



Supplementary Figure S1: SB-induced mutagenesis was performed in the *Ptch1* heterozygous mouse model and transposon CIS were identified. The local protein network for each CIS-derived candidate cancer gene was generated from experimentally determined protein interaction data and these local protein networks integrated to generate a PPI network comprising the CISs and their interacting proteins. Human MB transcriptomics data was used to identify differentially expressed genes common to all non-WNT MB, which was used to refine our protein interaction network to include only over-expressed genes and their directly interacting proteins. Drugs and their molecular targets were mapped to this network, with subsequent validation of these novel druggable proteins in PDX models of MB