# Transcriptome of rhesus macaque (*Macaca mulatta*) exposed to total-body irradiation

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[$]YL and JS have made equal contributions to this study.

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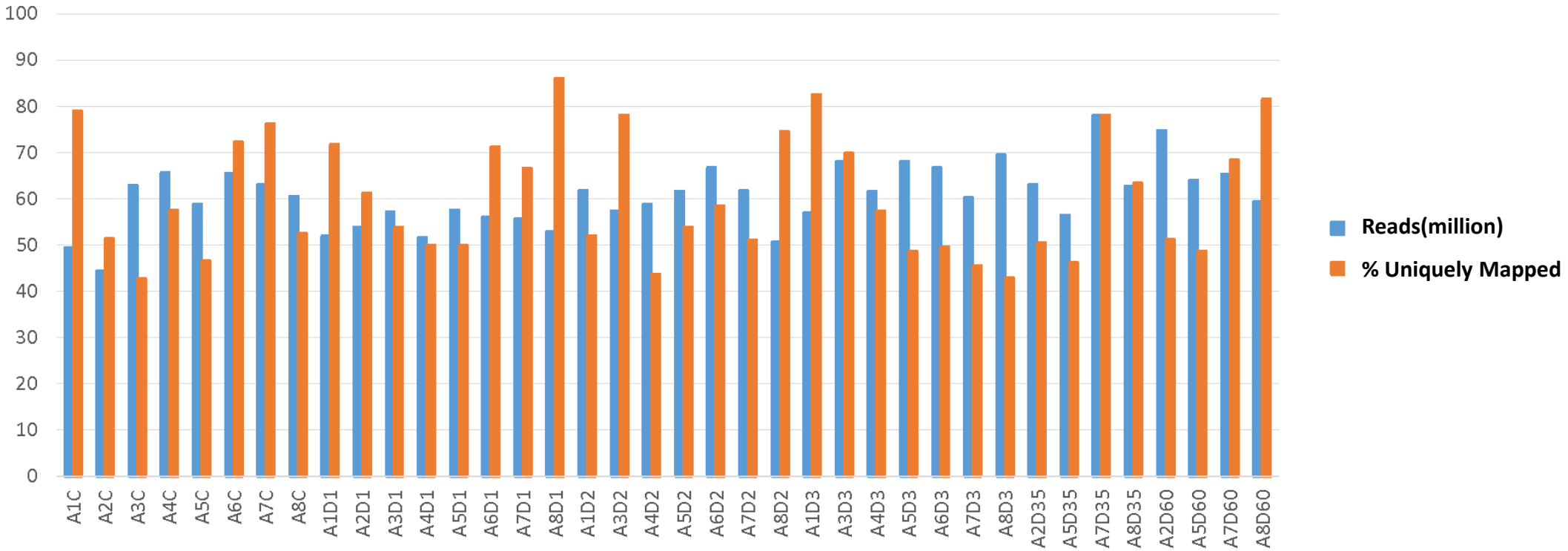
**Supplementary Figure 1.** Uniquely mapped reads (mapping efficiency) of samples as a percent of the reference genome (ranging from 43% to 86%). The X-axis displays sample IDs by acquisition sequence.



**Supplementary Figure 2.** 6-way Venn diagram of differentially expressed genes (DEGs) (fold change ≥ 2, FDR <0.05, downregulated) in survivors D1 vs. Baseline (S_D1), Survivors D2 vs. Baseline (S_D2), Survivors D3 vs. Baseline (S_D3), Non-Survivors D1 vs. Baseline (NS_D1), Non-survivors D2 vs. Baseline (NS_D2), Non-survivors D3 vs. Baseline (NS_D3). The groups are color coded to denote significantly dysregulated genes within and across groups along with overlap details.