

**Table S1 Summary of sequence reads generated from mutant and wild type samples**

Sample	Total no. of reads	Read length in bases	Total MB	Coverage	No. of reads mapped to reference genome	% of reads mapped to reference genome
wt_3	108,513,967	51	5534	134x	105,047,645	96.8
pro32/fus	91,404,127	51	4662	114x	89,264,279	97.7