

Supplemental data files for

"Convergent organization of aberrant MYB complexes controls oncogenic gene expression in acute myeloid leukemia"

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MYBMIM Genome-wide CRISPR screen (Figure 1, S1, and Table S1)

01_MYBMIM_GeCKO_gene_summary.xlsx	Genome-wide GeCKO CRISPR screen in MYBMIM treated MOLM13 cells
02_Control_GeCKO_gene_summary.xlsx	Genome-wide GeCKO CRISPR screen in PBS treated MOLM13 cells

RNA-seq and GSEA with CRYBMIM and CREBMIM (Figure 5, 10, Table S4 and S5)

03_RNAseq_DESeq2_CRYBMIM_1hr-vs-PBS_1hr_SignificantAll.xlsx	Excel file of differentially expressed genes measured by RNA-seq in 1 hr CRYBMIM vs PBS treated MV411
04_RNAseq_DESeq2_CRYBMIM_4hr-vs-PBS_4hr_SignificantAll.xlsx	Excel file of differentially expressed genes measured by RNA-seq in 4 hr CRYBMIM vs PBS treated MV411
05_RNAseq_DESeq2_CREBMIM_1hr-vs-PBS_1hr_SignificantAll.xlsx	Excel file of differentially expressed genes measured by RNA-seq in 1 hr CREBMIM vs PBS treated MV411
06_RNAseq_DESeq2_CREBMIM_4hr-vs-PBS_4r_SignificantAll.xlsx	Excel file of differentially expressed genes measured by RNA-seq in 4 hr CREBMIM vs PBS treated MV411
07_gsea_report_for_na_pos_1552361301359_CRYBMIM-vs-PBS_1hr.xlsx	Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 1 hr CRYBMIM vs PBS (positive enrichment)
08_gsea_report_for_na_neg_1552361301359_CRYBMIM-vs-PBS_1hr.xlsx	Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 1 hr CRYBMIM vs PBS (negative enrichment)
09_gsea_report_for_na_pos_1552361302266_CRYBMIM-vs-PBS_4hr.xlsx	Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 4 hr CRYBMIM vs PBS (positive enrichment)
10_gsea_report_for_na_neg_1552361302266_CRYBMIM-vs-PBS_4hr.xlsx	Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 4 hr CRYBMIM vs PBS (negative enrichment)

11_gsea_report_for_na_pos_1552361302042_CREBMIM-vs-PBS_1hr.xlsx

Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 1 hr CREBMIM vs PBS (positive enrichment)

12_gsea_report_for_na_neg_1552361302042_CREBMIM-vs-PBS_1hr.xlsx

Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 1 hr CREBMIM vs PBS (negative enrichment)

13_gsea_report_for_na_pos_1552361302044_CREBMIM-vs-PBS_4hr.xlsx

Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 4 hr CREBMIM vs PBS (positive enrichment)

14_gsea_report_for_na_neg_1552361302044_CREBMIM-vs-PBS_4hr.xlsx

Gene set enrichment analysis for differentially expressed genes measured by RNA-seq in 4 hr CREBMIM vs PBS (negative enrichment)

ChIP-seq analysis for MYB and CBP (Figure 6, 12 and 13)

15_ChIPseq_DESeq2_Named_SignificantIncrease_All_CRYBMIM-vs-PBS_1hr_MYB.xlsx

Differentially increased peaks measured by MYB ChIP-seq in 1hr CRYBMIM vs PBS treated MV411

16_ChIPseq_DESeq2_Named_SignificantDecrease_All_CRYBMIM-vs-PBS_1hr_MYB.xlsx

Differentially decreased peaks measured by MYB ChIP-seq in 1hr CRYBMIM vs PBS treated MV411

17_ChIPseq_DESeq2_Named_SignificantIncrease_All_CRYBMIM-vs-PBS_1hr_CBP.xlsx

Differentially increased peaks measured by CBP ChIP-seq in 1hr CRYBMIM vs PBS treated MV411

18_ChIPseq_DESeq2_Named_SignificantDecrease_All_CRYBMIM-vs-PBS_1hr_CBP.xlsx

Differentially decreased peaks measured by CBP ChIP-seq in 1hr CRYBMIM vs PBS treated MV411

19_ChIPseq_DESeq2_Named_SignificantIncrease_All_CRYBMIM-vs-PBS_4hr_MYB.xlsx

Differentially increased peaks measured by MYB ChIP-seq in 4hr CRYBMIM vs PBS treated MV411

20_ChIPseq_DESeq2_Named_SignificantDecrease_All_CRYBMIM-vs-PBS_4hr_MYB.xlsx

Differentially decreased peaks measured by MYB ChIP-seq in 4hr CRYBMIM vs PBS treated MV411

21_ChIPseq_DESeq2_Named_SignificantIncrease_All_CRYBMIM-vs-PBS_4hr_CBP.xlsx

Differentially increased peaks measured by CBP ChIP-seq in 4hr CRYBMIM vs PBS treated MV411

22_ChIPseq_DESeq2_Named_SignificantDecrease_All_CRYBMIM-vs-PBS_4hr_CBP.xlsx

Differentially decreased peaks measured by CBP ChIP-seq in 4hr CRYBMIM vs PBS treated MV411

MYB and CBP IP-MS data (Figure 7 and Table S6)

23_IP-MS_MYB_IgG_protein_list.xlsx

List of proteins identified by IP-MS of IgG control and MYB complex purifications from MV411 cell nuclei

24_IP-MS_CBP_IgG_protein_list.xlsx

List of proteins identified by IP-MS of IgG control and CBP complex purifications from MV411 cell nuclei

RNA-seq analysis with CRYBMIM in 5 AML cell lines (Figure 10)

25_RNAseq_expression_all_coding_5AML_celllines.xlsx

All coding gene expression changes measured by RNA-seq in 1 hr CRYBMIM vs PBS treated MV411, HL-60, Kasumi-1, OCI-AML3 and U937

ChIP-seq analysis for multiple TFs (Figure 12, 13 and Table S8)

26_ChIPseq_DESeq2_FilteredNormalizedCounts_PeakNorm_CRYBMIM-vs-PBS_1hr_allTFs.xlsx

Differentially increased peaks measured by multiple TF ChIP-seq in 1hr CRYBMIM vs PBS treated MV411

27_ChIPseq_pathway_analysis_9_clusters.xlsx

Pathway analysis for 9 clusters of transcription factor-remodeled genes measured by ChIP-seq