

# Report

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

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

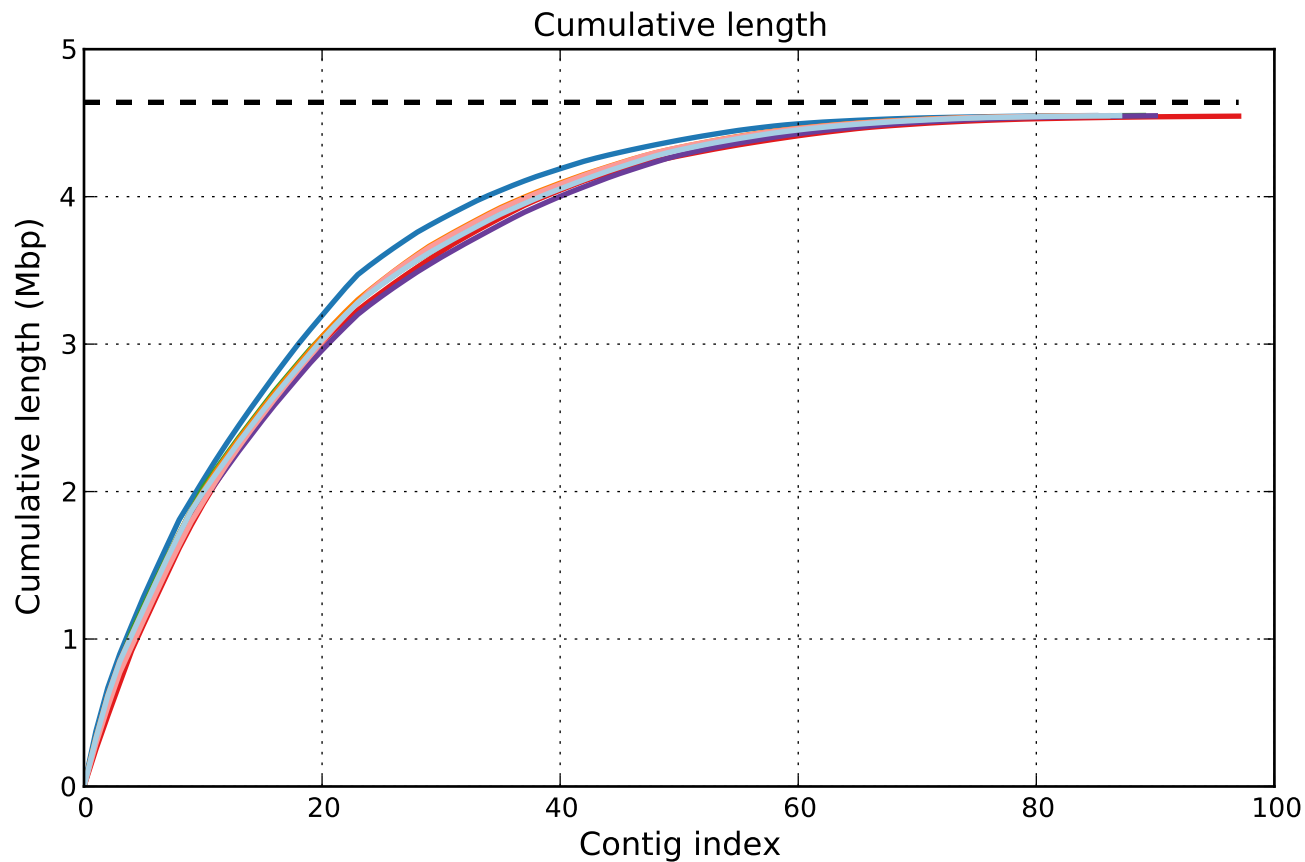
	velvet.10M_contigs	velvet.20M_contigs	velvet.40M_contigs	velvet.60M_contigs	velvet.120M_contigs	velvet.240M_contigs	velvet.2400M_contigs
misassemblies	20	29	24	21	22	21	23
# relocations	20	29	24	21	22	21	23
# translocations	0	0	0	0	0	0	0
# inversions	0	0	0	0	0	0	0
misassembled contigs	11	15	13	12	13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

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

Unaligned report

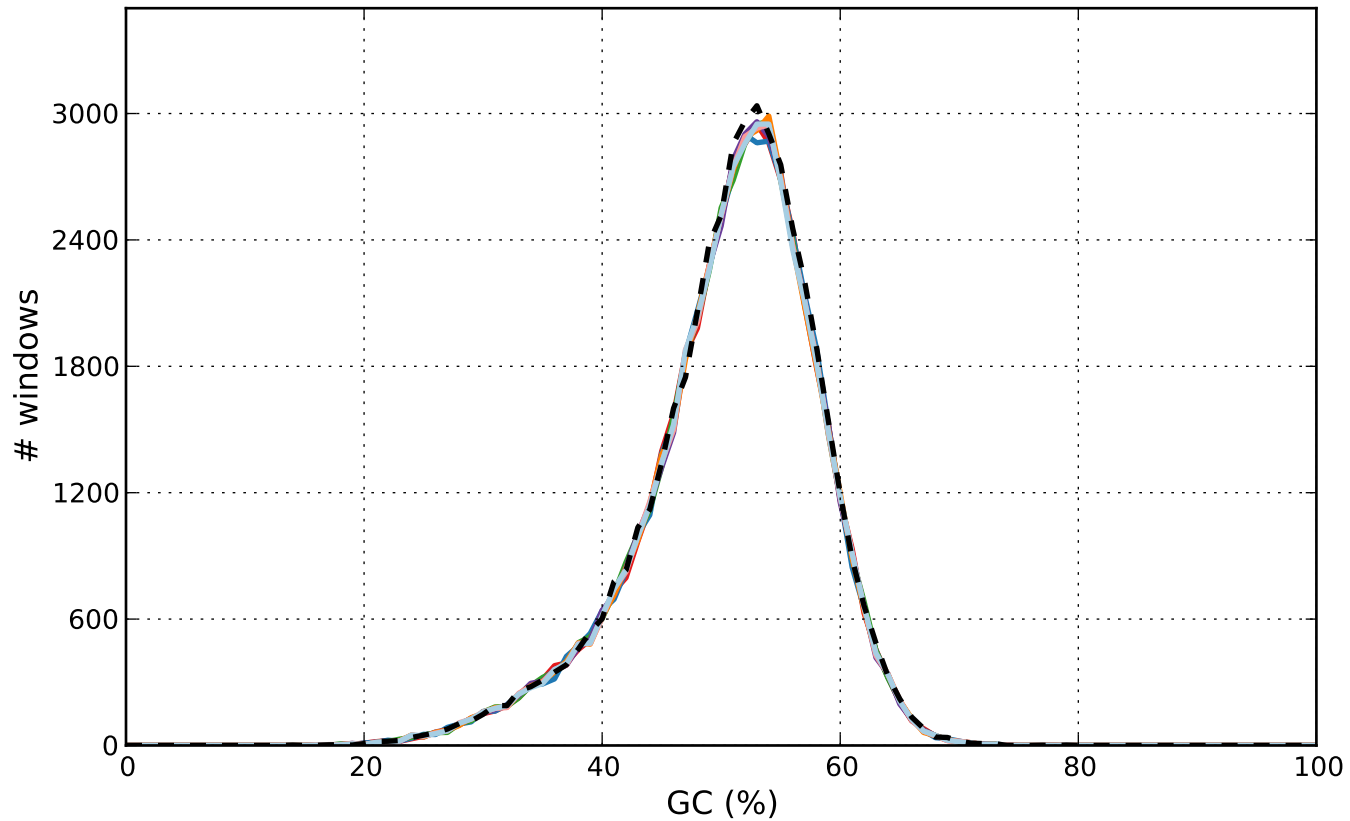
	velvet.10M_contigs	velvet.20M_contigs	velvet.40M_contigs	velvet.60M_contigs	velvet.120M_contigs	velvet.240M_contigs	velvet.2400M_contigs
# fully unaligned contigs	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0
# partially unaligned contigs	1	1	0	0	0	0	0
# with misassembly	0	1	0	0	0	0	0
# both parts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

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contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



velvet.10M_contigs	velvet.40M_contigs	velvet.120M_contigs	velvet.240M_contigs
velvet.20M_contigs	velvet.60M_contigs	velvet.240M_contigs	Reference

GC content



velvet.10M\_contigs

velvet.40M\_contigs

velvet.120M\_contigs

velvet.240M\_contigs

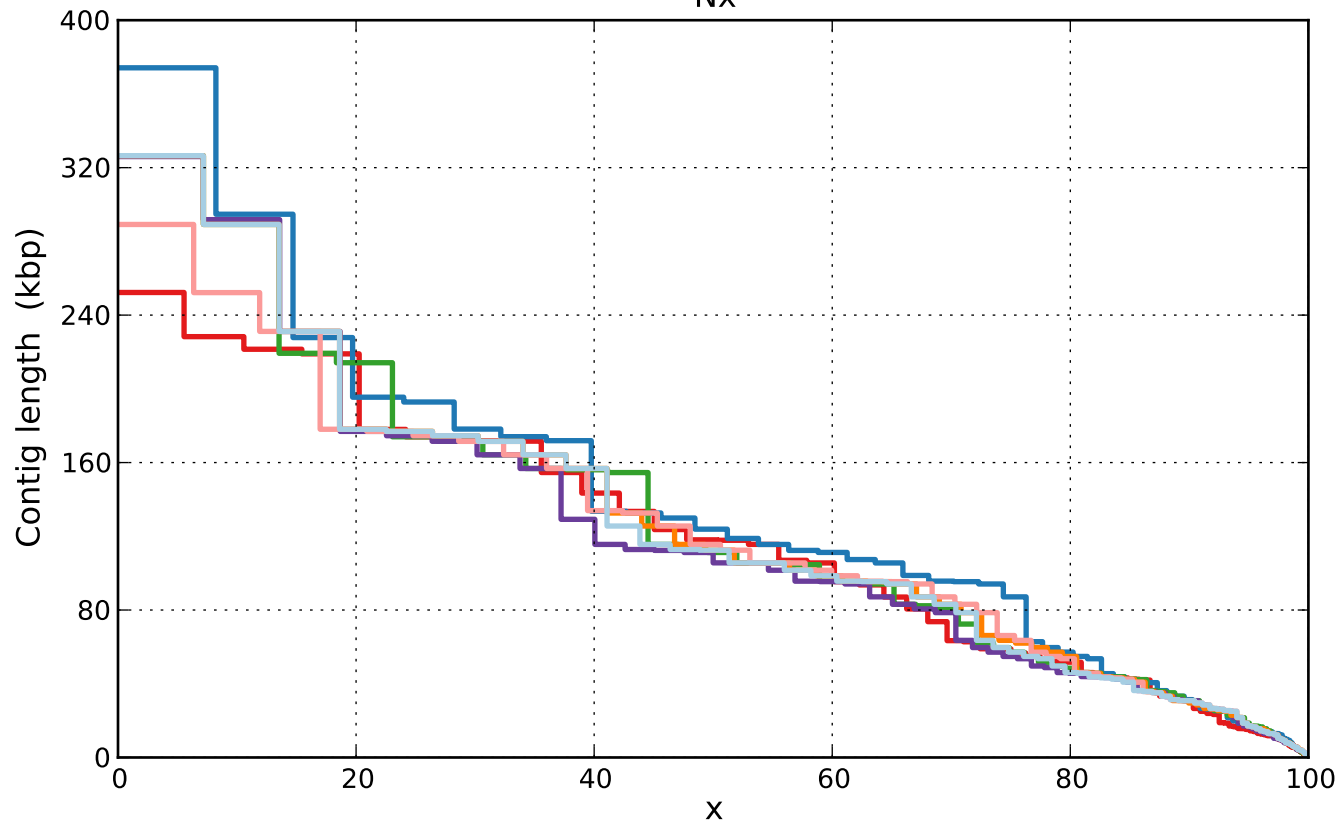
velvet.20M\_contigs

velvet.60M\_contigs

velvet.240M\_contigs

Reference

Nx



velvet.10M\_contigs

velvet.40M\_contigs

velvet.120M\_contigs

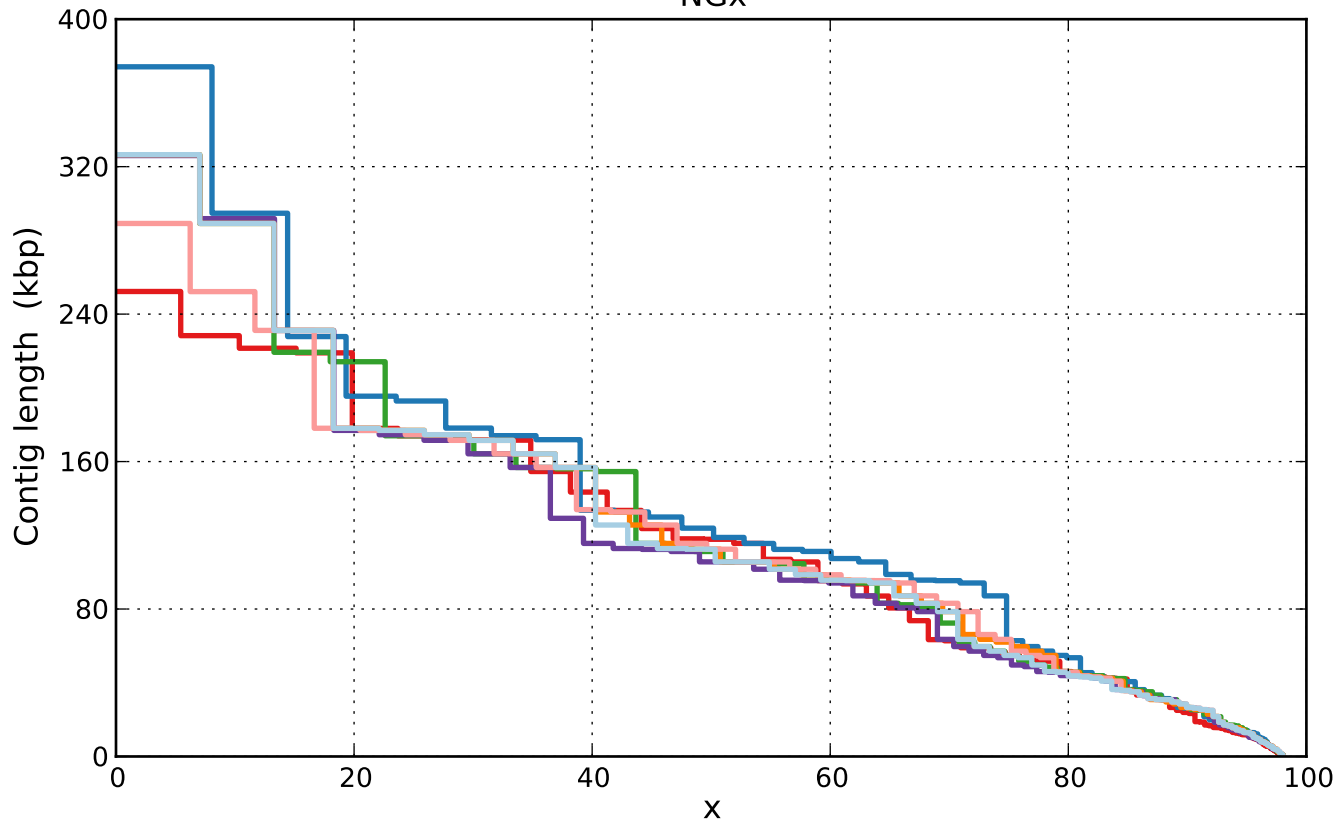
velvet.240M\_contigs

velvet.20M\_contigs

velvet.60M\_contigs

velvet.240M\_contigs

NGx



velvet.10M\_contigs

velvet.40M\_contigs

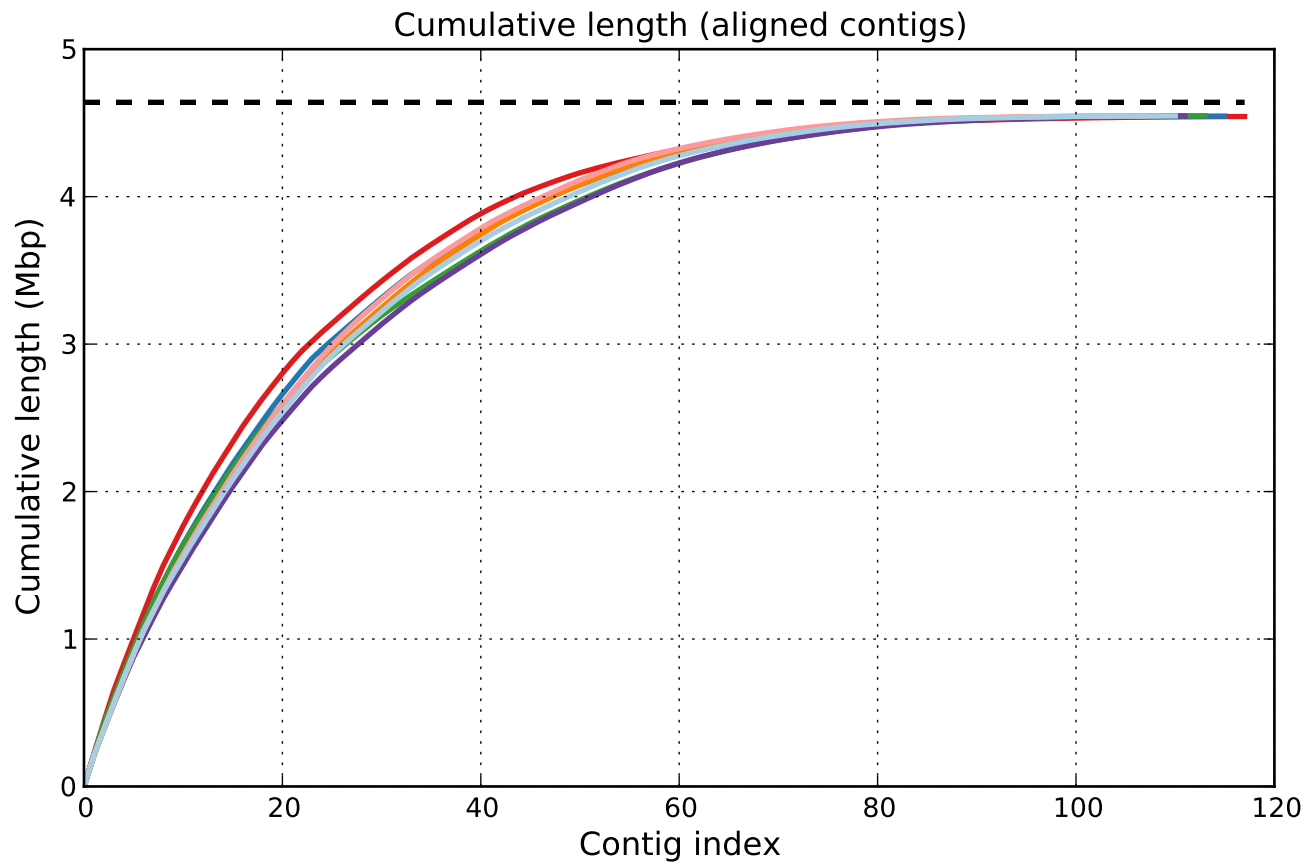
velvet.120M\_contigs

velvet.2400M\_contigs

velvet.20M\_contigs

velvet.60M\_contigs

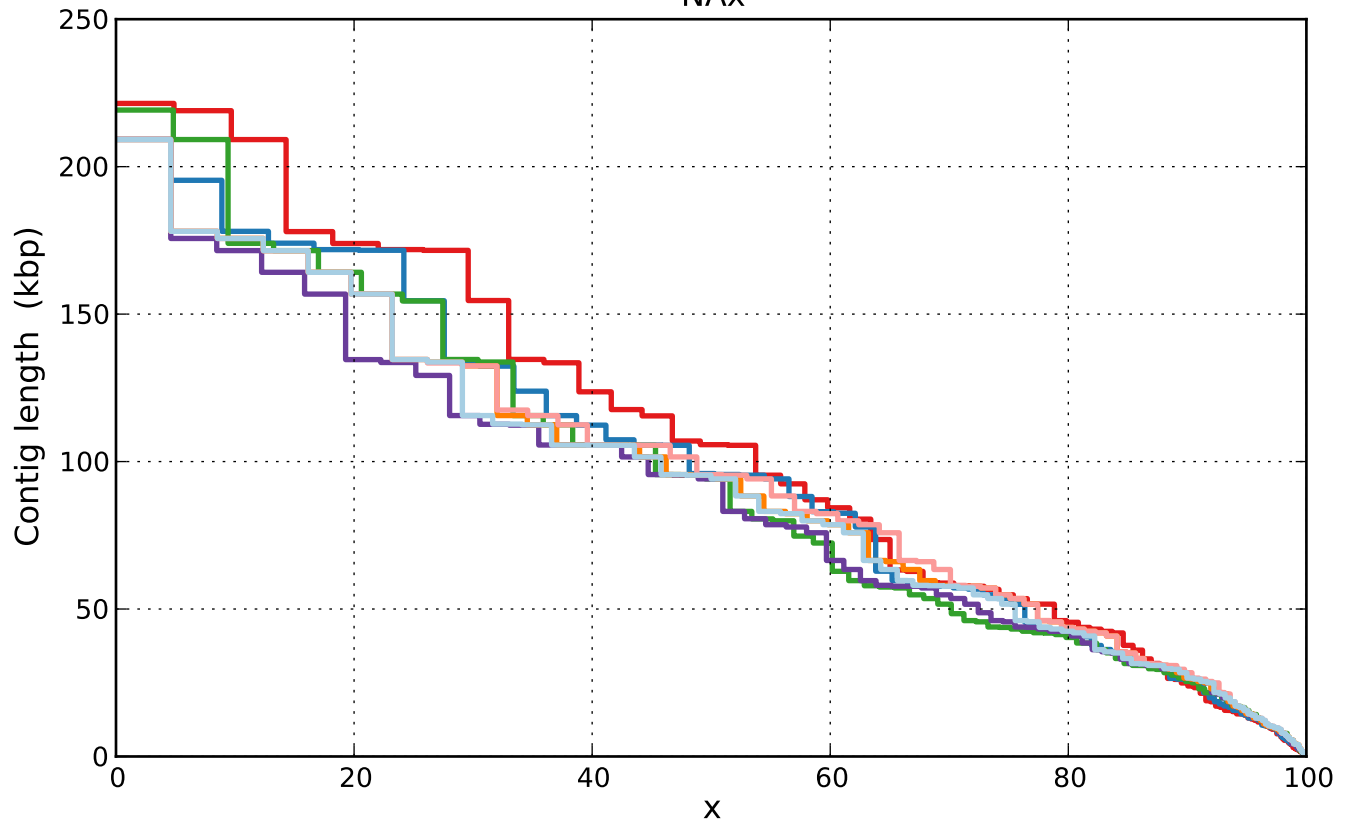
velvet.240M\_contigs



velvet.10M_contigs	velvet.40M_contigs	velvet.120M_contigs	velvet.240M_contigs
velvet.20M_contigs	velvet.60M_contigs	velvet.240M_contigs	Reference



NAx



velvet.10M\_contigs

velvet.40M\_contigs

velvet.120M\_contigs

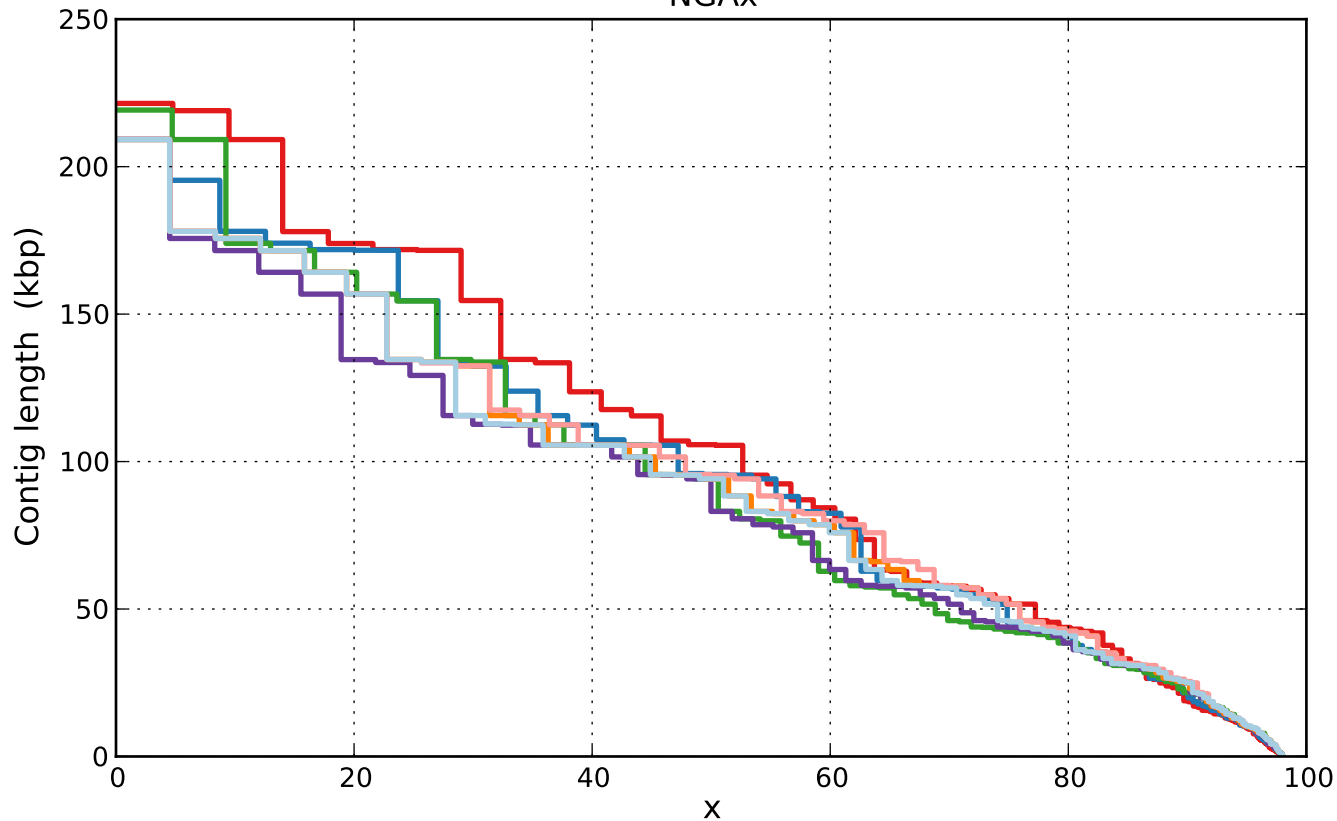
velvet.240M

velvet.20M\_contigs

velvet.60M\_contigs

velvet.240M\_contigs

# NGAx



velvet.10M\_contigs

velvet.40M\_contigs

velvet.120M\_contigs

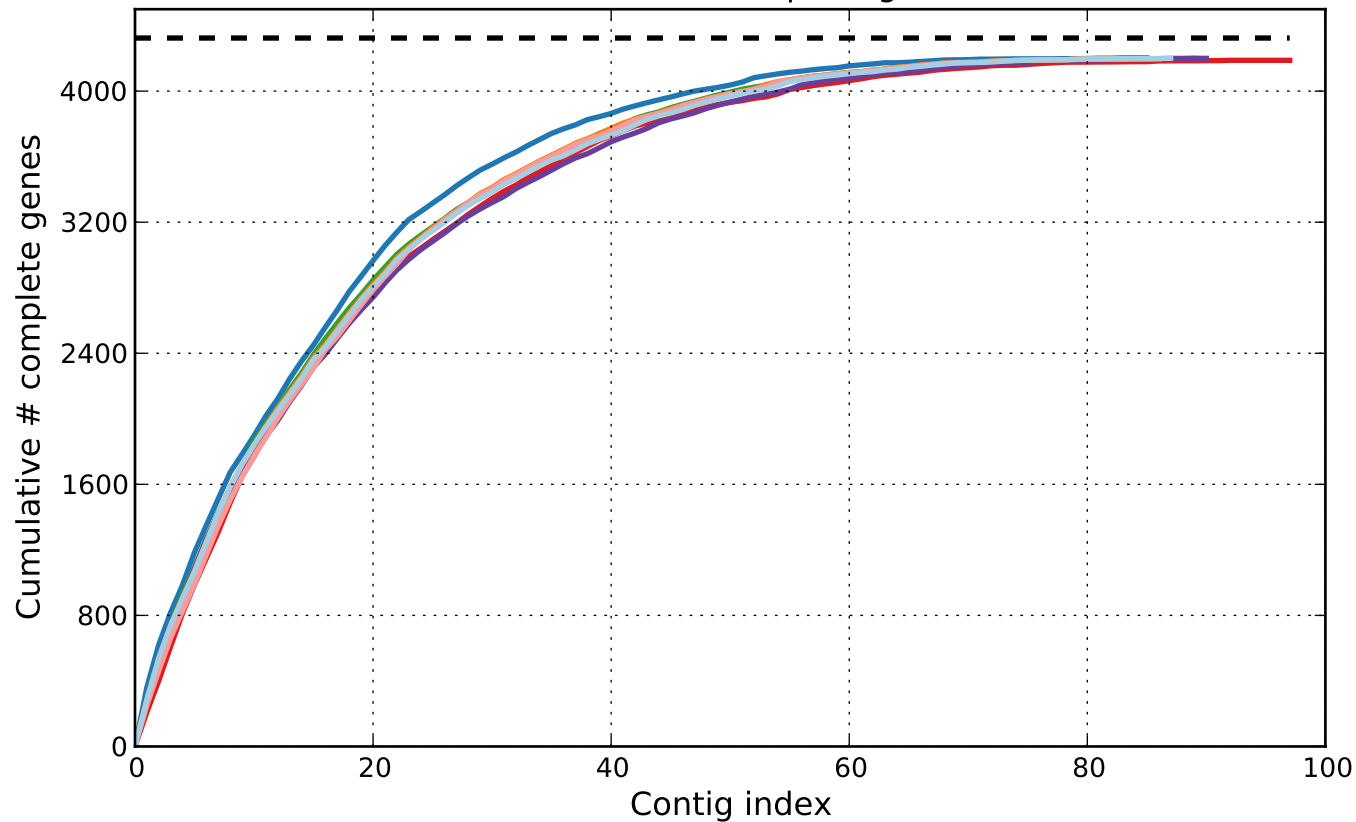
velvet.240M\_contigs

velvet.20M\_contigs

velvet.60M\_contigs

velvet.240M\_contigs

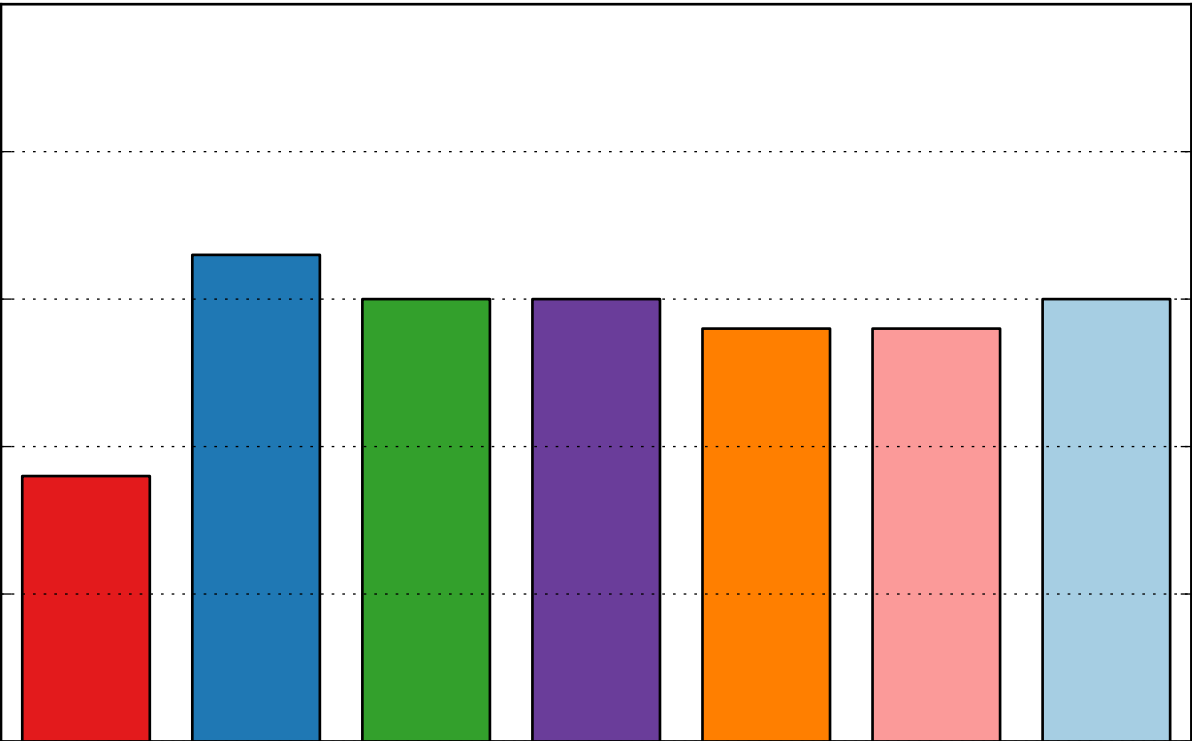
Cumulative # complete genes



velvet.10M_contigs	velvet.40M_contigs	velvet.120M_contigs	velvet.240M_contigs
velvet.20M_contigs	velvet.60M_contigs	velvet.240M_contigs	Reference

# complete genes

4220  
4210  
4200  
4190  
4180  
4170



velvet.10M\_contigs



velvet.40M\_contigs



velvet.120M\_contigs



velvet.240M\_contigs

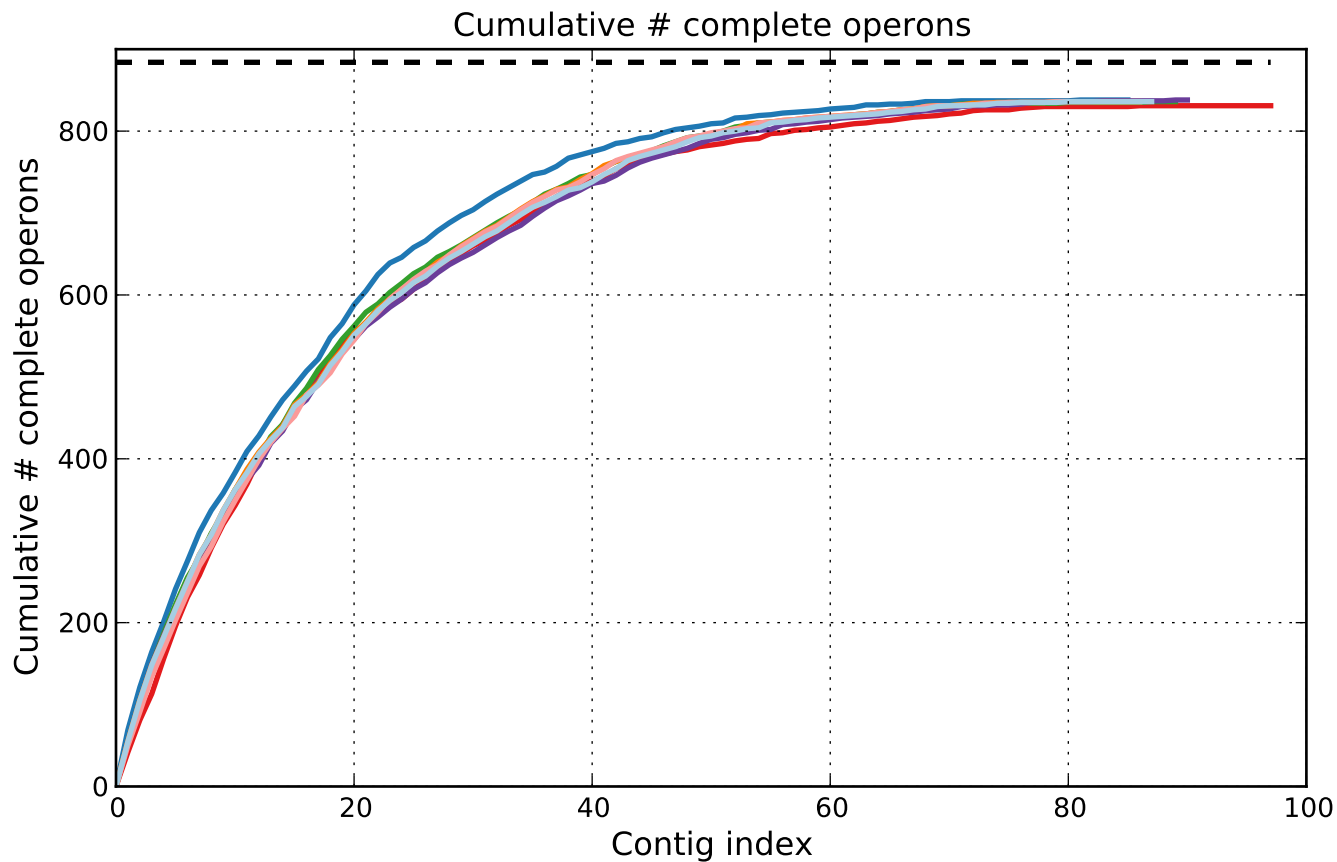
velvet.20M\_contigs



velvet.60M\_contigs

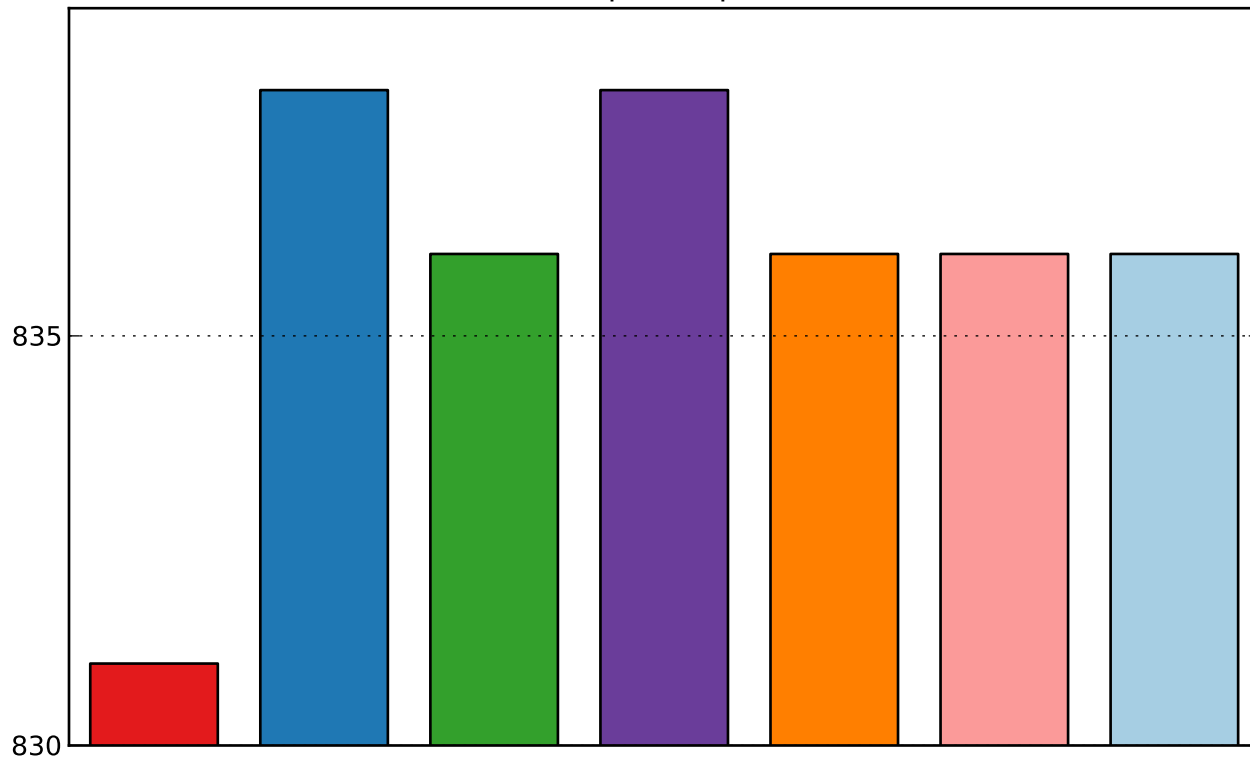


velvet.240M\_contigs



velvet.10M_contigs	velvet.40M_contigs	velvet.120M_contigs	velvet.240M_contigs
velvet.20M_contigs	velvet.60M_contigs	velvet.240M_contigs	Reference

# complete operons



velvet.10M\_contigs



velvet.40M\_contigs



velvet.120M\_contigs



velvet.240M\_contigs

velvet.20M\_contigs



velvet.60M\_contigs



velvet.240M\_contigs

