Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 01:27:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617699.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_SRR8617699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617699_1.fastq.gz SRR8617699_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 01:27:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,069,220
Mapped reads	55,174,318 / 98.4%
Unmapped reads	894,902 / 1.6%
Mapped paired reads	55,174,318 / 98.4%
Mapped reads, first in pair	27,788,405 / 49.56%
Mapped reads, second in pair	27,385,913 / 48.84%
Mapped reads, both in pair	54,620,548 / 97.42%
Mapped reads, singletons	553,770 / 0.99%
Secondary alignments	0
Supplementary alignments	700,488 / 1.25%
Read min/max/mean length	30 / 150 / 150.59
Duplicated reads (estimated)	17,909,812 / 31.94%
Duplication rate	24.4%
Clipped reads	25,020,624 / 44.62%

2.2. ACGT Content

Number/percentage of A's	2,190,456,045 / 29.24%
Number/percentage of C's	1,421,061,426 / 18.97%
Number/percentage of T's	2,245,063,647 / 29.97%
Number/percentage of G's	1,633,379,688 / 21.81%
Number/percentage of N's	305,910 / 0%

GC Percentage	40.78%

2.3. Coverage

Mean	2.4211
Standard Deviation	25.1383

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	71,628.61
Standard Deviation	2,526,403.23
P25/Median/P75	220 / 275 / 346

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	82,938,944
Insertions	1,167,099
Mapped reads with at least one insertion	2.01%
Deletions	2,530,250
Mapped reads with at least one deletion	4.43%
Homopolymer indels	47.38%

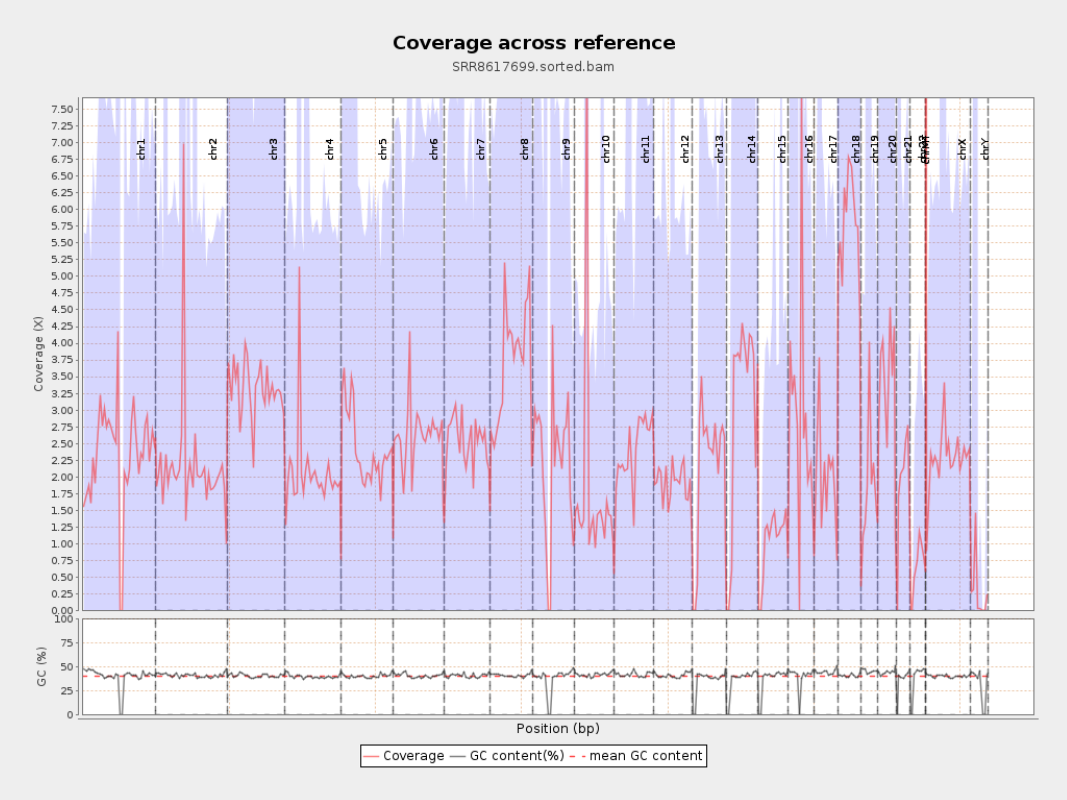
2.7. Chromosome stats

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

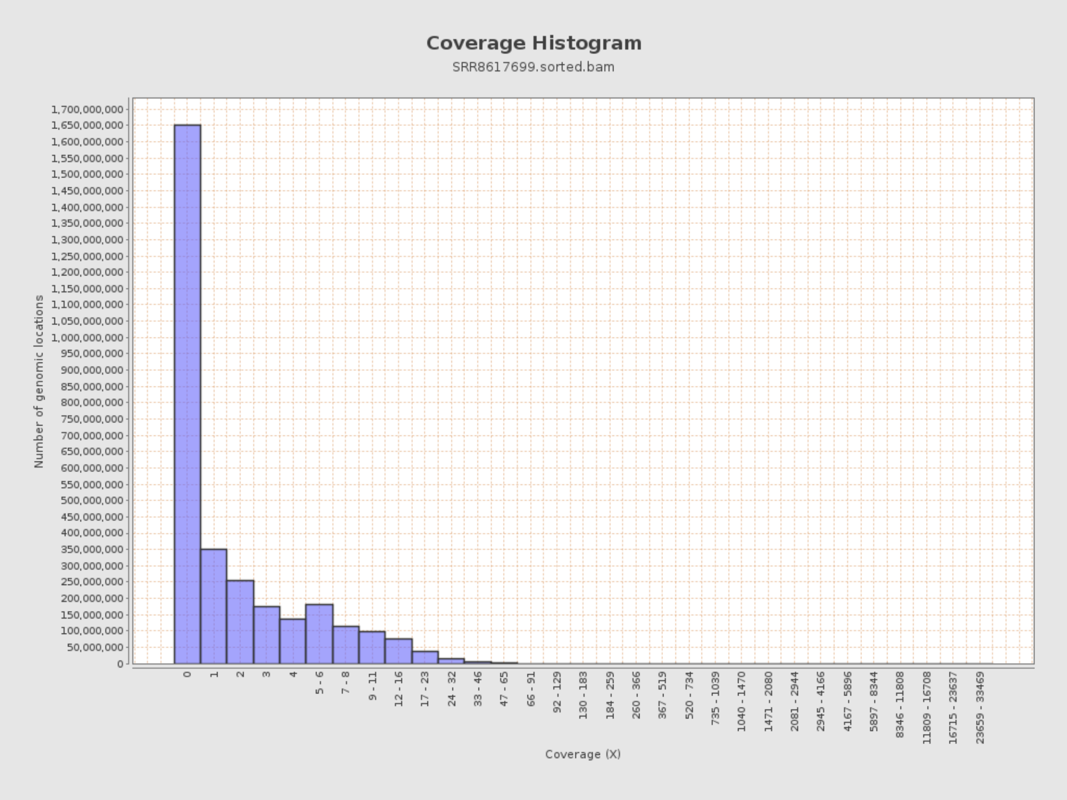
		bases	**coverage**	**deviation**
chr1	249250621	581386740	2.3325	31.2199
chr2	243199373	524577415	2.157	31.1318
chr3	198022430	654805868	3.3067	5.3534
chr4	191154276	395550731	2.0693	24.2302
chr5	180915260	435715414	2.4084	4.8205
chr6	171115067	450217795	2.6311	17.7555
chr7	159138663	401049633	2.5201	18.7509
chr8	146364022	542236397	3.7047	13.5762
chr9	141213431	312817789	2.2152	52.0841
chr10	135534747	234554871	1.7306	54.7475
chr11	135006516	320374846	2.373	15.718
chr12	133851895	254854153	1.904	7.2046
chr13	115169878	250736657	2.1771	4.1585
chr14	107349540	327288157	3.0488	5.7396
chr15	102531392	105430408	1.0283	3.7148
chr16	90354753	254594082	2.8177	37.6626
chr17	81195210	166531897	2.051	29.7318
chr18	78077248	456099479	5.8416	36.7831
chr19	59128983	110835082	1.8745	16.8824
chr20	63025520	219106252	3.4765	8.8306
chr21	48129895	92194937	1.9155	10.9027
chr22	51304566	34023099	0.6632	2.2582
chrMT	16571	835286	50.4065	30.6239
chrX	155270560	351860176	2.2661	9.5978

chrY	59373566	17291118	0.2912	23.265

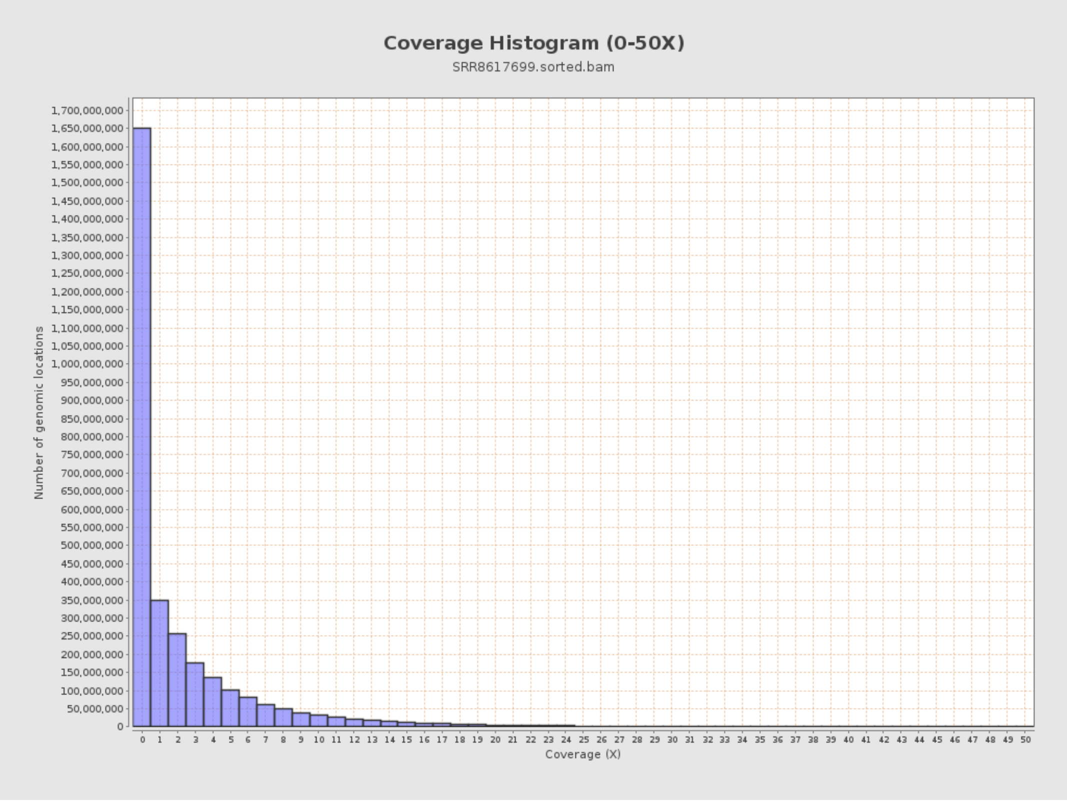
3. Results : Coverage across reference



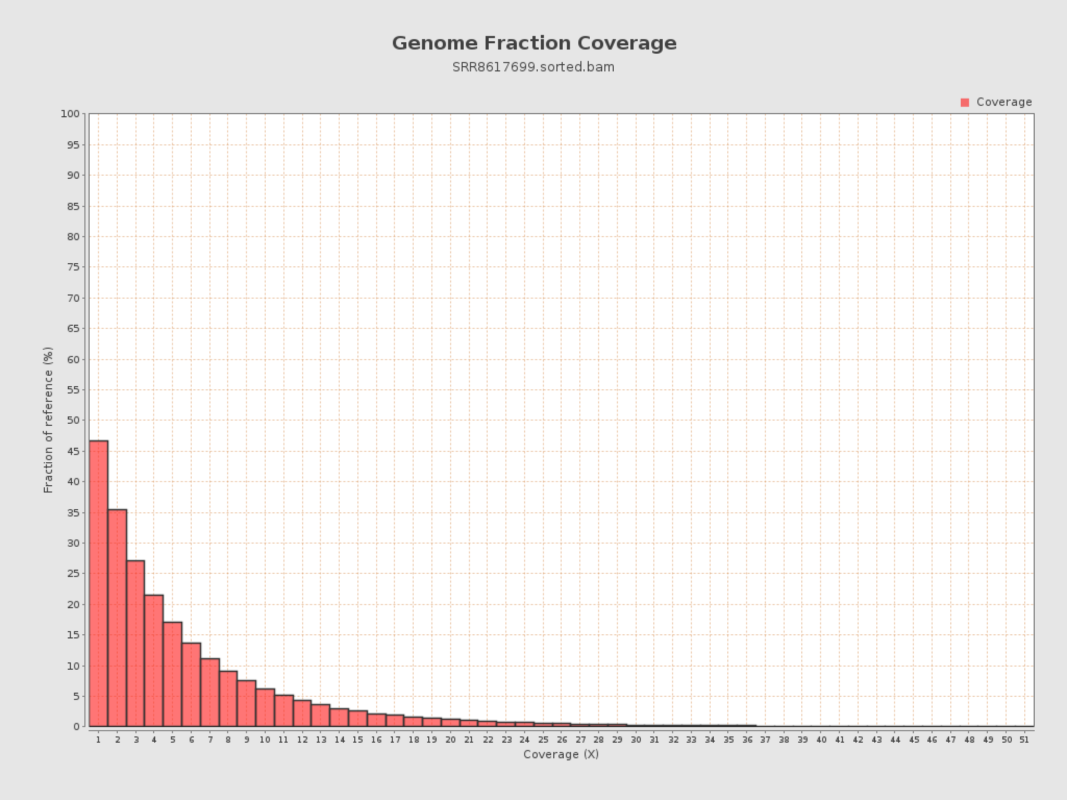
4. Results : Coverage Histogram



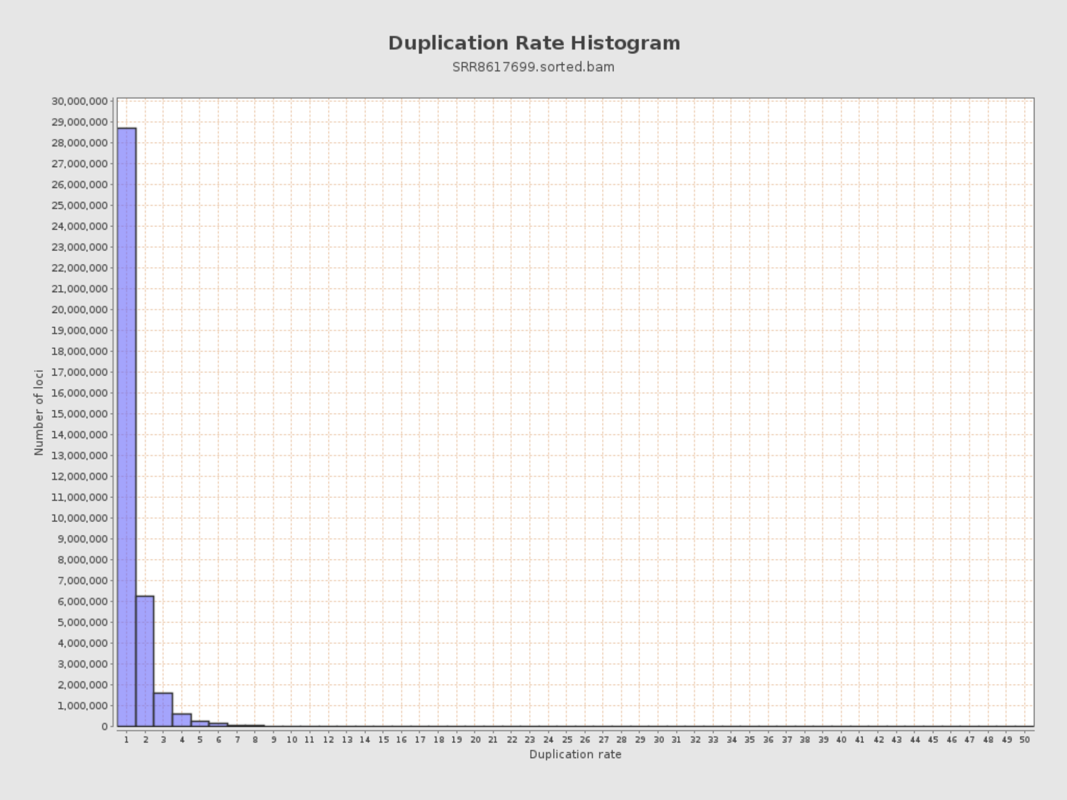
5. Results : Coverage Histogram (0-50X)



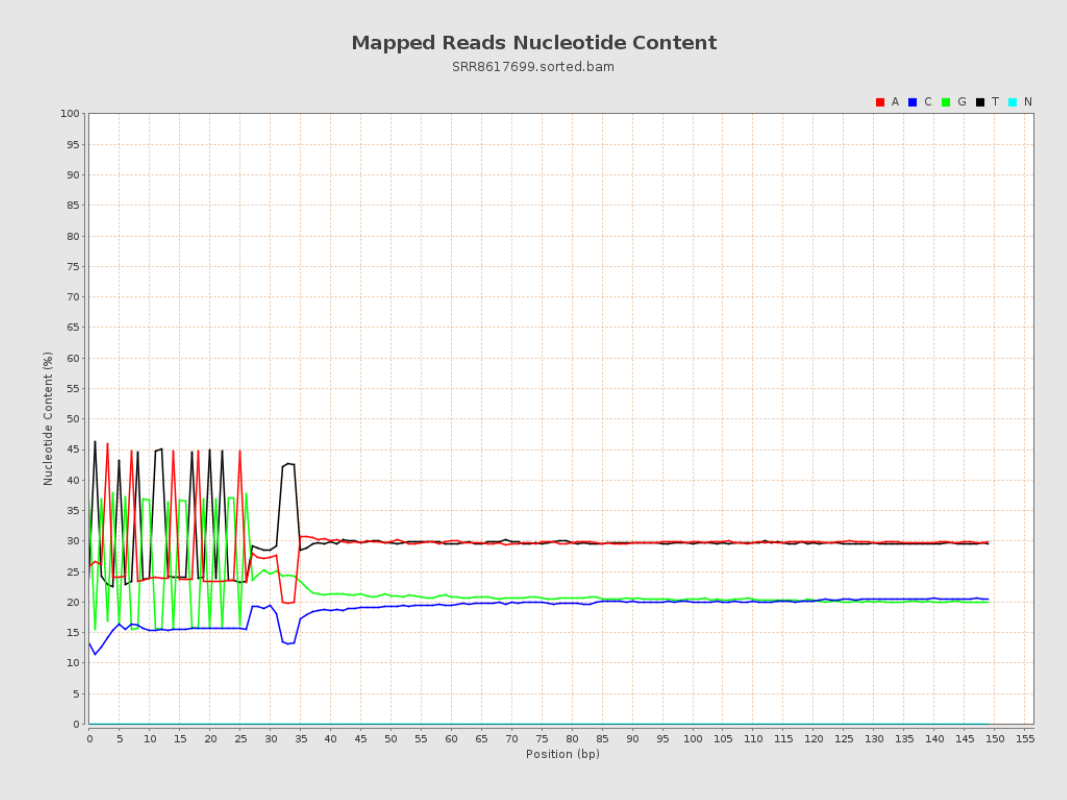
6. Results : Genome Fraction Coverage



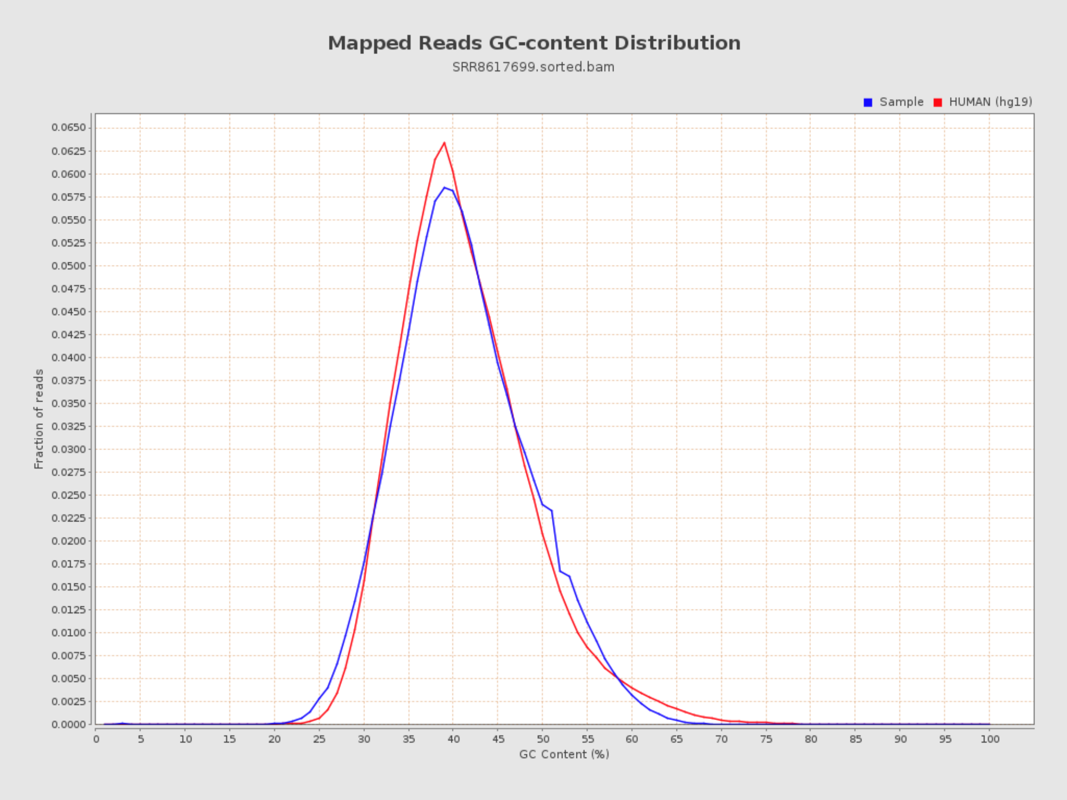
7. Results : Duplication Rate Histogram



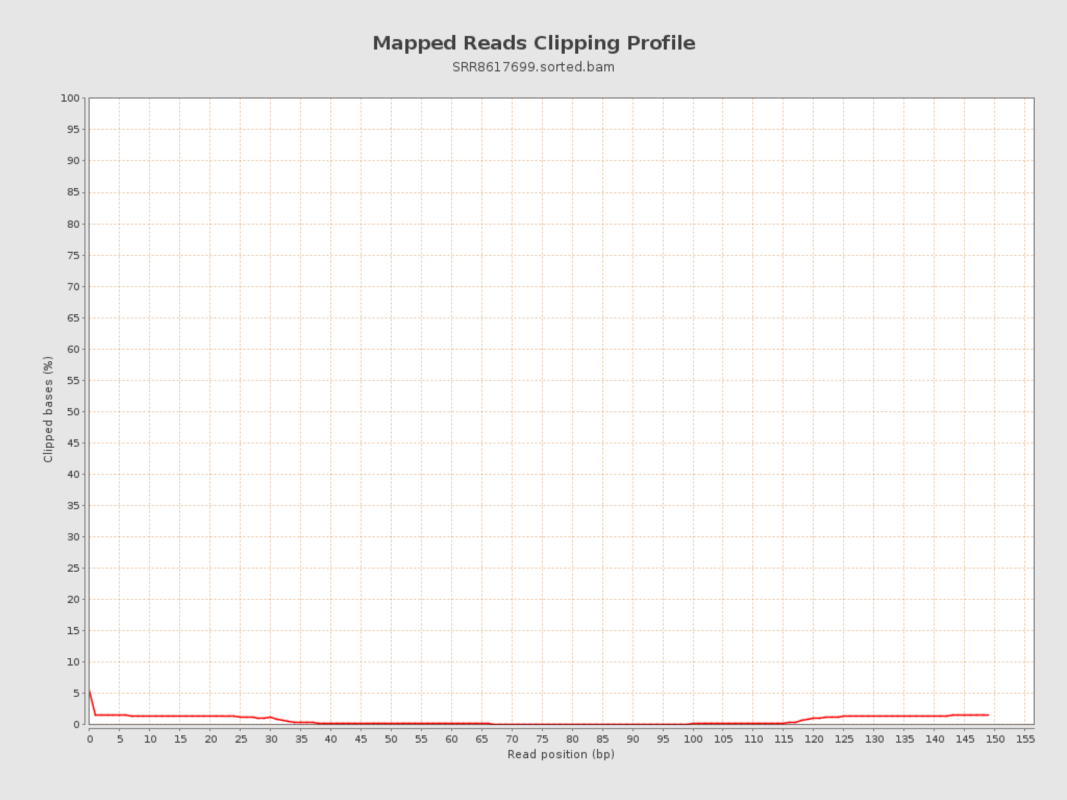
8. Results : Mapped Reads Nucleotide Content



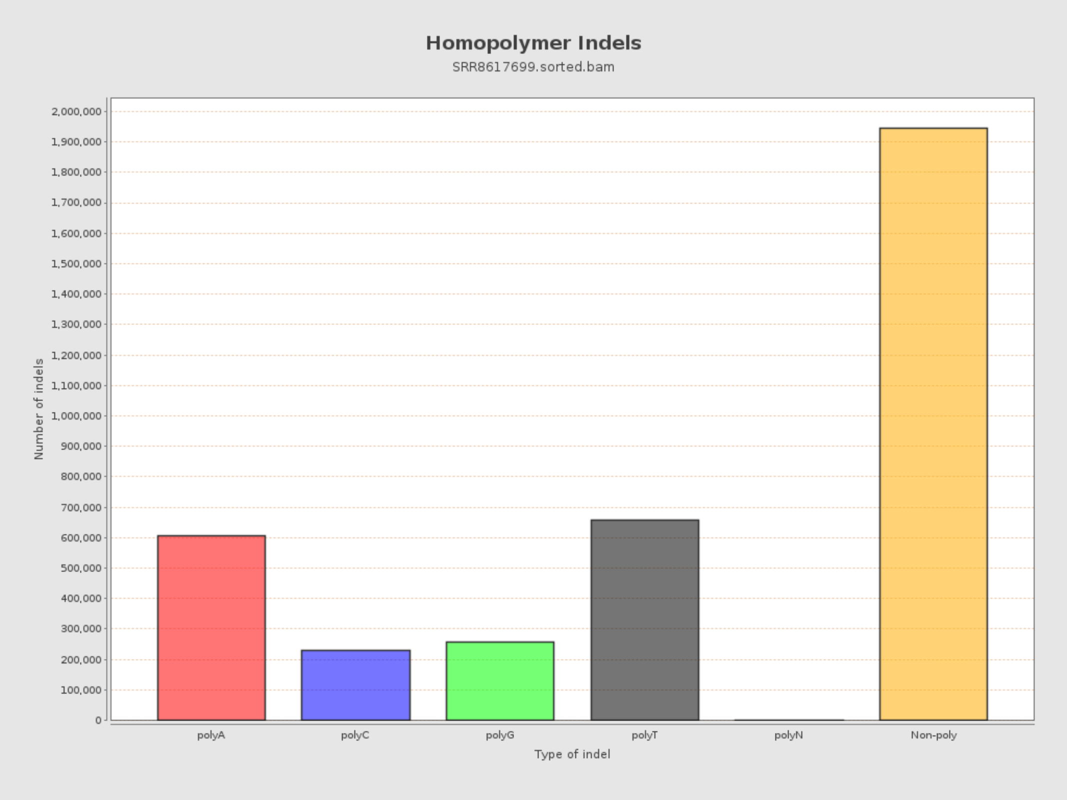
9. Results : Mapped Reads GC-content Distribution



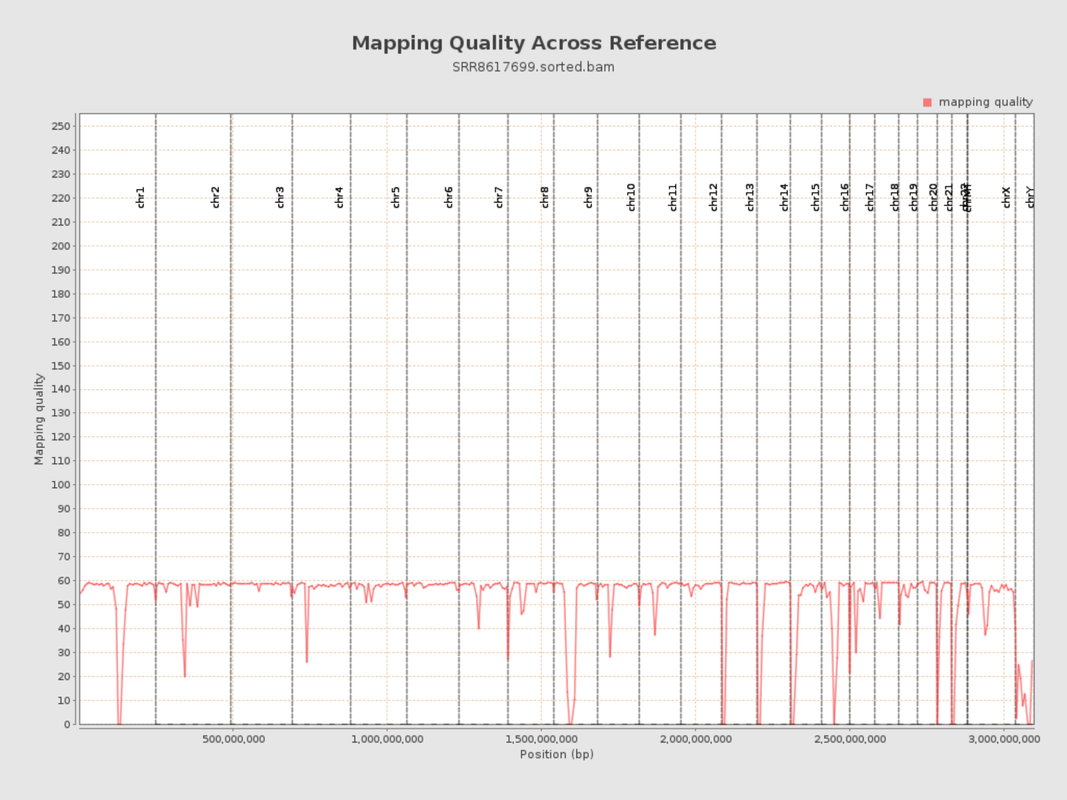
10. Results : Mapped Reads Clipping Profile



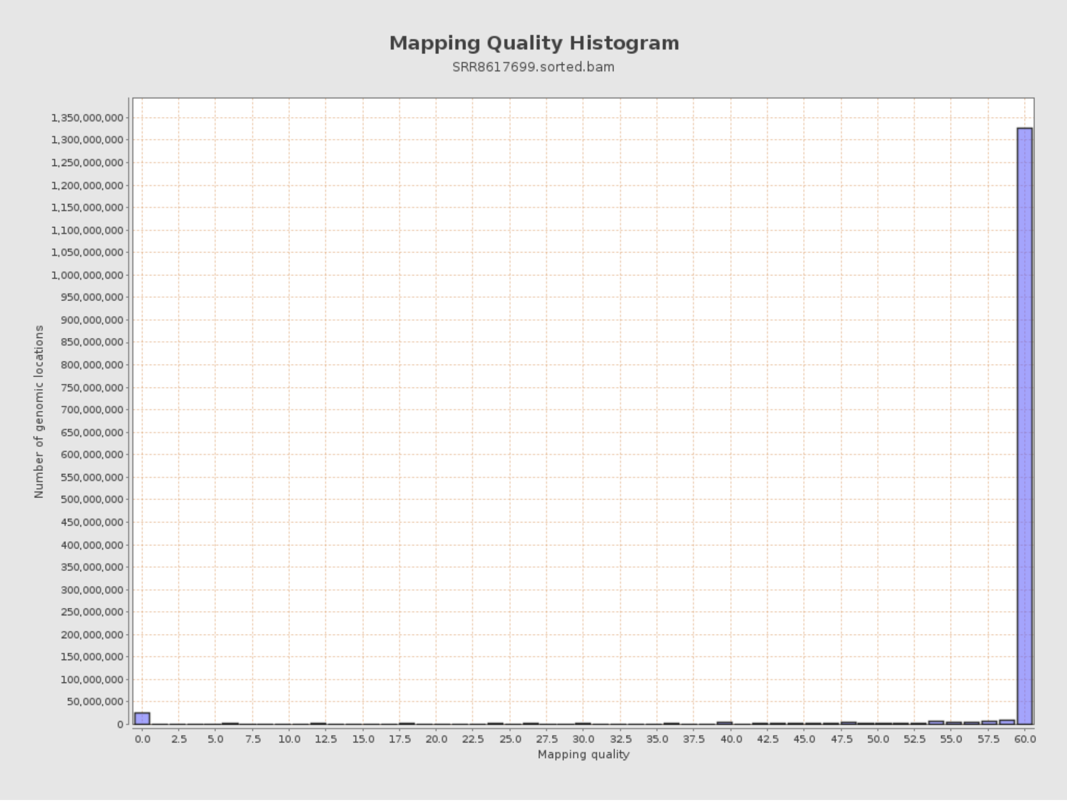
11. Results : Homopolymer Indels



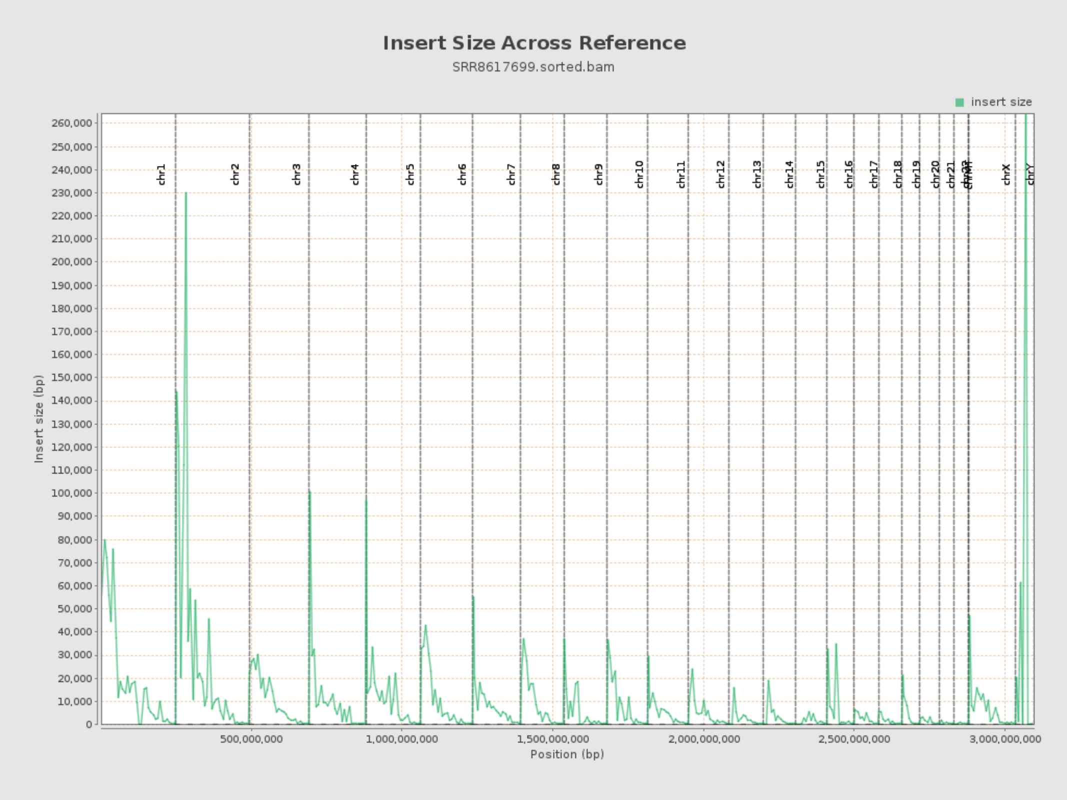
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram