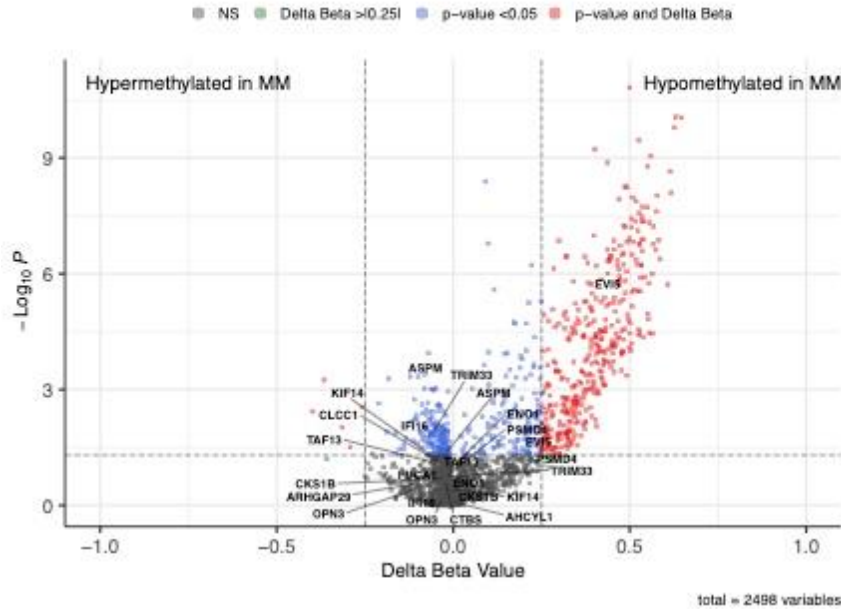


Supplemental Figure 17. Differential methylation of MM relevant genes. Volcano plots of the CpG probes (probes=2498) across chromosome 1 between MM (n=161) and normal PC (n=3), as a result there are 378 probes (genes=360) that are significantly hypomethylated in MM on in comparison to the normal phenotype and 5 probes (genes=7) are significantly hypermethylated. The plot is further annotated to show the probe associated with **A.** the GEP70 genes located on chromosome 1 (n=20, p-arm=12, q-arm=8), and **B.** genes that have been previously implicated as driver genes of the gain/1amp(1q) phenotype in MM (n=20, p-arm=7, q-arm=13).

A. GEP70 Genes on Chr1 (n=20)
EnhancedVolcano



B. Previously Implicated Driver Genes on Chr1 (n=20)
EnhancedVolcano

