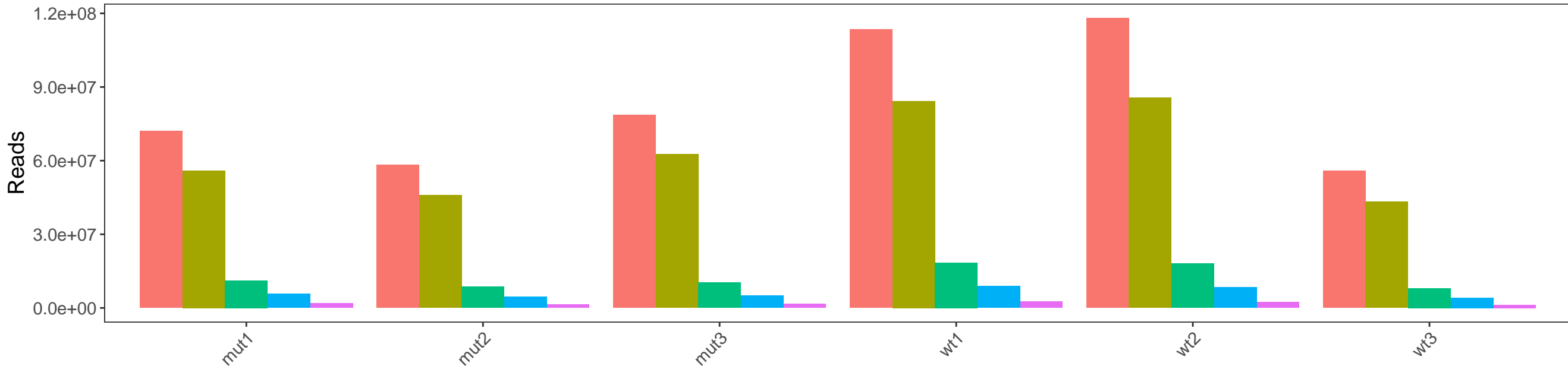
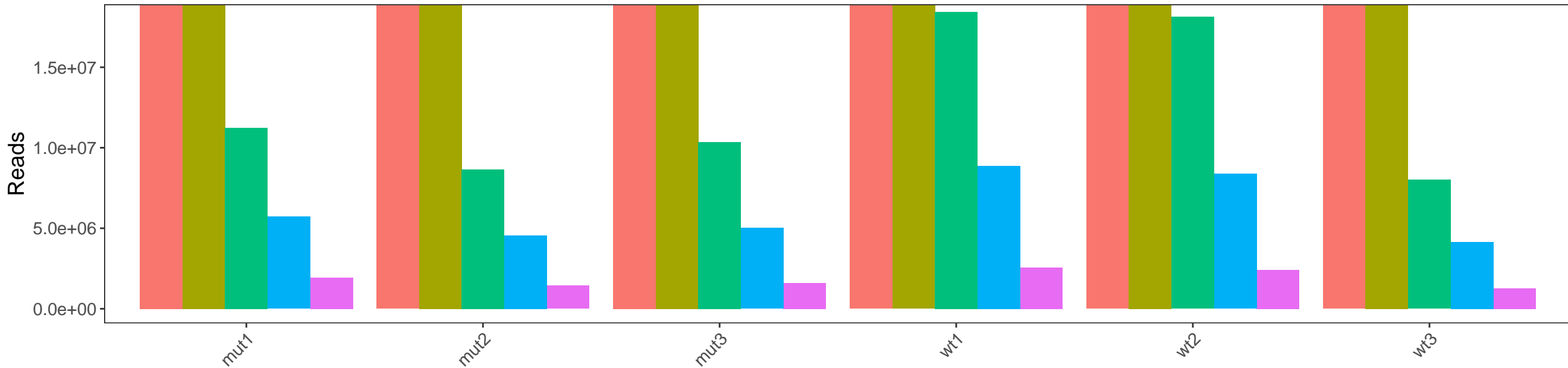


read\_counts\_per\_step



read\_counts\_per\_step



sample total\_reads after\_rRNA\_depletion after\_dedup genome\_aligned CDS\_reads