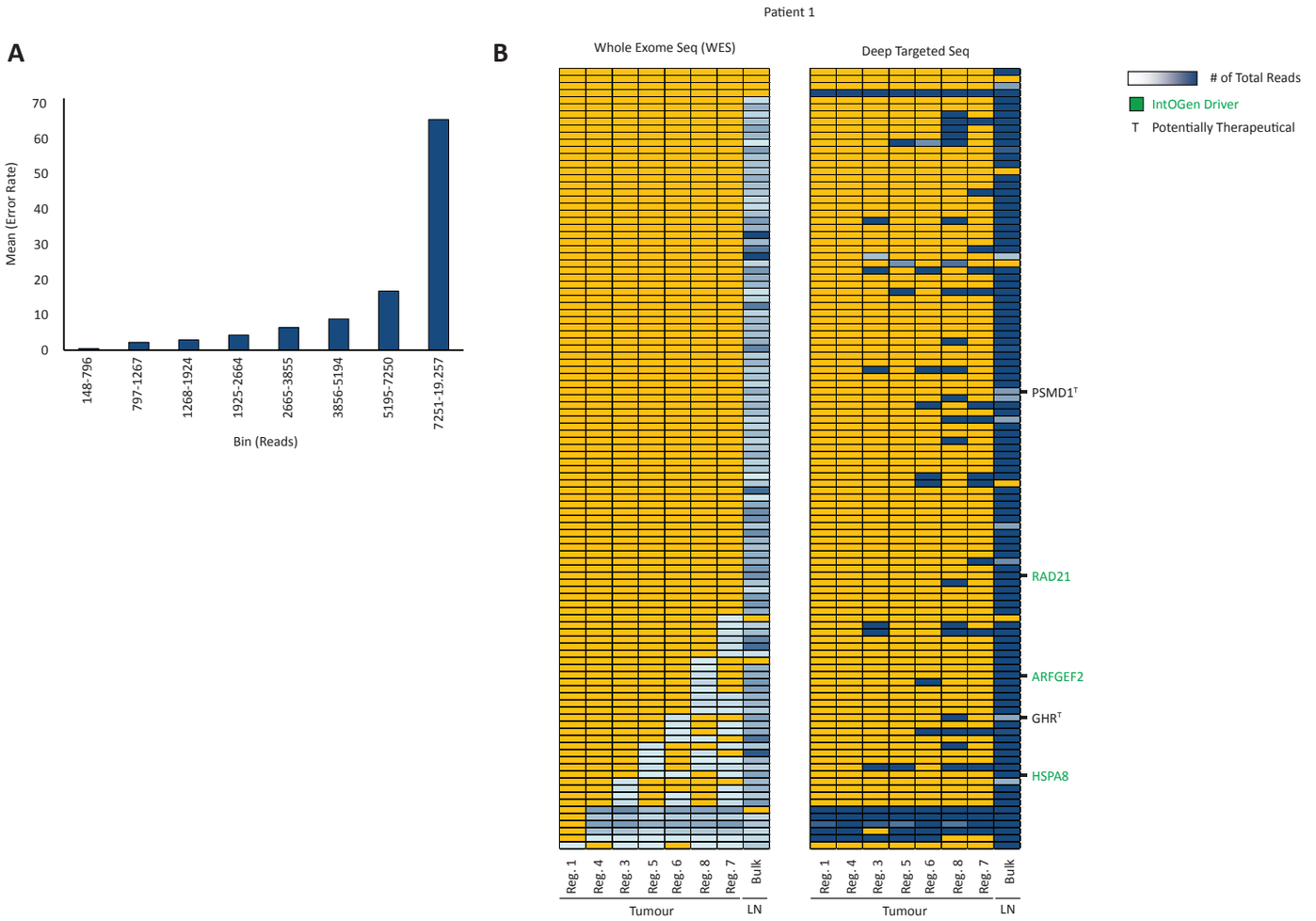
Supplementary Figure S4



Supplementary Figure S4 - Validation of mutations by deep targeted sequencing. (A) Number of reads for all positions were ranked and divided into 8 bins of 110 positions each. For each bin we counted the number of times different bases than the reference and the WES called mutated base was observed (estimated error rate). The mean estimated error rate for each bin is shown. (B) Heat map of allele frequencies of WES called mutations (left) and corresponding deep targeted sequencing (right). In the deep targeted sequencing experiment we required at least 10 reads in all samples for a given position, which resulted in 110 mutations for the comparison. We regarded a mutation as being present if the WES called mutation was present more than 2x the mean of the estimated error rate for the bin covering the given read depth of the position; otherwise it was regarded as not present. Yellow: mutation present, white: less than 10 reads in the given position, blue range: mutation not present (presented with number of reads ranging from 11-19.257 reads excluding the lower and upper 10% quartiles) with dark blue equaling high amount of total reads. Samples are ordered according to number of mutations. Reg.: Region, LN: Lymph node metastasis.