
218724_s_at	TGIF2	NM_021809	Hs.292281	2.12	1.13
202902_s_at	CTSS	NM_004079	Hs.181301	2.12	1.00
207110_at	KCNJ12	NM_021012	Hs.200629	2.12	0.70
229468_at	CDK3	NM_001258	Hs.584745	2.11	0.95
208284_x_at	GGT1	NM_001032364	Hs.444164	2.11	1.06
236657_at	cDNA YI37C01		Hs.432924	2.11	0.85
225220_at	ACA24 snoRNA gene		Hs.535762	2.11	1.75
1554014_at	CHD2	NM_001271	Hs.220864	2.11	1.80
210190_at	STX11	NM_003764	Hs.118958	2.10	0.91
235414_at	ZNF383	NM_152604	Hs.567750	2.10	1.31
211468_s_at	RECQL5	NM_001003715	Hs.514480	2.10	1.28
1558212_at	FLJ35024	XM_379622	Hs.416043	2.10	1.96
1557257_at	IMAGE:1628131			2.10	0.89
211605_s_at	RARA	NM_000964	Hs.535499	2.10	0.94
205807_s_at	TUFT1	NM_020127	Hs.489922	2.09	1.31
235062_at	LOC120379	NM_138789	Hs.420662	2.09	1.16
227347_x_at	HES4	NM_021170	Hs.154029	2.09	1.01
238624_at	NLK	NM_016231	Hs.208759	2.09	1.34
201008_s_at	TXNIP	NM_006472	Hs.533977	2.09	0.88
206044_s_at	BRAF	NM_004333	Hs.324250	2.08	1.39
235116_at	TRAF1	NM_005658	Hs.531251	2.08	1.01
202684_s_at	RNMT	NM_003799	Hs.8086	2.08	1.10
242827_x_at	transcribed locus		Hs.272159	2.08	0.88
204015_s_at	DUSP4	NM_001394	Hs.417962	2.08	1.13
220382_s_at	ARHGAP28	NM_001010000	Hs.183114	2.07	0.78
240983_s_at	CARS	NM_001014437	Hs.274873	2.07	1.44
228250_at	KIAA1961	NM_001008738	Hs.483329	2.07	0.99
227452_at	LOC440462	XM_498681	Hs.157726, H	2.07	1.17
205931_s_at	CREB5	NM_001011666	Hs.437075	2.07	1.23
226462_at	STXBP6	NM_014178	Hs.508958	2.07	0.93
209324_s_at	RGS16	NM_002928	Hs.413297	2.07	0.71
1554274_a_at	SSH1	NM_018984	Hs.199763	2.07	1.01
220370_s_at	USP36	NM_025090	Hs.464243	2.07	1.08
212665_at	TIPARP	NM_015508	Hs.12813	2.07	1.70
216262_s_at	TGIF2	NM_021809	Hs.292281	2.06	0.89

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
242727_at	ARL8	NM_178815	Hs.25362	2.06	1.11
226991_at	NFATC2	NM_012340	Hs.356321	2.06	0.94
224739_at	PIM3	NM_001001852	Hs.530381	2.06	1.03
204420_at	FOSL1	NM_005438	Hs.283565	2.06	0.83
221308_at	FRS2	NM_006654	Hs.334831	2.06	0.88
207046_at	HIST2H4	NM_003548	Hs.534370	2.05	5.75
207082_at	CSF1	NM_000757	Hs.173894	2.05	0.96
235558_at	RBMS2	NM_002898	Hs.505729	2.05	0.84
228442_at	NFATC2	NM_012340	Hs.356321	2.04	0.92
1553986_at	RASEF	NM_152573	Hs.129136	2.04	1.08
211527_x_at	VEGF	NM_001025366	Hs.73793	2.04	1.01
31846_at	RHOD	NM_014578	Hs.15114	2.04	0.86
211416_x_at	GGTLA4	NM_080920	Hs.355394	2.04	1.20
228856_at	MGC2474	NM_023931	Hs.460604	2.03	1.60
206388_at	PDE3A	NM_000921	Hs.386791	2.03	1.11
236631_at	C21orf125	NM_194309	Hs.146127	2.03	1.00
1559929_at	IMAGE:4042121		Hs.350952	2.03	1.02
228230_at	PRIC285	NM_033405	Hs.517180	2.03	0.83
213556_at	LOC390940	XM_372732	Hs.22049	2.03	1.05
205590_at	RASGRP1	NM_005739	Hs.511010	2.03	1.05
223937_at	FOXP1	NM_001012505	Hs.431498	2.03	1.04
235456_at	HIST1H2BD	NM_021063	Hs.130853	2.02	1.49
202912_at	ADM	NM_001124	Hs.441047	2.01	0.99
228298_at	MGC16044	NM_138371	Hs.258002	2.01	1.02
201044_x_at	DUSP1	NM_004417	Hs.171695	2.01	0.96
239678_at	AP1GBP1	NM_007247	Hs.101480	2.01	1.27
209239_at	NFKB1	NM_003998	Hs.431926	2.01	1.03
236302_at	PPM1E	NM_014906	Hs.245044	2.01	1.25
1553962_s_at	RHOB	NM_004040	Hs.502876	2.01	0.81
209230_s_at	P8	NM_012385	Hs.513463	2.00	2.63
211674_x_at	CTAG1A, CTAG1B	NM_001327	Hs.534310	2.00	1.03
1554140_at	WDR78	NM_024763	Hs.49421	1.25	4.64
230763_at	LOC128153	NM_138796	Hs.171130	0.91	4.61
215071_s_at	HIST1H2AC	NM_003512	Hs.484950	1.52	4.05
230142_s_at	CIRBP	NM_001280	Hs.25489	1.62	3.86
1553494_at	TDH	NR_001578	Hs.130610	0.96	3.81
230815_at	LOC389765	XM_372122	Hs.160561	1.54	3.57
205278_at	GAD1	NM_000817	Hs.420036	1.27	3.54
223714_at	ZNF256	NM_005773	Hs.288736	1.01	3.41
1562309_s_at	PHF21B	NM_138415	Hs.254097	0.76	3.21
230861_at	CHRNA7			0.90	3.17
222612_at	PSPC1	NM_018282	Hs.213198	1.59	3.05
232611_at	LOC92497		Hs.524660	1.46	3.03
231945_at	FILIP1	NM_015687	Hs.526972	0.94	3.00
1555151_s_at	TDH	NR_001578	Hs.130610	0.84	2.97
236706_at	LOC129530	NM_174898	Hs.164589	1.28	2.97
207166_at	GNGT1	NM_021955	Hs.555871	1.23	2.97
218371_s_at	PSPC1	NM_018282	Hs.213198	1.45	2.96
230795_at	HIST2H4	NM_003548	Hs.55468	1.42	2.95
219455_at	FLJ21062	NM_024788	Hs.521012	1.49	2.89
1561759_at	LOC441038	XM_376342	Hs.535008	1.08	2.84
1561761_x_at	LOC441038	XM_376342	Hs.535008, H	1.61	2.81
239282_at	CCDC41	NM_016122	Hs.279209	0.91	2.73
241348_at	ZNF654	NM_018293	Hs.27595	1.00	2.72
209602_s_at	GATA3	NM_001002295	Hs.524134	1.00	2.65
242586_at	FSD1CL	NM_207647	Hs.136901	1.03	2.64
228209_at	clone NT2NE2013189		Hs.537031	1.24	2.60
242807_at	FSD1L	NM_207647	Hs.136901	1.38	2.59
202086_at	MX1	NM_002462	Hs.517307	1.71	2.57
220366_at	ELSPBP1	NM_022142	Hs.104894	1.12	2.55

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
224165_s_at	FLJ12476	NM_001031715	Hs.444535	1.58	2.55
213938_at	CAST1	NM_015576		0.77	2.54
208886_at	H1F0	NM_005318	Hs.226117	1.04	2.49
234040_at	HELLS	NM_018063	Hs.463677	1.77	2.46
1562904_s_at	Clone PP1195		Hs.571462	1.04	2.46
204919_at	PRR4	NM_007244	Hs.533634	1.02	2.43
1564282_a_at	LOC285708			0.89	2.39
1558651_at	CCDC28A	NM_015439	Hs.412019	1.15	2.39
205185_at	SPINK5	NM_006846	Hs.331555	1.11	2.39
233141_s_at	ST7L	NM_017744	Hs.201921	1.98	2.37
226164_x_at	FAM80B	NM_020734	Hs.504670	1.88	2.35
214079_at	DHRS2	NM_005794	Hs.272499	1.16	2.35
1564474_at	LOC285711	XM_211988	Hs.161338	1.02	2.35
205896_at	SLC22A4	NM_003059	Hs.310591	1.15	2.33
242639_at	NARG2	NM_001018089	Hs.200943	1.19	2.31
222728_s_at	MGC5306	NM_024116	Hs.355750	1.95	2.31
215559_at	ABCC6	NM_001171	Hs.442182	1.13	2.31
232158_x_at	NPAL1	NM_207330	Hs.134190	0.63	2.29
230536_at	PBX4	NM_025245	Hs.466257	1.08	2.28
1554614_a_at	PTBP2	NM_021190	Hs.269895	1.72	2.26
219635_at	ZNF606	NM_025027	Hs.287629	1.01	2.25
223589_at	ZNF416	NM_017879	Hs.247711	1.85	2.24
1568838_at	clone CS0DF033YE17		Hs.498519	1.10	2.24
206463_s_at	DHRS2	NM_005794	Hs.272499	1.43	2.24
222161_at	NAALAD2	NM_005467	Hs.503560	0.90	2.23
214016_s_at	SFPQ	NM_005066	Hs.355934	1.68	2.23
231953_at	FALZ	NM_004459	Hs.444200	1.04	2.21
239812_s_at	FLJ12476	NM_001031715	Hs.444535	1.00	2.21
244190_at	THAP5	NM_182529	Hs.290259	0.87	2.20
1552738_a_at	ST7L	NM_017744	Hs.201921	1.30	2.19
205432_at	OVGP1	NM_002557	Hs.1154	1.14	2.19
238658_at	transcribed locus		Hs.444083	1.01	2.19
202508_s_at	SNAP25	NM_003081	Hs.167317	1.53	2.18
230600_at	LRRC46	NM_033413	Hs.130767	0.94	2.17
203861_s_at	ACTN2	NM_001103	Hs.498178	0.84	2.17
1569366_a_at	ZNF569	NM_152484	Hs.511848	1.02	2.16
234907_x_at	POLB	NM_002690	Hs.521563	1.04	2.16
1556006_s_at	IMAGE:4619723		Hs.529862	1.40	2.16
228497_at	SLC22A15	NM_018420	Hs.125482	1.56	2.15
1557261_at	LOC339005, LOC440253	XM_370838	Hs.558967	1.12	2.15
238458_at	EFHA2	NM_181723	Hs.403594	1.09	2.15
231500_s_at	LOC388221	XM_370939	Hs.444600	1.22	2.15
220361_at	FLJ12476	NM_001031715	Hs.444535	0.85	2.14
226614_s_at	C8orf13	NM_053279	Hs.124299	0.72	2.14
238695_s_at	RAB39B	NM_171998	Hs.24970	1.02	2.13
241745_at	clone BRAWH3003343		Hs.571199	0.95	2.12
213908_at	LOC339005, LOC440253	XM_370838	Hs.558967	1.10	2.12
1561396_at	EPHA6	XM_114973	Hs.292059	1.10	2.10
228953_at	KIAA1971	XM_058720	Hs.377360	1.84	2.09
203895_at	PLCB4	NM_000933	Hs.472101	1.78	2.09
203896_s_at	PLCB4	NM_000933	Hs.472101	1.45	2.08
204726_at	CDH13	NM_001257	Hs.436040	1.00	2.08
242522_at	transcribed locus		Hs.120040	1.02	2.08
220369_at	KIAA2010	NM_017936	Hs.533887	1.60	2.07
223791_at	FAM27B, FAM27C	XM_499139	Hs.545934	1.60	2.07
225699_at	LOC285958		Hs.25892	1.86	2.06
216303_s_at	MTMR1	NM_003828	Hs.347187	0.96	2.06
207156_at	HIST1H2AG	NM_021064	Hs.51011	0.95	2.05
1554743_x_at	PMS1	NM_000534	Hs.111749	1.20	2.04
1569974_x_at	LOC441220	XM_496867	Hs.520804	1.38	2.03

Table SII

Name	Gene Symbol (Genedata An	RefSeq Transcrip	UniGene [A]	HeLa 500/0	Hek 500/0
205437_at	ZNF211	NM_006385	Hs.469694	1.40	2.03
209824_s_at	ARNTL	NM_001030272	Hs.65734	1.44	2.02
230837_at	IMAGE:286061			0.87	2.01
203862_s_at	ACTN2	NM_001103	Hs.498178	0.86	2.01
218683_at	PTBP2	NM_021190	Hs.269895	1.10	2.00
227359_at	C1orf102	NM_145047	Hs.202207	1.35	2.00
1554264_at	CKAP2	NM_018204	Hs.444028	0.81	2.00
203444_s_at	MTA2	NM_004739	Hs.173043	1.26	0.50
239351_at	IMAGE:1301821			0.95	0.49
228870_at	FAM84B	NM_174911	Hs.124951	1.02	0.49
237622_at	IMAGE:1690036			0.76	0.48
203505_at	ABCA1	NM_005502	Hs.429294	1.16	0.48
207390_s_at	SMTN	NM_006932	Hs.149098	1.22	0.48
1557062_at	IMAGE:4838183		Hs.434894	1.31	0.48
232282_at	WNK3	NM_001002838	Hs.92423	0.77	0.47
231259_s_at	CCND2	NM_001759	Hs.376071	0.89	0.46
1552658_a_at	NAV3	NM_014903	Hs.306322	1.09	0.46
216953_s_at	WT1	NM_000378	Hs.408453	0.66	0.43
236330_at	clone BRAMY3002120		Hs.444593	1.02	0.42
200952_s_at	CCND2	NM_001759	Hs.376071	0.95	0.40
235102_x_at	EPN2	NM_014964	Hs.514728	1.05	0.39
213854_at	SYNGR1	NM_004711	Hs.216226	0.90	0.37
238320_at	TncRNA		Hs.433995	0.28	0.69
232412_at	clone CAE10055		Hs.587911	0.33	0.95
230930_at	LOC338620		Hs.558072	0.34	1.12
117_at	HSPA6	NM_002155	Hs.3268	0.34	0.83
212177_at	C6orf111	NM_032870	Hs.520287	0.34	0.88
244503_at	BDNF	NM_001709	Hs.502182	0.35	0.88
234989_at	TncRNA		Hs.433995	0.36	0.89
213418_at	HSPA6	NM_002155	Hs.3268	0.38	0.88
234032_at	ZCCHC7	NM_032226	Hs.571599	0.39	0.97
214078_at	PAK3	NM_002578	Hs.390616	0.40	0.89
214587_at	COL8A1	NM_001850	Hs.134830	0.41	0.93
214807_at	clone DKFZp564O0862		Hs.99472	0.41	0.97
242191_at	LOC200030, LOC400781	NM_183372	Hs.125298	0.42	1.14
228620_at	PRKRA	NM_003690	Hs.405537	0.42	1.26
210602_s_at	CDH6	NM_004932	Hs.171054	0.43	1.04
239270_at	PLCXD3	NM_001005473	Hs.145404	0.44	1.00
235030_at	FAM55C	NM_145037	Hs.130195	0.44	0.93
235060_at	DKFZp547E087		Hs.531664	0.44	0.86
213517_at	PCBP2	NM_005016	Hs.546271	0.44	0.69
230629_s_at	EP400	NM_015409	Hs.507307	0.44	0.71
244043_at	IMAGE:1700929			0.45	0.85
215143_at	FLJ36166	NM_182634	Hs.148768	0.46	0.82
206100_at	CPM	NM_001005502	Hs.567251	0.46	0.77
240450_at	PAPPA	NM_002581	Hs.494928	0.47	1.08
236140_at	GCLM	NM_002061	Hs.315562	0.47	1.12
214605_x_at	GPR1	NM_005279	Hs.184907	0.47	1.11
1570482_at	SLC22A3	NM_021977	Hs.567337	0.48	0.94
224875_at	FLJ37562	NM_152409	Hs.406549	0.48	0.93
215470_at	GTF2H2	NM_001515	Hs.191356	0.48	0.98
1556331_a_at	IMAGE:5259142			0.48	1.21
203913_s_at	HPGD	NM_000860	Hs.77348	0.48	0.95
238635_at	FLJ21657	NM_022483	Hs.558531	0.49	1.40
239960_x_at	clone SKMUS2001014		Hs.508823	0.49	1.35
243308_at	MORN1	NM_024848	Hs.567585	0.49	1.06
204932_at	TNFRSF11B	NM_002546	Hs.81791	0.49	0.82
228353_x_at	STS-1	NM_032873	Hs.444075	0.49	1.17
1554513_s_at	FLJ14640	NM_032816	Hs.317590	0.49	0.95
1555778_a_at	POSTN	NM_006475	Hs.136348	0.49	1.02

Table SIII

name	sequence	product length (bp)	note
genotyping, T1 treatment and editing analysis			
MosE.fwd	GAGCAAGACGTTTGTAAGATCA	268	editing analysis
MosE.rev	TGCTCAAGGGGCTTCATGATGT		
Mos 3.fwd	CTCTTTTGGAATCACCCTAAGGG	317	transgene genotyping
MosIR+3.rev	GCTGTTTCATATACTGATGACCTCTTTAT		
MosIR.fwd	ACTCTTTTGGAATCACCCTAAGCC	316	
MosIR+3.rev	GCTGTTTCATATACTGATGACCTCTTTAT		
MosP.fwd	GAGCAAGACGTTTGTAAGATCA	241	
MosP.rev	AGATGGGGAGAGTGAAGACAAGA		
Egfp.fwd	GCACCATCTTCTTCAAGGACGAC	343	
Egfp.rev	TCTTTGCTCAGGGCGGACTG		
MosT1.Fwd	CAACGTGACTCTACACCAAGTC	204	amplification after RNase T1 treatment
MosT1.Rev	ATCTTACAAACGTCTTGCTCACTG		
qPCR mouse			
Mos.fwd	GGGAACAGGTATGTCTGATGCA	75	qPCR
Mos.rev	CACCGTGGTAAGTGGCTTTATACA		
Mos3.fwd	CTCTTTTGGAATCACCCTAAGGG	102	
MosIR+3q.rev	GCCAGAAGTCAGATGCTCAAGG		
CagI.fwd	GGCTCTGACTGACCGCGTTAC	176	
CagI.rev	GCTGAACTTGTGGCCGTTTACG		
Ifit.fwd	AGAGAGTCAAGGCAGGTTTCTGAG	190	
Ifit.fwd	TCTCACTTCCAAATCAGGTATGTCA		
Pkr.fwd	TCCTCAGAGAACGTGTTTACGAAC	169	
Pkr.rev	TGAAAACTTGACCAAATCCACCTA		
Oas1.fwd	AGACGTTGTGGAGTGAAGTTTGAG	335	
Oas1.rev	CCCAGCTTCTCCTTACACAGTTG		
Rig1.fwd	AGCTTACTCGGAGGTTTGAAGAAA	234	
Rig1.fwd	CAGTCAGTATGCCAGGCTTTAGAA		
Hprt.fwd	GCTACTGTAATGATCAGTCAACGG	213	qPCR - standard
Hprt.rev	CTGTATCCAACACTTCGAGAGGTC		
globin.fwd	GCAGCCACGGTGGCGAGTAT	257	
globin.rev	GTGGGAVAGGAGVTTGAAAT		
qPCR human			
IRF1.fwd	CTCTGAAGCTACAACAGATGAGGA	169	qPCR
IRF1.rev	CCTCCTTACAGCTAAAGTCTCCAT		
NMI.fwd	CCTTTGAAAAAGAAGAAGTTGCTC	130	
NMI.rev	ATAAACCTGGAATCTGACTCCTGAA		
GCH1.fwd	ATCTCAGATGTCCTAAACGATGCT	185	
GCH1.fev	GATTTCTACAATCCTCGCAAGTTT		
C1S.fwd	TACTATGTTGCCACAGACATAAATG	148	
C1S.rev	CAATTAACTCCGCAATTCTTCAT		
IFIT1.fwd	CTAAGCAAAACCCTGCAGAACG	179	
IFIT1.rev	GGAATTCAATCTGATCCAAGACTC		
PKR.fwd	GTGACCAGCACACTCGCTTCTG	217	
PKR.rev	CCATGCCAAACCTCTTGTCCACAG		
RIG-I.fwd	CATGTCCACCTTCAGAAGTGTCTG	137	
RIG-I.rev	GGTTTTTCCACAACCTGTAGGAGC		
HPRT.fwd	TGACCTTGATTTATTTTGCATACC	102	qPCR - standard
HPRT.rev	CGAGCAAGACGTTCAGTCCT		