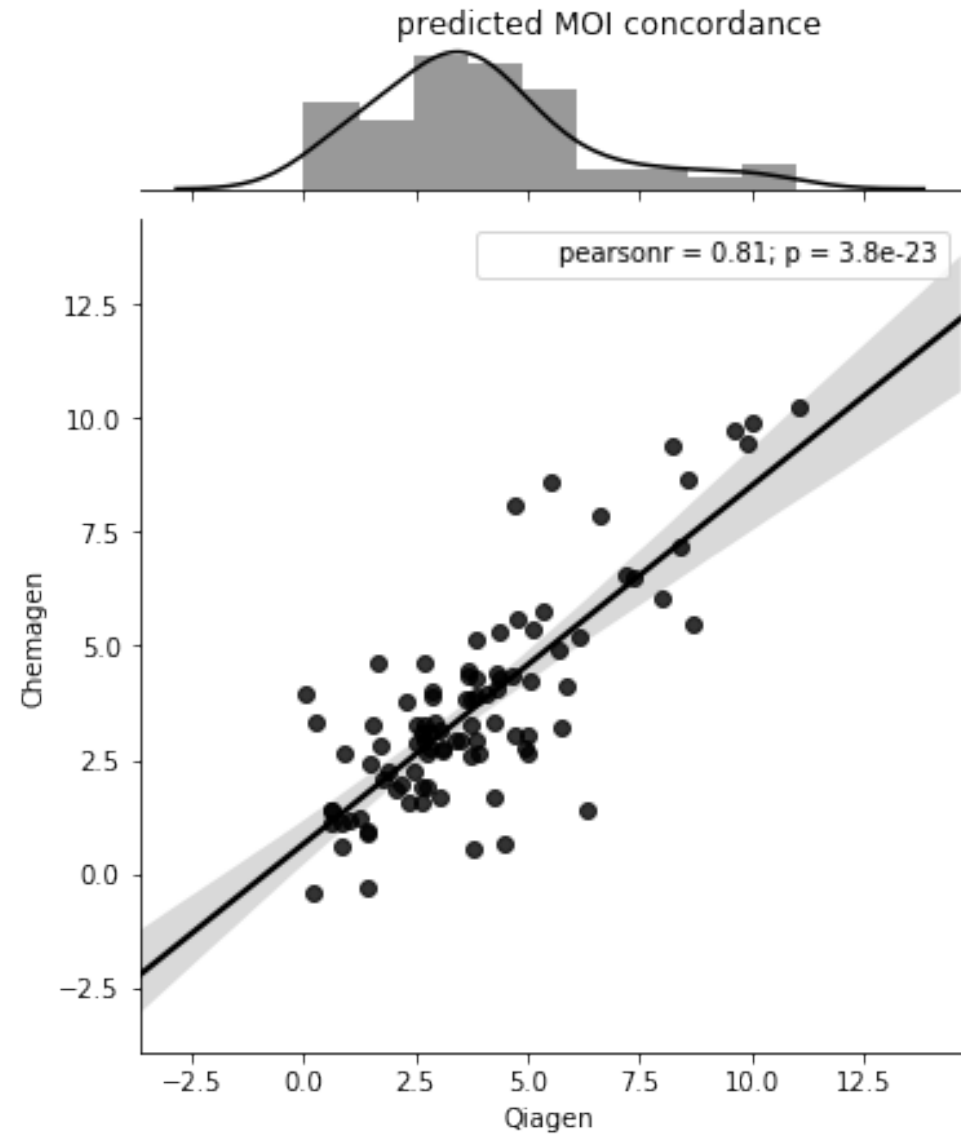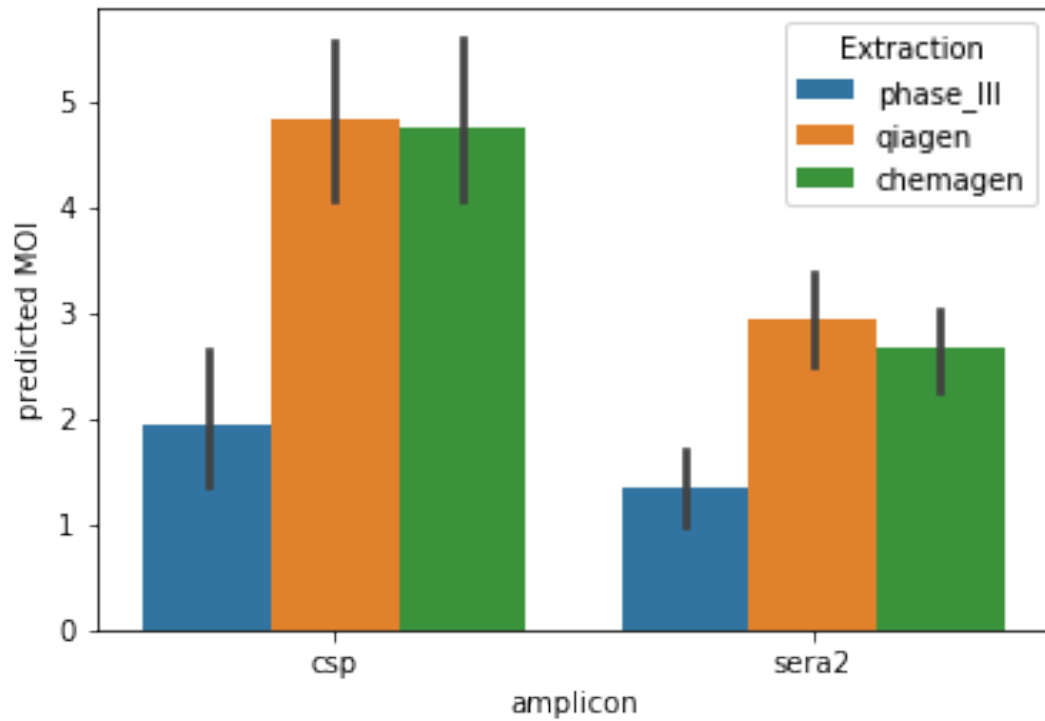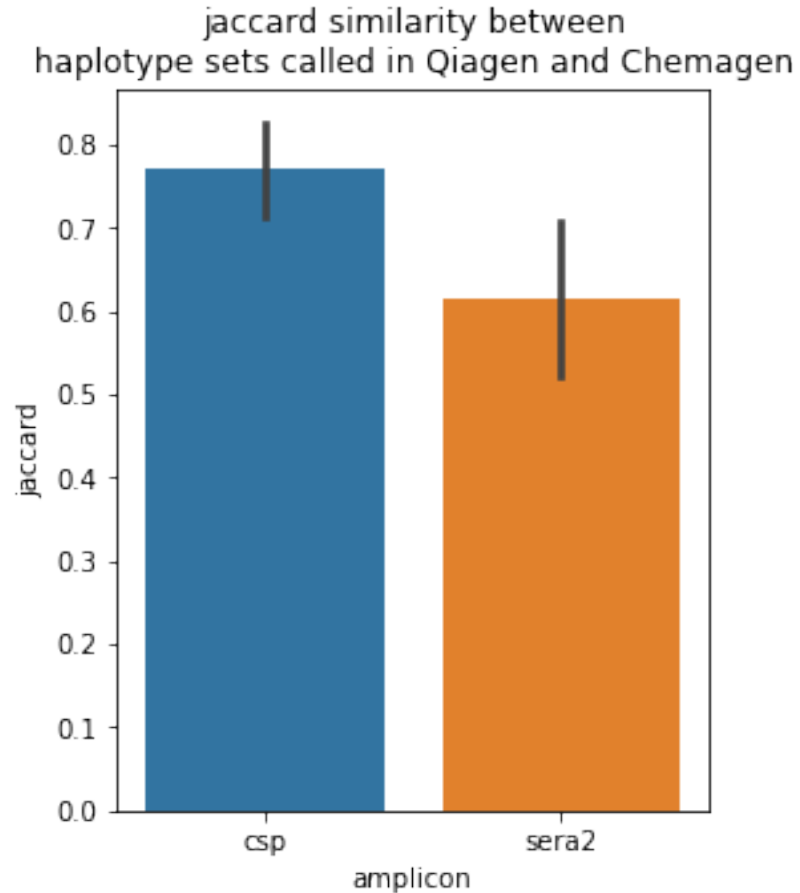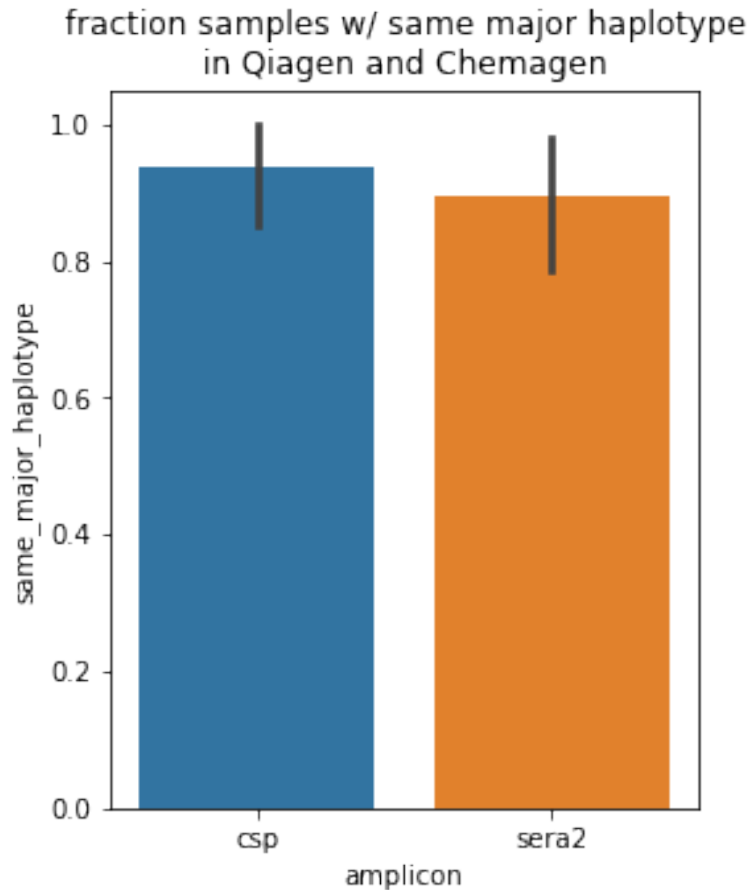# rtss amplicon

extractor testing 20180720

good agreement b/t Qiagen and Chemagen for predicted MOI

good concordance b/t haplotypes called

fraction samples w/ same major haplotype in Qiagen and Chemagen

jaccard similarity between haplotype sets called in Qiagen and Chemagen

Where jaccard similarity is a measure of similarity between 2 sets s1 and s2 defined as:

$$J = \frac{\text{length}(\text{intersection}(s1, s2))}{\text{length}(\text{union}(s1, s2))}$$

~90% agreement b/t major haplotypes

comparable to concordance b/t patient sample replicates in Jul 17 validation run

fraction same major haplotype called in patient sample replicates

jaccard similarity b/t haplotype sets called in patient sample replicates
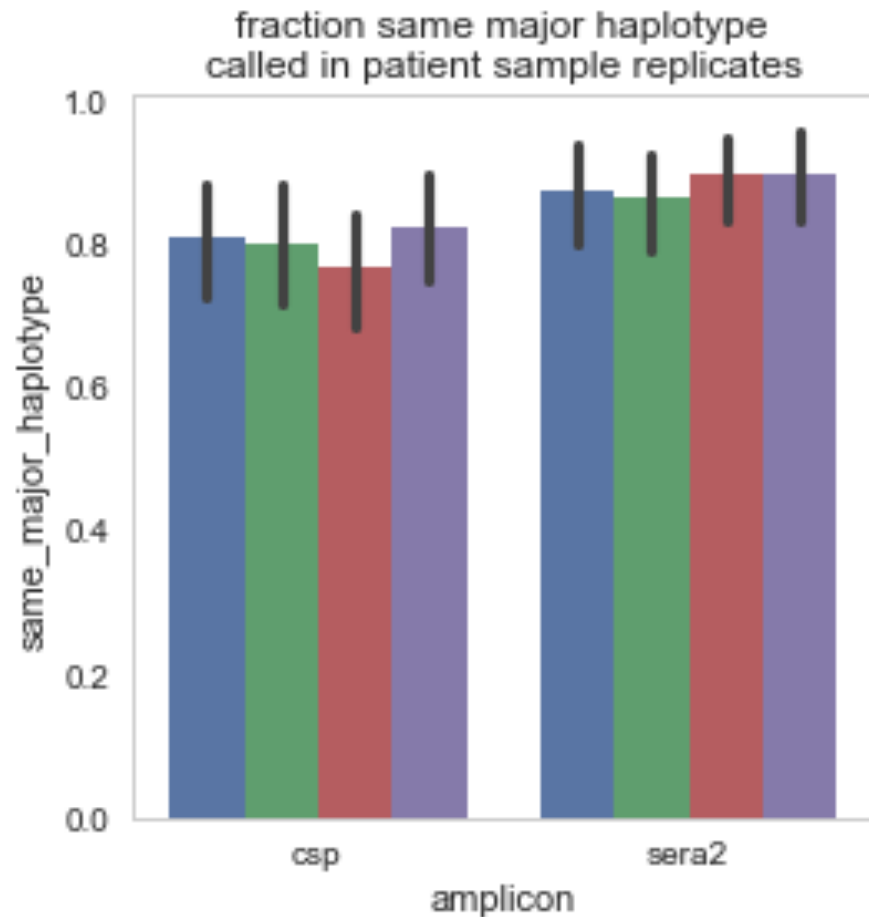
~80-90% agreement b/t major haplotypes for all tools
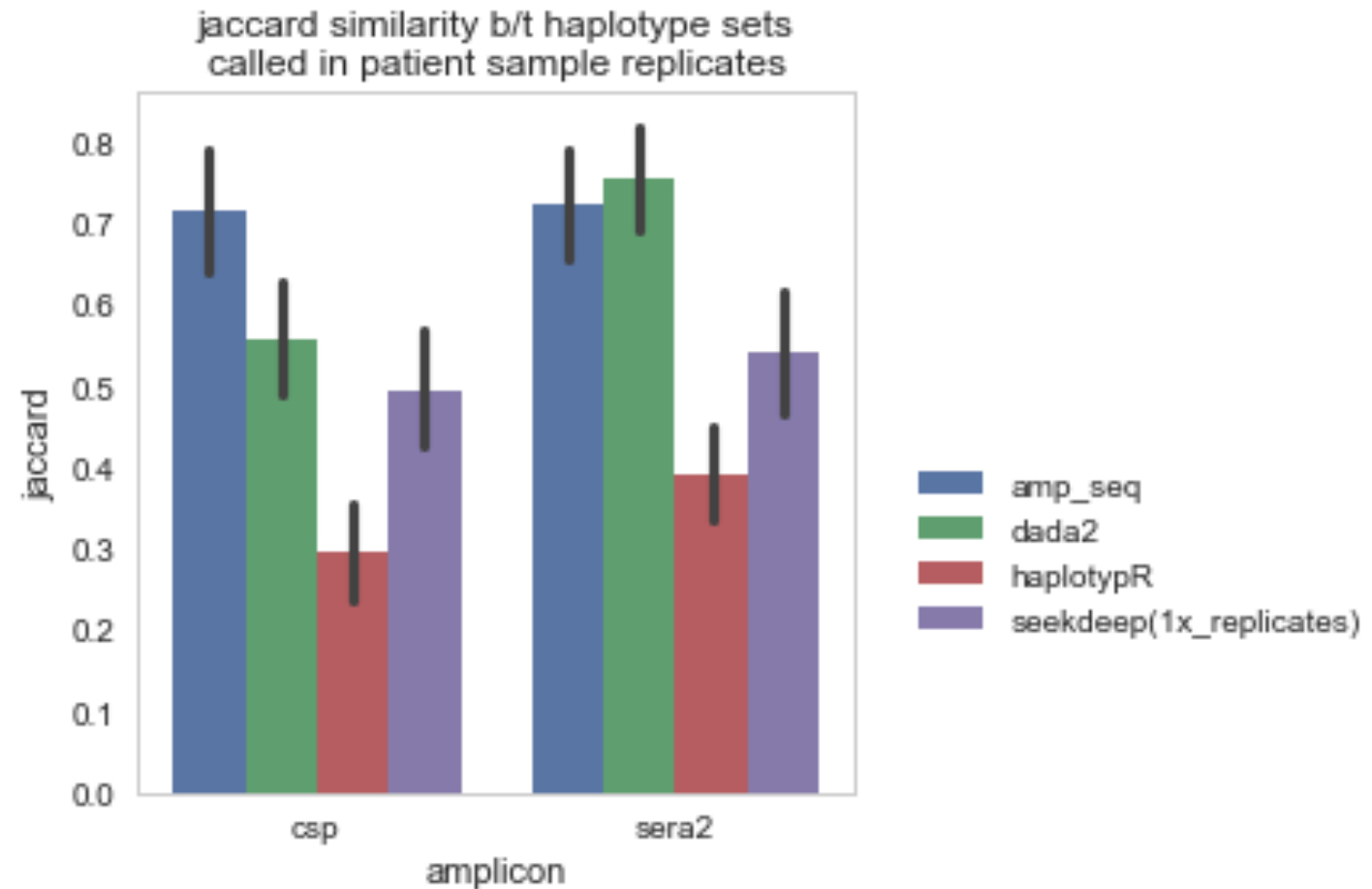
Better performing tools (amp_seq, dada2) agree more consistently between patient sample replicates

similar patterns b/t mock sample replicates in Jul 17 validation run