

**Table S1. Bioinformatics analysis of *RAD51C* variants with Max Ent Score.**

<b><i>RAD51C</i> VARIANTS<sup>1</sup></b>	<b>EXON/ INTRON</b>	<b>MES wt</b>	<b>MES mut</b>	<b>MES score change<sup>2</sup></b>	<b>MES <i>de novo</i> SS- mut vs. wt <sup>3</sup></b>	<b>MES score change<sup>2</sup></b>
c.146-8A>G	ivs1/Ex2	9.5	9.4	-0.2%		
c.146-4T>C	ivs1/Ex2	9.5	9.1	-3.4%		
<b>c.146-3C&gt;T</b>	ivs1/Ex2	9.5	8.7	-8.5%		
c.403T>C	Ex2	4.8	6.5	+36.3%		
<b>c.404G&gt;A</b>	Ex2	4.8	-3.5	-172.7%		
c.404+6delA	Ex2/ivs2	4.8	6.4	+33.8%		
c.404+13G>A	Ex2/ivs2	4.8	4.8	0%		
<b>c.405-6T&gt;A</b>	ivs2/Ex3	7.7	2.2	-72.2%	8.6 vs. 0.2	+4650% 4-nt upstream
<b>c.571+4A&gt;G</b>	Ex3/ivs3	10.5	8.1	-22.5%	5.5 vs. 0.9	+525% 4-nt downstream
<b>c.571+5G&gt;A</b>	Ex3/ivs3	10.5	5.8	-44.2%		
c.571+5G>T	Ex3/ivs3	10.5	6.6	-36.7%		
c.571+9G>C	Ex3/ivs3	10.5	10.5	0%		
c.572-8T>C	ivs3/Ex4	7.4	7.5	+0.4%		
c.572-7G>A	ivs3/Ex4	7.4	5.9	-21.3%		
<b>c.572-1G&gt;T</b>	ivs3/Ex4	7.4	-1.2	-115.6%		
c.572A>C	Ex4	7.4	6.3	-15.2%		
c.573A>G	Ex4	7.4	7.3	-1.4%		
<b>c.705G&gt;T</b>	Ex4	9.1	2.6	-72%		
<b>c.705+5G&gt;C</b>	Ex4/ivs4	9.1	7.2	-20.8%		
c.705+8T>C	Ex4/ivs4	9.1	9.1	0%		
c.706-7T>C	ivs4/Ex5	11.1	10.4	-6.4%		
<b>c.706-2A&gt;C</b>	ivs4/Ex5	11.1	3.1	-72.4%	3.3 vs. -2	+263.2% 10-nt downstream
<b>c.706-2A&gt;G</b>	ivs4/Ex5	11.1	3.1	-71.7%	3.2 vs. -2	+254.9% 10-nt downstream
c.837+1G>A	Ex5/ivs5	8.6	0.4	-95.6%		
<b>c.837+2T&gt;C</b>	Ex5/ivs5	8.6	0.8	-90.5%		

<b>RAD51C VARIANTS<sup>1</sup></b>	<b>EXON/ INTRON</b>	<b>MES wt</b>	<b>MES mut</b>	<b>MES score change<sup>2</sup></b>	<b>MES de novo SS- mut vs. wt <sup>3</sup></b>	<b>MES score change<sup>2</sup></b>
c.905-5C>G	ivs6/Ex7	8.2	6.6	-19.3%		
c.905-4T>C	ivs6/Ex7	8.2	8.1	-1.2%		
<b>c.905-3C&gt;G</b>	ivs6/Ex7	8.2	-4.9	-159.4%		
<b>c.905-2_905-1del</b>	ivs6/Ex7	8.2	0.6	-93.3%		
<b>c.905-2A&gt;C</b>	ivs6/Ex7	8.2	0.1	-98.3%		
<b>c.965+5G&gt;A</b>	Ex7/ ivs7	8.7	3.8	-56.6%		
c.966-8T>C	ivs7/Ex8	7.3	8.5	+17%		
<b>c.966-3C&gt;A</b>	ivs7/Ex8	7.3	4.4	-40%	5.4 vs. 5.7	-4.2% 3-nt upstream
<b>c.966-2A&gt;G</b>	ivs7/Ex8	7.3	-0.7	-109.5%	7 vs. 5.7	+22.6% 3-nt upstream
<b>c.966-2A&gt;T</b>	ivs7/Ex8	7.3	-1.1	-115.2%	7.6 vs. 5.7	+34% 3-nt upstream
c.967T>C	Ex8	7.25	6.5	-10.8%		
<b>c.1026+5_1026+7del</b>	Ex8/ivs8	<sup>2</sup> NNSplice: 0.8	- <0.1	-		
<b>c.1026+5G&gt;T</b>	Ex8/ivs8	<sup>2</sup> NNSplice: 0.8	- <0.1	-		
c.1027-8T>A	ivs8/Ex9	8.6	7.4	-14.5%		
c.1029T>C	Ex9	8.6	9.1	+6.3%	4 vs. 3.9	+2.3 6-nt downstream

<sup>1</sup> Selected variants are shown in red.

<sup>2</sup> MES score changes ( $\Delta\%$ ), wild type (wt) vs. mutant (mut).

<sup>3</sup> *De novo*: predicted creation of new alternative splice sites: mutant score vs. wild type score.

**Table S2. RNA and protein impact according to sequence ENST00000337432.9 of *RAD51C*.**

TRANSCRIPT <sup>1</sup>	RNA-HGVS	PROTEIN-HGVS	Diagrams of the splicing events <sup>2</sup>
▼(E2q27)	r. [404g>a,404_405ins404+1_404+27] PTC-NMD	p.Cys135*	
Δ(E2q175)	r.230_404del PTC-NMD	p.Gly77Valfs*6	
Δ(E2q22)	r. 383_404del PTC-NMD	p.Gly128Valfs*6	
Δ(E2)	r. 146_404del PTC-NMD	p.Glu49Valfs*6	
▼(E3p4)	r.404_405ins405-4_405-1 PTC-NMD	p. Cys135*	
Δ(E3)	r. 405_571del PTC-NMD	p.Cys135*	
▼(E3q4)	r.[571+4a>g,571_572ins571+1_571+4] PTC-NMD	p.Glu191Glyfs*13	
Δ(E3q114)	r. 458_571del	p.Gly153_Glu190del	
Δ(E4)	r. 572_705del PTC-NMD	p.Glu191Glyfs*16	
Δ(E5p10)	r. 706_715del PTC-NMD	p.Val236*	
Δ(E5p52)	r.706_757del PTC-NMD	p.Val236Metfs*10	

TRANSCRIPT <sup>1</sup>	RNA-HGVS	PROTEIN-HGVS	Diagrams of the splicing events <sup>2</sup>
<b>Δ(E5)</b>	r.706_837del	p.Arg237_Val280del	
<b>Δ(E4_5)</b>	r.572_837del PTC-NMD	p.Glu191Glyfs*12	
<b>Δ(E7)</b>	r.905_965del PTC	p.Glu303Trpfs*41	
<b>Δ(E7_8)</b>	r.905_1026del PTC	p.Gly302Alafs*5	
<b>Δ(E8)</b>	r.966_1026del PTC	p.Arg322Serfs*22	
<b>▼(E8p3)-a</b>	r.[966-3c>a,965_966ins966-3_966-1]	p.Arg322dup	
<b>▼(E8p3)-b</b>	r.[966-2a>g,965_966ins966-3_966-1]	p.Arg322delinsSerGly	
<b>▼(E8p3)-c</b>	r.[966-2a>u,965_966ins966-3_966-1]	p.Arg322delinsSerTrp	
<b>Δ(E8q18)</b>	r.1009_1026del	p.Val337_Lys342del	
<b>▼(E8q41)</b>	r.1026_1027ins[1026+1_1026+4;1026+8_1026+44] PTC	p.Pro343Valfs*4	
<b>▼(E8q44)</b>	r.1026_1027ins1026+1_1026+44 PTC	p.Pro343Valfs*5	

<sup>1</sup> Transcript annotation according to López-Perolio et al (2019) (see also in Materials and Methods).

<sup>2</sup> Anomalous exons and splicing events (broken lines) are indicated in red. Abnormal *de novo*/cryptic AG or GT sites are shown in red text.

**Table S3.** Mutagenesis primers for *RAD51C* variants

Variant	Exon/Intron	Primers (5'→3')
c.146-3C>T	ivs1	TTTTTTCTTATTTTACTTTTAGAAGTTGGGATATCTAAAG CTTTAGATATCCCAACTTCTAAAAGTAAAAAAGAAAAAAA
c.404G>A	Ex2	TGTTGGAAAAACACAATTATAGTAAAATAAAGTGTTCCT AGGAGAACTTTATTTTACTATAATTGTGTTTTCCAACA
c.405-6T>A	ivs2	GTTGTTTGTCTCTTTCTGTAGACAGTATGCAGTTGGCAGT ACTGCCAACTGCATACTGTCTACAGAAAGATGACAAACAAC
c.571+4A>G	ivs3	AAACACAAGGGAGAGGGTAGGTTAGTAAATGATCTTCTT AAGAAGATCATTTACTAACCTACCCTCTCCCTTGTTT
c.571+5G>A	ivs3	AACACAAGGGAGAGGGTAAATTAGTAAATGATCTTCTT AAAGAAGATCATTTACTAATTTACCCTCTCCCTTGTTT
c.572-1G>T	ivs3	AAGAGTGTGTTTGTGTTTCATAACACCGAAAAGCTTTGGAG CTCCAAAGCTTTTCGGTGTTATGAAACAACAAAACACTCTT
c.705G>T	Ex4	TTCTTTTCAGAACTCAAATGTATGAGTCAGACTACTGAA TTCAGTAGTCTGACTCATACATTTGAGTGTCTGAAAGGAA
c.705+5G>C	ivs4	TTCAGAACTCAAAGGTATCAGTCAGACTACTGAAATGTA TACATTTCACTAGTCTGACTGATACCTTTGAGTGTCTGAA
c.706-2A>C	ivs4	ATATTATCTCTTCTGTATTTTCGGTTCGACTAGTGATAGTGG CCACTATCACTAGTCGAACCGAAATACAGAAGAGATAATAT
c.706-2A>G	ivs4	ATATTATCTCTTCTGTATTTGGGTTTCGACTAGTGATAGTGG CCACTATCACTAGTCGAACCCAAATACAGAAGAGATAATAT
c.837+2T>C	ivs5	AAATAATCACAGATTAGCTGCAAGTATTAAGTAGTGAAGAG CTCTTCACTAGTTAATACTTGCAGCTAATCTGTGATTATTT
c.905-3C>G	ivs6	GTTATTATGTTTTTACTCTGAGGGGAAAGTTGGGGACATG CATGTCCCCAACTTTCCCCTCAGAGTAAAAAACATAATAAC
c.905-2A>C	ivs6	TTATTATGTTTTTACTCTCCGGGGAAAGTTGGGGACATGC GCATGTCCCCAACTTTCCCCGGAGAGTAAAAAACATAATAA
c.905-2_905-1del	ivs6	TACAGTTATTATGTTTTTACTCTCGGGAAAGTTGGGGACATGCTG CAGCATGTCCCCAACTTTCCCGAGAGTAAAAAACATAATAACTGTA
c.965+5G>A	ivs7	GGGACCGAAAGCAAAGGTCAATACAGAAACAAGTTAATAAC GTTATTAAGTTGTTTCTGTATTGACCTTTGCTTTTCGGTCCC
c.966-3C>A	ivs7	ATTTATTCTTTTTCTTTAAGAAGGTTGGCAACATTGTACAA TTGTACAATGTTGCCAACCTTCTTAAAGAAAAAGAATAAAT
c.966-2A>G	ivs7	TTTATTCTTTTTCTTTAAGCGGGTTGGCAACATTGTACAAG CTTGTACAATGTTGCCAACCCGCTTAAAGAAAAAGAATAAA

<b>c.966-2A&gt;T</b>	ivs7	TTTATTCTTTTTCTTTAAGCTGGTTGGCAACATTGTACAAG
		CTTGTACAATGTTGCCAACCAGCTTAAAGAAAAAGAATAAA
<b>c.1026+5_1026+7del</b>	ivs8	GAATGCACAGTACTGTTTCAAATCAAAGTCATTATTTGATTAGAGTGGGATTTTGATATT
		AATATCAAAATCCCACTCTAATCAAATAATGACTTTGATTTGAAACAGTACTGTGCATTC
<b>c.1026+5G&gt;T</b>	ivs8	ACTGTTTCAAATCAAAGTCATTATTATTTGATTAGAGTGGG
		CCCACTCTAATCAAATAATAATGACTTTGATTTGAAACAGT