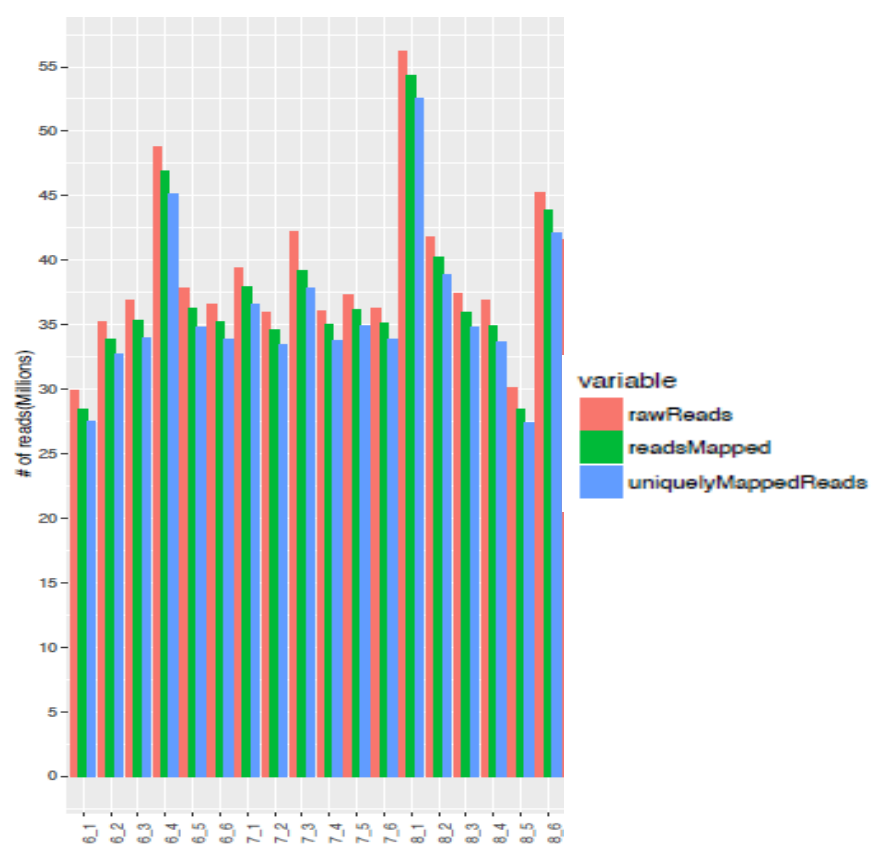
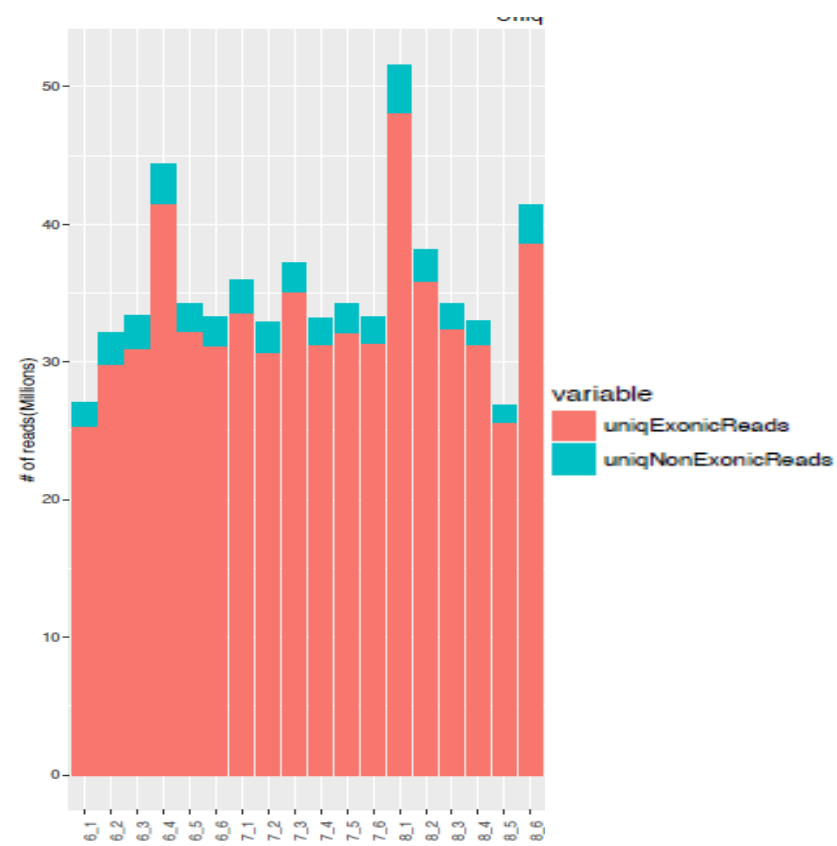


A



B



C



Supplementary Figure 2. Descriptive statistics of RNA-seq dataset 1. MDMs obtained from 3 different donors were treated or not with anti-CCL2 or control Ab (2.5 $\mu\text{g/ml}$) for 4 or 20 h. Total RNA was extracted, subjected to poly(A) selection followed by reverse transcription, generation of cDNA libraries, and sequencing. (A) Raw, mapped and uniquely mapped reads per sample. (B) Uniquely exonic and non-exonic reads per sample. (C) Protein-coding genes reads per sample. The samples numeric codes in the x axis identify the different donors (first number) and conditions (second number; 1 = nil 4 h, 2 = anti-CCL2 Ab 4 h, 3 = control Ab 4 h, 4 = nil 20 h, 5 = anti-CCL2 Ab 20 h, 6 = control Ab 20 h).