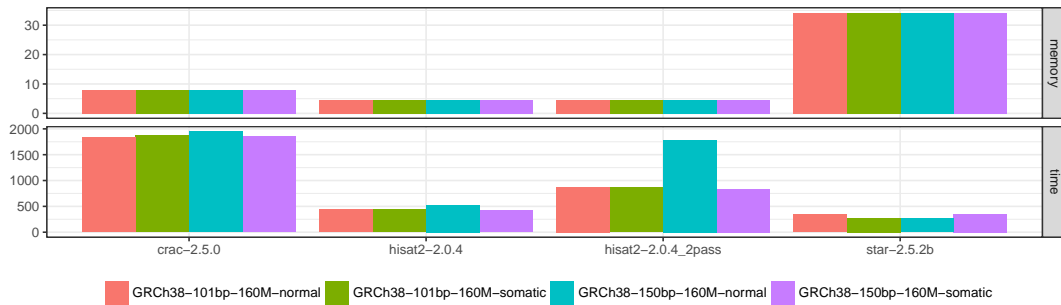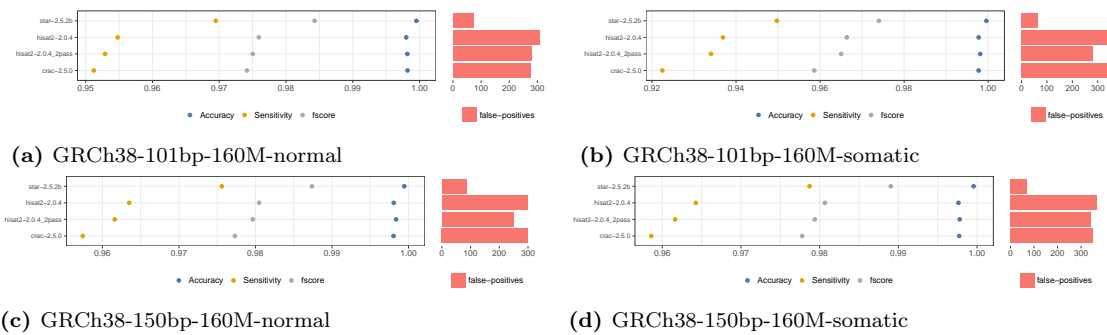# Supplemental Materials: A methodology and tools for evaluating the performance of RNA-Seq bioinformatic pipelines

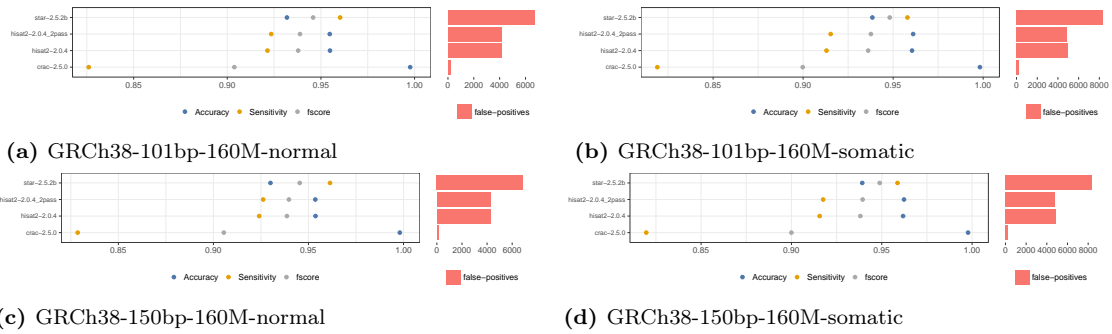

Supplementary Figure 1: Memory and time of mapping softwares
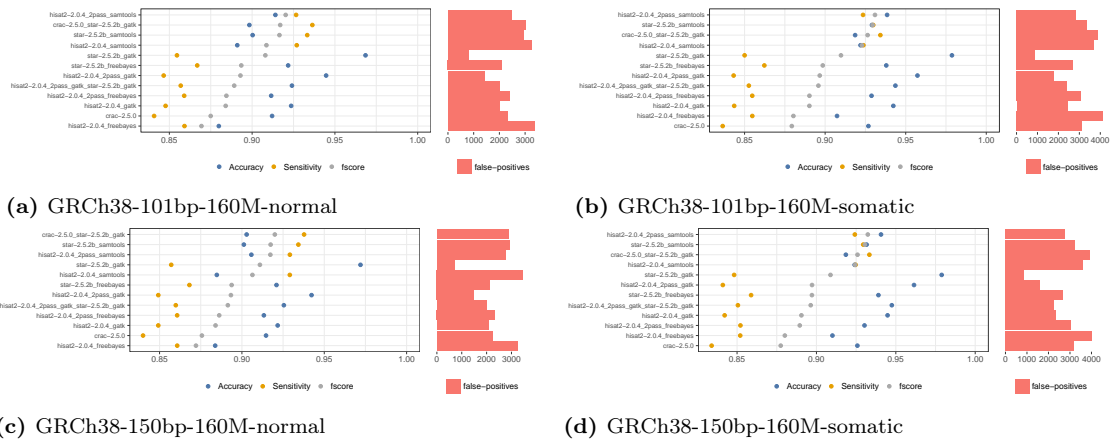Performances where measured with unix /usr/bin/time command. Mappers were run with 10 cores. Time is set to *user* time (in minutes), while memory is set to *max memory usage* (in Gb).
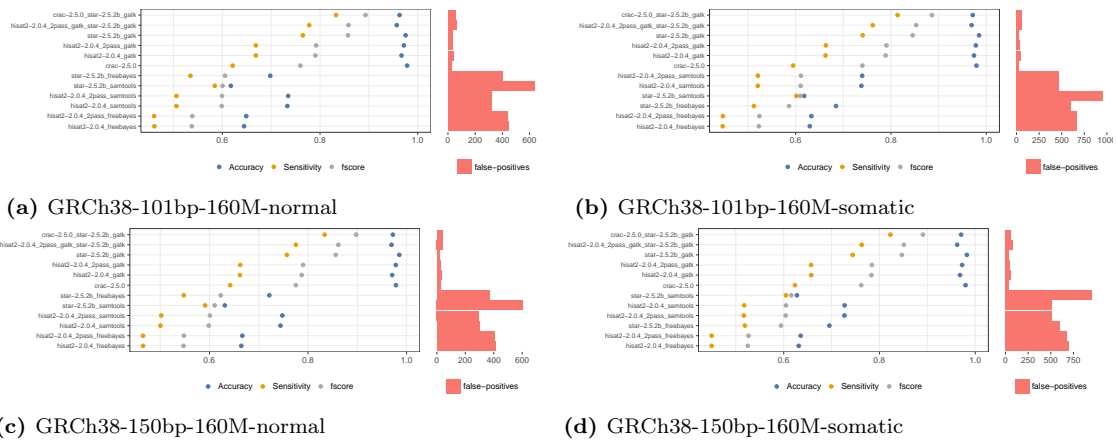

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic

Supplementary Figure 2: Accuracy sensitivity for alignments

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic

Supplementary Figure 3: Accuracy sensitivity for splices

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic

Supplementary Figure 4: Accuracy sensitivity for snps

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic

Supplementary Figure 5: Accuracy sensitivity for insertions

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic
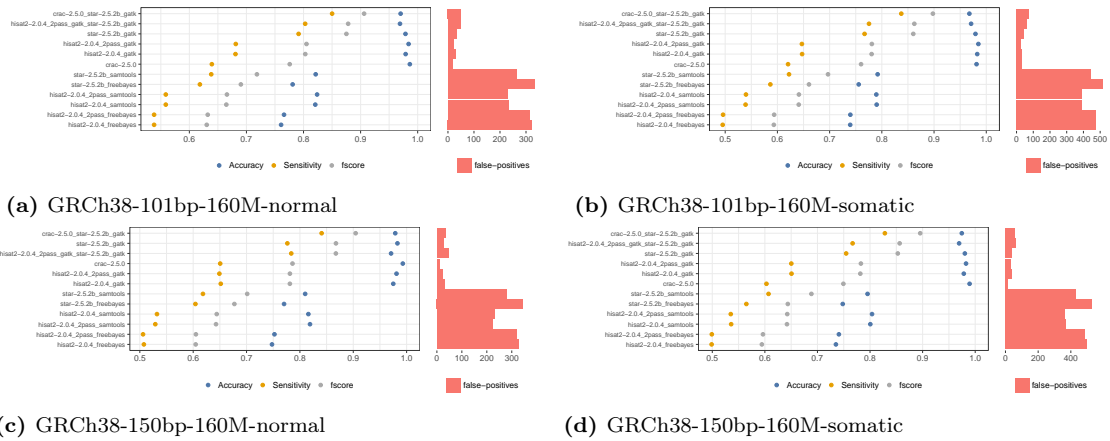
Supplementary Figure 6: Accuracy sensitivity for deletions

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic
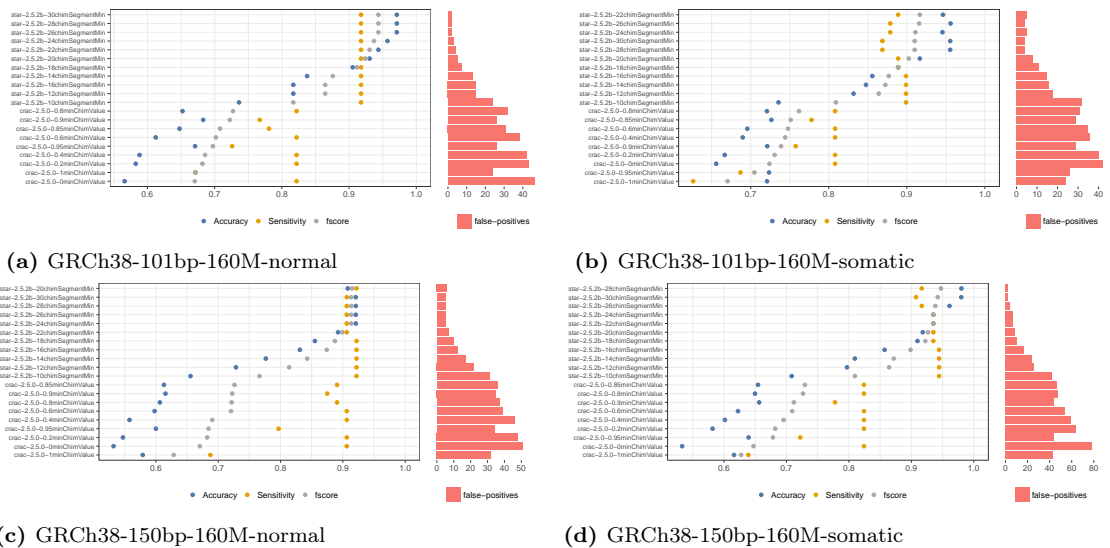
Supplementary Figure 7: Accuracy sensitivity for colinear_fusions

(a) GRCh38-101bp-160M-normal

(b) GRCh38-101bp-160M-somatic

(c) GRCh38-150bp-160M-normal

(d) GRCh38-150bp-160M-somatic
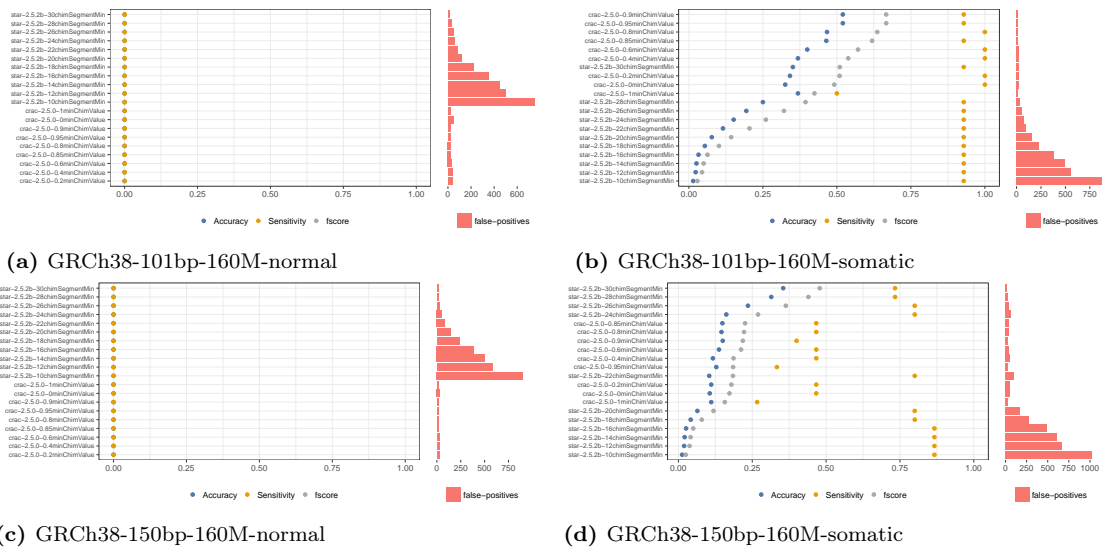
Supplementary Figure 8: Accuracy sensitivity for noncolinear_fusions