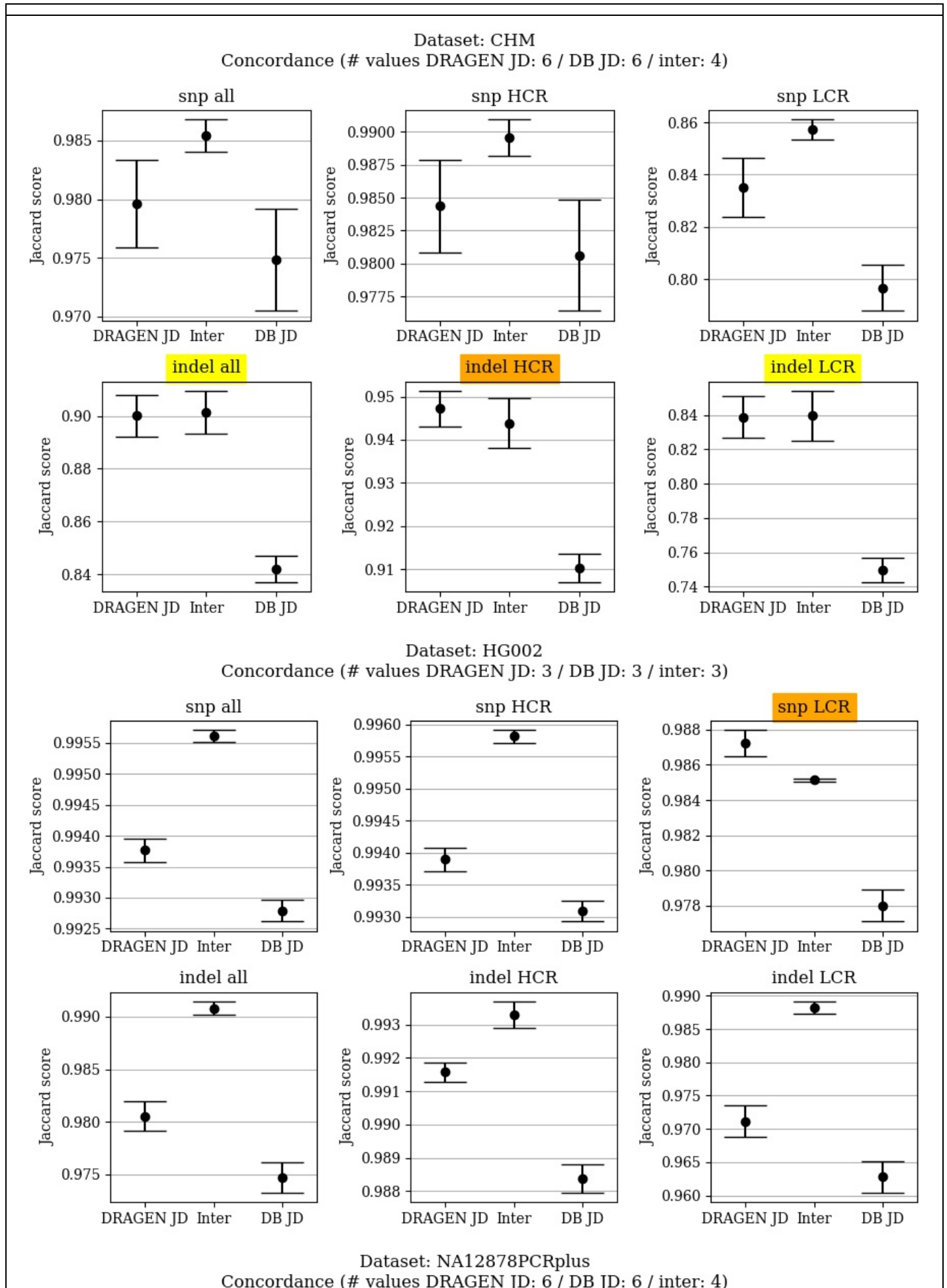
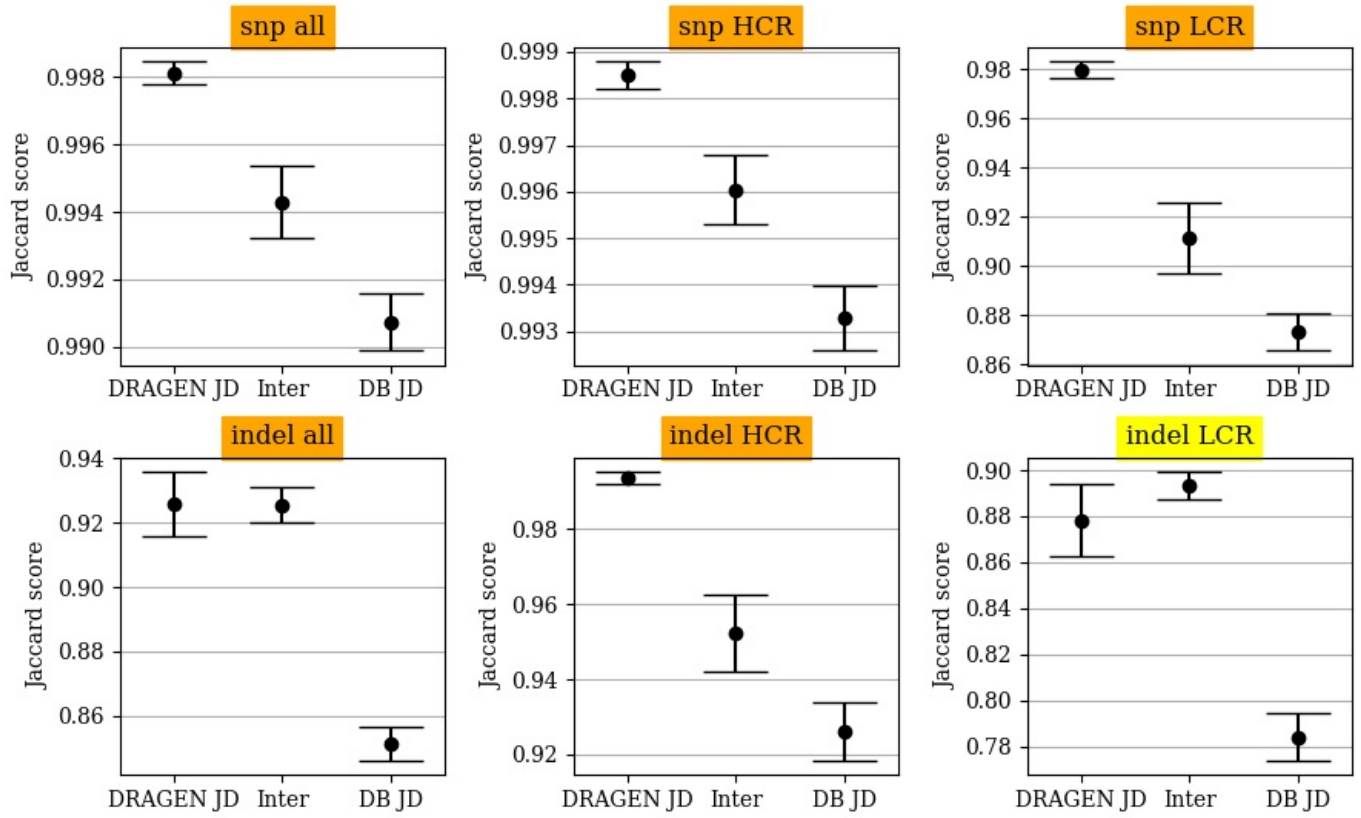


# The analysis suggests that the tools are NOT functionally equivalent.

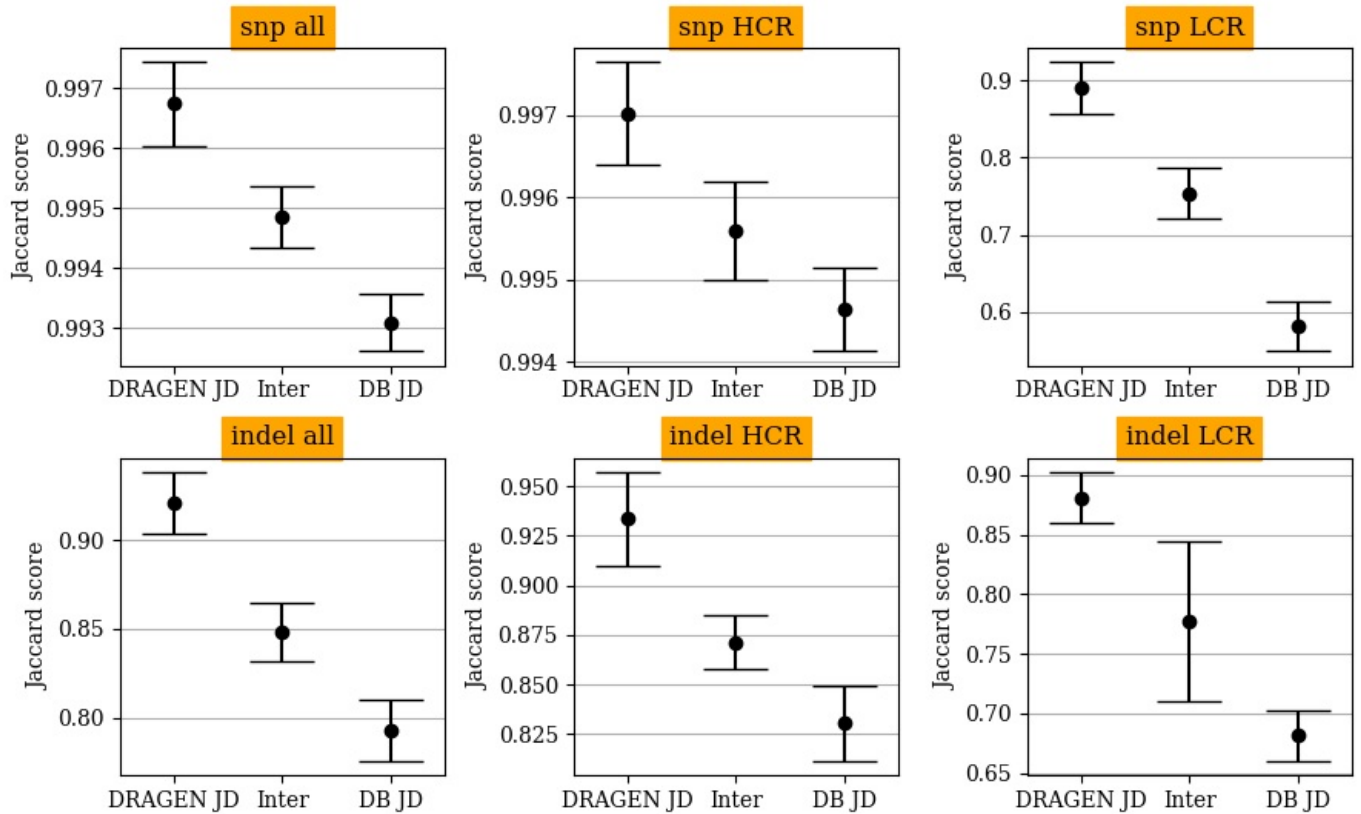
For more information about how to interpret the plots, please refer to the [documentation on GitHub](#).

## FE plots





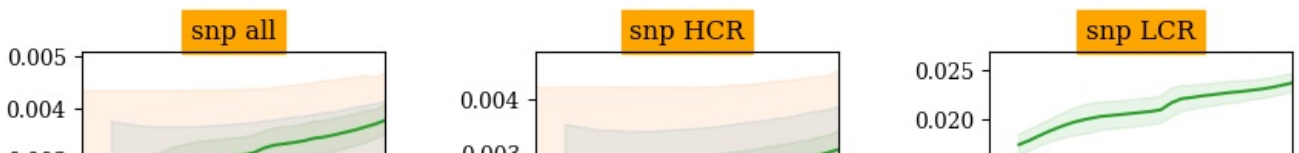
Dataset: NA12878PCRplusExome  
Concordance (# values DRAGEN JD: 6 / DB JD: 6 / inter: 4)

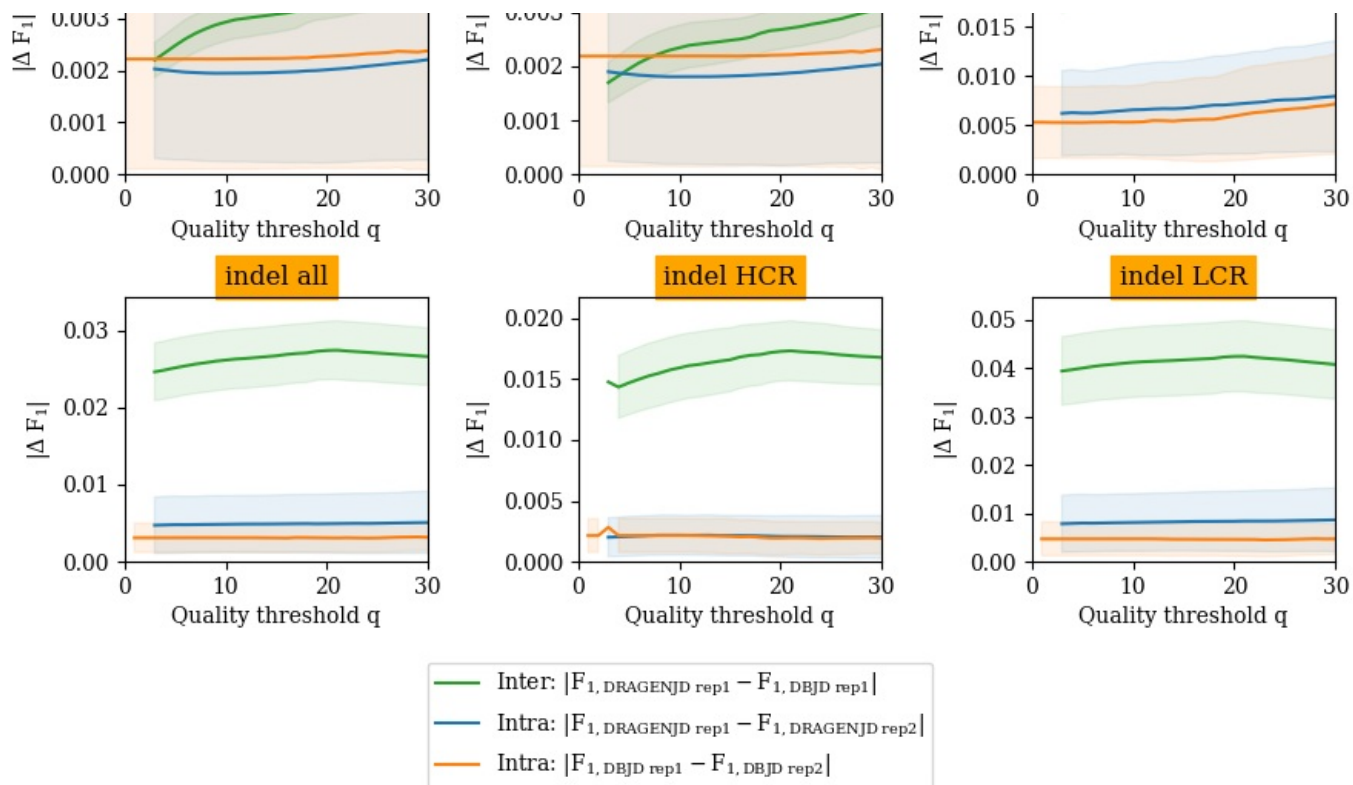


## F1 plots

Dataset: CHM

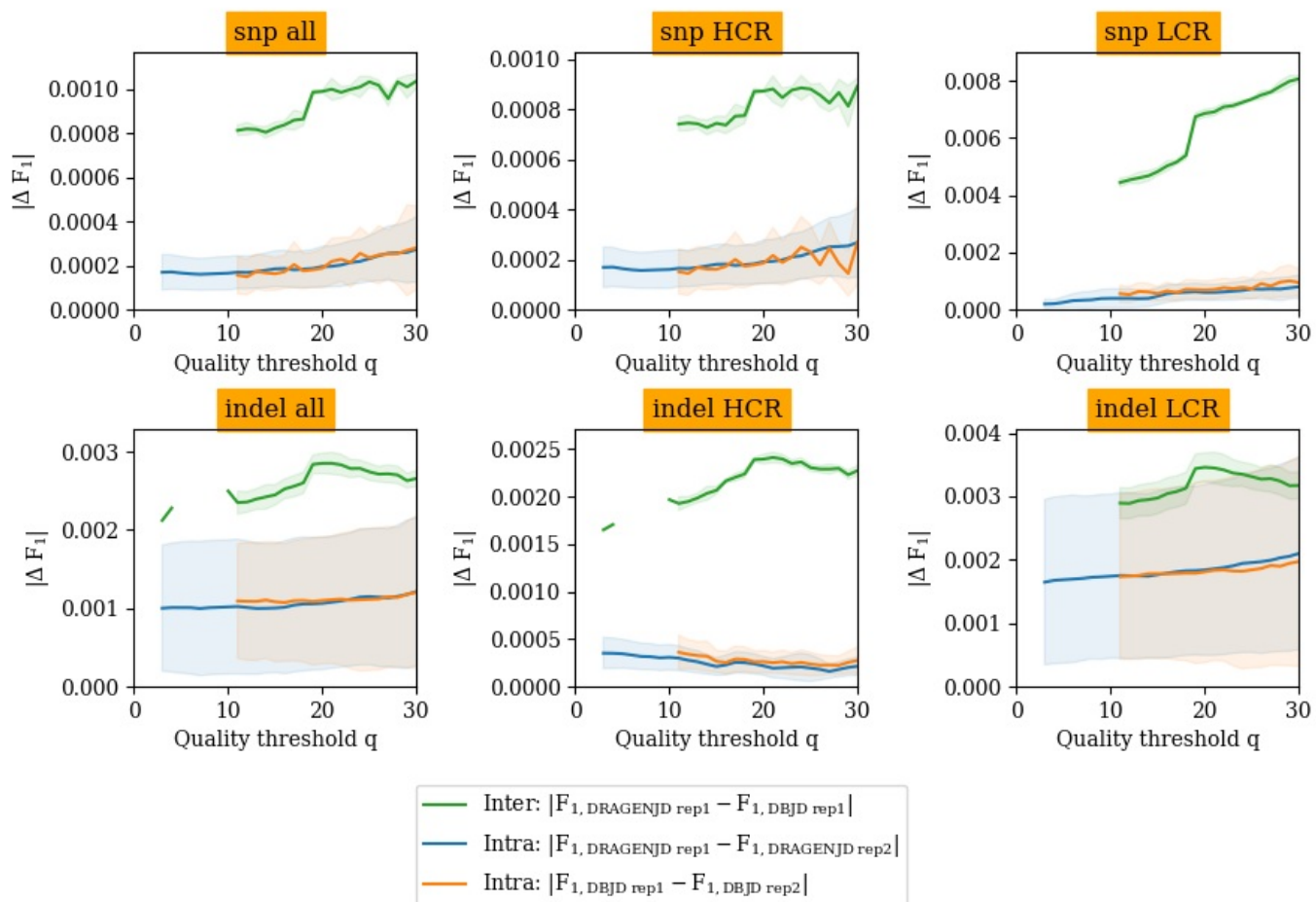
Absolute  $F_1 = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$  score differences for calls with  $QUAL \geq q$  (# replicates: 4)





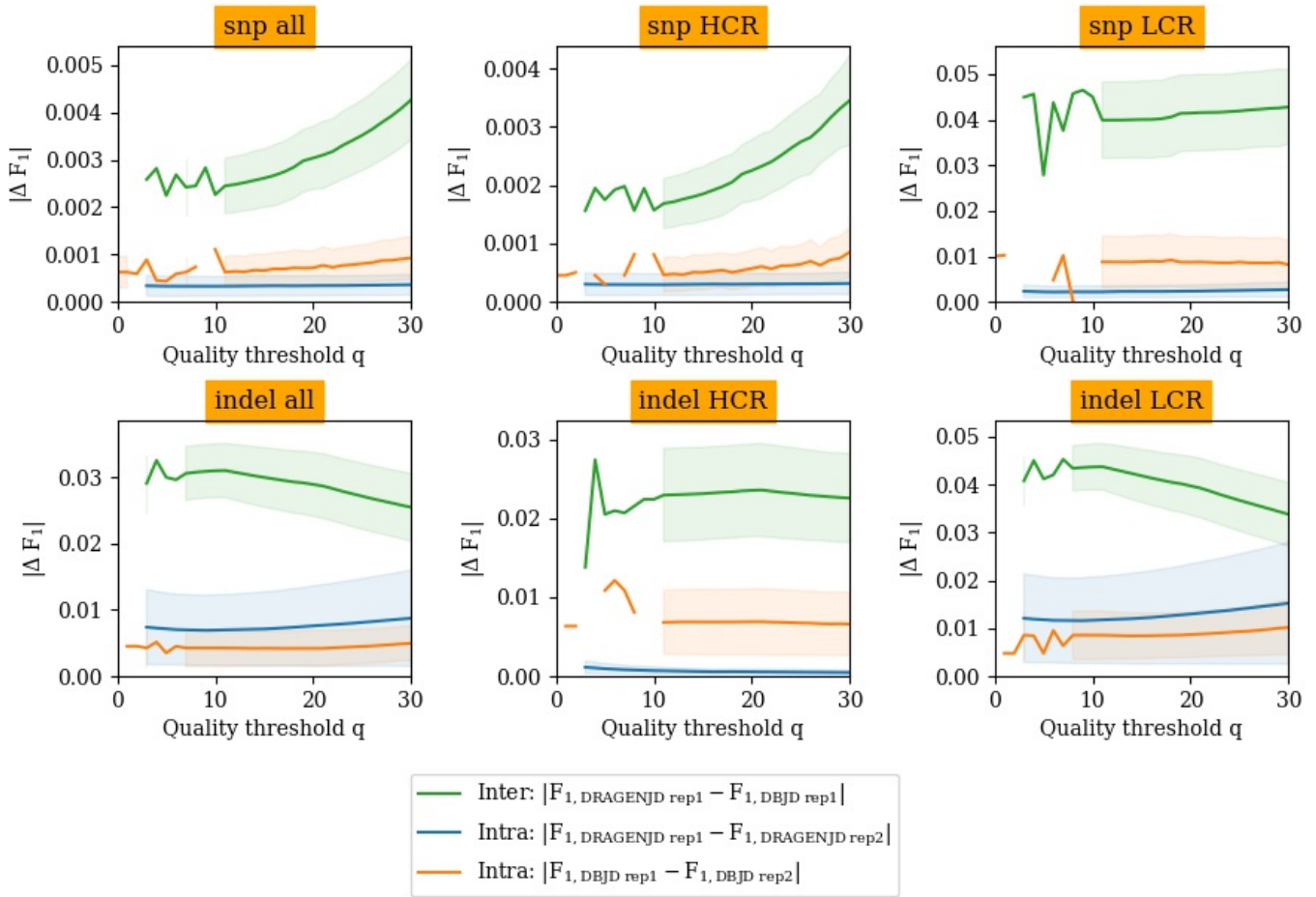
Dataset: HG002

Absolute  $F_1 = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$  score differences for calls with  $QUAL \geq q$  (# replicates: 3)



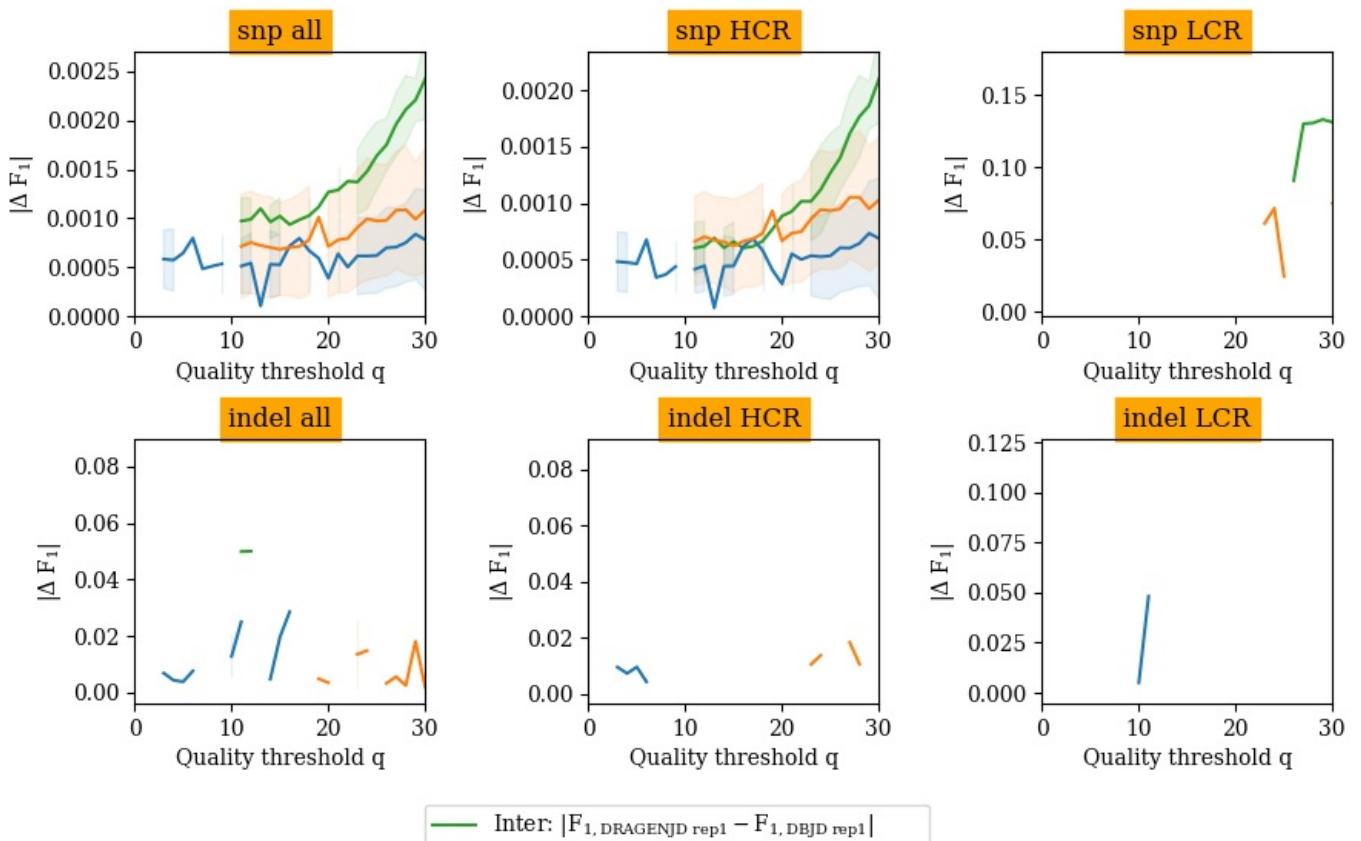
Dataset: NA12878PCRplus

Absolute  $F_1 = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$  score differences for calls with  $QUAL \geq q$  (# replicates: 4)



Dataset: NA12878PCRplusExome

Absolute  $F_1 = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$  score differences for calls with  $QUAL \geq q$  (# replicates: 4)



— Intra:  $|F_{1, \text{DRAGENJD rep1}} - F_{1, \text{DRAGENJD rep2}}|$   
— Intra:  $|F_{1, \text{DBJD rep1}} - F_{1, \text{DBJD rep2}}|$