

Supplementary TABLE. *Hprt* gene mutations of UV-C-exposed *Rev1^{B/B}*-254 and Wild type (WT) ES cells

Position ^A	Mutation	5'-sequence- 3' ^B	Amino acid change	# of mutants		Strand ^C
				WT	<i>Rev1^{B/B}</i>	
Single base pair substitutions at dipyrimidine sites						
<i>Transitions</i>						
74	GC > AT	TAC <u>C</u> TAA	Pro > Leu	3	1	NTS
113	GC > AT	TTC <u>C</u> TCA	Pro > Leu	3	3	NTS
119	GC > AT	ATG <u>G</u> ACT	Gly > Glu	2		TS
145	GC > AT	AGAC <u>T</u> TG	Leu > Phe	1	1	NTS
202	GC > AT	GTG <u>C</u> TCA	Leu > Phe	1		NTS
208	GC > AT	AAG <u>G</u> GGG	Gly > Arg	1	1	TS
325	GC > AT	GAT <u>C</u> AGT	Gln > Stop	1		NTS
400	GC > AT	GTT <u>G</u> AAG	Glu > Lys	1	1	TS
463	GC > AT	AGC <u>C</u> CCA	Pro > Ser	1		NTS
508	GC > AT	TCT <u>C</u> GAA	Arg > Stop		1	NTS
527	GC > AT	GGC <u>C</u> AGA	Pro > Leu	1		NTS
538	GC > AT	GTT <u>G</u> GAT	Gly > Arg		2	TS
539	GC > AT	TTG <u>G</u> ATT	Gly > Glu		1	TS
544	GC > AT	TTT <u>G</u> AAA	Glu > Ile	1	1	TS
551	GC > AT	TTC <u>C</u> AGA	Pro > Leu		1	NTS
599	GC > AT	TCAG <u>G</u> GA	Arg > Lys	5	2	TS
601	GC > AT	AGG <u>G</u> ATT	Asp > Asn	3	3	TS
635	GC > AT	CTG <u>G</u> AAA	Gly > Glu	5	2	TS
7	AT > GC	CCG <u>A</u> CCC	Thr > Ala	1		TS
146	AT > GC	GACT <u>T</u> GC	Leu > Pro	1		NTS
440	AT > GC	TGCT <u>T</u> TC	Leu > Pro	1		NTS
<i>Transversions</i>						
544	GC > TA	TTT <u>G</u> AAA	Glu > Stop	1		TS
550	GC > TA	ATT <u>C</u> CAG	Pro > Thr	1		NTS
29	AT > TA	TGAT <u>T</u> AG	Ile > Asn	1		NTS
62	AT > TA	ATT <u>T</u> GTT	Leu > Stop	1		NTS
125	AT > TA	TGAT <u>T</u> AT	Ile > Asn	1		NTS
374	AT > TA	CTT <u>T</u> AAC	Leu > Stop	3		NTS
548	AT > TA	AAAT <u>T</u> CC	Ile > Asn	1		NTS
637	AT > TA	GGAA <u>A</u> AG	Lys > Stop	1		TS
643	AT > TA	GCC <u>A</u> AAT	Lys > Stop	1		TS
656	AT > TA	CCTA <u>A</u> GA	Stop > Leu	1		TS
487	AT > CG	AGCT <u>T</u> GC	Leu > Val	1		NTS
Double base pair substitutions at dipyrimidine sites						
196/197	AT > TA	CTCT <u>G</u> TGT	Cys > Ser		1	NTS
	GC > TA		Cys > Phe			NTS
211/212	GC > TA	GGG <u>G</u> GCTA	Gly > Cys		1	TS

	GC > AT		Gly > Asp			TS
382/384	AT > GC	GGAA <u>AG</u> AA	Lys > Glu	1		TS
	GC > AT		no change			TS
568/569	GC > AT	GTTGGATA	Gly > Arg	1		TS
	GC > AT		Gly > Glu			TS
569/570	GC > AT	TTGGATAT	Gly > Glu		1	TS
	AT > TA		no change			TS
569/571	GC > AT	TTGGATAT	Gly > Glu		1	TS
	AT > TA		Tyr > Asn			TS
580/582	GC > AT	CTTGACTA	Asp > Asn		1	TS
	GC > TA		Asp > Glu			NTS
600/601	GC > AT	CAGGGGAT	no change	1	1	TS
	GC > AT		Asp > Asn			TS
601/603	GC > AT	AGGGATTT	Asp > Asn	1		TS
	AT > TA		Asp > Glu			NTS
632/634	GC > AT	AAACTGGA	Thr > Ile	1		NTS
	GC > TA		Gly > Stop			TS
Single base pair substitutions at non-dipyrimidine sites						
<i>Transversions</i>						
584	AT > CG	ACTATAA	Tyr > Ser		1	
611	AT > TA	ATCACGT	His > Leu		1	
617	GC > TA	TTTGTGT	Cys > Phe		1	
Frameshift mutation						
472	+T	TGG-TTA			1	
Double basepair substitutions at non-dipyrimidine sites						
183/185	GC > AT	TCACATTG	No change	1		
	-T					
406/407	AT > TA	GATATAAT	Ile > Leu		1	
	AT > TA		Ile > Lys			
Others						
Splice ^D				28	30	
No <i>Hprt</i>					8	
PCR						
No				2	1	
mutation						

^A Position 1 at adenine of the translational start codon ATG.

^B Non-transcribed strand. Nucleotide with underscore is affected.

^C Pyrimidine dimer-containing strand. NTS, non-transcribed strand; TS, transcribed strand.

^D Mutants lacking one or more exons in the *Hprt* mRNA, probably due to mutations affecting correct splicing