Qualimap Analysis Results

Multi-sample BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2019/09/23 13:20:52

1. Input data & parameters

1.1. Samples

9564	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/11_BT2_Bc_B05.10.dedup.rg.csorted_stats
B757-4	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/3_BT2_Bc_B05.10.dedup.rg.csorted_stats
9136	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/7_BT2_Bc_B05.10.dedup.rg.csorted_stats
9345	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/10_BT2_Bc_B05.10.dedup.rg.csorted_stats
9653	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/12_BT2_Bc_B05.10.dedup.rg.csorted_stats
8762	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/16_BT2_Bc_B05.10.dedup.rg.csorted_stats

8880	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/9_BT2_Bc_B05.10.de dup.rg.csorted_stats
8763	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/17_BT2_Bc_B05.10.d edup.rg.csorted_stats
214/99	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/1_BT2_Bc_B05.10.de dup.rg.csorted_stats
B402	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/19_BT2_Bc_B05.10.d edup.rg.csorted_stats
BGM_Pod_S.H-3	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/15_BT2_Bc_B05.10.d edup.rg.csorted_stats
9550	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/18_BT2_Bc_B05.10.d edup.rg.csorted_stats
9053	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/4_BT2_Bc_B05.10.de

	dup.rg.csorted_stats
B16-1	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/21_BT2_Bc_B05.10.d edup.rg.csorted_stats
TR9815	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/14_BT2_Bc_B05.10.d edup.rg.csorted_stats
10418	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/5_BT2_Bc_B05.10.de dup.rg.csorted_stats
B16-2	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/22_BT2_Bc_B05.10.d edup.rg.csorted_stats
B775-1	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/20_BT2_Bc_B05.10.d edup.rg.csorted_stats
8748	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces s_19_09_2019/8_BT2_Bc_B05.10.de dup.rg.csorted_stats
B589-2	/export/home/s2978925/data/Marzia/ B_cinerea_WGS/AGRF_CAGRF200 74_HFLHKDRXX/AGRF_BT2_proces

|	
	s_19_09_2019/2_BT2_Bc_B05.10.dedup.rg.csorted_stats
Kingsford2	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/6_BT2_Bc_B05.10.dedup.rg.csorted_stats
10412	/export/home/s2978925/data/Marzia/B_cinerea_WGS/AGRF_CAGRF20074_HFLHKDRXX/AGRF_BT2_process_19_09_2019/13_BT2_Bc_B05.10.dedup.rg.csorted_stats

2. Summary

2.1. Globals

Number of samples	22
Total number of mapped reads	620,052,720
Mean samples coverage	96.26
Mean samples GC-content	42.89
Mean samples mapping quality	38.64
Mean samples insert size	269.91

2.2. Sample statistics

Sample name	Coverage mean	Coverage std	GC percentage	Mapping quality mean	Insert size median
214/99	114.4971	115.1547	42.97	38.9758	289.0
B589-2	112.1055	141.5384	43.07	38.9921	276.0
B757-4	148.4225	197.159	42.87	39.139	303.0
9053	39.4021	40.802	43.07	39.35	273.0
10418	84.1911	114.407	42.57	39.2181	264.0
Kingsford2	127.9451	196.8198	43.27	38.9215	287.0
9136	12.7484	16.1927	42.69	39.5662	274.0
8748	88.6738	106.2827	42.78	38.361	270.0
8880	46.1346	62.2396	42.85	38.1331	259.0
9345	132.3911	184.2125	43.24	38.0319	284.0
9564	94.7355	108.1317	42.66	38.311	241.0
9653	59.62	75.6783	42.64	37.5839	245.0

10412	45.8917	66.2997	42.72	38.3598	265.0
TR9815	109.9548	130.9144	42.89	38.0175	253.0
BGM_Pod_S.H-3	106.1426	131.3938	42.53	39.0992	274.0
8762	128.4231	200.7594	43.25	37.9207	272.0
8763	140.693	154.4968	43.12	38.6097	263.0
9550	121.7113	176.1397	43.28	38.6755	275.0
B402	110.0094	157.0802	43.12	37.7879	267.0
B775-1	121.7621	169.9358	43.25	39.0952	268.0
B16-1	76.6804	100.9603	42.43	38.9779	269.0
B16-2	95.6601	134.0293	42.4	39.0051	267.0

3. Results : PCA
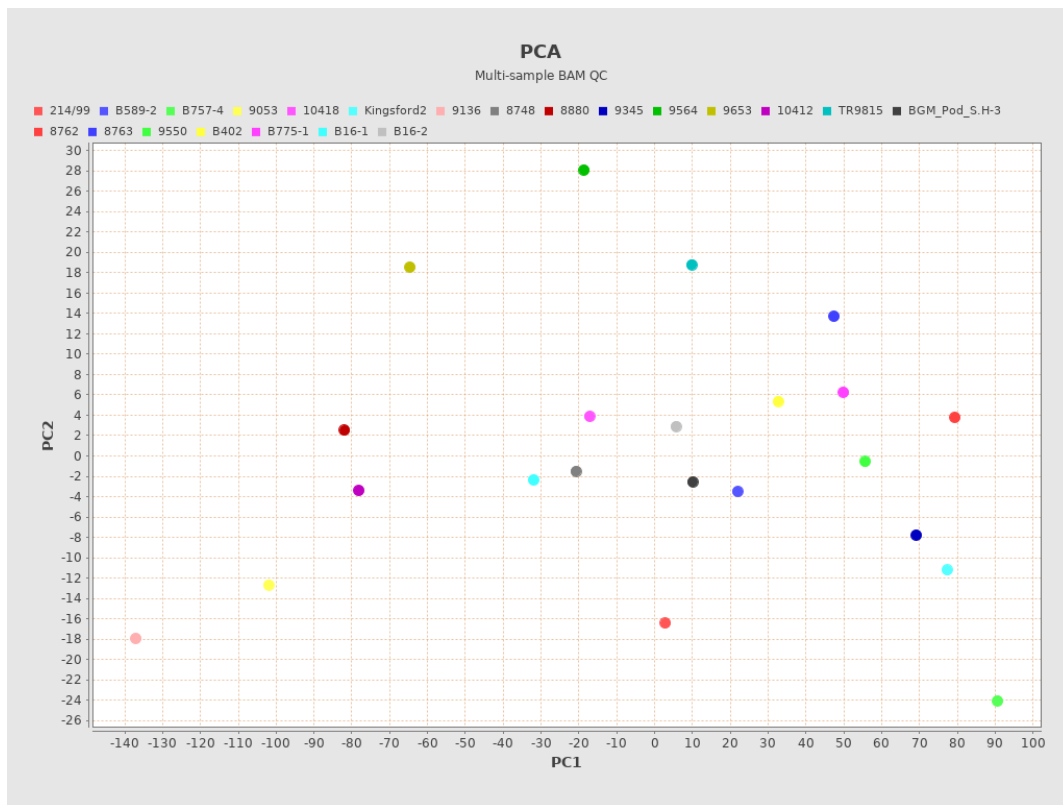
4. Results : Coverage Across Reference
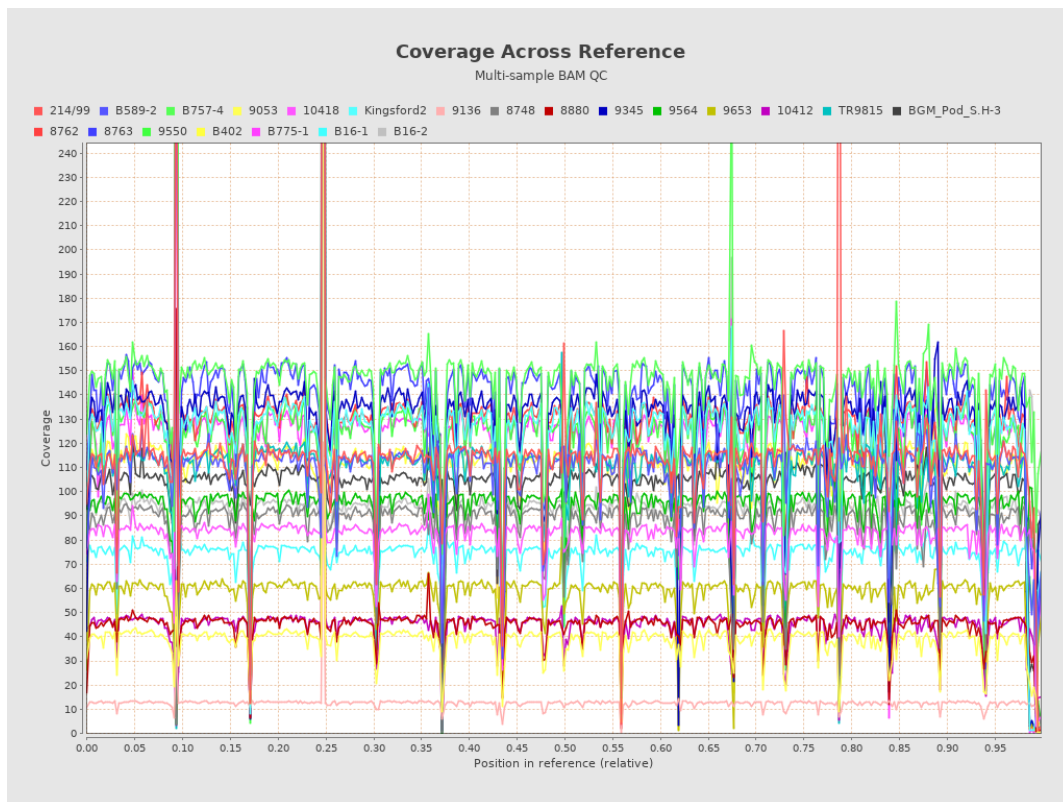
5. Results : Coverage Histogram (0 - 24233X)

Coverage Histogram (0 - 24233X)
Multi-sample BAM QC
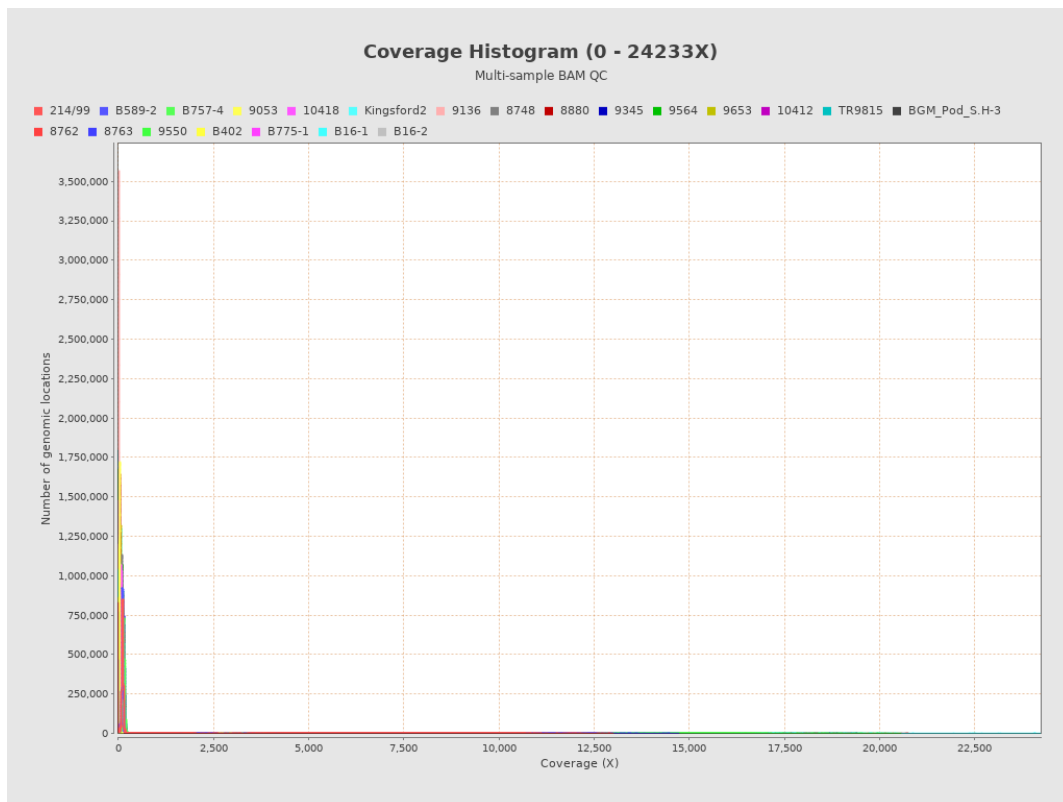
6. Results : Global Coverage Histogram

Global Coverage Histogram
Multi-sample BAM QC
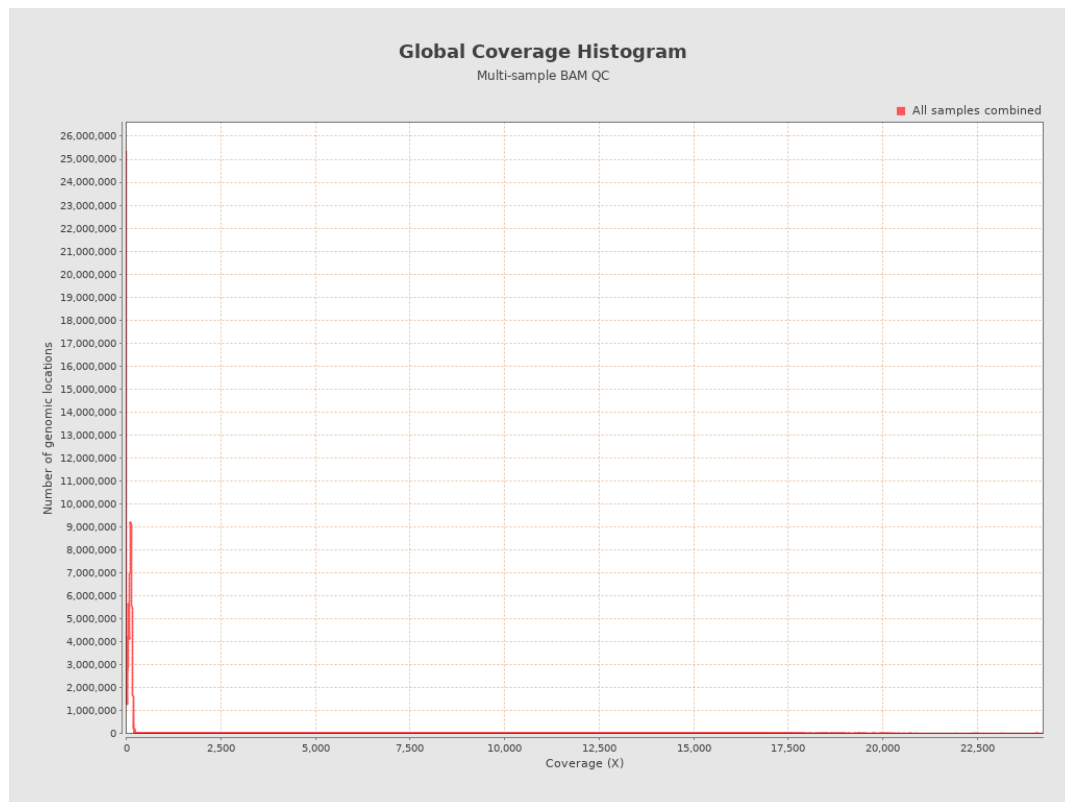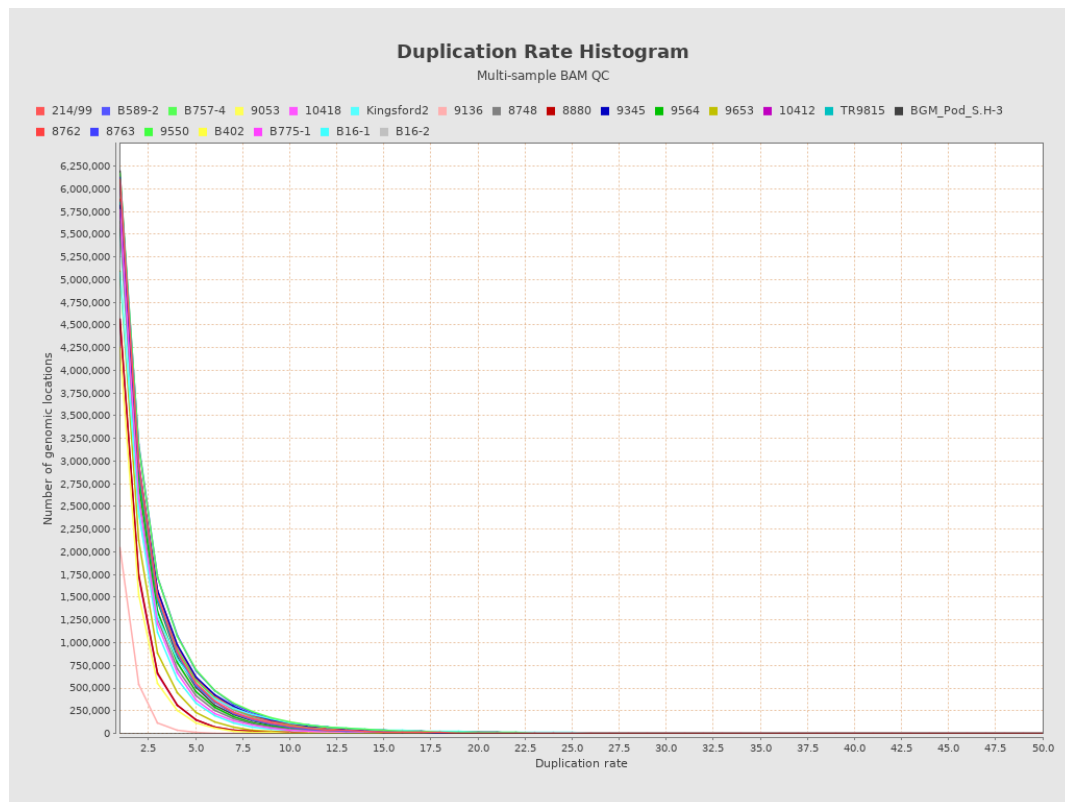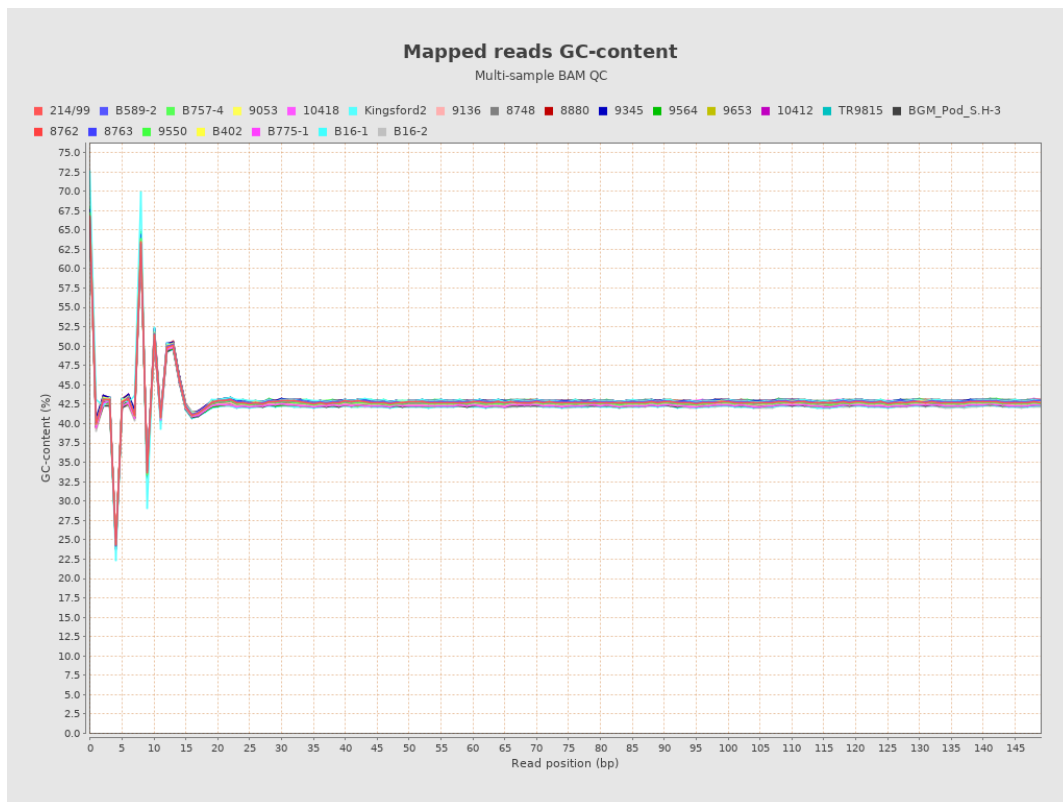
7. Results : Genome Fraction Coverage
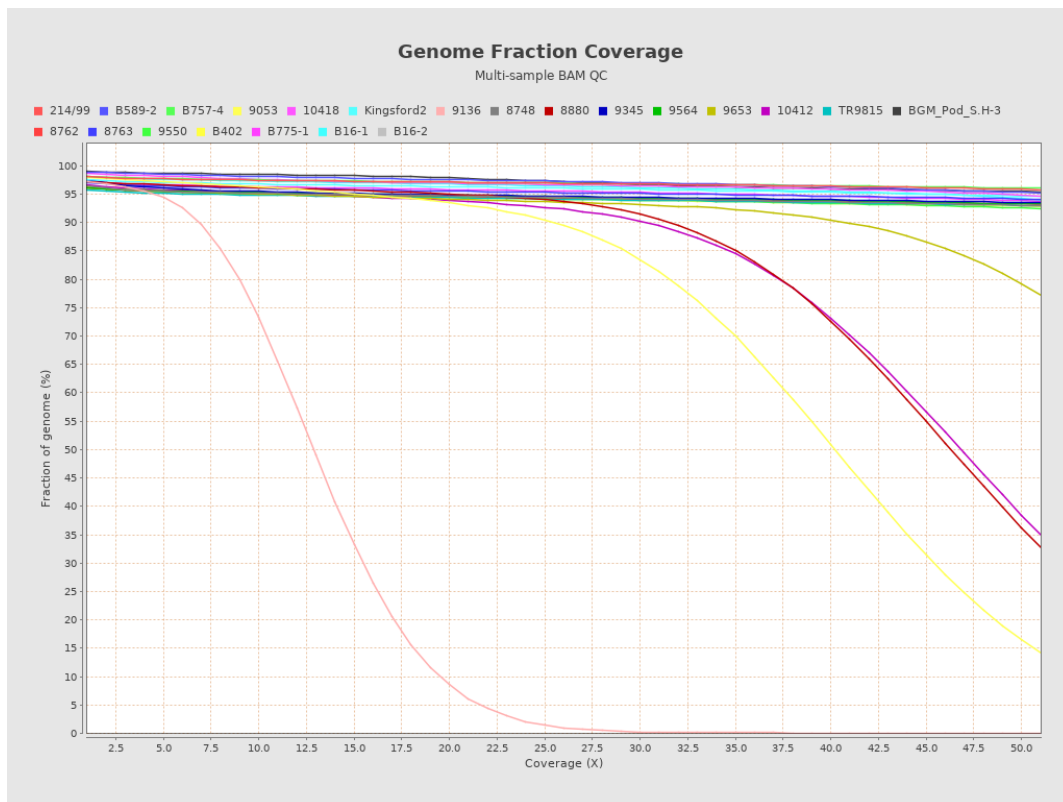
8. Results : Duplication Rate Histogram

9. Results : Mapped reads GC-content

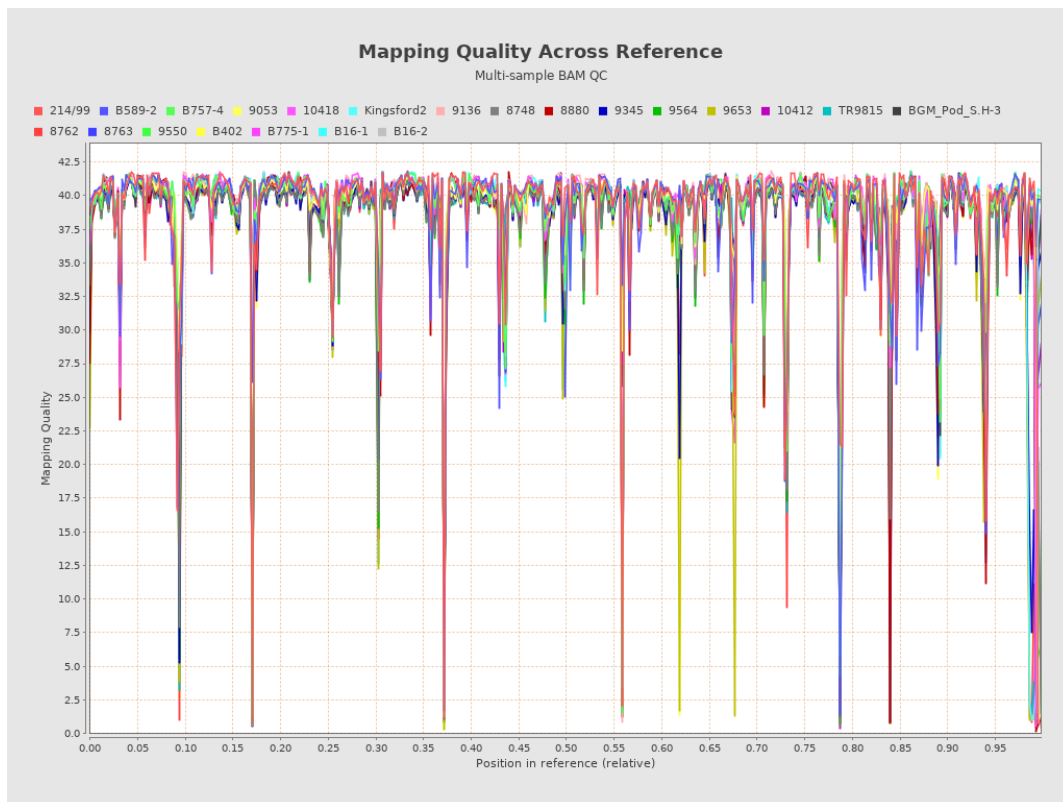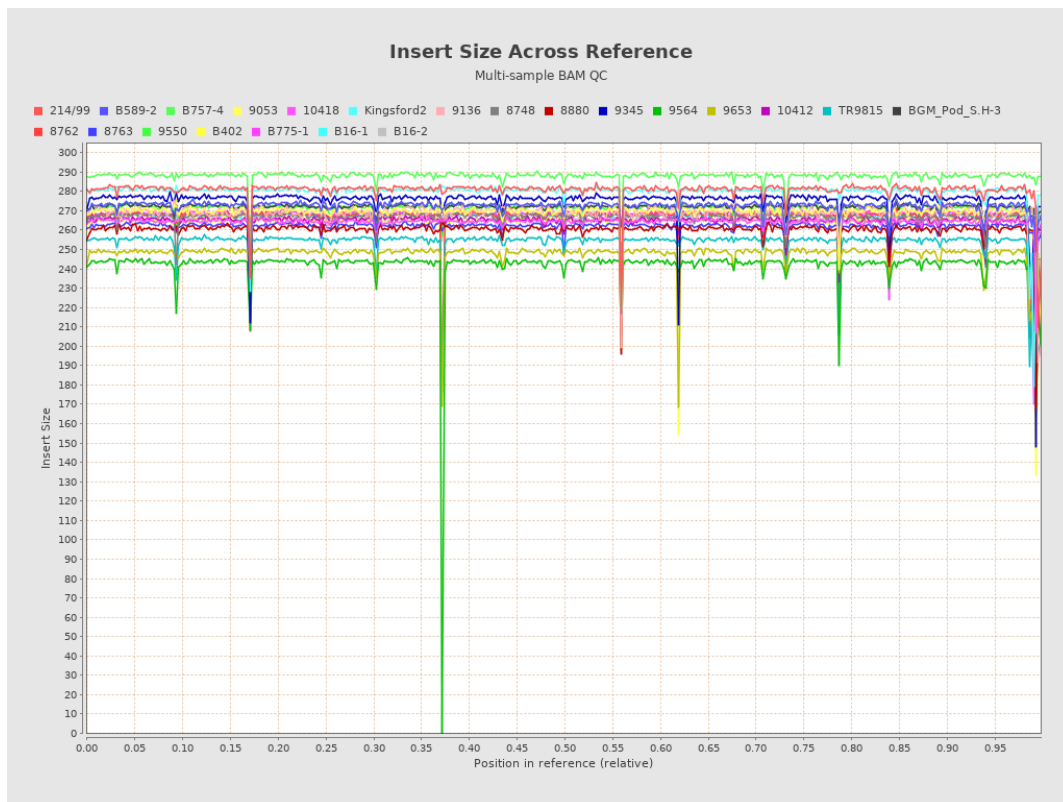# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile

Multi-sample BAM QC

No data available.

11. Results : Mapped Reads GC-content Distribution
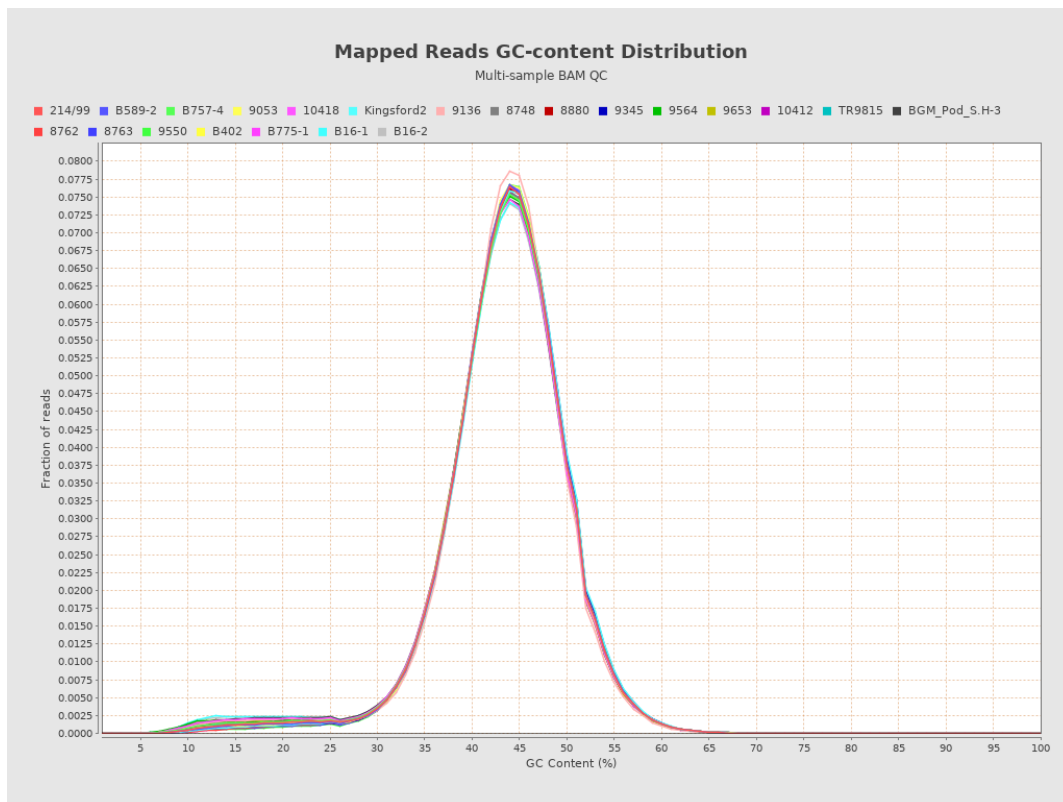
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
Multi-sample BAM QC

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram