

Report

	velvet.10M_contigs	velvet.20M_contigs	velvet.40M_contigs	velvet.60M_contigs	velvet.120M_contigs	velvet.240M_contigs	velvet.2400M_contigs	velvet.all_contigs
contigs (>= 0 bp)	207	181	193	194	199	199	200	255
contigs (>= 1000 bp)	88	78	84	86	82	82	83	96
total length (>= 0 bp)	4561014	4562410	4562796	4561972	4563242	4563160	4563142	4565607
total length (>= 1000 bp)	4539639	4544868	4546820	4545384	4546341	4546259	4546241	4539120
contigs	97	85	89	90	86	86	87	106
largest contig	252273	374170	326502	326019	326502	289177	326502	209551
total length	4545871	4550014	4550599	4548619	4549335	4549253	4549235	4546051
reference length	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675
C (%)	50.74	50.74	50.74	50.74	50.74	50.74	50.74	50.73
reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
50	118079	123869	111212	105592	112457	115595	112457	95446
650	117838	123869	111212	105592	112457	112457	112457	95446
75	58878	87139	57136	54810	63531	66164	57136	59505
675	54820	62823	54816	53576	62041	63531	54810	57603
0	13	12	13	14	13	13	13	17
50	14	12	13	14	13	14	13	17
5	26	23	26	27	25	25	26	32
75	28	24	27	28	26	26	27	33
misassemblies	20	29	24	21	22	21	23	9
misassembled contigs	11	15	13	12	13	12	13	6
misassembled contigs length	1004766	1827350	1437617	1531863	1667273	1518740	1642690	638588
local misassemblies	31	28	25	21	25	22	23	30
unaligned contigs	0 + 1 part	0 + 1 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
aligned length	158	719	0	0	0	0	0	0
genome fraction (%)	97.973	98.040	98.112	98.033	98.043	98.036	98.047	97.840
mplication ratio	1.001	1.001	1.000	1.000	1.000	1.000	1.000	1.002
N's per 100 kbp	104.34	90.13	74.96	64.28	68.67	64.63	64.58	168.39
mismatches per 100 kbp	5.85	4.53	6.35	5.21	4.53	4.59	4.55	6.45
indels per 100 kbp	2.16	1.76	1.69	1.58	1.36	1.34	1.36	3.28
genes	4188 + 34 part	4203 + 28 part	4200 + 32 part	4200 + 26 part	4198 + 26 part	4198 + 26 part	4200 + 26 part	4179 + 48 part
operons	831 + 24 part	838 + 20 part	836 + 25 part	838 + 19 part	836 + 21 part	836 + 21 part	836 + 21 part	829 + 32 part
largest alignment	221439	209250	219191	209212	209210	209262	209210	209062
A50	105725	95942	94124	94124	95381	95589	94124	86381
GA50	105725	95626	94124	83105	94124	95381	94124	86381
A75	54820	53554	43766	45659	54810	54810	51643	54762
GA75	53520	45487	42468	43766	51643	51643	46071	46182
50	15	16	17	18	17	17	18	18
GA50	15	17	17	19	18	18	18	18
75	30	32	35	36	33	32	34	34
GA75	31	34	37	38	35	34	35	36

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

Misassemblies report

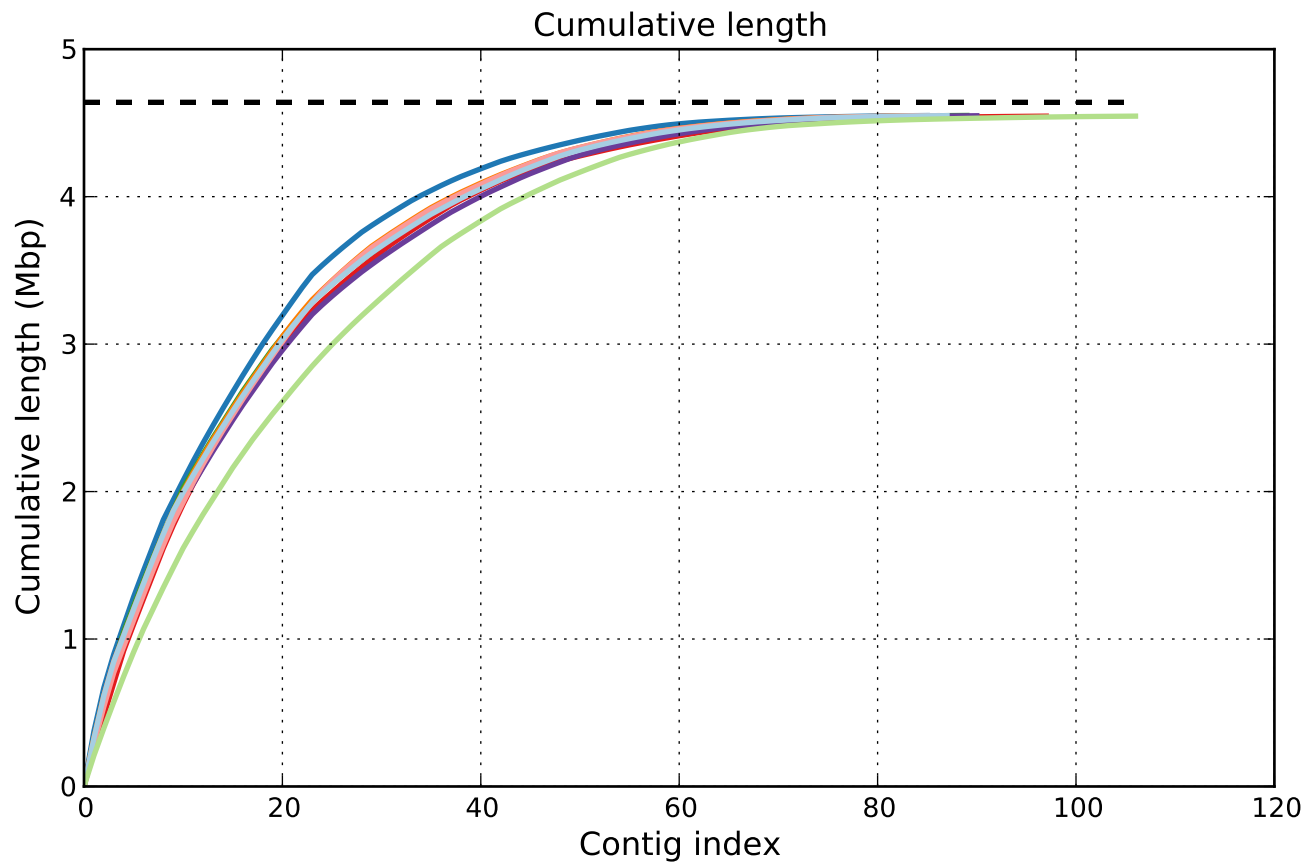
	velvet.10M_contigs	velvet.20M_contigs	velvet.40M_contigs	velvet.60M_contigs	velvet.120M_contigs	velvet.240M_contigs	velvet.2400M_contigs	velvet.all_contigs
misassemblies	20	29	24	21	22	21	23	9
# relocations	20	29	24	21	22	21	23	9
# translocations	0	0	0	0	0	0	0	0
# inversions	0	0	0	0	0	0	0	0
misassembled contigs	11	15	13	12	13	12	13	6
misassembled contigs length	1004766	1827350	1437617	1531863	1667273	1518740	1642690	638588
local misassemblies	31	28	25	21	25	22	23	30
mismatches	266	206	289	237	206	209	207	293
indels	98	80	77	72	62	61	62	149
# short indels	35	34	32	31	25	24	25	56
# long indels	63	46	45	41	37	37	37	93
indels length	1982	1451	1337	1096	1073	1038	1041	2865

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

Unaligned report

	velvet.10M_contigs	velvet.20M_contigs	velvet.40M_contigs	velvet.60M_contigs	velvet.120M_contigs	velvet.240M_contigs	velvet.2400M_contigs	velvet.all_contigs
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	1	1	0	0	0	0	0	0
# with misassembly	0	1	0	0	0	0	0	0
# both parts are significant	0	1	0	0	0	0	0	0
Partially unaligned length	158	719	0	0	0	0	0	0
# N's	4743	4101	3411	2924	3124	2940	2938	7655

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contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



velvet.10M_contigs

velvet.60M_contigs

velvet.240M_contigs

velvet.a

velvet.20M_contigs

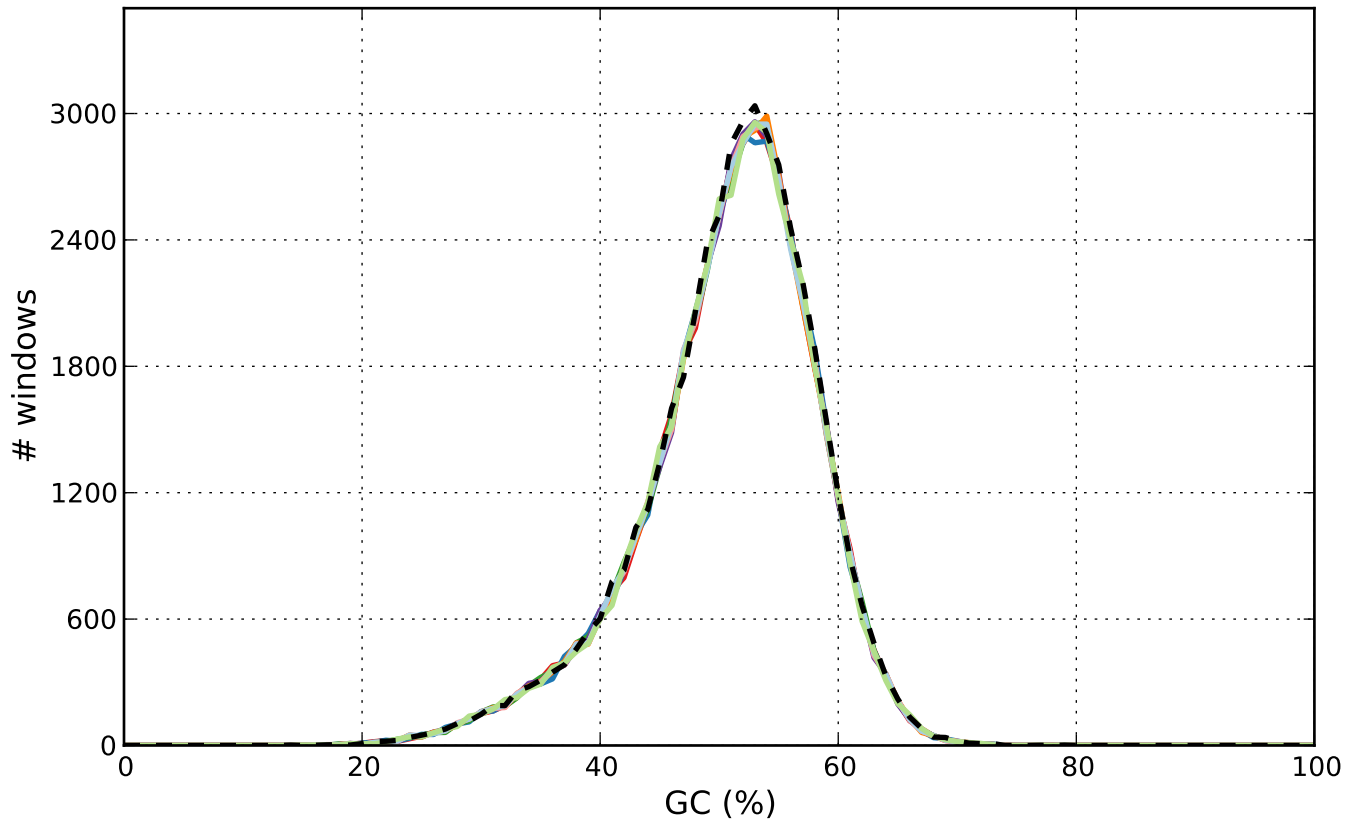
velvet.120M_contigs

velvet.2400M_contigs

Reference

velvet.40M_contigs

GC content



velvet.10M_contigs
velvet.20M_contigs
velvet.40M_contigs

velvet.60M_contigs

velvet.120M_contigs

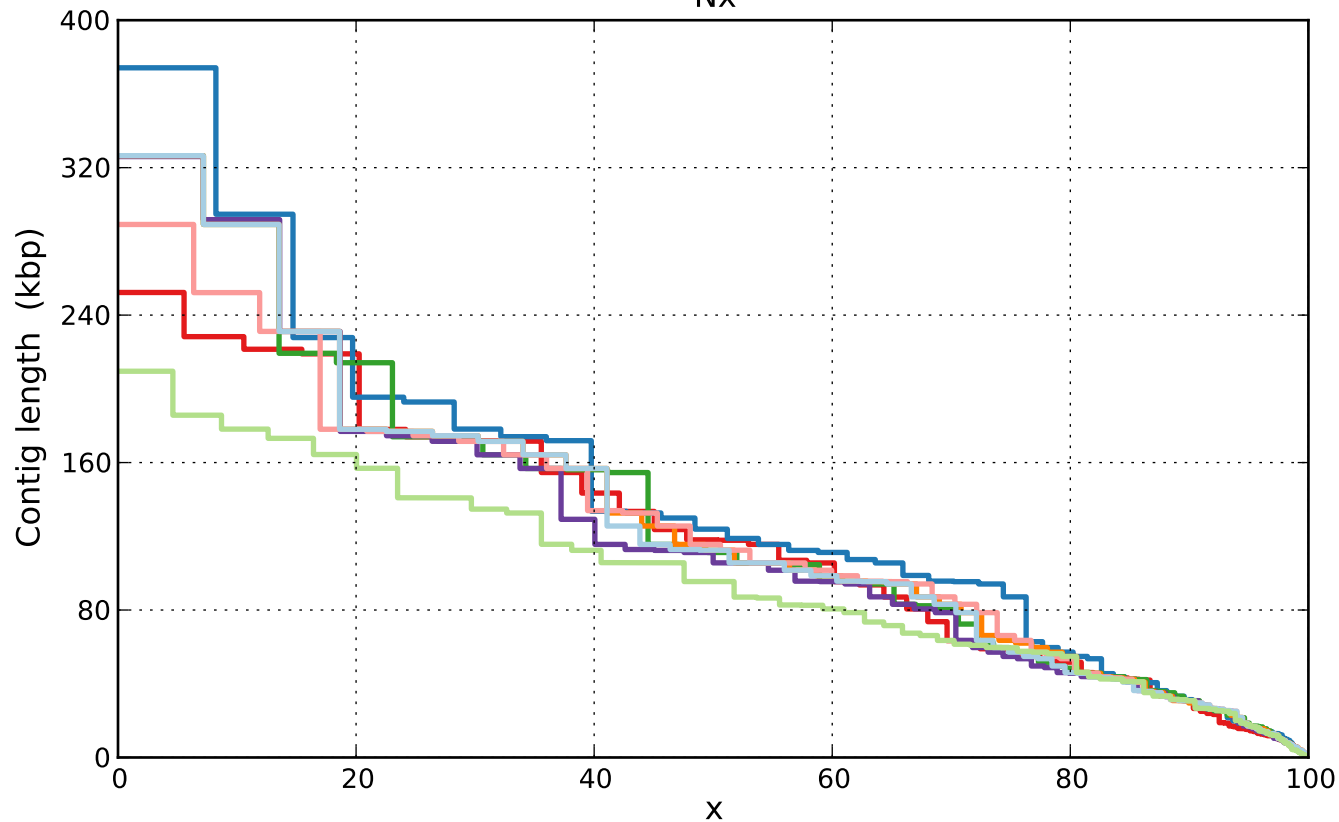
velvet.240M_contigs

velvet.2400M_contigs

velvet.a

Referen

Nx



velvet.10M_contigs

velvet.40M_contigs

velvet.120M_contigs

velvet.240M_contigs

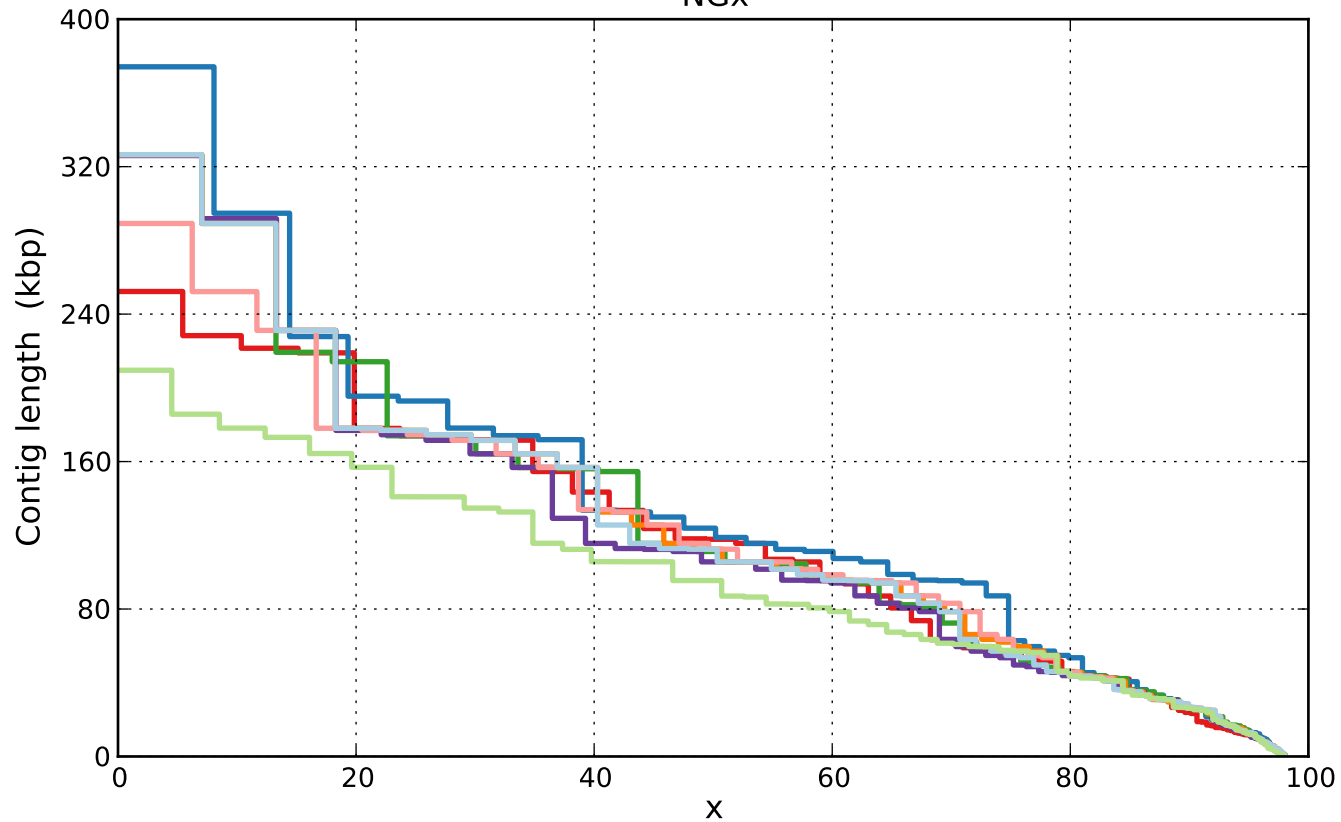
velvet.20M_contigs

velvet.60M_contigs

velvet.240M_contigs

velvet.all_c

NGx



velvet.10M_contigs

velvet.40M_contigs

velvet.120M_contigs

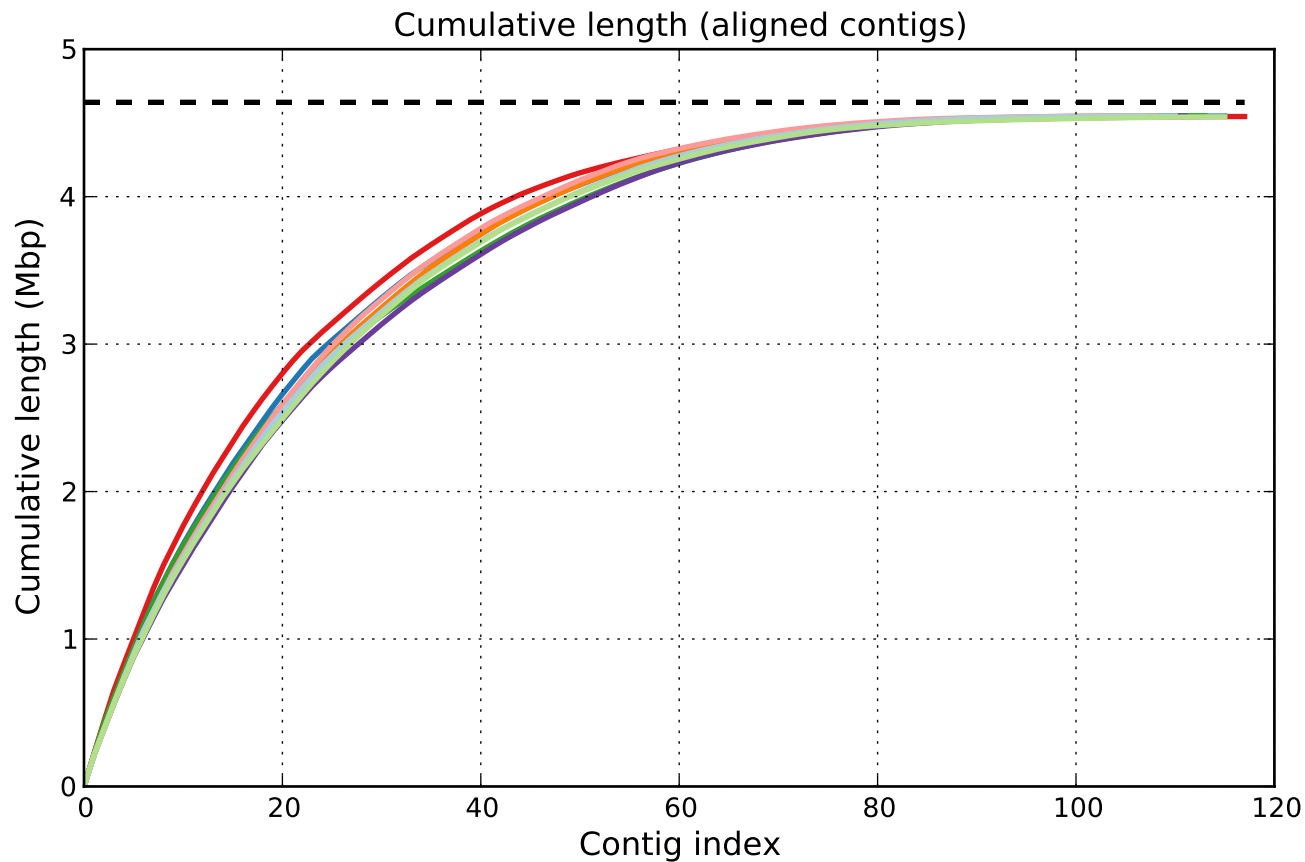
velvet.240M_contigs

velvet.20M_contigs

velvet.60M_contigs

velvet.240M_contigs

velvet.all_c



velvet.10M_contigs
velvet.20M_contigs
velvet.40M_contigs



velvet.60M_contigs



velvet.120M_contigs



velvet.240M_contigs



velvet.2400M_contigs

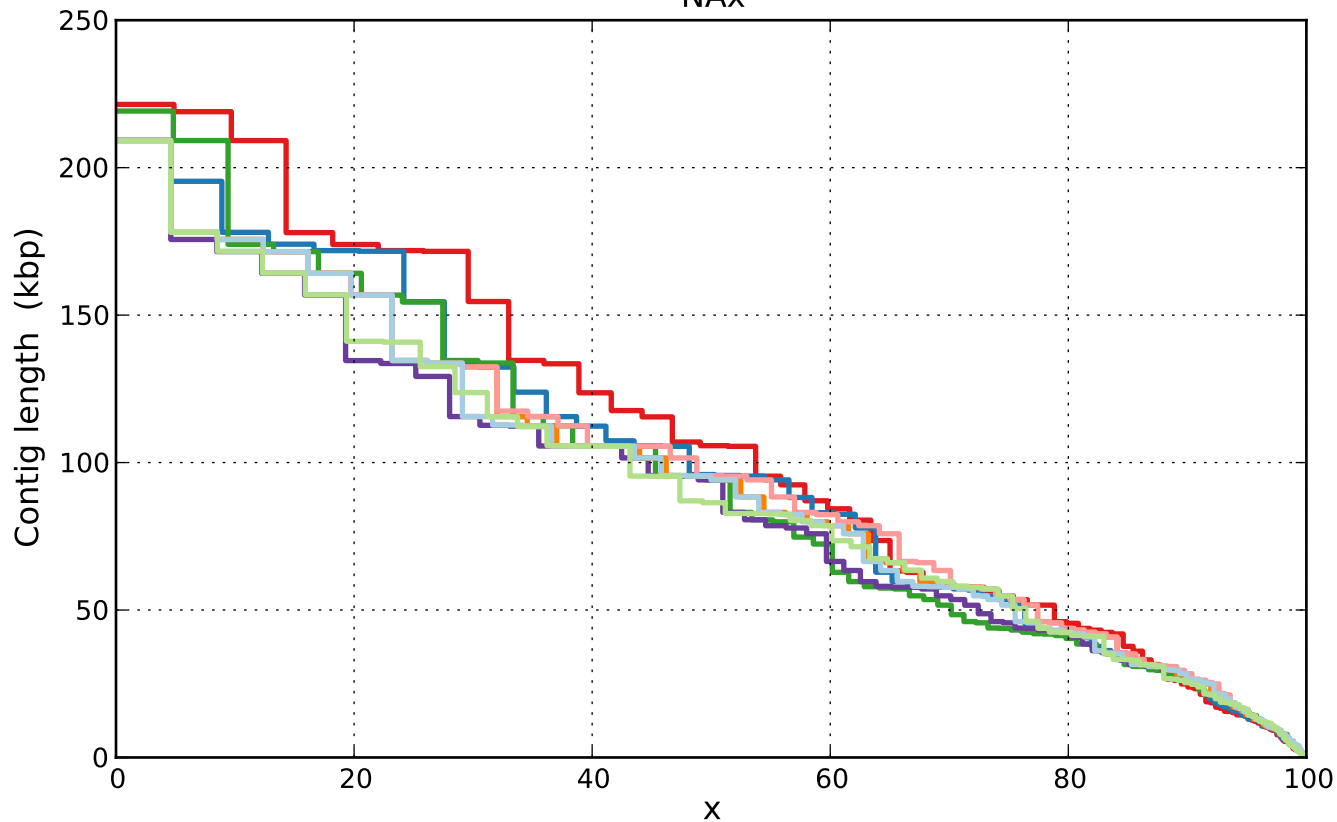


velvet.a



Referen

NAx



velvet.10M_contigs

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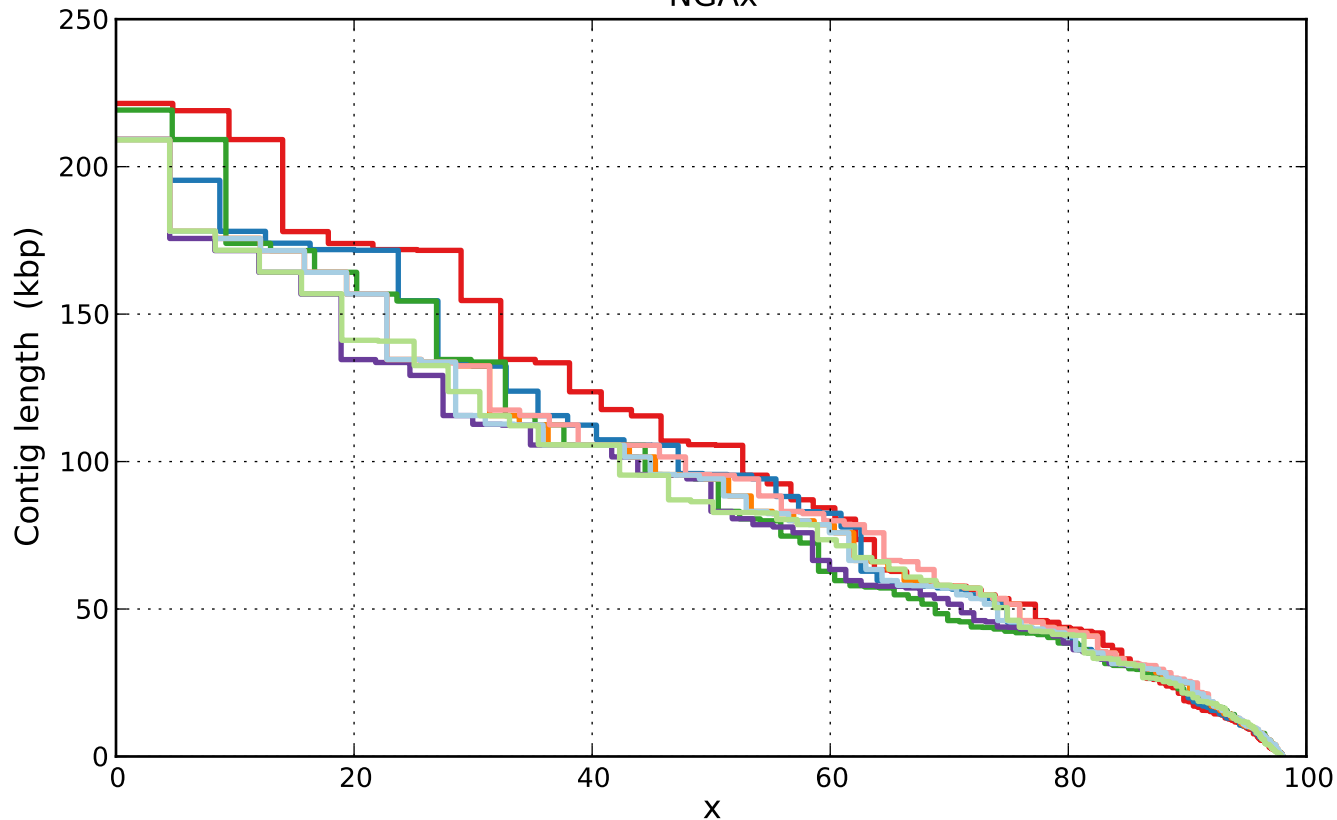
velvet.20M_contigs

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velvet.all_c

NGAx



velvet.10M_contigs

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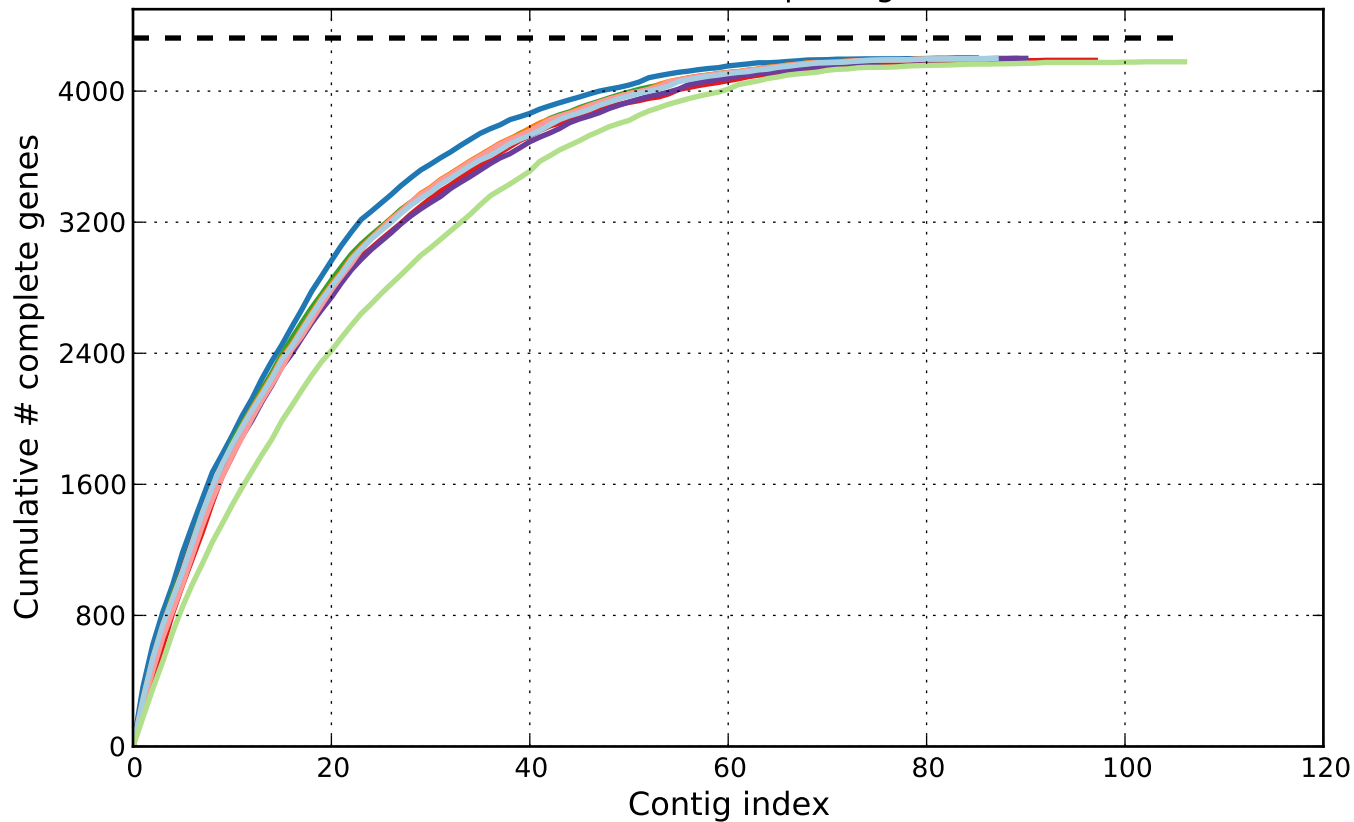
velvet.20M_contigs

velvet.60M_contigs

velvet.240M_contigs

velvet.all_c

Cumulative # complete genes



velvet.10M_contigs

velvet.60M_contigs

velvet.240M_contigs

velvet.a

velvet.20M_contigs

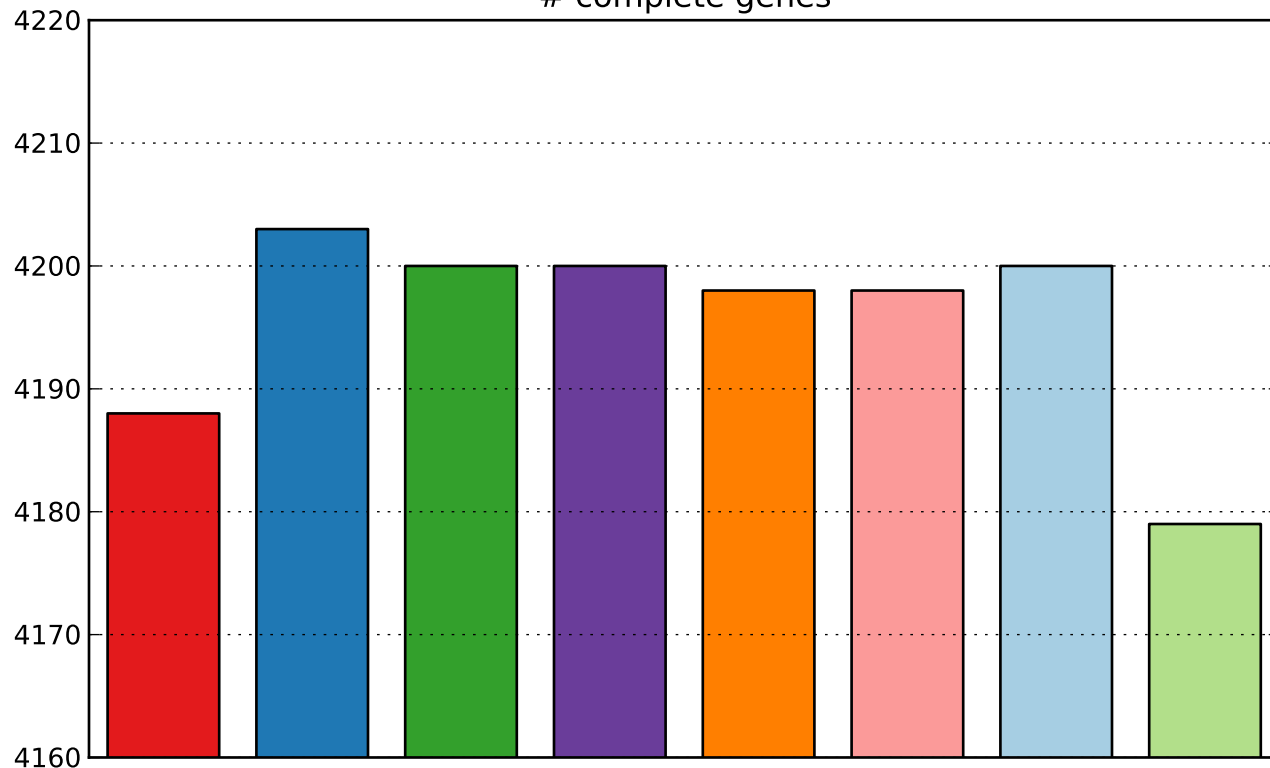
velvet.120M_contigs

velvet.2400M_contigs

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velvet.40M_contigs

complete genes



velvet.10M_contigs



velvet.40M_contigs



velvet.120M_contigs



velvet.240M_contigs

velvet.20M_contigs



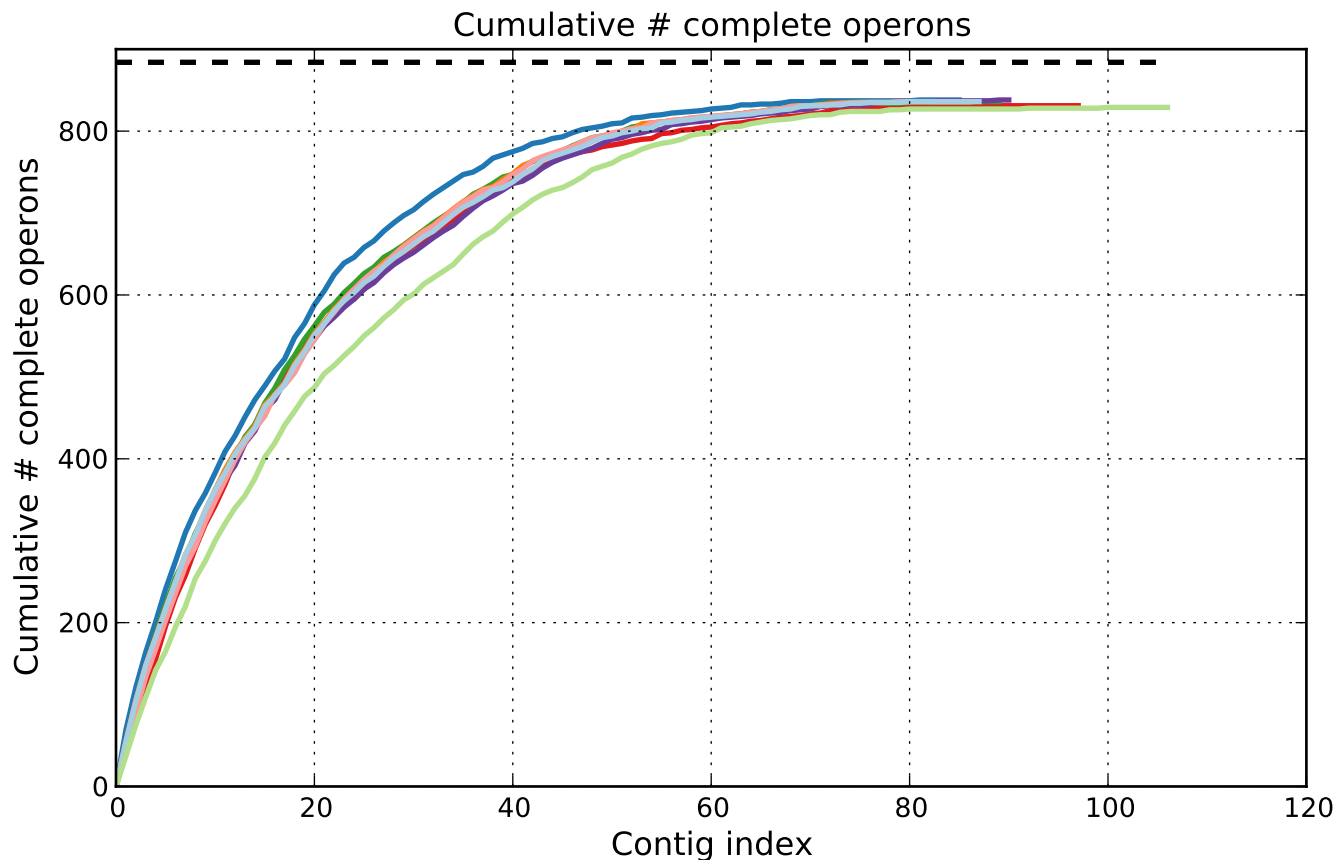
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velvet.240M_contigs



velvet.all_c



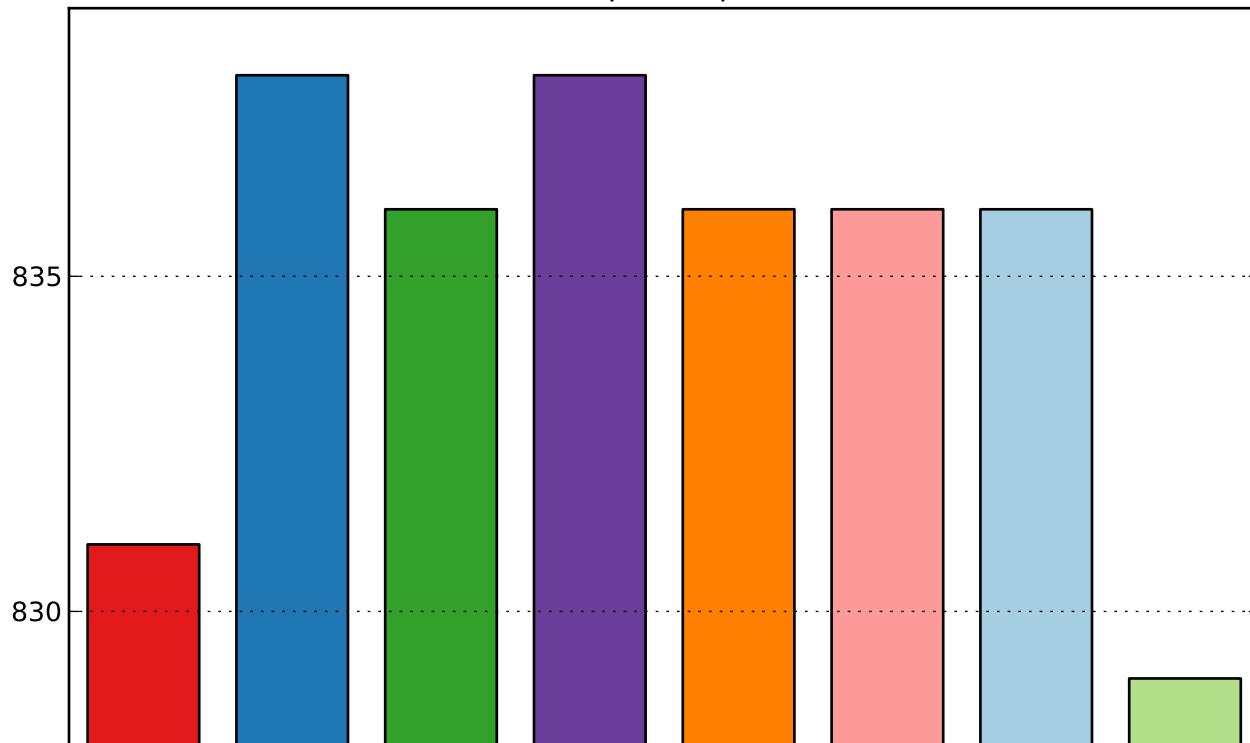
velvet.10M_contigs
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velvet.40M_contigs

velvet.60M_contigs
velvet.120M_contigs

velvet.240M_contigs
velvet.2400M_contigs

velvet.a
- - Referen

complete operons



velvet.10M_contigs



velvet.40M_contigs



velvet.120M_contigs



velvet.240M_contigs

velvet.20M_contigs



velvet.60M_contigs



velvet.240M_contigs



velvet.all_c

