# **Graph construction report for** graph5

#### Generated on Wed 12:01 28 October 2020

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#### Computational resources

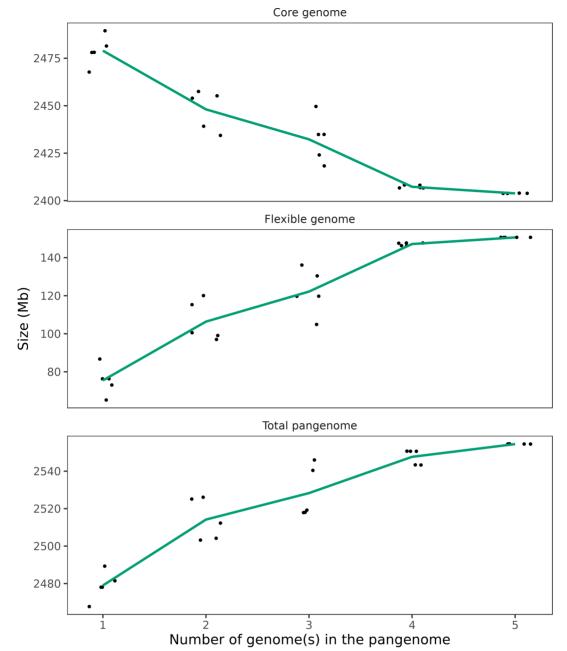
Statistics	Val(Mb/sec)	Val(GB/mins)
CPU time	10844.93	180.75
max mem	90396	88.28
average mem	42898.73	41.89
Run time	978	16.30

### Graph statistics

Graph parameters	Count	Length (bp)
All nodes	176,037	2,554,462,759
Reference nodes	119,284	2,489,385,779
Non-reference nodes	56,753	65,076,980
Added from Angus	8,515	12,997,145
Added from Highland	4,695	7,175,045
Added from Brahman	12,820	12,326,594
Added from Yak	30,723	32,578,196
Edge RefRef	136,305	0
Edge RefNonref	109,044	0
Edge NonrefNonref	3,201	0

## Core - flexible genome analysis

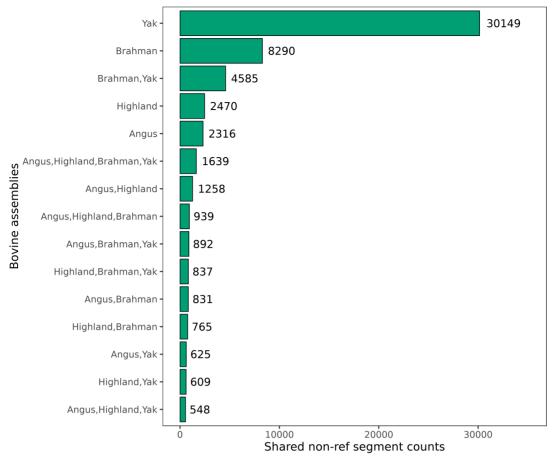
Pangenome component	Length	Proportion
core	2,403,833,363	94.10%
flexible	150,629,396	5.90%
flexible_shared	91,923,908	3.60%
private	58,705,488	2.30%



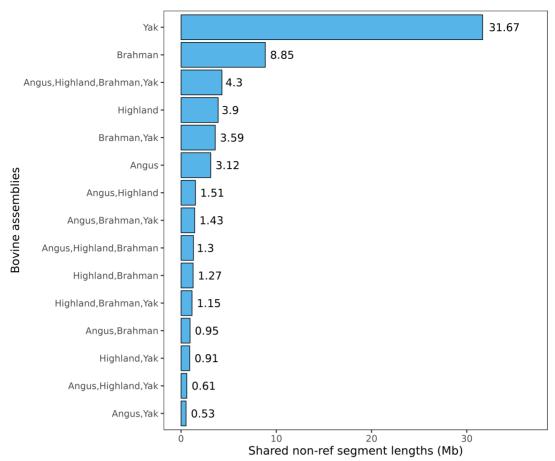
Pangenome size as sample increased

### Non-reference sequences

Non-ref sequences	Node count	Total sequence length
Angus	9,048	13,744,385
Brahman	18,778	22,833,008
Highland	9,065	14,944,012
Yak	39,884	44,184,846



Pangenome nonref sharing count



Pangenome nonref sharing length

### Structural variations analysis

#### Biallelic variations

Mutation type	SV count	SV total length	SV mean length
AltDel	12752	10,829,643	849
AltIns	14768	12,391,969	839
Deletion	14854	15,994,388	1077
Insertion	19343	20,788,858	1075

#### Multiallelic variations

Mutation type	SV count	SV total length	SV mean length
Deletions	4631	12,609,337	2723
Insertions	4306	10,327,422	2398