Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Maximal fold changes for RNA-seq differential gene expression profile. 2 genes (March 1 and March 2) were represented by 2 transcripts each with maximal fold changes per gene provided in the table. Only genes with a fold change of at least 2 are presented. Differential expression was obtained by using “limma” package, p-values were adjusted for multiple testing with BH method with p-<0.05 considered significant. Pathway analysis was performed using the Reactome tool (https://reactome.org/PathwayBrowser/#TOOL=AT), and only terms yielding FDR < 0.05 were considered to be significant and were used for further examination.

File Name: Supplementary Data 2

Description: Differential pathway networks enrichment. Upregulated and downregulated pathways between Wnt, Group 3, and Group 4 MBs or L807mts- and PBS control-treated samples. Differential expression was obtained by using “limma” package, p-values were adjusted for multiple testing with BH method with p-<0.05 considered significant. Pathway analysis was performed using the Reactome tool (https://reactome.org/PathwayBrowser/#TOOL=AT), and only terms yielding FDR < 0.05 were considered to be significant and were used for further examination.