Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 07:52:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617667.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR617667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617667_1.fastq.gz SRR617667_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 07:52:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,139,578 / 94.19%
Unmapped reads	1,860,422 / 5.81%
Mapped paired reads	30,139,578 / 94.19%
Mapped reads, first in pair	15,155,286 / 47.36%
Mapped reads, second in pair	14,984,292 / 46.83%
Mapped reads, both in pair	29,544,598 / 92.33%
Mapped reads, singletons	594,980 / 1.86%
Secondary alignments	0
Supplementary alignments	144,400 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,861,502 / 21.44%
Duplication rate	10.61%
Clipped reads	6,345,767 / 19.83%

2.2. ACGT Content

Number/percentage of A's	872,712,981 / 29.84%
Number/percentage of C's	581,719,351 / 19.89%
Number/percentage of T's	869,980,277 / 29.75%
Number/percentage of G's	597,662,155 / 20.44%
Number/percentage of N's	2,140,652 / 0.07%

GC Percentage	40.33%

2.3. Coverage

Mean	0.9452
Standard Deviation	10.7013

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	32,983.62
Standard Deviation	1,659,685.94
P25/Median/P75	178 / 221 / 285

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	44,983,992
Insertions	453,978
Mapped reads with at least one insertion	1.48%
Deletions	1,068,257
Mapped reads with at least one deletion	3.47%
Homopolymer indels	47.6%

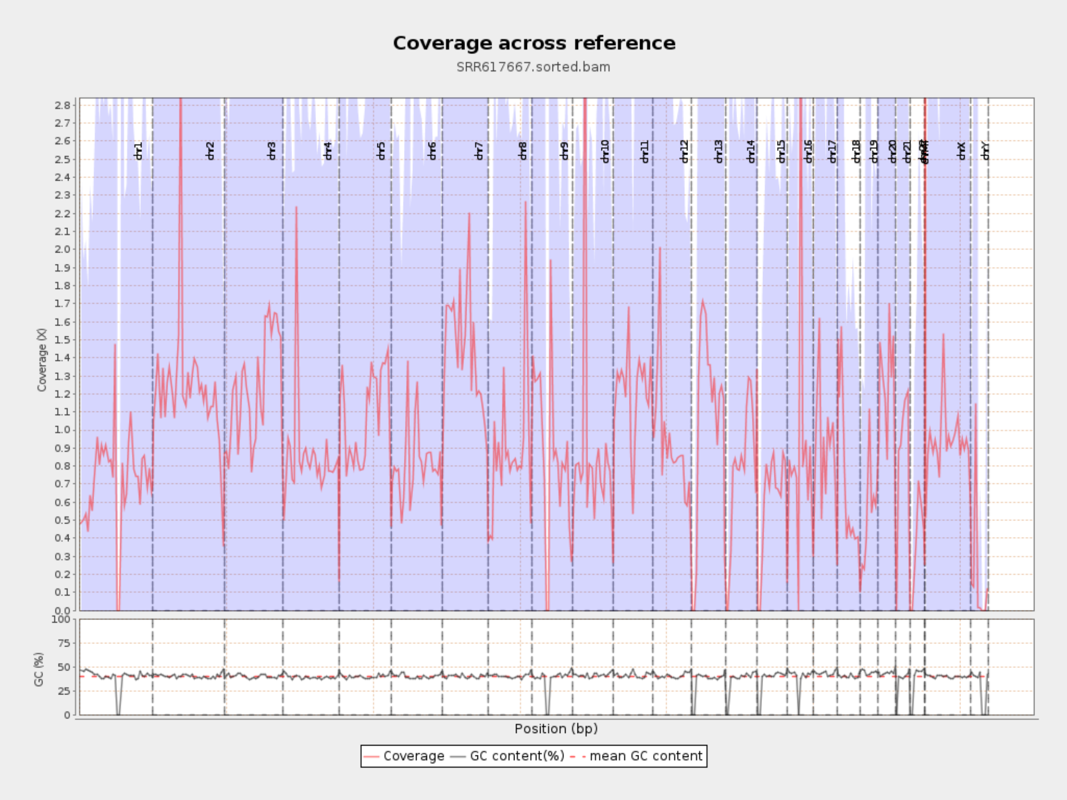
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

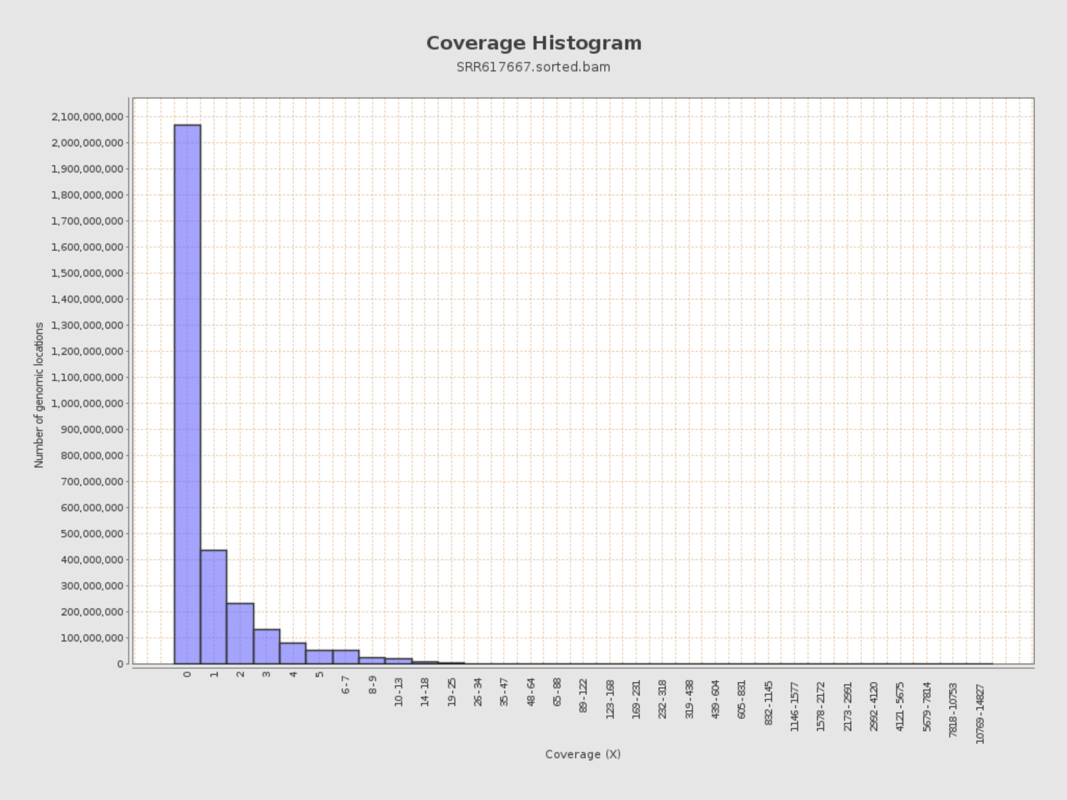
		bases	coverage	deviation
chr1	249250621	178990164	0.7181	10.247
chr2	243199373	302583623	1.2442	12.2063
chr3	198022430	245036216	1.2374	2.4716
chr4	191154276	163986848	0.8579	8.2787
chr5	180915260	193723136	1.0708	2.3205
chr6	171115067	141805615	0.8287	5.7464
chr7	159138663	229203854	1.4403	13.5565
chr8	146364022	130263227	0.89	4.0948
chr9	141213431	120128940	0.8507	20.6684
chr10	135534747	124156730	0.9161	21.8862
chr11	135006516	160871001	1.1916	12.0923
chr12	133851895	124988706	0.9338	2.1536
chr13	115169878	126044391	1.0944	2.2876
chr14	107349540	83536851	0.7782	2.4423
chr15	102531392	62351827	0.6081	1.5762
chr16	90354753	81379755	0.9007	17.0586
chr17	81195210	71533372	0.881	12.9041
chr18	78077248	54070215	0.6925	18.4569
chr19	59128983	30791707	0.5208	6.0323
chr20	63025520	78604891	1.2472	2.9906
chr21	48129895	42801594	0.8893	4.4026
chr22	51304566	18724405	0.365	1.2692
chrMT	16571	3058360	184.561	129.0223
chrX	155270560	145523155	0.9372	4.3483

chrY	59373566	11821201	0.1991	17.536

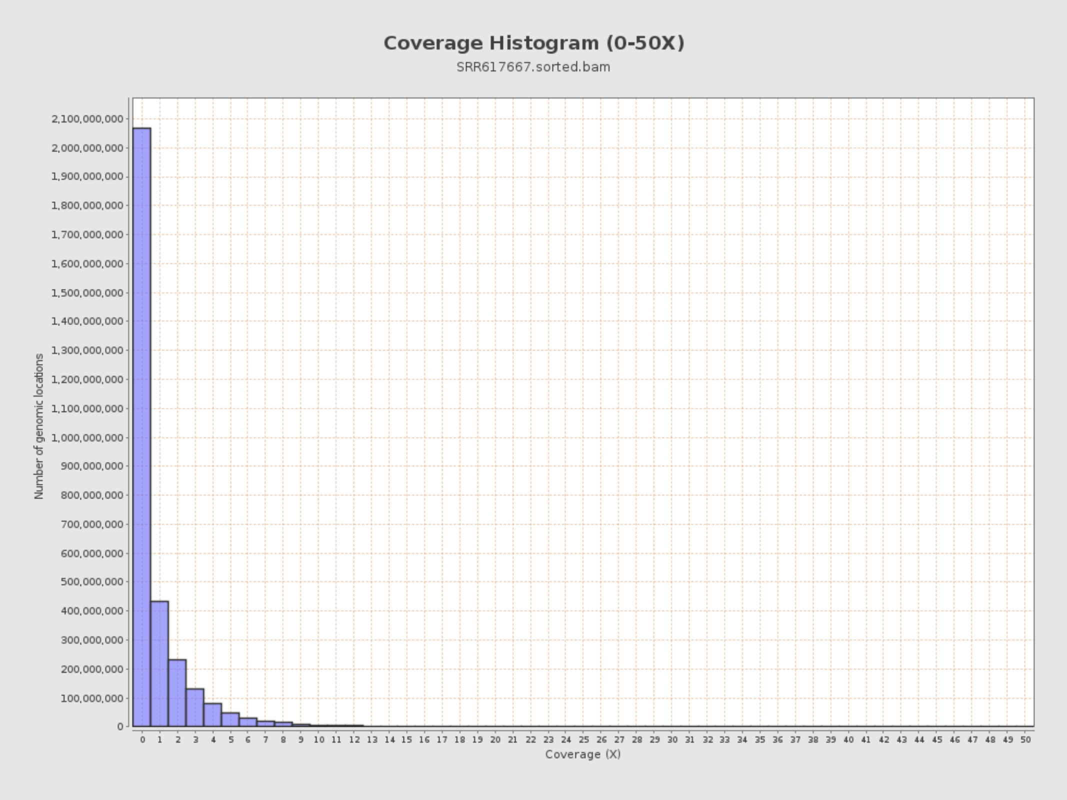
3. Results : Coverage across reference



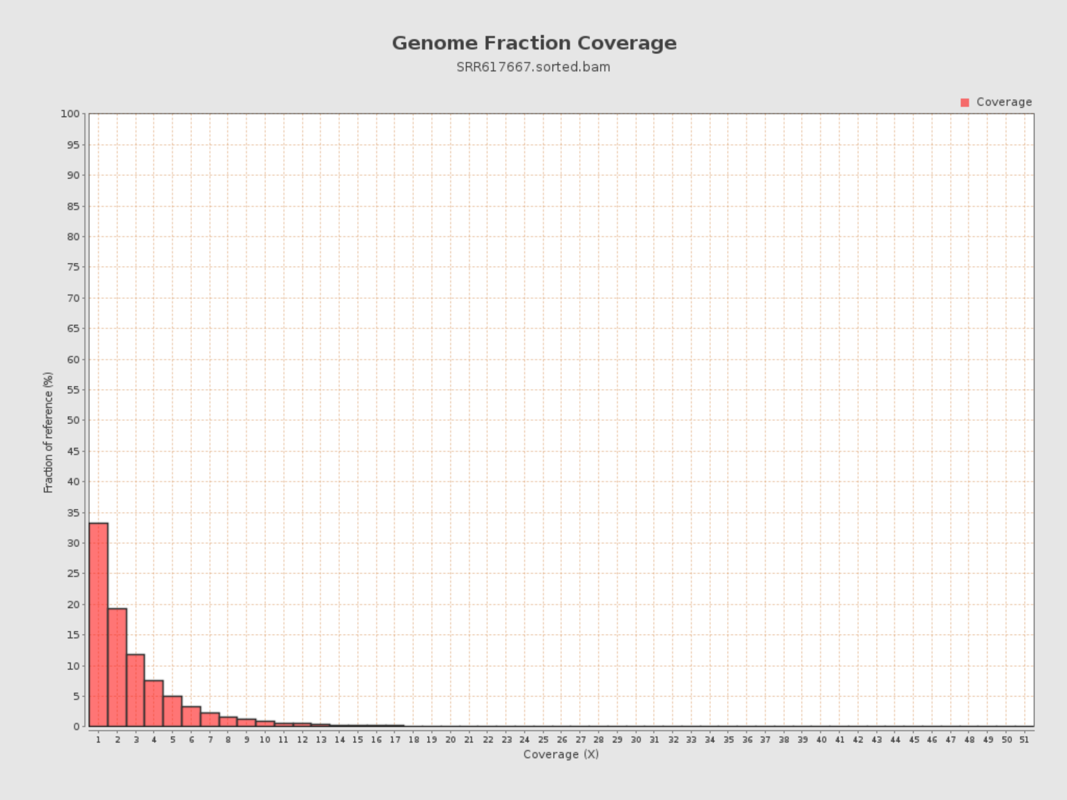
4. Results : Coverage Histogram



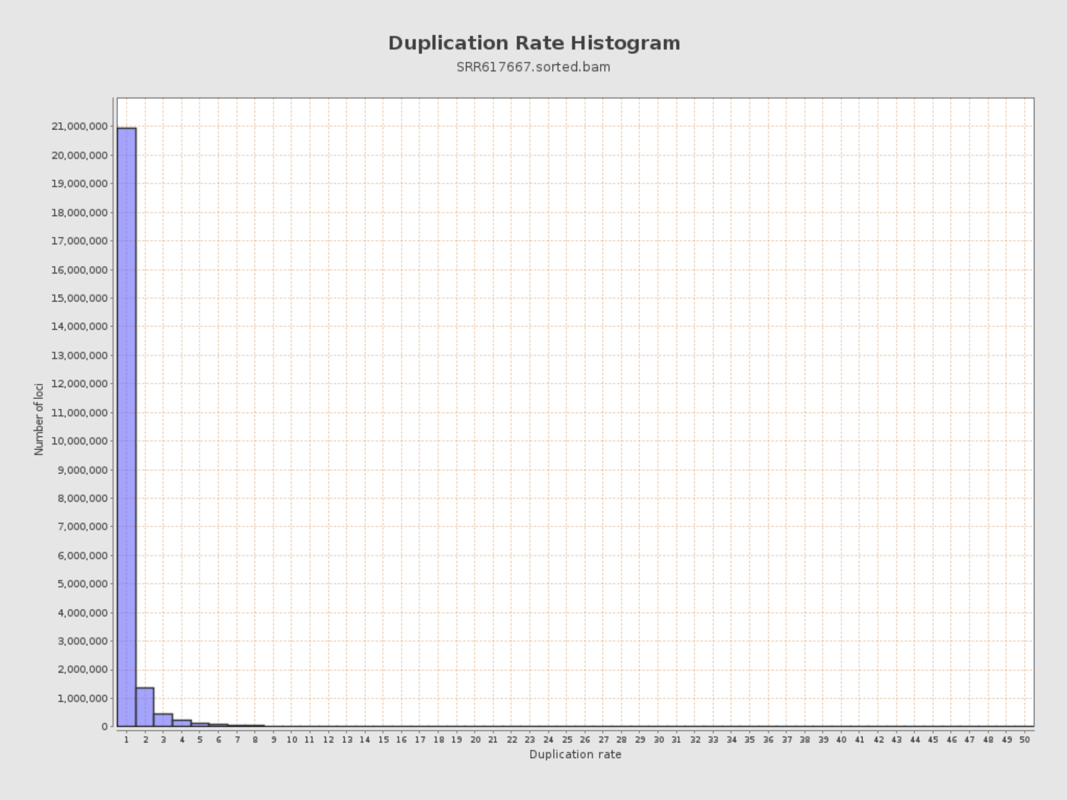
5. Results : Coverage Histogram (0-50X)



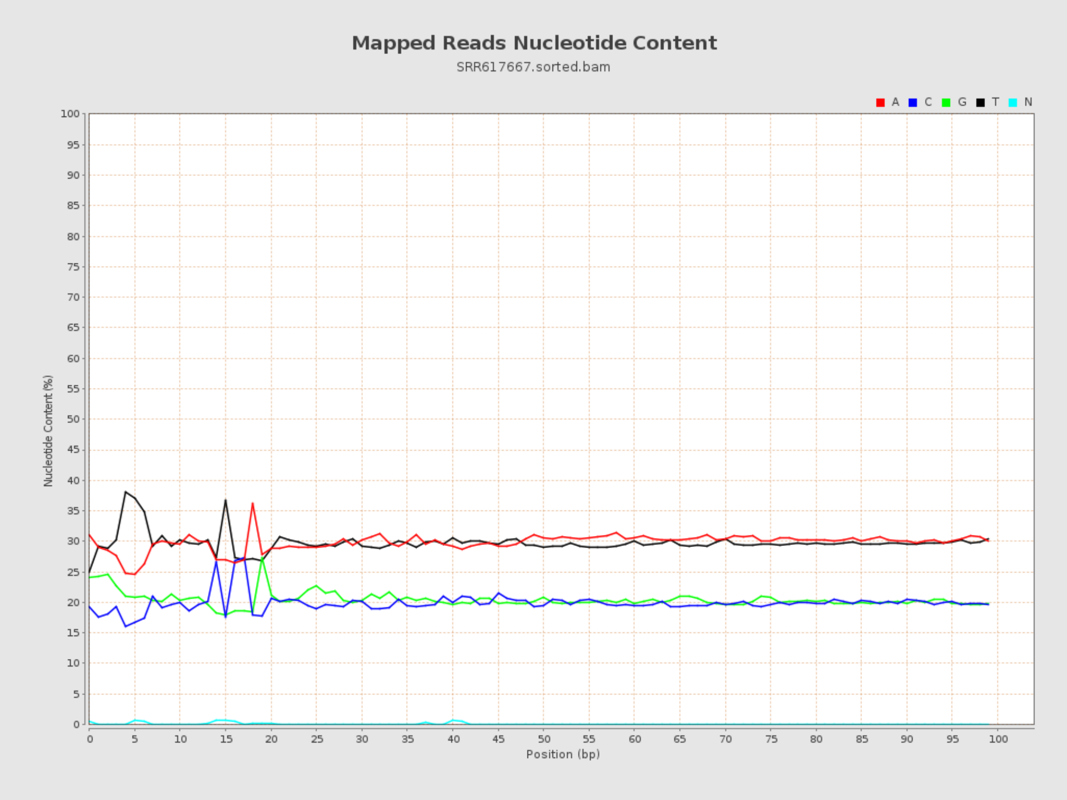
6. Results : Genome Fraction Coverage



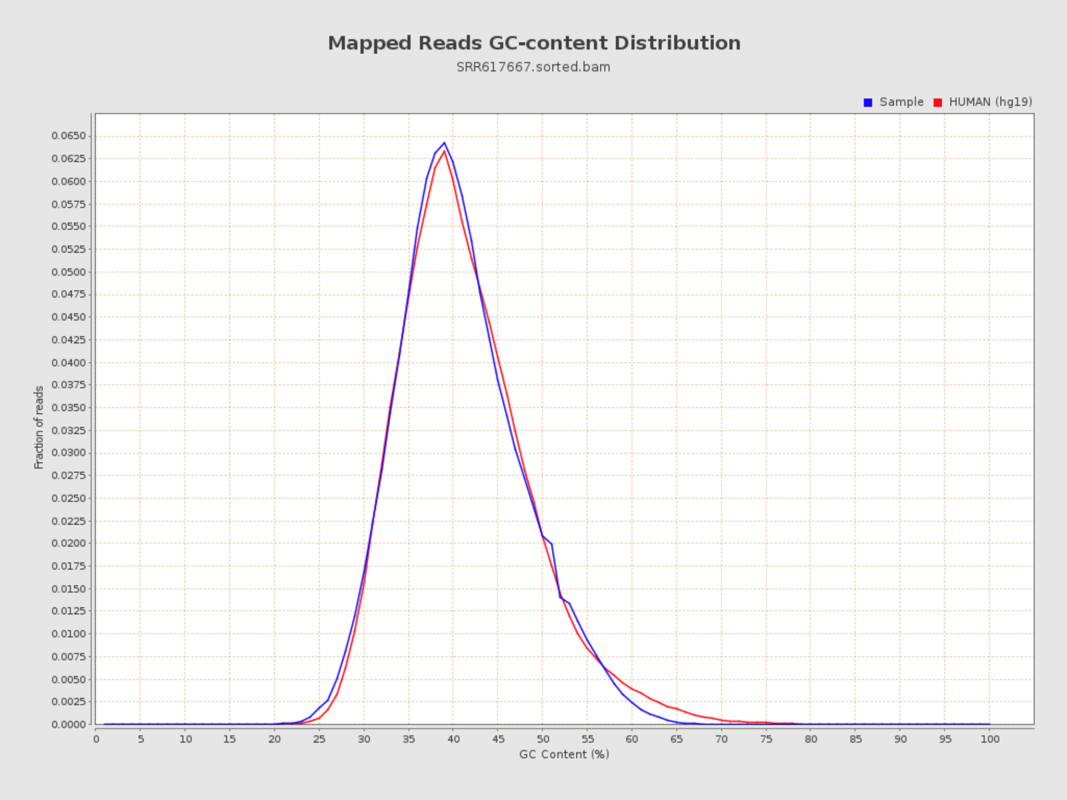
7. Results : Duplication Rate Histogram



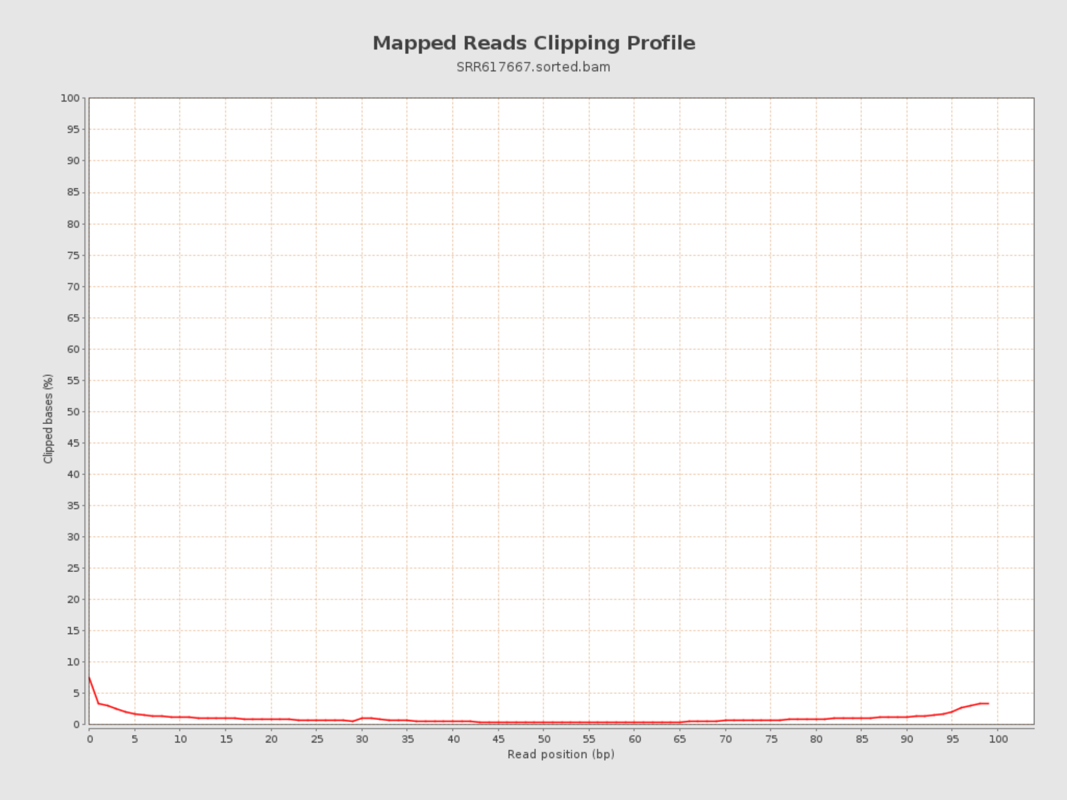
8. Results : Mapped Reads Nucleotide Content



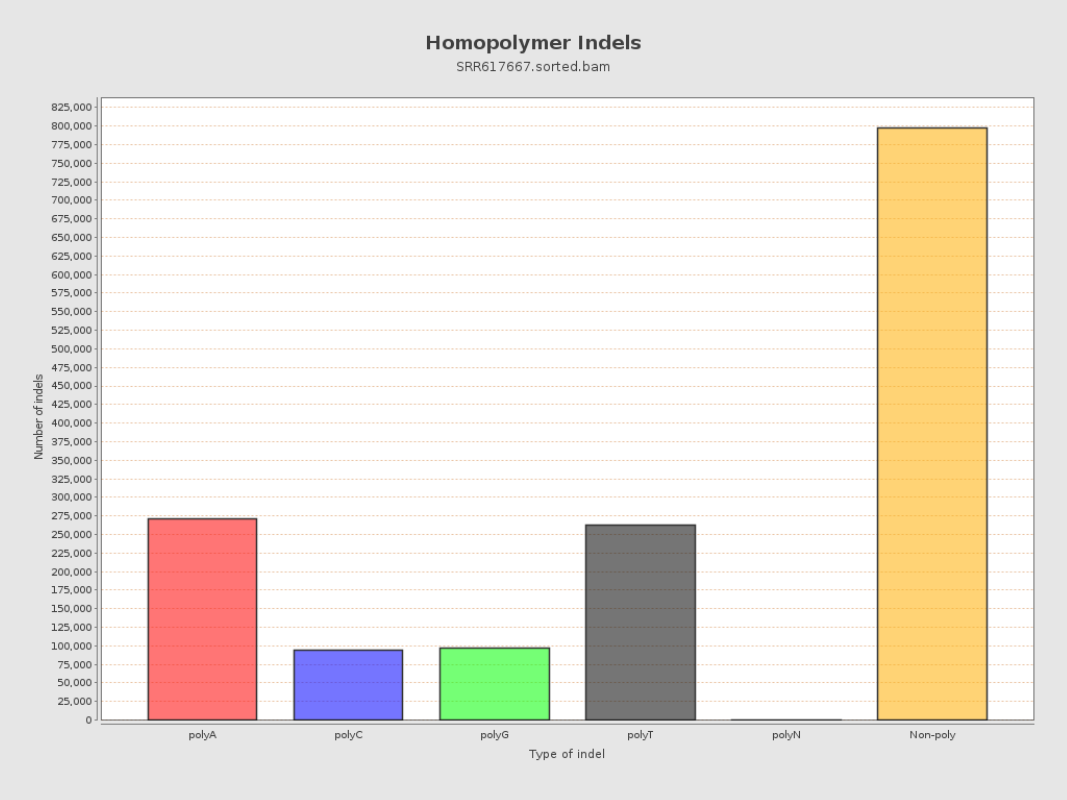
9. Results : Mapped Reads GC-content Distribution



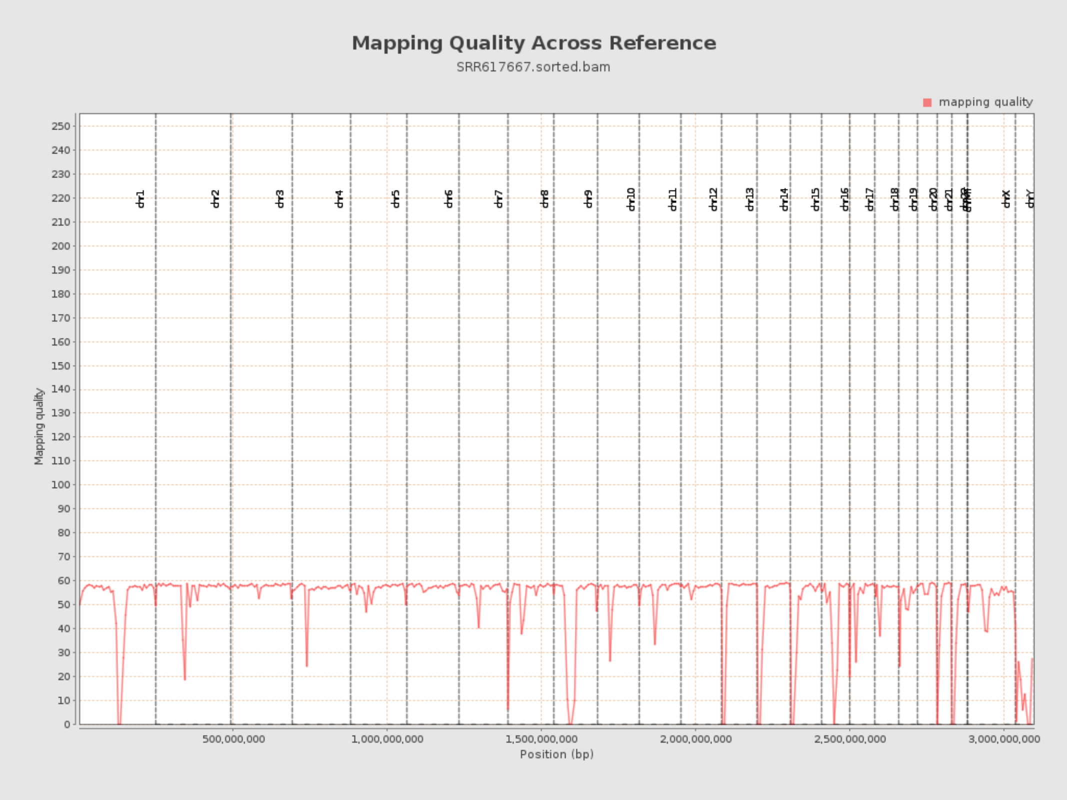
10. Results : Mapped Reads Clipping Profile



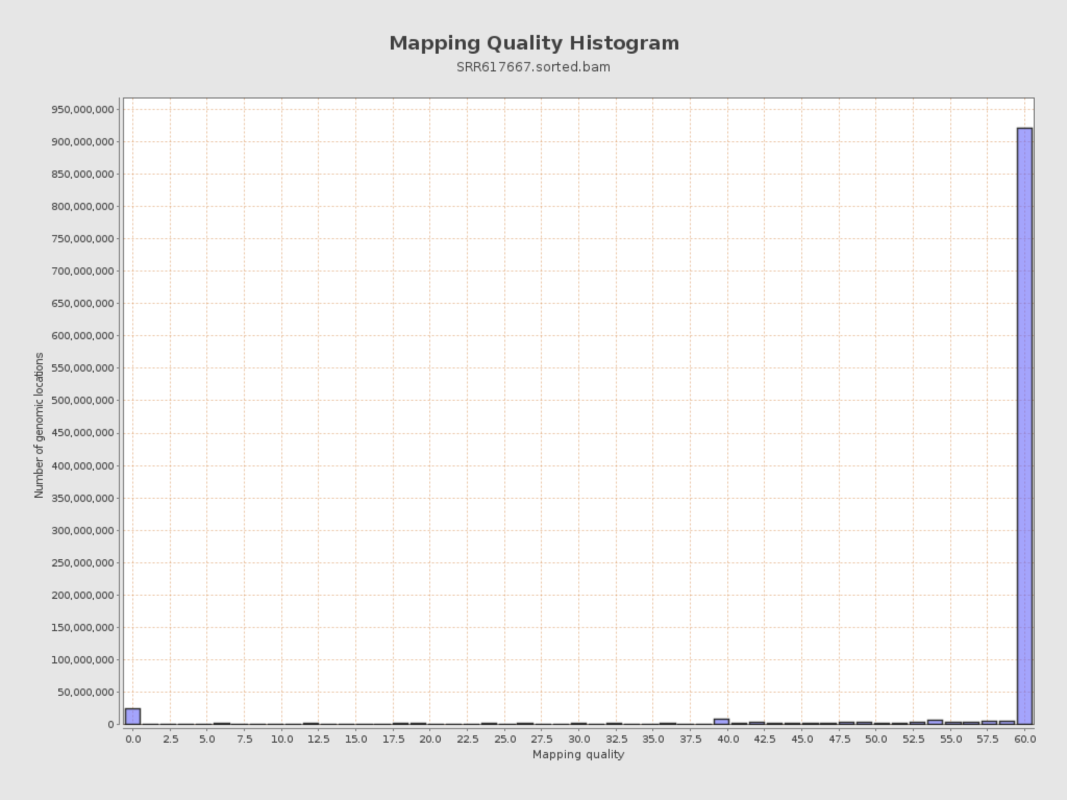
11. Results : Homopolymer Indels



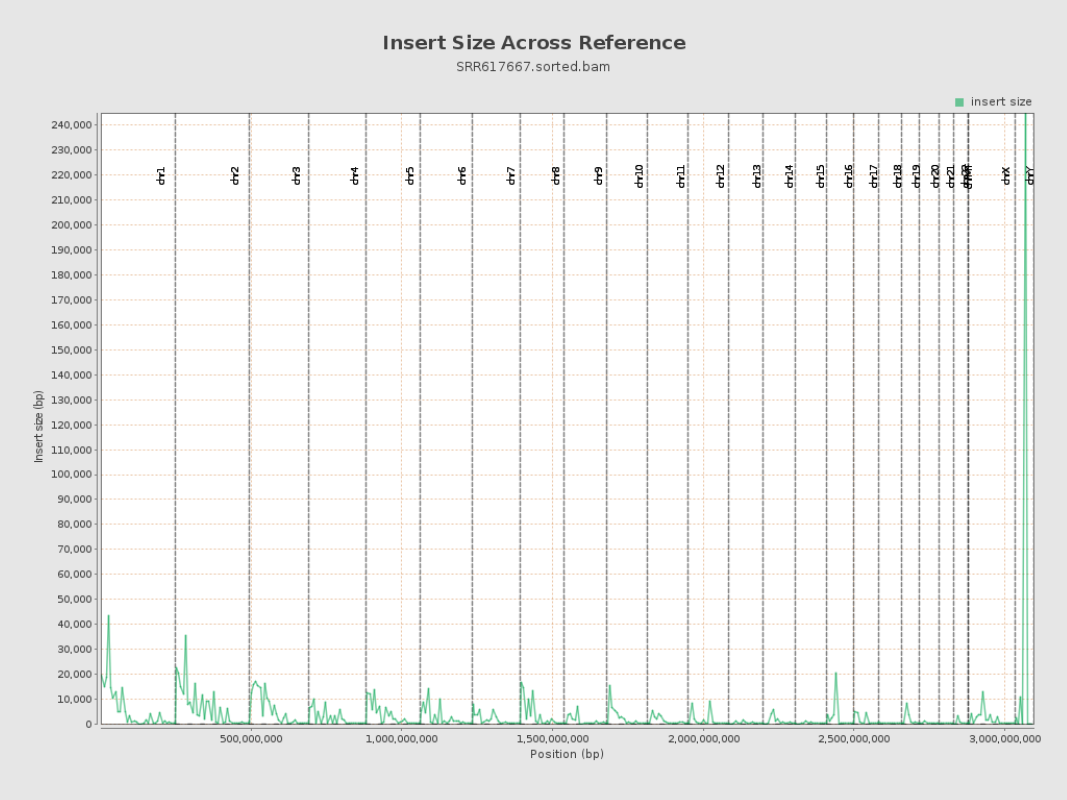
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram