

Supplemental Figure 13. CRISPR dependencies on chromosome 1. Nineteen myeloma cell lines and 15 random non-myeloma cell lines were identified and CERES dependencies for genes located on chr1 recorded. A total of 1701 genes were analyzed. Cell lines did not cluster according to their copy number profile but tended to cluster according to disease type. Common dependencies genes with gene dependencies < -1 clustered together and comprised proteasome subunit coding genes (*PSMA5*, *PSMB2*, *PSMB4*), three regulators of ubiquitin-protein transferase activity (*RPL5*, *RPL11*, *CDC20*), splicing factors (*SF3B4*, *SF3A3*, *SFPQ*, *RNPC3*, *SRNPE*, *PRPF38A*, *PRPF38B*) and *DTL*. The second clade could be further subdivided into two clades (n2.1=125 and n2.2=1594). The second of these two clades could further be divided into two clades (n2.2.1=105 and n2.2.2=1489). Clades 2.1 and 2.2.0 included genes with significant dependencies in some cell lines but not the others. Genes in these clusters include suspected drivers such as *ADAR* alongside more unexpected genes such as *CD30*. The tumor suppressor genes commonly found in deleted regions on 1p such as *CDKN2C*, or *FAF1* were commonly found in clade with no dependency.

