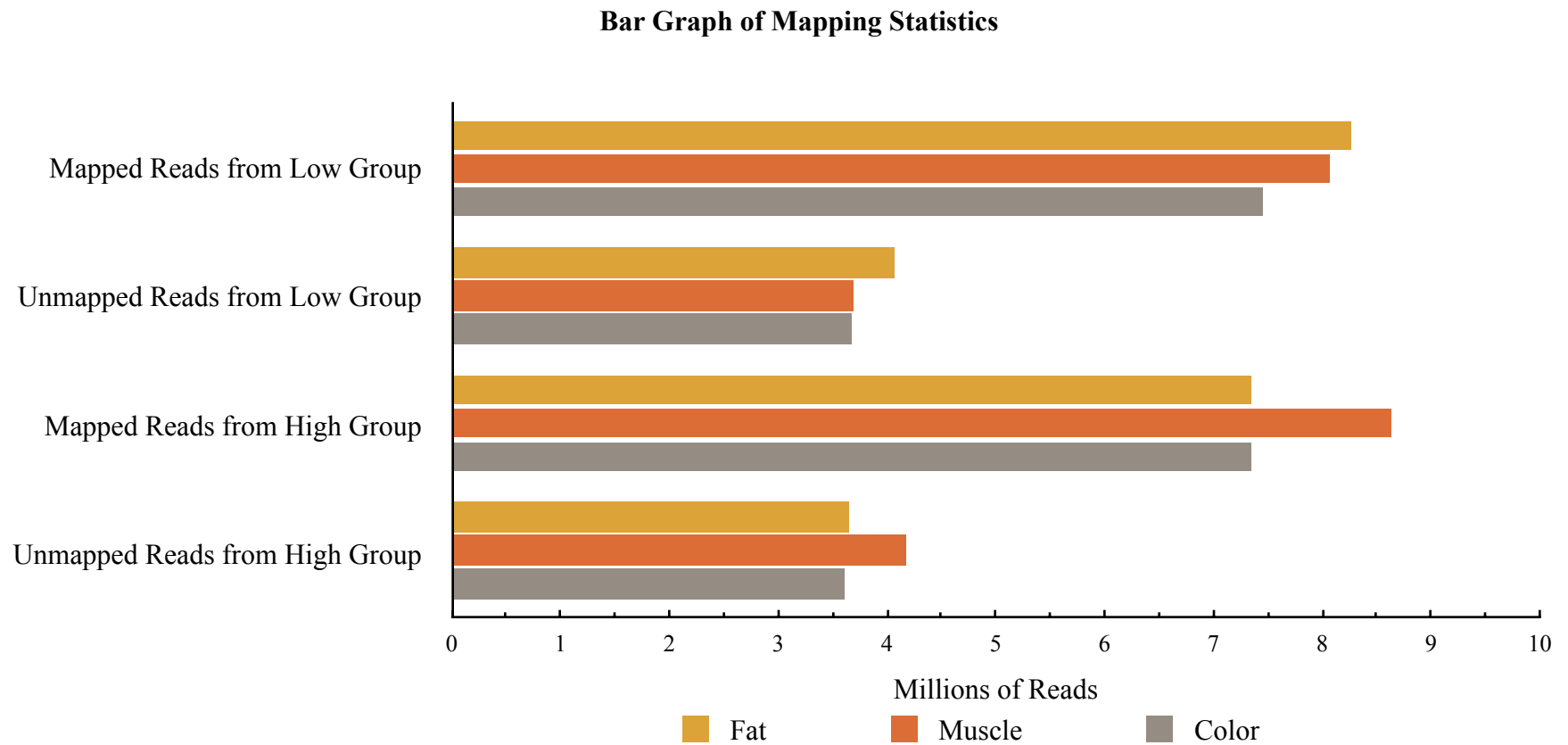


FIGURE 2



This bar graph shows the mapping statistics of the reads of high and low-ranked families. Reads were mapped to the previously generated reference transcriptome. An average of 8,600,000 reads were mapped per group.