Supporting information for Ogi *et al.* (2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.223377899

Table 2. Mutation spectrum at the *Hprt* locus in wild-type and *Polk*$^{-/-}$ ES cells

Mutant no.*	Position†	Mutation‡	Sequence§	Purine strand	Amino acid change
Polk$^{+/+}$ (TT2)					
25-56	134	G→ A	cagGtta	NT	G16D
25-2	152	A→ G	caaAaca	T	F22S
20-10	175	**G→ T**	gccGagg	NT	E30STOP
19-1	204	A→ T	tccAtga	T	H39Q
*19-6	206	G→A	atgGact	NT	G40E
25-55	208	G→ C	tcaGtcc	T	L41V
*12-14	217	G→ C	atgGaca	NT	D44H
25-26	217	**G→ T**	atgGaca	NT	D44Y
25-54	218	A→ G	tggAcag	NT	D44G
25-15	284	G→A	tctGtgt	NT	C66Y
25-52	295	G→ A	aagGggg	NT	G70R
14-2	318	**G→T**	cagGtca	T	D77E
*14-9	319	G→ A	gcaGgtc	T	No change
14-6	319	G→ C	gcaGgtc	T	L78V
25-19	320	A→G	cgaAggt	T	L78P
20-1	328	A→ G	tgtAatc	T	Y81H
*14-9	457	A→G	tcaActt	NT	T124A
14-1	479	A→ G	atcAaga	T	L131S
25-16	499	**G→ T**	attGaca	NT	D138Y
25-10	551	G→ C	ttgGggc	T	P155R
25-51	573	G→ C	caaGctt	T	S162R
25-8	583	A→ G	gtgAaaa	NT	K166E
15-1	608	A→ C	gatAcag	NT	Y174S
15-6	635	A→ G	ggaAttt	T	I183T
25-18	649	**G→ T**	tttGttg	NT	V188F
25-17	656	**G→ T**	ttgGata	NT	G190V
6-4	688	**G→ T**	aggGatt	NT	D201Y
15-9	713	**G→T**	ttaGtga	NT	S209I
25-52	713	**G→ T**	ttaGtga	NT	S209I
*19-6	717	A→ G	tgaAact	NT	No change
25-13	722	G→A	ctgGaaa	NT	G212E
7-2	274	-1G	attGtgg	NT	Frameshift
15-2	586-587	G2 > G1	aaaGGacc	NT	Frameshift
25-9	667	-1G	cttGact	NT	Frameshift
25-7	?	v			Deletion of 91 bp at 3′ of exon 1
16-2	?				Complete deletion of exons 2 and 3
20-7	?				Complete deletion of exon 3
25-1	?				Deletion of 111 bp at 3′ of exon 3
25-5					Complete deletion of exons 7 and 8
*12-14	?				SINE insertion in exon 2
Polk$^{-/-}$ (A71)					
30-4	127	**G→ T**	gatGaac	NT	E14STOP
30-1	175	**G→ T**	gccGagg	NT	E30STOP
23-4	183	**G→ T**	tttGgaa	NT	L32F
30-6	190	G→ A	aaaGtgt	NT	V35M

30-38	200	**G→ T**	tgaGgaa	T	P38H
23-14	200	G→ A	tgaGgaa	T	P38L
30-10	205	**G→T**	catGgac	NT	E40STOP
18-3	217	**G→ T**	atgGaca	NT	D44Y
30-7	221	**G→ T**	acaGgac	NT	R45M
*17-2	239	G→ C	ctcGaga	NT	R51P
30-23	253	**G→ T**	aagGaga	NT	Q56STOP
17-5	259	**G→ T**	atgGgag	NT	G58STOP
30-18	265	**G→ T**	gatGgcc	T	H60N
30-2	270	**G→ T**	aatGtga	T	H61Q
*17-7	278	**G→ T**	aggGcca	T	A64D
8-5	295	**G→ T**	aaggGggg	NT	G70W
30-40	298	**G→ T**	gggGgct	NT	G70C
30-34	316	**G →T**	gctGacc	NT	E77Y
30-20	382	A→ G	ataAaat	T	P99S
17-6	449	A→ G	atgAtct	NT	D121G
30-30	480	**G→ T**	cttGatt	NT	L131P
*30-13	481	A→ C	ttgAttg	NT	I132L
30-12	506	**G→ T**	ctgGtaa	NT	G119V
30-28	516	**G→ T**	aatGcaa	NT	M143I
30-8	551	**G → T**	ttgGggc	T	P155H
*30-13	564	**G → T**	taaGgtt	NT	K159N
30-24	568	**G→ T**	gttGcaa	NT	A161S
30-32	625	**G → T**	gttGgat	NT	G180STOP
20-2	649	**G →T**	tttGttg	NT	V188F
*17-7	652	**G →T**	gttGttg	NT	V189F
30-22	655	**G → T**	gttGgat	NT	G190STOP
*18-2	666	A →G	gtcAagg	T	No change
21-8	686	G →T	tcaGgga	NT	R200M
18-9	687	**G →T**	cagGgat	NT	R200S
18-4	713	**G →T**	ttaGtga	NT	S209I
8-6	291	-1G	cttGagc	T	Frameshift
18-5	327-328	A2 → A1	tgtAAtcc	T	Frameshift
30-3	420-424	G5 →G4	aacGGGG Gaca	NT	Frameshift
18-6	721-722	G2 → G1	actGGaaa	NT	Frameshift
21-2	727	-1G	aaaGcca	NT	Frameshift
*17-2	?				Complete deletion of exon 2
*18-2	?				Complete deletion of exons 2 and 3
17-4	?				No mutation found

NT, nontranscribed strand; T, transcribed strand; boldface, G→T transversion, the most frequent type of B[*a*]P-induced mutation. ?, for large deletions, the position where the large alteration had occurred was not determined exactly.

*A mutant in which multiple mutations were found.

[†]The base position is numbered according to the GenBank entry J00423.

[‡]The strand containing purine at the altered site.

[§]Uppercase letters indicate the base or sequence altered by the mutation and lowercase letters indicate the surrounding sequence.