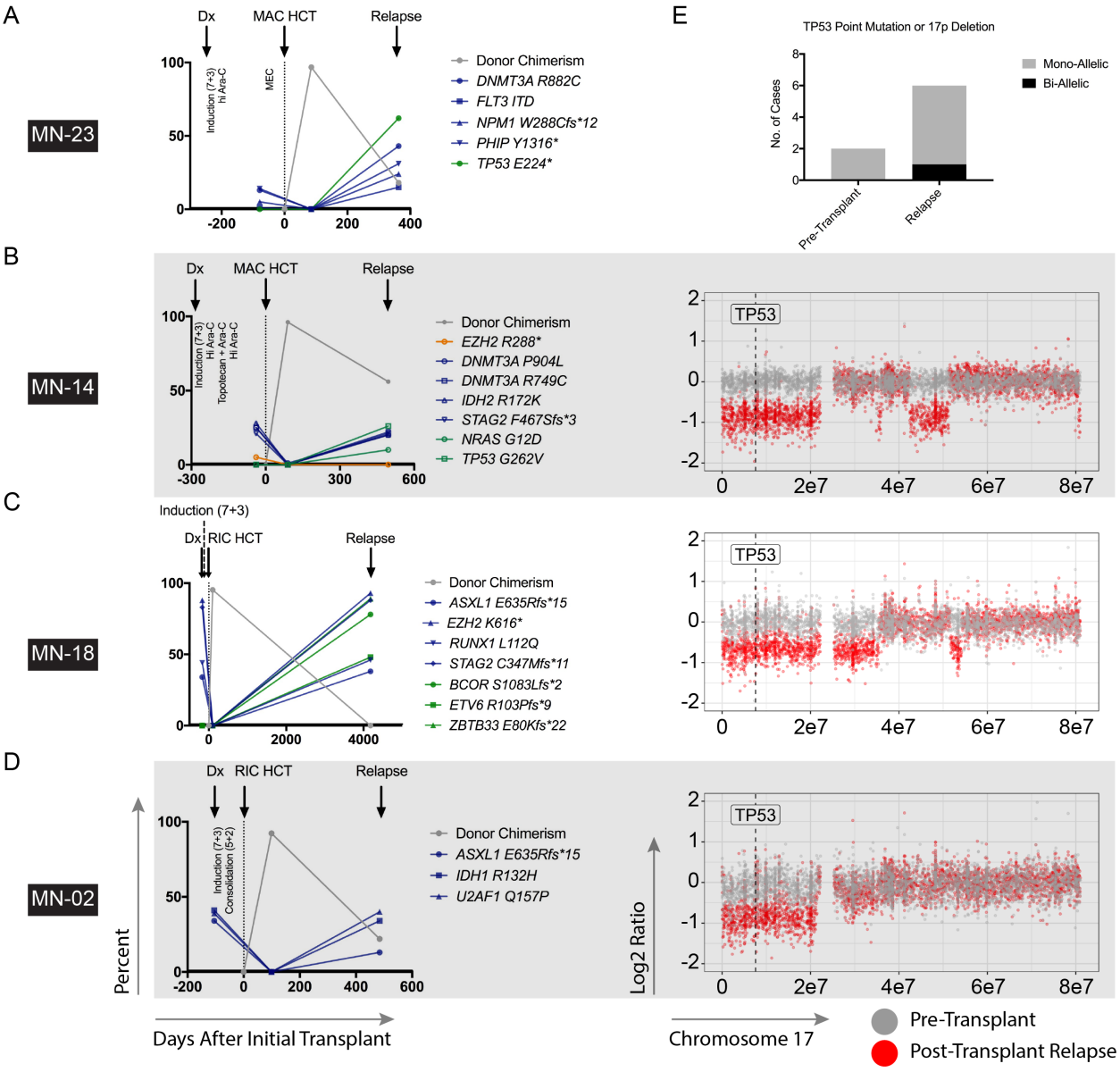
Supplemental Figure 1: Relapse-specific *TP53* mutations and chromosome 17p deletions.

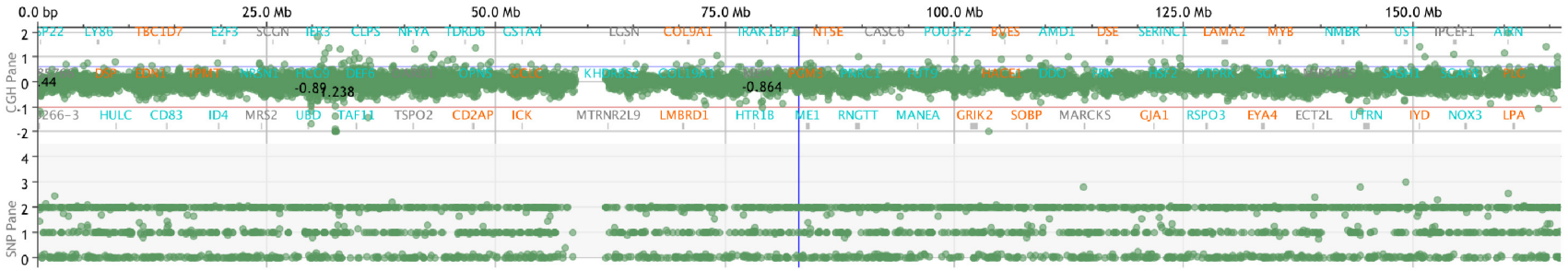
(A-D left) Mutation variant allele and donor chimerism percentage determined from serial targeted sequencing. Pre-transplant-specific mutations in orange, relapse-specific mutations in green, and mutations identified at both timepoints in blue. (B-D right) CGH microarray analysis of chromosome 17. (E) *TP53* alterations detected pre-transplant and at post-transplant relapse.



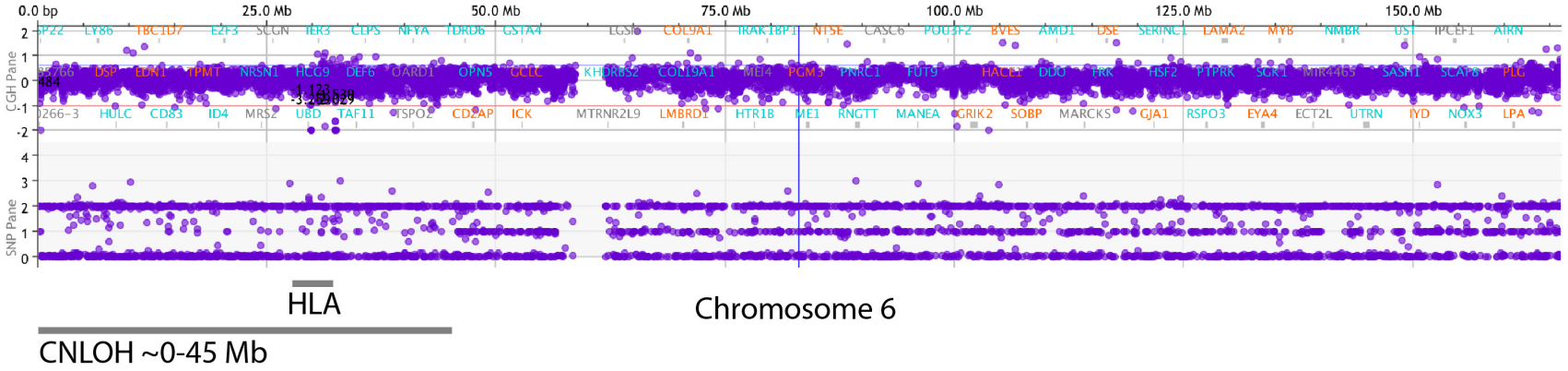
Supplemental Figure 2: 6p copy neutral loss of heterozygosity at post-transplantation relapse.

Copy number and SNP microarray analysis of chromosome 6 in pre-transplant and post-transplant relapse tumor samples from case MN-04 presented from Agilent Cytogenomics software analysis. Copy number is presented in the upper panel. SNP uncut allele number is presented in the lower panel.

Pre-Transplant

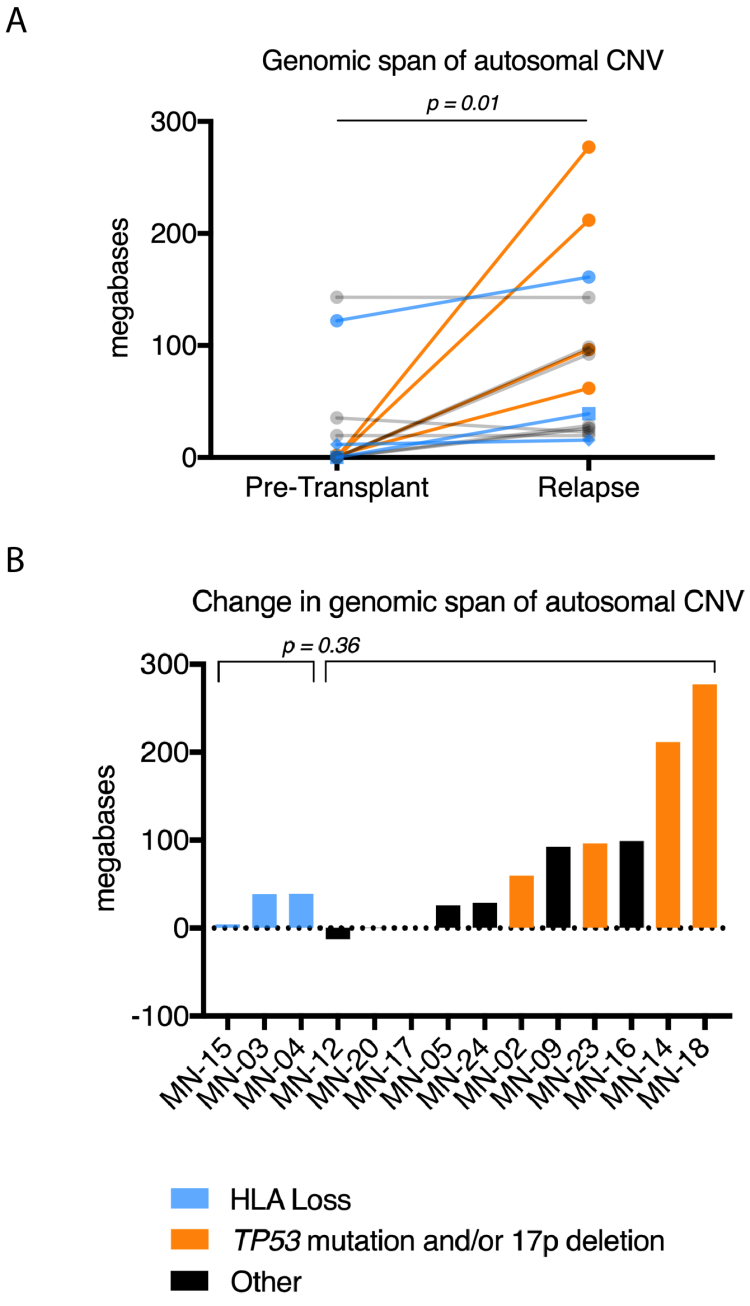


Post-Transplant Relapse



Supplemental Figure 3: Relationship between genome-wide copy number variation, HLA loss, and *TP53* status.

The genomic span of autosomal copy number variations (CNV) identified by CGH+SNP microarray were plotted as matched pre-transplant and post-transplant relapse specimens (**A**) and as the change in genomic span from pre-transplant to post-transplant relapse (**B**). The genomic span of autosomal CNV was greater in relapse versus pre-transplant (p = 0.01, two-tailed Student's t-test). The change in genomic span of autosomal CNV did not significantly vary between HLA loss and non-HLA loss cases (p = 0.36, two-tailed Student's t-test).



Supplemental Table 1: Clinical characteristics of patients included in this study.

Supplemental Table 2: Genes targeted for capture and sequencing.

Supplemental Table 3: Criteria for variant evaluation among genes recurrently mutated in myeloid malignancies.

Supplemental Table 4: Class I HLA typing by targeted sequencing analysis, clinical HLA typing, and amplicon next-generation sequence-based HLA typing of class I and class II HLA alleles.

Supplemental Table 5: Single nucleotide variant and insertion/deletion variants detected via targeted capture sequencing.

Supplemental Table 6: Copy number variants identified by CGH+SNP microarray analysis and summary of clinical cytogenetic analysis.