

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	372	1167	61	779	1208
# contigs (>= 5000 bp)	228	61	0	0	65
# contigs (>= 10000 bp)	126	5	0	0	7
# contigs (>= 25000 bp)	33	2	0	0	1
# contigs (>= 50000 bp)	1	0	0	0	0
Total length (>= 1000 bp)	3623092	2833024	71344	1101157	2916180
Total length (>= 5000 bp)	3246574	468764	0	0	504782
Total length (>= 10000 bp)	2512192	116130	0	0	123688
Total length (>= 25000 bp)	1106480	73874	0	0	41118
Total length (>= 50000 bp)	74984	0	0	0	0
# contigs	403	1728	1101	2441	1807
Largest contig	74984	46742	1591	4028	41118
Total length	3644954	3247639	740863	2272898	3357249
Reference length	3664641	3664641	3664641	3664641	3664641
GC (%)	68.14	67.72	68.29	68.02	68.25
Reference GC (%)	68.12	68.12	68.12	68.12	68.12
N50	15743	2437	657	984	2366
NG50	15645	2149	-	664	2178
N75	8559	1433	570	719	1423
NG75	8271	1108	-	-	1177
L50	71	408	452	815	419
LG50	72	500	-	1676	486
L75	150	839	754	1492	877
LG75	152	1087	-	-	1054
# misassemblies	0	5	0	0	0
# misassembled contigs	0	5	0	0	0
Misassembled contigs length	0	11886	0	0	0
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 162 part	0 + 0 part	0 + 1 part	0 + 92 part
Unaligned length	0	220596	0	98	199420
Genome fraction (%)	99.463	81.767	20.199	61.982	85.265
Duplication ratio	1.000	1.010	1.001	1.001	1.011
# N's per 100 kbp	0.00	0.00	0.00	118.75	0.00
# mismatches per 100 kbp	0.00	116.34	0.68	232.01	406.80
# indels per 100 kbp	0.00	1.03	0.00	42.44	3.49
Largest alignment	74984	11230	1591	4028	16031
NA50	15743	2147	657	984	2105
NGA50	15645	1903	-	664	1887
NA75	8559	1169	570	719	1203
NGA75	8271	821	-	-	964
LA50	71	471	452	815	492
LGA50	72	574	-	1676	570
LA75	150	979	754	1492	1019
LGA75	152	1296	-	-	1233

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	347	1419	191	58	1032
# relocations	165	194	78	13	151
# translocations	114	582	96	42	328
# inversions	15	4	5	1	8
# interspecies translocations	53	639	12	2	545
# possibly misassembled contigs	197	207	177	98	234
# misassembled contigs	195	1235	113	57	916
Misassembled contigs length	8338532	11608967	7268947	267742	10567448
# local misassemblies	136	122	168	44	115
# structural variations	111	64	63	21	60
# mismatches	242529	239771	164253	168262	340117
# indels	8070	7047	4985	11614	7839
# short indels	6717	6156	4441	6346	6858
# long indels	1353	891	544	5268	981
Indels length	30143	21304	14403	89675	24869

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	8181	4137	3487	5995	4452
Fully unaligned length	17337884	13024959	11177988	11501862	13151827
# partially unaligned contigs	320	884	143	555	1627
# with misassembly	49	50	49	2	50
# both parts are significant	112	134	104	91	159
Partially unaligned length	2788721	2921554	2880327	238930	3106444
# N's	126	0	6072	23728	6852

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	56168	27909	112149	261972	51346
# contigs (>= 1000 bp)	9713	9863	6814	13327	10383
# contigs (>= 5000 bp)	2676	2109	1162	1848	2190
# contigs (>= 10000 bp)	1360	1116	687	700	1166
# contigs (>= 25000 bp)	491	445	318	113	437
# contigs (>= 50000 bp)	203	193	155	22	169
Total length (>= 0 bp)	97196568	75596305	72039857	87289689	82359499
Total length (>= 1000 bp)	80954951	66269212	45124735	43342137	66084435
Total length (>= 5000 bp)	66609038	50077730	34912924	21341840	49170265
Total length (>= 10000 bp)	57307002	43171375	31611613	13399664	42077060
Total length (>= 25000 bp)	43872072	32595589	25609380	4811011	30569801
Total length (>= 50000 bp)	33989240	23949778	19860544	1795083	21248231
# contigs	20004	17716	17884	28240	19945
Largest contig	2780101	800397	560953	202548	514709
Total length	88077239	71707572	52656365	53726740	72643866
Reference length	183474340	183474340	183474340	183474340	183474340
N50	24752	19377	23276	3140	16577
N75	5231	3548	2055	1211	3116
L50	498	594	348	3259	719
L75	2569	2995	2678	10554	3544
# misassemblies	347	1419	191	58	1032
# misassembled contigs	195	1235	113	57	916
Misassembled contigs length	8338532	11608967	7268947	267742	10567448
# local misassemblies	136	122	168	44	115
# structural variations	111	64	63	21	60
# unaligned contigs	8181 + 320 part	4137 + 884 part	3487 + 143 part	5995 + 555 part	4452 + 1627 part
Unaligned length	20126605	15946513	14058315	11740792	16258271
Genome fraction (%)	38.014	32.809	20.672	25.138	33.480
Duplication ratio	1.127	1.021	1.056	1.002	1.020
# N's per 100 kbp	0.14	0.00	11.53	44.16	9.43
# mismatches per 100 kbp	347.73	398.32	433.08	364.82	553.69
# indels per 100 kbp	11.57	11.71	13.14	25.18	12.76
Largest alignment	2780101	800397	560953	202541	505955
NA50	11158	6120	2335	1771	4994
NA75	542	554	-	574	545
LA50	989	1311	1587	4941	1638
LA75	11266	12693	-	19108	14336

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	342	1405	187	58	1017
# relocations	168	196	80	13	153
# translocations	118	587	97	42	330
# inversions	15	4	5	1	8
# interspecies translocations	41	618	5	2	526
# possibly misassembled contigs	192	207	176	96	232
# misassembled contigs	194	1223	112	57	905
Misassembled contigs length	8337812	11587897	7268287	267742	10550406
# local misassemblies	134	122	168	44	115
# structural variations	111	64	63	21	60
# mismatches	234523	237883	163329	167497	338615
# indels	7922	6915	4914	11598	7770
# short indels	6570	6024	4370	6330	6789
# long indels	1352	891	544	5268	981
Indels length	29953	21150	14314	89652	24788

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	8478	4169	3493	6016	4481
Fully unaligned length	17773626	13243040	11380695	11534814	13383083
# partially unaligned contigs	235	884	139	544	1624
# with misassembly	50	47	49	2	48
# both parts are significant	107	134	103	89	157
Partially unaligned length	2543826	2731724	2686243	219816	2898497
# N's	126	0	6072	23728	6852

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	20004	17716	17884	28240	19945
# contigs (>= 1000 bp)	9713	9863	6814	13327	10383
# contigs (>= 5000 bp)	2676	2109	1162	1848	2190
# contigs (>= 10000 bp)	1360	1116	687	700	1166
# contigs (>= 25000 bp)	491	445	318	113	437
# contigs (>= 50000 bp)	203	193	155	22	169
Total length (>= 0 bp)	88077239	71707572	52656365	53726740	72643866
Total length (>= 1000 bp)	80954951	66269212	45124735	43342137	66084435
Total length (>= 5000 bp)	66609038	50077730	34912924	21341840	49170265
Total length (>= 10000 bp)	57307002	43171375	31611613	13399664	42077060
Total length (>= 25000 bp)	43872072	32595589	25609380	4811011	30569801
Total length (>= 50000 bp)	33989240	23949778	19860544	1795083	21248231
# contigs	20004	17716	17884	28240	19945
Largest contig	2780101	800397	560953	202548	514709
Total length	88077239	71707572	52656365	53726740	72643866
Reference length	95264179	95264179	95264179	95264179	95264179
N50	24752	19377	23276	3140	16577
N75	5231	3548	2055	1211	3116
L50	498	594	348	3259	719
L75	2569	2995	2678	10554	3544
# misassemblies	342	1405	187	58	1017
# misassembled contigs	194	1223	112	57	905
Misassembled contigs length	8337812	11587897	7268287	267742	10550406
# local misassemblies	134	122	168	44	115
# structural variations	111	64	63	21	60
# unaligned contigs	8478 + 235 part	4169 + 884 part	3493 + 139 part	6016 + 544 part	4481 + 1624 part
Unaligned length	20317452	15974764	14066938	11754630	16281580
Genome fraction (%)	72.964	63.117	39.756	48.373	64.421
Duplication ratio	1.127	1.021	1.056	1.002	1.020
# N's per 100 kbp	0.14	0.00	11.53	44.16	9.43
# mismatches per 100 kbp	337.40	395.63	431.25	363.48	551.76
# indels per 100 kbp	11.40	11.50	12.97	25.17	12.66
Largest alignment	2780101	800397	560953	202541	505955
NA50	11158	6120	2333	1770	4993
NA75	524	552	-	573	543
LA50	989	1311	1588	4941	1638
LA75	11367	12711	-	19116	14352

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	5	0	0	0
# relocations	0	0	0	0	0
# translocations	0	5	0	0	0
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	64	0	0	34
# misassembled contigs	0	5	0	0	0
Misassembled contigs length	0	11886	0	0	0
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# mismatches	0	3486	5	5270	12711
# indels	0	31	0	964	109
# short indels	0	29	0	414	96
# long indels	0	2	0	550	13
Indels length	0	69	0	7755	412

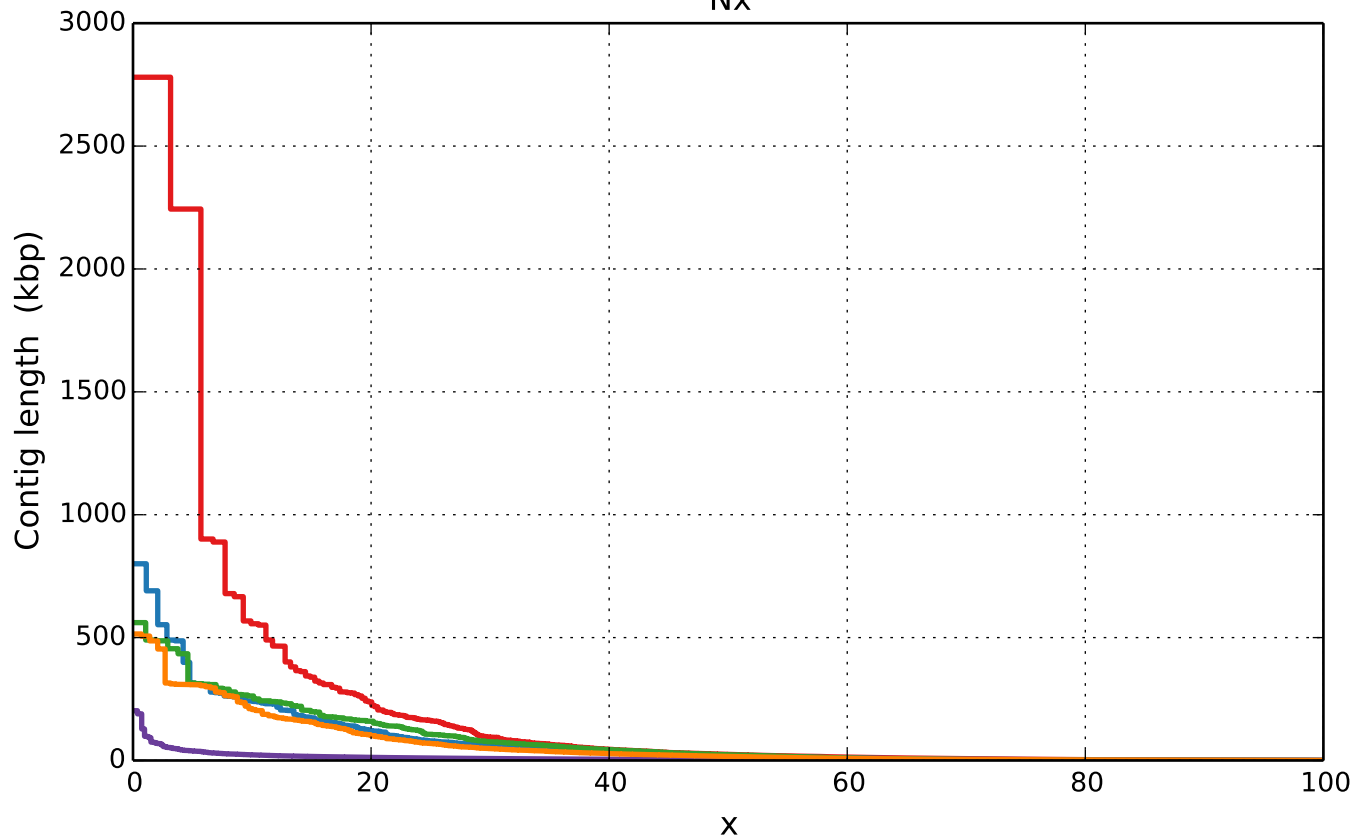
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	162	0	1	92
# with misassembly	0	1	0	0	1
# both parts are significant	0	62	0	0	34
Partially unaligned length	0	220596	0	98	199420
# N's	0	0	0	2699	0

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



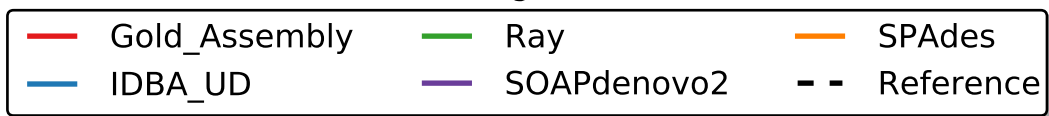
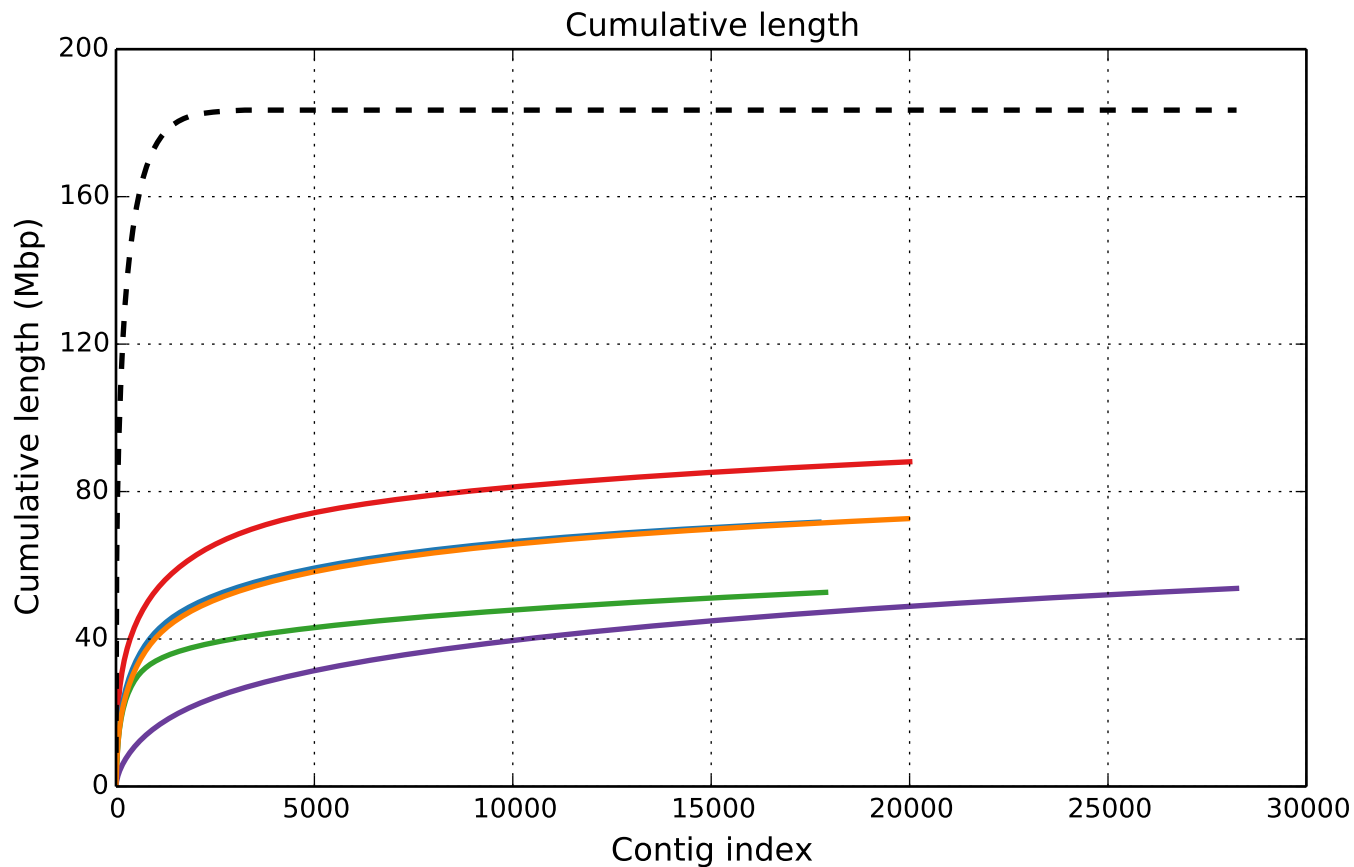
Gold_Assembly

Ray

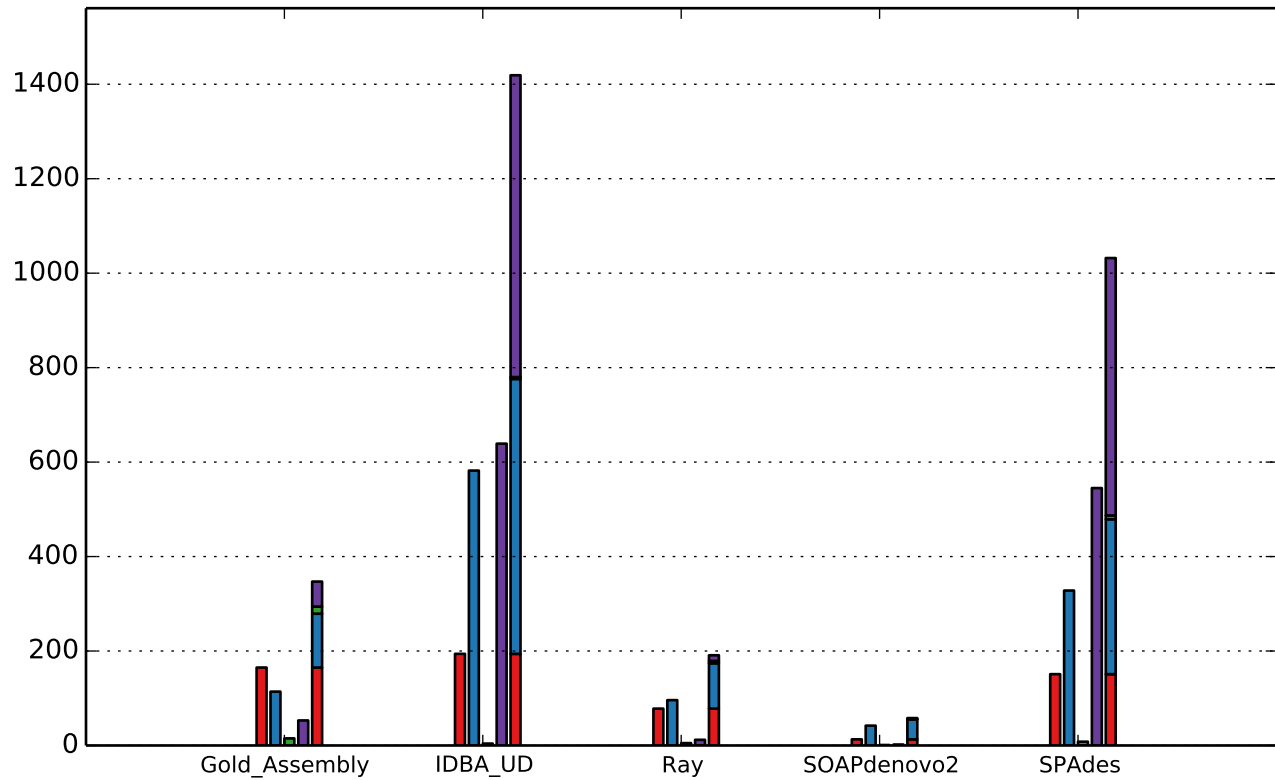
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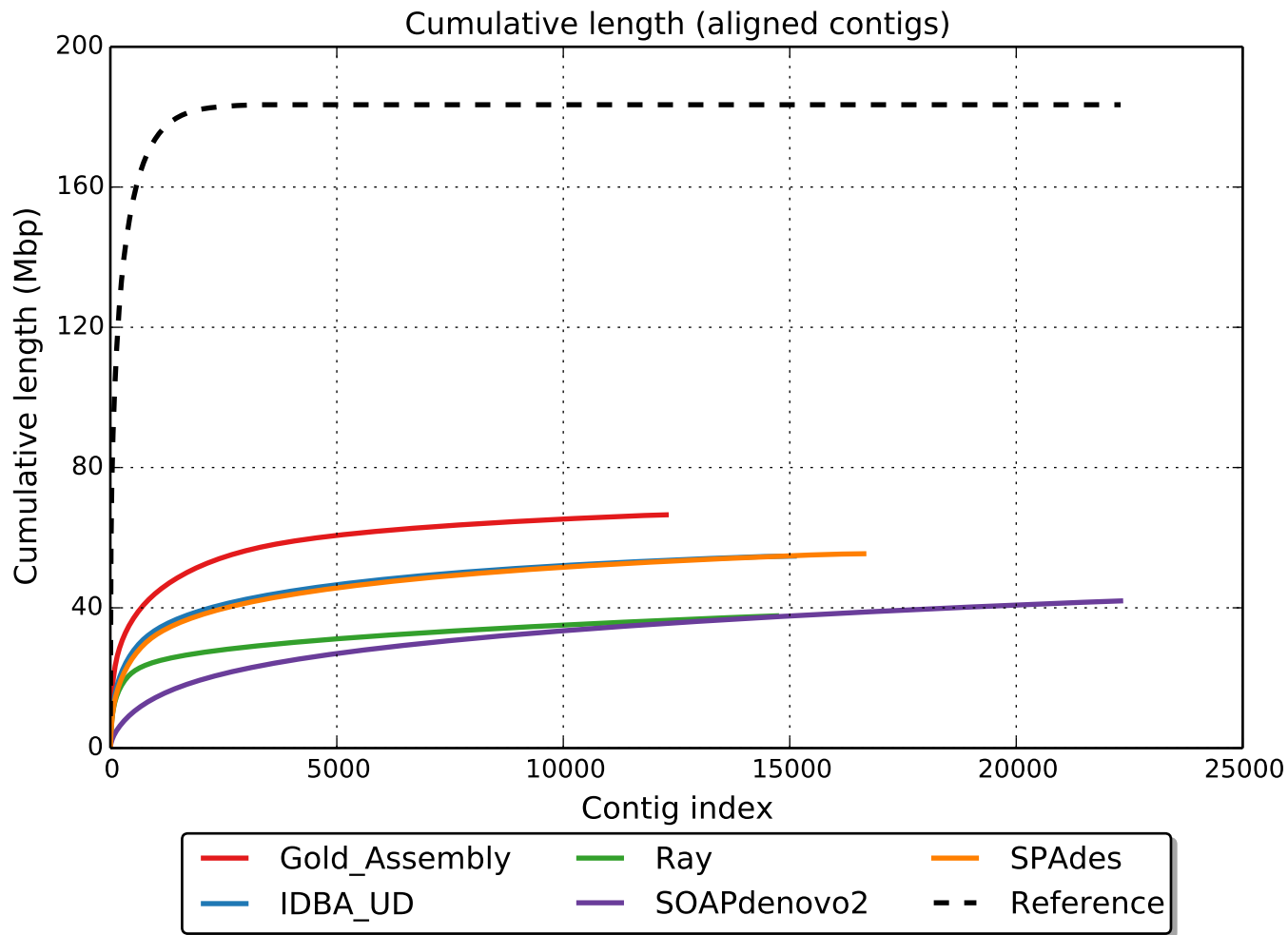
IDBA_UD

SOAPdenovo2

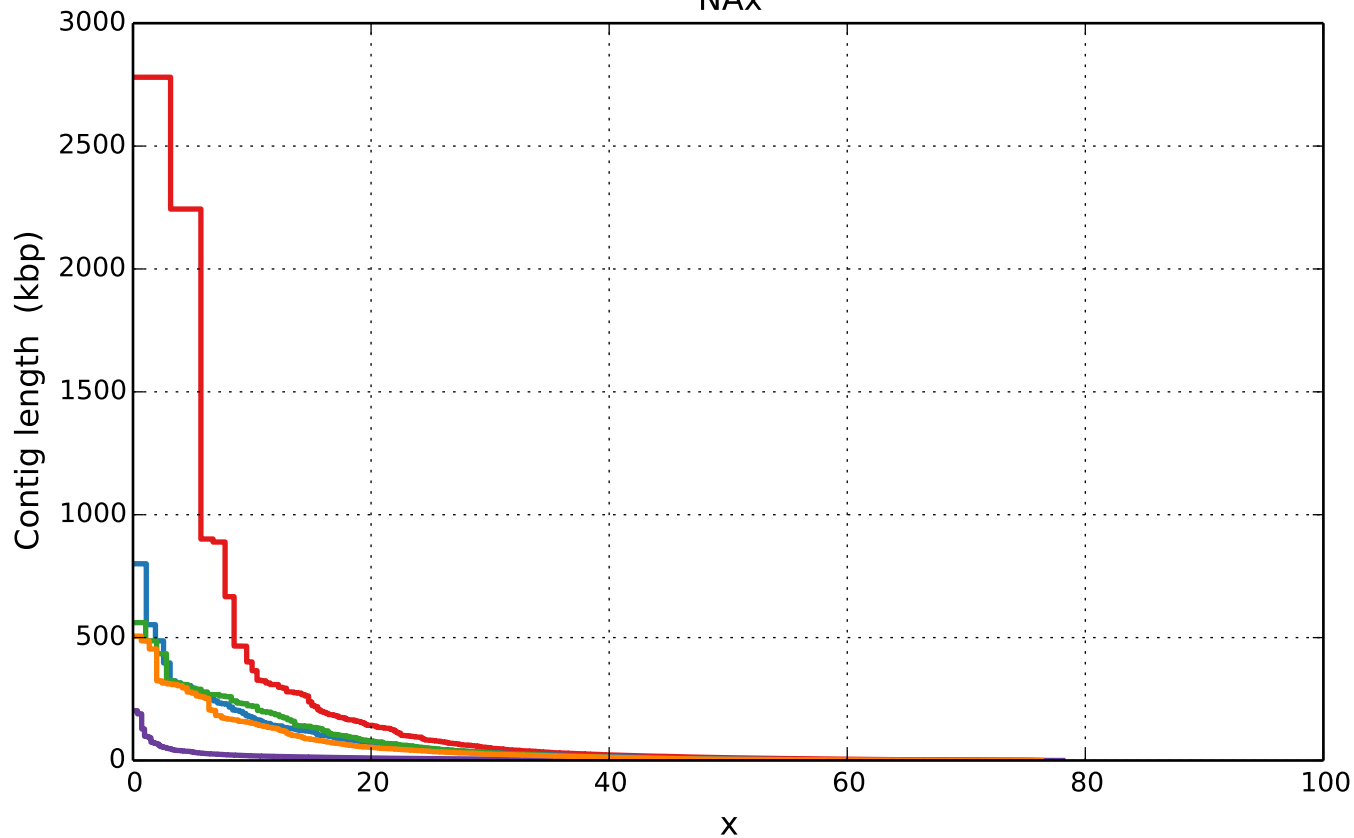


Misassemblies





NAx



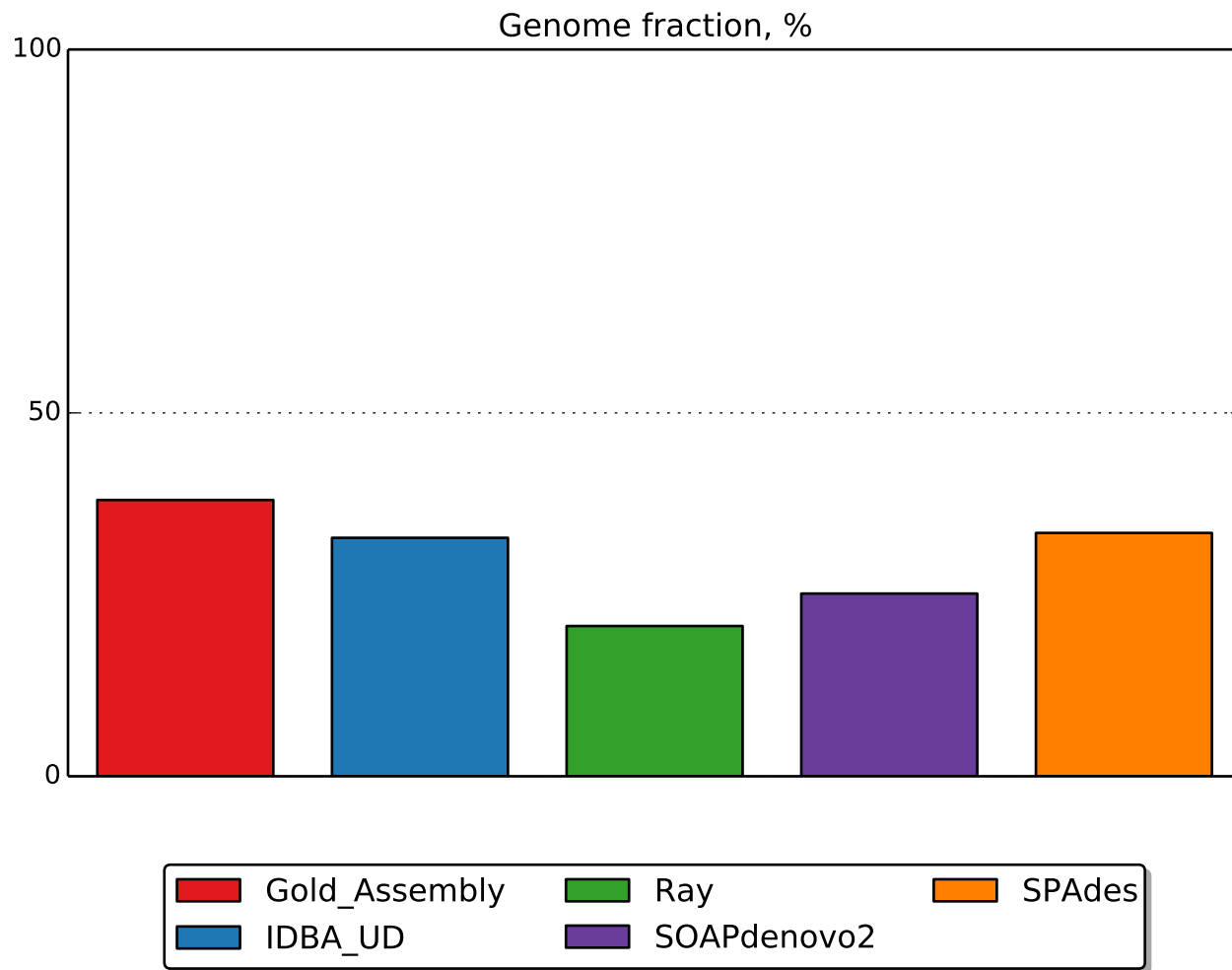
Gold_Assembly

Ray

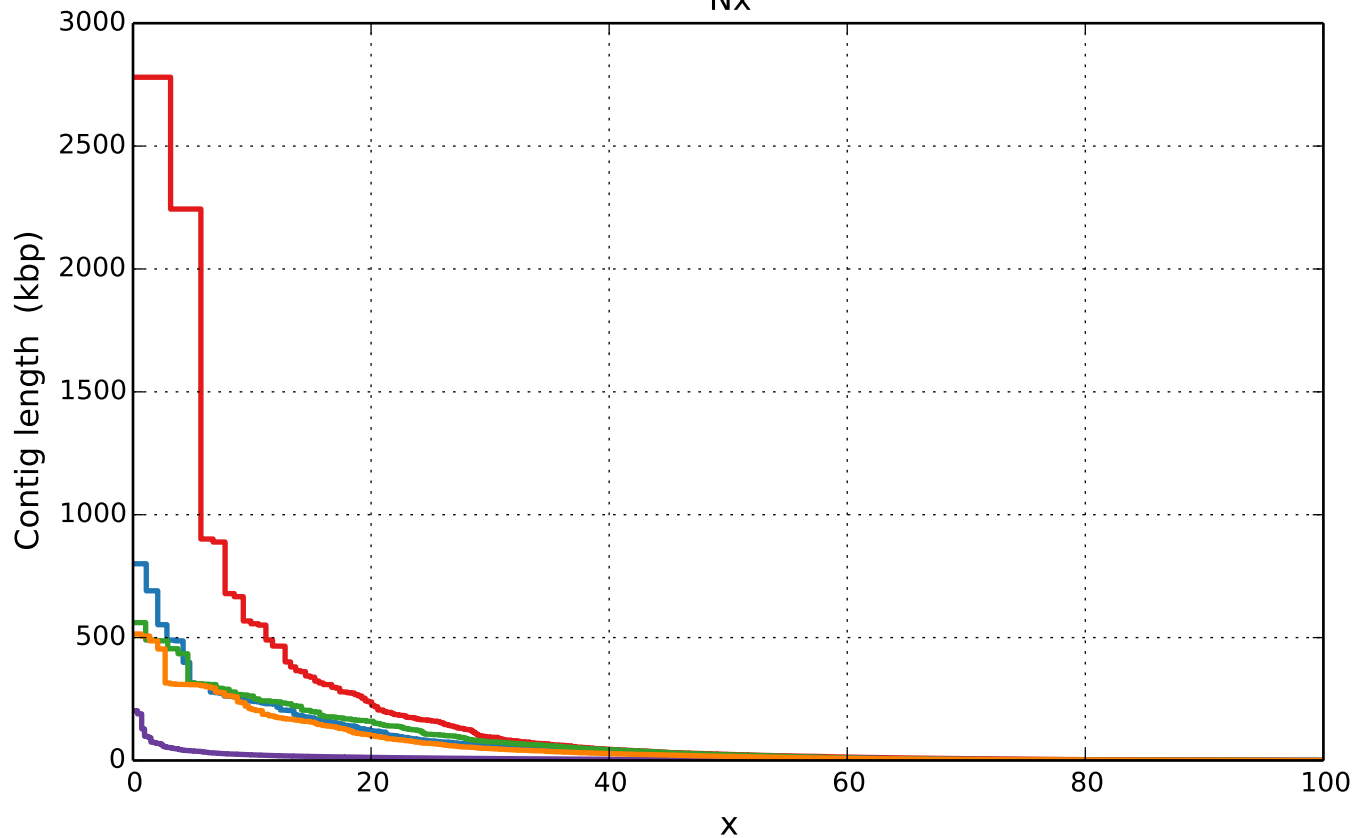
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IDBA_UD

SOAPdenovo2



Nx



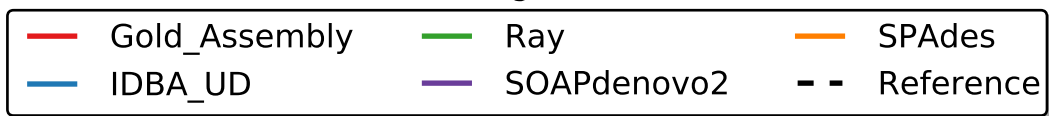
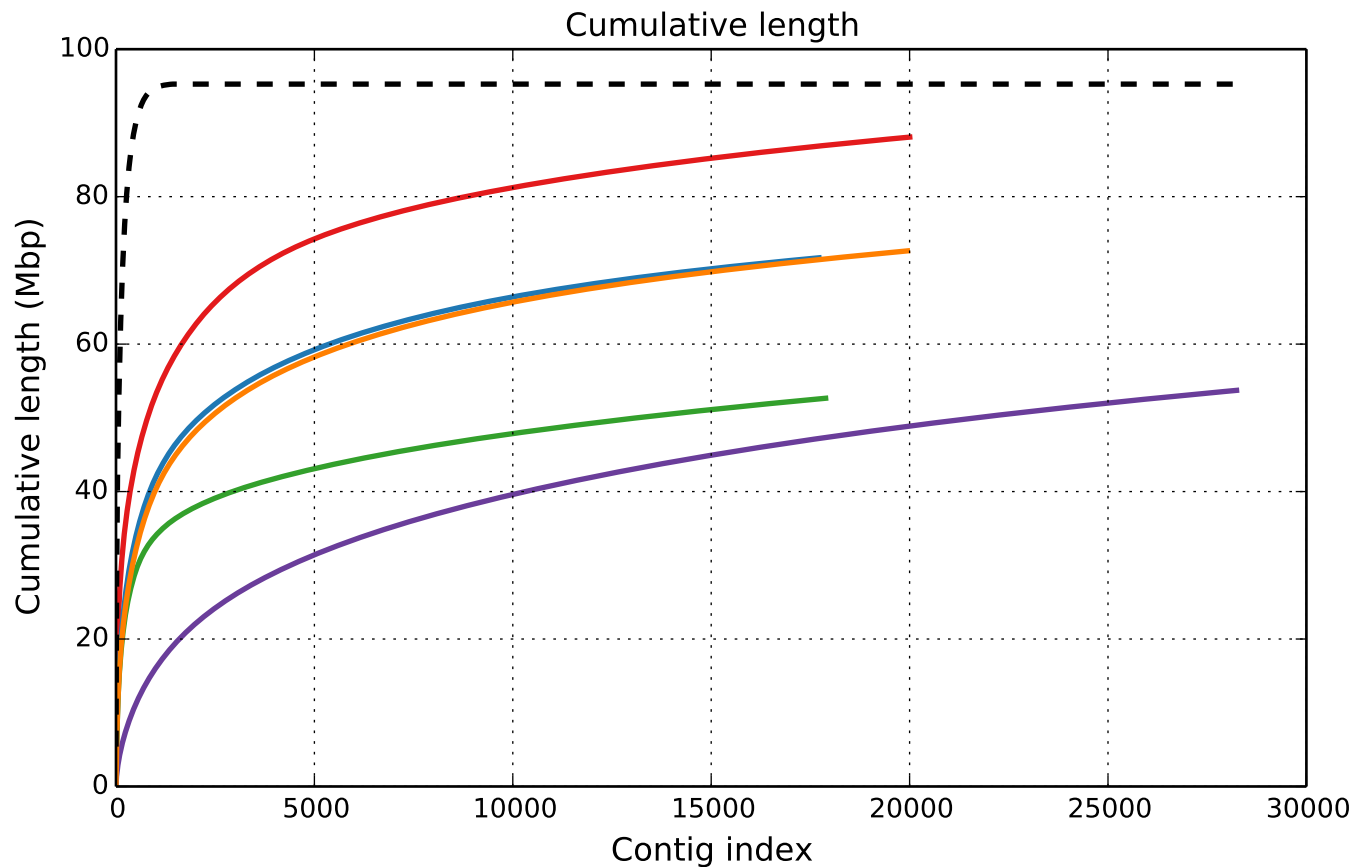
Gold_Assembly

Ray

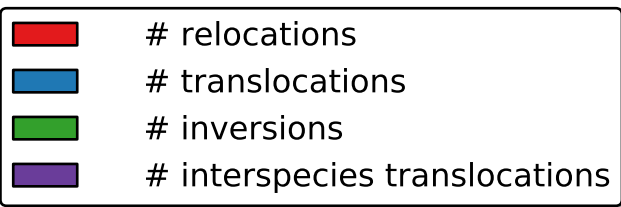
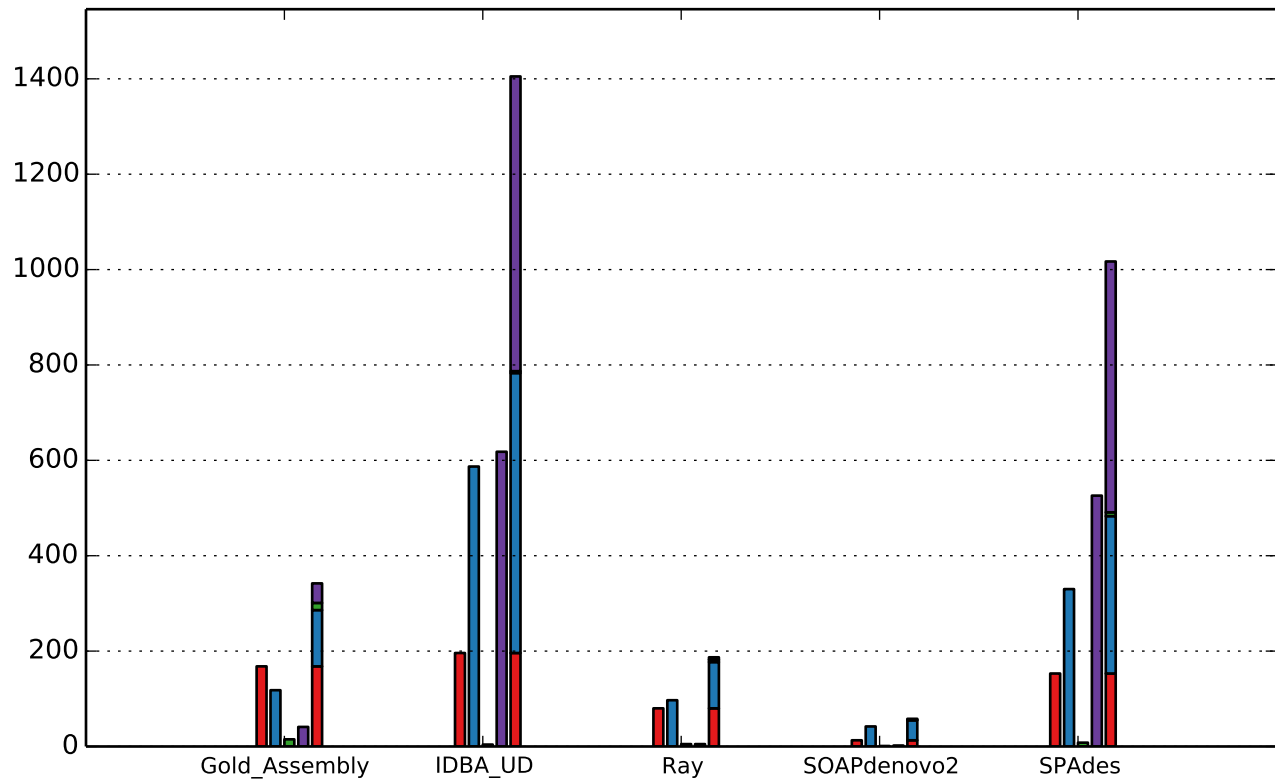
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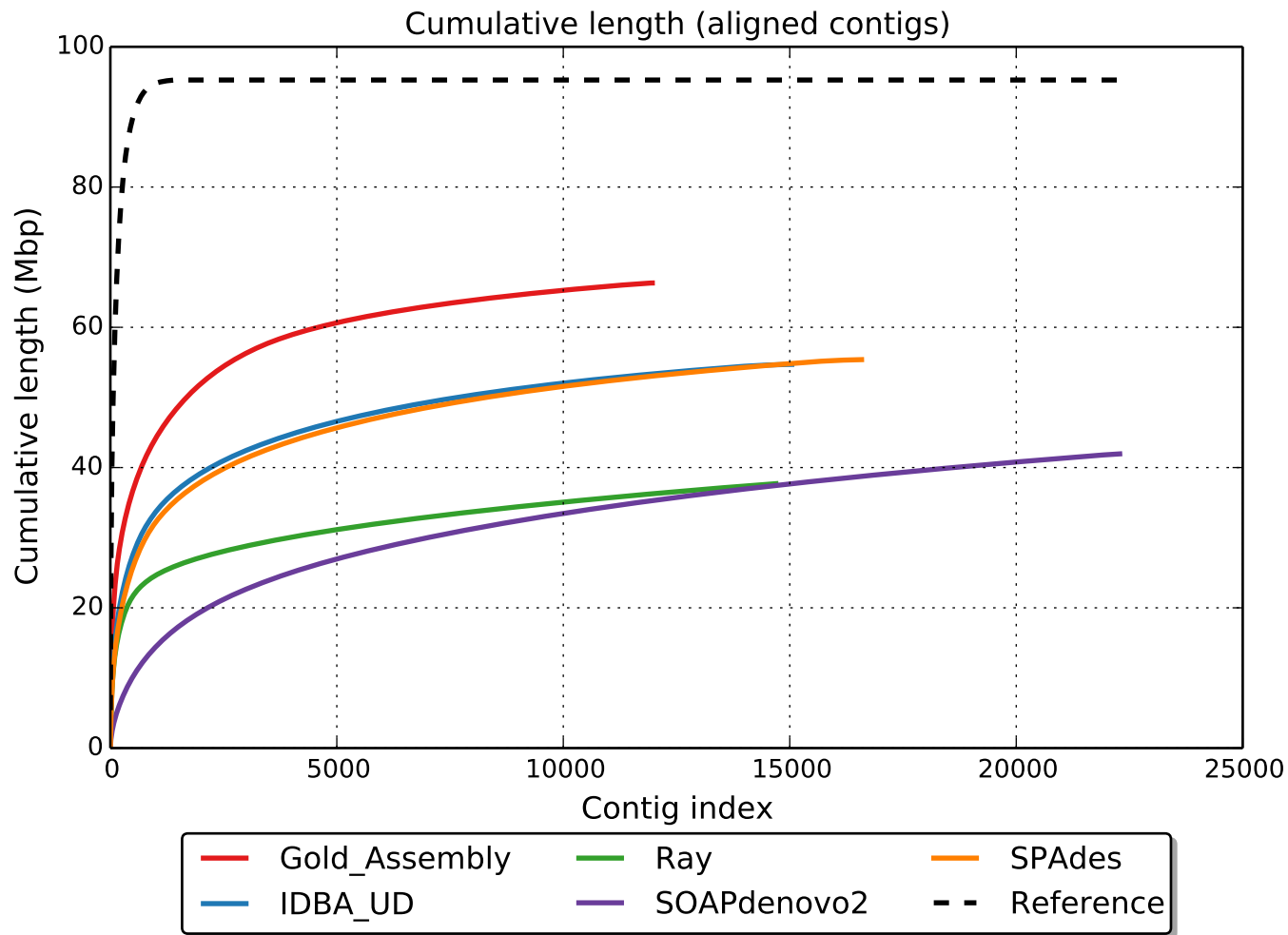
IDBA_UD

SOAPdenovo2

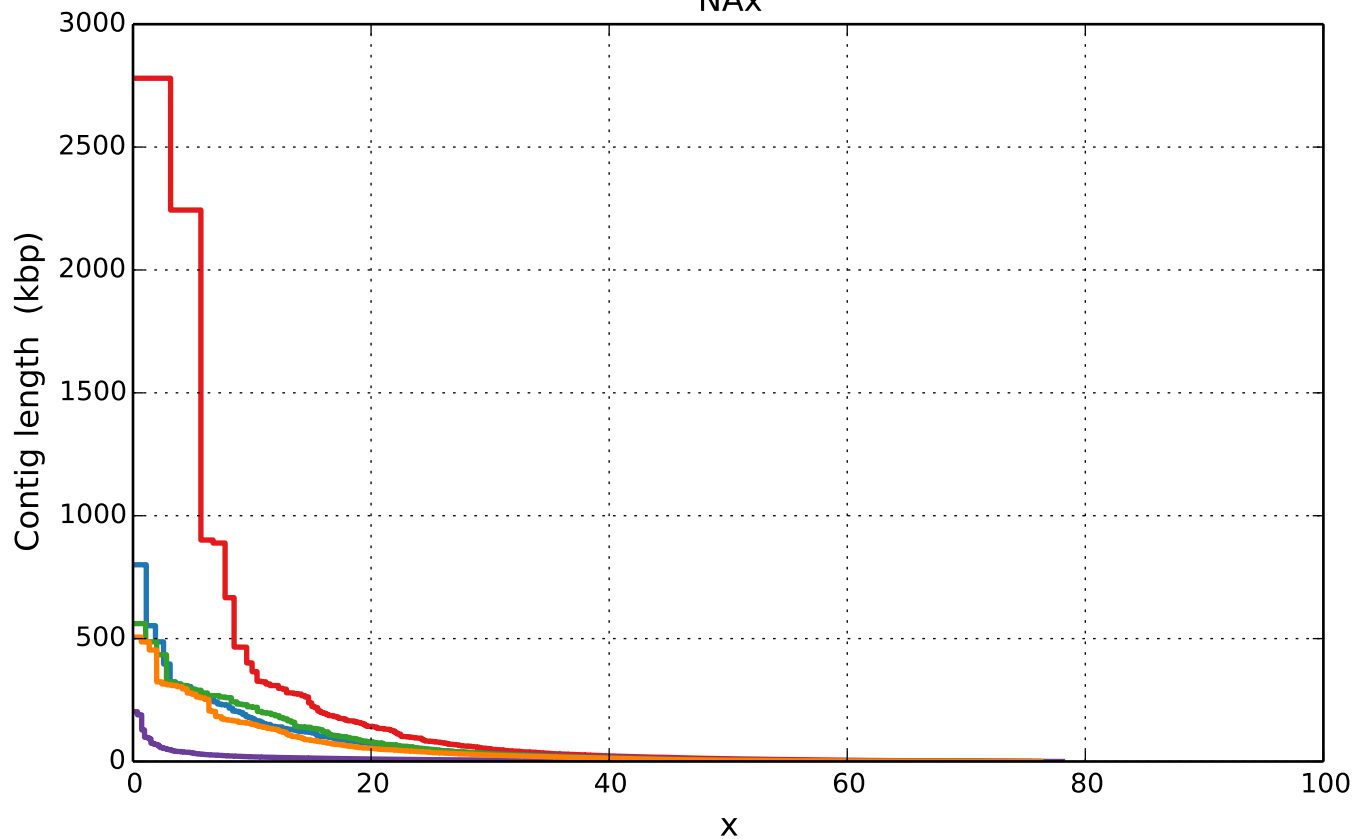


Misassemblies





NAx



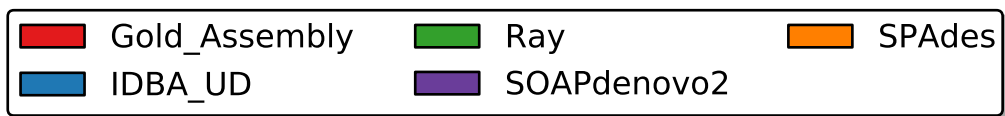
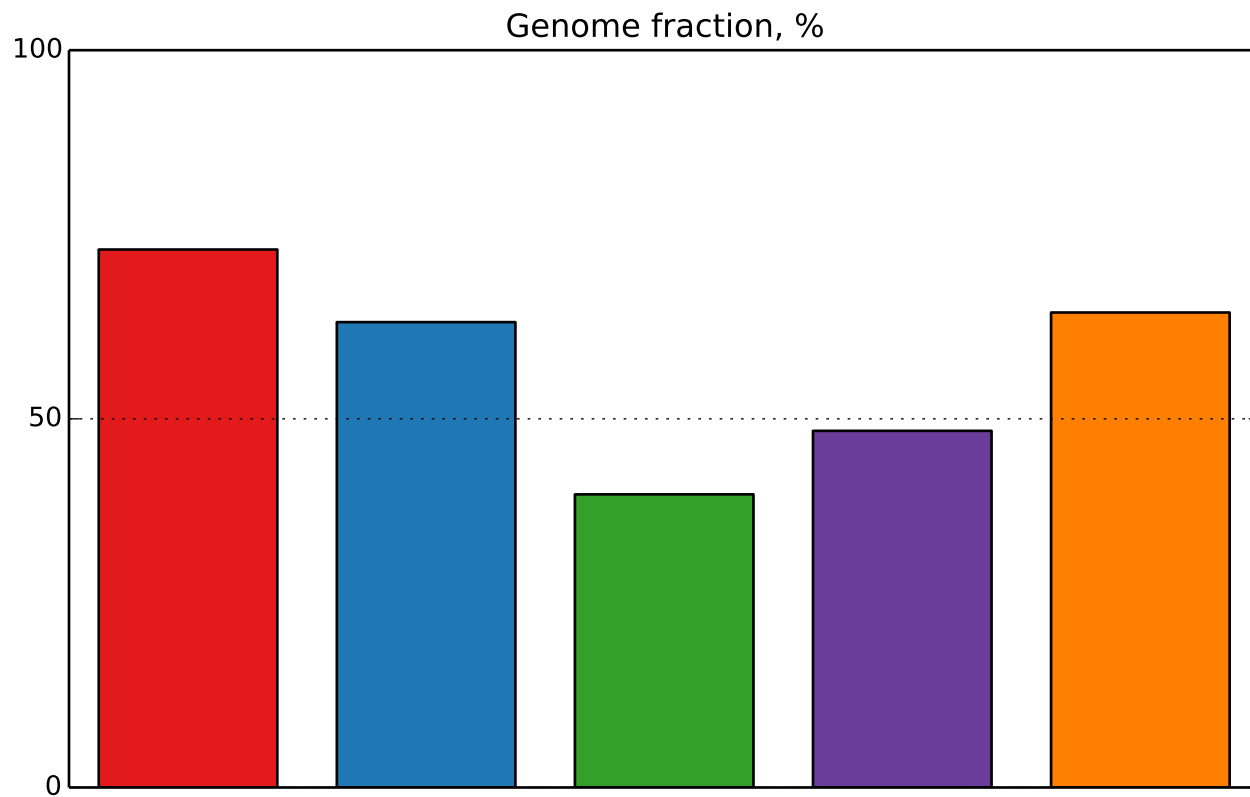
Gold_Assembly

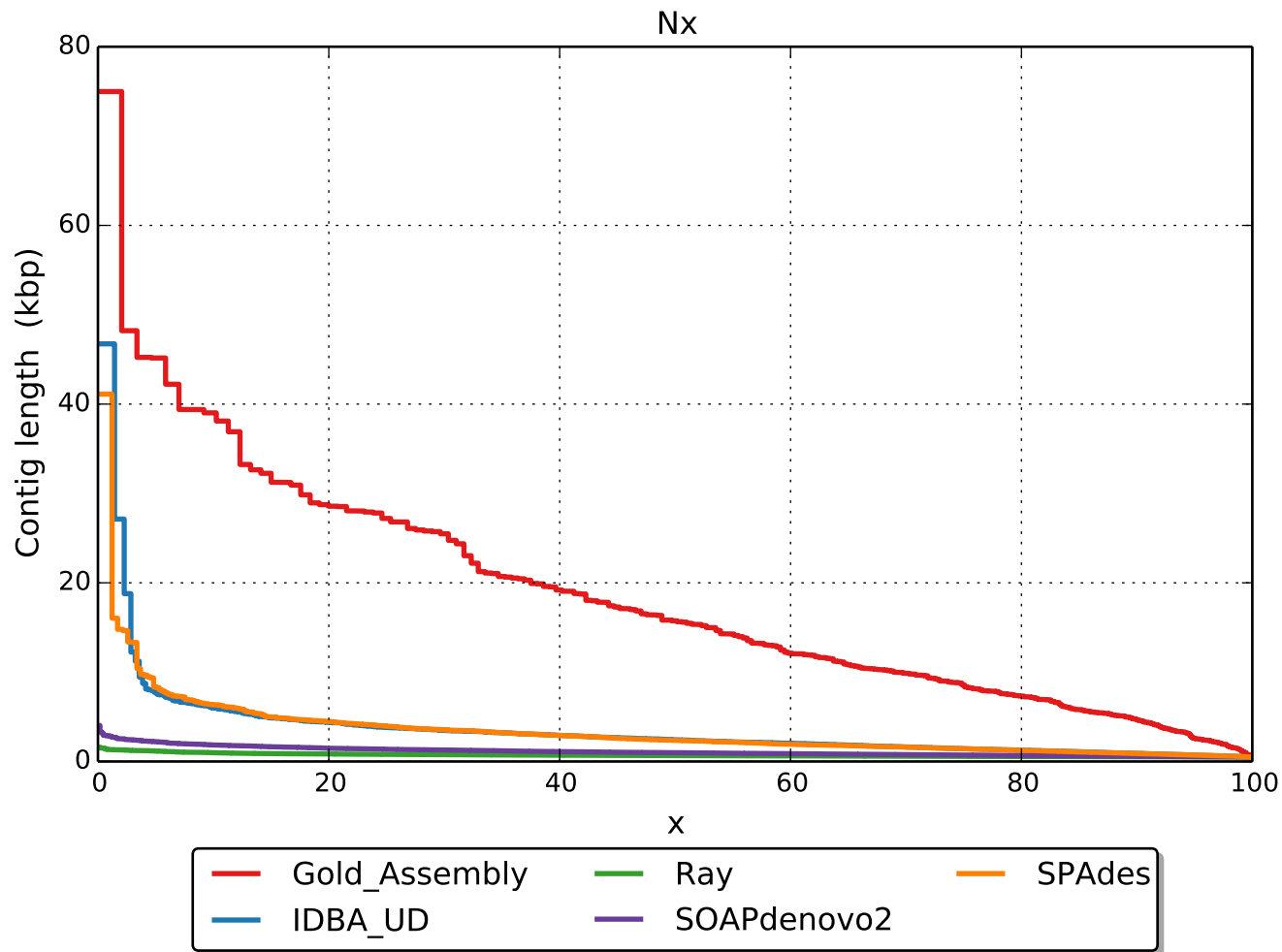
Ray

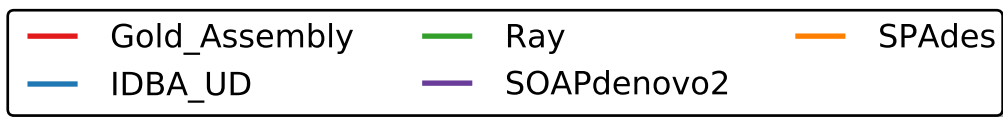
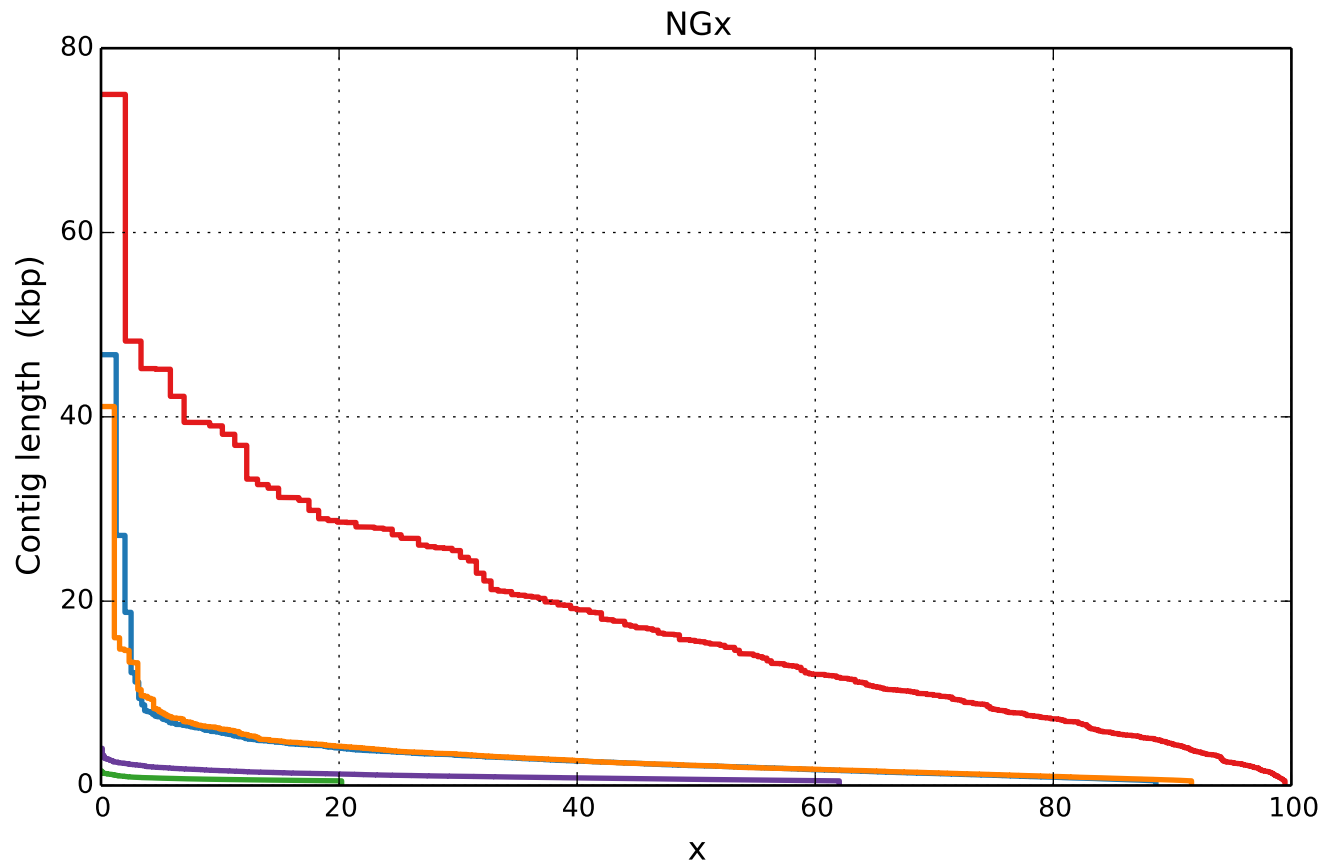
SPAdes

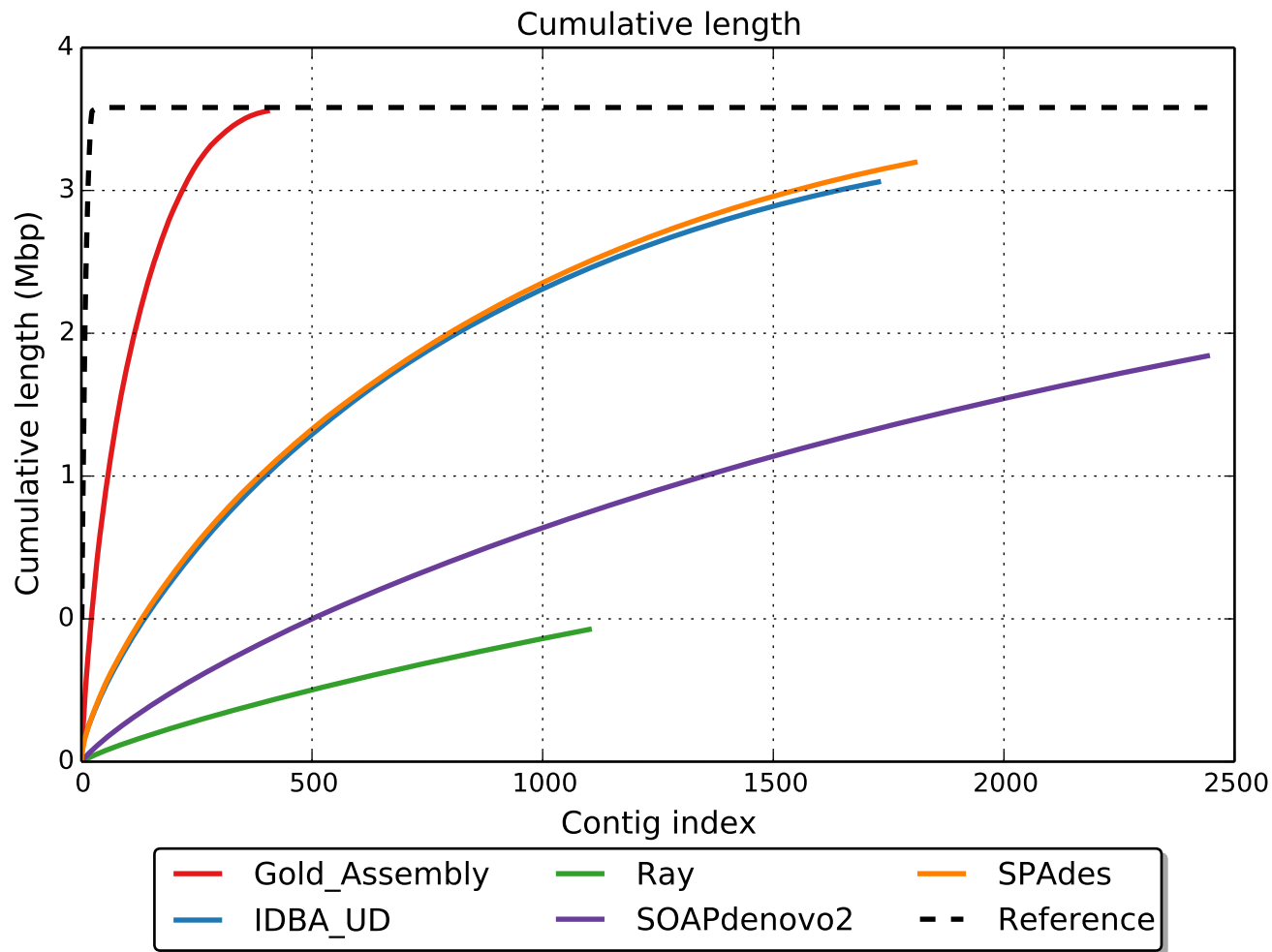
IDBA_UD

SOAPdenovo2

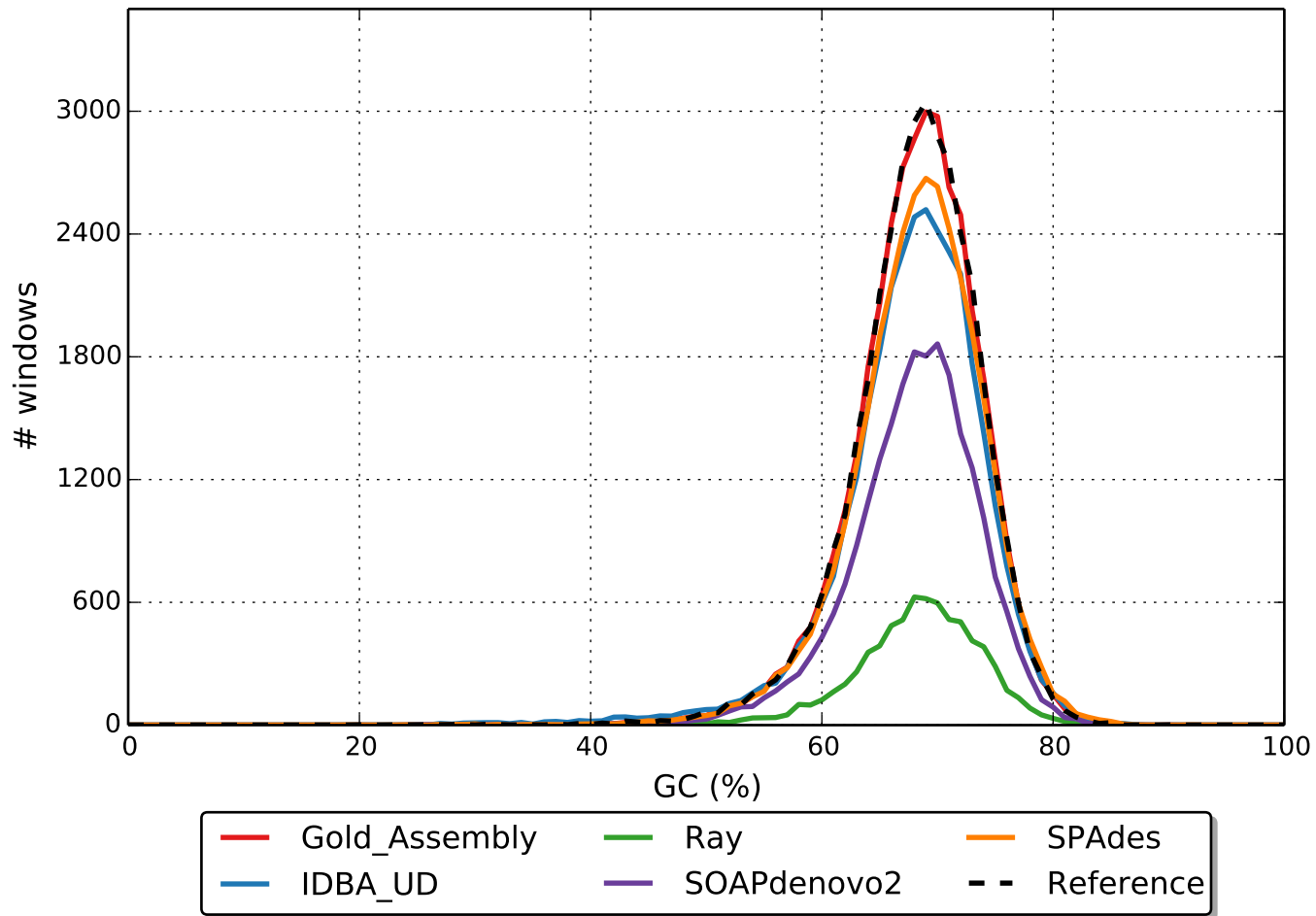


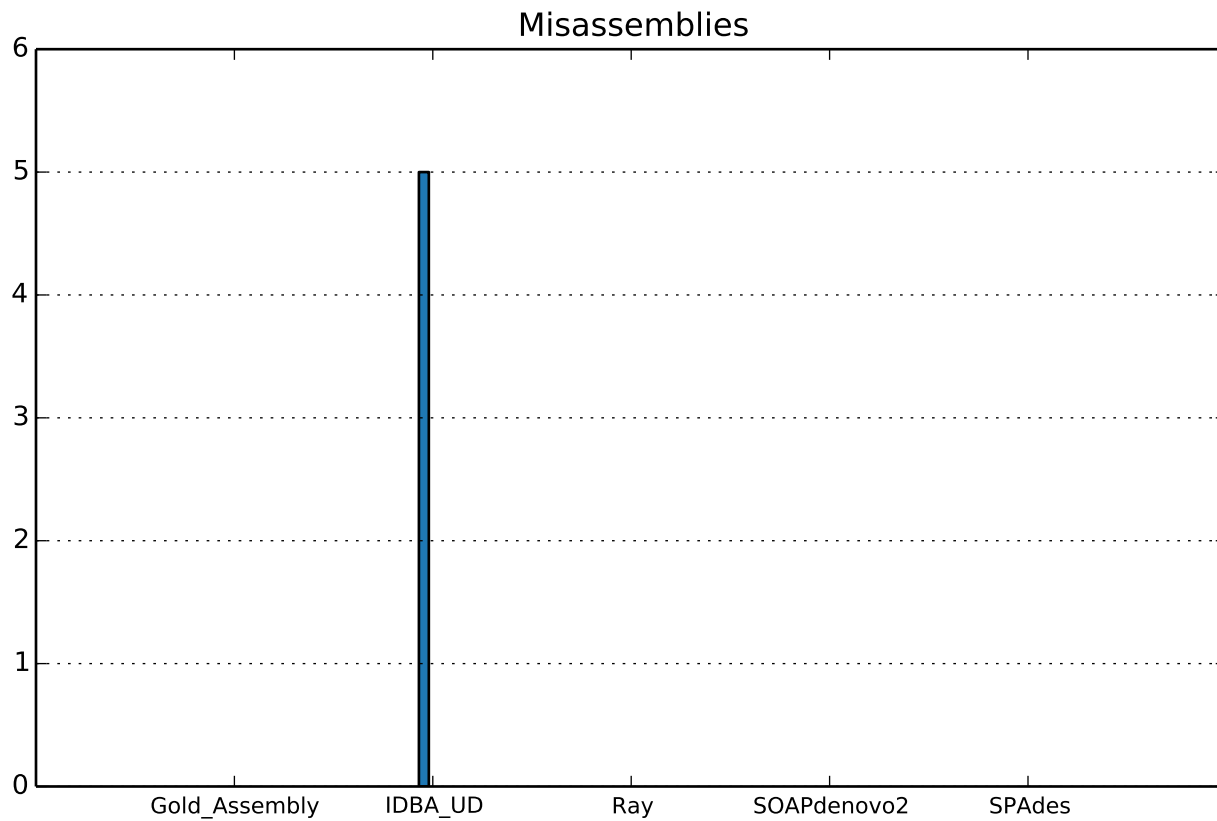





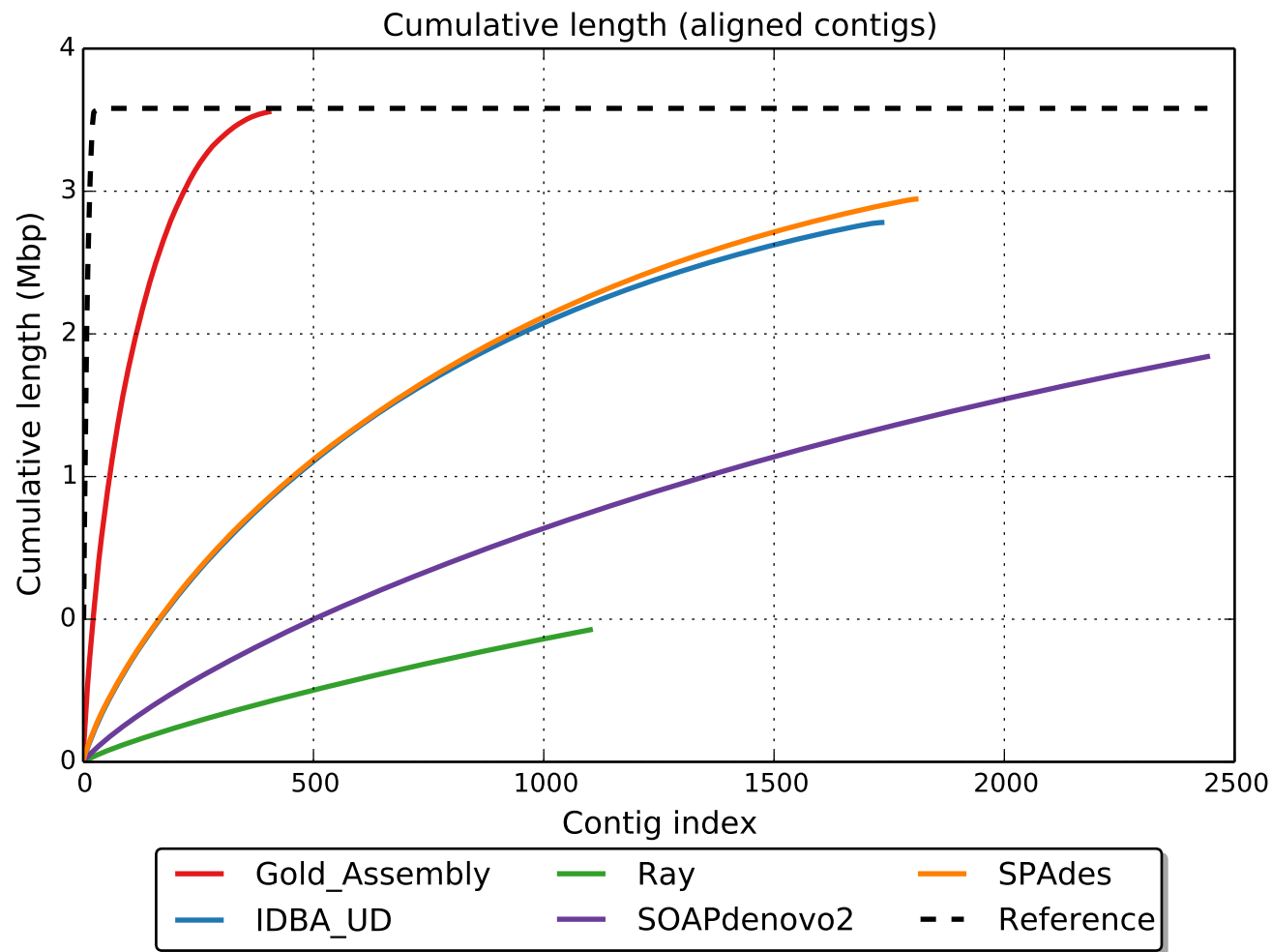


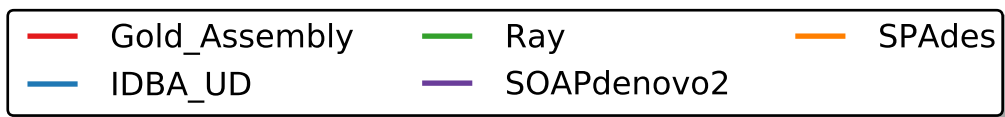
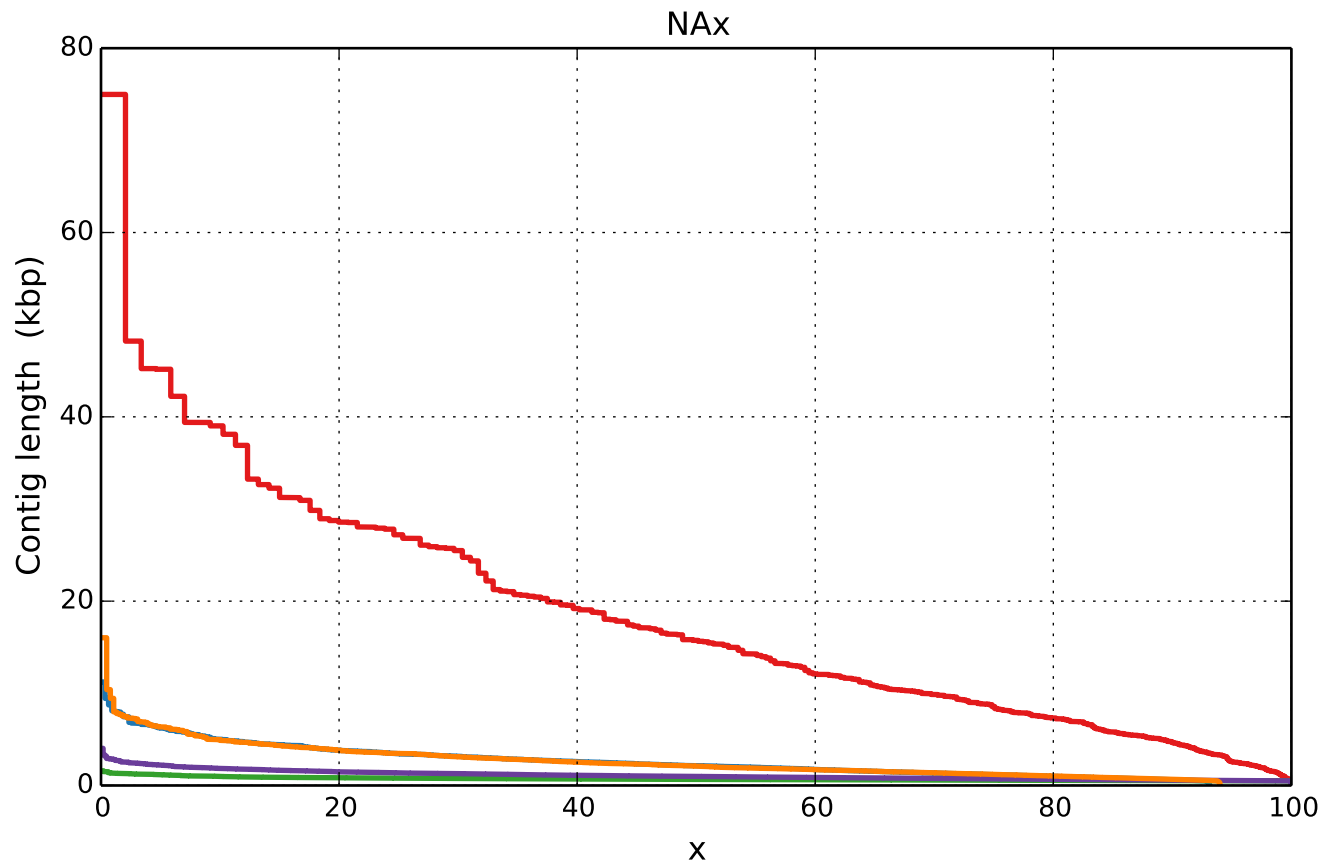
GC content





 # translocations





NGAx

