

Supplementary information

ORIGINAL RESEARCH

Short running header: Differential radiation response between normal and glioma cell

Liang Gong et al

**Differential radiation response between normal and glioma cell
revealed by comparative transcriptome analysis**

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Supplementary Figures

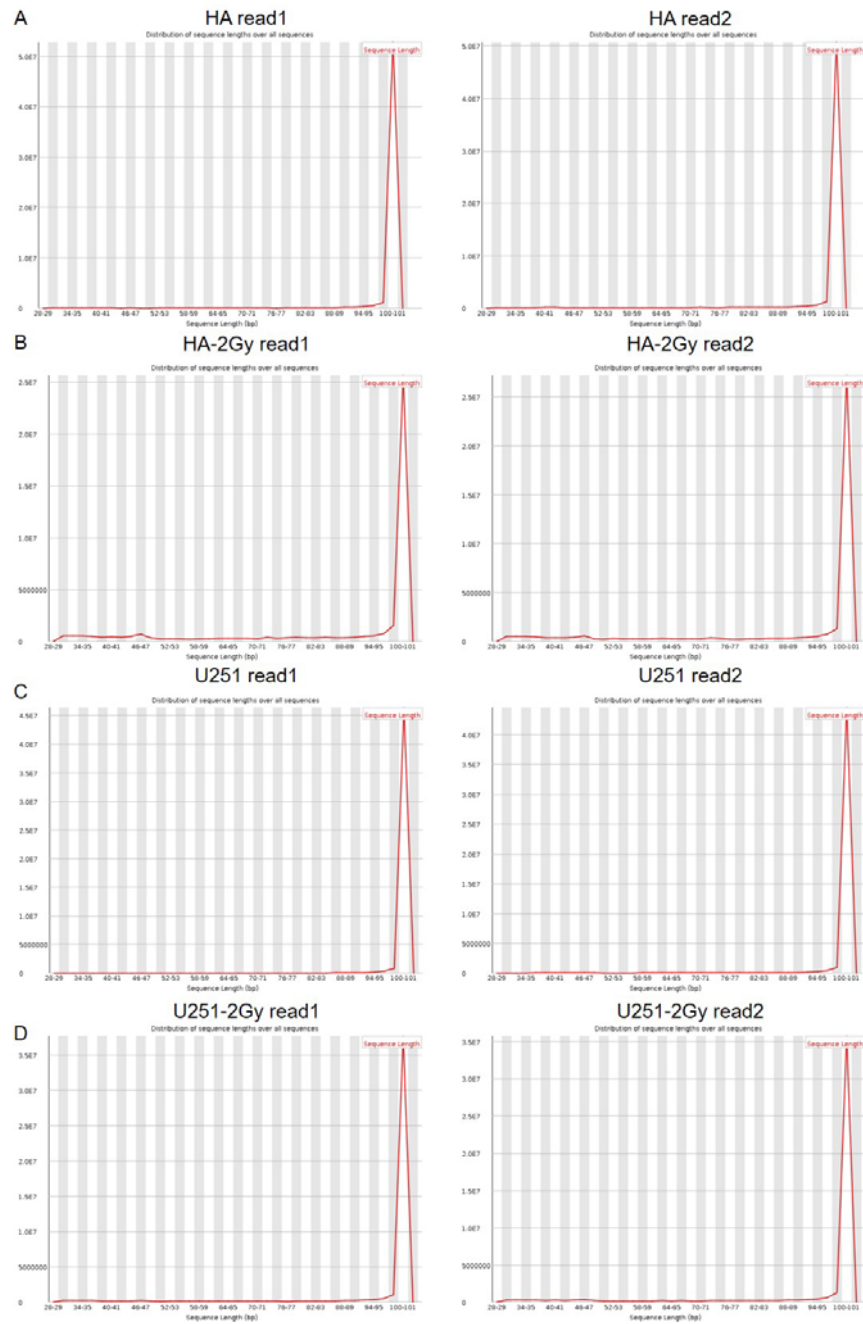


Figure S1 Distribution of read length.

Notes: Read length distribution of the RNA sequencing data from normal HA cell (**A**), radiation-treated HA cell (**B**), normal U251 cell (**C**), radiation-treated U251 cell (**D**). (**Left:** read 1, **Right:** read 2).

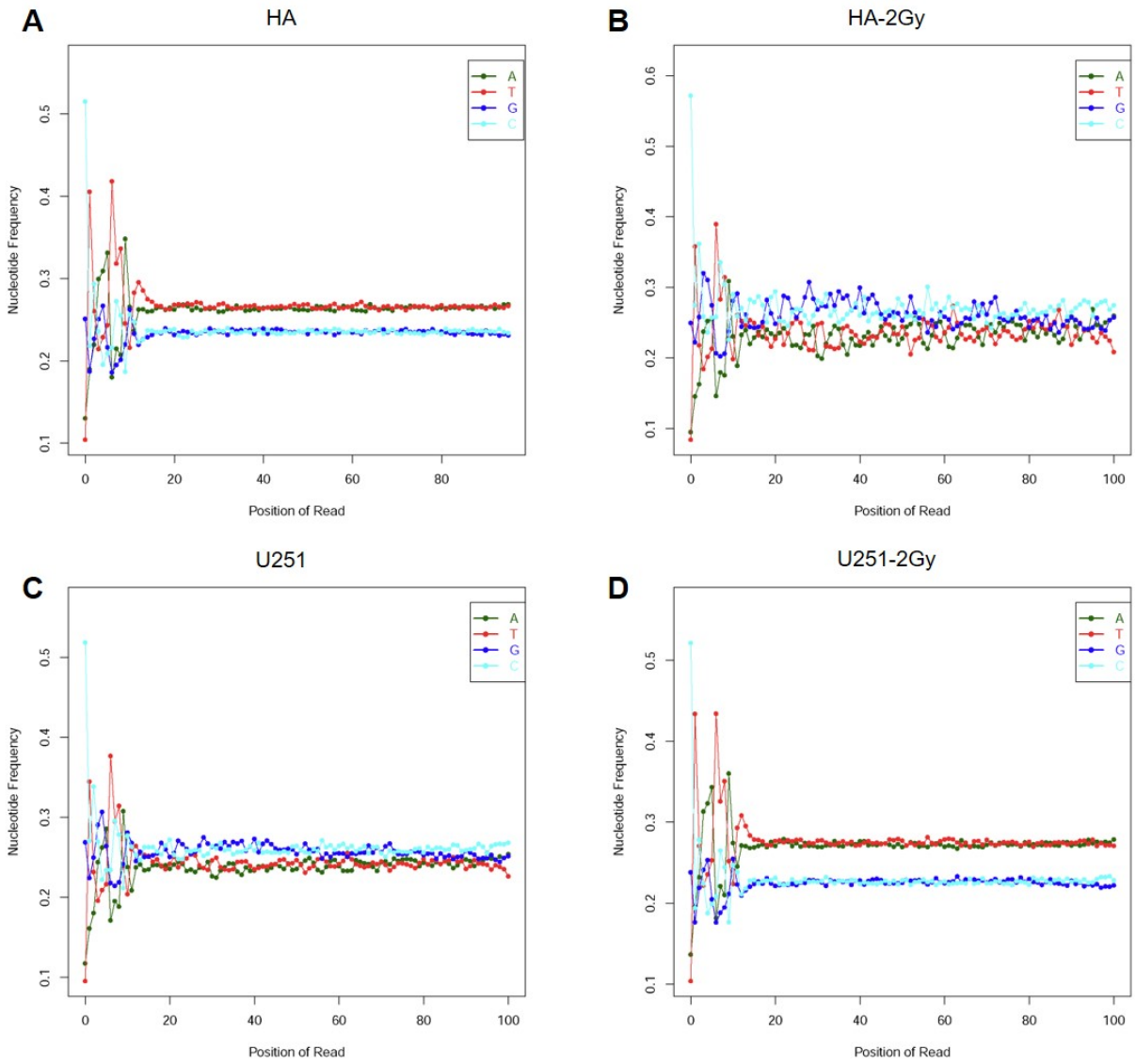


Figure S2 Nucleotide distribution across all reads.

Notes: Nucleotide distribution of the RNA sequencing data from normal HA cell (**A**), radiation-treated HA cell (**B**), normal U251 cell (**C**), radiation-treated U251 cell (**D**). (**Left:** read 1, **Right:** read 2).

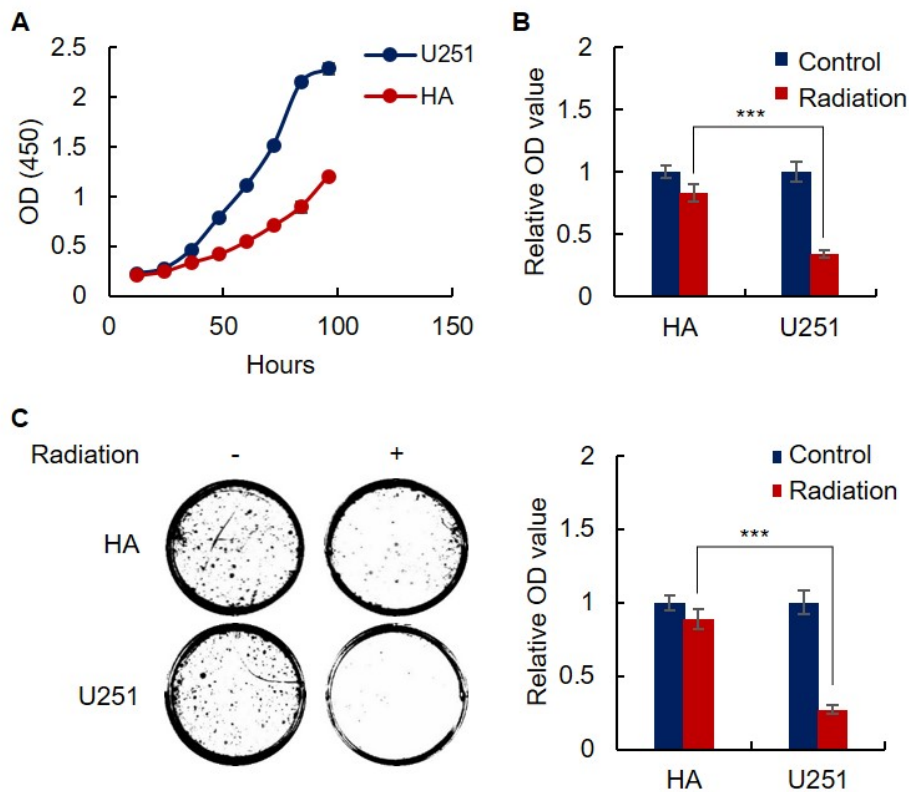


Figure S3 HA cells are more resistant to radiation than U251 cells.

Notes: **(A)** Growth curves of HA and U251 cells. The cells were plated in the well of 96 well plate at a density of 3,000 cells / well. Every 12 h, the cells in the wells of three parallel plates were subjected to CCK-8 analysis. **(B)** CCK-8 assay showed the cell viability of HA and U251 cells after radiation treatment. HA and U251 cells were treated with (radiation group) or without (control group) 10 Gy of radiation. The cells were then cultured in complete culture media for 48 h. The cell number was measured by CCK-8 kits. Data were normalized to control group. *** P < 0.001. **(C)** Colony formation assay showed the radiation-induced cytotoxicity on HA and U251. The cells were pretreated with or without 30Gy of radiation followed by 15 days culture. The colonies were visualized by crystal violet and the colonies with > 50 cells were counted under a dissecting scope. The statistics was shown on the right (The number of colonies were normalized to control group). *** P < 0.001.

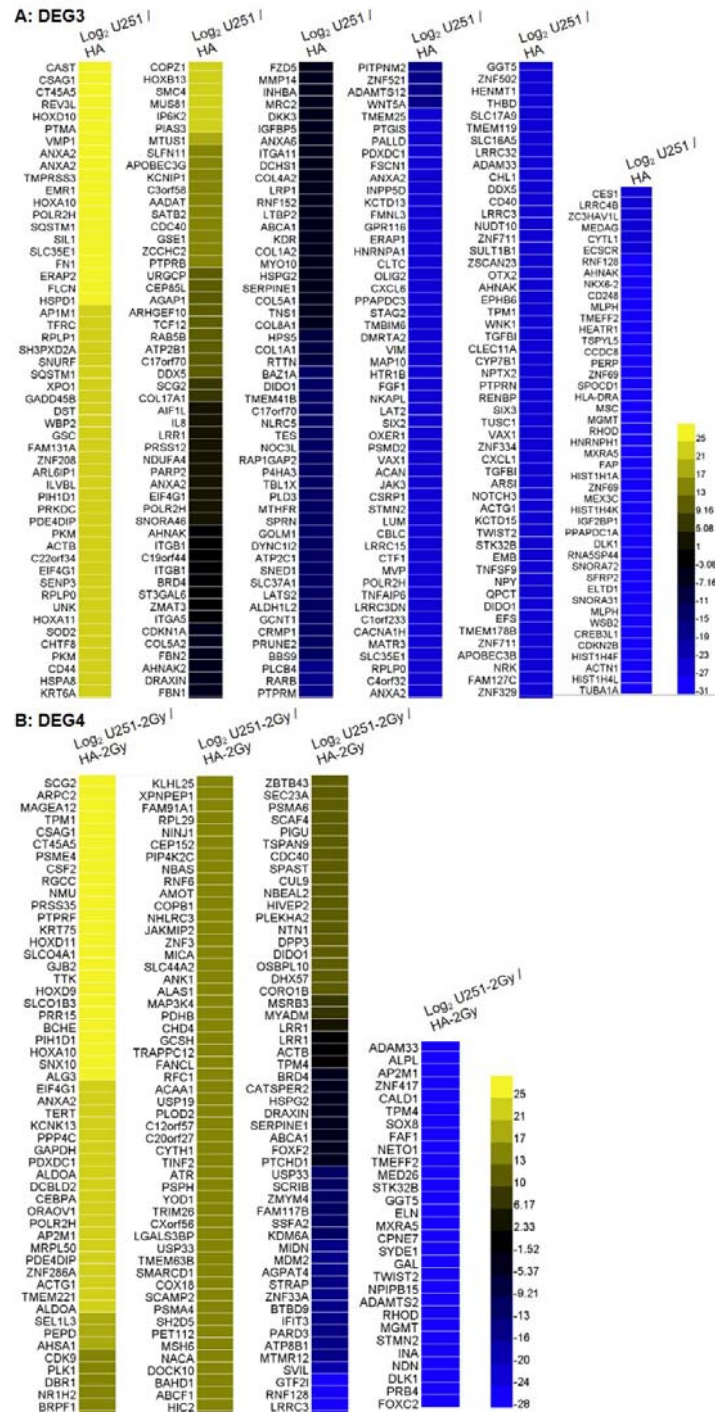


Figure S4 Differentially expressed genes between untreated HA and U251 cells and between radiation-treated HA and U251.

Notes: (A) Total RNAs were extracted from HA and U251 cells under normal culture condition. The mRNA expression profile was generated by next-generation sequencing. The differentially expressed genes

between untreated HA and U251 cells were listed. **(B)** HA and U251 cells were treated with 2Gy of radiation. One hour after treatment, the total mRNA of the cells were then extracted to produce mRNA expression profile. The differentially expressed genes between between these two radiation-treated cells were presented.

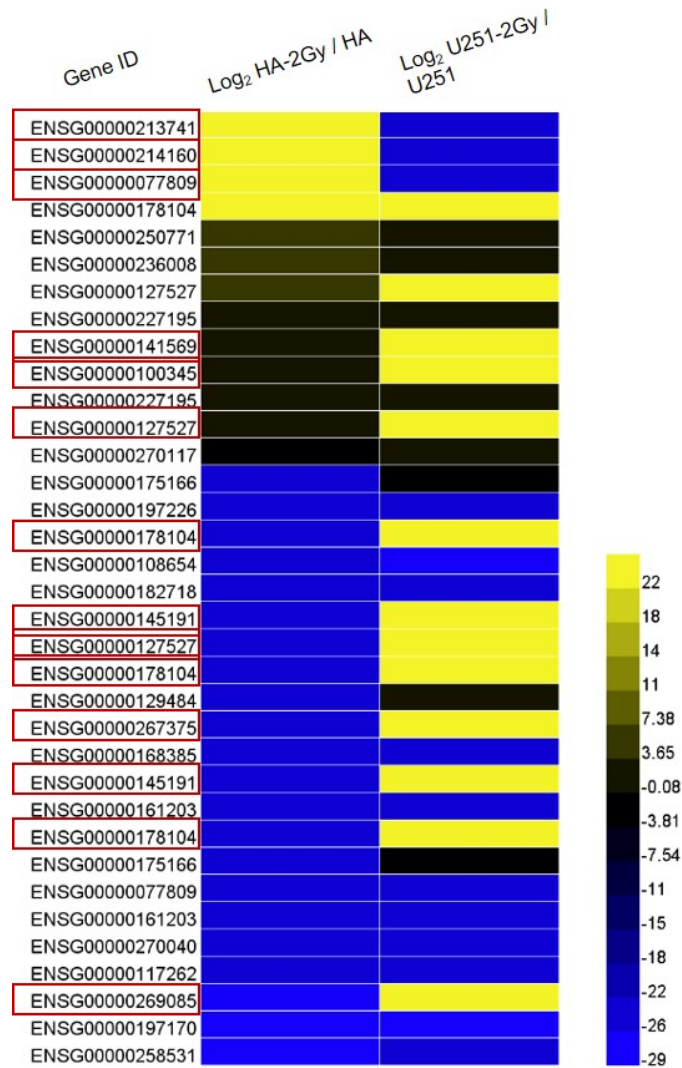


Figure S5 LncRNAs regulated by radiation in both HA and U251 cells.

Notes: LncRNAs oppositely regulated by radiation were highlighted.

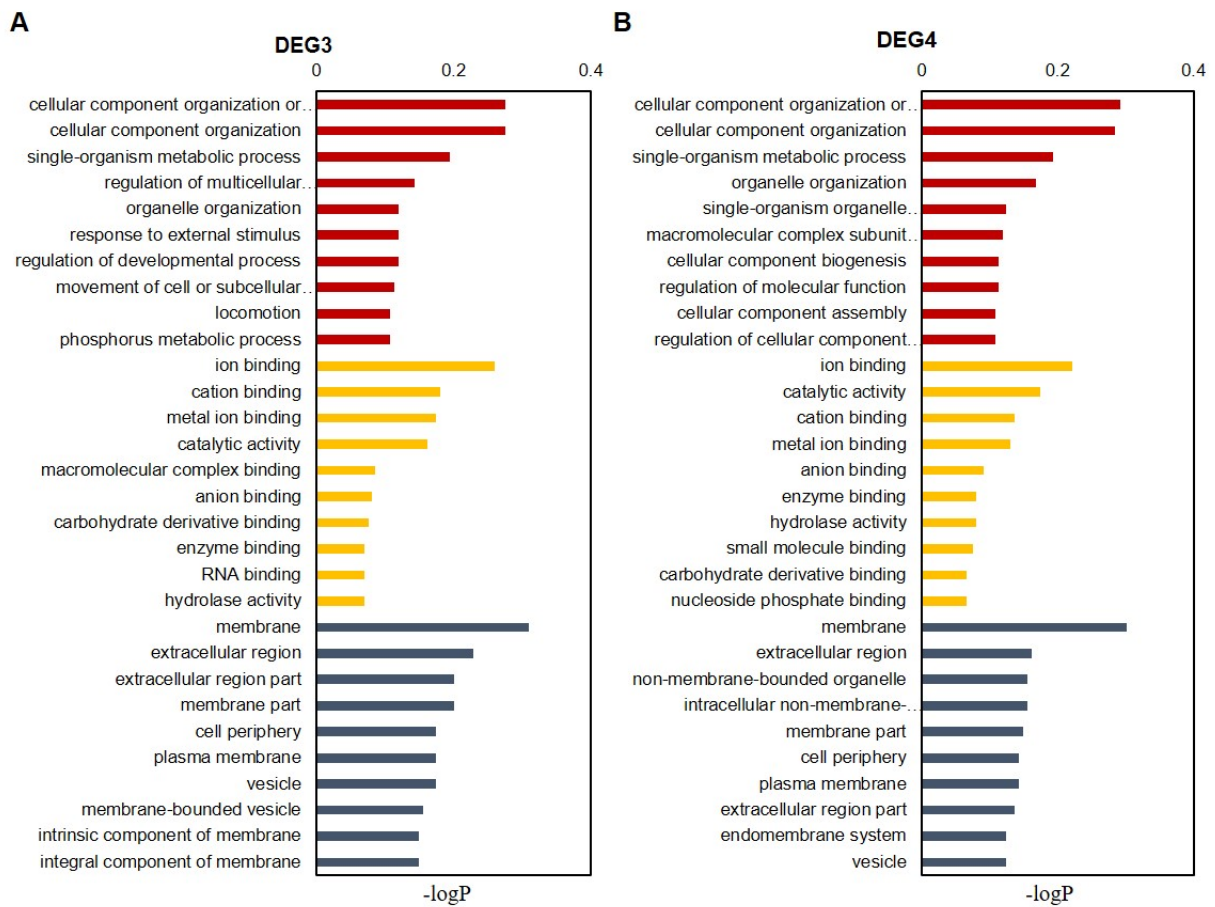


Figure S6 Gene ontology analysis of genes differentially expressed between HA and U251 cells.

Notes: Genes differentially expressed between nontreated HA and U251 cells **(A)** and radiation-treated HA and U251 cells **(B)** were subjected to ipathwayGuide online software for gene ontology analysis. Top ten gene ontology terms in cellular components (Red), molecular function (Yellow) and biological process (blue) category were listed.

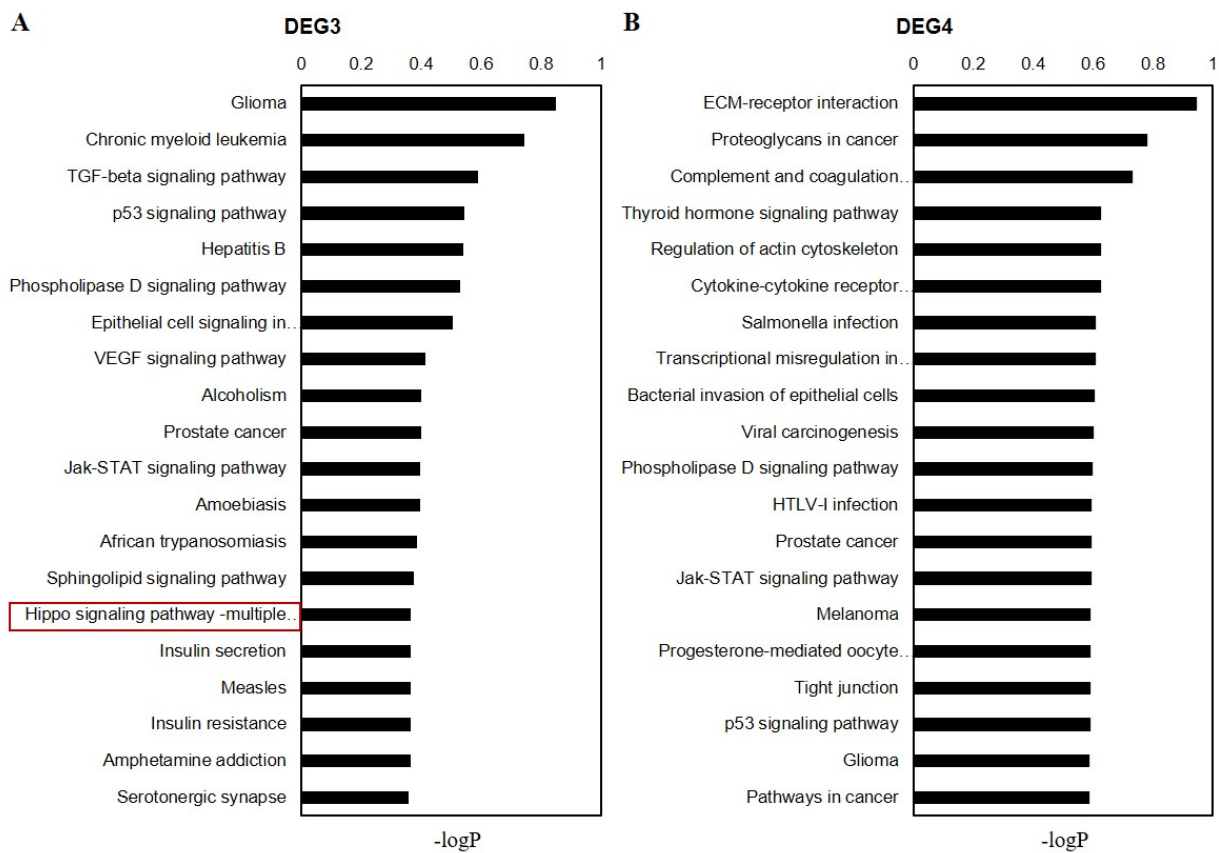


Figure S7 Pathway analysis of genes differentially expressed between HA and U251 cells.

Notes: Genes differentially expressed between nontreated HA and U251 cells (**A**) and radiation-treated HA and U251 cells (**B**) were subjected to ipathwayGuide online software for pathway analysis. Top twenty impact signaling pathway were listed.

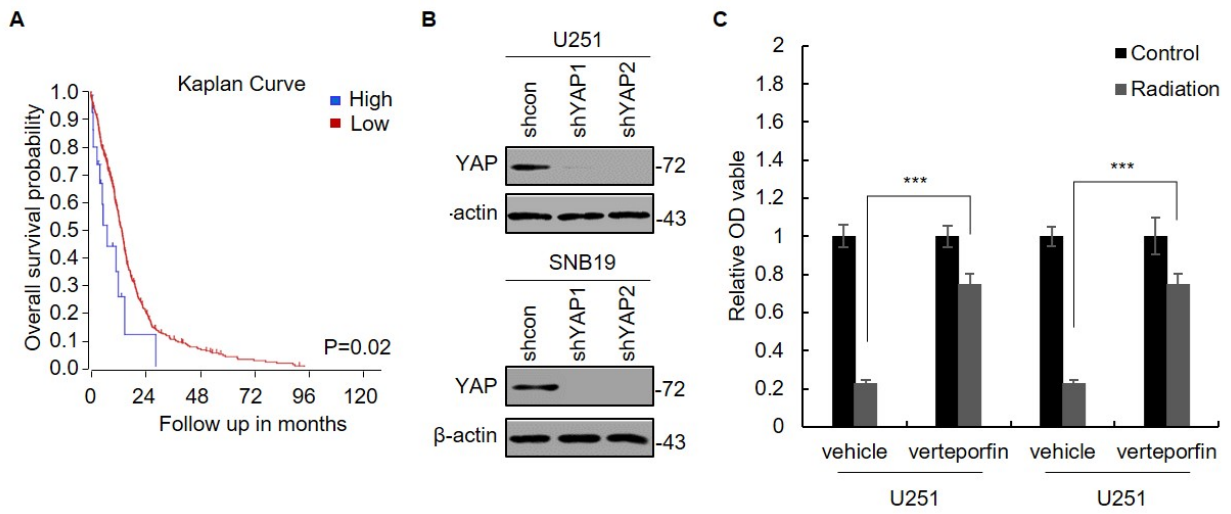


Figure S8 Suppression of YAP induces radiation-resistance of glioma cells.

Notes: (A) High expression of YAP predicts poor prognosis of patients with glioma. (B) Characterization of YAP-knockdown U251 and SNB19 cells. (C) Verteporfin reduced cytotoxic effect of radiation on U251 and SNB19 cells.

Supplemental table:

Table S1. The number of reads and high quality reads ratio.

Sample	Raw reads	Raw bases	Raw read pairs	Trim reads	Trim read pairs	Trim bases	Average length	Trim reads %	Trim bases %
HA	124,202,714	12,544,474,114	62,101,357	118,116,766	5,905,8383	11,536,800,280	97.7	95.1%	92.0%
HA-2Gy	102,304,860	10,332,790,860	51,152,430	82,337,002	41,168,501	7,285,391,087	88.5	80.5%	70.5%
U251	103,158,346	10,418,992,946	51,579,173	99,650,342	49,825,171	9,853,757,013	98.9	96.6%	94.6%
U251-2Gy	101,871,032	10,288,974,232	50,935,516	91,884,582	45,942,291	8,694,726,105	94.6	90.2%	84.5%

Table S2. Alignment of preprocessing and reference genome sequence

Sampl e	Total Reads	Total mapped	Multiple mapped	Unique mapped	Read-1	Read-2	Reads map to '+'	Reads map to '-'	Non-Splice reads	Splice reads	Reads Proper pair
HA	118,116,76	101,152,21	3,222,44	97,929,77	49,090,87	48,838,90	48,881,38	49,048,39	82,920,70	15,009,07	86,633,49
HA-2Gy	82,337,002	42,531,119	2,231,55	40,299,56	20,163,95	20,135,61	19,770,61	20,528,95	38,684,75	1,614,814	34,185,53
U251	99,650,342	54,789,048	2,094,78	52,694,26	26,390,48	26,303,77	26,302,98	26,391,28	43,055,97	9,638,295	42,031,52
U251-2Gy	91,884,582	49,067,481	2,023,83	47,043,64	23,566,67	23,476,97	23,276,55	23,767,09	40,282,28	6,761,358	41,168,62

Table S3 Primer sequences used in this study

Quantitative real-time reverse-transcription PCR			
CTGF	F: 5'-CAGCATGGACGTTTCGTCTG-3'	AREG	F: 5'-GTGGTGCTGTGCGCTCTTGATA-3'
	R: 5'-AACCACGGTTTGGTCCTTGG-3'		R: 5'-CCCCAGAAAATGGTTCACGCT-3'
GAPDH	F: 5'-GTCATCCAACGGGAATGCA-3'		
	R: 5'-TGATCGGTTACCGTGATCAAAA-3'		

Table S4. shRNAs used in this study

shRNAs	Sequence
shYAP#1	5'- TGCTGTTGACAGTGAGCGCAGGGTTCATAACAGGCATAAATAGTGAAGCCACAGATGTATTTATGCCT GTTATGAACCCTTGCCTACTGCCTCGGA -3'
shYAP#2	5'-

	TGCTGTTGACAGTGAGCGCGGAACTATTTGAACAGCTGAATAGTGAAGCCACAGATGTATTCAGCTGT TCAAATAGTTCCTTGCCTACTGCCTCGGA -3'
<i>shcon</i>	5'- CCTAAGGTTAAGTCGCCCTCGCTCGAGCGAGGGCGACTTAACCTTAGG -3'

Table S5. Antibodies used in this study.

<i>Antigen</i>	<i>Application</i>	<i>Supplier</i>	<i>Catalog #</i>	<i>Dilution</i>
YAP	immunoblotting	Abcam	Ab52771	2000
p-YAP	immunoblotting	Abcam	Ab76252	1000
Lamin2	immunoblotting	Abcam	Ab16048	2000
β-actin	IB immunoblotting	Abcam	Ab6276	1000

Table S6. LncRNAs regulated by radiation treatment in HA cells (DEG1).

<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>
CAPNS1	-30.43	TERF2	-25.25	SMIM7	-24.55	RP11-946L20.4	4.03
RP11-408I18.9	-29.77	PTRH2	-25.24	HDLBP	-24.55	SLX1A	4.08
FN1	-28.63	ITGA3	-25.21	PDE4DIP	-24.51	RP11-259O2.3	4.12
BANF1P1	-27.99	EIF4G2	-25.20	FTX	-24.49	FSIP2	4.25
PSMD12	-27.99	SPARC	-25.19	APOPT1	-24.49	AC007743.1	4.29
MACF1	-27.65	DST	-25.19	EPS15L1	-24.48	TMEM45A	4.32
FLNA	-27.59	CALD1	-25.17	FLNC	-24.47	XXbac- BPG154L12.4	4.41
RP11- 572P18.1	-27.42	PDE4DIP	-25.17	MYL6	-24.47	AC011747.4	4.45
ACTB	-27.34	COL4A2	-25.16	EIF2B5	-24.46	RP11-703G6.1	4.57
RP11-122C9.1	-27.26	EEF2	-25.13	RPL3	-24.46	CYSLTR1	4.58
VCL	-27.24	DNAJC19P5	-25.12	CLTC	-24.45	COL1A1	4.65
COL1A2	-27.21	COL1A2	-25.12	SCAND2P	-24.44	RP11-153M7.3	4.73
CTB-108O6.2	-27.03	FN1	-25.10	GART	-24.44	MIPOL1	4.83
MDM2	-27.03	ITGA10	-25.09	ANXA2	-24.44	RP11-47122.3	4.99
CTD- 2033D15.1	-26.96	DVL3	-25.09	TRIO	-24.43	LINC00887	6.16
FN1	-26.85	SVIL	-25.08	AC090602.2	-24.42	DDX6	11.00
FAT1	-26.76	RPL17P26	-25.07	REV3L	-24.42	TAF10	11.17
CTD- 3222D19.10	-26.55	AP1M1	-24.99	RP11-180I22.2	-24.42	ZNF521	11.97

COL1A2	-26.52	SVIL	-24.98	UBE2Q2P1	-24.41	CORO1B	12.14
MACF1	-26.47	RP11- 517B11.7	-24.97	HMGB1P24	-24.41	GTPBP10	12.21
THBS1	-26.37	AP2M1	-24.97	RP11-351I24.3	-24.41	RP11-15H20.5	12.39
GAPDH	-26.34	CANX	-24.97	DDX5	-24.41	TCTN1	12.88
CTD- 2145A24.3	-26.26	CLTC	-24.95	SLC35E1	-24.40	BCAS2	13.29
CTNNA1	-26.25	RNF213	-24.94	PDE4DIP	-24.40	MFSD2A	14.75
PKM	-26.17	EIF2B5	-24.94	TP53BP2	-24.40	WDR76	15.08
AC005776.1	-26.10	VMP1	-24.92	TBC1D9B	-24.38	BFAR	17.25
PSMD2	-26.09	2-Sep	-24.92	PSMD2	-24.38	MGAT4B	24.46
GPR89A	-26.06	SMIM7	-24.91	TRIO	-13.93	CTD-2587H19.1	24.46
TPM4	-26.05	ACOX1	-24.90	METTL16	-12.69	AKAP8	24.48
RP11- 416A14.1	-26.02	STAG3L2	-24.85	RP11- 1017G21.4	-3.01	BAIAP2	24.65
AP2M1	-26.00	JPX	-24.83	VIM-AS1	-3.00	PDE4DIP	24.66
COL8A1	-25.96	HDLBP	-24.83	FN1	-2.72	PDE4DIP	24.66
CALD1	-25.88	RP11- 640M9.2	-24.82	AP000769.7	-2.13	RP11-640M9.1	24.71
COL5A1	-25.88	CYFIP2	-24.80	RPS29	-2.07	HTN1	24.71
BOLA2B	-25.81	PMS2P5	-24.80	MYH9	-1.11	RP11-242F24.1	24.84
VIM	-25.78	RP11- 231C14.4	-24.79	BRD4	1.11	CPM	24.87
CALD1	-25.76	RP11- 479G22.7	-24.79	EPS15L1	1.33	ALG3	25.11
EIF4G1	-25.74	RP11- 148G20.1	-24.77	PARP2	1.53	PIWIL3	25.45
AC004257.3	-25.73	CHERP	-24.76	COL4A2	1.56	RP11-386I8.6	25.46
NOMO3	-25.68	C19orf44	-24.76	PARP2	1.70	OR6K1P	25.75
RNF213	-25.68	AC007283.4	-24.74	COL1A1	1.73	ENTHD2	25.80
LPP	-25.64	AC005785.2	-24.73	MIR663A	1.76	GTF2I	25.91
CALD1	-25.64	AP1M1	-24.70	MYH9	1.92	KCTD13	25.92
CTC-429P9.4	-25.63	AC133106.2	-24.66	RP11- 309L24.2	2.12	AD000685.1	25.93
DVL3	-25.58	RP11- 19G24.2	-24.65	COL1A1	2.16	ALG3	25.94
SMARCC2	-25.56	KIF22	-24.64	AKAP8L	2.30	RPS29	26.04
TCF25	-25.54	BCL9	-24.64	SLC38A10	2.42	AC003973.6	26.10
AC009133.12	-25.54	CHMP4A	-24.62	RP11-572O6.1	2.42	RP11-138I18.2	26.17
NBPF9	-25.53	RBM8A	-24.62	TRIM65	2.48	KCTD13	26.50
NMT1	-25.50	CTB-186G2.4	-24.61	RP11- 763B22.7	2.52	RP11-347C12.3	26.53

TTC3	-25.49	TADA2A	-24.58	COL5A1-AS1	2.55	RP11-654A16.1	26.61
GTF2I	-25.48	PARP2	-24.58	MIR663A	2.92	FLNA	27.18
PSMD2	-25.44	RP6-206117.3	-24.57	COL4A2	3.01	HSPH1	27.28
FBN1	-25.44	INO80E	-24.57	CHRD	3.12	RP11-864I4.3	27.60
RP11-640M9.1	-25.36	SNHG9	-24.56	VIM	3.30	CTD-2340E1.2	27.84
AC002454.1	-25.25	PSMD2	-24.56	EPS15L1	3.71		

Table S7. LncRNAs regulated by radiation treatment in U251 cells (DEG2).

<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log2(FC)</i> <i>HA2Gy/HA</i>
SCARNA22	-30.0155	HSPA8	-23.3263	PARP2	3.10556	FASN	23.68874
DDX5	-29.9317	ZWILCH	-23.3138	CTD- 2328D6.1	3.13144	AC006483.5	23.74222
PSMD12	-27.6677	PSMD2	-23.2836	ANKRD30BL	3.43068	CTB-186G2.4	23.74438
ATP5O	-26.8594	GPR89A	-23.2514	MIR663A	3.52212	POLR3C	23.81528
RPS23P8	-26.4378	YPEL3	-23.2387	LINC00273	4.43776	RP11-162D9.3	23.82959
USMG5P1	-25.74	AL590762.11	-23.1821	MFSD9	13.0223	ATP5J2-PTCD1	23.90626
RPS29	-25.3528	TBL2	-23.1494	OAZ1	13.4426	RP11-184D12.1	23.95601
RAB8A	-25.3249	RNF207	-23.0443	PLXNA2	13.7878	ABCF3	23.96374
2-Sep	-25.3249	RPL13	-23.0322	RHPN2	13.854	GABPB1	24.00406
RPLP0	-25.3177	TBC1D9B	-23.0288	BTN3A1	14.1938	UBR4	24.06994
PSMD2	-24.8473	VPS33B	-23.0192	ABHD16A	14.7986	UNC13D	24.12676
RP3-462E2.5	-24.8204	MRPL38	-23.004	HEXB	23.05634	RP11-865I6.2	24.25135
WDR45B	-24.5878	KIAA1191	-14.6666	VWA5B2	23.13719	CTD-2050E21.1	24.26486
GTF2I	-24.0057	AC007620.3	-14.0265	AC027269.2	23.2164	AC115522.3	24.27991
RP11-420K8.2	-23.9733	CASP8AP2	-12.4365	RFC2	23.24102	MYH9	24.30176
EEF1G	-23.9163	EEF1A1P5	-4.14512	PDE4DIP	23.24506	CTA-398F10.2	24.63527
ANXA2	-23.7862	PARP2	-2.59873	EPS15L1	23.26094	RP11-455F5.4	24.7512
ALG3	-23.7836	PSMD2	-1.6855	AC009093.1	23.27225	EIF2B5-AS1	24.80933
DPYSL3	-23.744	ABCF3	-1.46869	EIF4A1	23.29967	EMC1	24.93209
DONSON	-23.7107	AP000769.7	1.49345	EIF2B5	23.32114	RP1-122K4.3	25.02645
ORAOV1	-23.6768	RP5- 1125K23.1	1.52442	LMNA	23.36141	CTD- 3222D19.10	25.03803
ABCF3	-23.6492	PARP2	1.73633	TRIM65	23.41965	UBR4	25.28273
SRP68	-23.5887	ABCF3	1.82254	HIRIP3	23.41976	MYH9	25.84102
RP11- 416A14.1	-23.5108	AC011747.4	2.3247	ZWILCH	23.44719	RP11-644F5.16	25.95554
AP2M1	-23.424	RP11-703G6.1	2.51541	RP11-87N3.6	23.54499	WDR1	28.37899
BANF1P1	-23.3787	ALDOA	2.63702	FLII	23.62151		
RP11-666A1.4	-23.3604	RP11-	3.05309	BMP2KL	23.65707		

		153M7.3					
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Table S8. IncRNAs differentially expressed between HA and U251 cells under normal condition (DEG3)

<i>symbol</i>	<i>log₂(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log₂(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log₂(FC)</i> <i>HA2Gy/HA</i>	<i>symbol</i>	<i>log₂(FC)</i> <i>HA2Gy/HA</i>
MLPH	-29.2015	ILVBL	-24.7192	ACOX1	-23.7864	CTC-429P9.4	24.10049
MT1L	-28.4803	APP	-24.6827	SSR3	-23.7815	HEXB	24.13299
CTD-2231H16.1	-28.4733	TSEN15P2	-24.6696	EFTUD2	-23.7813	SQSTM1	24.20294
FLNA	-28.1115	RBM8A	-24.5926	POLR3F	-10.2467	NIP7	24.22725
MYH9	-27.9512	POLR3C	-24.5607	RBM38	-10.1846	SMIM7	24.24529
SPOCD1	-27.7548	ARL8B	-24.553	MICAL2	-5.63051	VPS33B	24.27437
MYH9	-27.5076	AC093375.1	-24.5323	MYH9	-4.66108	TBC1D9B	24.28278
FAT1	-27.2818	AC068831.3	-24.5248	FAT1	-3.33572	CD44	24.28678
KIAA1755	-27.134	CTNNA1	-24.5239	CTD-2033D15.1	-3.153	RNF207	24.29753
CTD-3222D19.10	-27.0733	NOTCH3	-24.5183	AP000769.7	-3.00381	VWA5B2	24.29759
COL4A2	-26.8118	FXR2	-24.5103	AC005776.1	-2.65238	HEXB	24.36722
AC112721.2	-26.6869	RP4-565E6.1	-24.4907	FLNA	-2.50678	PIH1D1	24.41431
FAT1	-26.4584	VCL	-24.4843	AC113189.5	-2.47135	MRPL38	24.45645
AC004702.2	-26.3229	ECH1	-24.4812	MIR663A	-2.36666	CCT7P2	24.49198
ZSCAN23	-26.2232	STX1A	-24.4794	CTB-51J22.1	-1.93264	YPEL3	24.49355
RP11-757F18.5	-26.1742	DYNC1H1	-24.4787	AP2M1	-1.84344	KIAA0430	24.51462
CALD1	-26.165	ENC1	-24.4597	CRYZL1	-1.72518	PSMD2	24.53784
CTC-429P9.4	-26.158	MOK	-24.4168	AC004257.1	-1.46716	KCTD13	24.55584
ITGA3	-26.0399	RP11-33N16.2	-24.4012	MAPK3	-1.45407	RP11-666A1.4	24.61527
TTC3	-26.0179	RP11-426C22.6	-24.3727	AP1M1	-1.34573	RP11-654A16.1	24.6315
ITGA3	-25.9098	ELN	-24.3606	MIR663A	-1.11117	GATAD2A	24.6812
MYH9	-25.8099	SAT2	-24.3092	CTD-2013N17.4	-1.1023	IFT80	24.75091
RP11-1017G21.3	-25.801	CRYZL1	-24.3058	ZNF29P	1.06187	COL21A1	24.75163
KMT2A	-25.7313	EEFSEC	-24.2791	LRR1	1.1036	PXDN	24.78932
SPARC	-25.7148	EFEMP2	-24.2787	EIF4G1	1.21695	TFRC	24.8536
LINC00982	-25.7018	RP11-562A8.5	-24.2779	RP11-666A1.3	1.23804	DDX5	24.89092
CALD1	-25.6969	ACTG1	-24.2627	POLR2H	1.27504	RP1-309F20.3	24.91432
RPL7L1P9	-25.6942	TBL2	-24.2596	PARP2	1.61236	RP4-535B20.1	24.92749
COL4A2	-25.6841	LMNA	-24.2489	ALDOA	1.68529	HEXB	24.95792
DVL3	-25.6106	NOTCH3	-24.2388	RPL17P40	1.69656	DRG2	24.98775

PDE4DIP	-25.5274	PRPF8	-24.2003	AP000226.9	1.7079	DPYSL3	24.99824
ACOX1	-25.4248	RP11-455F5.4	-24.1812	LRR1	1.72236	ALG3	25.03783
TPM4	-25.353	IGF2BP3	-24.167	AC113189.5	1.74535	AP000705.8	25.18554
RP11-479G22.7	-25.3009	ALG3	-24.1643	RHOQP1	1.81572	RP11-144N1.1	25.1897
AC005785.2	-25.2563	RUVBL1	-24.1559	ALG3	2.34809	ATM	25.1985
MYLK	-25.2004	MRTO4	-24.1474	PSMD2	2.67755	AC005838.2	25.22047
KIF22	-25.1687	GTF2I	-24.1281	ABCF3	2.79102	BRD4	25.22907
RP11-490G2.2	-25.1628	LIMK1	-24.0878	PARP2	2.83259	ALG3	25.25269
CHMP4A	-25.1489	CTD- 2562J15.4	-24.0863	RP11-778D9.4	2.93158	GTF2I	25.25969
CTB-186G2.4	-25.1333	SAT2	-24.0787	POLR2H	2.96147	EIF2B5	25.27774
ITGAV	-25.1226	ILVBL	-24.0735	ABHD11	3.09964	BTF3L4P4	25.33309
STX1A	-25.0993	TP53BP2	-24.0569	ANXA2	3.42844	RFC2	25.46723
VCAN	-25.0821	WBSCR22	-24.0507	ALDOA	3.57036	EIF3FP3	25.55061
RNF213	-25.039	FAM126A	-24.0417	RPL4	3.85583	RP11-479I1.4	25.658
OGT	-25.0353	TENC1	-24.0398	NEFL	5.65781	FUBP1	25.73963
TRIO	-24.9507	SIL1	-24.0042	UBXN4	12.8754	DOCK5	25.79471
AC090602.2	-24.9469	RP11- 344E13.1	-23.9985	KDM3B	13.0363	WDR45B	25.84205
UBE2Q2P1	-24.9381	MED13	-23.9794	HNRNPH1	23.79187	CTC-471F3.4	25.85342
CBR4	-24.9206	ZMYM3	-23.9758	GART	23.82223	EIF2B5	25.86542
TP53BP2	-24.9205	APLP2	-23.9738	RPS2	23.8296	PSMD2	26.10155
PIAS3	-24.8931	6-Mar	-23.9539	ANXA2	23.83998	PES1P1	26.39679
PSAP	-24.8851	YPEL3	-23.9527	NONO	23.85205	TUFMP1	26.53343
HDLBP	-24.8784	C5orf45	-23.9293	EIF2B5	23.86454	RPLP0	26.573
WDR20	-24.8576	EPS15L1	-23.9229	TADA2A	23.88655	RAB8A	26.57901
PRPF40B	-24.848	RP4-565E6.1	-23.9194	LGALS1	23.89706	RPS29	26.60707
KIAA0430	-24.8124	RP13- 766D20.2	-23.8998	HAUS1	23.92448	RP11- 281P11.1	26.88395
CTA-797E19.1	-24.8079	SNX14	-23.8907	PRC1	23.92737	AL022344.2	26.92266
GANAB	-24.767	CYFIP2	-23.8905	PDCD2L	23.94498	USMG5P1	26.99399
MACF1	-24.7624	POLR3C	-23.8814	RPL8	23.94548	ACTB	27.07713
NBPF9	-24.7552	ELN	-23.8779	2-Sep	23.94772	RP11- 123O22.1	27.10826
PGM3	-24.7444	SLC43A2	-23.8711	AP005482.1	24.01806	RP11- 698N11.2	27.18091
AP001439.2	-24.7372	WDR20	-23.8678	SERF2	24.04399	RPS2P55	27.4532
COL4A2	-24.7326	RUNX1	-23.8283	APLP2	24.05669	RP11- 734I18.1	27.84075
SLC17A9	-24.73	PDE4DIP	-23.8082	API5	24.07051	ATP5O	28.11362
CTD-2334D19.1	-24.7263	ELN	-23.797	AC113189.5	24.07155		

Table S9. lncRNAs differentially expressed between HA and U251 cells under normal condition (DEG4).

<i>symbol</i>	<i>log2(FC)</i> HA2Gy/HA	<i>symbol</i>	<i>log2(FC)</i> HA2Gy/HA	<i>symbol</i>	<i>log2(FC)</i> HA2Gy/HA	<i>symbol</i>	<i>log2(FC)</i> HA2Gy/HA
CTD-2231H16.1	-28.2181	PAN3	-14.1816	RFC2	24.16873	COL21A1	24.88169
CPNE7	-27.8603	MRPS16	-12.3834	ABHD11	24.18164	MATR3	24.89958
RP5-1057J7.7	-26.9442	TCEA1	-12.3534	RAB8A	24.20729	AC005838.2	24.92428
RP11-86414.3	-26.8267	CD63	-11.8018	RP11-231C14.4	24.2635	EMC1	24.92677
HSPH1	-26.5167	AC123886.2	-5.544	AP2M1	24.28745	EIF4G1	24.97057
ITGA3	-26.4081	TFPI	-5.19127	MACF1	24.3554	PSMD2	24.97591
COL6A1	-26.3143	PKNOX2	-4.82487	AC005776.1	24.39108	ITGA3	25.00214
RP11-431N15.2	-26.11	COL4A2	-4.37694	RPL31P7	24.4062	CTD-3222D19.10	25.03808
RP11-654A16.1	-25.8393	MYH9	-3.49144	MACF1	24.40914	AC009133.12	25.05195
RPS29	-25.2727	AD000685.1	-3.31155	ABHD11	24.4444	PPP4C	25.26687
COL4A2	-25.2431	SLX1A	-3.08958	PKM	24.46281	UBR4	25.2808
SMIM7	-25.1991	AKAP8L	-2.59452	N4BP2L2	24.46434	PSMD2	25.32212
TBC1D9B	-25.1878	COL4A2-AS1	-2.29782	ZNF286A	24.49903	PES1P1	25.35494
ALG3	-25.1726	KCTD13	-2.08093	FLCN	24.53618	GTF2I	25.38061
GTF2I	-25.1383	EPS15L1	-1.83786	PMS2P5	24.5381	TUFMP1	25.44116
RP11-390M11.1	-25.059	GTF2I	-1.83462	AC004257.3	24.55405	INO80E	25.50898
VIM	-24.8474	AP1M1	-1.7975	RPEP4	24.57506	MRTO4	25.73303
DVL3	-24.7793	RP4-778K6.1	-1.58012	MSMP	24.61587	SNHG9	25.8286
CTB-51J22.1	-24.6695	MYH9	-1.53901	LRR1	24.64955	EIF4G1	25.90119
RP11-46H11.12	-24.5855	RP11-572O6.1	-1.50144	MACF1	24.66835	CTC-429P9.4	25.94586
ELN	-24.455	ILVBL	1.26417	EEF2	24.72192	FAM129B	26.02729
POLR3GL	-24.3864	RHOQP1	1.44822	CLTC	24.73609	LINC00052	26.04174
ZSCAN2	-24.376	RPS29	2.7986	EIF4G1	24.77778	DVL3	26.34607
ALG3	-24.3463	UNC13D	4.8658	RP11-469N6.1	24.79228	GAPDH	26.80652
CD302	-16.4904	TRIO	12.1751	AP1M1	24.79631	AC011330.6	27.45099
RAB7L1	-15.9894	DNTTIP2	16.7251	RP11-317P15.4	24.834	SNORD3B-2	27.64554
CDKN1A	-15.598	ILVBL	24.15179	SYNE2	24.8575	RPS2P55	27.74419