Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 18:25:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617599.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_SRR8617599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617599_1.fastq.gz SRR8617599_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 18:25:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,890,948
Mapped reads	55,285,885 / 98.92%
Unmapped reads	605,063 / 1.08%
Mapped paired reads	55,285,885 / 98.92%
Mapped reads, first in pair	27,797,112 / 49.73%
Mapped reads, second in pair	27,488,773 / 49.18%
Mapped reads, both in pair	54,878,416 / 98.19%
Mapped reads, singletons	407,469 / 0.73%
Secondary alignments	0
Supplementary alignments	816,951 / 1.46%
Read min/max/mean length	30 / 150 / 150.7
Duplicated reads (estimated)	14,911,313 / 26.68%
Duplication rate	20.59%
Clipped reads	25,940,862 / 46.41%

2.2. ACGT Content

Number/percentage of A's	2,197,760,608 / 29.38%
Number/percentage of C's	1,398,083,995 / 18.69%
Number/percentage of T's	2,261,273,385 / 30.23%
Number/percentage of G's	1,622,955,647 / 21.7%
Number/percentage of N's	296,510 / 0%

GC Percentage	40.39%

2.3. Coverage

Mean	2.4177
Standard Deviation	31.8923

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	89,515.19
Standard Deviation	2,906,490.38
P25/Median/P75	226 / 281 / 352

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	73,946,264
Insertions	1,017,875
Mapped reads with at least one insertion	1.76%
Deletions	2,143,381
Mapped reads with at least one deletion	3.75%
Homopolymer indels	46.73%

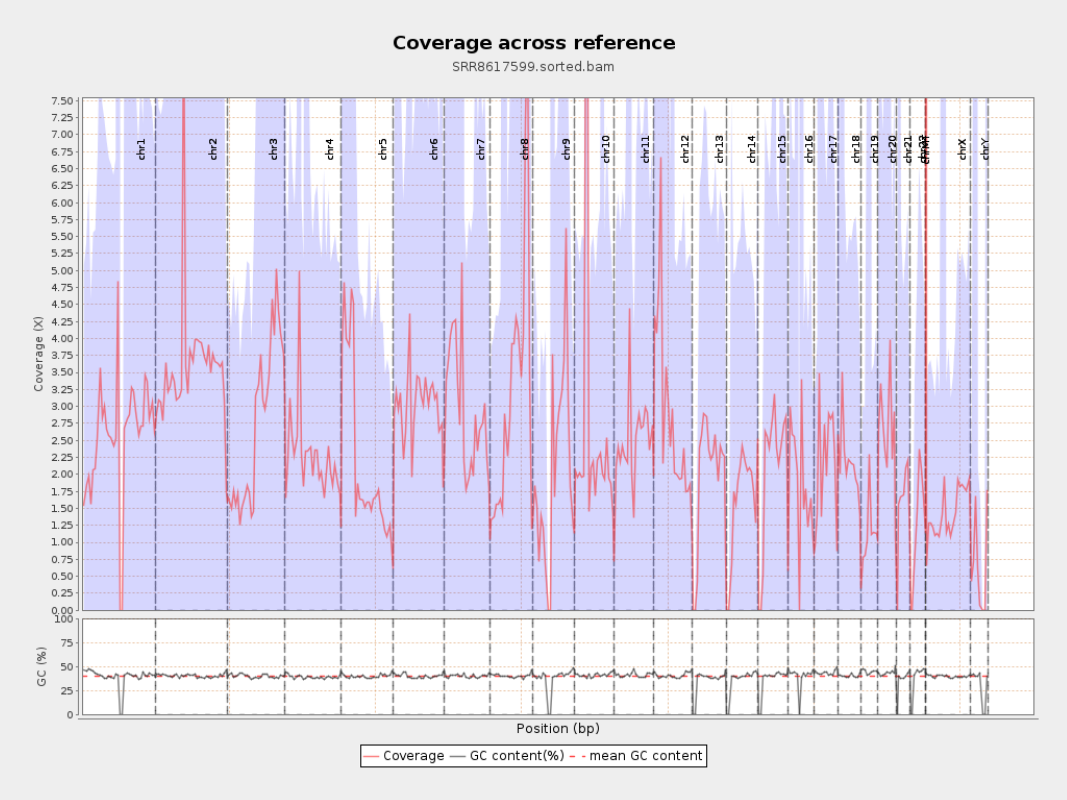
2.7. Chromosome stats

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

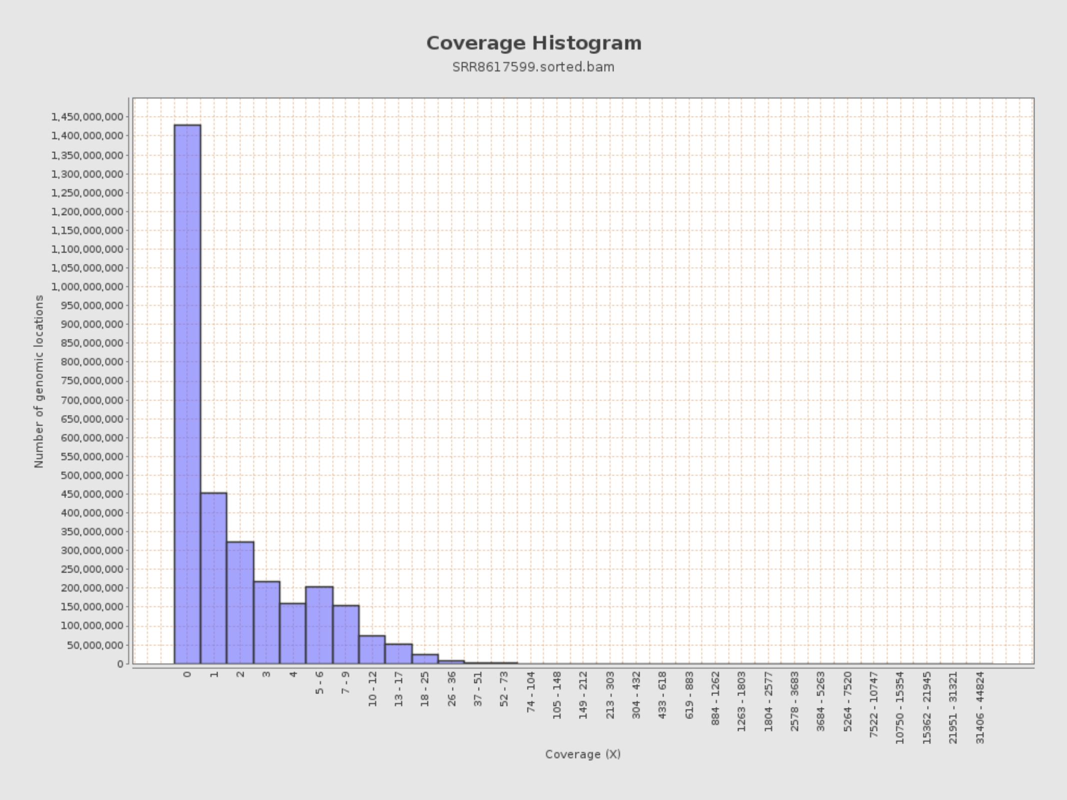
		bases	coverage	deviation
chr1	249250621	637115694	2.5561	33.2693
chr2	243199373	883267011	3.6319	34.4561
chr3	198022430	534952767	2.7015	4.7914
chr4	191154276	436925326	2.2857	19.8182
chr5	180915260	394906741	2.1828	4.2613
chr6	171115067	520378661	3.0411	12.5868
chr7	159138663	462703122	2.9075	45.6516
chr8	146364022	473673302	3.2363	9.1017
chr9	141213431	288526910	2.0432	47.2617
chr10	135534747	355899466	2.6259	99.2252
chr11	135006516	338052583	2.504	37.2684
chr12	133851895	385107170	2.8771	7.8387
chr13	115169878	229690412	1.9944	3.3922
chr14	107349540	171532058	1.5979	3.425
chr15	102531392	212296142	2.0705	4.6633
chr16	90354753	163864325	1.8136	15.7244
chr17	81195210	179301301	2.2083	34.444
chr18	78077248	171979639	2.2027	37.1142
chr19	59128983	67419944	1.1402	17.723
chr20	63025520	171070155	2.7143	6.6092
chr21	48129895	76153294	1.5822	7.6311
chr22	51304566	65754792	1.2817	3.0369
chrMT	16571	2663617	160.7397	99.5899
chrX	155270560	221608416	1.4272	8.2895

chrY	59373566	39737265	0.6693	16.6571

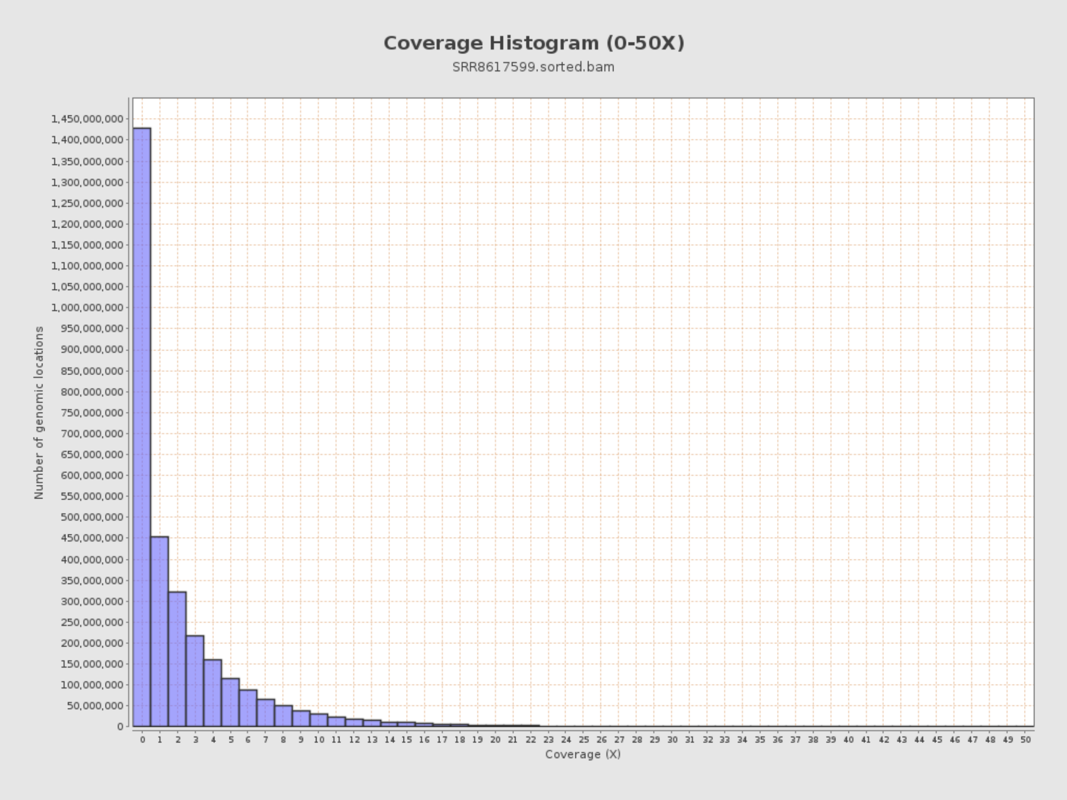
3. Results : Coverage across reference



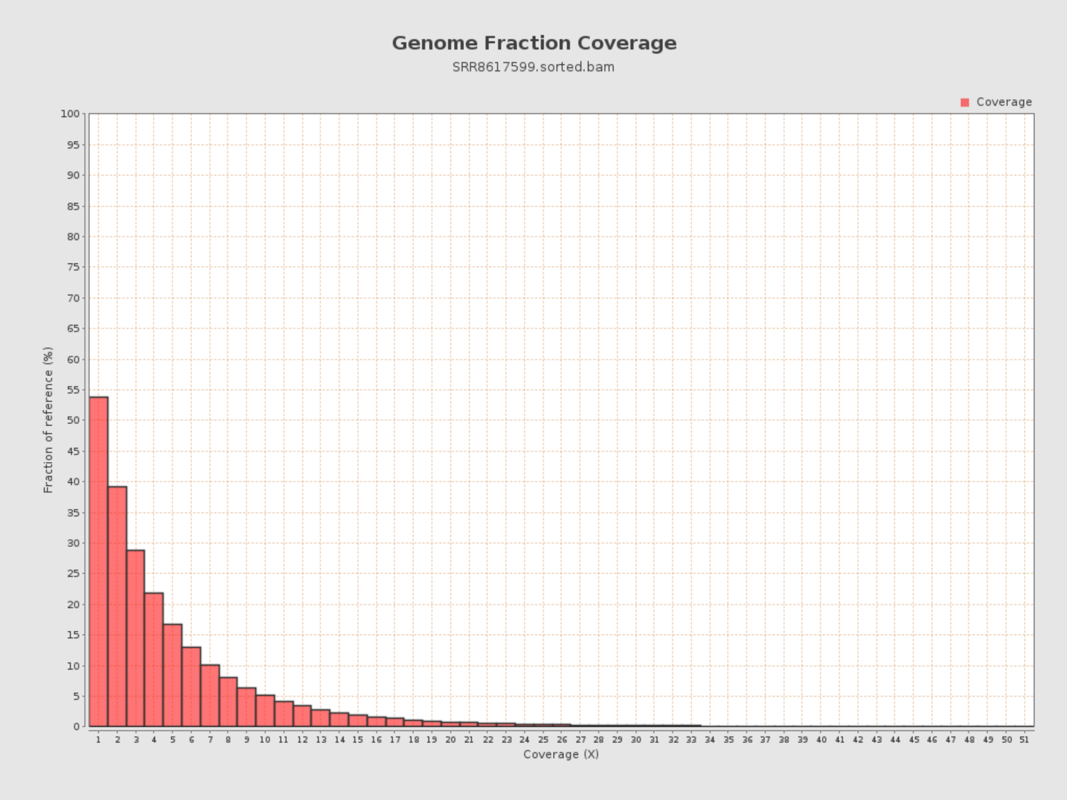
4. Results : Coverage Histogram



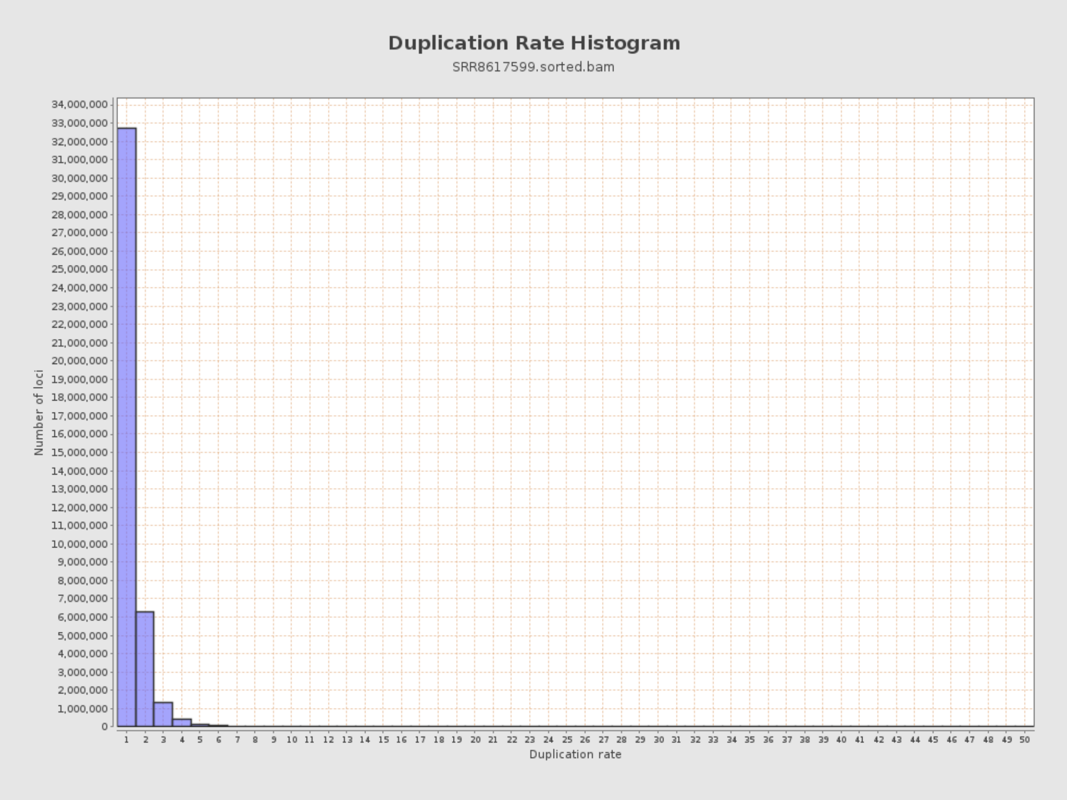
5. Results : Coverage Histogram (0-50X)



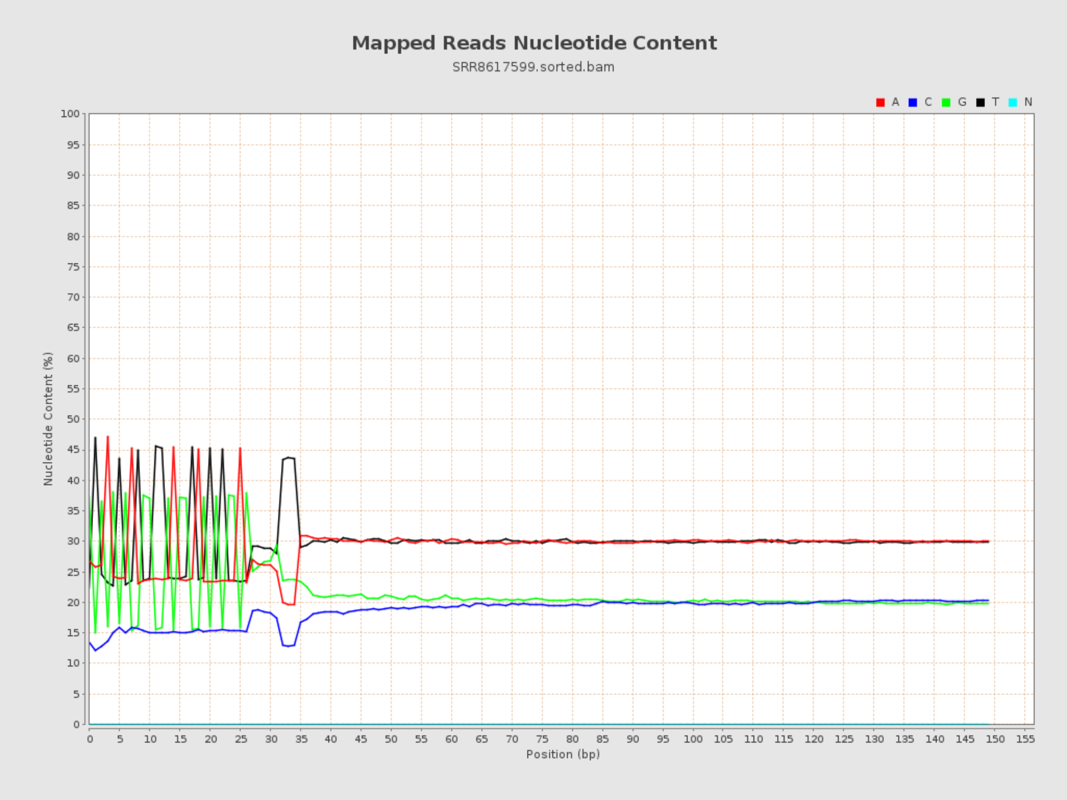
6. Results : Genome Fraction Coverage



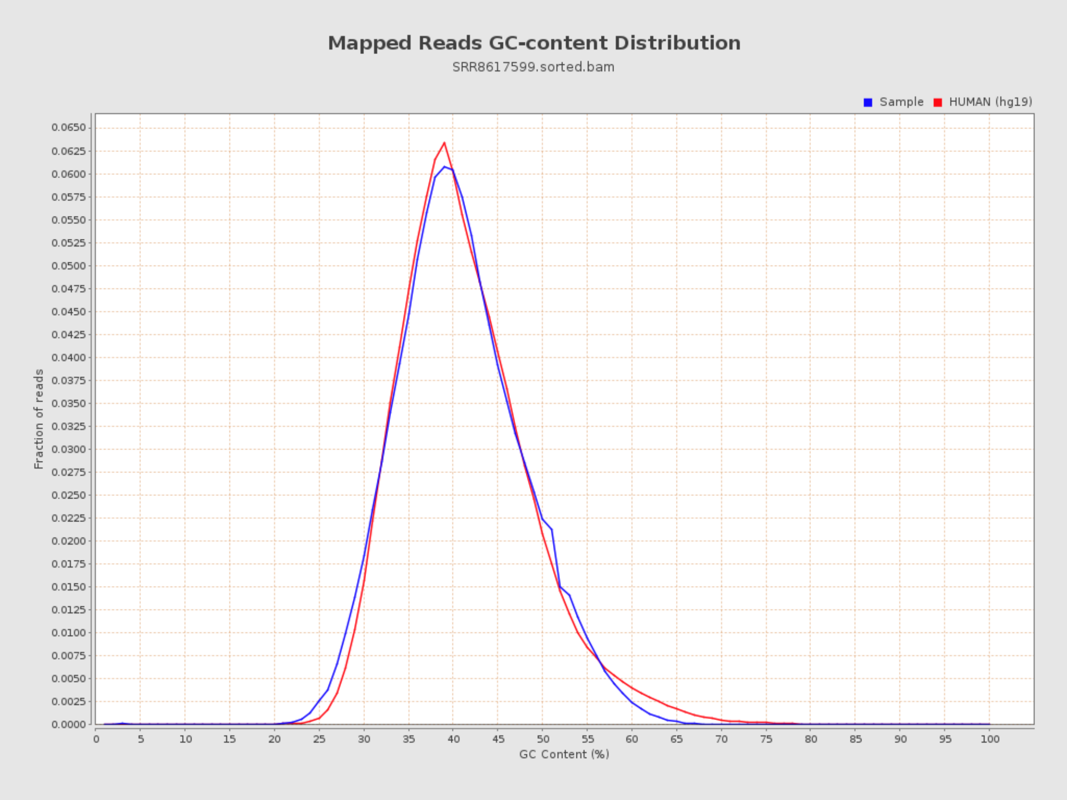
7. Results : Duplication Rate Histogram



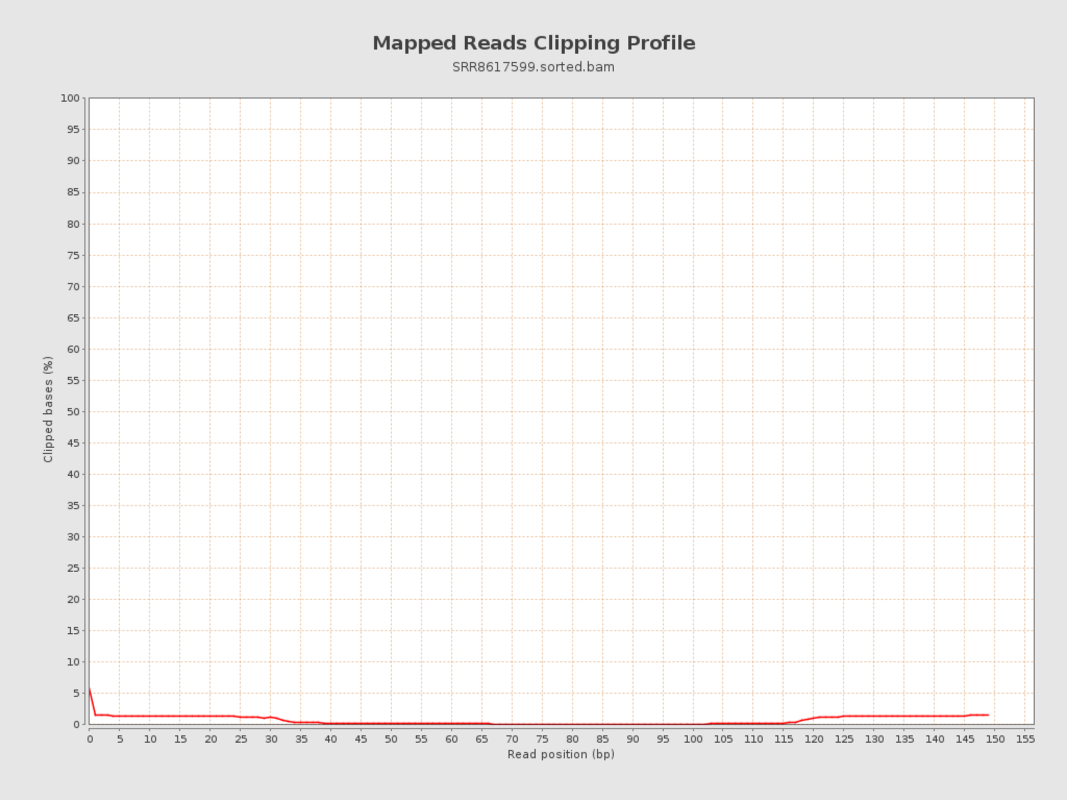
8. Results : Mapped Reads Nucleotide Content



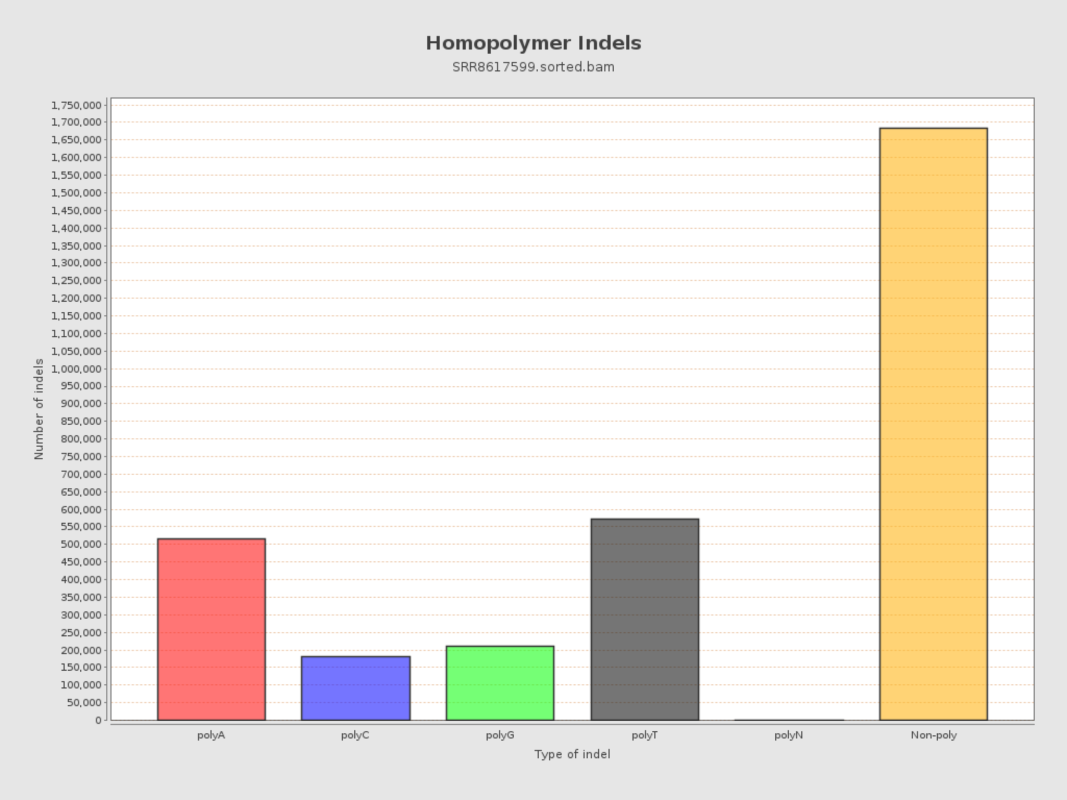
9. Results : Mapped Reads GC-content Distribution



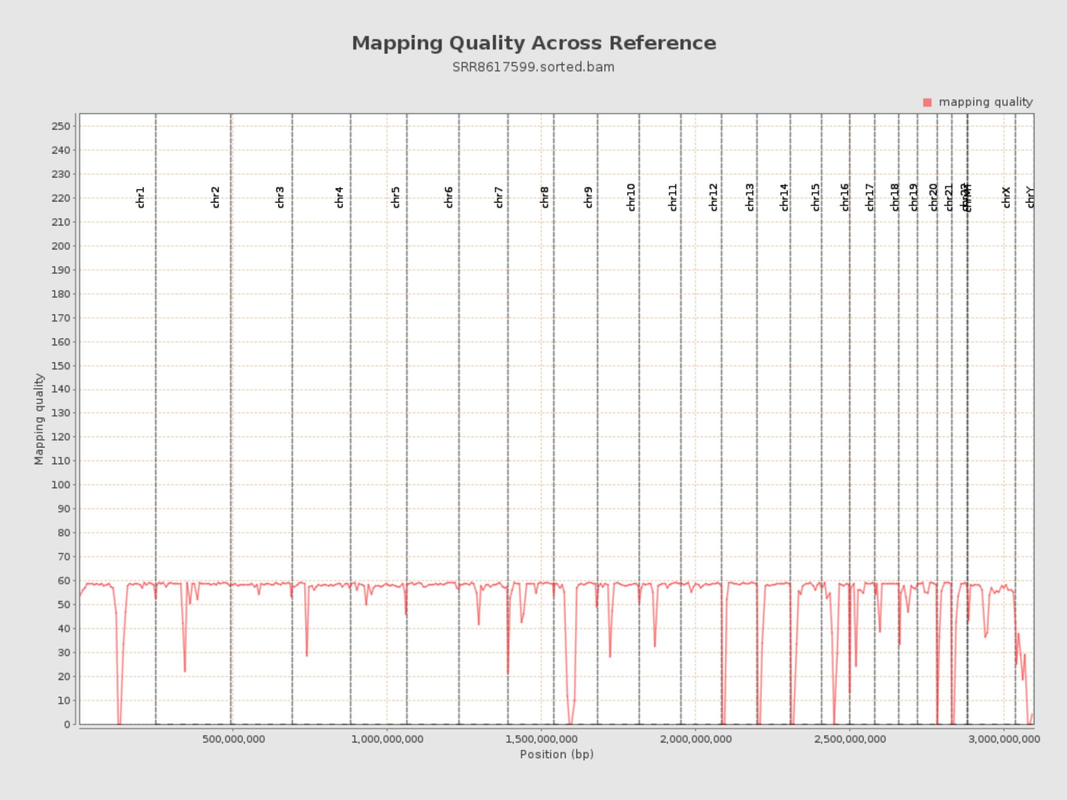
10. Results : Mapped Reads Clipping Profile



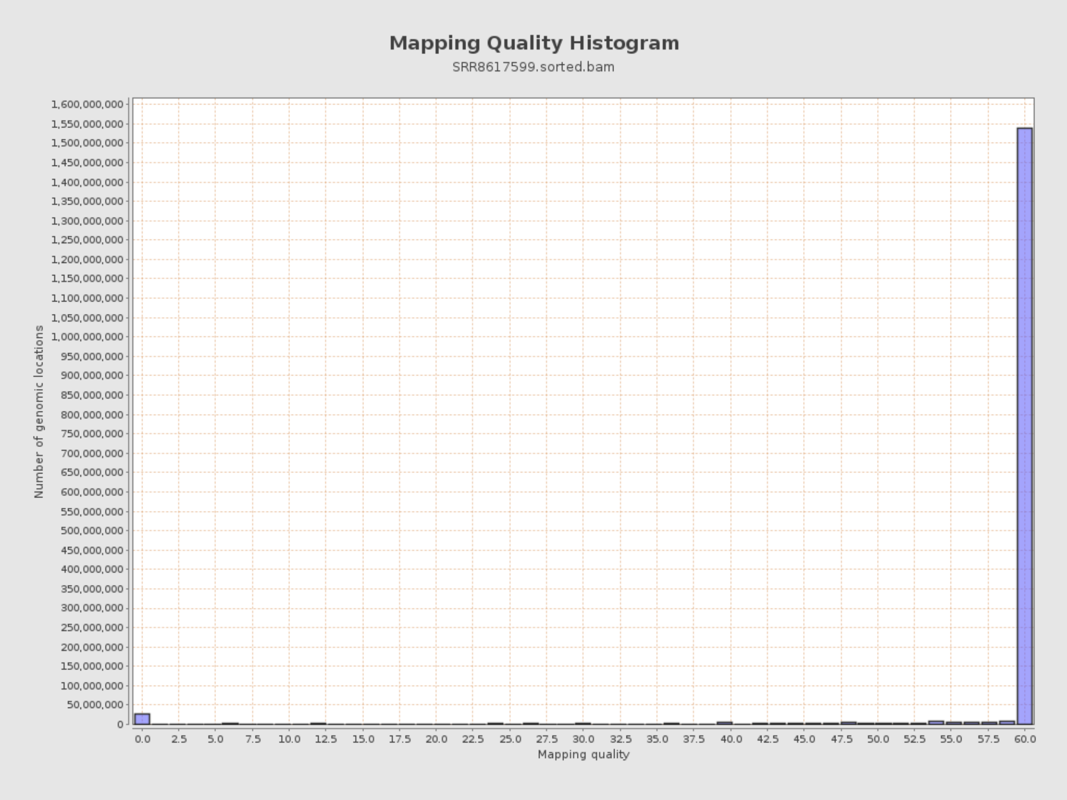
11. Results : Homopolymer Indels



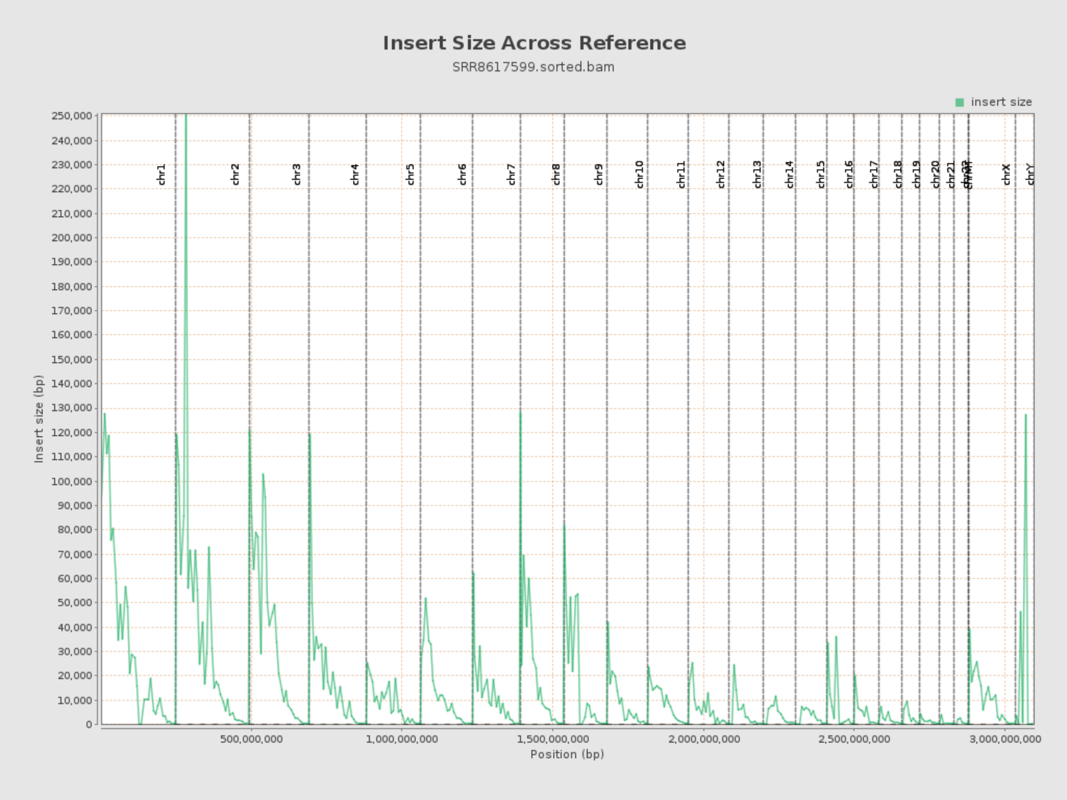
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram