**Supplementary Figure 1. Mre11 exon 16 was deleted using site-directed mutagenesis and confirmed by Sanger DNA sequencing**

Alignment of Sequences: [Translation of MRE11\_Full length] with [Translation of MRE11 Δexon16]

Similarity : 679/708 (95.90 %)

MRE11 FL MSTADALDDENTFKILVATDIHLGFMEKDAVRGNDTFVTLDEILRLAQENEVDFILLGGD 60

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MRE11 Δexon16 MSTADALDDENTFKILVATDIHLGFMEKDAVRGNDTFVTLDEILRLAQENEVDFILLGGD 60

MRE11 FL LFHENKPSRKTLHTCLELLRKYCMGDRPVQFEILSDQSVNFGFSKFPWVNYQDGNLNISI 120

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MRE11 Δexon16 LFHENKPSRKTLHTCLELLRKYCMGDRPVQFEILSDQSVNFGFSKFPWVNYQDGNLNISI 120

MRE11 FL PVFSIHGNHDDPTGADALCALDILSCAGFVNHFGRSMSVEKIDISPVLLQKGSTKIALYG 180

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MRE11 Δexon16 PVFSIHGNHDDPTGADALCALDILSCAGFVNHFGRSMSVEKIDISPVLLQKGSTKIALYG 180

MRE11 FL LGSIPDERLYRMFVNKKVTMLRPKEDENSWFNLFVIHQNRSKHGSTNFIPEQFLDDFIDL 240

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MRE11 Δexon16 LGSIPDERLYRMFVNKKVTMLRPKEDENSWFNLFVIHQNRSKHGSTNFIPEQFLDDFIDL 240

MRE11 FL VIWGHEHECKIAPTKNEQQLFYISQPGSSVVTSLSPGEAVKKHVGLLRIKGRKMNMHKIP 300

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MRE11 Δexon16 VIWGHEHECKIAPTKNEQQLFYISQPGSSVVTSLSPGEAVKKHVGLLRIKGRKMNMHKIP 300

MRE11 FL LHTVRQFFMEDIVLANHPDIFNPDNPKVTQAIQSFCLEKIEEMLENAERERLGNSHQPEK 360

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MRE11 Δexon16 LHTVRQFFMEDIVLANHPDIFNPDNPKVTQAIQSFCLEKIEEMLENAERERLGNSHQPEK 360

MRE11 FL PLVRLRVDYSGGFEPFSVLRFSQKFVDRVANPKDIIHFFRHREQKEKTGEEINFGKLITK 420

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MRE11 Δexon16 PLVRLRVDYSGGFEPFSVLRFSQKFVDRVANPKDIIHFFRHREQKEKTGEEINFGKLITK 420

MRE11 FL PSEGTTLRVEDLVKQYFQTAEKNVQLSLLTERGMGEAVQEFVDKEEKDAIEELVKYQLEK 480

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MRE11 Δexon16 PSEGTTLRVEDLVKQYFQTAEKNVQLSLLTERGMGEAVQEFVDKEEKDAIEELVKYQLEK 480

MRE11 FL TQRFLKERHIDALEDKIDEEVRRFRETRQKNTNEEDDEVREAMTRARALRSQSEESASAF 540

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MRE11 Δexon16 TQRFLKERHIDALEDKIDEEVRRFRETRQKNTNEEDDEVREAMTRARALRSQSEESASAF 540

MRE11 FL SADDLMSIDLAEQMANDSDDSISAATNKGRGRGRGRRGGRGQNSASRGGSQRGRADTGLE 600

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MRE11 Δexon16 SADDLMSIDLAEQMANDSDDSISAATNKGRGRGRGRRGGRGQNSASRGGSQRGR------ 594

MRE11 FL TSTRSRNSKTAVSASRNMSIIDAFKSTRQQPSRNVTTKNYSEVIEVDESDVEEDIFPTTS 660

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MRE11 Δexon16 -----------------------FKSTRQQPSRNVTTKNYSEVIEVDESDVEEDIFPTTS 631

MRE11 FL KTDQRWSSTSSSKIMSQSQVSKGVDFESSEDDDDDPFMNTSSLRRNRR 708

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MRE11 Δexon16 KTDQRWSSTSSSKIMSQSQVSKGVDFESSEDDDDDPFMNTSSLRRNRR 679

**Supplementary Table 1. Enrichment analysis and additional isoform information used in the TCGA analysis.** Sheet 1: pairwise enrichment analysis (P-values of Wilcoxon on-sided unpaired test on increase of relative isoform abundance of mutant vs. WT, pairwise for each isoform). Sheet 2: Overview on used isoform annotations for quantification and P-values for increased relative abundance of one isoform (P-values of Wilcoxon on-sided unpaired test on increase of relative isoform abundance mutant vs. WT, each isoform against all other isoforms). Sheet 3: overview of allele frequencies in different studies from dbGAP.





