Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data

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Supplementary Figure S2: Comparison of time and computational memory, used by software packages on the mixed dataset. **BE**: Bellerophontes, **ER**: EricScript, **NF**: nFuse, **FC**: FusionCatcher, **FH**: FusionHunter, **FM**: FusionMap, **JA**: JAFFA, **MS**: MapSplice, **TF**: TopHat-Fusion.

Supplementary Figure S3: Overlapping and unique fusions among the six best tools on the test dataset. **ER**: EricScript, **FC**: FusionCatcher, **JA**: JAFFA, **MS**: MapSplice, **SF**: SOAPfuse, **TF**: TopHatFusion.

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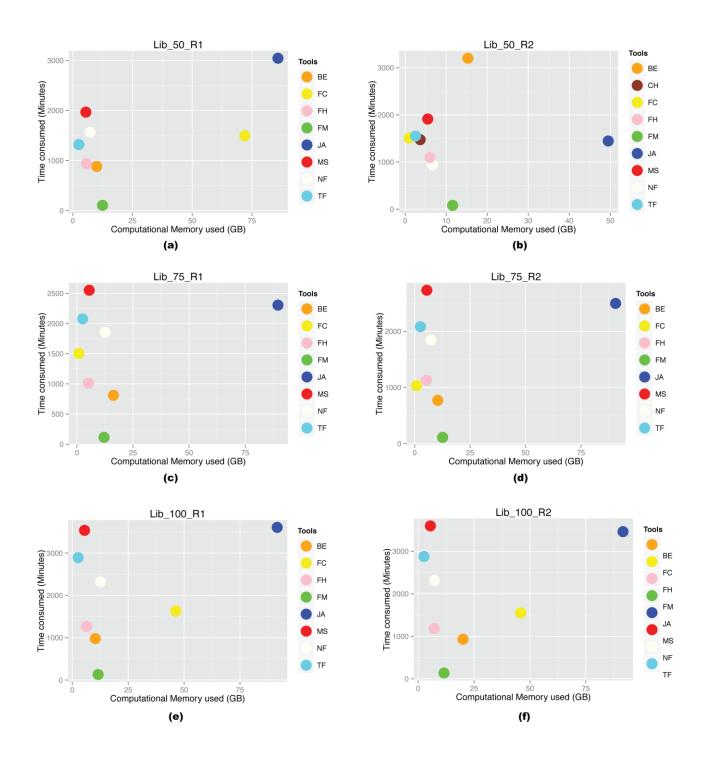
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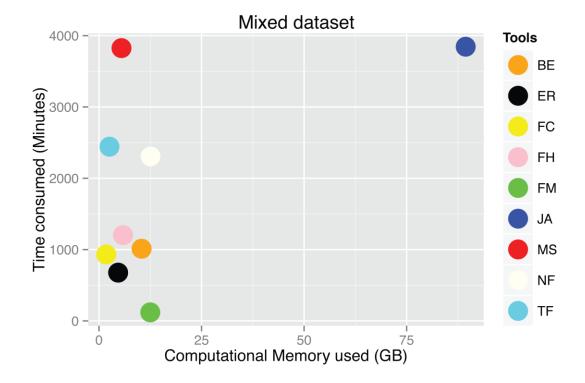
Tools	Lib_50_R1	Lib_50_R2	Lib_75_R1	Lib_75_R2	Lib_100_R1	Lib_100_R2
Bellerophontes	0	15465	0	0	0	0
		(15430)				
BreakFusion	*	*	*	*	*	*
Chimerascan	*	1600	*	*	*	*
		(1540)				
EricScript	*	*	*	*	*	*
FusionCatcher	0	0	0	0	0	0
FusionHunter	0	842 (767)	0	0	0	0
FusionMap	93	27	24	27	81	83
JAFFA	0	51(48)	0	0	0	0
MapSplice	0	152	33	30	45	42
nFuse	5	70(67)	39 (35)	31 (29)	54 (53)	78 (70)
SOAPfuse	*	*	*	*	*	*
TopHat-	0	29 (25)	0	0	0	0
Fusion						

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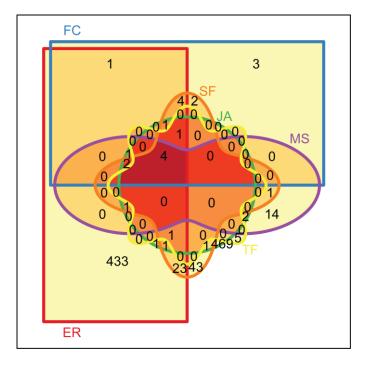
Tools	BE	BF	СН	ER	FC	FH	FM	JA	MS	NF	SF	TF
BE	1820	0	0	2	0	0	0	0	0	2	1	0
BF	0	1401	5	4	0	173	1	2	2	1	3	0
СН	0	5	463	43	9	5	7	14	7	1	42	5
ER	2	4	43	474	14	1	9	13	8	1	38	6
FC	0	0	13	14	19	0	11	14	11	1	19	9
FH	0	173	5	1	0	287	0	0	0	1	2	0
FM	0	1	7	9	7	0	16	10	9	1	8	5
JA	0	2	14	13	9	0	10	485	10	1	12	6
MS	0	2	7	8	7	0	9	10	25	2	8	4
NF	2	1	1	1	1	1	1	1	2	150	1	2
SF	1	3	42	38	14	2	8	12	8	1	85	6
TF	0	0	5	6	5	0	5	6	4	2	6	11



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Supplementary Figure S2: Comparison of time and computational memory, used by software packages on the mixed dataset. BE: Bellerophontes, ER: EricScript, NF: nFuse, FC: FusionCatcher, FH: FusionHunter, FM: FusionMap, JA: JAFFA, MS: MapSplice, TF: TopHat-Fusion.



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