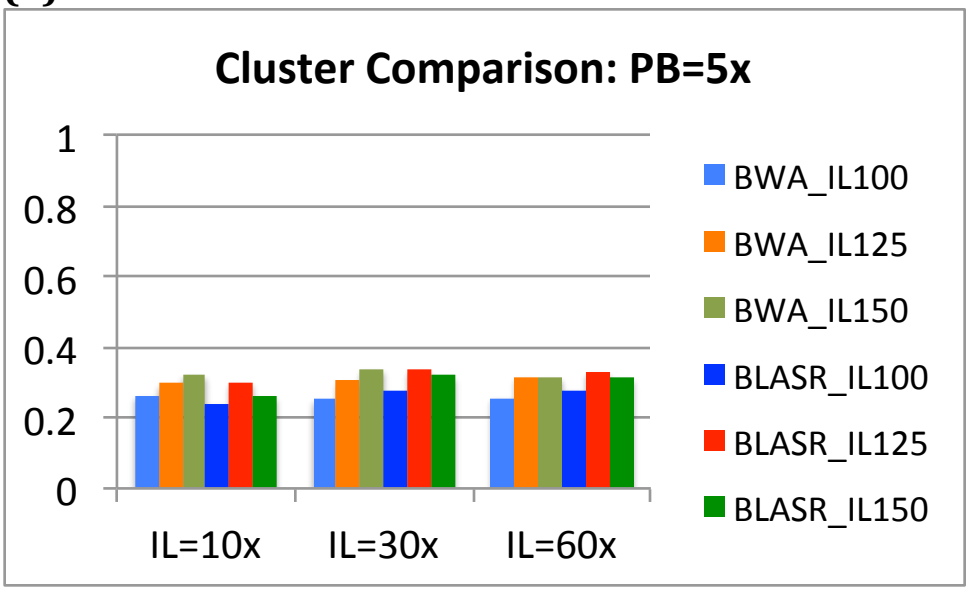
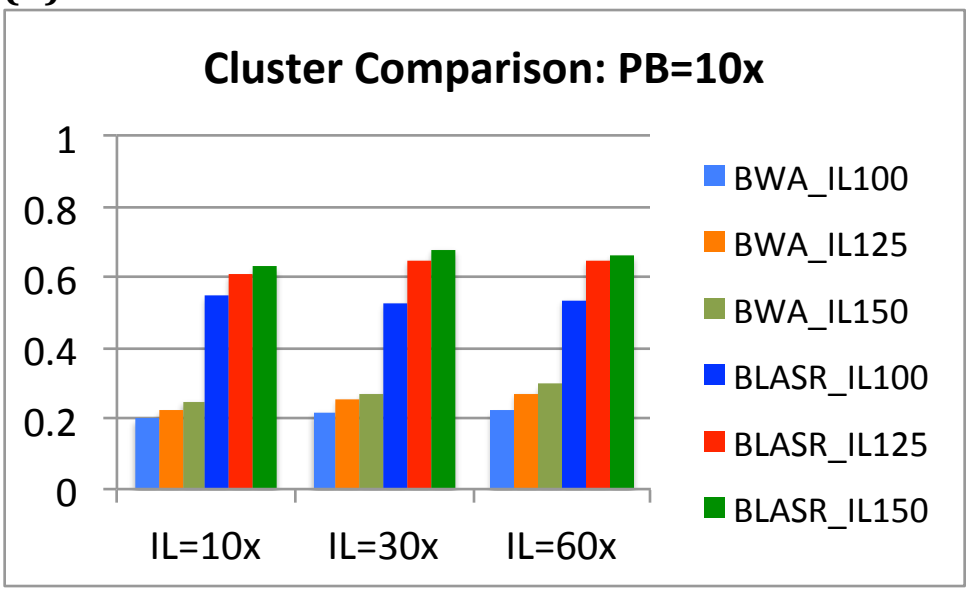
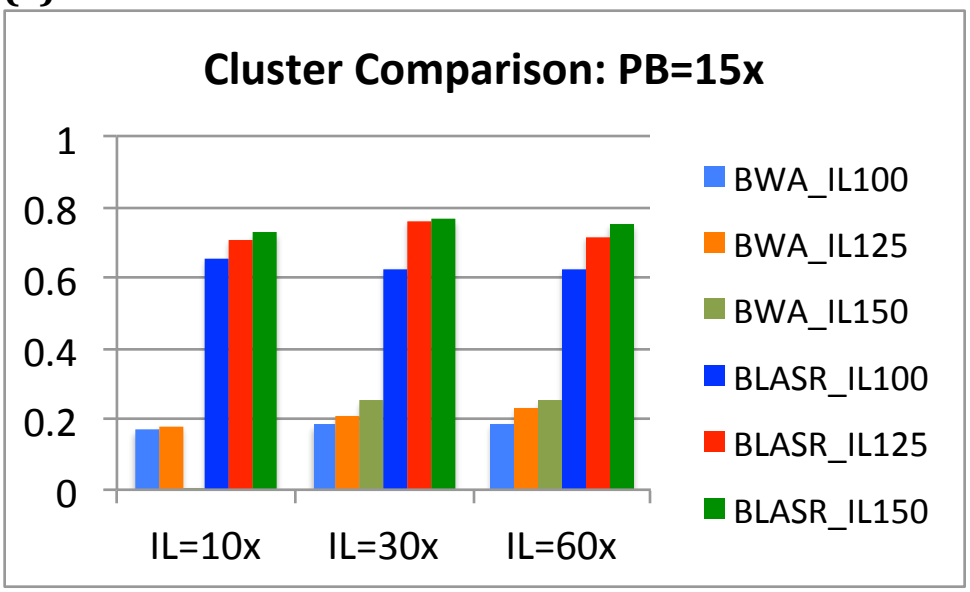
(a)


Cluster Comparison: PB=5x
1
0.8
0.6
0.4
0.2
0
IL=10x
IL=30x
IL=60x
BWA_IL100
BWA_IL125
BWA_IL150
BLASR_IL100
BLASR_IL125
BLASR_IL150

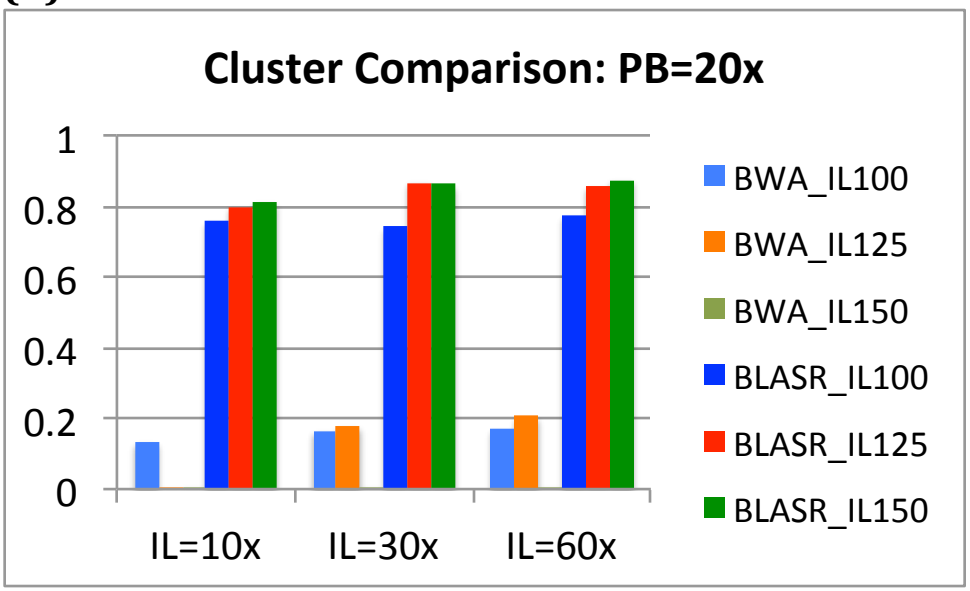
(b)


Cluster Comparison: PB=10x
1
0.8
0.6
0.4
0.2
0
IL=10x
IL=30x
IL=60x
BWA_IL100
BWA_IL125
BWA_IL150
BLASR_IL100
BLASR_IL125
BLASR_IL150

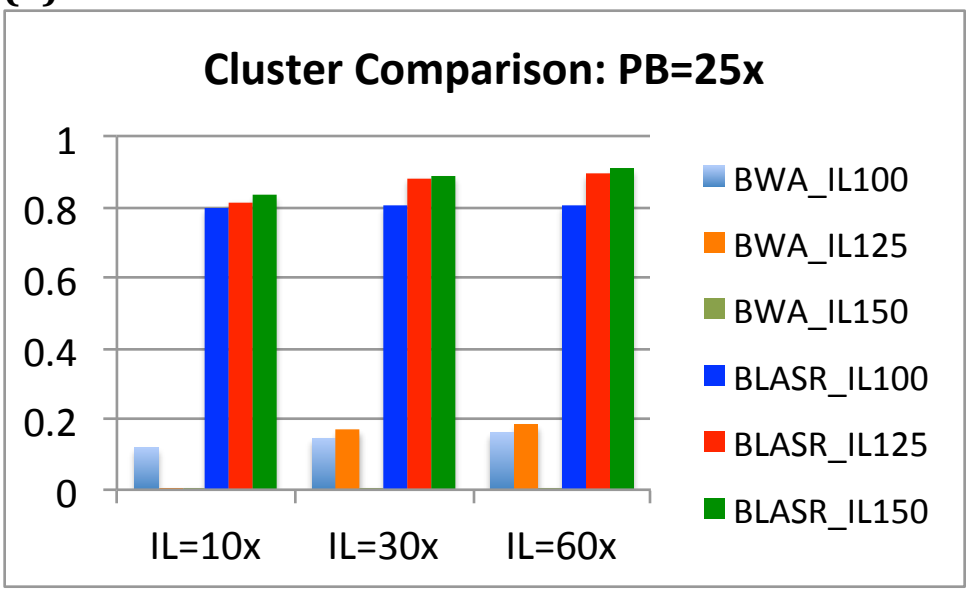
(c)


Cluster Comparison: PB=15x
1
0.8
0.6
0.4
0.2
0
IL=10x
IL=30x
IL=60x
BWA_IL100
BWA_IL125
BWA_IL150
BLASR_IL100
BLASR_IL125
BLASR_IL150

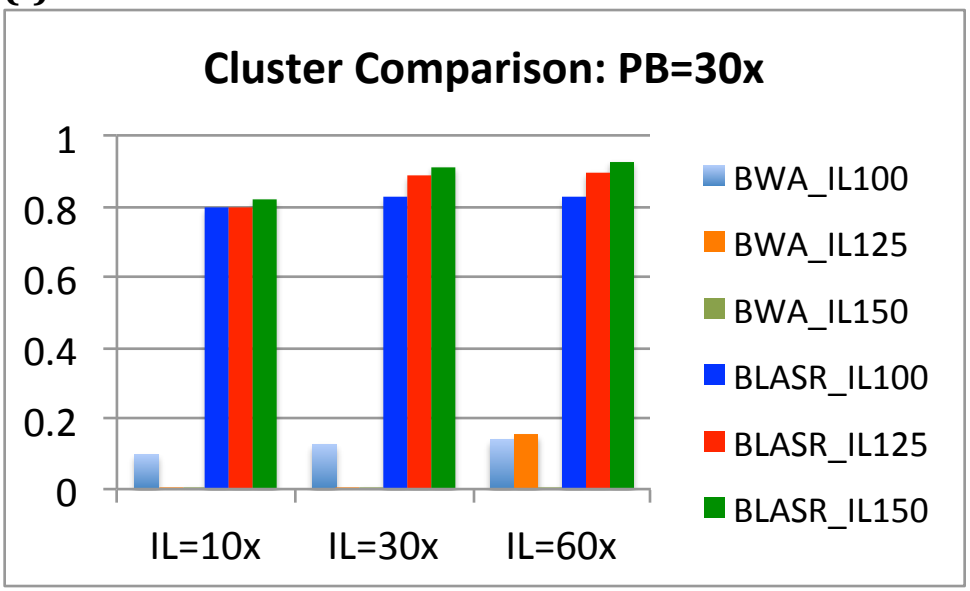
(d)


Cluster Comparison: PB=20x
1
0.8
0.6
0.4
0.2
0
IL=10x
IL=30x
IL=60x
BWA_IL100
BWA_IL125
BWA_IL150
BLASR_IL100
BLASR_IL125
BLASR_IL150

(e)



(f)



Supplemental Fig. 1 Quality of clusters computed on alignments obtained by BWA and BLASR. Each of the six panels, (a) – (f), corresponds to a different PacBio read coverage, N×, as indicated by the "PB=N×". Each panel has three groups of bars, corresponding, from left to right, to Illumina coverage of 10×, 30×, and 60×, respectively. Within each group, the results for BWA and BLASR are shown for three different Illumina read lengths. The y-axis measures the quality of the clustering using the Jaccard index (see Methods). Note that results obtained from BWA are near zero in several instances.