

Qualimap Analysis Results

Multi-sample BAM QC analysis

Generated by Qualimap v.2.3

2023/09/27 05:48:29

1. Input data & parameters

1.1. Samples

PE2	/home/abhinavmishra/sars-project/pair2/minimap2-illumina.sorted_stats
PE1	/home/abhinavmishra/sars-project/pair1/minimap2-illumina.sorted_stats
PE3	/home/abhinavmishra/sars-project/pair3/minimap2-illumina.sorted_stats

2. Summary

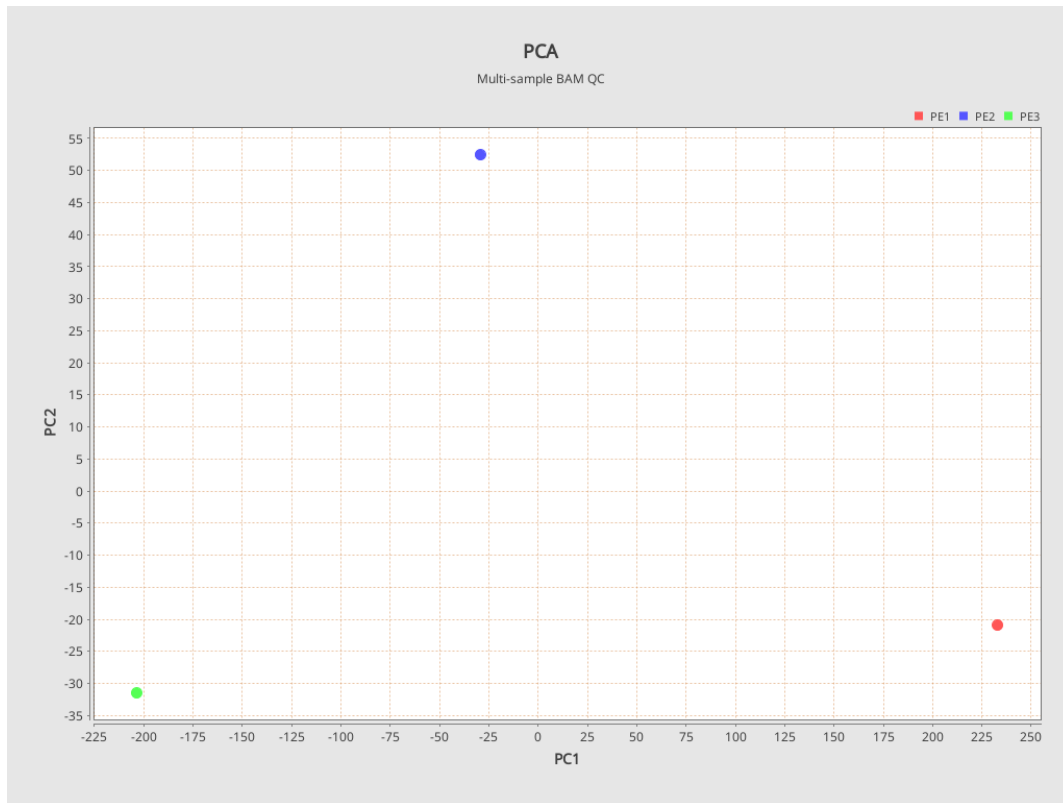
2.1. Globals

Number of samples	3
Total number of mapped reads	116,879
Mean samples coverage	154.08
Mean samples GC-content	31.05
Mean samples mapping quality	44.95
Mean samples insert size	110

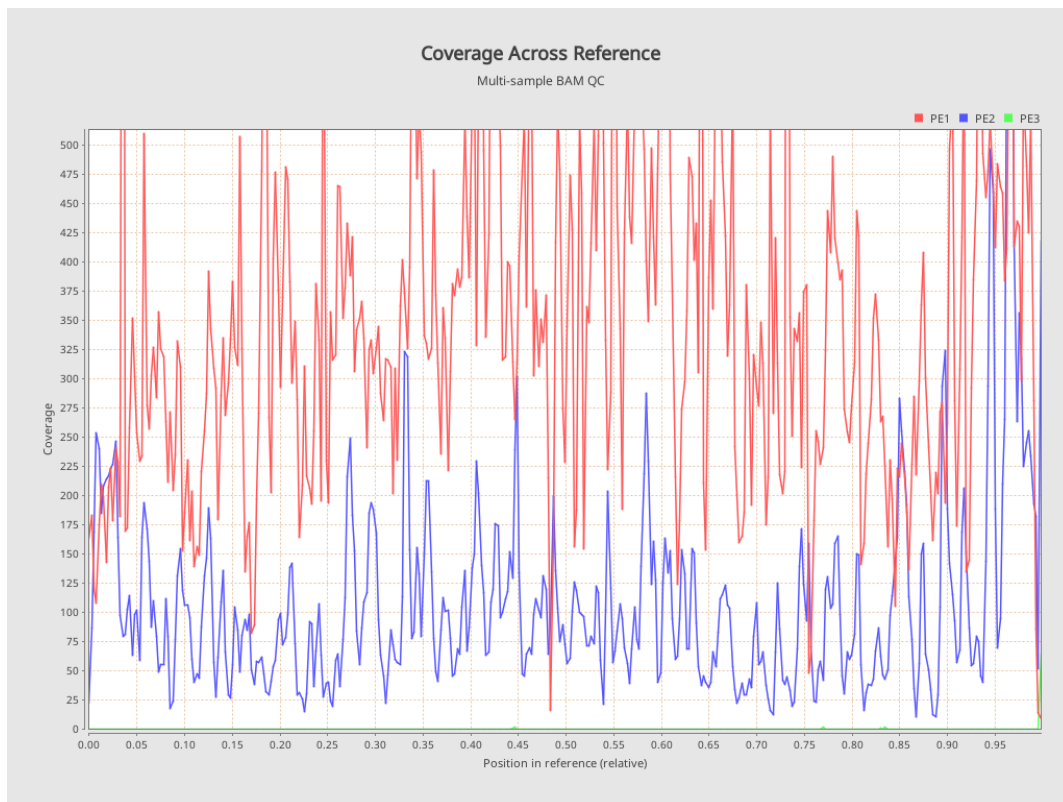
2.2. Sample statistics

Sample name	Coverage mean	Coverage std	GC percentage	Mapping quality mean	Insert size median
PE1	351.2866	232.7568	37.87	54.9977	149.0
PE2	110.8722	104.7774	40.6	56.285	148.0
PE3	0.0714	3.9842	14.67	23.5644	33.0

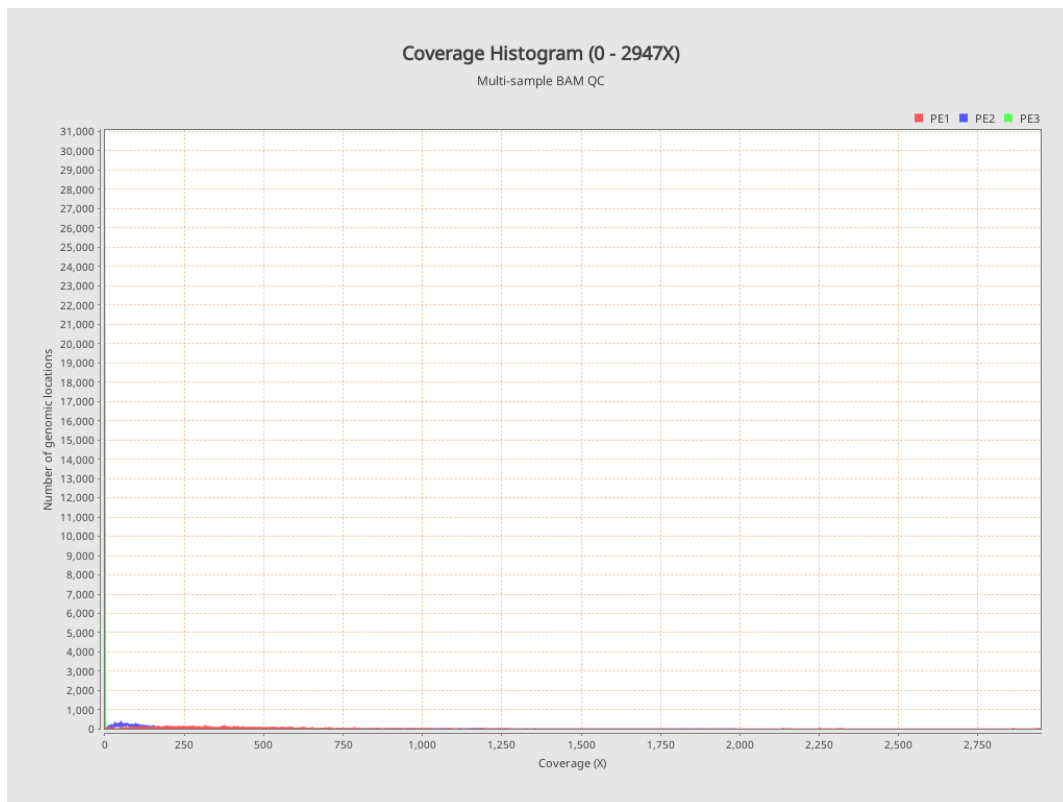
3. Results : PCA



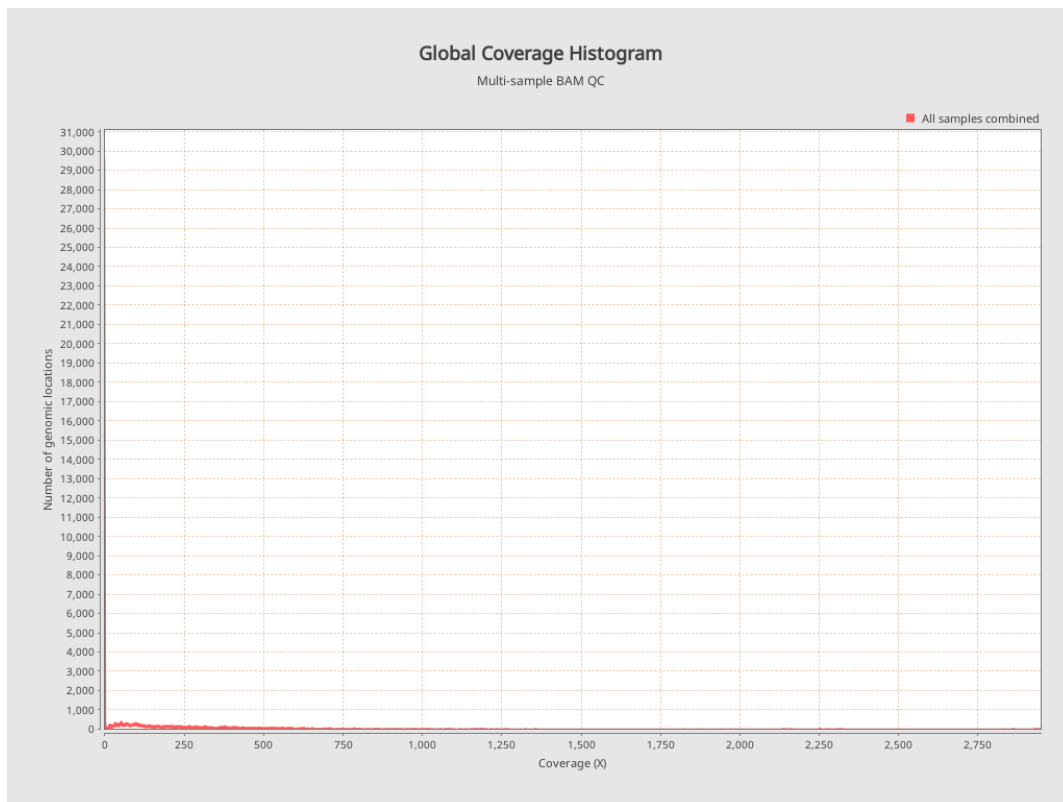
4. Results : Coverage Across Reference



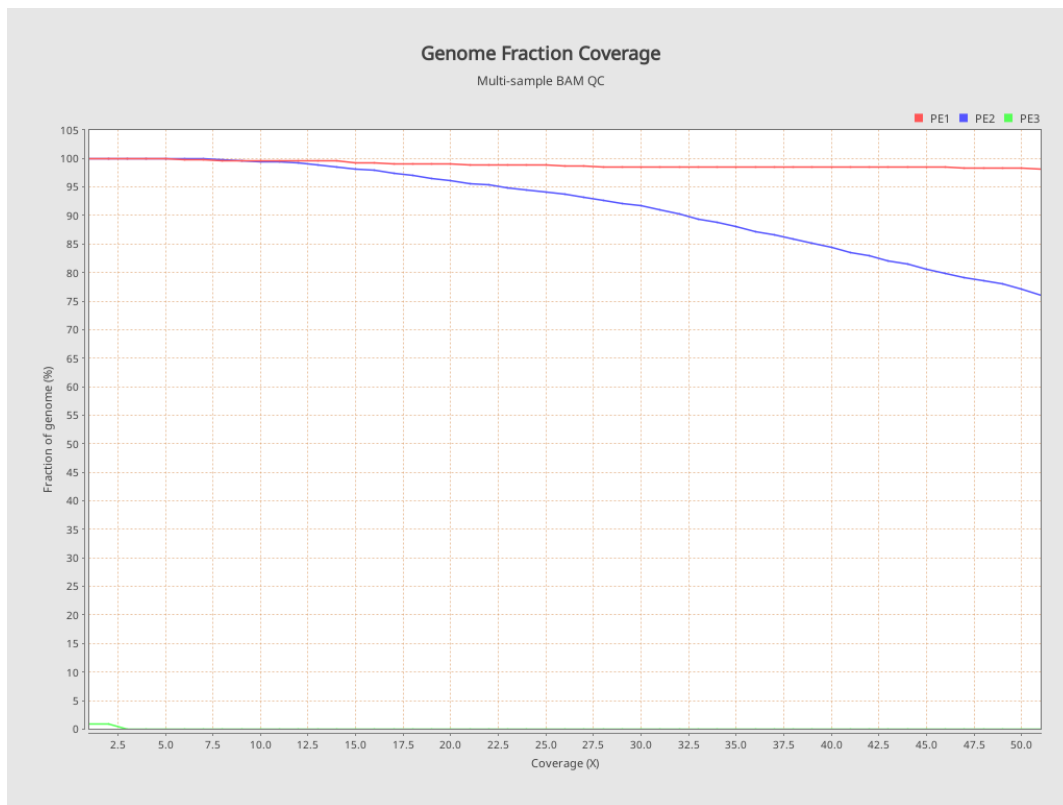
5. Results : Coverage Histogram (0 - 2947X)



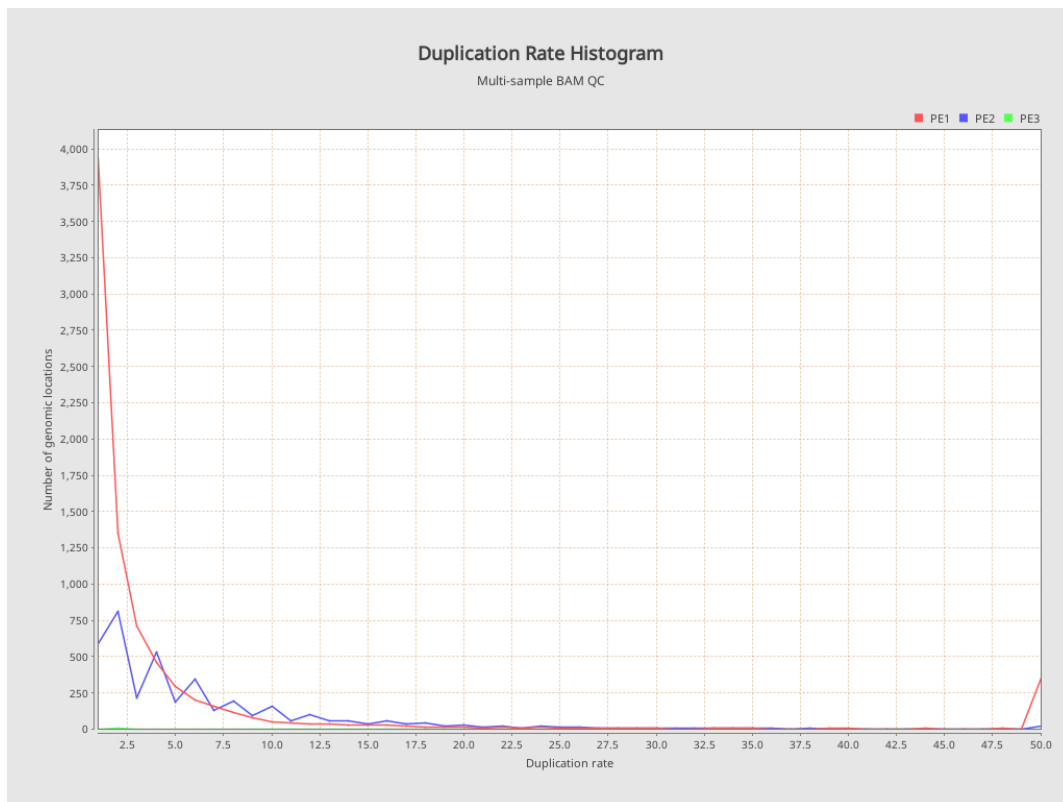
6. Results : Global Coverage Histogram



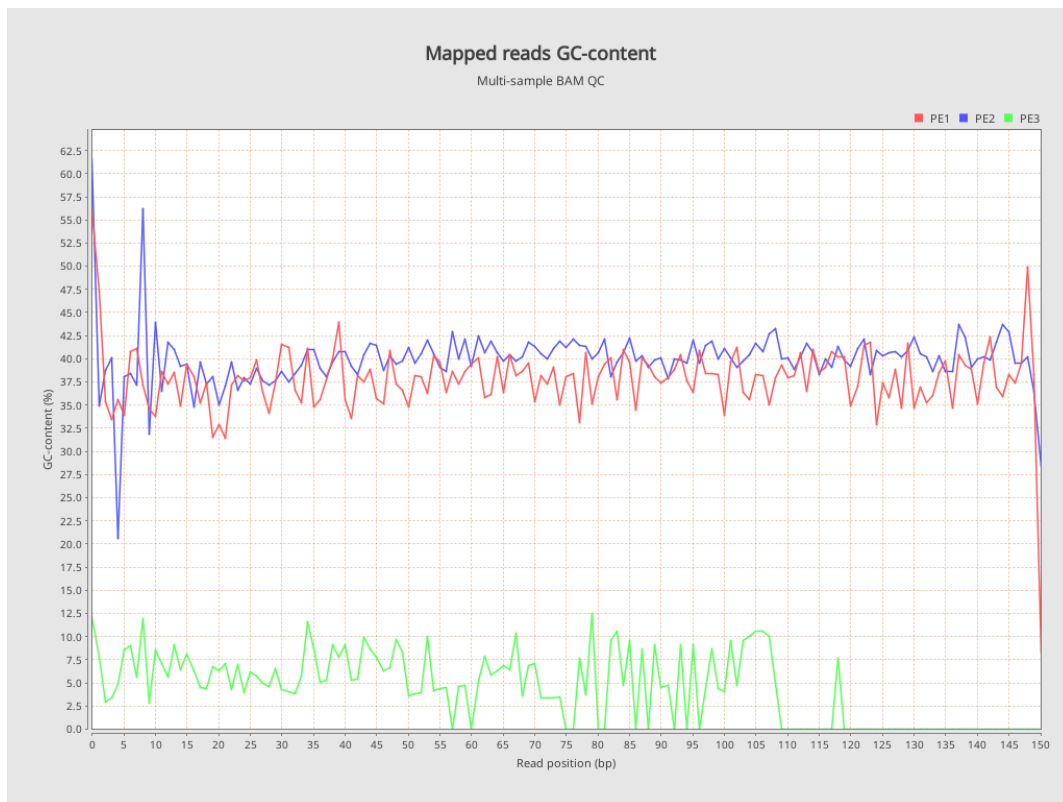
7. Results : Genome Fraction Coverage



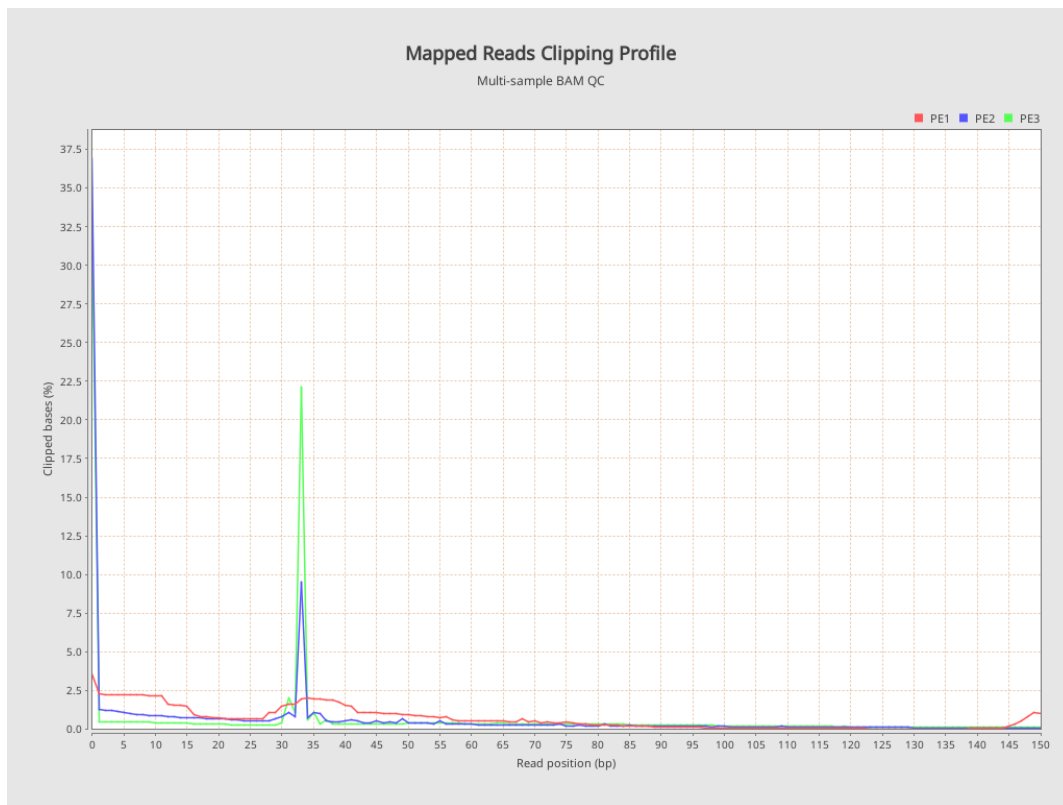
8. Results : Duplication Rate Histogram



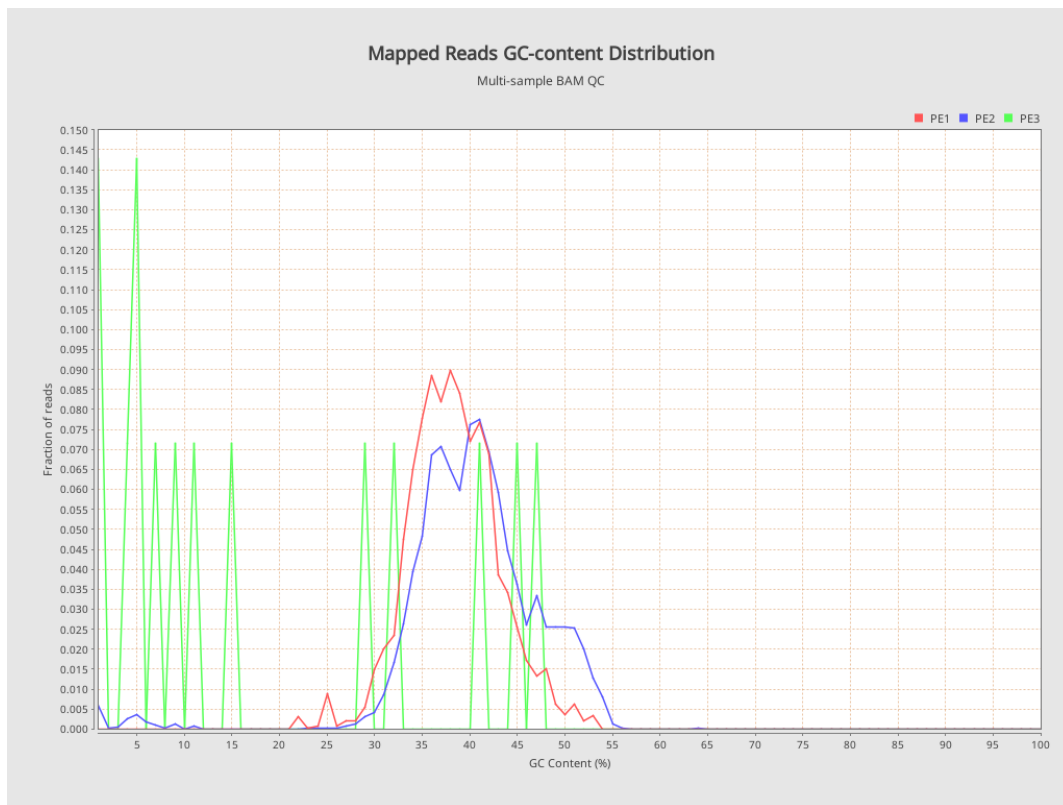
9. Results : Mapped reads GC-content



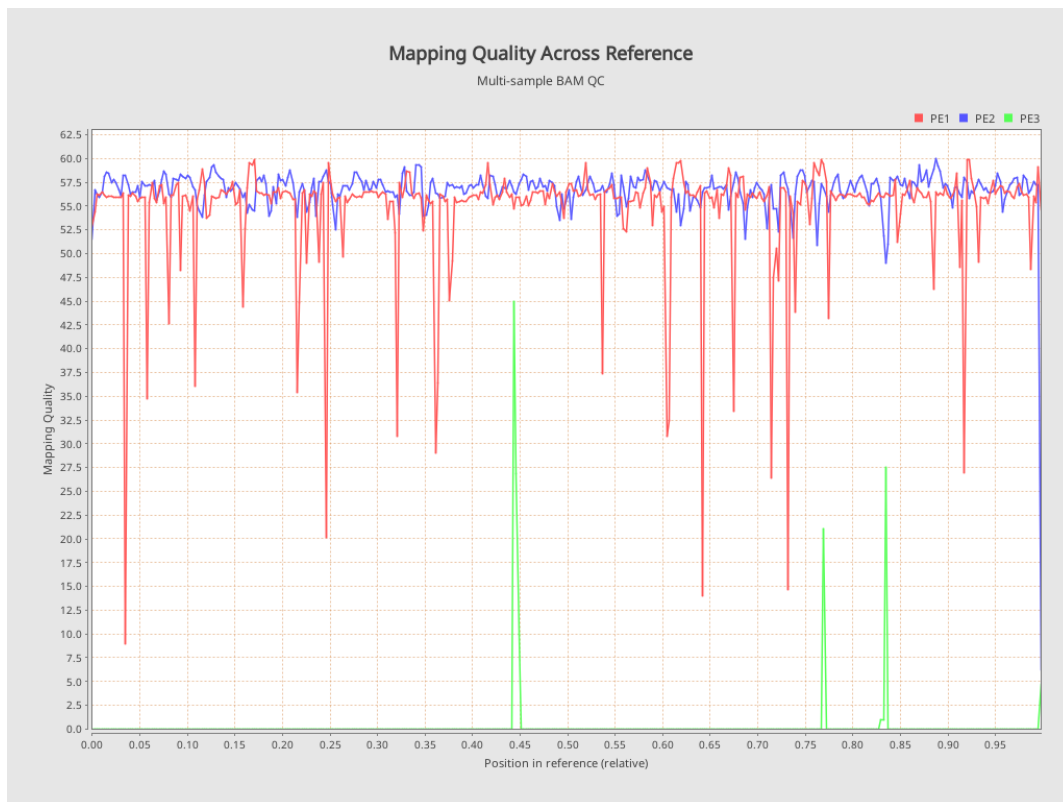
10. Results : Mapped Reads Clipping Profile



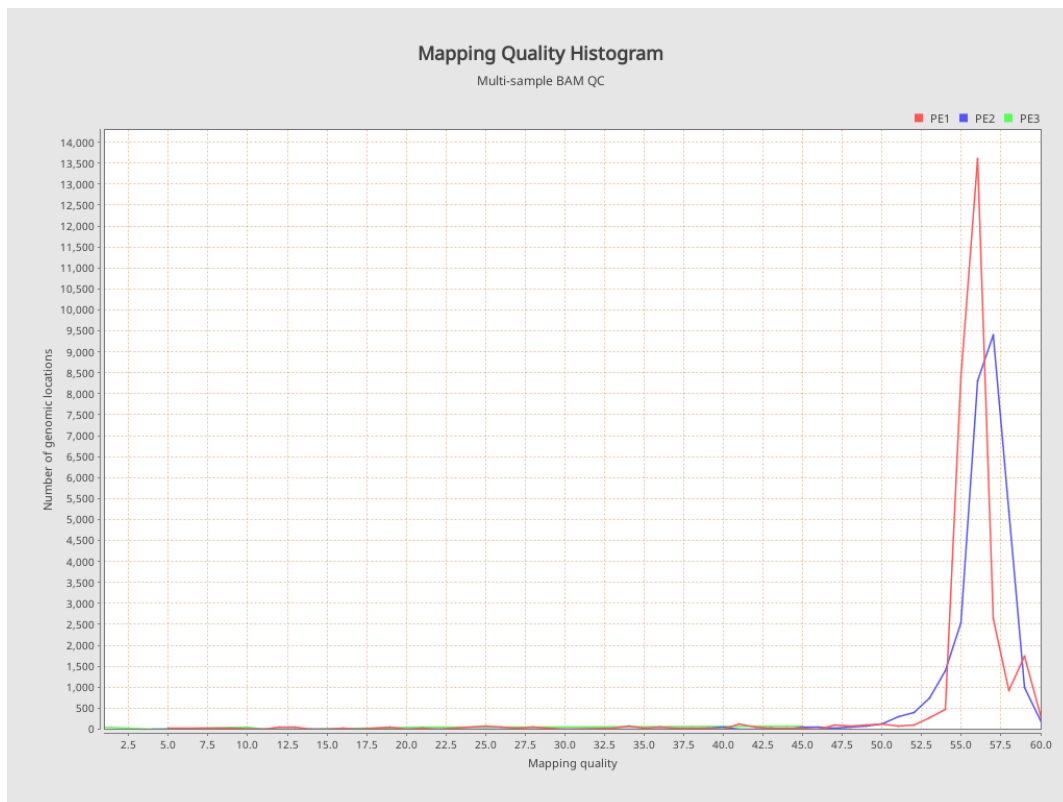
11. Results : Mapped Reads GC-content Distribution



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

