

A

WT	GATCGACGTGGCAGAGGAGGATATGACCGGGGCGGCTACCGGGGCCGAGGAG
F29-24	GATCGACGTGGCAGAGGAGGATATGACCGGGGCGGCTACCGGGGCCGAGGAG
	Exon 14
WT	GGGACCGTGGGGGCTTCAGAGGGGGCCGGGGTGGTGGGGACAGAGGCGGTTT
F29-24	GGGACCGTGGGGGCTTCAGAGGGGGCCGGGGTGGTGGGGACAGAGGCGGTTT
	Exon 14
WT	TGGCCCTGGCAAGATGGACTCCAGGGGCGAGCACAGAC-AGGATCGCAGGGA
F29-24	TGGCCCTGGCAAGATGGACTCCAGGGGCGAGCACAGAC-AGGATGCAGGGA
	Exon 14 Exon 15
	TALEN-Fus 15A* R513G
WT	GAGGCCATATTAGCCTGGCTCCTGAAGTTCTGGAACCTTTCCTGTACCCAGT
F29-24	GAGGCCATATTAGCCTGGCTCCTGAAGTTCTGGAACCTTTCCTGTACCCAGT
	Exon 15 3' UTR
	TALEN-Fus 15B Stop codon
WT	GTTACCCTTGTTATTTTGTAAACTTACAATTCAGGATCGCTCATGGATATTT
F29-24	GTTACCCTTGTTATTTTGTAAACTTACAATTCAGGATCGCTCATGGATATTT
	3' UTR
WT	TTTTTTGGGGGGGTGGGGCGGTTGTGTGTGTATGTGTGTGTGTGTGTCA
F29-24	TTTTTTGGGGGGGTGGGGCGGTTGTGTGTGTATGTGTGTGTGTGTGTCA
	3' UTR
WT	GACTACCCTAATTGTAACCA
F29-24	GACTACCCTAATTGTAACCA
	3' UTR

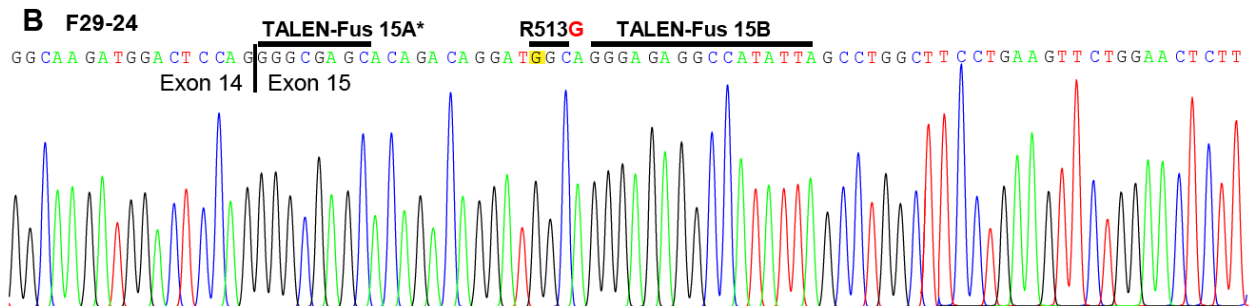


Figure S4 Sequence analysis of *Fus*^{R513G} cDNA.

(A) Sequence comparison of the cloned PCR product representing 341 bp of the *Fus* cDNA sequence, including exon 14, exon 15 and 3'UTR sequences, derived from the mutant pup F29-24 in comparison to wildtype cDNA sequence. **(B)** Chromatogram showing the sequencing peaks of the cloned PCR product covering the *Fus* codon 513 (nucleotide replacement highlighted in yellow). The positions of exon 14, exon 15, exon boundary, stop codon, 3' UTR, TALEN binding sites and of the R513G replacement are indicated.