Highly sensitive and ultrafast read mapping for RNA-seq analysis

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Supplementary Tables

Supplementary Table 1. Benchmarking for the simulated dataset containing 10 million single-end reads simulated with the *dwgsim* program. First column, RL, indicated read length in bps. Second column represents the mutation rate (MR). For each program the table contains the following columns with the percentages of: IMR: incorrectly mapped reads, RNM: reads not mapped, CMR: correctly mapped reads covering the corresponding splice junctions. The last column, T, represent runtimes to produce a BAM file in minutes.

		HPG Aligner 1				**HISAT**				**STAR 2**				**TopHat 2 + Bowtie 2**				**MapSplice 2**			
RL	**MR**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**
50	0.1	5.09	2.80	92.11	2.80	1.02	18.39	80.59	2.68	10.34	3.06	86.60	6.62	1.81	11.33	86.86	292.00	3.35	4.96	91.69	24.20
	1	5.59	4.46	89.95	3.90	1.10	24.40	74.5	2.74	10.44	4.98	84.58	6.90	1.70	18.37	79.93	395.00	3.27	8.88	87.85	23.70
	2	6.86	6.31	86.83	3.60	1.14	31.22	67.64	2.83	10.43	7.64	81.93	10.90	1.57	27.14	71.29	443.00	3.17	14.01	82.82	25.40
75	0.1	4.50	0.61	94.89	3.80	0.58	8.19	91.23	3.10	11.91	1.36	86.73	6.83	1.08	22.90	76.02	53.50	5.46	1.45	93.09	29.60
	1	5.26	1.17	93.57	3.60	0.60	13.60	85.8	3.20	12.44	2.64	84.92	6.60	0.92	35.19	63.89	54.30	6.90	3.35	89.75	28.50
	2	6.26	2.30	91.44	5.00	0.60	20.98	78.42	3.28	12.77	4.53	82.70	10.50	0.76	48.42	50.82	56.00	8.57	6.48	84.95	32.10
100	0.1	4.13	0.34	95.53	5.30	0.43	8.90	90.67	3.97	11.94	0.98	87.08	7.75	0.72	36.71	62.57	75.20	7.48	0.58	91.94	36.40
	1	4.92	0.65	94.43	5.60	0.46	16.00	83.54	4.18	12.67	2.24	85.09	7.08	0.57	52.44	46.99	80.30	11.75	1.33	86.92	38.30
	2	5.96	1.42	92.62	5.50	0.44	25.85	73.71	4.16	13.19	4.14	82.67	10.20	0.43	66.93	32.64	85.50	16.05	2.63	81.32	40.15
150	0.1	4.27	0.40	95.33	5.90	0.34	15.13	84.53	5.26	12.38	0.53	87.09	8.18	0.35	62.07	37.58	130.60	19.87	0.69	79.44	47.50
	1	5.08	0.78	94.14	6.50	0.31	28.65	71.04	5.13	13.38	1.54	85.08	9.07	0.23	77.82	21.95	142.40	25.53	1.06	73.41	47.00
	2	6.02	1.43	92.55	6.00	0.16	45.27	54.57	5.14	15.33	3.26	81.41	13.00	0.10	88.56	11.34	84.50	21.49	1.54	76.97	43.40
250	0.1	4.09	0.70	95.21	9.00	0.15	39.01	60.84	6.38	11.38	0.63	87.99	11.95	0.08	89.67	10.25	252.00	42.49	0.26	57.25	61.95
	1	4.87	1.66	93.47	9.30	0.10	63.40	36.5	4.28	13.76	2.09	84.15	12.33	0.04	96.55	3.41	208.00	47.02	0.32	52.66	62.20
	2	6.42	3.15	90.43	8.00	0.04	82.18	17.78	6.00	16.90	5.08	78.02	16.70	0.01	99.06	0.93	155.00	40.22	0.38	59.40	58.40
400	0.1	3.98	1.23	94.79	9.60	0.02	78.75	21.23	8.06	14.30	1.57	84.13	19.40	0.02	99.00	0.98	374.20	56.35	0.04	43.61	81.10
	1	4.89	3.37	91.74	10.00	0.01	93.82	6.17	8.11	18.28	6.56	75.16	20.20	0.00	99.87	0.13	382.40	57.41	0.05	42.54	83.00
	2	6.51	6.59	86.90	12.80	0.00	98.78	1.22	8.31	22.23	18.59	59.18	21.40	0.00	99.99	0.01	271.00	56.83	0.05	43.12	85.20

Supplementary Table 2. Benchmarking for the simulated dataset containing 10 million paired-end reads simulated with the dwgsim program. First column, RL, indicated read length in bps. Second column represents the mutation rate (MR). For each program the table contains the following columns with the percentages of: IMR: incorrectly mapped reads, RNM: reads not mapped, CMR: correctly mapped reads covering the corresponding splice junctions. The last column, T, represent runtimes to produce a BAM file in minutes.

		HPG Aligner 1				**HISAT**				**STAR 2**				**TopHat 2 + Bowtie 2**				**MapSplice 2**			
RL	**MR**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**	**IMR**	**RNM**	**CMR**	**T**
50	0.1	4.23	5.03	90.74	5.50	1.02	6.44	92.54	5.72	10.92	7.25	81.83	8.10	1.17	15.00	83.83	702.30	3.03	4.80	92.17	48.20
	1	4.49	6.33	89.18	5.90	1.14	10.21	88.65	5.86	10.87	10.96	78.17	8.05	1.04	23.83	75.13	848.20	3.33	8.33	88.34	49.20
75	0.1	3.89	1.66	94.45	6.10	0.59	5.70	93.71	6.54	12.81	1.14	86.05	9.13	0.67	33.26	66.07	107.00	4.84	1.39	93.77	60.80
	1	4.48	2.19	93.33	7.00	0.64	10.00	89.36	6.60	13.69	2.13	84.18	9.55	0.53	47.40	52.07	110.00	6.15	3.02	90.83	62.50
100	0.1	3.68	1.45	94.87	7.40	0.51	7.54	91.95	8.38	13.18	1.19	85.63	11.17	0.47	48.73	50.80	151.80	6.62	0.74	92.64	73.40
	1	4.38	1.35	94.27	8.30	0.53	14.33	85.14	8.52	14.17	1.14	84.69	12.18	0.34	63.56	36.10	161.80	9.12	1.26	89.62	76.70
150	0.1	4.02	0.82	95.16	10.10	0.4	14.40	85.20	10.53	13.09	0.26	86.65	14.87	0.25	70.37	29.38	253.00	14.63	0.73	84.64	91.50
	1	4.87	1.21	93.92	10.50	0.36	28.38	71.26	10.67	15.02	0.89	84.09	15.62	0.16	82.38	17.46	277.35	19.37	1.10	79.53	95.10
250	0.1	4.08	0.96	94.96	11.70	0.18	39.63	60.19	13.71	16.33	1.81	81.86	25.40	0.06	91.13	8.81	506.50	35.71	0.95	63.34	130.70
	1	4.95	1.91	93.14	17.90	0.11	64.33	35.56	13.51	19.98	8.45	71.57	26.47	0.03	96.80	3.17	541.00	39.80	1.05	59.15	126.90
400	0.1	3.99	1.41	94.60	16.00	0.03	79.44	20.53	18.02	22.30	24.15	53.55	78.20	0.01	99.03	0.96	751.20	52.48	1.56	45.96	179.10
	1	4.96	3.60	91.44	19.00	0.01	94.06	5.93	17.86	13.85	56.28	29.87	82.70	0.01	99.86	0.13	778.00	53.54	1.53	44.93	117.90