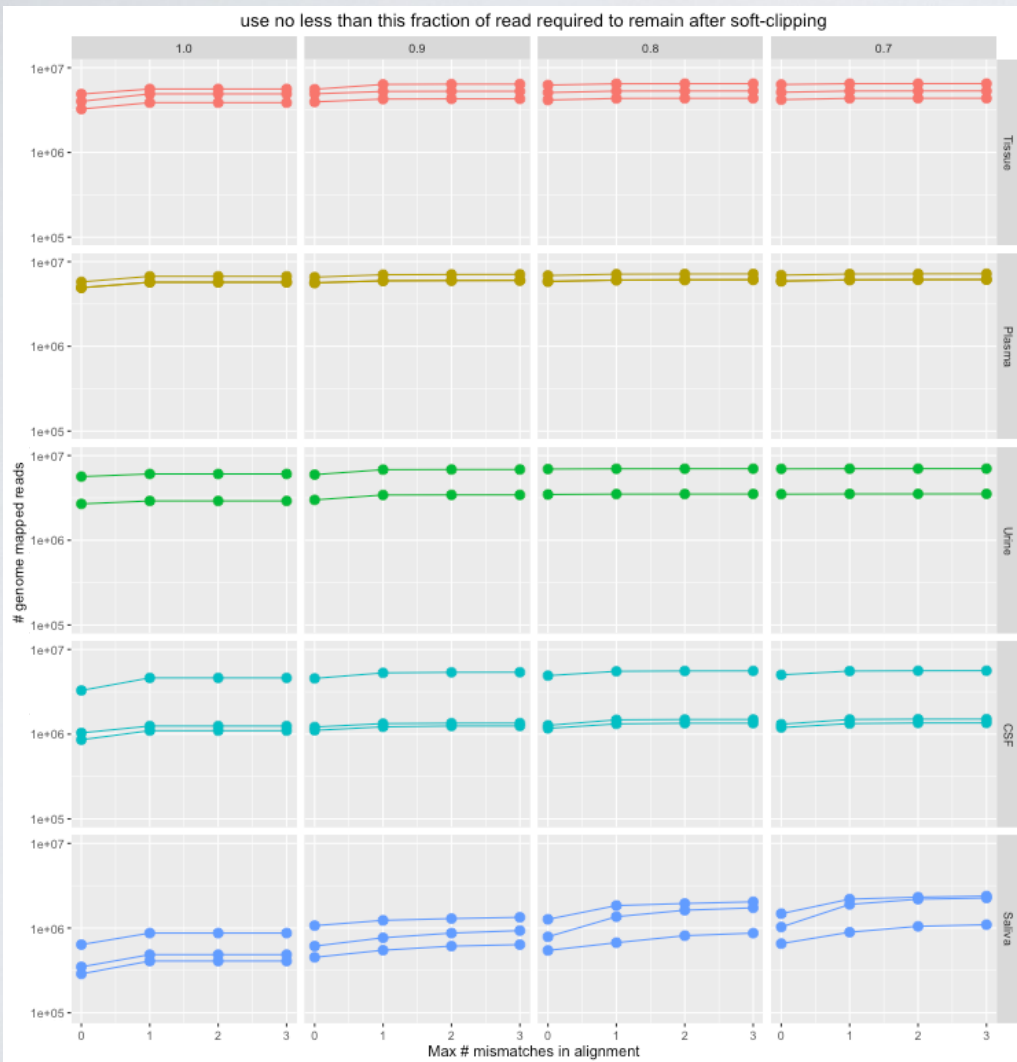


source-specific alignment stats

genome mapped reads

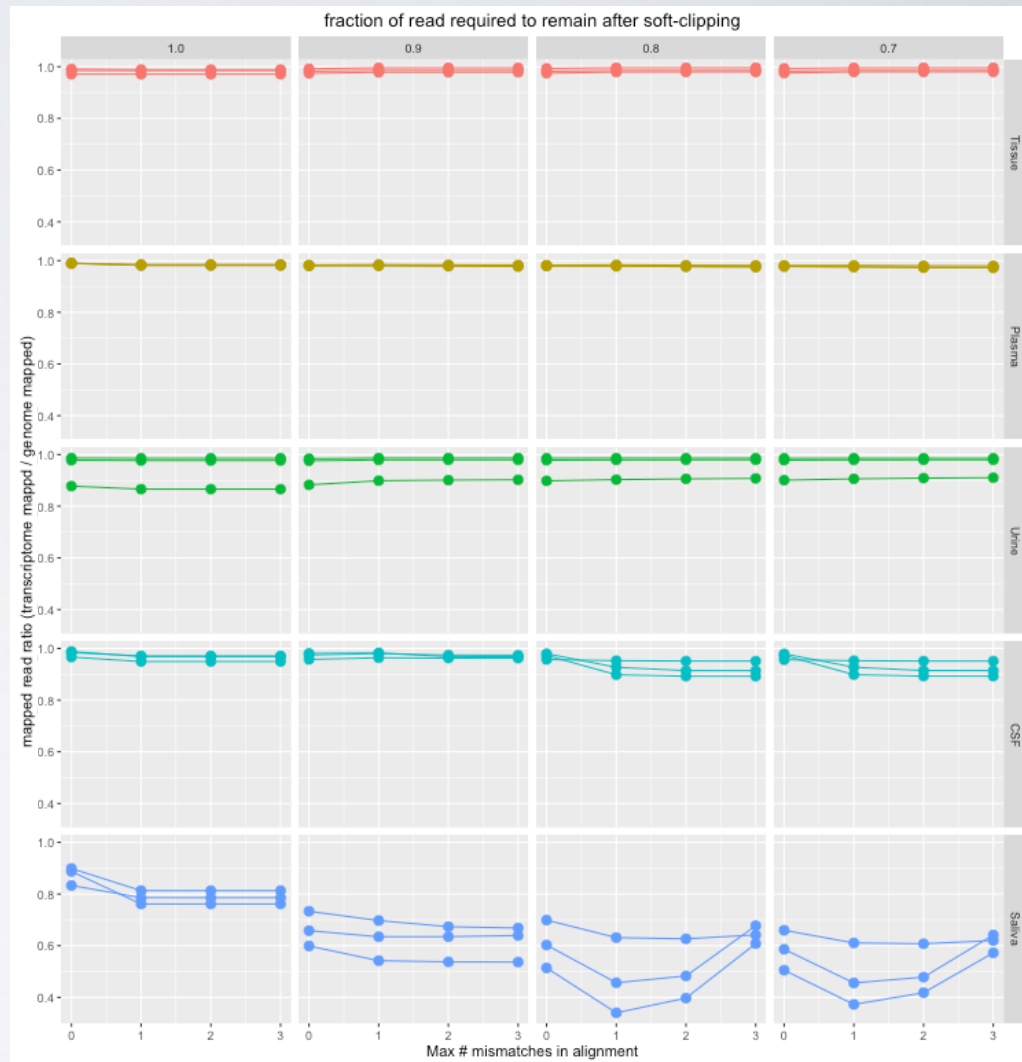


stringent

alignment mode

lenient

$\frac{\text{\# transcriptome mapped reads}}{\text{\# genome mapped reads}}$

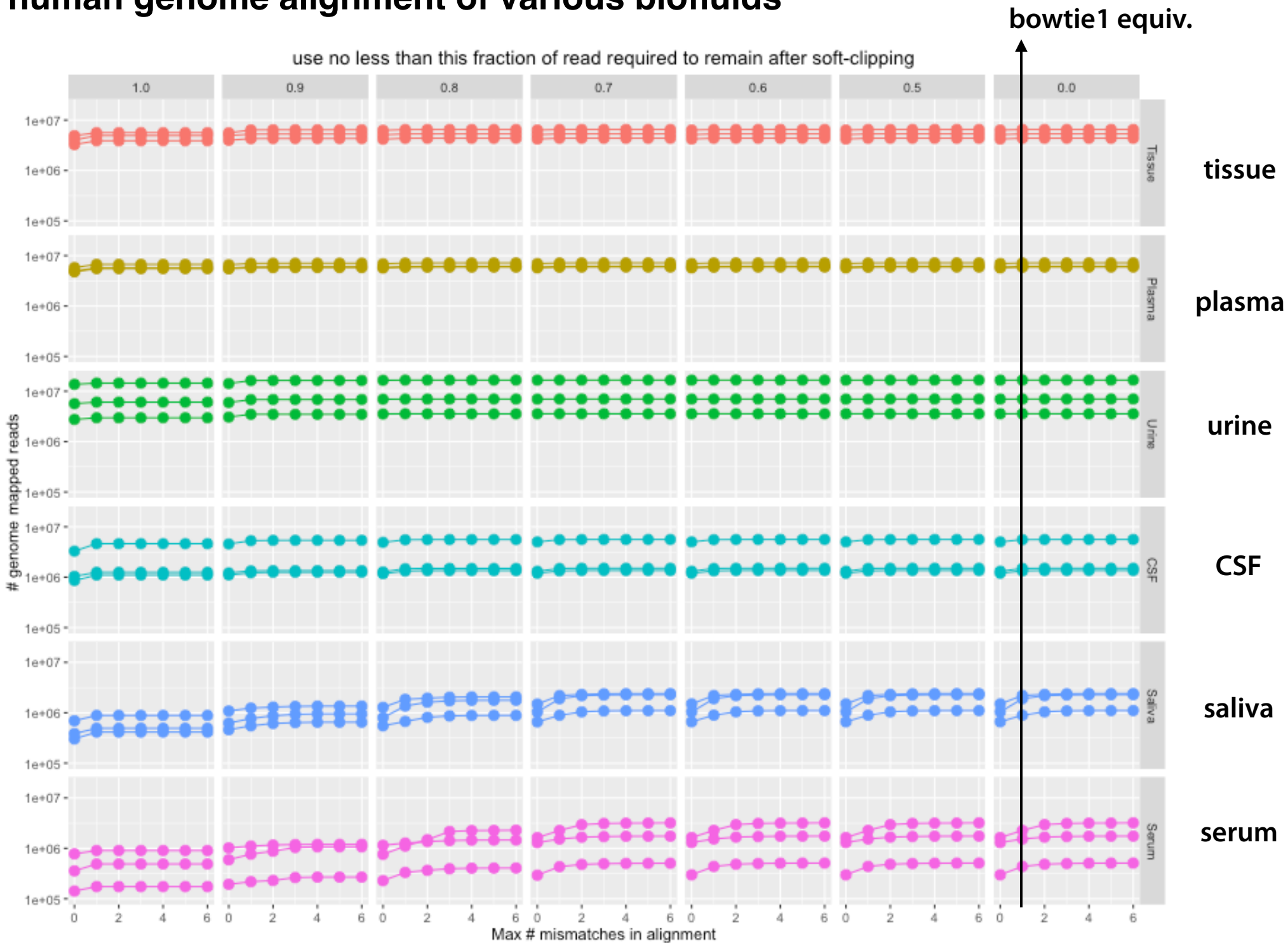


stringent

alignment mode

lenient

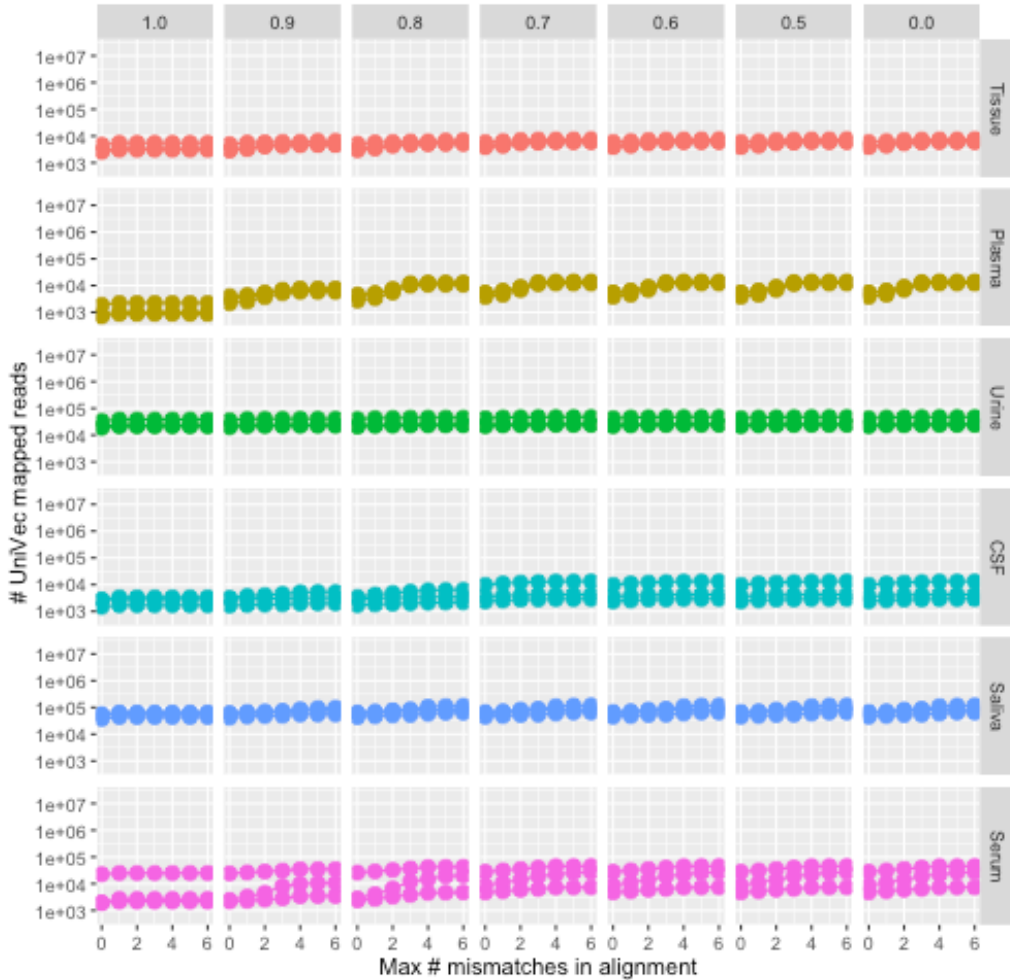
human genome alignment of various biofluids



contaminant alignment of various biofluids

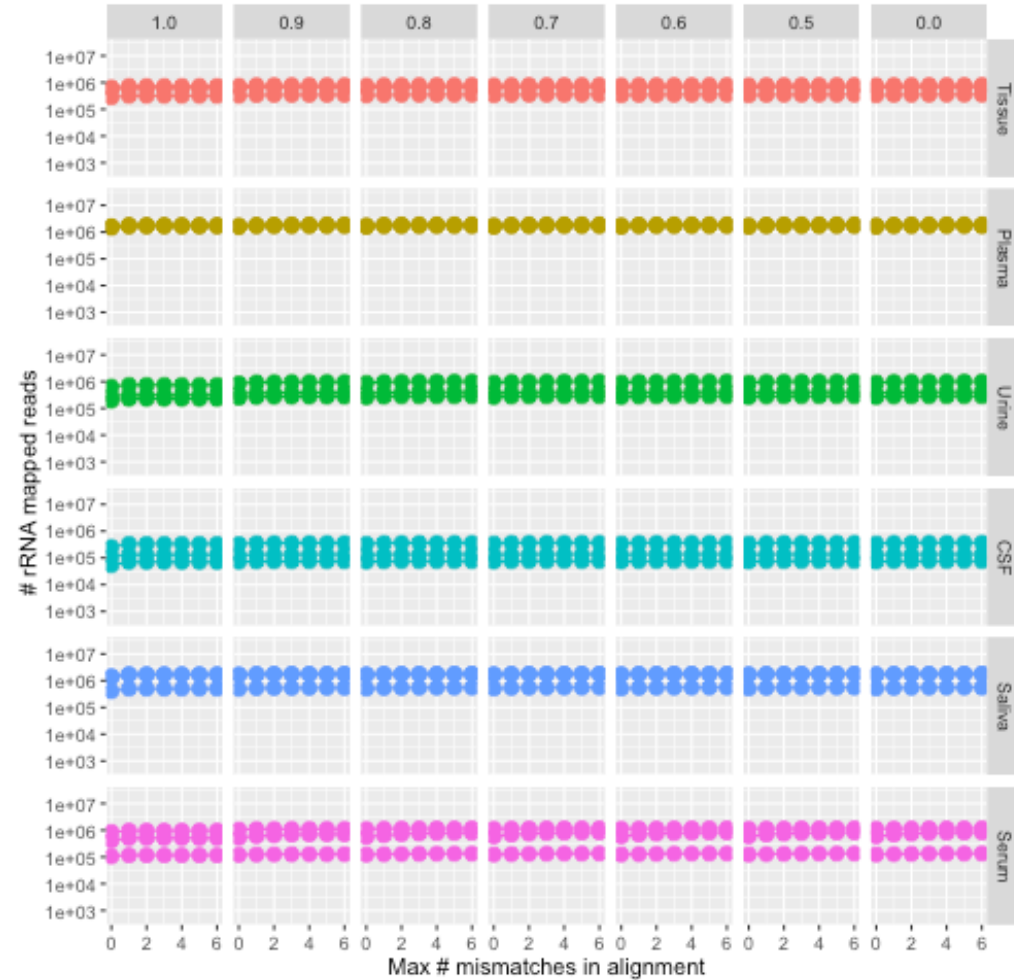
UniVec contaminants

use no less than this fraction of read required to remain after soft-clipping

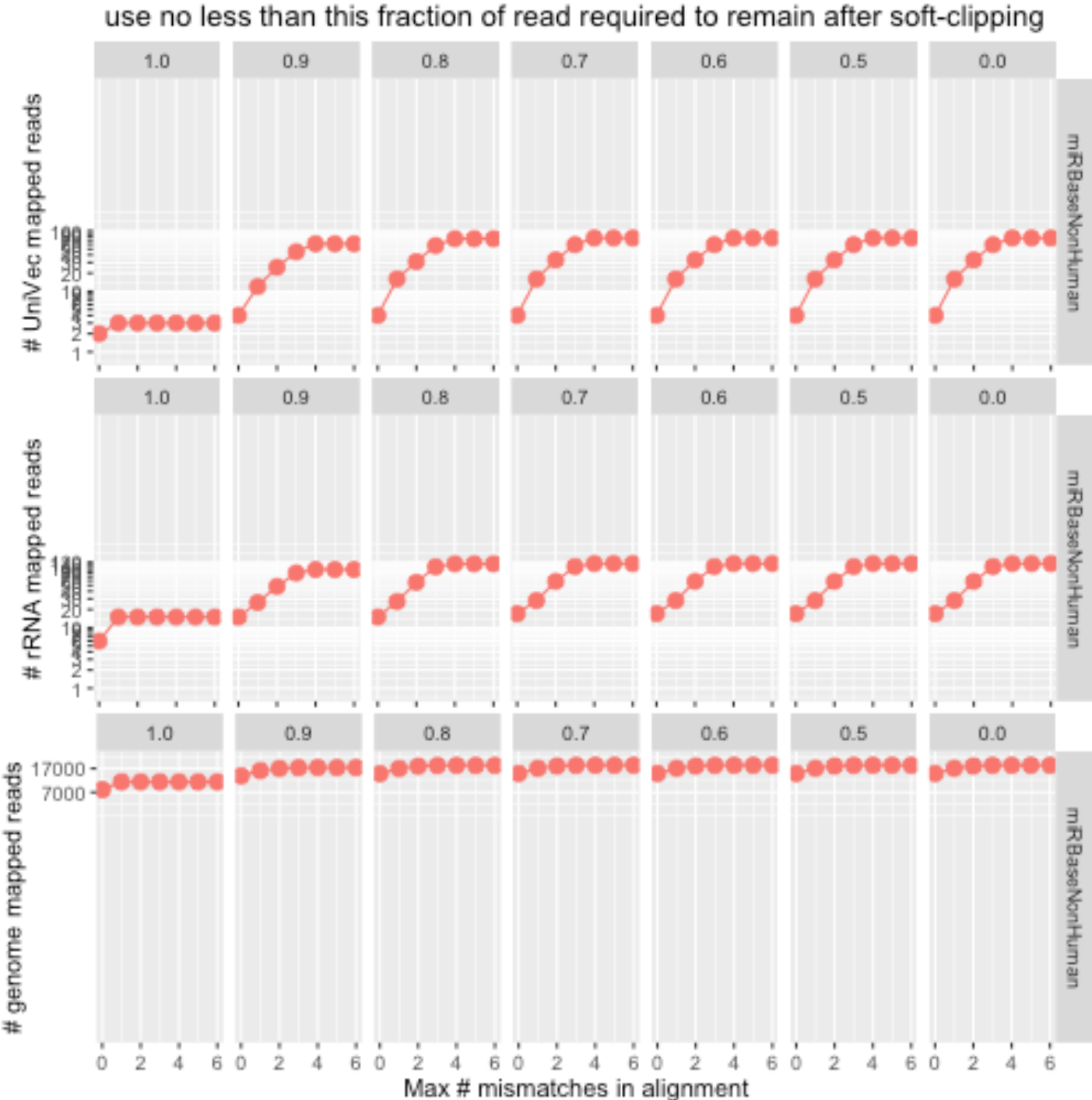


rRNA

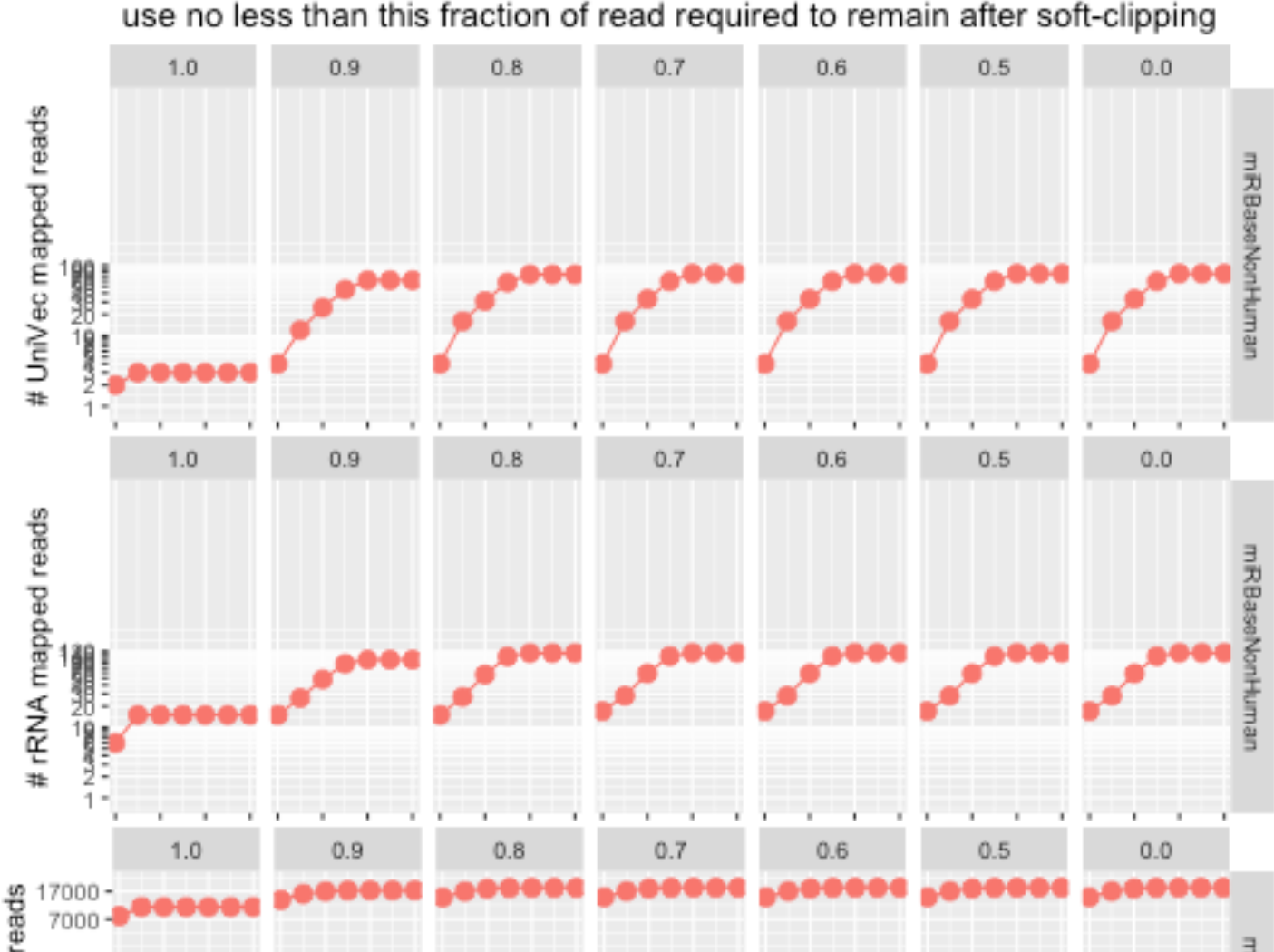
use no less than this fraction of read required to remain after soft-clipping



exogenous miRBase miRNAs



exogenous miRBase miRNAs



33,240 non-human mature miRNAs in miRBase
2 miRNAs with 100% identity to UniVec contaminants
6 miRNAs with 100% identity to human rRNA
7,747 miRNAs with 100% identity to human genome
10,336 miRNAs with 1mm to human genome

transcriptome / genome ratio

