

Supplementary Information 7: Chromosome coordinates and mutations

Table A Chromosome Coordinates of Promoter Fragments

Code	Contig	Start	Stop	Direction
100	AC078910.4.99755.114023	9493	9816	F
101	AP000926.5.1.196973	39985	40264	R
104	AL162590.15.1.98271	24390	25282	F
106	AC005326.1.1.122130	22551	23215	F
110	AC107219.5.1.187431	88019	89215	R
112	AF134726.1.1.180283	90277	90509	R
113	AC107219.5.1.187431	88019	88490	R
121*	AF134726.1.1.180283	90277	90582	R
122*	AC005326.1.1.122130	22551	23215	F
127	AC009004.6.1.39608	25591	26138	F
136	AC009004.6.1.39608	25948	26138	F
137	AL162590.15.1.98271	24957	25282	F
140 [†]	AF134726.1.1.180283	90277	90582	R
152*	AL137142.20.1.113850	62895	63071	R
154*	AC009004.6.1.39608	25948	26138	F
158*	AL162590.15.1.98271	24957	25282	F
160	AC078910.4.99755.114023	9493	9739	F
162*	AP000926.5.1.196973	39985	40264	R
163*	AP000926.5.1.196973	39985	40264	R
188	AL137142.20.1.113850	62895	63391	R
197	AC078910.4.99755.114023	9347	9816	F
198	AP000926.5.1.196973	39985	41137	R
199	AL137142.20.1.113850	62895	63071	R

according to Ensembl version 7.29a

* mutated as detailed in Table B

[†] corresponding sequence for *HSP70-1* is AF134726.1.1.180283: 102478-102783 (R) and is identical at 281/305 nucleotides

Supplementary Information 7 continued: Chromosome coordinates and mutations

Table B Introduced Mutations

Code	Sequence Targeted	Mutations Introduced
121*	CCCTGGAATATTCCCG	CCgTGcAATATTgCCc
122 [†]	TGATGAAAC	TGcgctcAC
152	TTCTGGAAA	gaCTGtctA
154	CTCTGGAAG	gaCTGtctG
158	CTCCAGAAG	gaCCA tctG
162	TTCTGGAAG	gaCTGtctG
163	TTCTGGAAG	TTgTGcAAG

* mutated in accordance with Kamano and Klempnauer (1997)

[†] mutated in accordance with Siu et al. (2001)