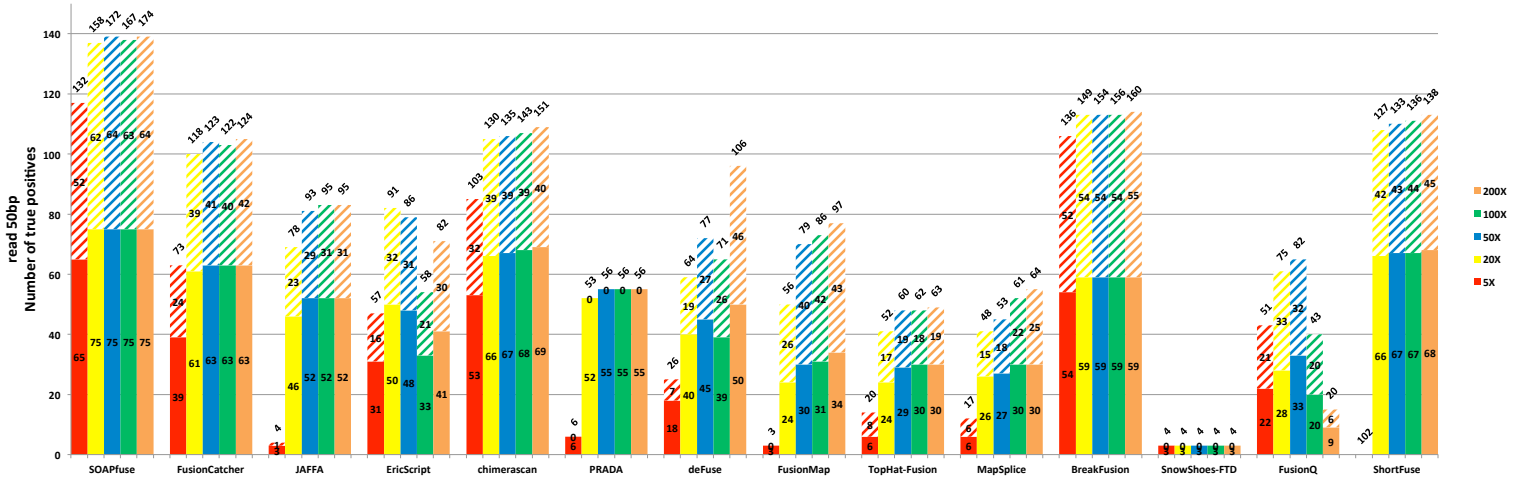


A



B

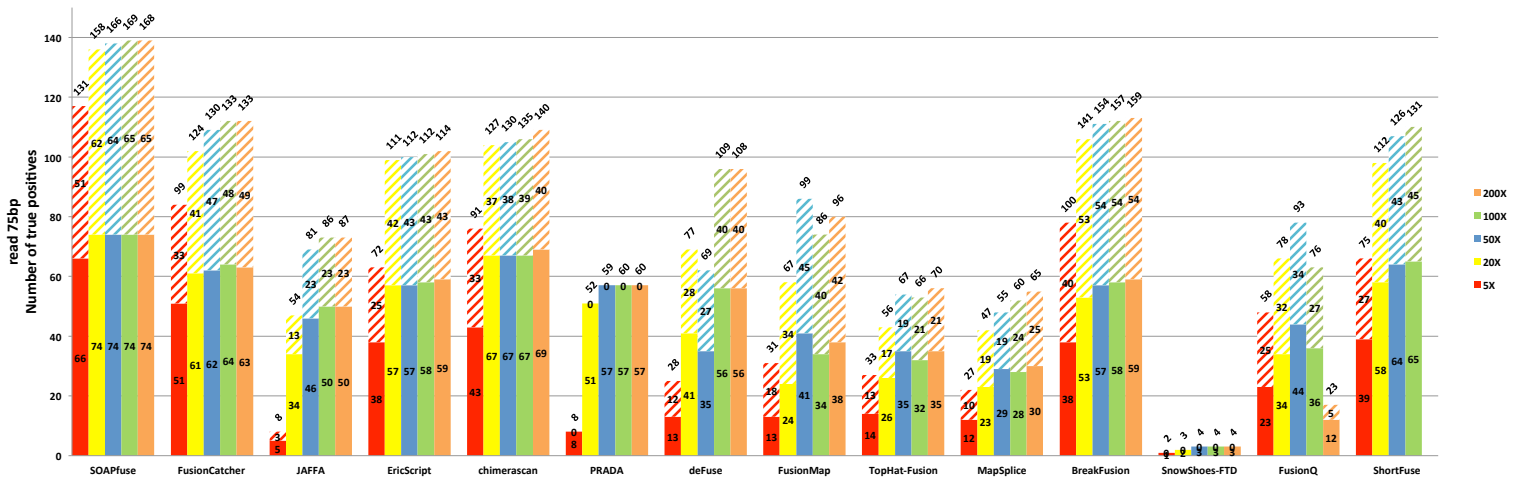
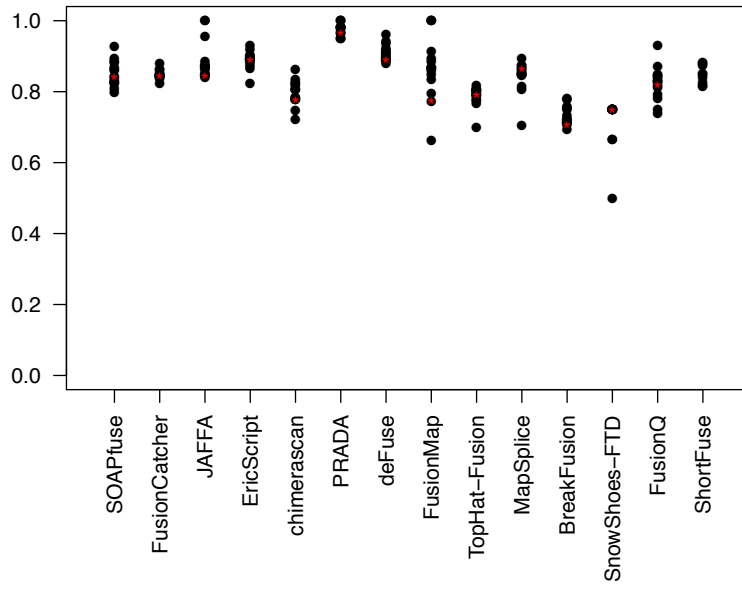
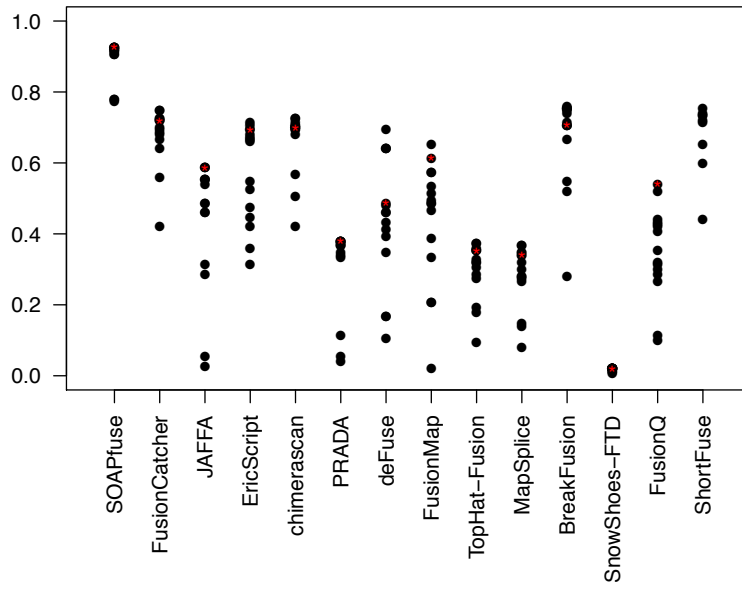


Figure S1: Fusion transcript detection results for type-1A synthetic datasets. The y-axis bars show the number of true detected positives, among them IE-type and BE-type fusions are shown in solid and slashed rectangles. The total numbers of fusion detections are shown on top of the bars. (A) results for read length 50 bp (B) results for read length 75 bp.

A



B



C

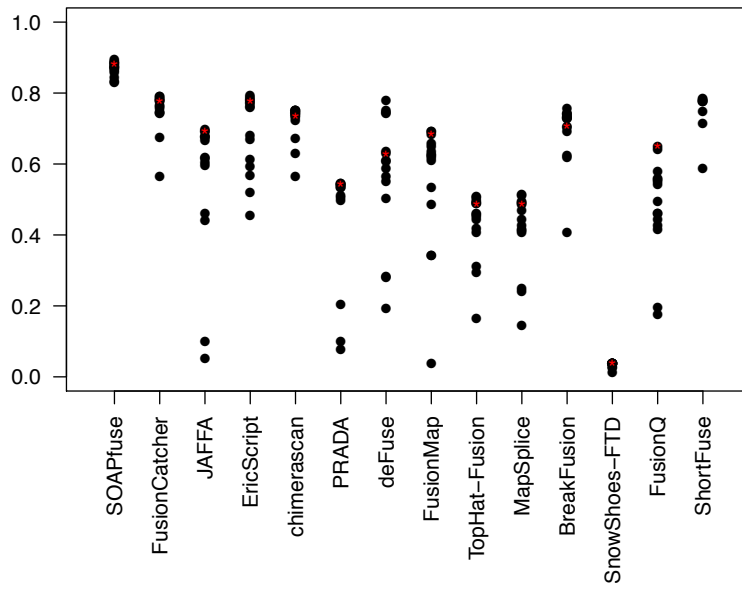
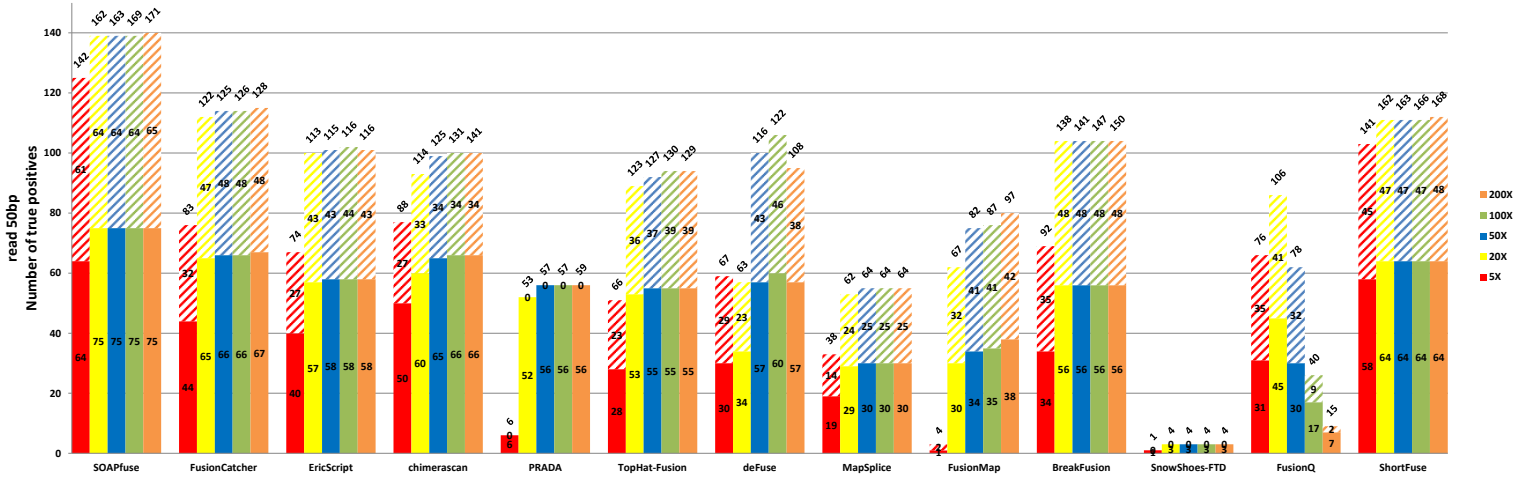


Figure S2: Precision, recall and F-measure for type-1A synthetic data. Results for read 100 bp & 100X are marked as red star.

A



B

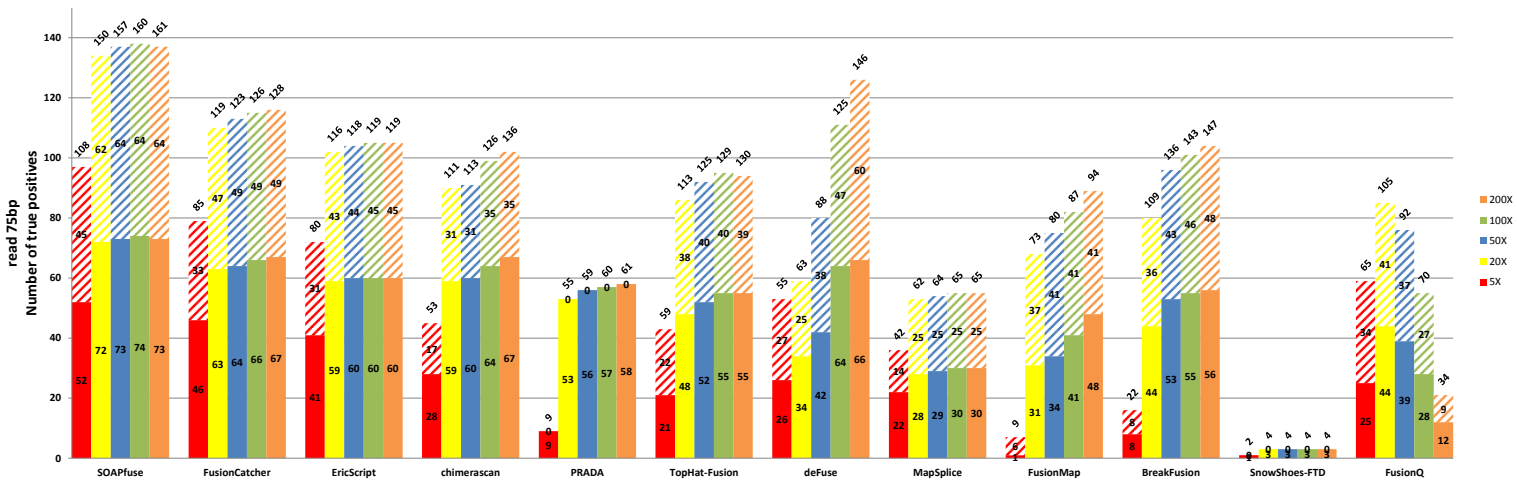
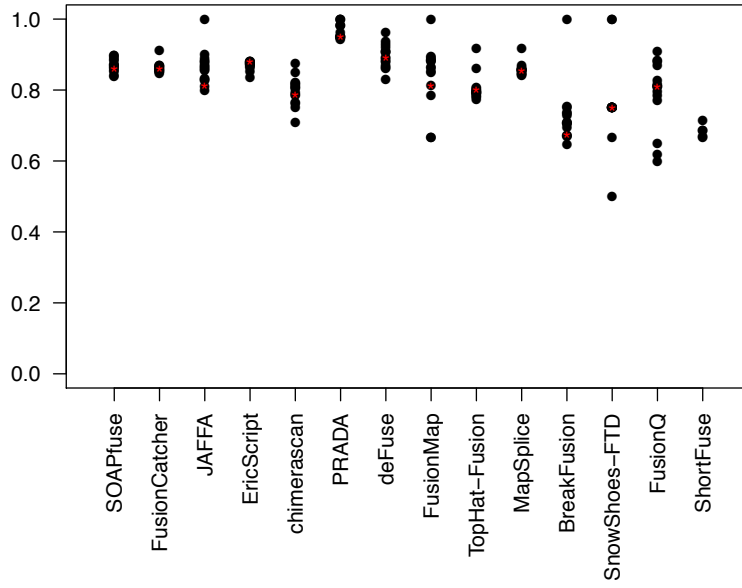
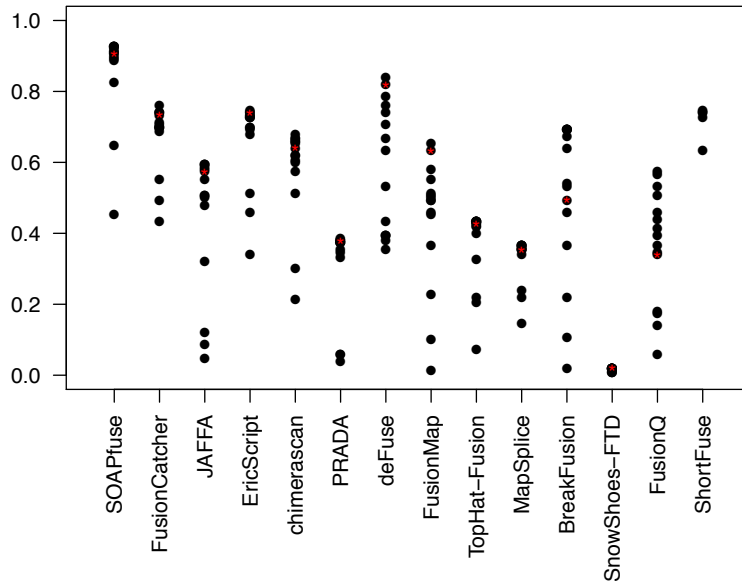


Figure S3: Fusion transcript detection results for type-1B synthetic datasets. The y-axis bars show the number of true detected positives, among them IE-type and BE-type fusions are shown in solid and slashed rectangles. The total numbers of fusion detections are shown on top of the bars. (A) results for read length 50 bp (B) results for read length 75 bp.

A



B



C

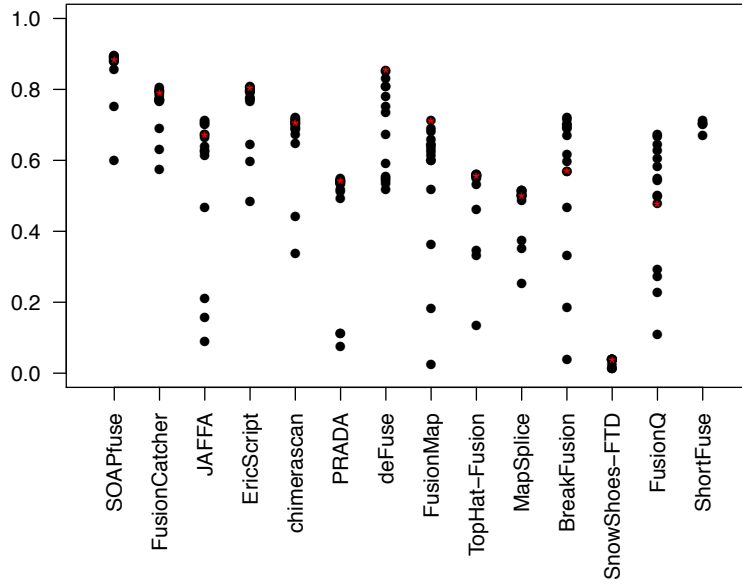
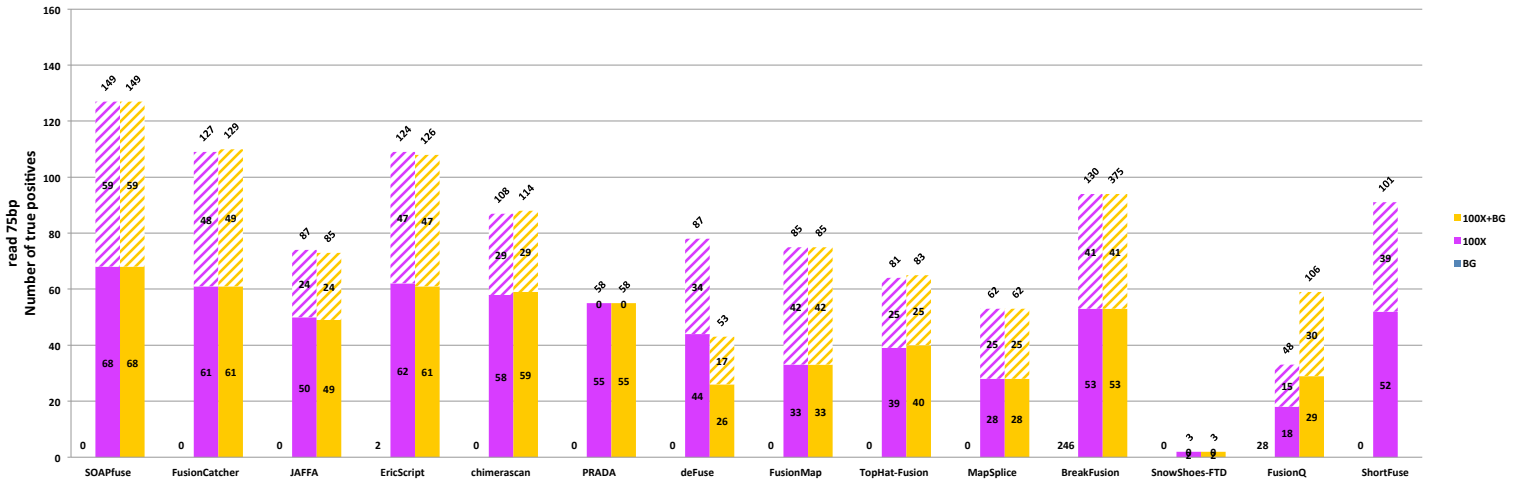


Figure S4: Precision, recall and F-measure for type-1B synthetic data. Results for read 100 bp & 100X are marked as red star.

A



B

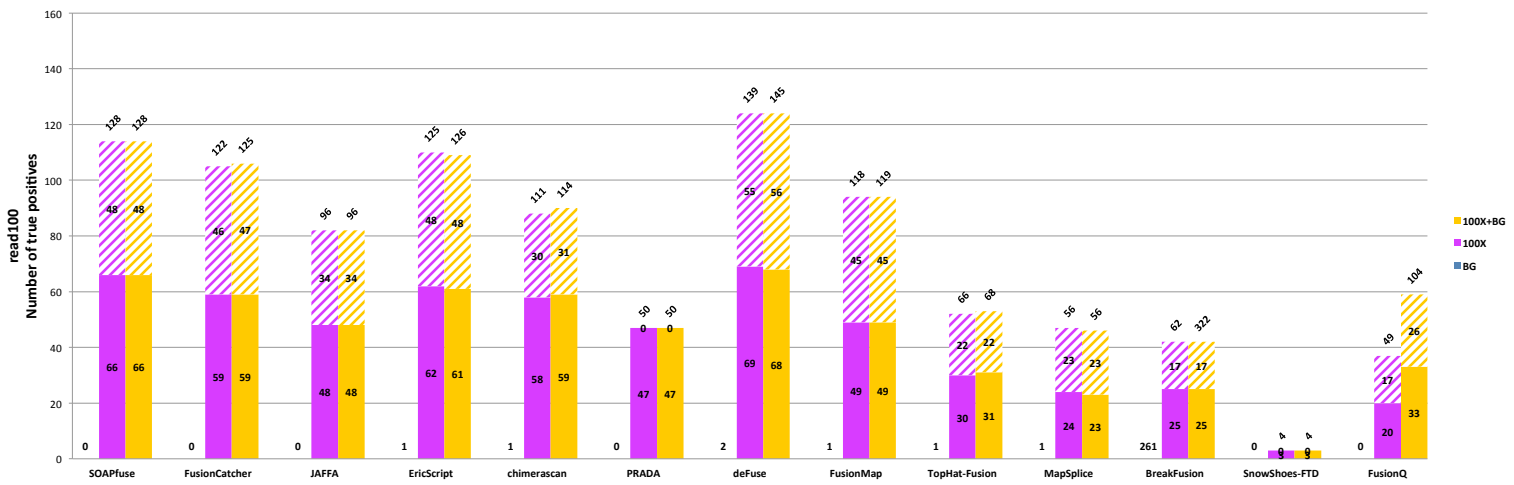


Figure S5: Fusion transcript detection results for type-2, type-3A and type-3B (lung sample) synthetic datasets on lung sample. The y-axis bars show the number of true detected positives, among them IE-type and BE-type fusions are shown in solid and slashed rectangles. The total numbers of fusion detections are shown on top of the bars. (A) results for read length 75 bp (B) results for read length 100 bp.

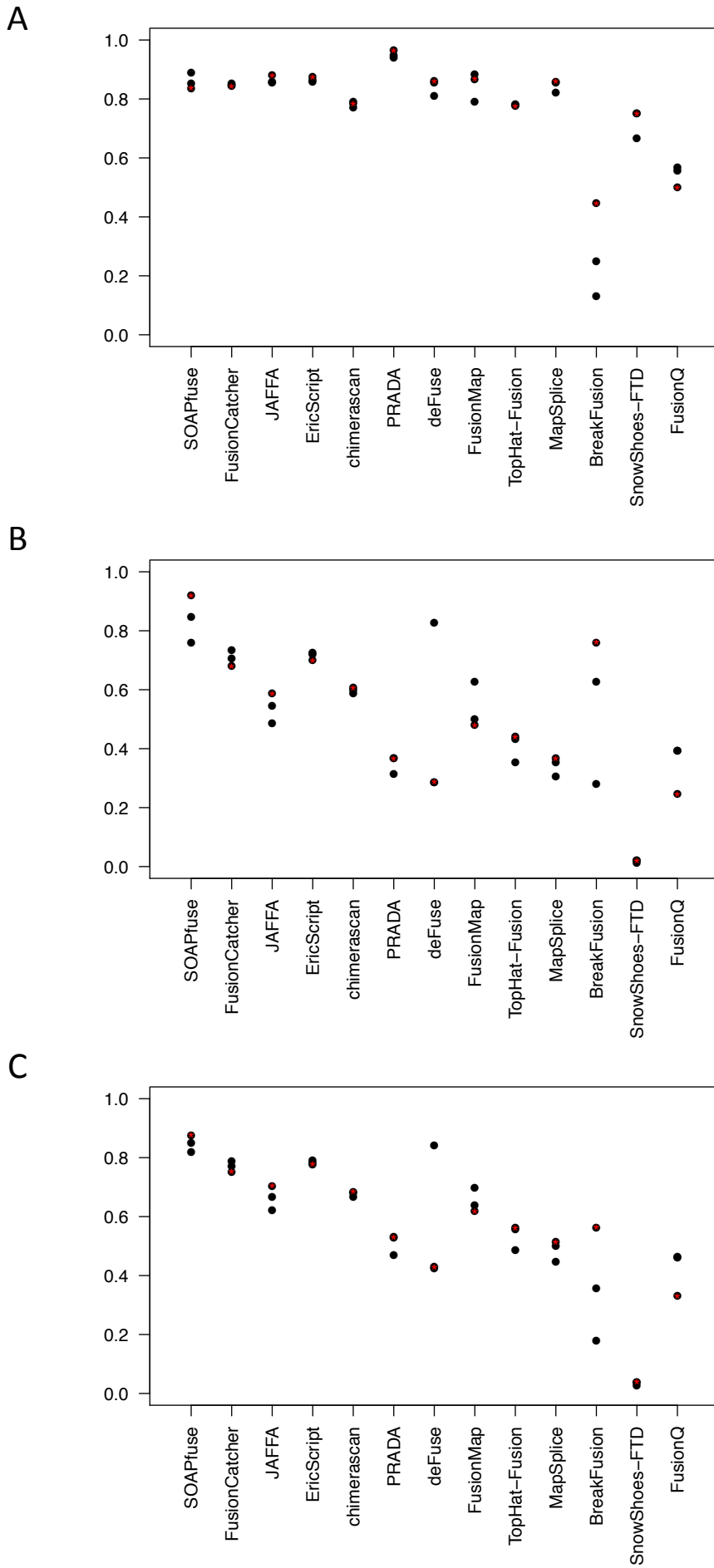


Figure S6: Precision, recall and F-measure for type-3B (lung sample) synthetic data. Results for read 50 bp are marked as red star.

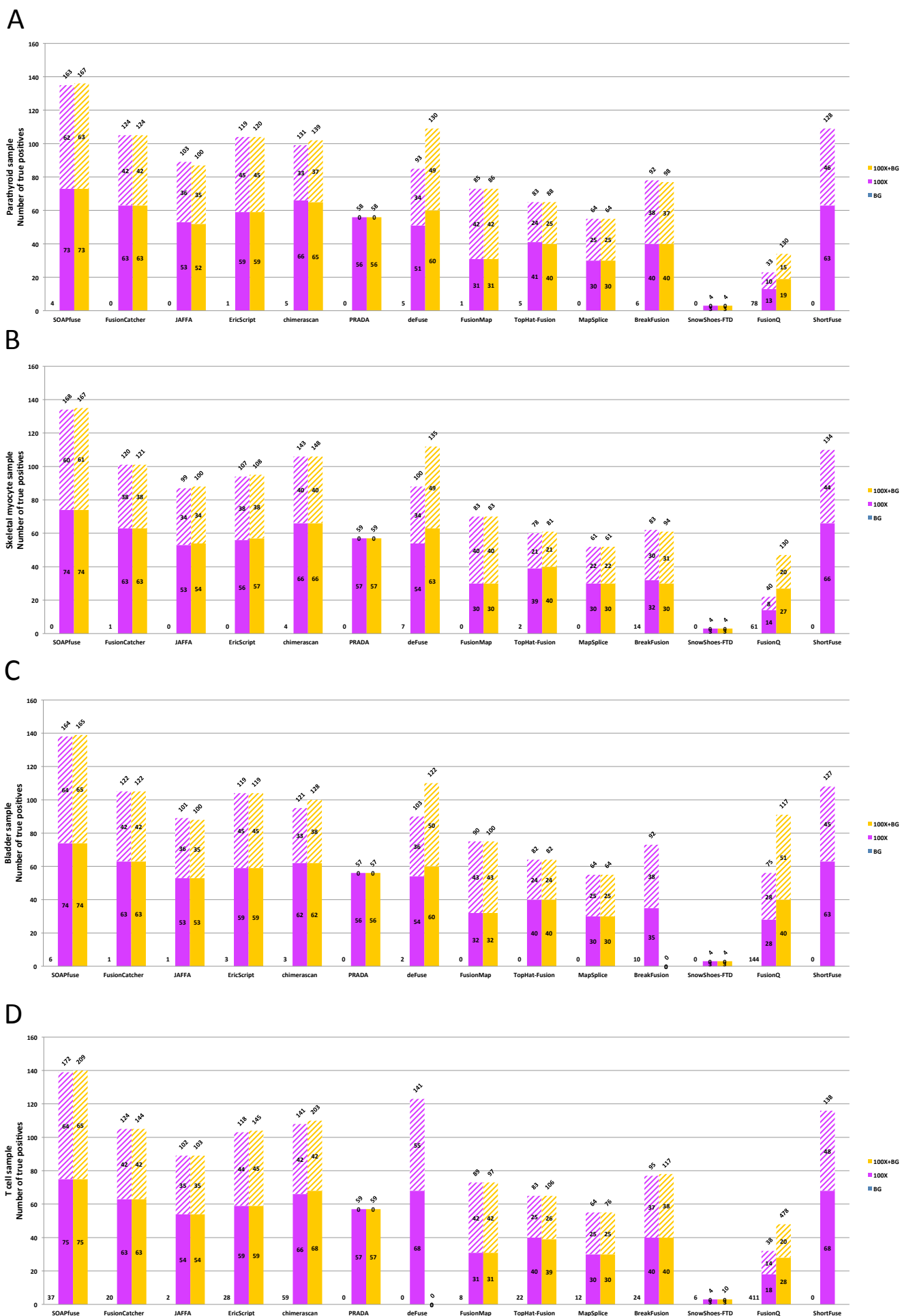


Figure S7: Fusion transcript detection results for type-2, type-3A and type-3B (lung sample) synthetic datasets on (A) Parathyroid sample (B) Skeletal myocyte sample (C) Bladder sample and (D) T cell sample for read length 50 bp. The y-axis bars show the number of true detected positives, among them IE-type and BE-type fusions are shown in solid and slashed rectangles. The total numbers of fusion detections are shown on top of the bars.

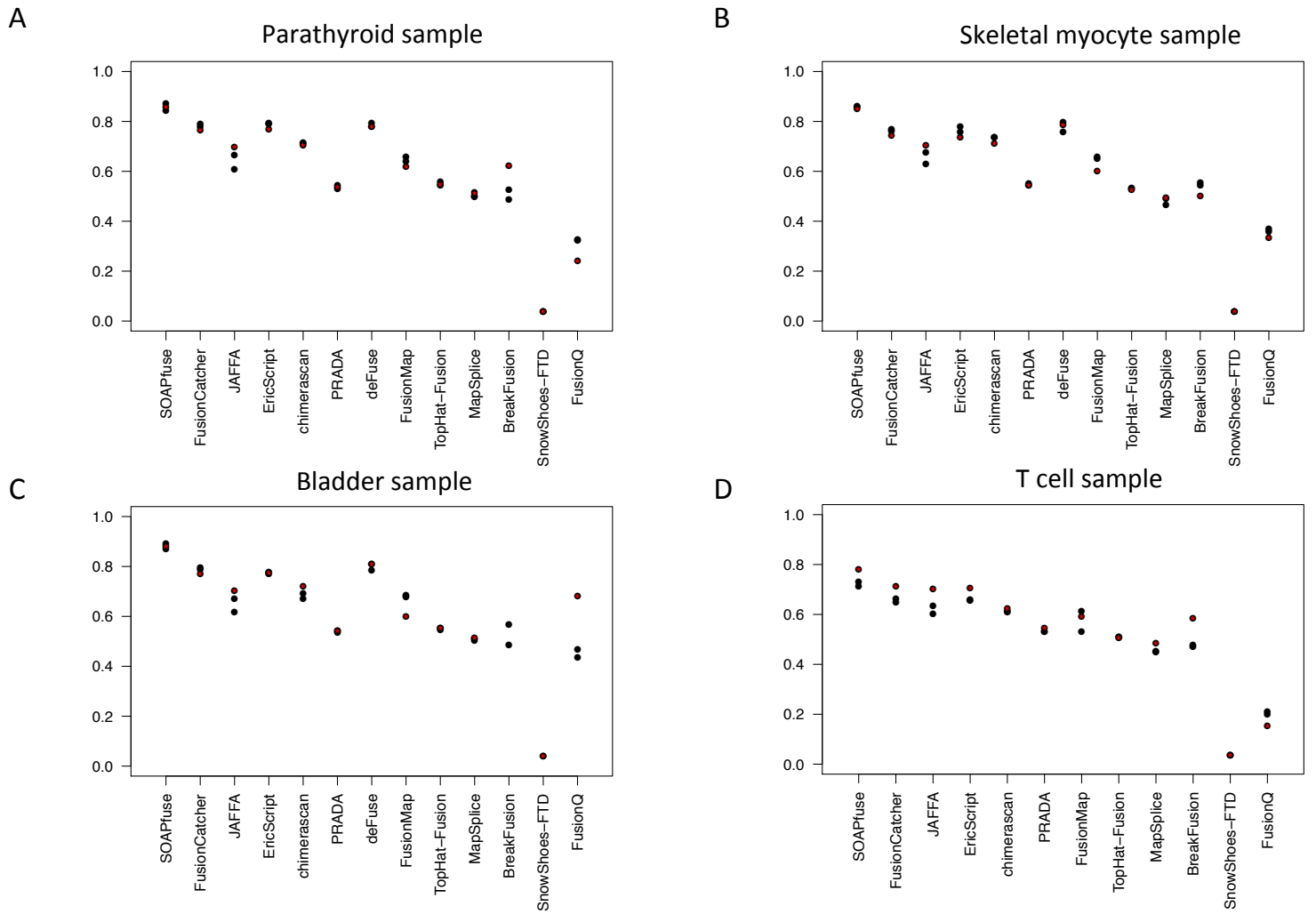


Figure S8: F-measure for type-3B synthetic data on (A) Parathyroid sample (B) Skeletal myocyte sample (C) Bladder sample and (D) T cell sample. Results for read 50 bp are marked as red star.



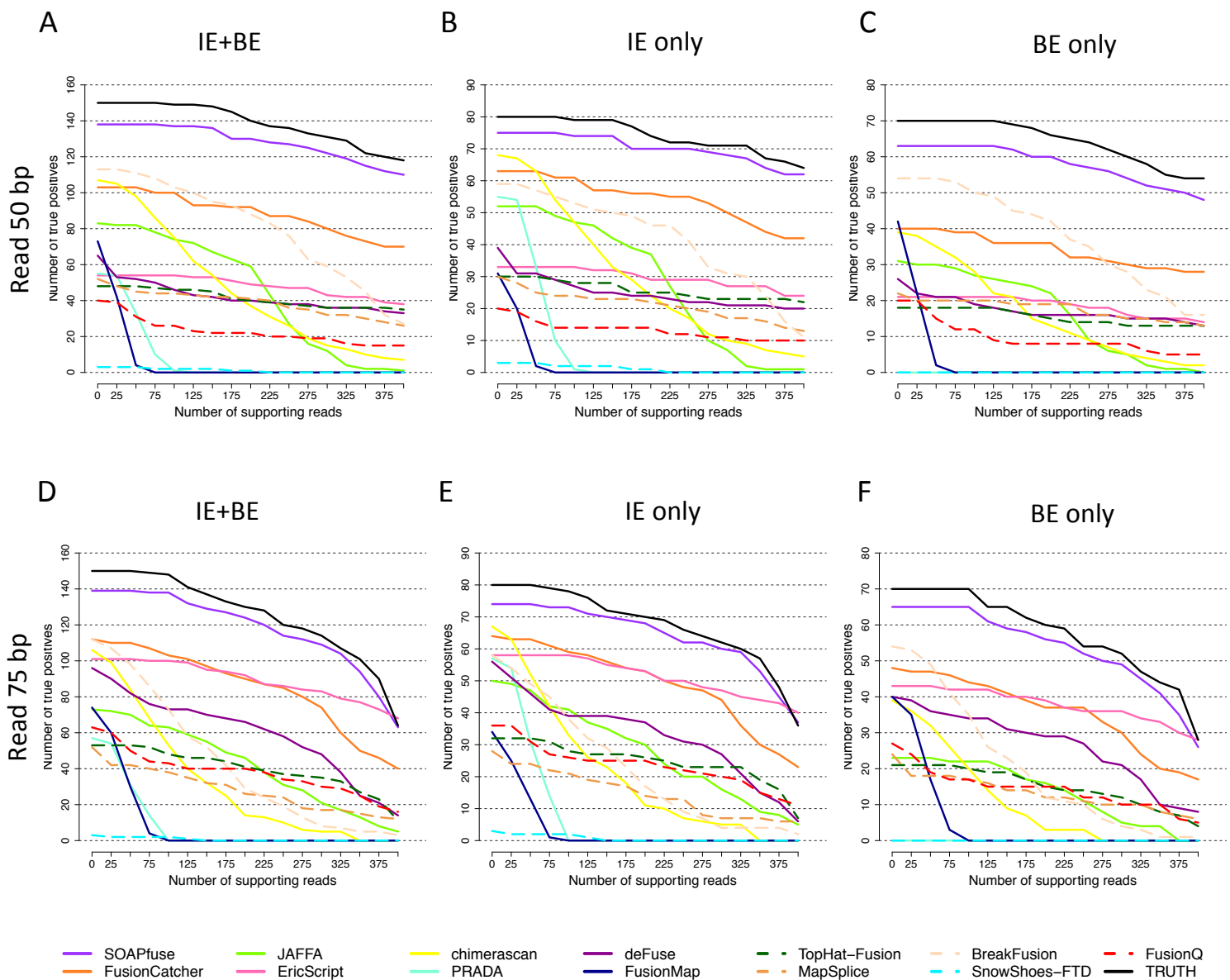


Figure S9: Distribution plots for alignment performance and similarity across tools for type-1A synthetic data with 50 and 75 bp read length & 100X. Number of true positives (y-axis) with detected supporting reads greater than the threshold on the x-axis. (A-C) results for read 50 bp. (D-F) results for read 75 bp. (A) and (D): results for all 150 true fusion transcripts. (B) and (E): results for only IE-type fusion transcripts. (C) and (F): results for only BE-type fusion transcripts.

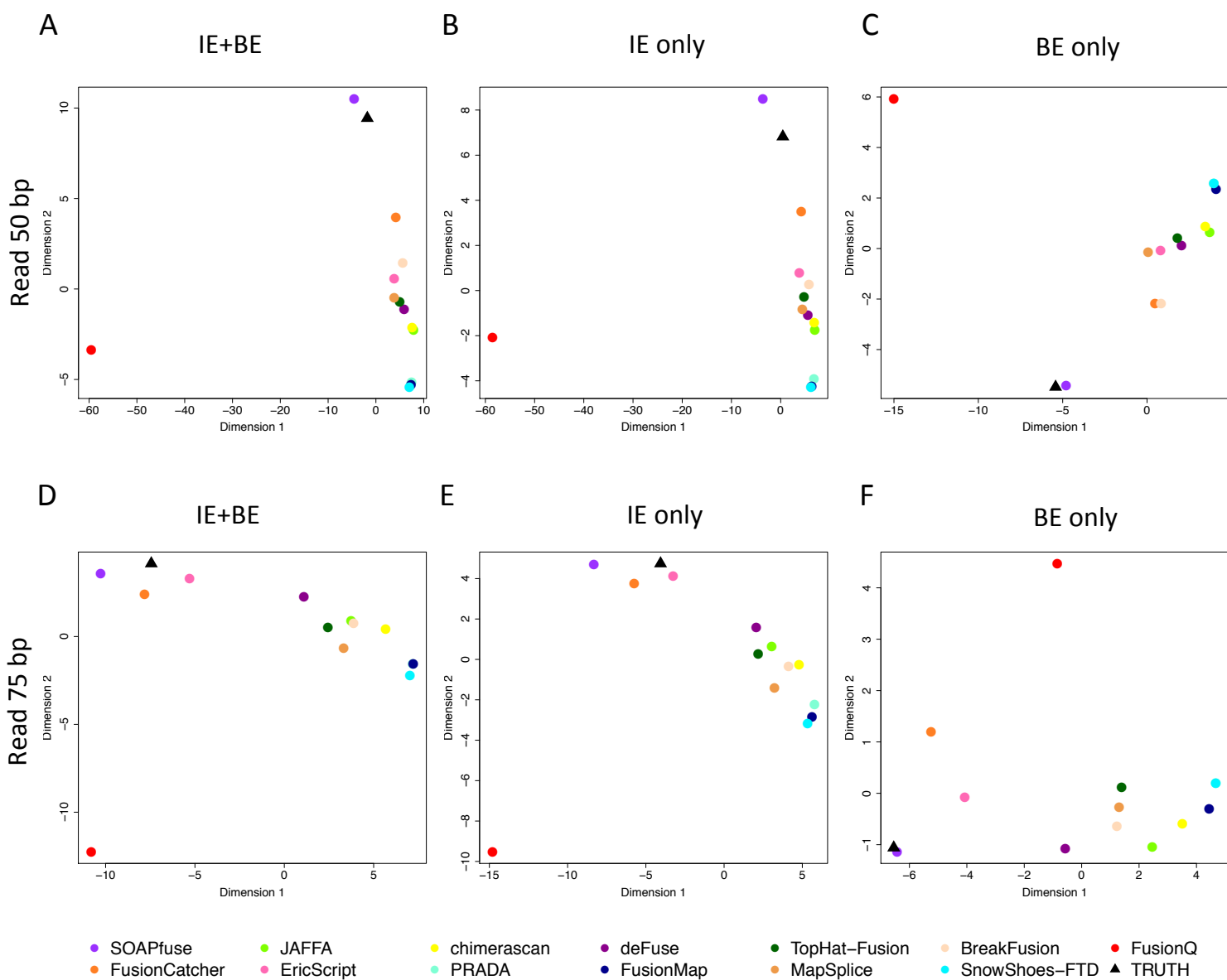


Figure S10: Multi-dimensional scaling (MDS) plots to demonstrate pairwise similarity of detection results from 14 tools and the underlying truth. (A-C) results for read 50 bp. (D-F) results for read 75 bp. (A) and (D): results for all 150 true fusion transcripts. (B) and (E): results for only IE-type fusion transcripts. (C) and (F): results for only BE-type fusion transcripts.

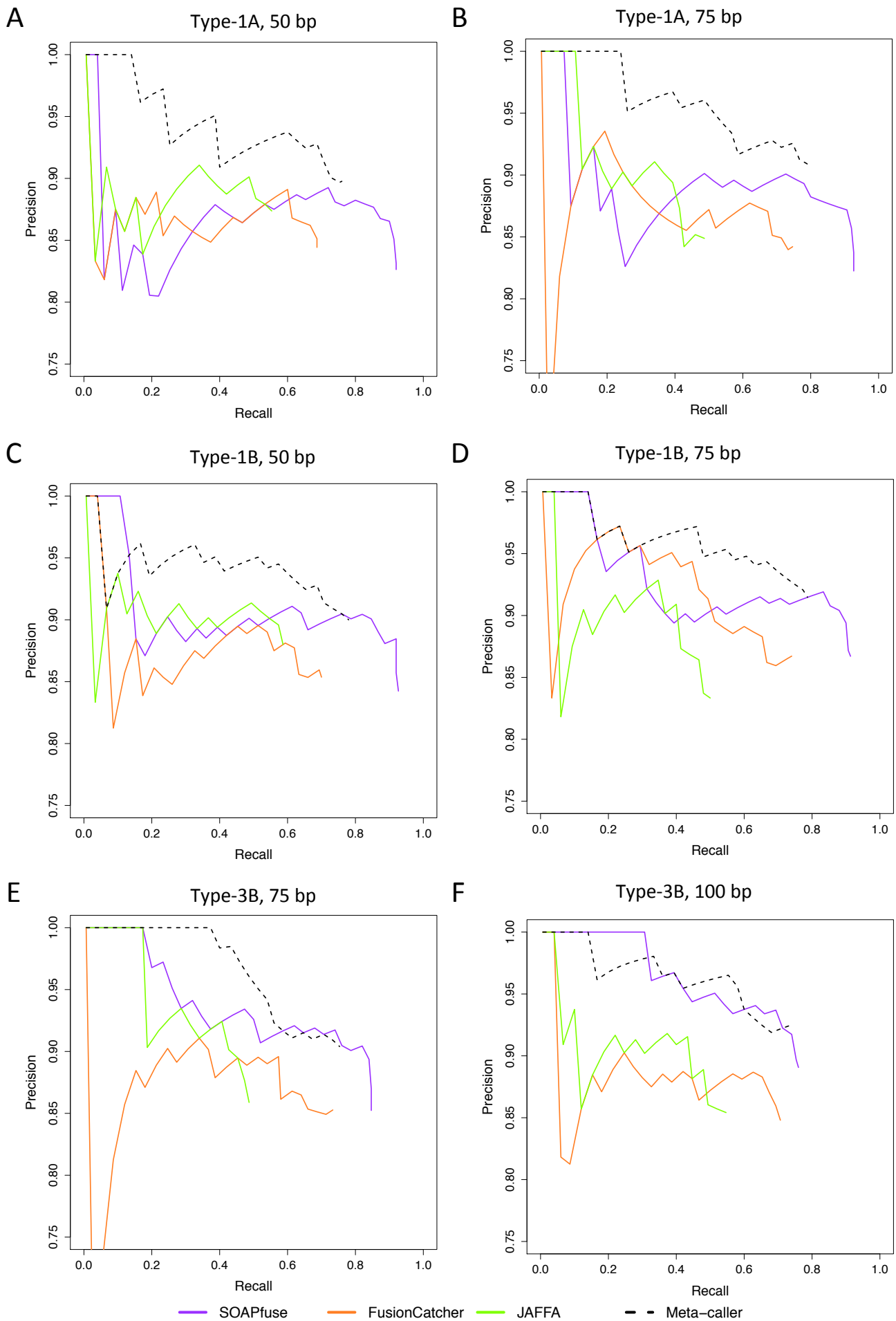


Figure S11: Precision-recall curves of top 3 performing tools and meta-caller. (A)-(B) Type-1A synthetic data with read length 50 and 75 bp. (C)-(D) Type-1B synthetic data with read length 50 and 75 bp. (E)-(F) Type-3B synthetic data (lung sample) with read length 75 and 100 bp.

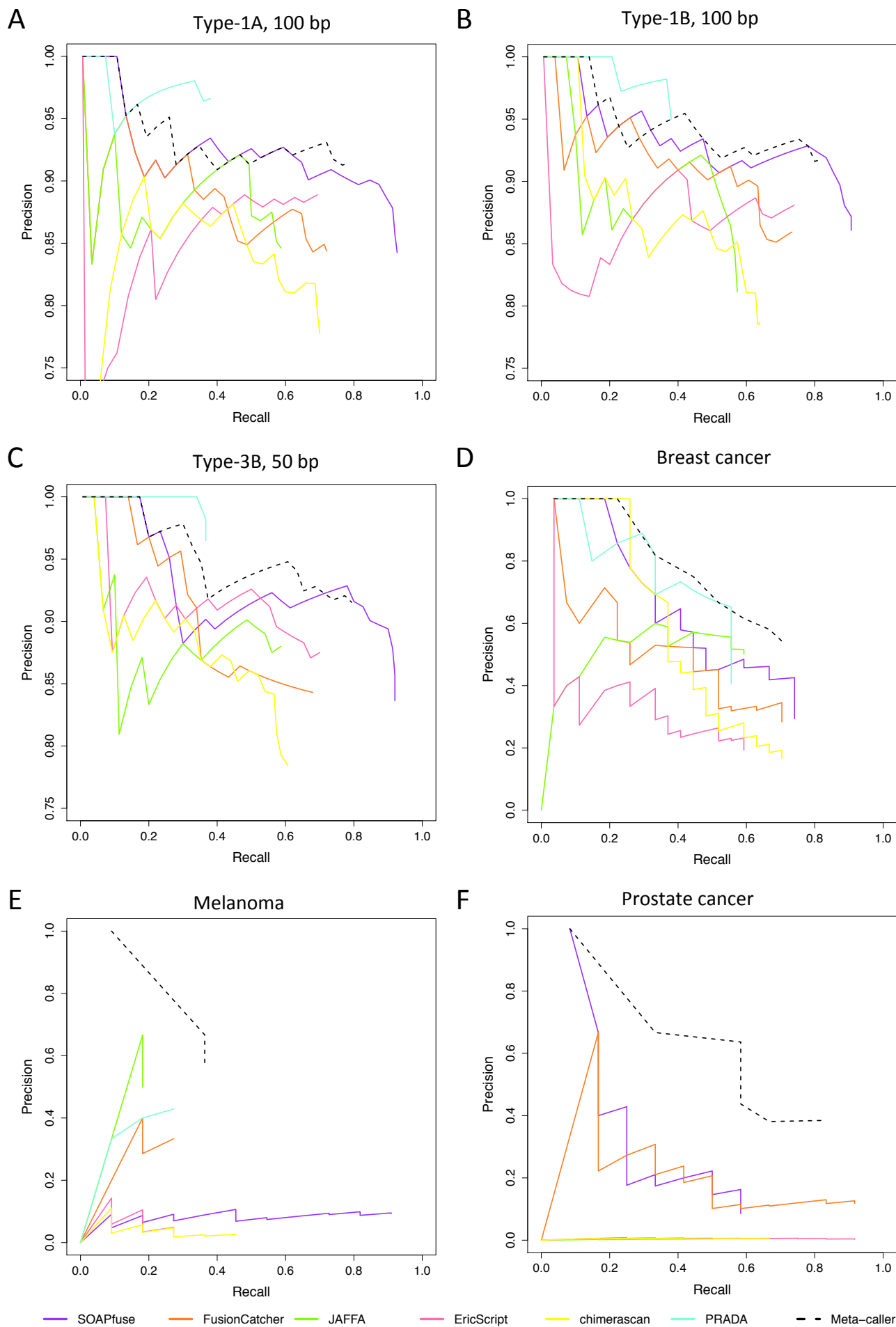


Figure S12: Precision-recall curves of top 6 performing tools and meta-caller. (A)-(C): Type-1A, type-1B and type-3B (lung sample) synthetic data with 100X coverage and 100, 100 and 50 bp read length respectively. (D)-(F): Three real datasets: breast cancer, melanoma and prostate cancer.

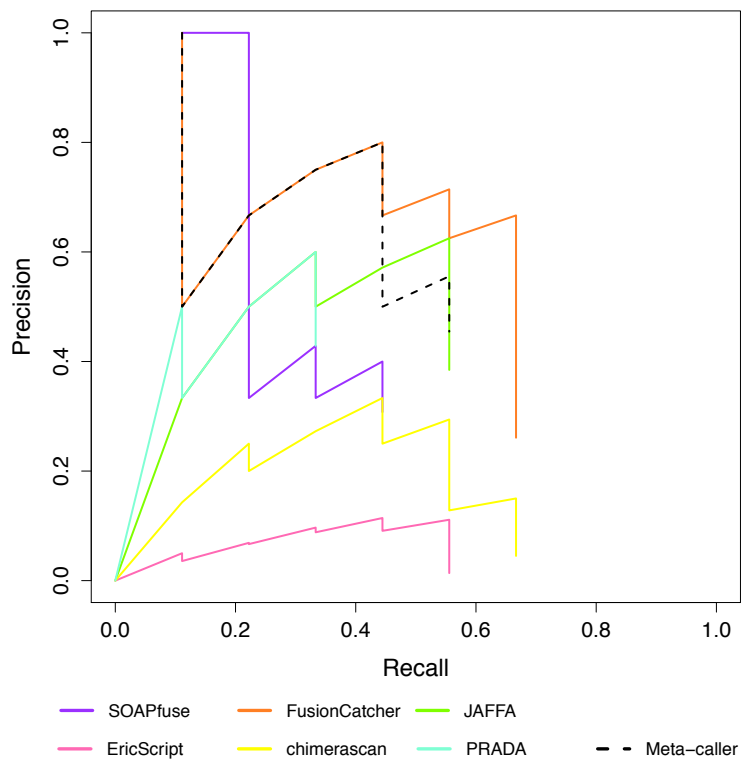


Figure S13: Precision-recall curves of top-6 performing tools and meta-caller (with majority vote=3) on validation data.