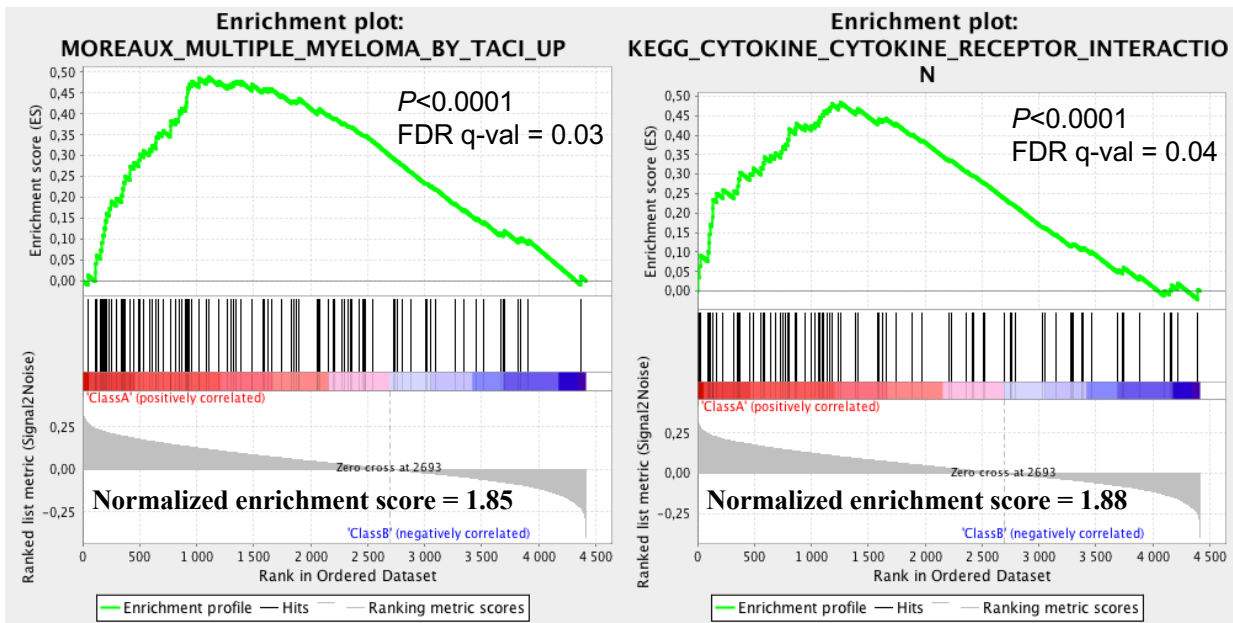
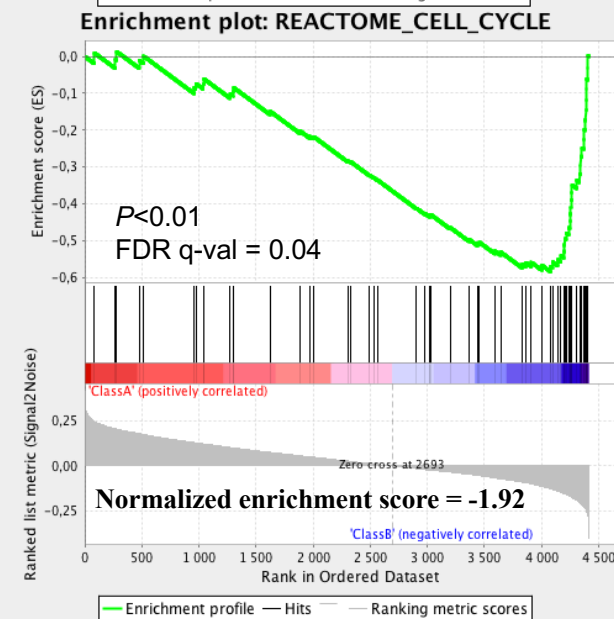
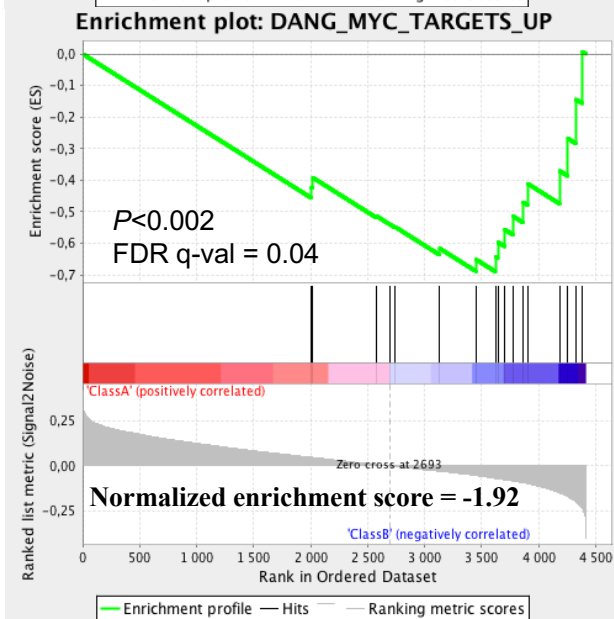
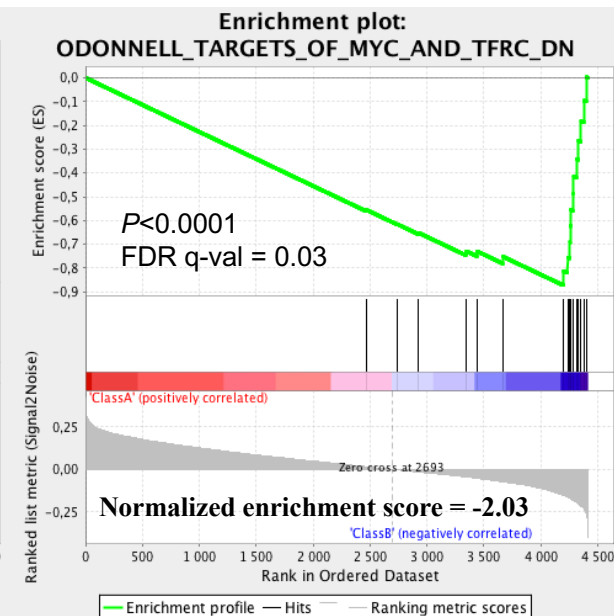
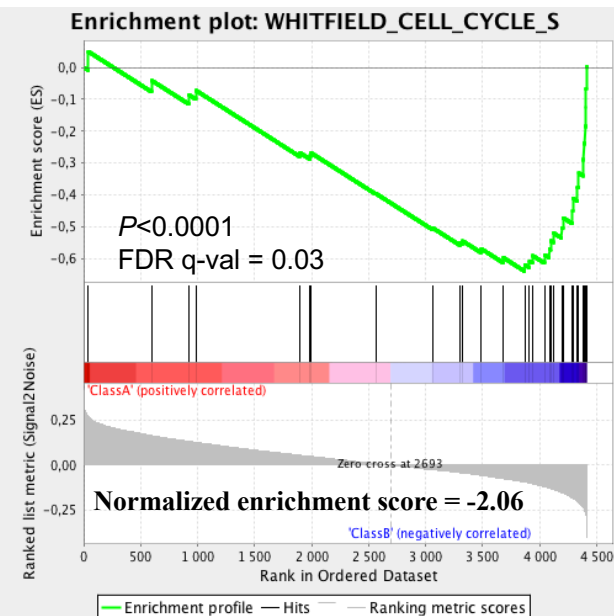
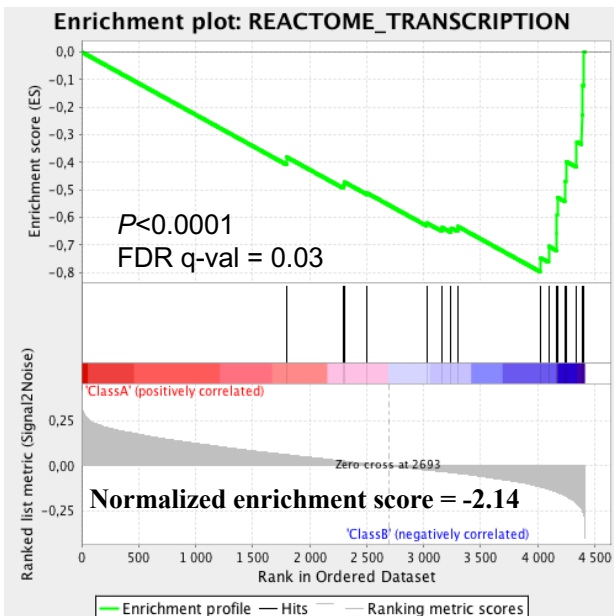


Supplementary Figure S1: The Combo score was computed for MMCs of patients belonging to the 8 groups of the UAMS molecular classification of multiple myeloma, using UAMS-TT2 cohort. PR: proliferation, LB: low bone disease, MS: MMSET, HY: hyperdiploid, CD1: Cyclin D1-D3, CD2: Cyclin D1-D3, MF: MAF, MY: myeloid. * Indicate that the score value is significantly higher in the group compared to all the patients of the cohort ($P < .05$). ** Indicate that the score value is significantly lower in the group compared to all the patients of the cohort ($P < .05$).

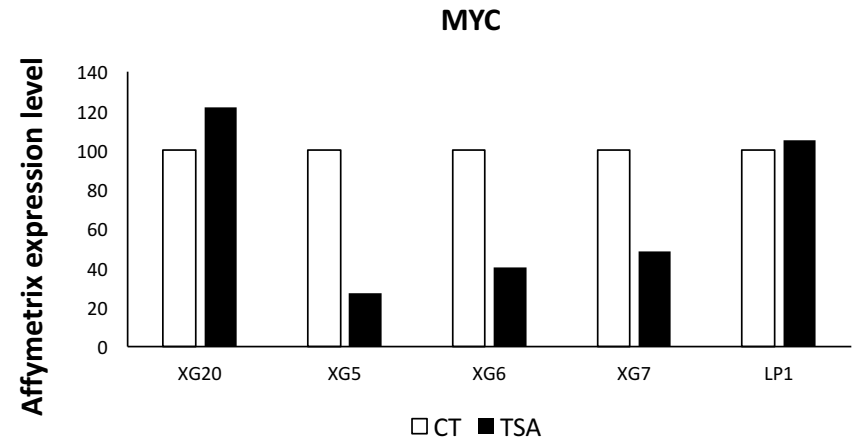
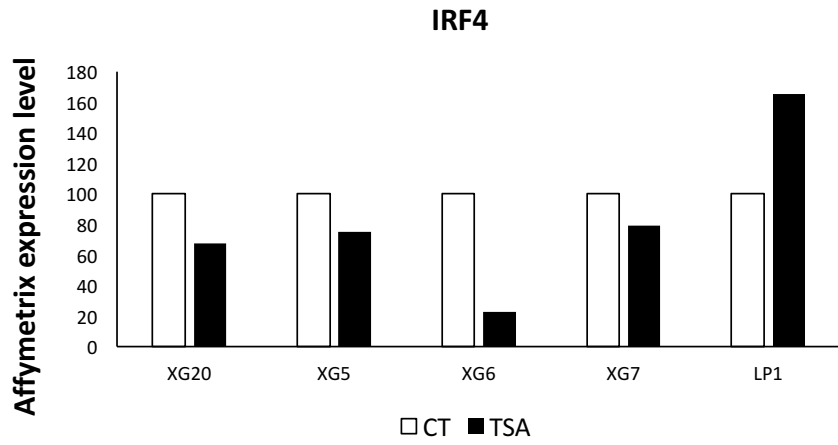
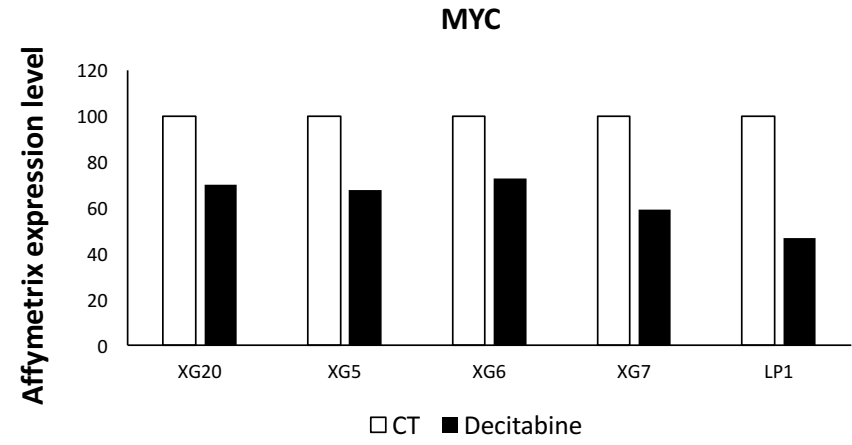
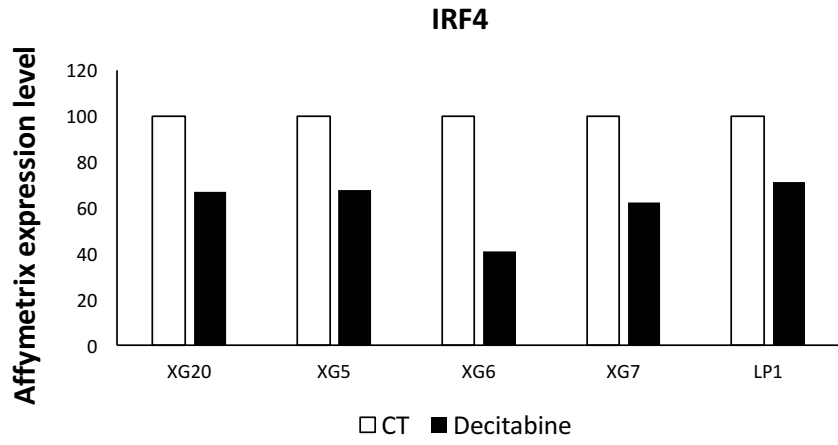


Supplementary Figure S2. Top gene set significantly associated with low Combo Score in MM. GSEA enrichment plot with the absolute enrichment p value and the normalized enrichment score of the gene set.

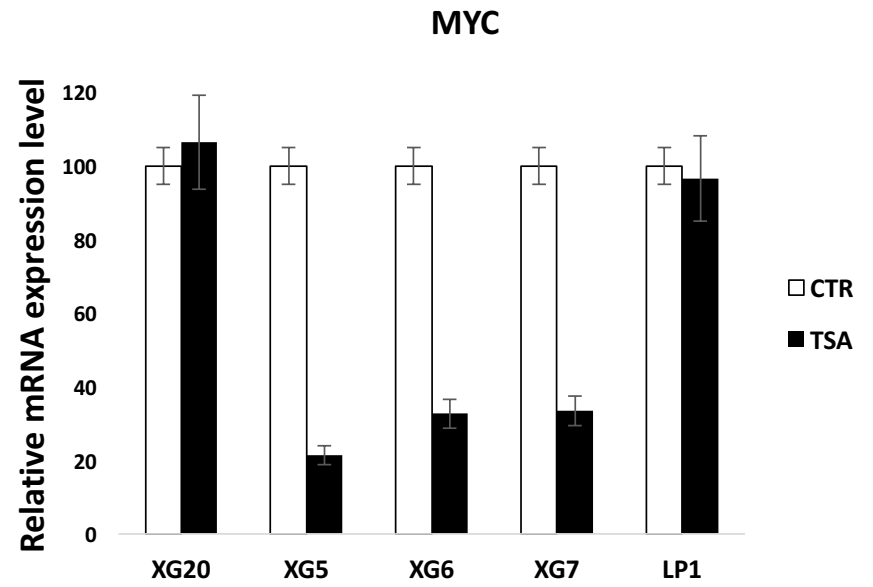
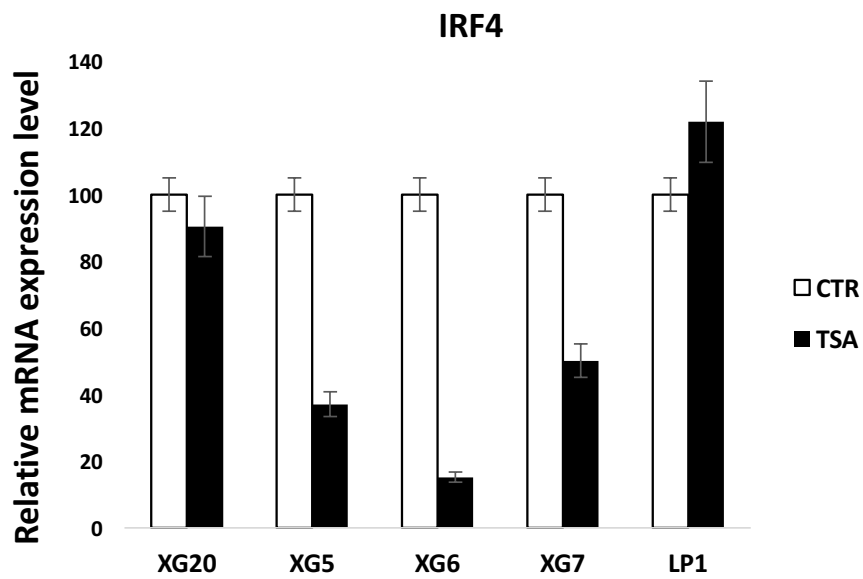
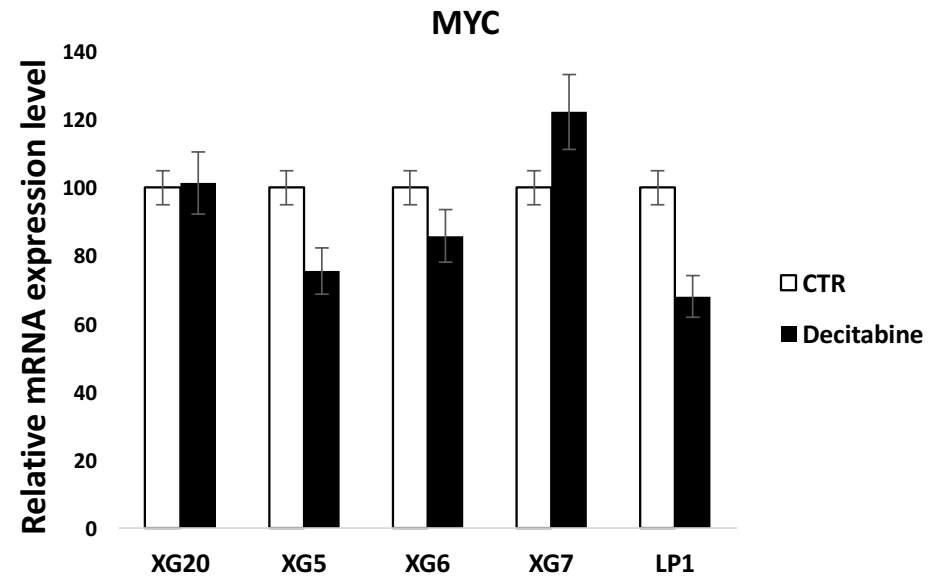
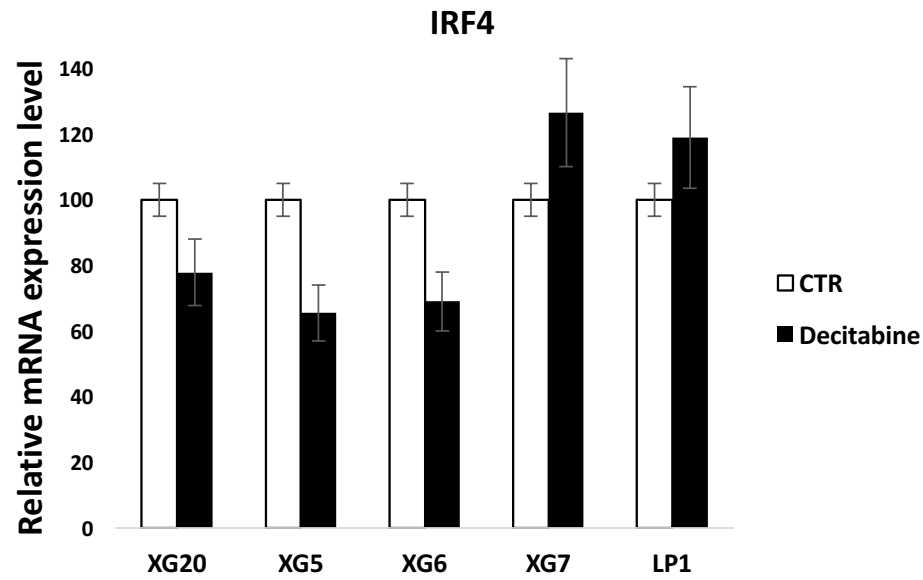


Supplementary Figure S3. Top gene set significantly associated with high Combo Score in MM.
GSEA enrichment plot with the absolute enrichment p value and the normalized enrichment score of the gene set.

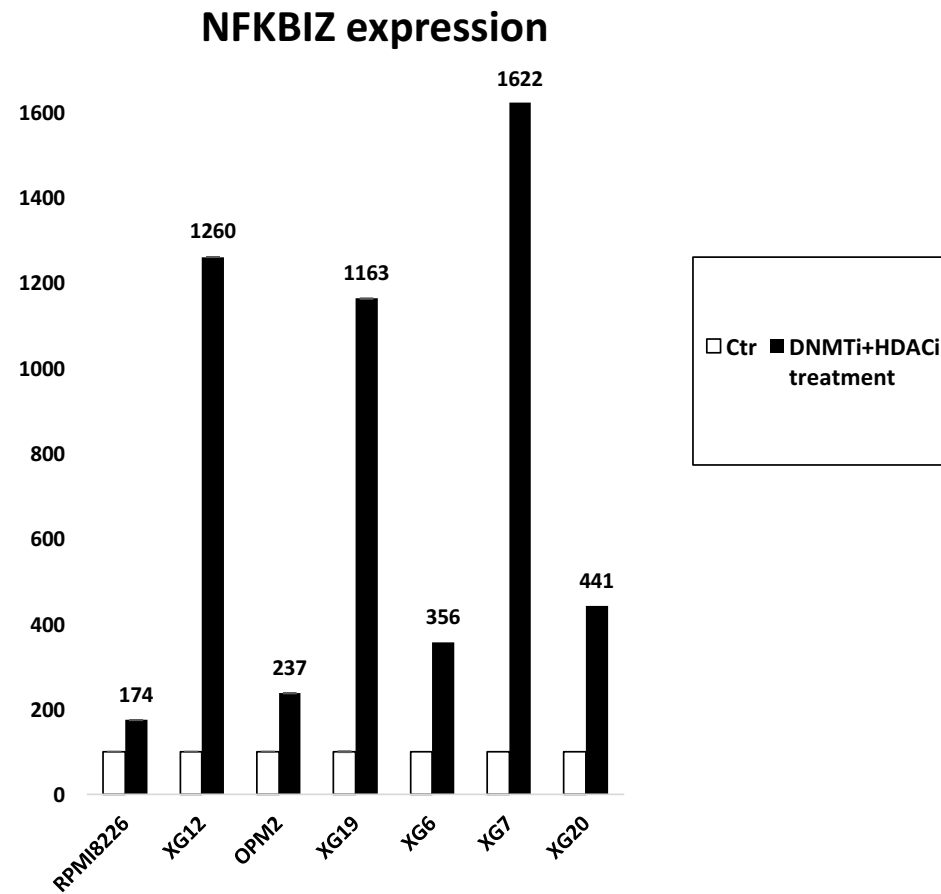
A



B



Supplementary Figure S4. *IRF4* and *MYC* gene expression in untrated (CT) and DNMTi or HDACi treated HMCLs using Affymetrix microarrays (A) and real time PCR (B).



Supplementary Figure S5. *NFKBIZ* gene expression in untreated (CT) and DNMTi/HDACi treated HMCLs was assayed using real time PCR.