

Somatic Mutation	Residue	WT AA	Mutant AA	Sector	Compensating Mutation	Residue	WT AA	Mutant AA	Sector	Number of Sequences with Compensatory Mutation Pair
	180	Glu	Gln	1		49	Asn	Gap	0	26
	200	Asn	Gap	1		56	Thr	Asp	0	25
	200	Asn	Gap	1		56	Thr	Gap	0	17
	200	Asn	Gap	1		59	Asn	Thr	0	23
	200	Asn	Gap	1		108	Val	Gly	0	36
	200	Asn	Gap	1		291	Val	Pro	0	35
	220	Tyr	His	1		108	Val	Gly	0	15
	220	Tyr	His	1		291	Val	Pro	0	18
	235	Asn	Ser	1		100	Val	Thr	0	21
	240	Ser	Gly	1		81	Thr	Pro	0	22
	240	Ser	Gly	1		111	Met	Ile	0	24
	270	Phe	Val	1		76	Met	Thr	0	18
	270	Phe	Val	1		80	Ser	Pro	0	27
	270	Phe	Val	1		81	Thr	Pro	0	27
	270	Phe	Val	1		94	Gln	Ile	0	19
	270	Phe	Val	1		111	Met	Ile	0	29
	270	Phe	Val	1		131	Asp	Lys	0	29
	363	Arg	Lys	5		73	Cys	Ser	0	17
	363	Arg	Lys	5		73	Cys	Gap	0	15
	363	Arg	Lys	5		76	Met	Thr	0	21
	363	Arg	Lys	5		80	Ser	Pro	0	35
	363	Arg	Lys	5		81	Thr	Pro	0	26
	363	Arg	Lys	5		90	Val	Met	0	15
	363	Arg	Lys	5		94	Gln	Ile	0	19
	363	Arg	Lys	5		111	Met	Ile	0	23
	363	Arg	Lys	5		111	Met	Leu	0	20
	363	Arg	Lys	5		131	Asp	Asn	0	23
	363	Arg	Lys	5		131	Asp	Lys	0	22

**Table 1.** Compensatory Mutation Candidates. This list of compensatory mutation candidates was generated from the coevolution matrix and somatic mutation list. There is no mutation in sector 2, 3, 4, or 6 that is compensated by other mutations, based on the criteria we used for screening.