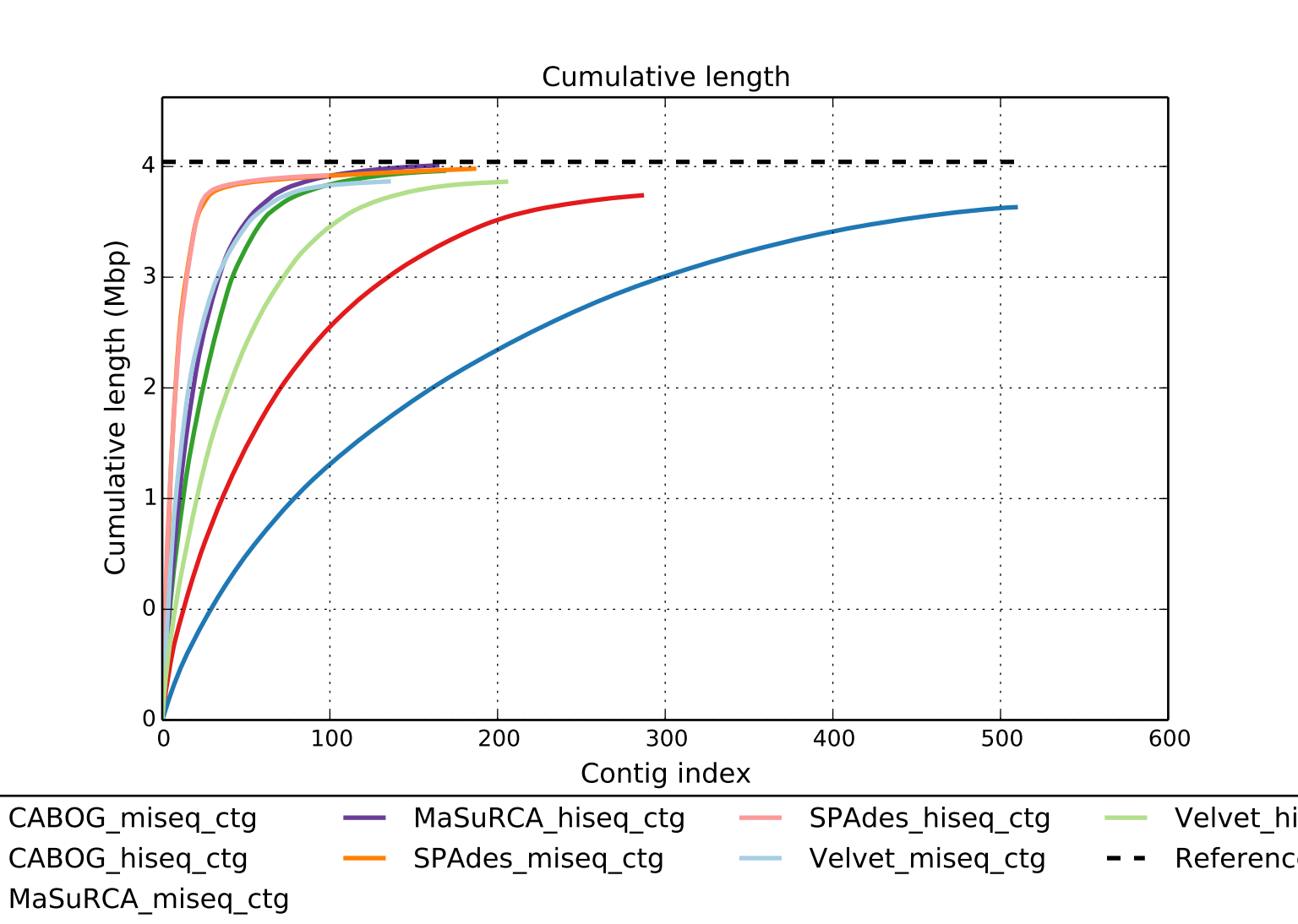
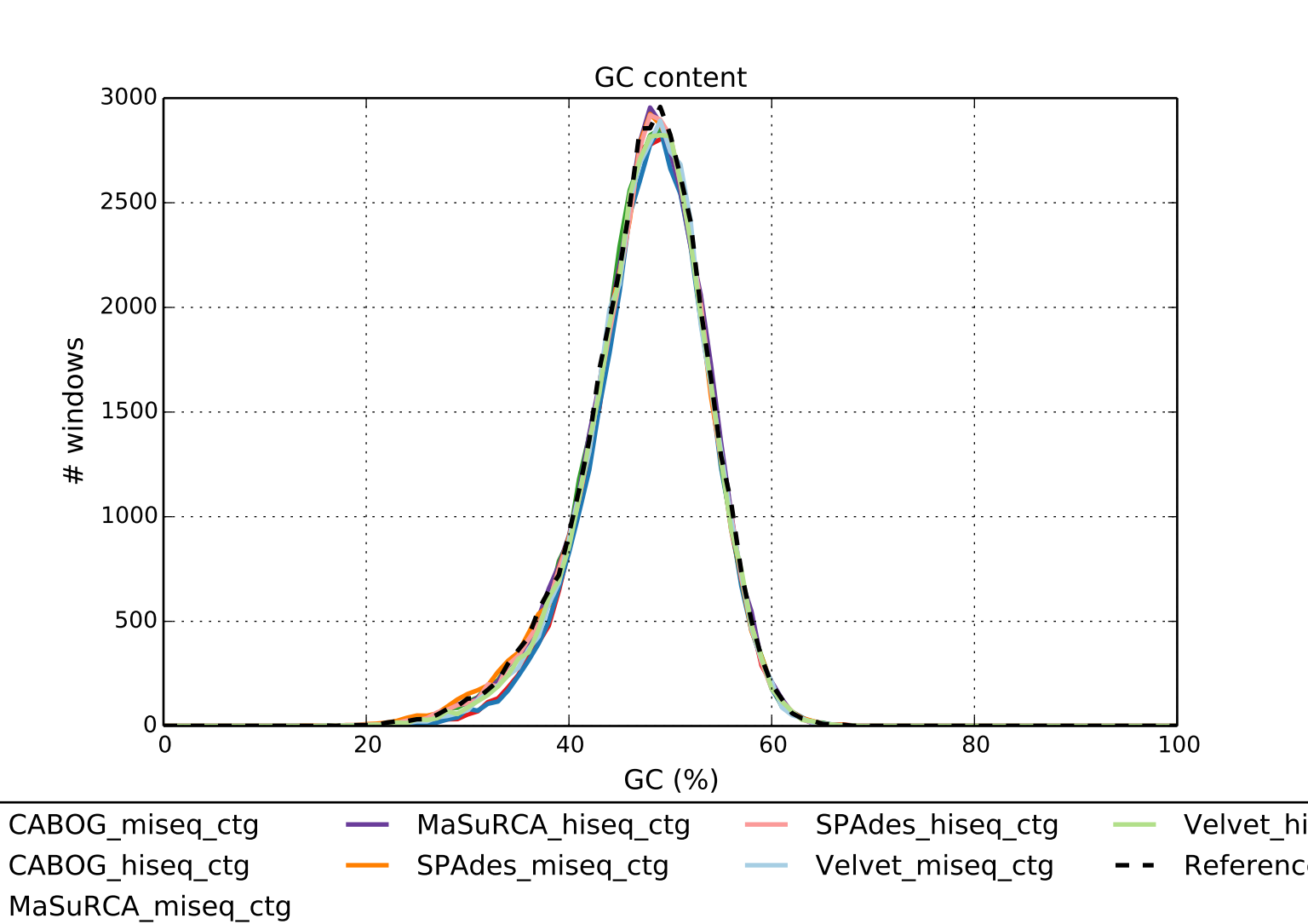
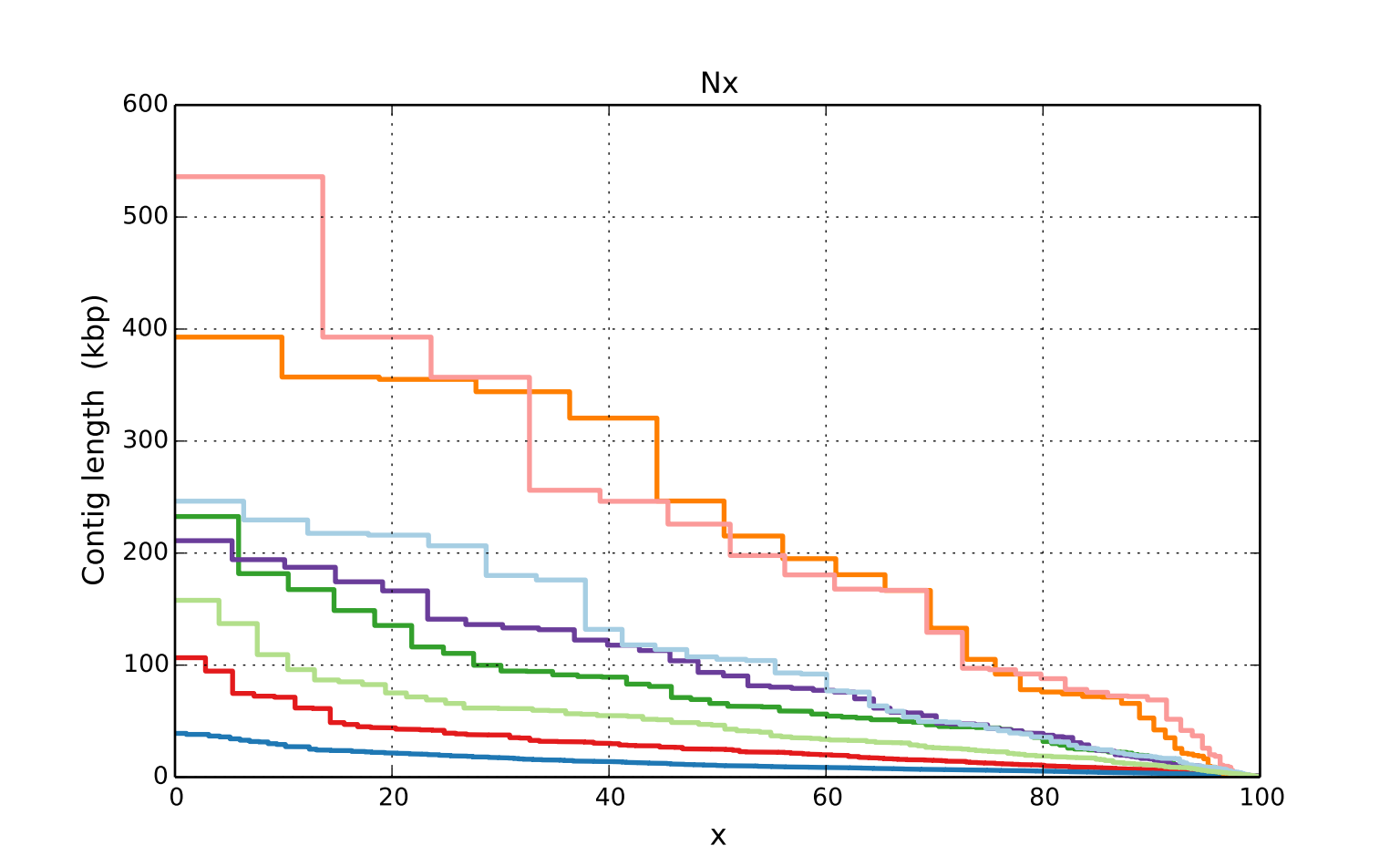
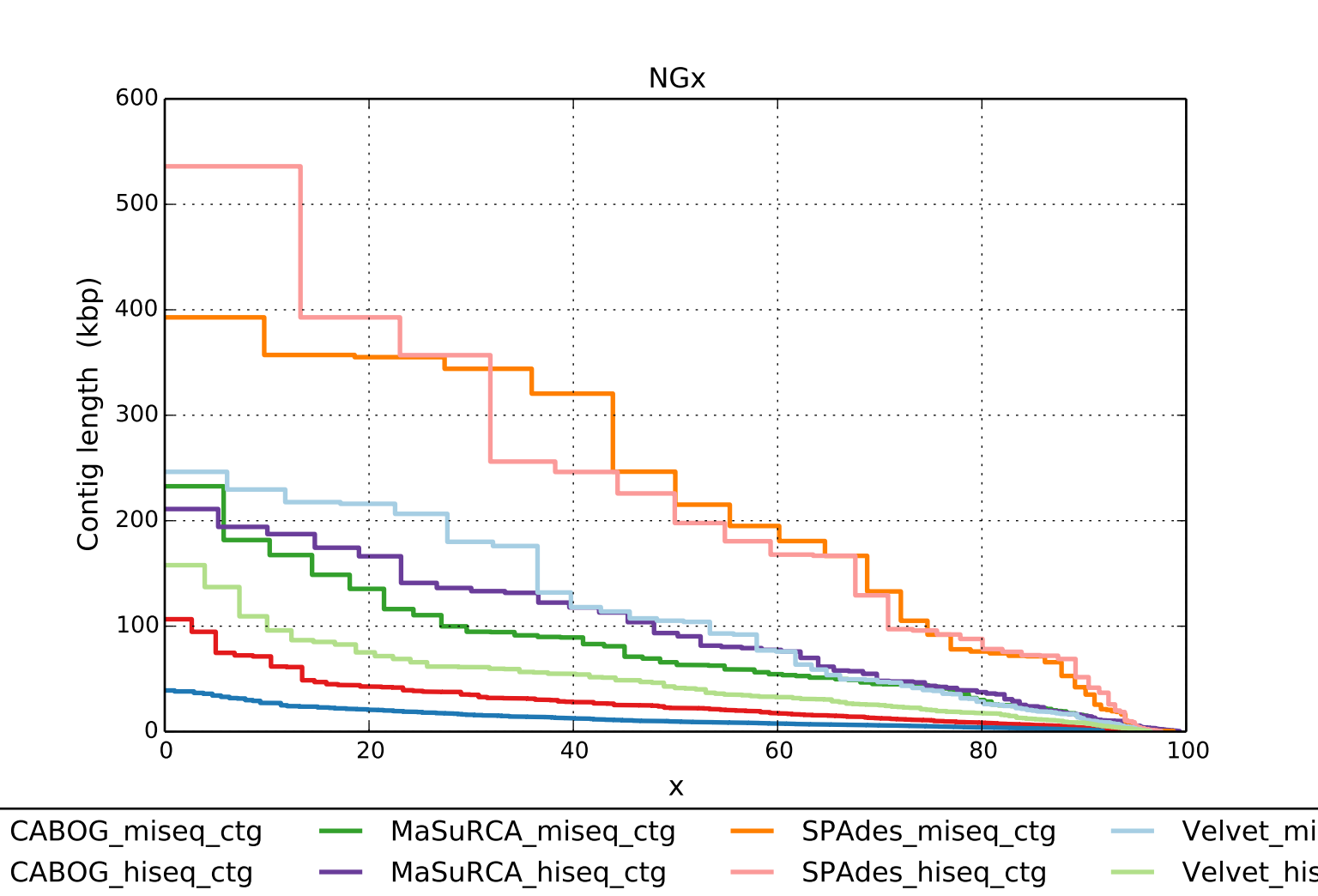
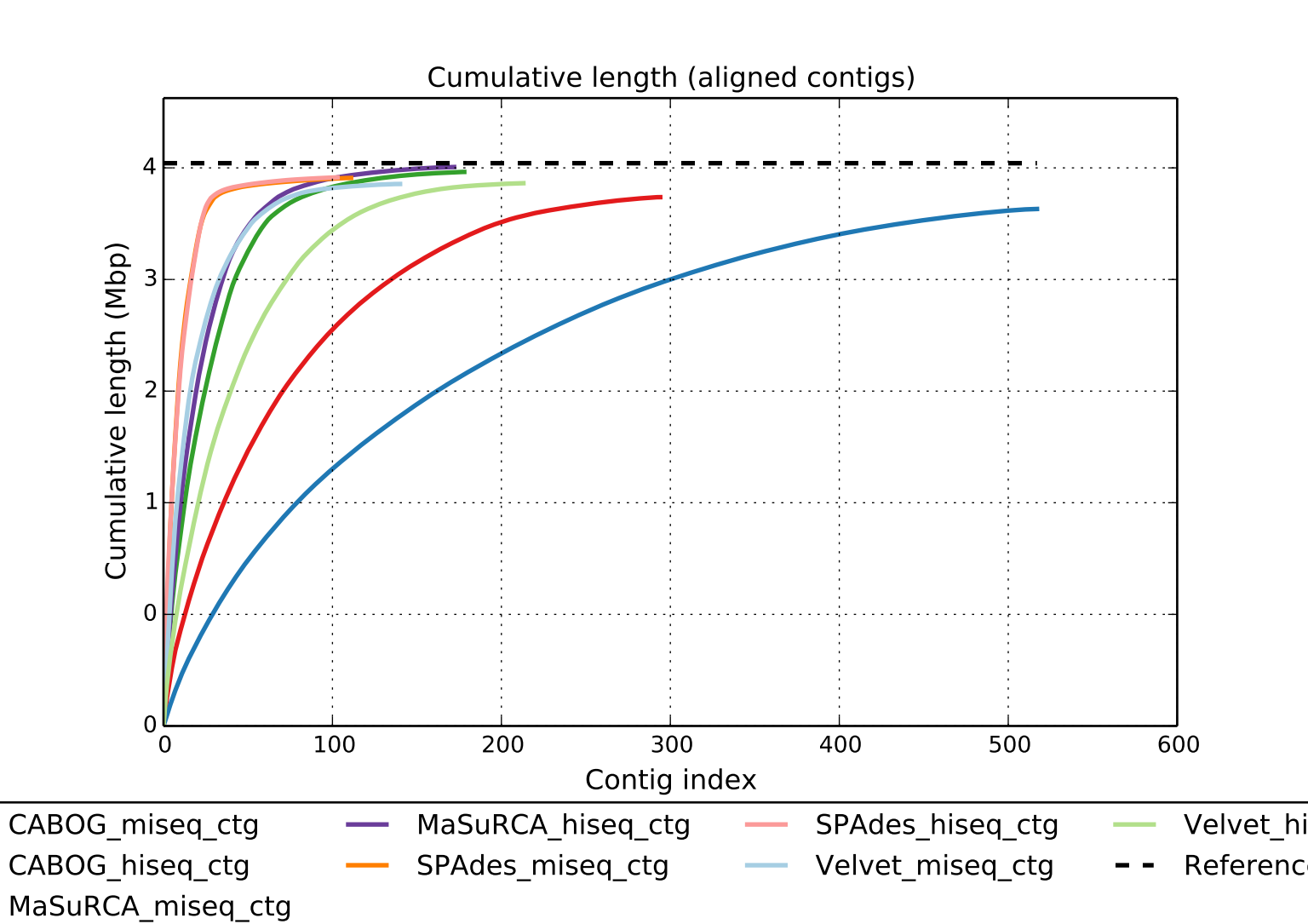
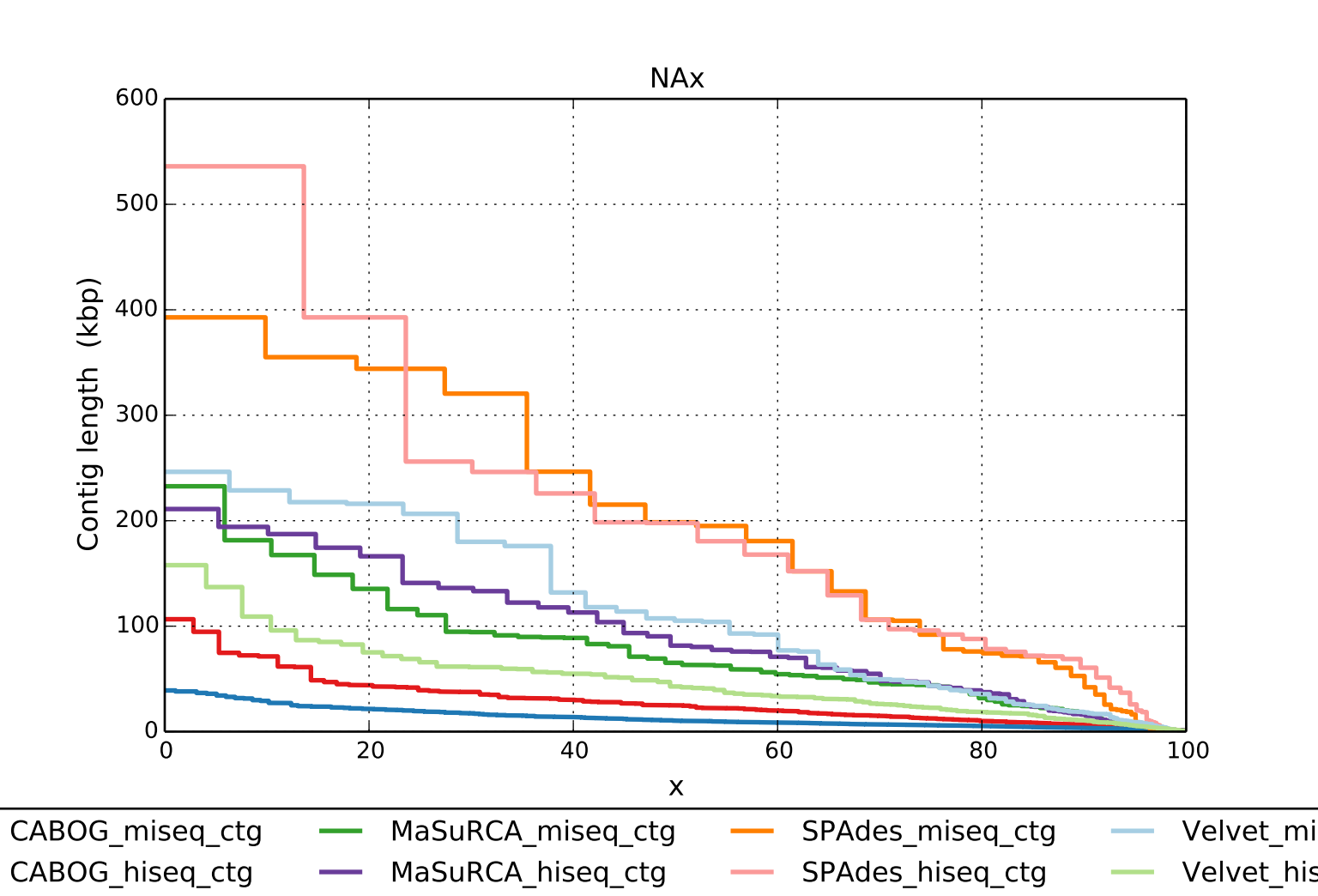

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
100
200
300
400
500
600
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_miseq_ctg
Velvet_hi
Referenc

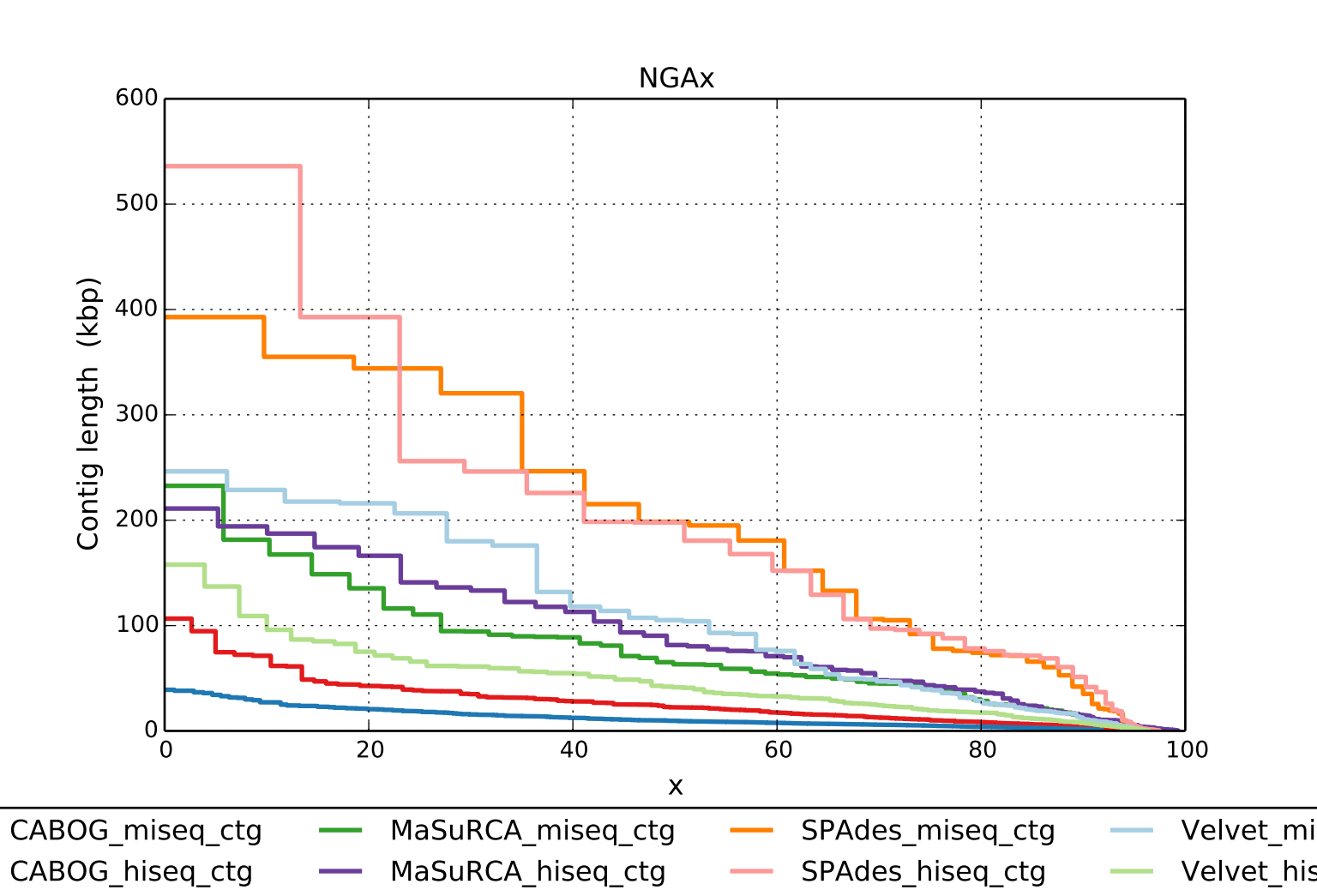

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_miseq_ctg
Velvet_hi
Referenc

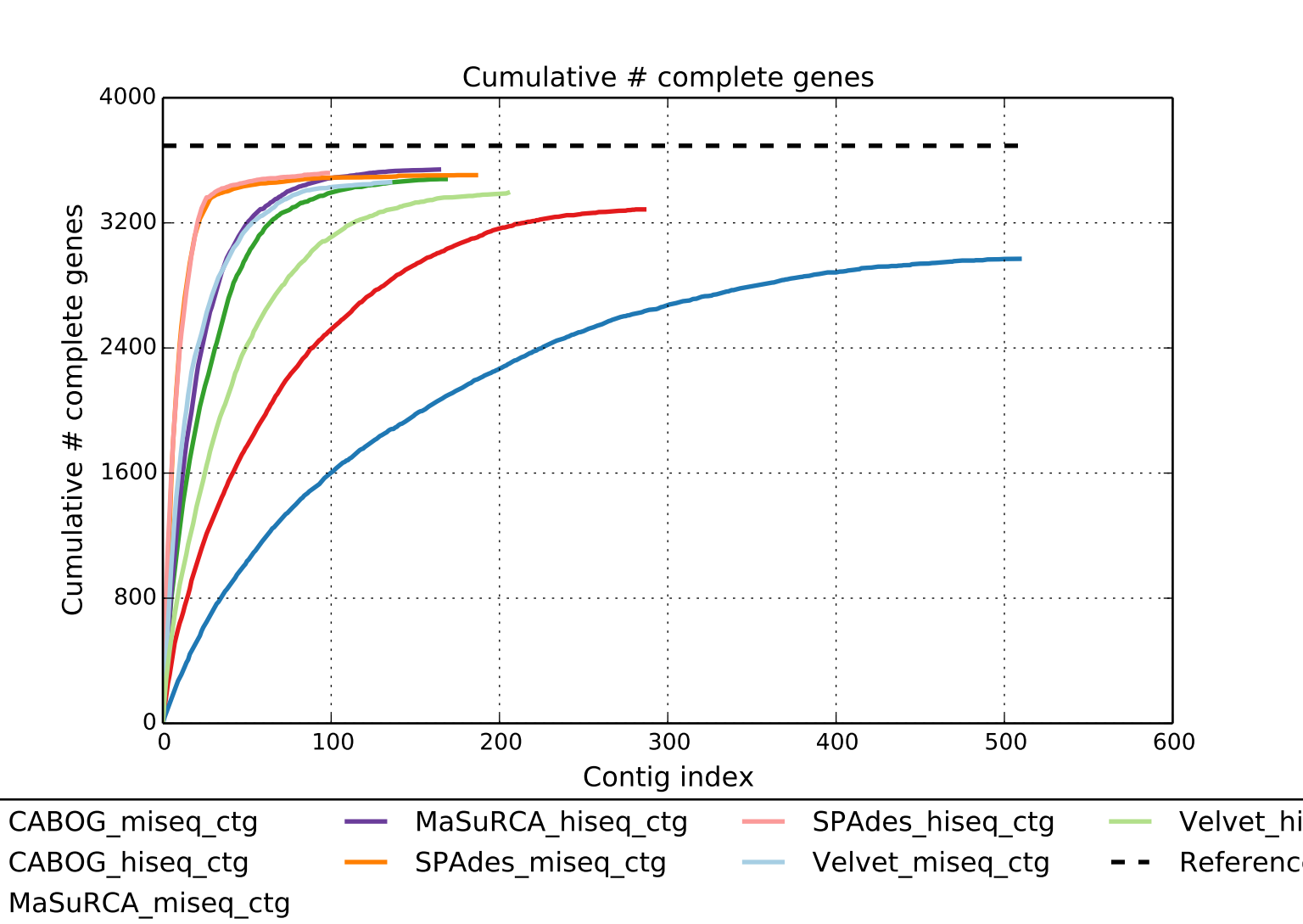

Nx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his

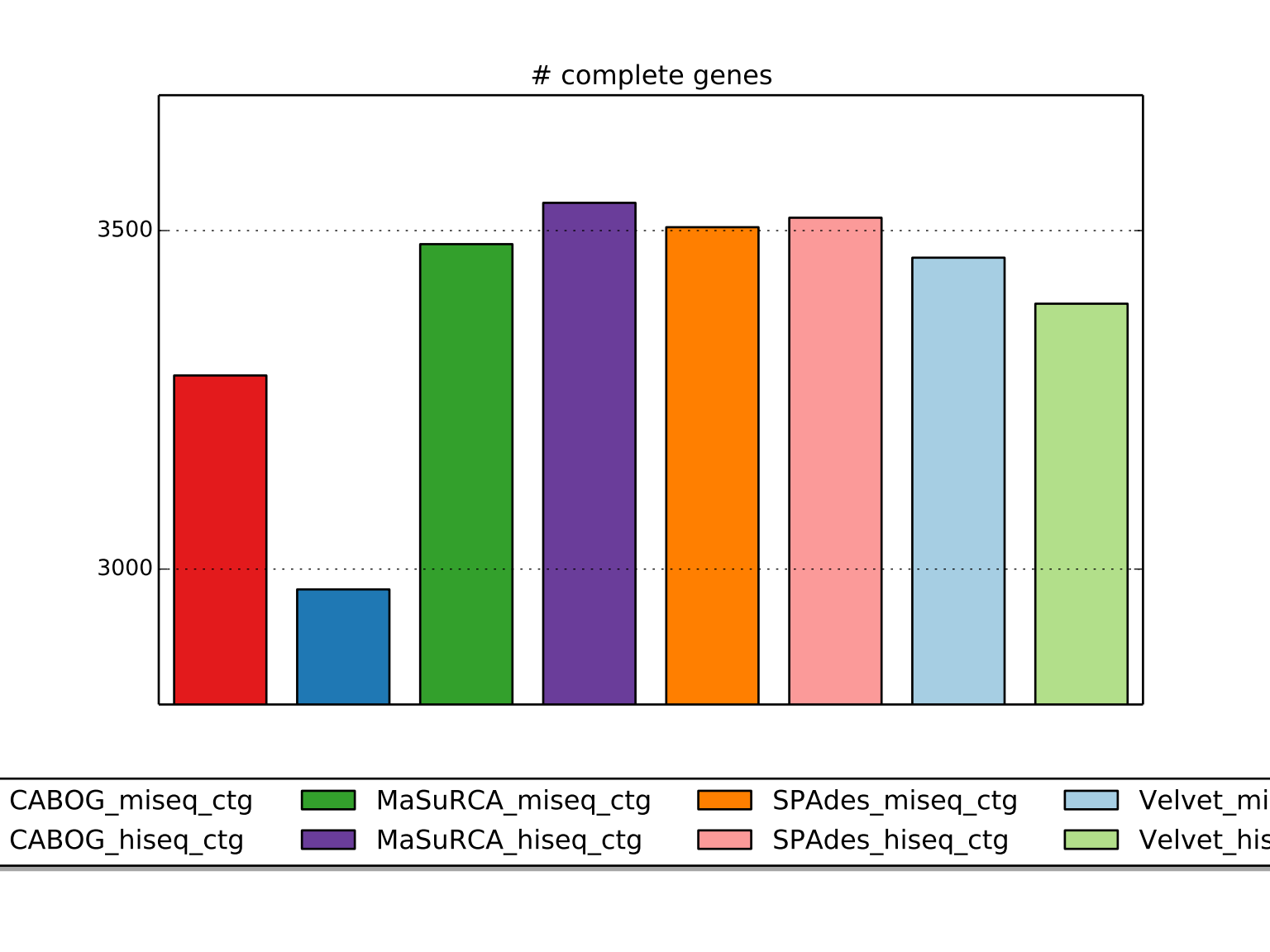

NGx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his

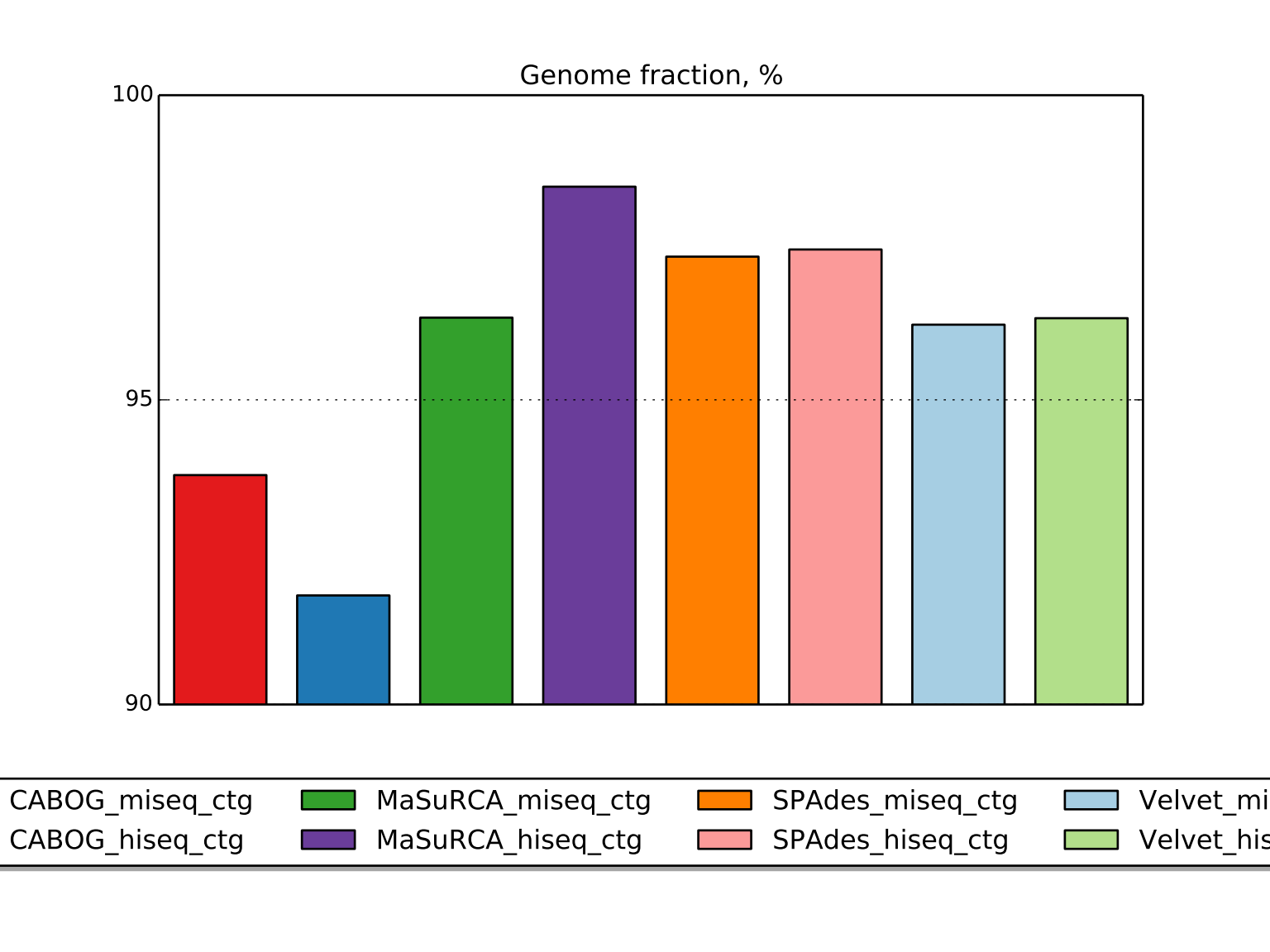

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
100
200
300
400
500
600
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_miseq_ctg
Velvet_hi
Referenc


NAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his


NGAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his


Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
100
200
300
400
500
600
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_miseq_ctg
Velvet_hi
Referenc


complete genes
3500
3000
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his


Genome fraction, %
100
95
90
CABOG_miseq_ctg
CABOG_hiseq_ctg
MaSuRCA_miseq_ctg
MaSuRCA_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_mi
Velvet_his