Graph construction report for taurus

Generated on Thu 15:09 05 November 2020

Computational resources

Statistics	Val(Mb/sec)	Val(GB/mins)
CPU time	8888.71	148.15
max mem	61880	60.43
average mem	34883.07	34.07
Run time	1502	25.03

Graph statistics

Graph parameters	Count	Length (bp)
All nodes	50,741	2,521,524,321
Reference nodes	34,876	2,489,385,779
Non-reference nodes	15,865	32,138,542
Added from OBV	8,388	21,181,957
Added from Angus	4,327	5,472,469
Added from Highland	3,150	5,484,116
Edge RefRef	40,988	0
Edge RefNonref	30,299	0
Edge NonrefNonref	1,054	0

Core - flexible genome analysis

Pangenome component	Length	Proportion
core	2,445,456,326	96.98%
flexible	76,067,995	3.02%
flexible_shared	47,858,670	1.90%
private	28,209,325	1.12%

Pangenome size as sample increased
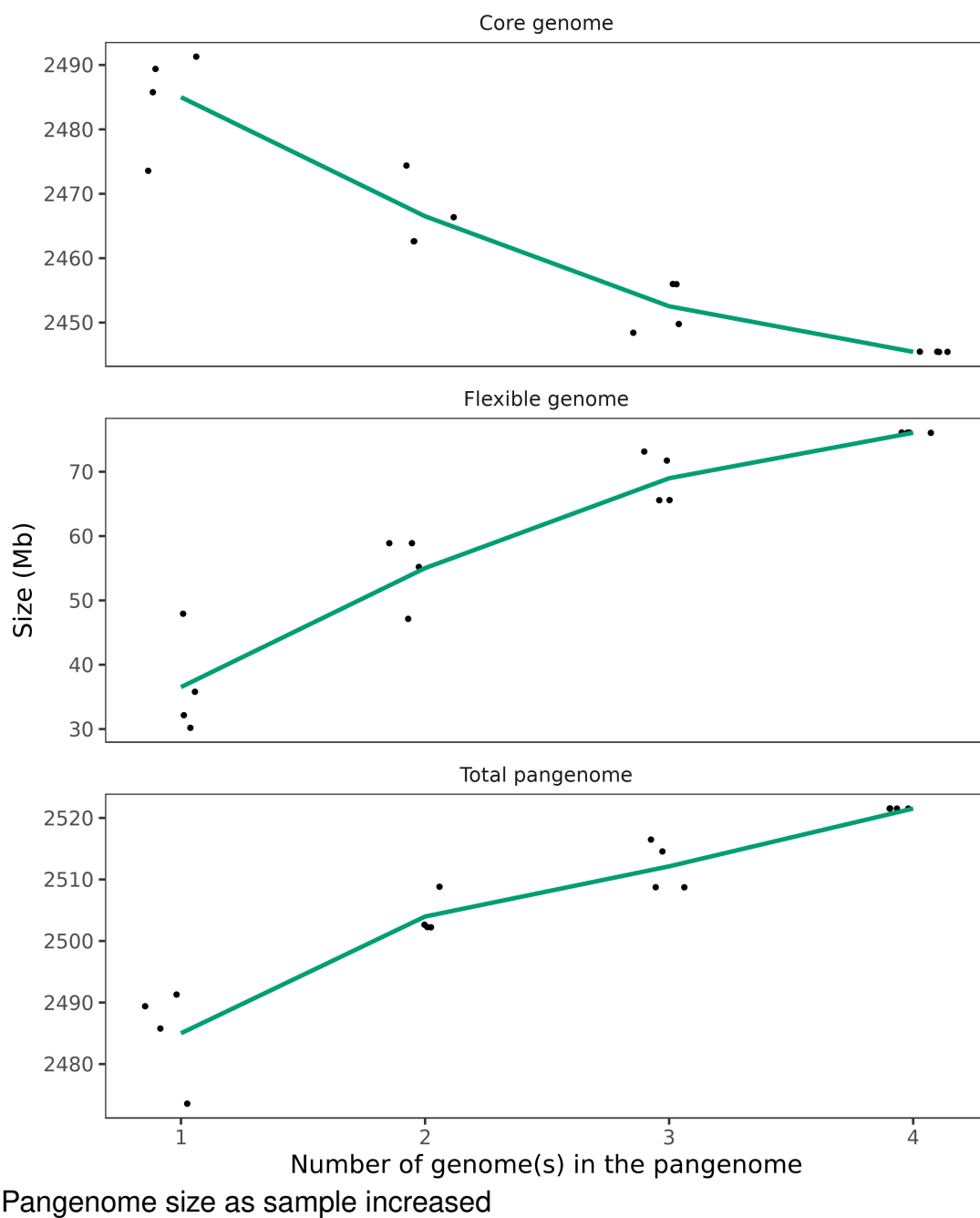
Non-reference sequences

Non-ref sequences	Node count	Total sequence length
Angus	8,308	18,181,891
Highland	8,328	19,414,397
OBV	8,672	21,781,129
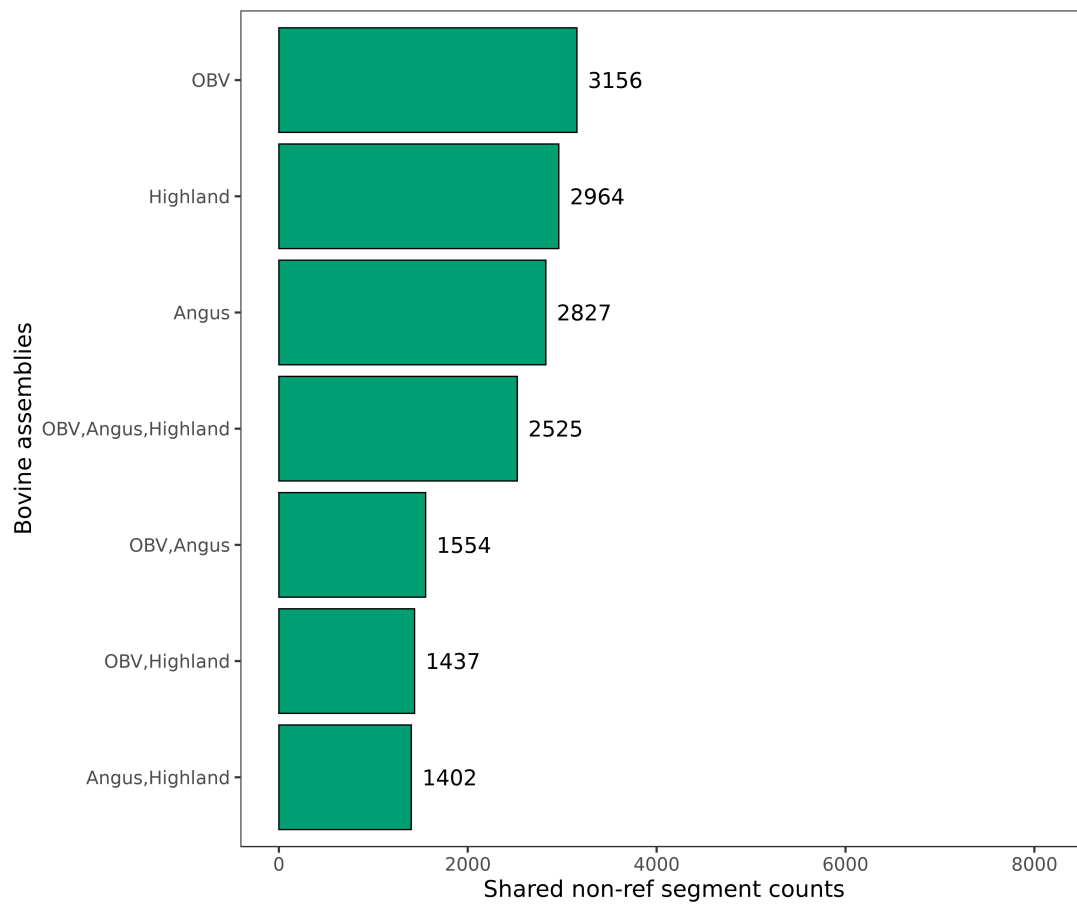
Pangenome nonref sharing count
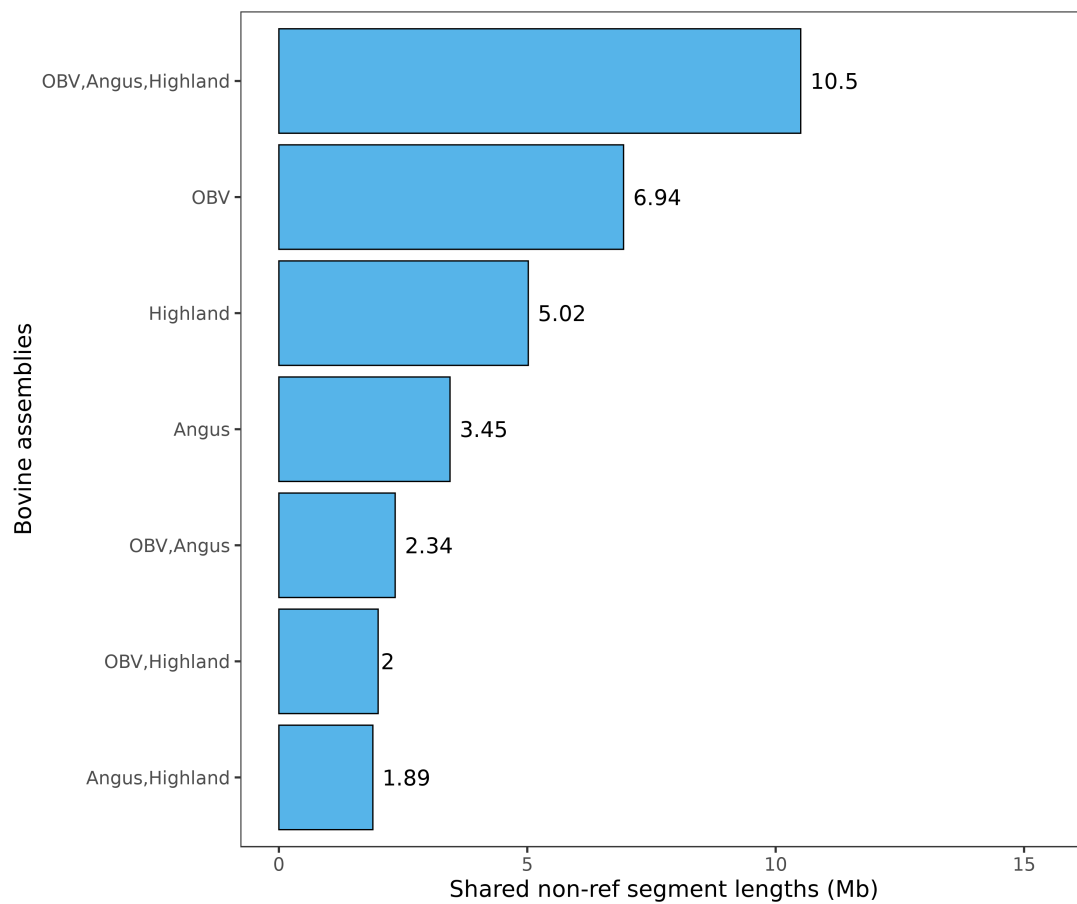
Pangenome nonref sharing length

Structural variations analysis

Annotations stats

Sequence Features	Count
intergenic	14,218
intronic	5,638
exon	63
CDS	74

Biallelic variations

Mutation type	SV count	SV total length	SV mean length
AltDel	3296	4,466,538	1355
AltIns	3642	4,176,361	1147
Deletion	5518	8,826,017	1599
Insertion	6437	9,185,182	1427

Multiallelic variations

Mutation type	SV count	SV total length	SV mean length
Deletions	1020	4,201,997	4120
Insertions	1124	6,173,053	5492

Functional analysis

Gene model prediction

Gene model features	Statistics
Total novel genes (distinct SV)	920(702)
Complete novel genes	428(284)
Transcript length	11370.42 (116891 - 267)
Exon length	895.75 (9096 - 13)
Exon length/gene	3260.71 (10241 - 267)
Exon count/gene	3.64 (25 - 1)
CDS length	330.4 (9066 - 2)
CDS length/gene	1083.08 (10036 - 199)
protein length	361.03 (3345.33 - 66.33)