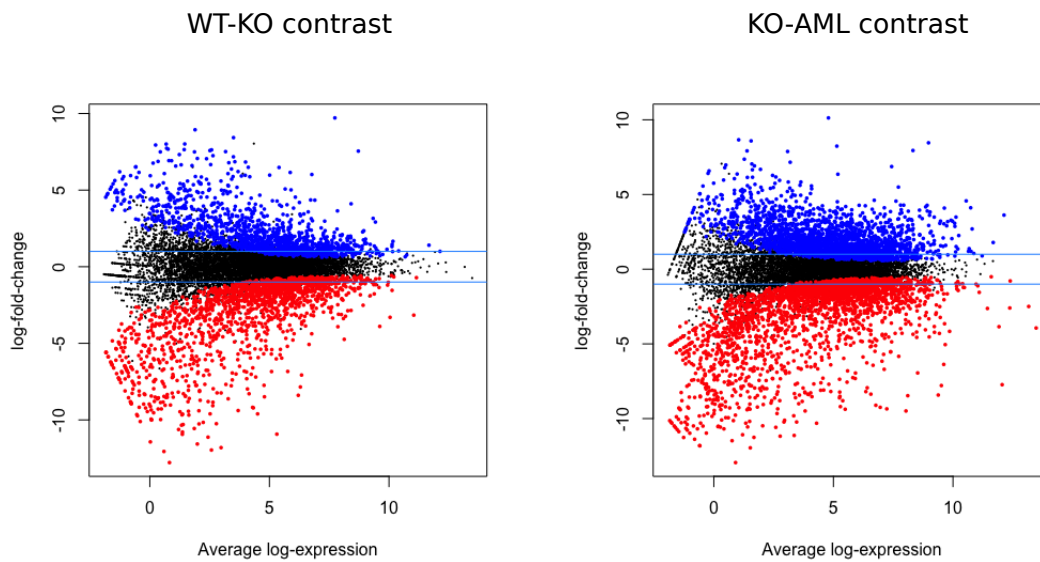


A



B

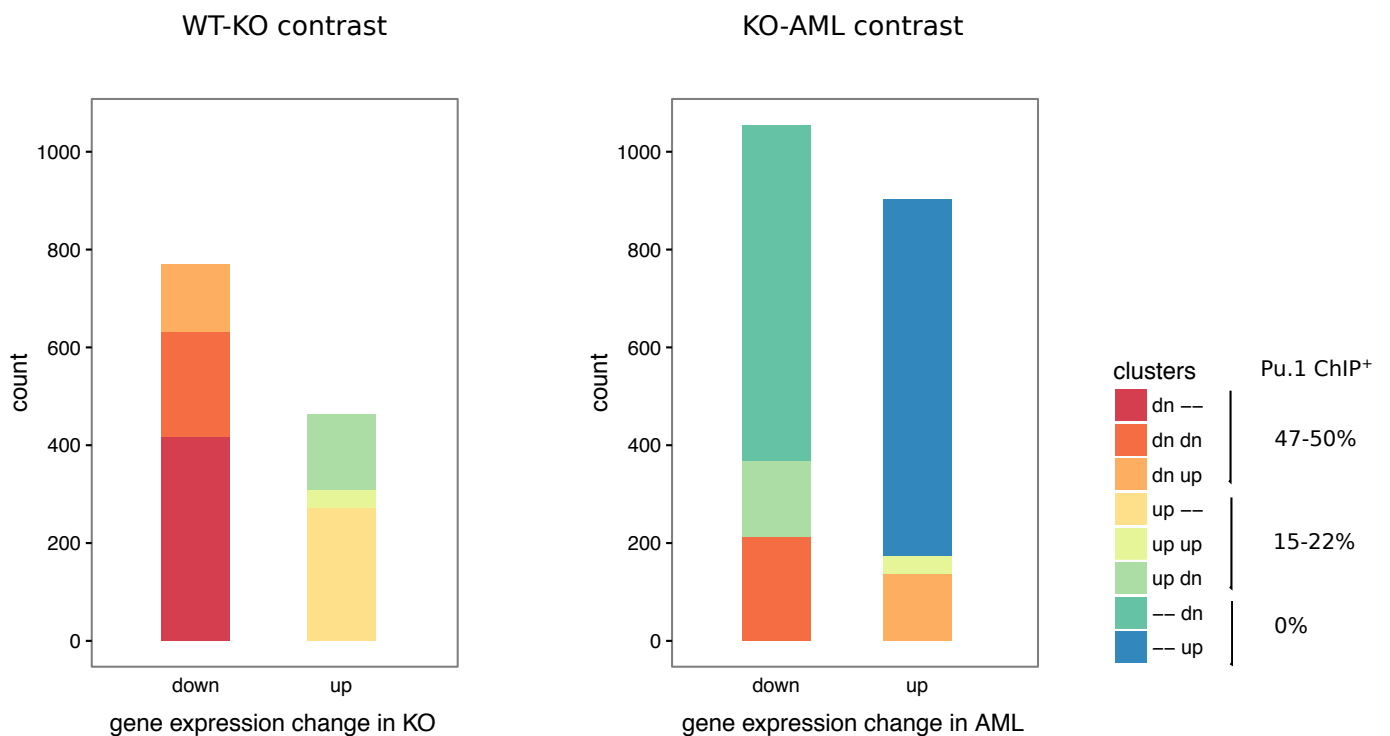


Fig 1.1. A: The spread of differential expression with respect to abundance. (Significantly DE genes are chosen with adjusted p-value < 0.01, a cutoff used in gene set tests) (red = downregulated, blue = upregulated in each contrast) (blue line demarkates two-fold change in expression in each direction)

B: Total number of differentially expressed genes across the two comparisons. Genes differentially expressed in KO, AML or both can be grouped in 8 broad clusters, according to their expression across the three conditions (WT, KO and AML) Proportion of genes in the clusters with detected Pu.1 binding in the broad promoter region is shown in the legend.