

SUPPORTING INFORMATION

The Fanconi Anemia Protein, FANCG, Binds to the ERCC1-XPF Endonuclease via its Tetratricopeptide Repeats and the Central Domain of ERCC1

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Table S1: Primers used to amplify cDNAs for the domains of ERCC1

ERCC1 constructs (residues)	domains	primer sequences (5'-3')
1-297	full-length	GCGCGAATTCATGGACCCTGGGAAGGACAA GCGCCTCGAGTCAGGGTACTTTCAAGAAGG
1-96	N-terminal	GCGCGAATTCATGGACCCTGGGAAGGACAA CTCGAGTCATGCCCCGGGTTTCAGGGCCT
88-297	central+HhH ₂	GAATTCCCAACCAGGCCCTGAAACC GCGCCTCGAGTCAGGGTACTTTCAAGAAGG
120-220	central(-Nt) ^a	GAATTCCCCTGGGAATTTGGCGACGT CTCGAGTCACGCTGGTTTCTGCTCATAGG
214-297	HhH ₂	GAATTGCCTATGAGCAGAAACCAGC GCGCCTCGAGTCAGGGTACTTTCAAGAAGG

^aThe central domain of ERCC1 minus its N-Terminal (-Nt)

Table S2: Primers used to amplify the cDNAs of TPR motifs mutated in FANCG

TPR motif mutated in FANCG	mutation	primer sequences (5'-3')
TPR1	G216Q	CAACTCCAGGAGCTGATCACAGG TTGGCGGTAGGCAAATGCTG
TPR2	G253Q	CAGTCCTGTCACCGTAAGATGGGAAATC CAGTGCTGTGTACACCTGGACCA
TPR3	A351Q	CAGAGCAGGTGCCTACAGACGGG TAGTATGTGCTTGGTCTGGCTCTG
TPR5	G460Q	CAGCAGGCCTGGGTTCAACTGGG CTGAAGCAGGTGGGTGGCAGAG
TPR6	G521Q	CAGCTGGAATGGGTAGCCAGCGG ACGACTAATTAGGGCGGCTGCC
TPR7a	R563E	GAGAGGGATGAGGCCACTGCACT ATCTAGCCTCTTCAGAGTCTGAAG
TPR7b	A567Q	CAGACTGCACTCTGGTGGAGGCT CTCATCCCTCCGATCTAGCCTC

Table S3: Wild-type and mutated TPR motifs in human FANCG ¹

TPR motif in FANCG	wild-type/ mutated	sequence (5'-3') ^a
TPR1	wild-type	209 - TAFAYRQGLQELITGNPDKALSSLHEAASGLCPR - 242
	mutated	209 - TAFAYRQQLQELITGNPDKALSSLHEAASGLCPR - 242
TPR2	wild-type	246 - VQVYTALGSCHRKMGNPQRALLYLVAALKEGSAW - 279
	mutated	246 - VQVYTALQGSCHRKMGNPQRALLYLVAALKEGSAW - 279
TPR3	wild-type	344 - SQTKHILASRCLQTGRAGDAAEHYDLLALLLDS - 377
	mutated	344 - SQTKHILQSRCLQTGRAGDAAEHYDLLALLLDS - 377
TPR5	wild-type	453 - SATHLLQGQAWVQLGAQKVAISEFSRCLELLFRA - 486
	mutated	453 - SATHLLQQAWVQLGAQKVAISEFSRCLELLFRA - 486
TPR6	wild-type	514 - AAALISRGLEWVASGQDTKALQDFLLSVQMCPGN - 547
	mutated	514 - AAALISRQLEWVASGQDTKALQDFLLSVQMCPGN - 547
TPR7a	wild-type	548 - RDTYFLLQTLKRLDRRDEATALWWRLEAQTKGS - 581
	mutated	548 - RDTYFLLQTLKRLDERDEATALWWRLEAQTKGS - 581
TPR7b	wild-type	548 - RDTYFLLQTLKRLDRRDEATALWWRLEAQTKGS - 581
	mutated	548 - RDTYFLLQTLKRLDRRDEQATALWWRLEAQTKGS - 581

^a Conserved residues are highlighted in grey and mutated residues are highlighted in black. These TPR motifs were identified in FANCG by Blom et al. (38).