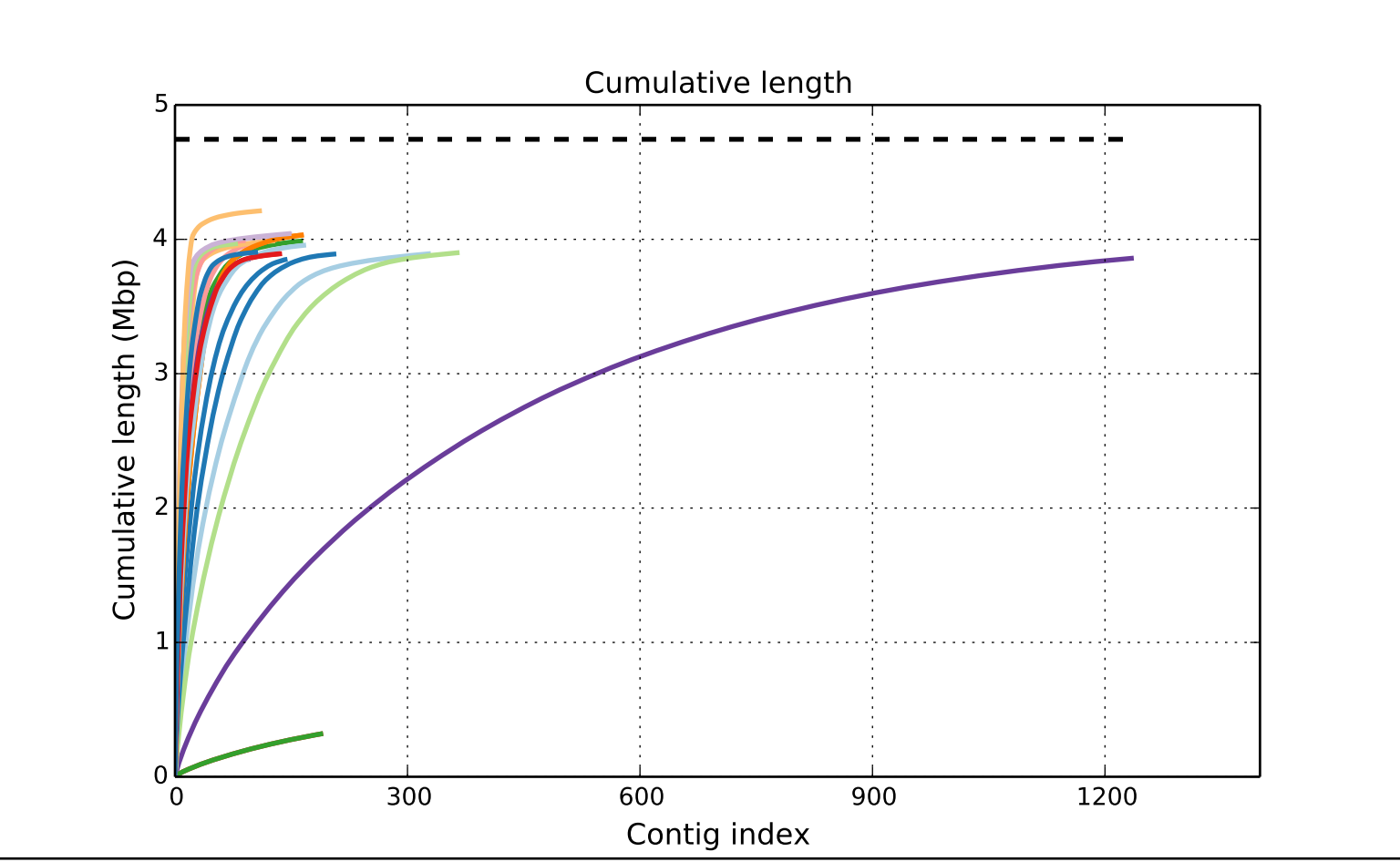
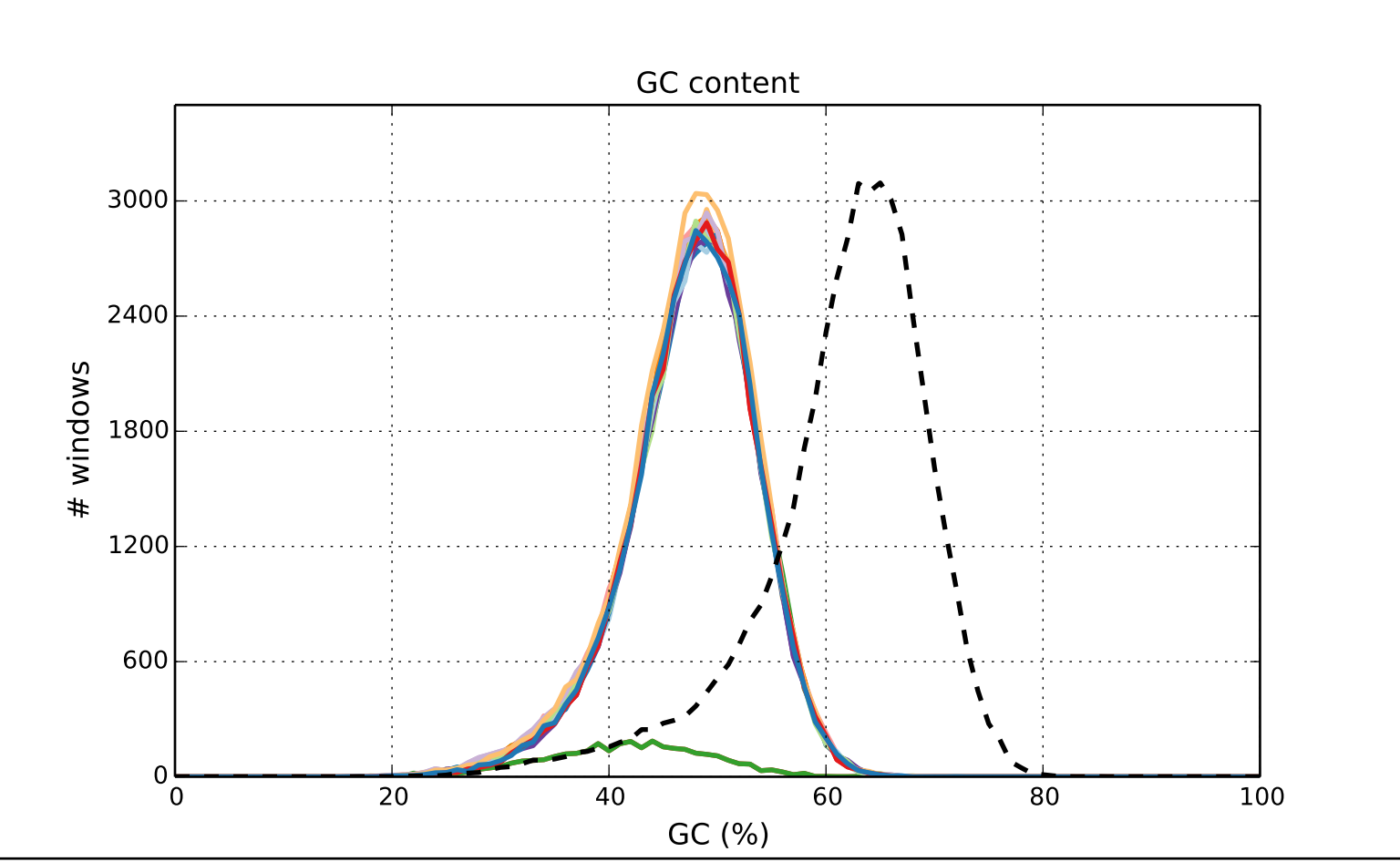
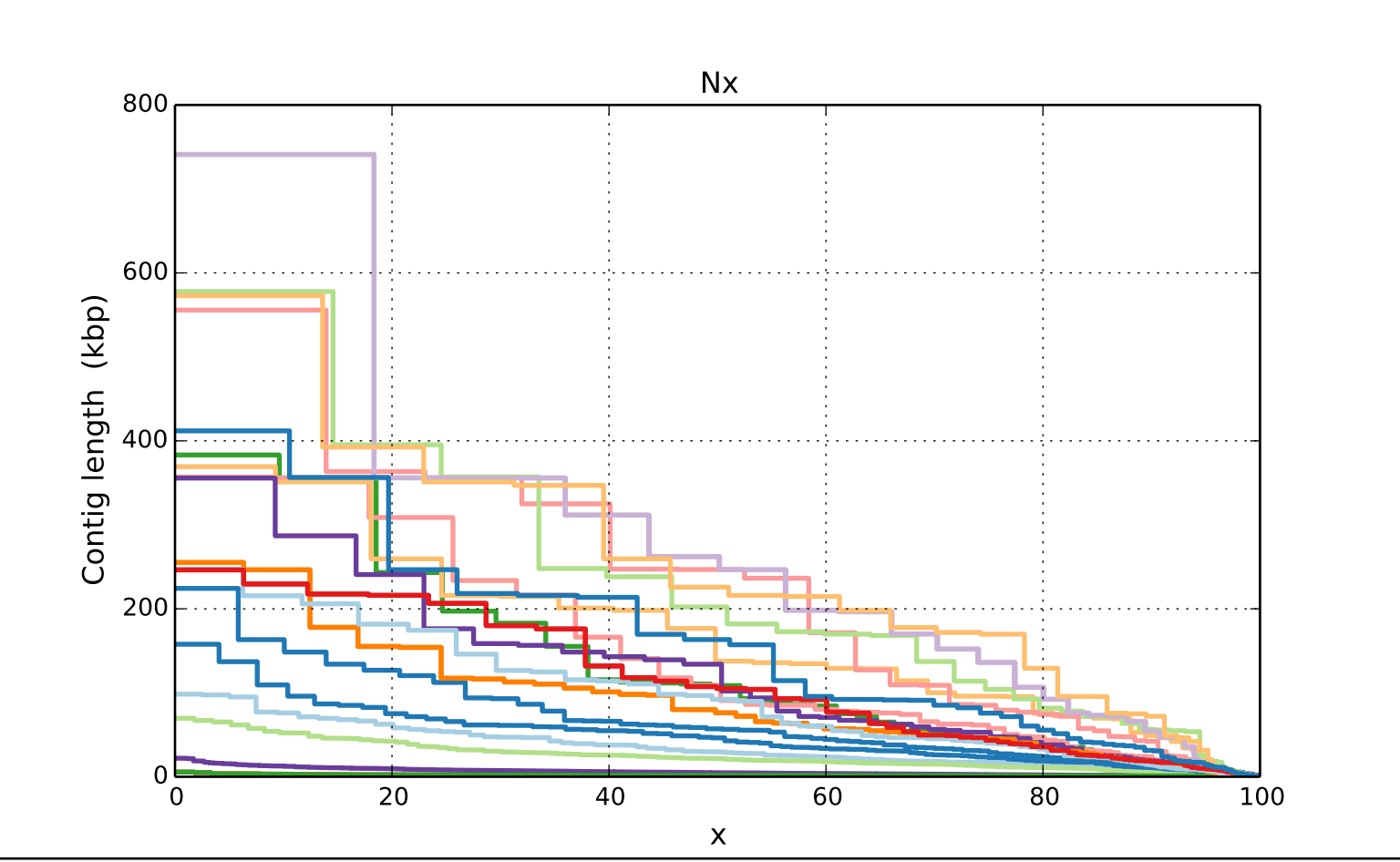
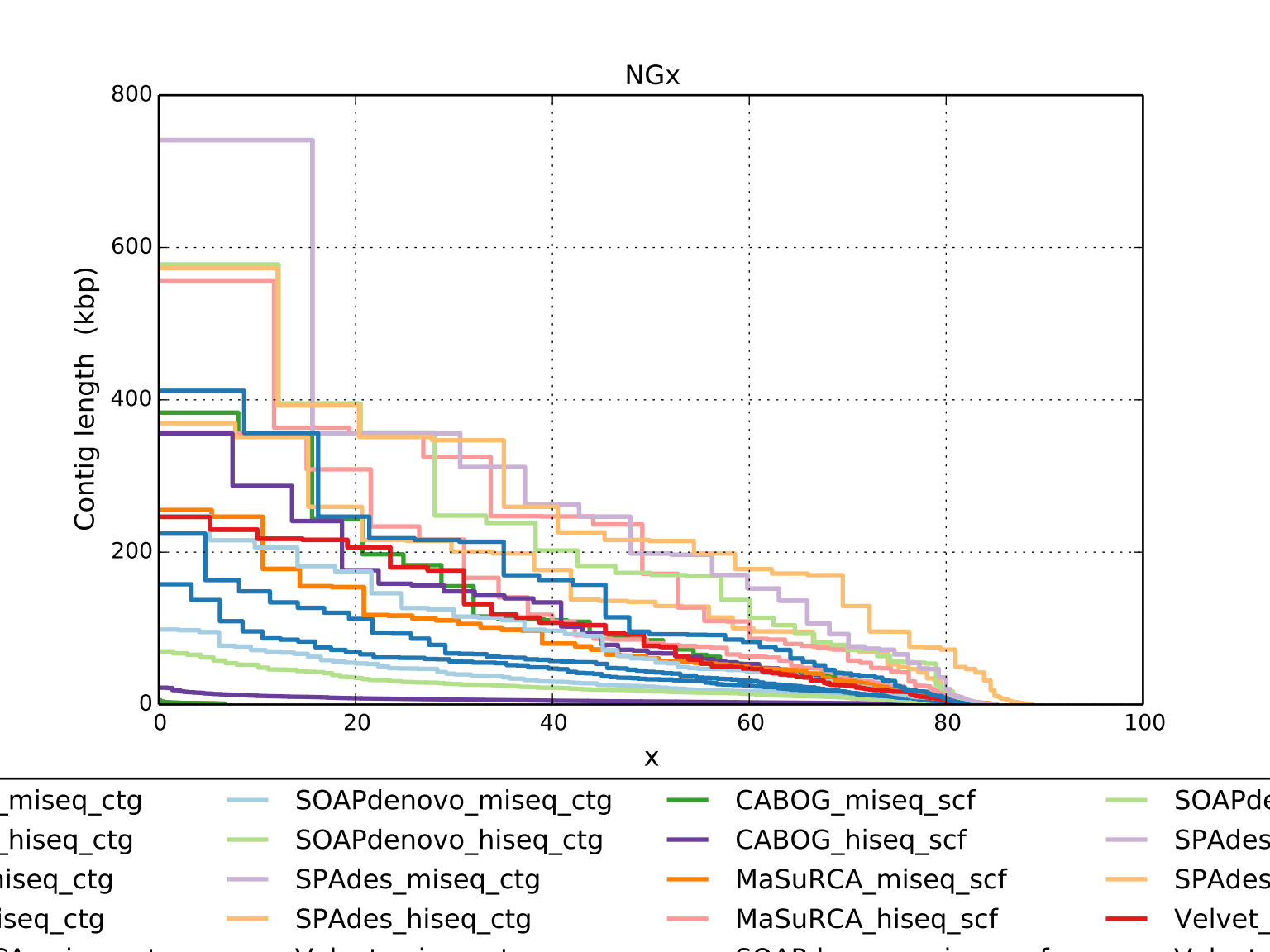
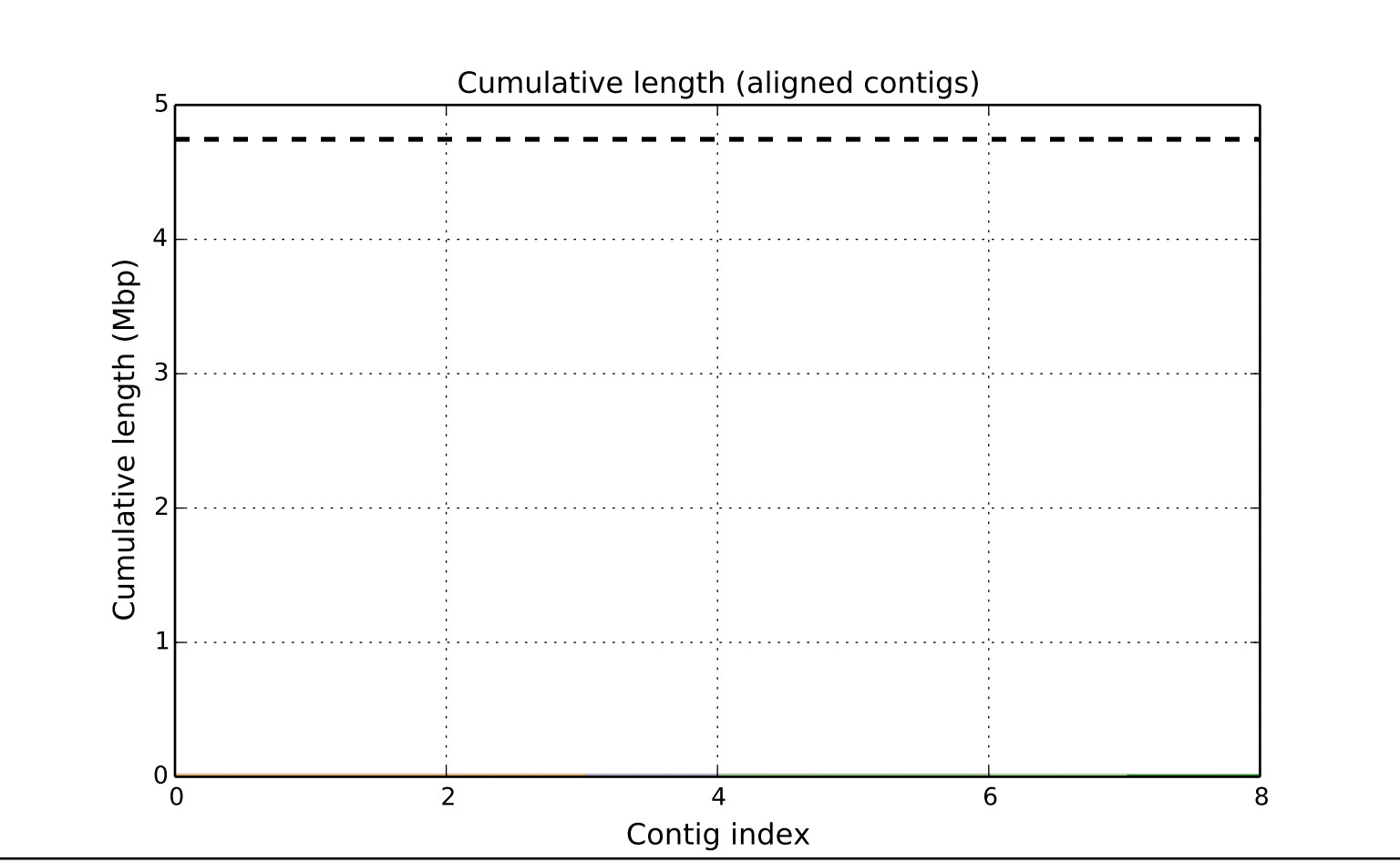
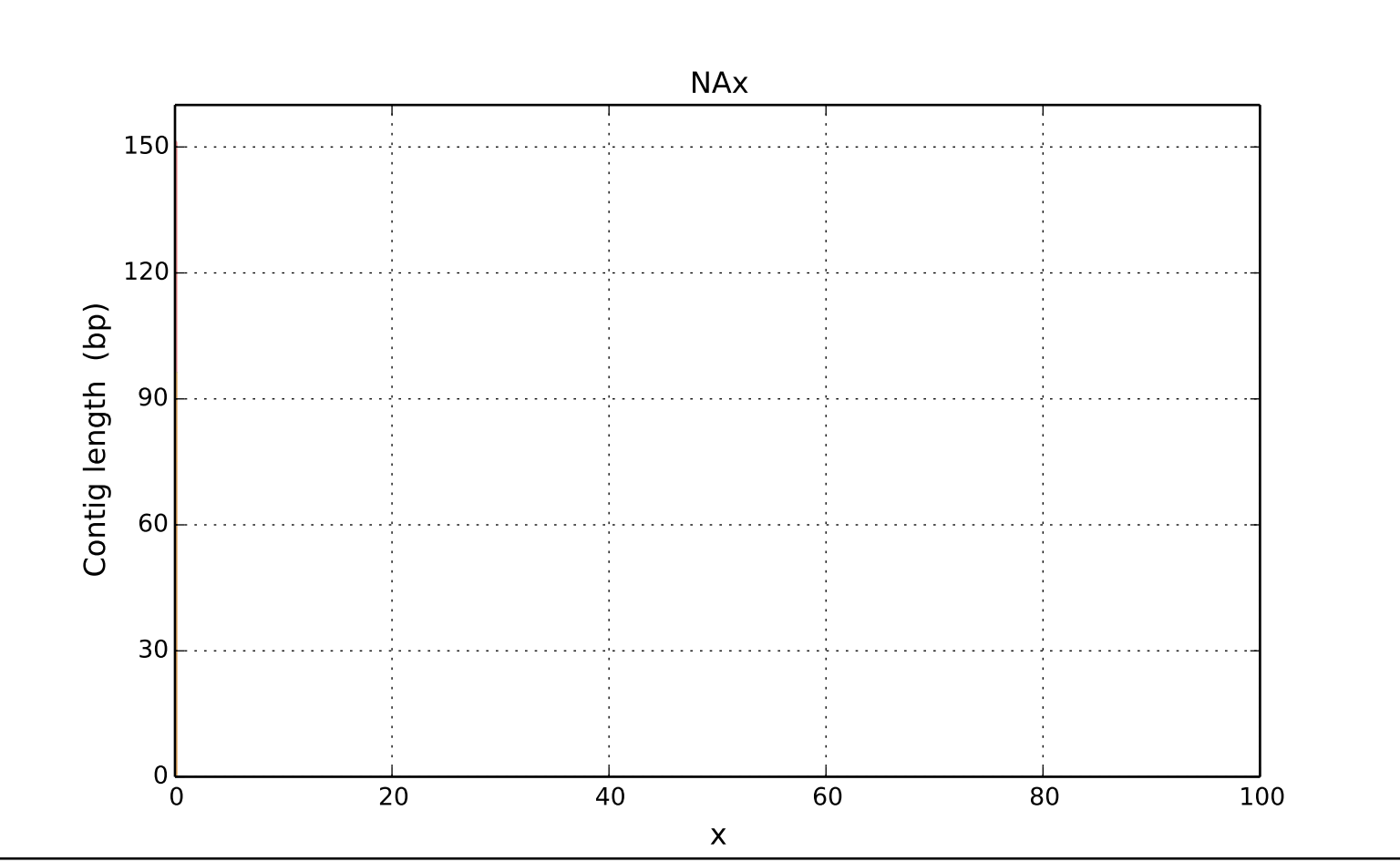

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
300
600
900
1200
OG_miseq_ctg
OG_hiseq_ctg
_miseq_ctg
_hiseq_ctg
SOAPdenovo_miseq_ctg
SOAPdenovo_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
CABOG_miseq_scf
CABOG_hiseq_scf
MaSuRCA_miseq_scf
MaSuRCA_hiseq_scf
SPAd
SPAd
Velve
Velve

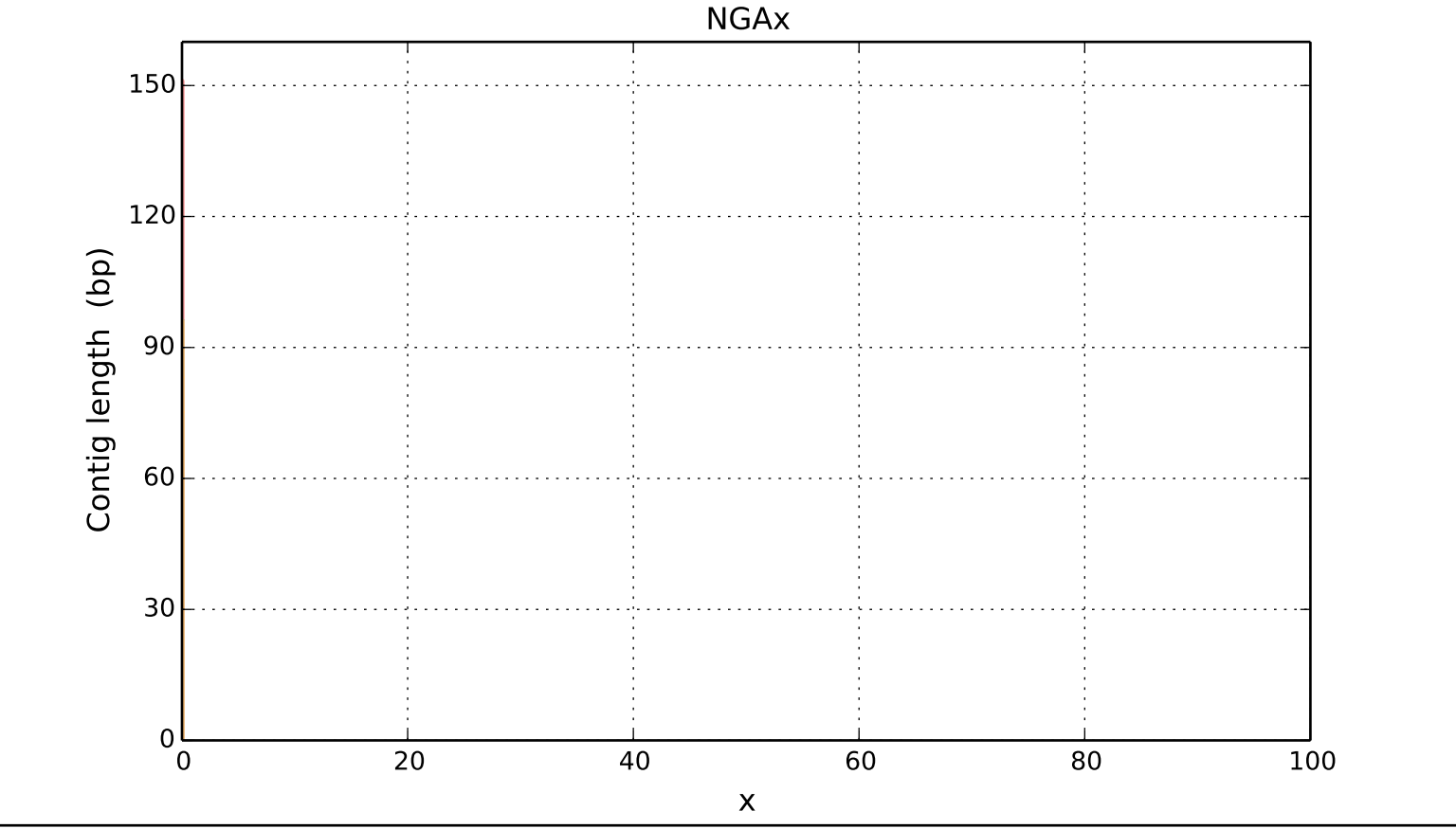

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
OG_miseq_ctg
OG_hiseq_ctg
_miseq_ctg
_hiseq_ctg
SOAPdenovo_miseq_ctg
SOAPdenovo_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
CABOG_miseq_scf
CABOG_hiseq_scf
MaSuRCA_miseq_scf
MaSuRCA_hiseq_scf
SPAd
SPAd
Velve
Velve

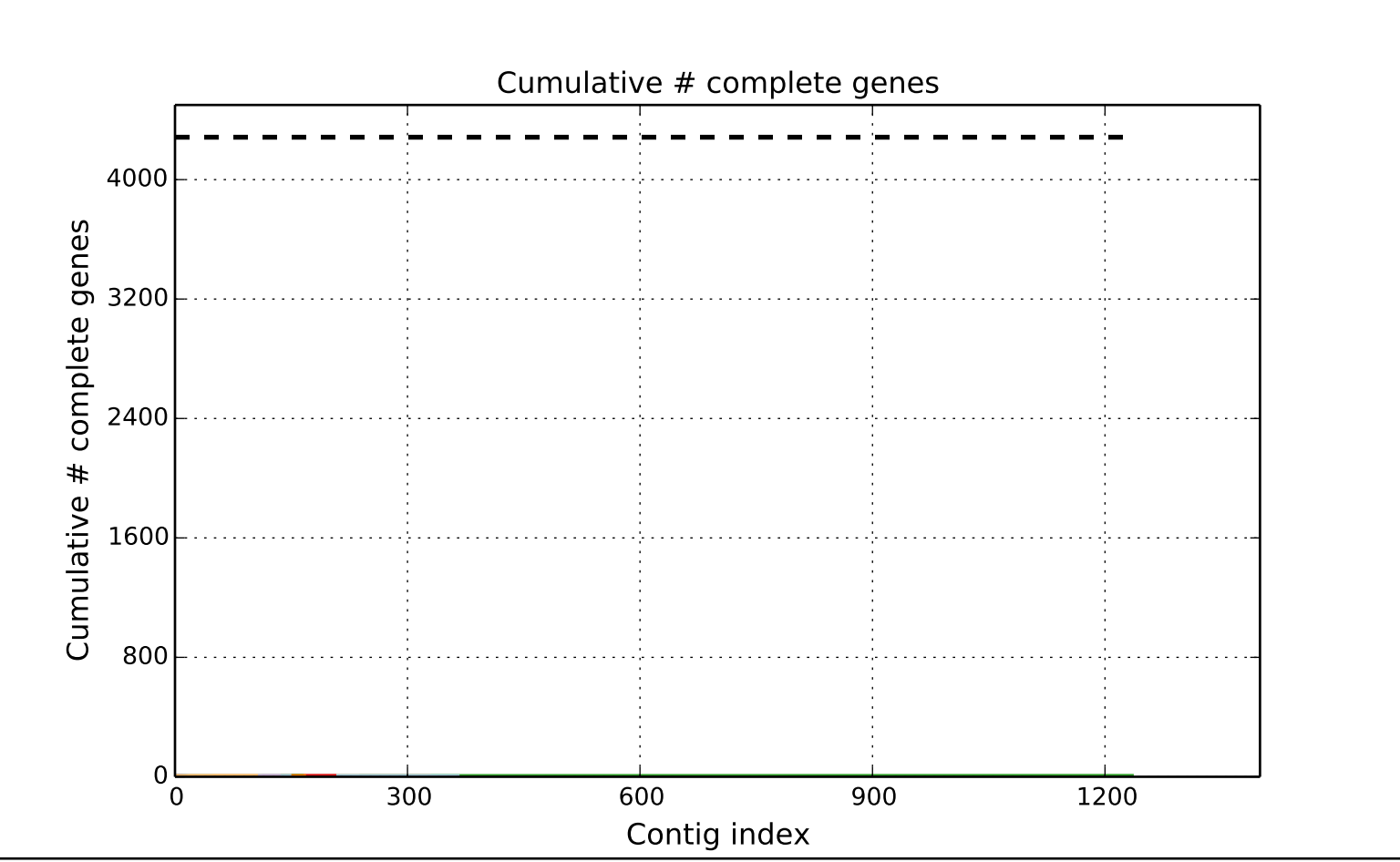

Nx
Contig length (kbp)
x
0
200
400
600
800
0
20
40
60
80
100
_miseq_ctg
_hiseq_ctg
iseq_ctg
iseq_ctg
SOAPdenovo_miseq_ctg
SOAPdenovo_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
CABOG_miseq_scf
CABOG_hiseq_scf
MaSuRCA_miseq_scf
MaSuRCA_hiseq_scf
SOAPde
SPAdes
SPAdes
Velvet_

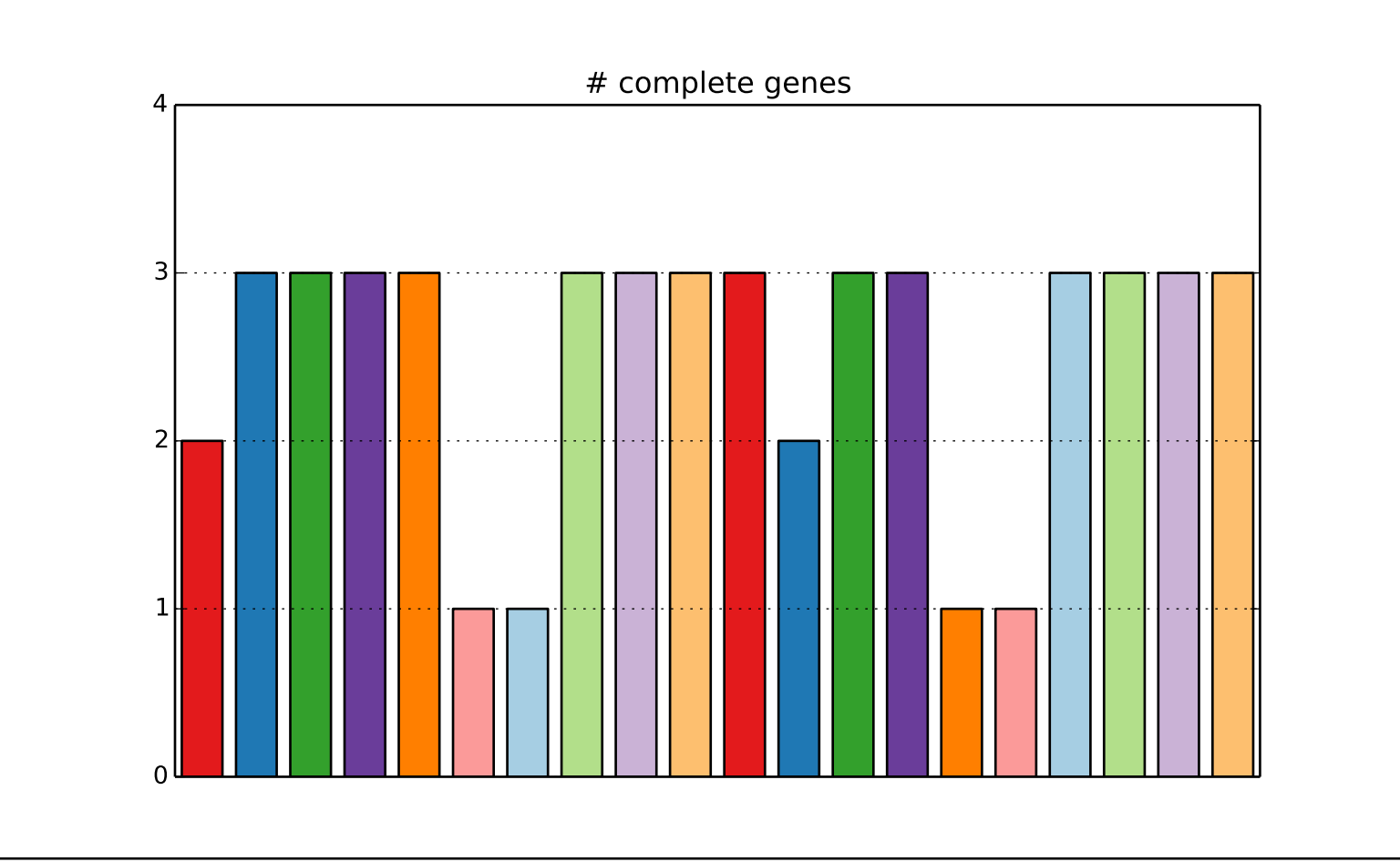

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
_miseq_ctg
_hiseq_ctg
iseq_ctg
iseq_ctg
SOAPdenovo_miseq_ctg
SOAPdenovo_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
CABOG_miseq_scf
CABOG_hiseq_scf
MaSuRCA_miseq_scf
MaSuRCA_hiseq_scf
SOAPde
SPAdes
SPAdes
Velvet_

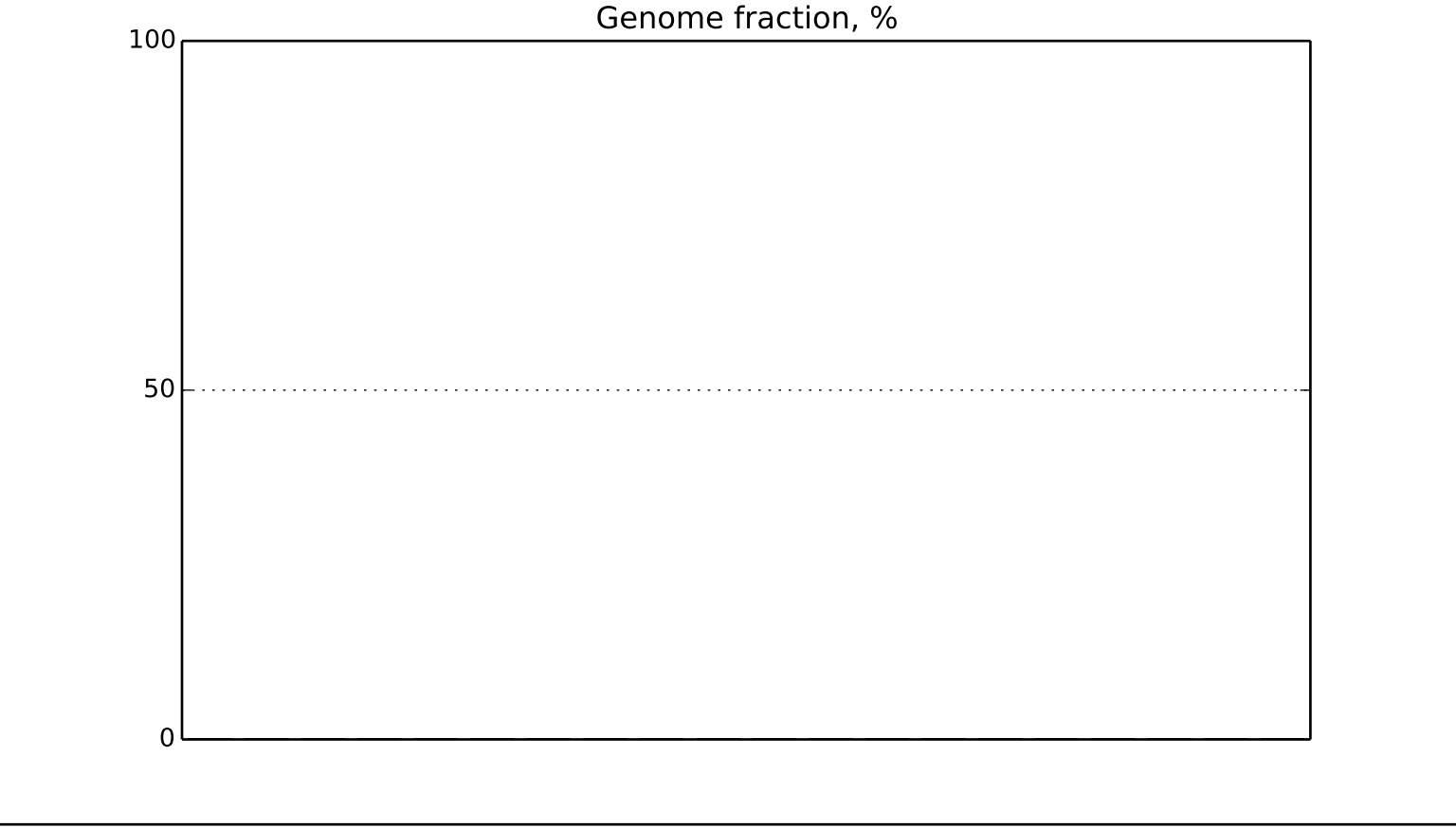

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
2
4
6
8
G_hiseq_ctg
miseq_ctg
hiseq_ctg
RCA_miseq_ctg
SOAPdenovo_hiseq_ctg
SPAdes_miseq_ctg
SPAdes_hiseq_ctg
Velvet_miseq_ctg
CABOG_hiseq_scf
MaSuRCA_miseq_scf
MaSuRCA_hiseq_scf
SOAPdenovo_miseq_scf
SPA
SPA
Velv
Velv


NAx
Contig length (bp)
150
120
90
60
30
0
0
20
40
60
80
100
x
_hiseq_ctg
SOAPdenovo_miseq_ctg
Velvet_hiseq_ctg
SOAPde
hiseq_ctg
SOAPdenovo_hiseq_ctg
CABOG_hiseq_scf
SPAdes
iseq_ctg
SPAdes_miseq_ctg
MaSuRCA_miseq_scf
SPAdes
CA_miseq_ctg
SPAdes_hiseq_ctg
MaSuRCA_hiseq_scf
Velvet_


NGAx
Contig length (bp)
150
120
90
60
30
0
0
20
40
60
80
100
x
_hiseq_ctg
SOAPdenovo_miseq_ctg
Velvet_hiseq_ctg
SOAPde
iseq_ctg
SOAPdenovo_hiseq_ctg
CABOG_hiseq_scf
SPAdes
iseq_ctg
SPAdes_miseq_ctg
MaSuRCA_miseq_scf
SPAdes
CA_miseq_ctg
SPAdes_hiseq_ctg
MaSuRCA_hiseq_scf
Velvet_


Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
300
600
900
1200
Contig index
G_hiseq_ctg
SOAPdenovo_hiseq_ctg
CABOG_hiseq_scf
SPA
miseq_ctg
SPAdes_miseq_ctg
MaSuRCA_miseq_scf
SPA
hiseq_ctg
SPAdes_hiseq_ctg
MaSuRCA_hiseq_scf
Velv
RCA_miseq_ctg
Velvet_miseq_ctg
SOAPdenovo_miseq_scf
Velv


complete genes
4
3
2
1
0
_hiseq_ctg
SOAPdenovo_miseq_ctg
Velvet_hiseq_ctg
SOAPde
iseq_ctg
SOAPdenovo_hiseq_ctg
CABOG_hiseq_scf
SPAdes
iseq_ctg
SPAdes_miseq_ctg
MaSuRCA_miseq_scf
SPAdes
CA_miseq_ctg
SPAdes_hiseq_ctg
MaSuRCA_hiseq_scf
Velvet_


Genome fraction, %
100
50
0
_hiseq_ctg
SOAPdenovo_miseq_ctg
Velvet_hiseq_ctg
SOAPde
iseq_ctg
SOAPdenovo_hiseq_ctg
CABOG_hiseq_scf
SPAdes
iseq_ctg
SPAdes_miseq_ctg
MaSuRCA_miseq_scf
SPAdes
CA_miseq_ctg
SPAdes_hiseq_ctg
MaSuRCA_hiseq_scf
Velvet_