

FIG.S1. The FSC: SSC profile and gating parameters. The flow cytometry data was gated for live cells based on forward and side scatter parameters. The orange represents RG⁺ SH-SY5Y cells upon KSHV infection. The grey represents the added uninfected cells as internal control for auto-fluorescence.

FIG.S2. Single cell soft agar cloning of uninfected, GFP⁺ and RG⁺ SH-SY5Y infected cells. (A) Single cells of the uninfected control (NC), GFP⁺ and RG⁺ cells were seeded in soft agar and pictures were taken at day 12 after seeding to show the number of clones formed by each type of cells. (B) The number of clones for each of the three groups were counted, and the numbers are shown in the Y-axis.

FIG.S3. Significantly regulated cellular genes exclusively in an infected population. Gene expression levels are illustrated in the log₂ scale range from white (0) to dark red (higher than 10) and fold changes are in the log₂ scale range from dark blue (less than 12) to dark red (greater than 12). (A) Significantly up-regulated genes uniquely expressed in the RG⁺ infected cell population. (B) Significantly down regulated genes expressed in the RG⁺ infected cell population. (C) Continuation of part B. (D) Significant up-regulated genes uniquely expressed in the GFP⁺ infected cell population. (E) Significantly downregulated genes expressed in the RG⁺ infected cell population.

FIG.S4. Significantly regulated cellular genes among GFP⁺ and RG⁺ infected cell populations. Genes expression levels are illustrated in the log₂ scale range from white (0) to dark red (higher than 10) and fold changes (GFP⁺/NC and RG⁺/NC) are in the log₂ scale range from dark blue (less than 12) to dark red (greater than 12). (A) Significantly up-regulated genes expressed in both infected populations. (B) Continuation of part A. (C) Significant downregulated genes expressed in both infected populations. (D) Continuation of part C.

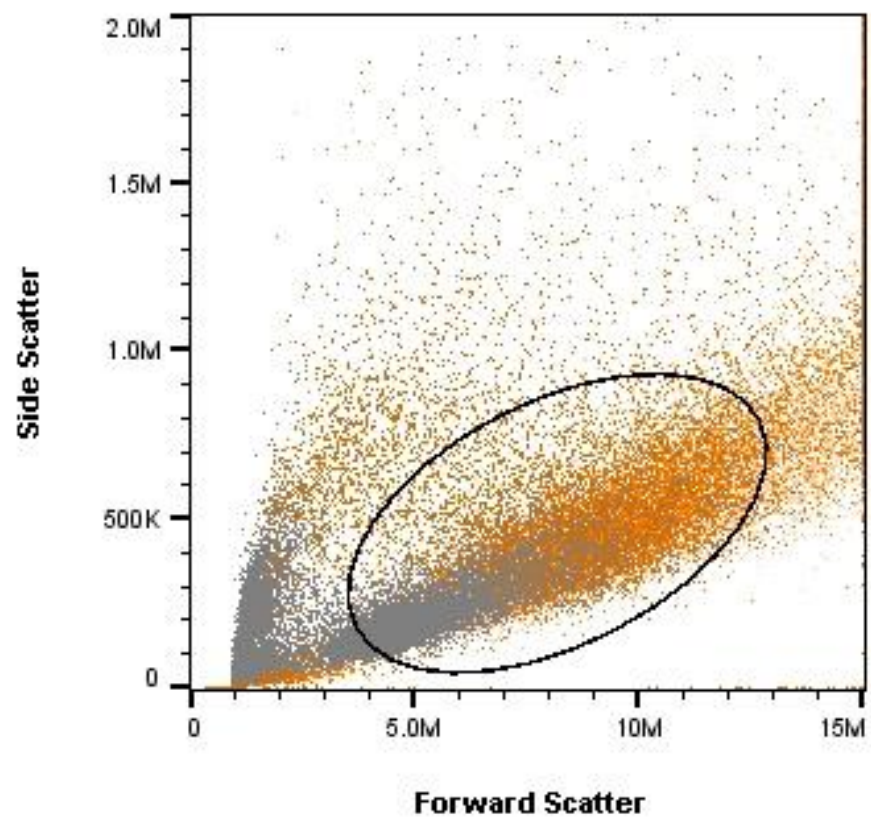
FIG.S5. KEGG pathways involved in the KSHV infection across two groups of GFP⁺ and RG⁺ infected cell populations. (A)

Venn diagram showing KEGG intersected pathways across the GFP⁺ and RG⁺ infected cells. (B) KEGG pathways associated with the GFP⁺ and RG⁺ cell populations, and individually or common pathways shared by both RG⁺ and GFP⁺ infected cell populations.

FIG.S6. Comparison of significant regulated genes in GFP⁺ and RG⁺ population with the significantly regulated genes from

the infected TIME cell. (A) The number of common significant regulated genes between each group. (B) The 44 common genes across all groups that have more log₂ fold or more changes. (C) The fold changes of 27 genes that were shared between two cell types.

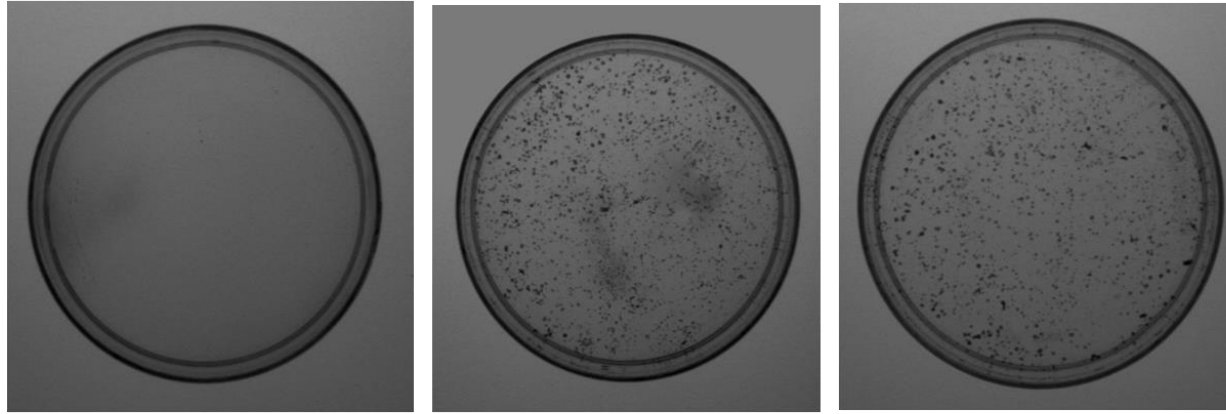
Thirteen significant regulated genes were found in common between TIME and GFP⁺, and 14 genes between RG⁺ and TIME.



	Sample Name	Subset Name	Count	\$DATE
■	B01 negative.fcs	Ungated	14304	22-MAR-2017
■	B05 RG.fcs	Ungated	8785	10-MAR-2017
■	B05 RG.fcs	Ungated	16734	13-MAR-2017
■	B05 RG.fcs	Ungated	16577	16-MAR-2017
■	B05 RG.fcs	Ungated	13199	22-MAR-2017

Fig.S1

A



NC

GFP+

RG+

B

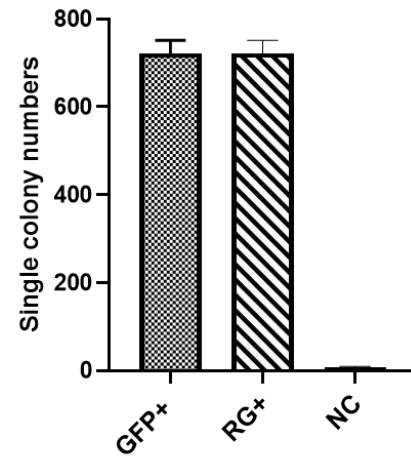


Fig.S2

A

GeneID	Expression levels log ₂ (FPKM _s +1)			Fold Change (log ₂) RG+/NC
	NC	RG+	NC	
RP6-24A23.3		0	3.117	Inf
USP43		0	2.466	Inf
MICB		0	2.160	Inf
HOXB13		0	2.073	Inf
APOBEC3B		0	1.953	Inf
NKX6-1		0	1.947	Inf
BARX2		0	1.840	Inf
WNT10B		0	1.594	Inf
USHIC		0	1.534	Inf
RASGEF1B		0	1.467	Inf
LTK		0	1.457	Inf
SP9		0	1.456	Inf
SIM1		0	1.423	Inf
LG12		0	1.407	Inf
EMX2OS		0	1.267	Inf
SOX21		0	1.229	Inf
INHBB		0	1.168	Inf
EFEMP1		0	1.130	Inf
RP11-138J23.1		0	1.097	Inf
PAX2		0	1.094	Inf
AC073043.1	0.015	1.303	7.158	
NLR5	0.305	2.169	3.893	
MI-NDS	8.621	10.422	1.804	

B

GeneID	Expression levels log ₂ (FPKM _s +1)			Fold Change (log ₂) RG+/NC
	NC	RG+	NC	
TAGLN3		5.832	0	-Inf
DTX3		5.745	0	-Inf
ACTL6B		5.194	0	-Inf
FAM155A		4.659	0	-Inf
ZNF43		4.214	0	-Inf
TMEM119		4.209	0	-Inf
CSRP1		4.189	0	-Inf
SEZ6L		3.881	0	-Inf
NAT16		3.783	0	-Inf
ARMCX1		3.683	0	-Inf
RP11-197K6.1		3.679	0	-Inf
LINC00599		3.649	0	-Inf
RP11-161D15.3		3.487	0	-Inf
MAATS1		3.459	0	-Inf
VAT1L		3.406	0	-Inf
CTC-338M12.9		3.326	0	-Inf
RP1-310O13.12		3.185	0	-Inf
DOCK10		3.155	0	-Inf
SERPINA5		3.080	0	-Inf
PLXNA4		3.044	0	-Inf
RP11-166D19.1		3.000	0	-Inf
ZFP82		2.985	0	-Inf
C7		2.967	0	-Inf
AC012354.6		2.861	0	-Inf
PDE6B		2.758	0	-Inf
SRRM4		2.727	0	-Inf
FSTL5		2.695	0	-Inf
CTD-2335A18.1		2.637	0	-Inf
FAM111B		2.627	0	-Inf
MIR137HG		2.532	0	-Inf
ZNF665		2.483	0	-Inf
SCRT1		2.441	0	-Inf
PEAR1		2.322	0	-Inf
ZFP3		2.281	0	-Inf
XKR7		2.215	0	-Inf
LINC00202-2		2.119	0	-Inf
PTH2R		2.109	0	-Inf
AKRIE2		1.994	0	-Inf
CX3CL1		1.977	0	-Inf
GUCA1A		1.880	0	-Inf
CALB1		1.862	0	-Inf
CHRM1		1.861	0	-Inf
SLC1A2		1.803	0	-Inf
ST6GAL2		1.771	0	-Inf
LRFN2		1.728	0	-Inf
CSMD2		1.657	0	-Inf
RP11-1038A11.1		1.602	0	-Inf
PTPRR		1.426	0	-Inf
PCDH9		1.219	0	-Inf
RP11-923H1.6		1.196	0	-Inf
AC092198.1		1.189	0	-Inf
AGAP7		1.160	0	-Inf
GLYATLIP2		1.154	0	-Inf
RP11-161D15.1		1.066	0	-Inf

C

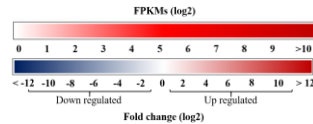
GeneID	Expression levels log ₂ (FPKM _s +1)			Fold Change (log ₂) RG+/NC
	NC	RG+	NC	
ELMO1		4.656	0.001	-16.030
RIMS2		3.244	0.0004	-14.859
ABCA12		5.168	0.058	-9.724
KCNMA1		2.280	0.014	-8.650
CELF4		3.455	0.098	-7.141
SNAP91		5.129	0.444	-6.560
STRA6		4.162	0.329	-6.042
DUSP4		5.459	0.751	-5.975
MYD88		3.640	0.313	-5.565
PCOLCE		7.728	2.668	-5.301
NREP		6.905	2.012	-5.293
NEFASC		2.752	0.199	-5.278
CNTN1		6.438	2.002	-4.834
GATA2		8.052	3.864	-4.285
MCF2L		4.555	1.139	-4.227
PDE2A		2.861	0.421	-4.208
DPYSL2		5.904	2.111	-4.148
TNFRSF25		3.748	0.823	-4.014
CACNA1G		1.484	0.160	-3.941
GLCCII		7.399	3.971	-3.515
ADAM22		5.056	1.970	-3.468
MLLT6		5.548	2.661	-3.104
LPIN1		5.594	2.775	-3.017
KIF1A		5.980	3.245	-2.873
MYO1B		6.627	4.145	-2.551

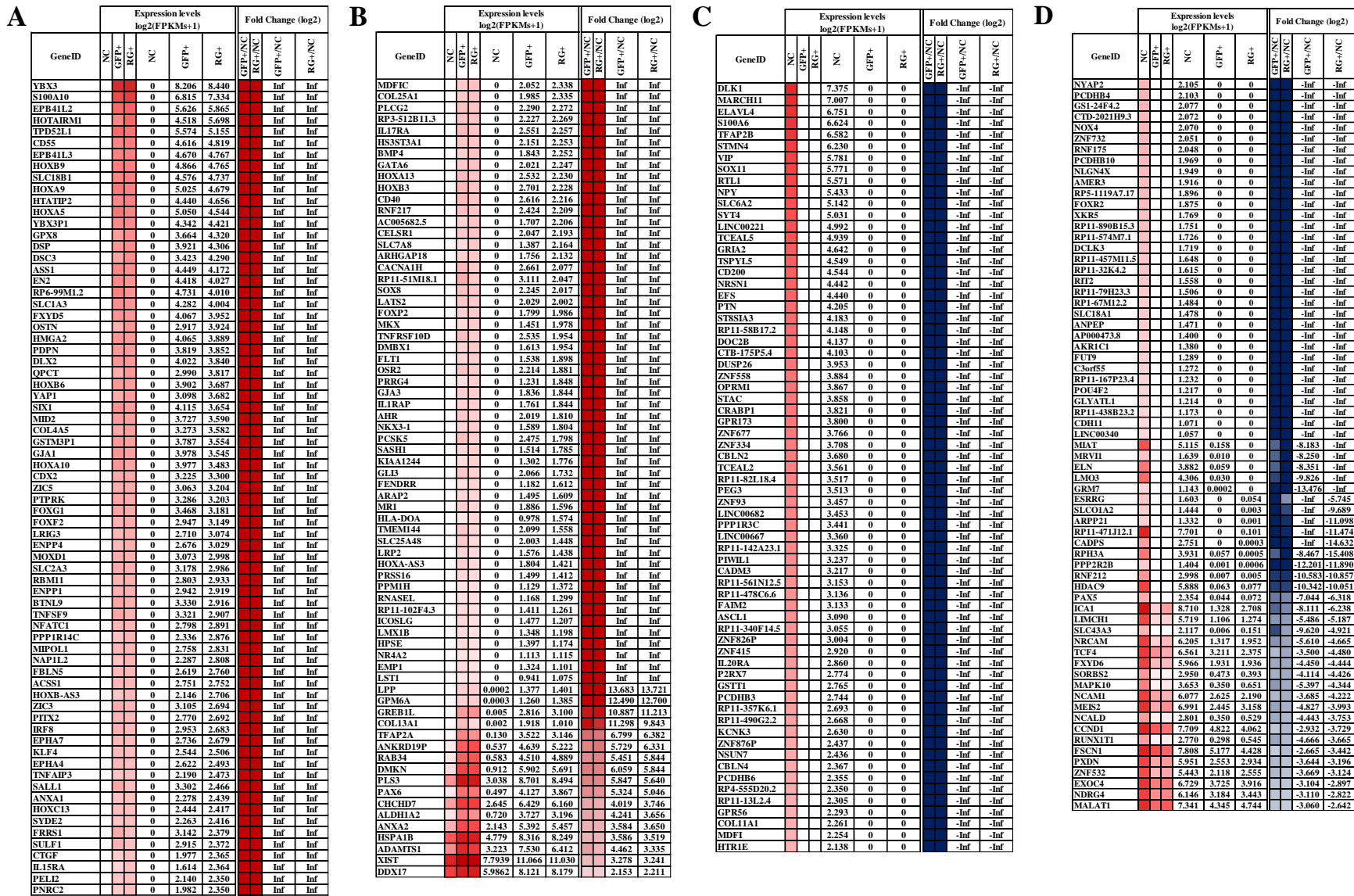
D

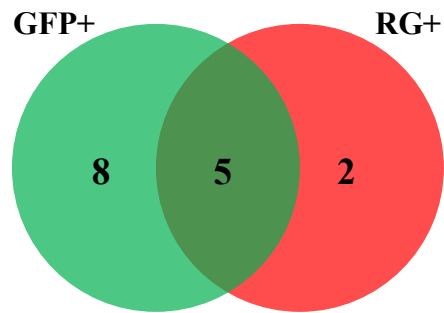
GeneID	Expression levels log ₂ (FPKM _s +1)			Fold Change (log ₂) GFP+/NC
	NC	GFP+	NC	
OCLAD2		8.363	0	-Inf
PFOX2B		6.107	0	-Inf
CPXMI		5.879	0	-Inf
DDC		5.709	0	-Inf
ARMCX2		4.969	0	-Inf
SLC18A3		4.391	0	-Inf
GPX7		4.311	0	-Inf
PDE4B		4.297	0	-Inf
SVOP		4.133	0	-Inf
PLCXD3		4.120	0	-Inf
SGIP1		4.119	0	-Inf
EPMAIP1		3.835	0	-Inf
JAKMIP2		3.638	0	-Inf
PDGFRB		3.628	0	-Inf
ZNF439		3.484	0	-Inf
SLITRK6		3.151	0	-Inf
MGMT		3.142	0	-Inf
RP11-293B20.1		3.055	0	-Inf
LAMP5		2.994	0	-Inf
PCDHB14		2.635	0	-Inf
LINGO2		2.608	0	-Inf
UNC80		2.433	0	-Inf
DNER		2.289	0	-Inf
KCNJ9		2.218	0	-Inf
ZNF844		2.104	0	-Inf
ZNF69		2.076	0	-Inf
CCDC169		2.062	0	-Inf
NPAS4		2.043	0	-Inf
CNTNAP5		2.002	0	-Inf
CACNG2		1.909	0	-Inf
CES4A		1.906	0	-Inf
RP11-764K9.4		1.867	0	-Inf
SHISA9		1.727	0	-Inf
AC073479.1		1.705	0	-Inf
MARCH4		1.678	0	-Inf
RP4-791K14.2		1.676	0	-Inf
Clorf173		1.633	0	-Inf
RP11-553L6.5		1.536	0	-Inf
RP11-461O7.1		1.320	0	-Inf
CNR1		1.275	0	-Inf
LINC00578		1.249	0	-Inf
C2CD2		1.100	0	-Inf
MUC19		0.959	0	-Inf
NRXN1		2.255	0.001	-11.979
MLH1		4.657	0.013	-11.395
PTPRN2		3.497	0.027	-9.070
RGL3		3.665	0.058	-8.163
NES		6.053	1.012	-6.006
EML5		6.596	1.996	-5.001
ZNF704		6.267	2.251	-4.337
CYB561		6.234	2.724	-3.728
MYEF2		6.396	3.042	-3.523
STMN1		10.765	8.303	-2.466

E

GeneID	Expression levels log ₂ (FPKM _s +1)			Fold Change (log ₂) GFP+/NC
	NC	GFP+	NC	
GS1-600G8.5		0	3.236	Inf
RP4-792G4.2		0	2.715	Inf
MAFA		0	2.233	Inf
CAV1		0	2.191	Inf
CT4SA5		0	2.159	Inf
HLA-DRB1		0	1.904	Inf
SMPDL3A		0	1.879	Inf
LOXLL-AS1		0	1.863	Inf
AC079135.1		0	1.841	Inf
GYPC		0	1.738	Inf
TFAP2C		0	1.737	Inf
EN1		0	1.605	Inf
NPIPL2		0	1.593	Inf
LHX1		0	1.497	Inf
SALL3		0	1.390	Inf
DOCK8		0	1.366	Inf
CEBPD		0	1.334	Inf
ARMC4		0	1.286	Inf
GIPC3		0	1.145	Inf
TGM2		0	1.098	Inf
LEF1		0.322	3.435	5.296
HLA-C		3.044	7.462	4.596
ATPIA1		5.466	7.846	2.407

**Fig. S3**

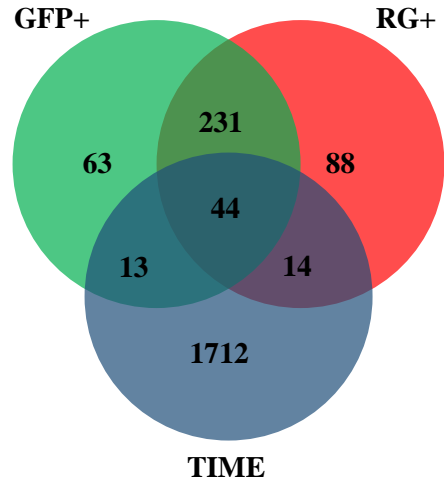


A**B**

Samples	#	KEGG Pathways
GFP+, RG+	5	hsa04390: Hippo signaling pathway
		hsa04974: Protein digestion and absorption
		hsa04672: Intestinal immune network for IgA production
		hsa05202: Transcriptional misregulation in cancer
		hsa04514: Cell adhesion molecules (CAMs)
GFP+	8	hsa05416: Viral myocarditis
		hsa04728: Dopaminergic synapse
		hsa05330: Allograft rejection
		hsa05169: Epstein-Barr virus infection
		hsa04940: Type I diabetes mellitus
		hsa05200: Pathways in cancer
		hsa05320: Autoimmune thyroid disease
		hsa04024: cAMP signaling pathway
RG+	2	hsa04060: Cytokine-cytokine receptor interaction
		hsa04925: Aldosterone synthesis and secretion

Fig. S5

A



B

GeneID	Fold Change (log2)					
	GFP+	RG+	TIME	GFP+	RG+	TIME
ENPP4				Inf	Inf	3.807
EPHA4				Inf	Inf	3.782
HOXB9				Inf	Inf	2.918
FLT1				Inf	Inf	2.570
CD40				Inf	Inf	2.467
NAP1L2				Inf	Inf	2.279
ADAMTS1				4.462	3.335	2.108
BMP4				Inf	Inf	1.907
SLC2A3				Inf	Inf	1.843
SIX1				Inf	Inf	1.637
CD55				Inf	Inf	1.620
HOXA-AS3				Inf	Inf	1.586
PDPN				Inf	Inf	1.531
IL15RA				Inf	Inf	1.265
NKX3-1				Inf	Inf	1.143
PCSK5				Inf	Inf	1.085
COL13A1				11.298	9.843	0.894
CSDA				Inf	Inf	0.709
CHCHD7				4.019	3.746	0.648
HOXA9				Inf	Inf	0.645
TNFAIP3				Inf	Inf	-0.736
ARHGAP18				Inf	Inf	-0.880
EPB41L3				Inf	Inf	-0.919
CTGF				Inf	Inf	-0.974
ENPP1				Inf	Inf	-1.008
FBLN5				Inf	Inf	-1.072
SYDE2				Inf	Inf	-1.530
KLF4				Inf	Inf	-1.731
TCF4				-3.500	-4.480	0.715
CD200				-Inf	-Inf	2.829
HDAC9				-10.342	-10.051	1.603
LIMCH1				-5.486	-5.187	1.218
MRVII				-8.250	-Inf	1.064
NRCAM				-5.610	-4.665	0.987
MALAT1				-3.060	-2.642	0.762
ZNF677				-Inf	-Inf	0.619
FSCN1				-2.665	-3.442	-0.628
AKR1C1				-Inf	-Inf	-0.656
S100A6				-Inf	-Inf	-0.684
SORBS2				-4.114	-4.426	-0.685
SLC43A3				-9.620	-4.921	-0.747
PPP1R3C				-Inf	-Inf	-1.252
RUNX1TI				-4.666	-3.665	-1.996
CADM3				-Inf	-Inf	-2.108

Legend: Not Significant (black), Down-regulated (blue), Up-regulated (red). Scale: Fold change (log2) from <-6 to >6.

C

GeneID	Fold Change (log2)					
	GFP+	RG+	TIME	GFP+	RG+	TIME
CPXM1				-Inf		5.973
CEBPD				Inf		2.961
RGL3				-8.163		1.921
CYB561				-3.728		1.192
STMN1				-2.466		-0.600
CAV1				Inf		-0.608
GYPC				Inf		-0.670
NES				-6.006		-0.715
MYEF2				-3.523		-0.966
ZNF704				-4.337		-2.002
CNR1				-Inf		-2.251
PDGFRB				-Inf		-2.289
MARCHF4				-Inf		-2.542
MYO1B					-2.551	1.574
LIG2					Inf	3.441
PCOLCE					-5.301	1.617
ADAM22					-3.468	1.423
SERPINA5					-Inf	1.316
PTPRR					-Inf	1.033
NLRC5					3.893	0.888
MYD88					-5.565	0.783
PEAR1					-Inf	-0.729
SIMI					Inf	-0.816
FAM111B					-Inf	-0.837
DOCK10					-Inf	-0.867
CSRP1					-Inf	-1.089
APOBEC3B					Inf	-1.305

Fig. S6

Table S1. List of oligonucleotide primers and probes

Target Gene	ID	Sequence (5'-3')
Primers		
ORF 26 for PCR	Forward	AGCCGAAAGATTCCACCAT
	Reverse	TCCGTGTTGTCTACGTCCAG
ORF 26 for dd PCR	Forward	CGAATCCAACGGATTTGACCTC
	Reverse	CCCATAAATGACACATTGGTGGTA
LANA for PCR	Forward	GGAAGAGCCCATAATCTTGC
	Reverse	GCCTCATAACGAACTCCAGGT
LANA for dd PCR	Forward	AGCCACCGGTAAAGTAGGAC
	Reverse	GATGTGACCTTGGCGATGAC
β -actin for PCR	Forward	TTCTACAATGAGCTGCGTGT
	Reverse	GCCAGACAGCACTGTGTTGG
β -globin for dd PCR	Forward	TCCACGTTACCTTGCCC
	Reverse	CAACCTCAAACAGACACCATGG
LANA for qPCR	Forward	TGGATCTCGTCTTCATCCTTTCCC
	Reverse	CCAACAACCACCGGTCCCTT
ORF59 for qPCR	Forward	GCCCACATCCACCGACTTC
	Reverse	AACACATGGTGTCAAATCAGG
GAPDH	Forward	GAGTCCACTGGCGTCTTCAC
	Reverse	ATGACGAACATGGGGGCATC
Probes		
ORF 26 for qPCR		5'FAM/CCCATGGTCGTGCCGCAGCA/3'BHQ-1
ORF 26 for dd PCR		5'FAM/CCATGGTCGTGCCGCACGCA/3'BHQ-1
LANA for dd PCR		5'FAM/CATGTCGCCGACTCCGTCTGA/3'BHQ-1
β -globin for dd PCR		5'HEX/CTCCTGAGGAGAAGTCTGCCGTTACTGCC/3'BHQ1

Table S2. ATCC Report on SHSY5Y Verification

Test Results for Submitted Sample				ATCC Reference Database Profile			
Locus	Query Profile: SHSY5Y			Database Profile: SH-SY5Y; Neuroblastoma; Human (Homo sapiens)			
TH01	7	10		7	10		
D5S818	12			12			
D13S317	11			11			
D7S820	7	10		7	10		
D16S539	8	13		8	13		
CSF1PO	11			11			
Amelogenin	X			X			
vWA	14	18		14	18		
TPOX	8	11		8	11		
Number of shared alleles between query sample and database profile:							9
Total number of alleles in the database profile:							9
Percent match between the submitted sample and the database profile:							100

Explanation of Test Results

Cell lines with 80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

X

The submitted profile is an exact match for the following ATCC human cell line(s) in the ATCC STR database (8 core loci plus Amelogenin): CRL-2266

Additional Comments:

Submitted sample, STRB5050 (SHSY5Y), is an exact match to ATCC cell line CRL-2266 (SH-SY5Y).