Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/05 06:58:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1768995.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_SRR1768995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1768995_1.fastq.gz SRR1768995_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 05 06:58:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1768995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	378,276,896
Mapped reads	340,669,333 / 90.06%
Unmapped reads	37,607,563 / 9.94%
Mapped paired reads	340,669,333 / 90.06%
Mapped reads, first in pair	172,464,508 / 45.59%
Mapped reads, second in pair	168,204,825 / 44.47%
Mapped reads, both in pair	334,153,546 / 88.34%
Mapped reads, singletons	6,515,787 / 1.72%
Secondary alignments	0
Supplementary alignments	305,113 / 0.08%
Read min/max/mean length	30 / 80 / 80.03
Duplicated reads (estimated)	40,837,693 / 10.8%
Duplication rate	7.15%
Clipped reads	13,423,676 / 3.55%

2.2. ACGT Content

Number/percentage of A's	7,806,347,722 / 28.91%
Number/percentage of C's	5,665,562,825 / 20.98%
Number/percentage of T's	7,846,012,896 / 29.06%
Number/percentage of G's	5,674,975,705 / 21.02%
Number/percentage of N's	7,361,527 / 0.03%

GC Percentage	42%

2.3. Coverage

Mean	8.724
Standard Deviation	83.8561

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	29,890.48
Standard Deviation	1,646,635.14
P25/Median/P75	201 / 264 / 336

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	130,885,295
Insertions	2,336,617
Mapped reads with at least one insertion	0.67%
Deletions	3,063,720
Mapped reads with at least one deletion	0.88%
Homopolymer indels	43.84%

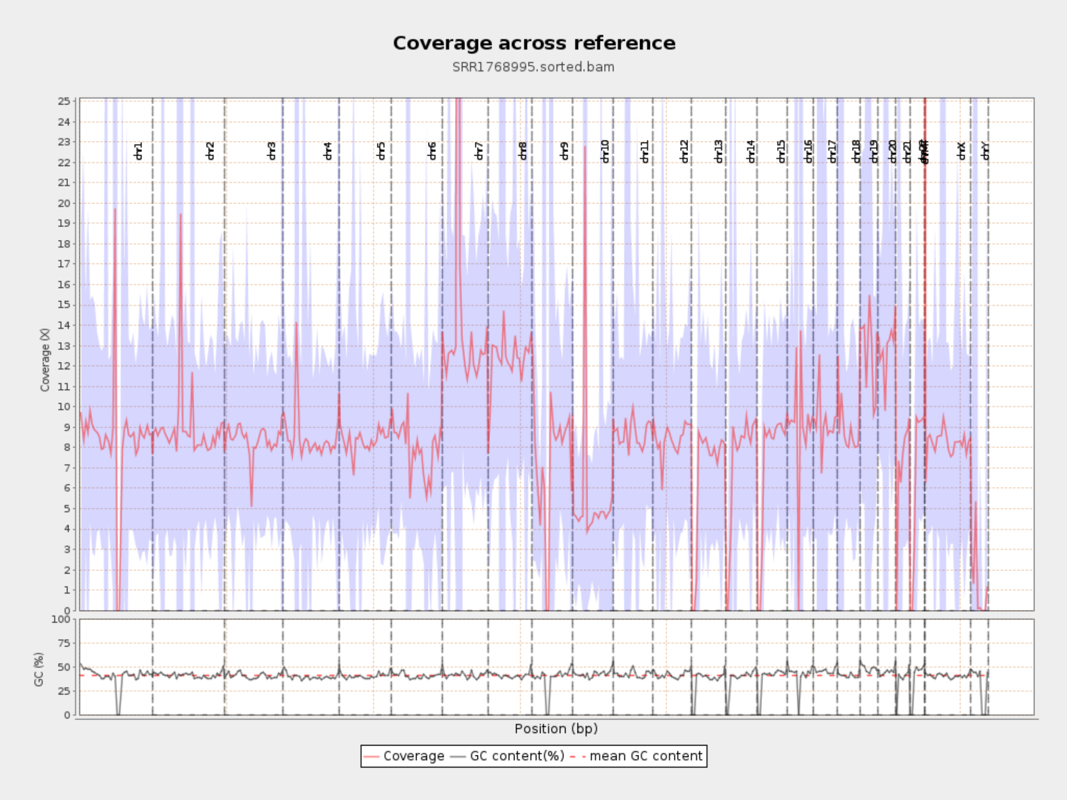
2.7. Chromosome stats

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

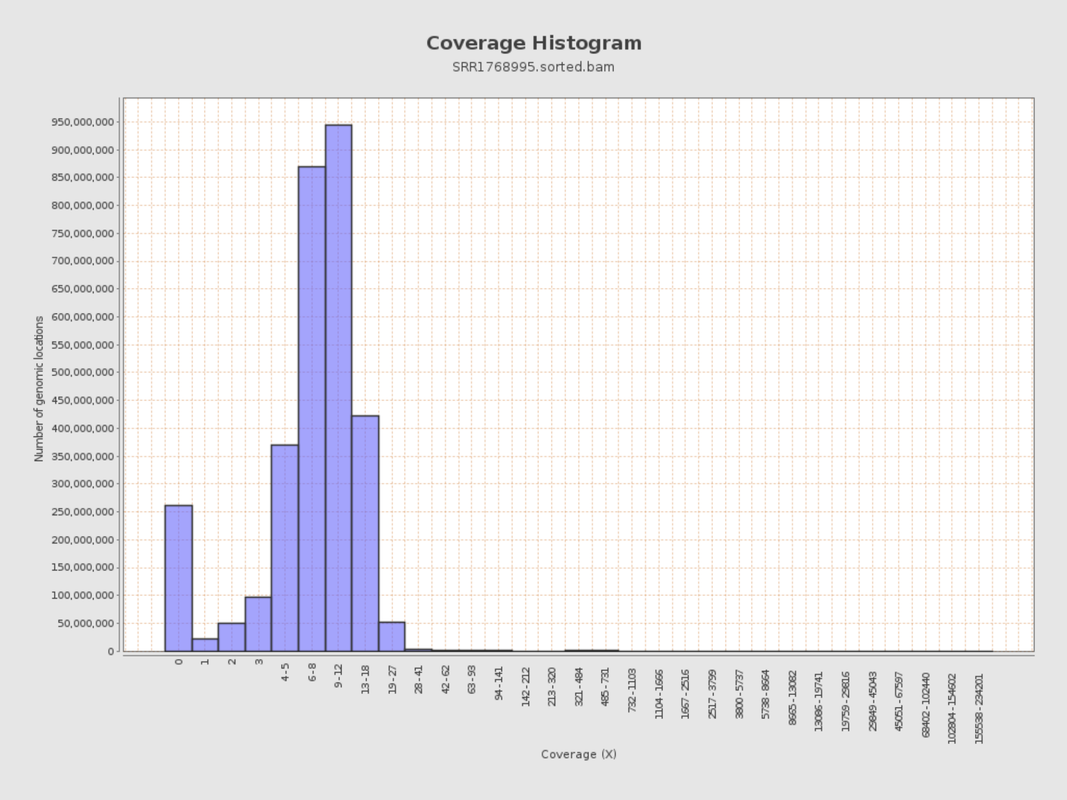
		bases	**coverage**	**deviation**
chr1	249250621	2106911421	8.453	226.0096
chr2	243199373	2189353329	9.0023	63.1386
chr3	198022430	1656446856	8.3649	6.8137
chr4	191154276	1618925108	8.4692	39.1107
chr5	180915260	1516522248	8.3825	6.9959
chr6	171115067	1366449391	7.9856	29.7927
chr7	159138663	2493874965	15.6711	107.1155
chr8	146364022	1825083718	12.4695	76.0361
chr9	141213431	1038611371	7.3549	73.6692
chr10	135534747	766721823	5.657	121.707
chr11	135006516	1175423904	8.7064	29.067
chr12	133851895	1125172469	8.4061	7.6607
chr13	115169878	777833583	6.7538	5.848
chr14	107349540	775720382	7.2261	10.7719
chr15	102531392	732642109	7.1455	5.5037
chr16	90354753	820990949	9.0863	44.9239
chr17	81195210	747742248	9.2092	42.2363
chr18	78077248	688172032	8.814	91.0243
chr19	59128983	743616149	12.5762	117.8639
chr20	63025520	806591989	12.7979	12.5735
chr21	48129895	346614553	7.2016	20.7134
chr22	51304566	332328721	6.4776	6.6744
chrMT	16571	5534047	333.9597	39.9966
chrX	155270560	1275086628	8.212	18.1561

chrY	59373566	74544585	1.2555	44.535

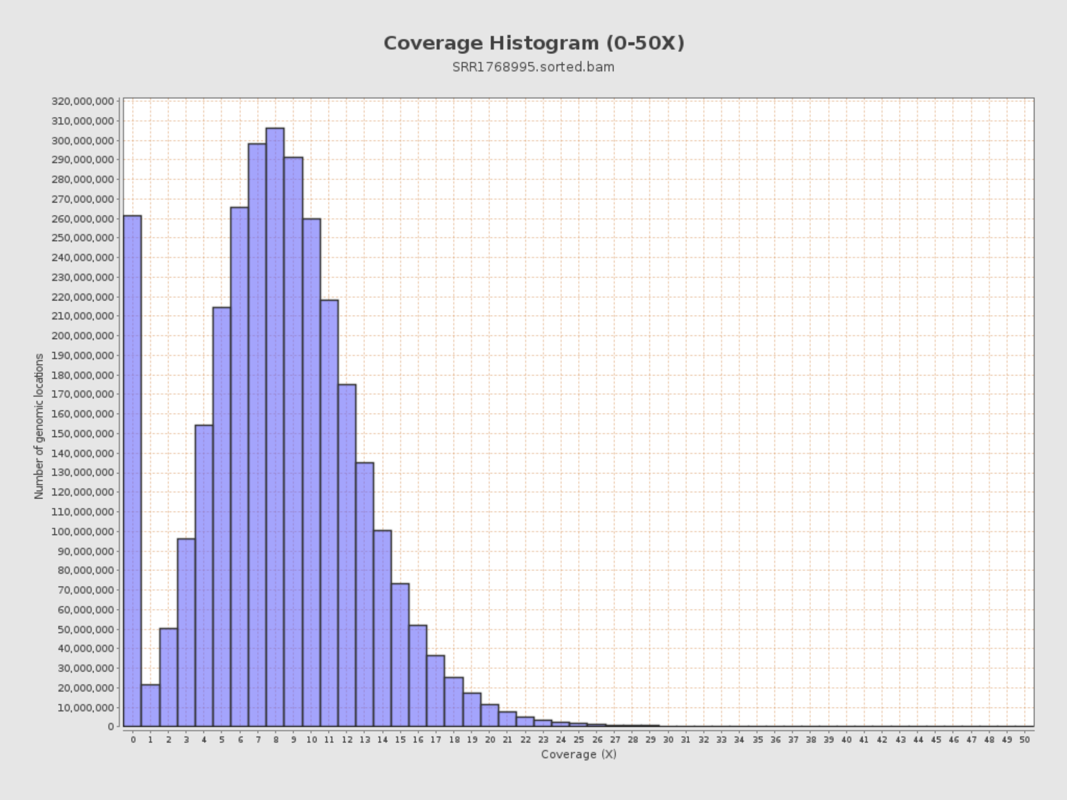
3. Results : Coverage across reference



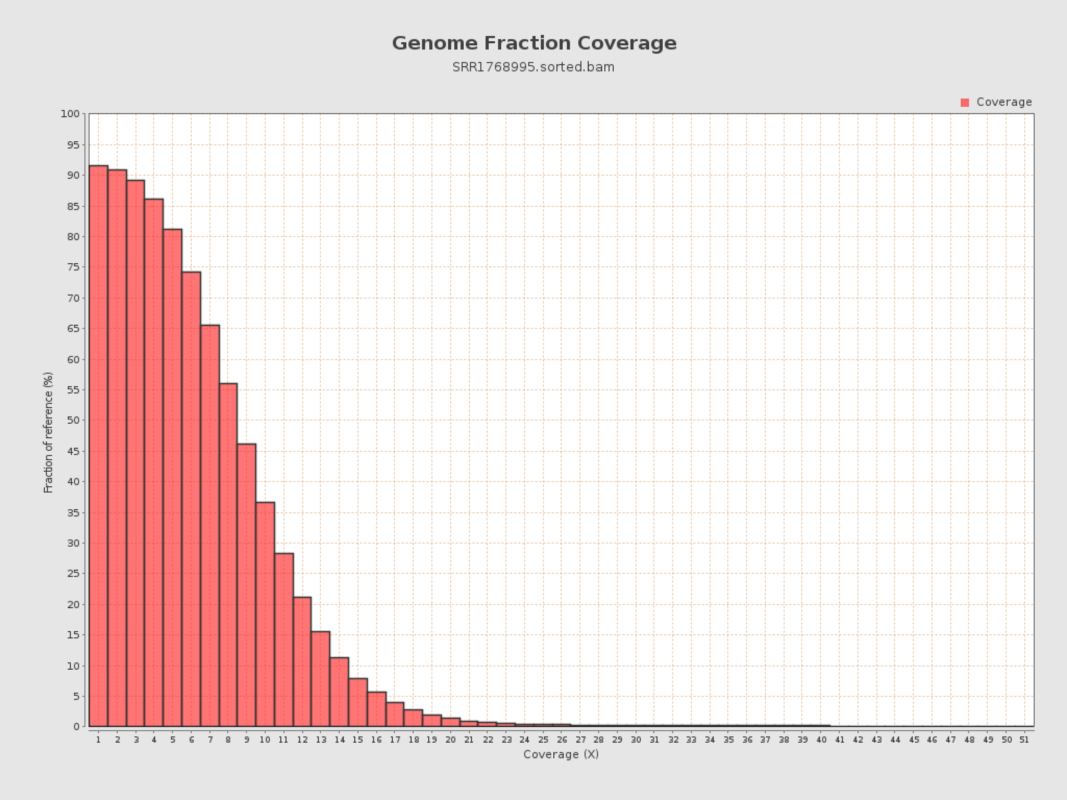
4. Results : Coverage Histogram



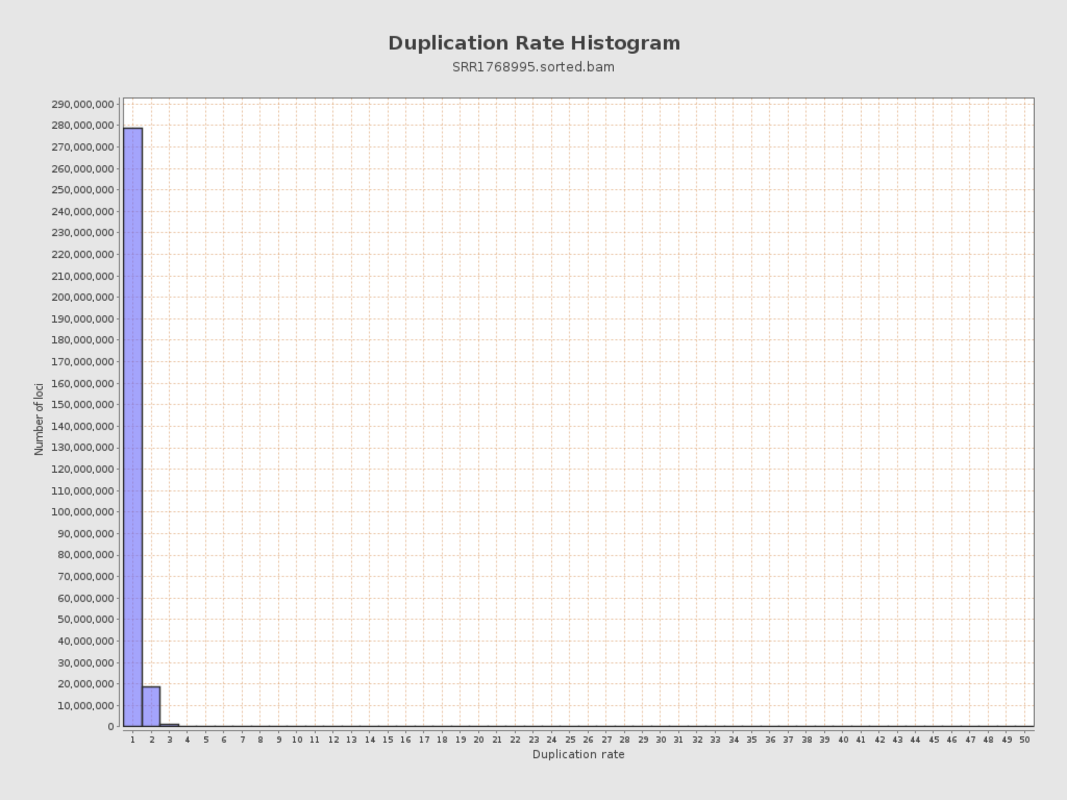
5. Results : Coverage Histogram (0-50X)



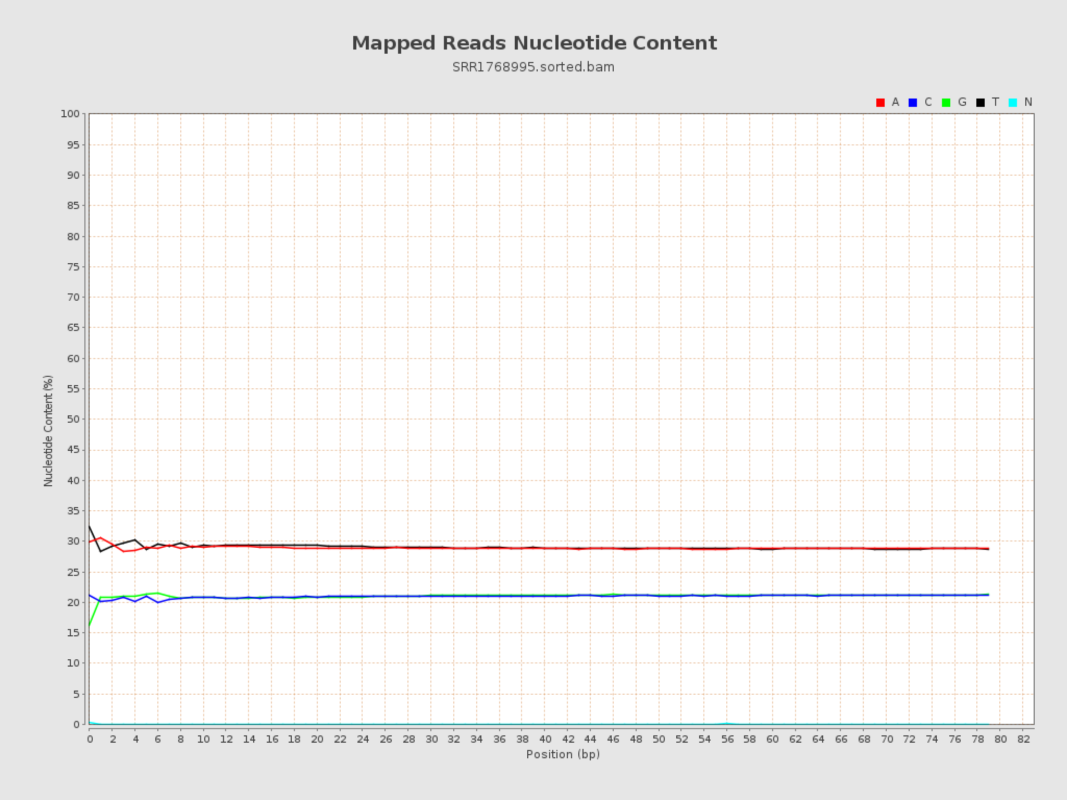
6. Results : Genome Fraction Coverage



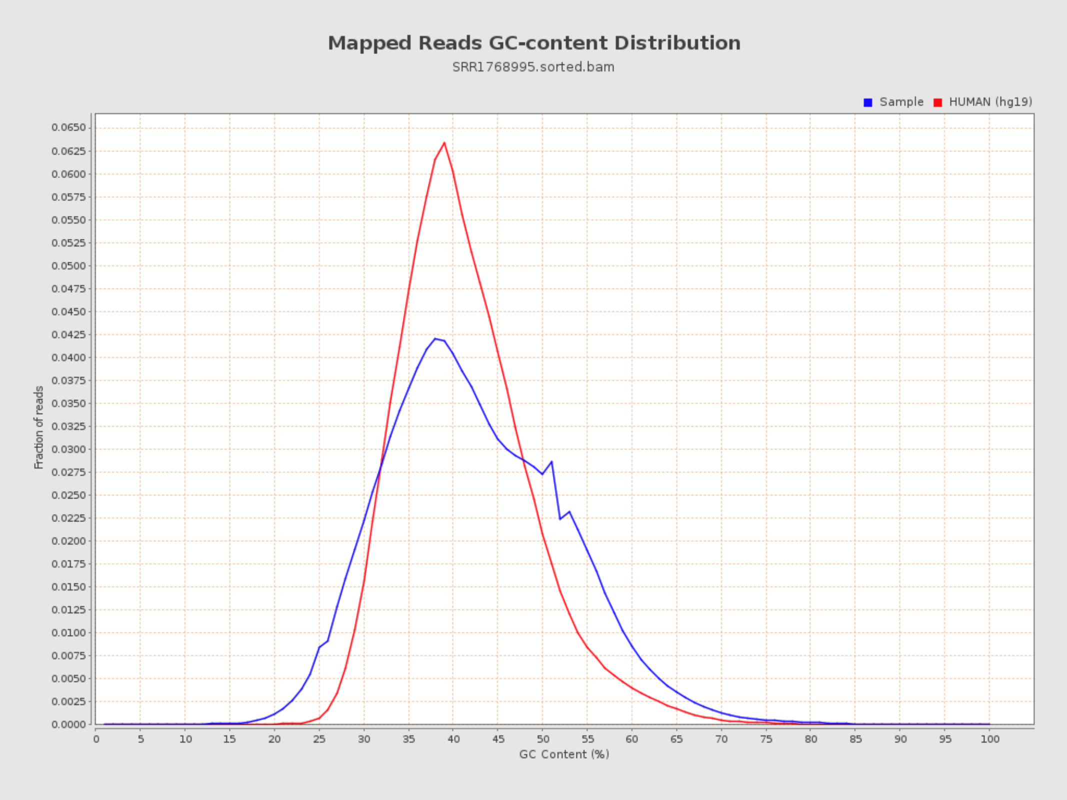
7. Results : Duplication Rate Histogram



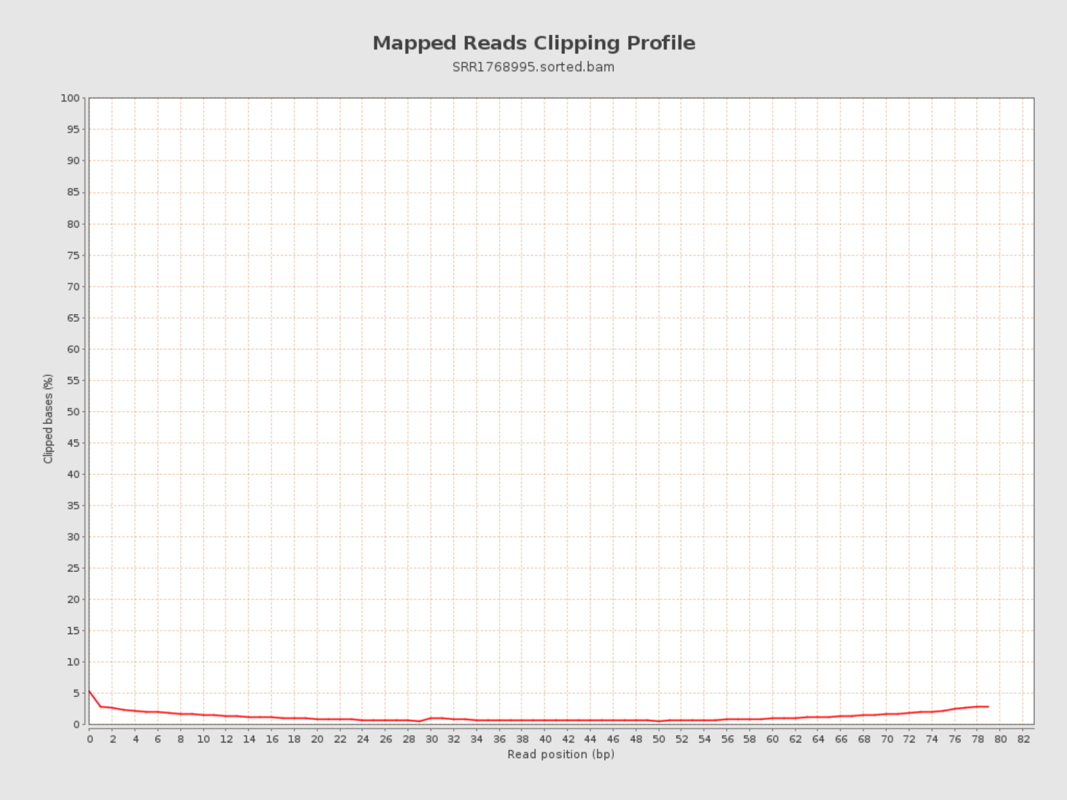
8. Results : Mapped Reads Nucleotide Content



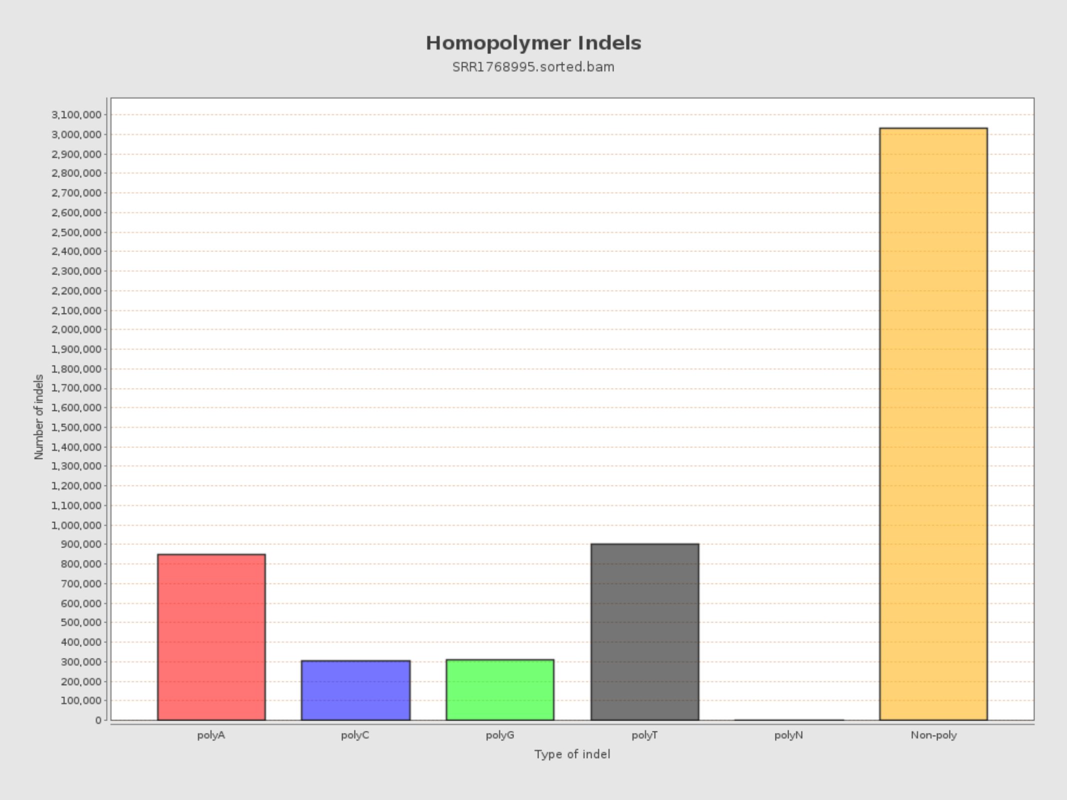
9. Results : Mapped Reads GC-content Distribution



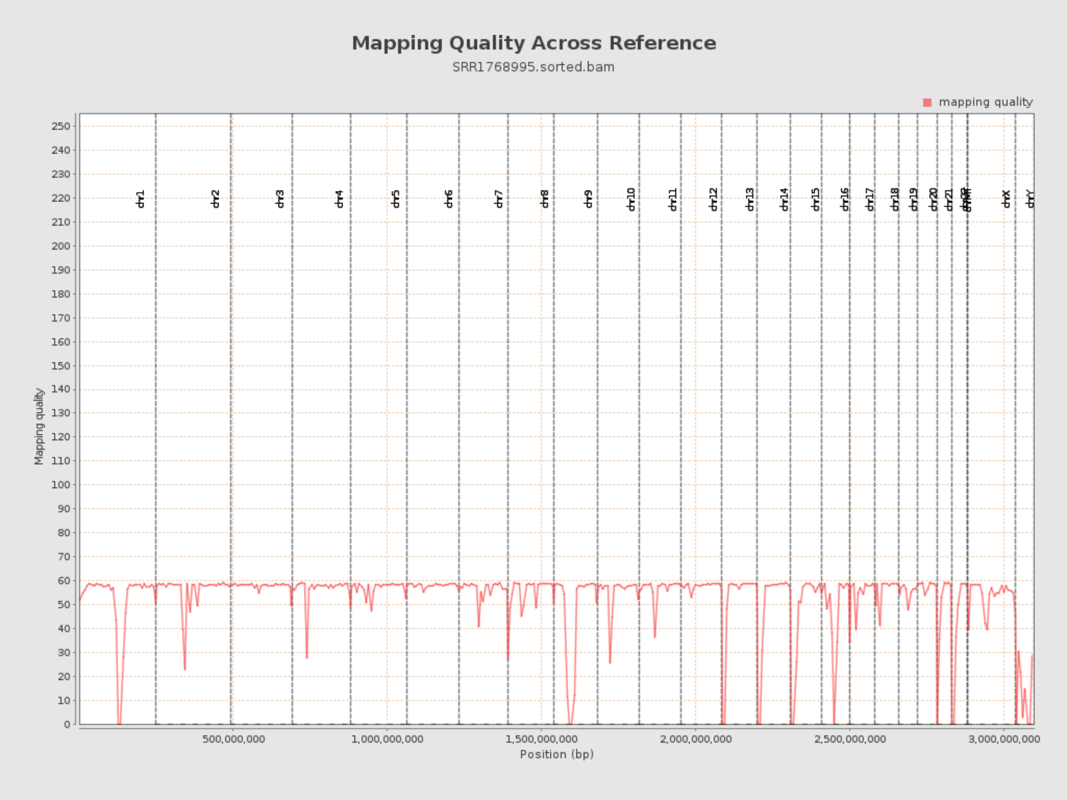
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



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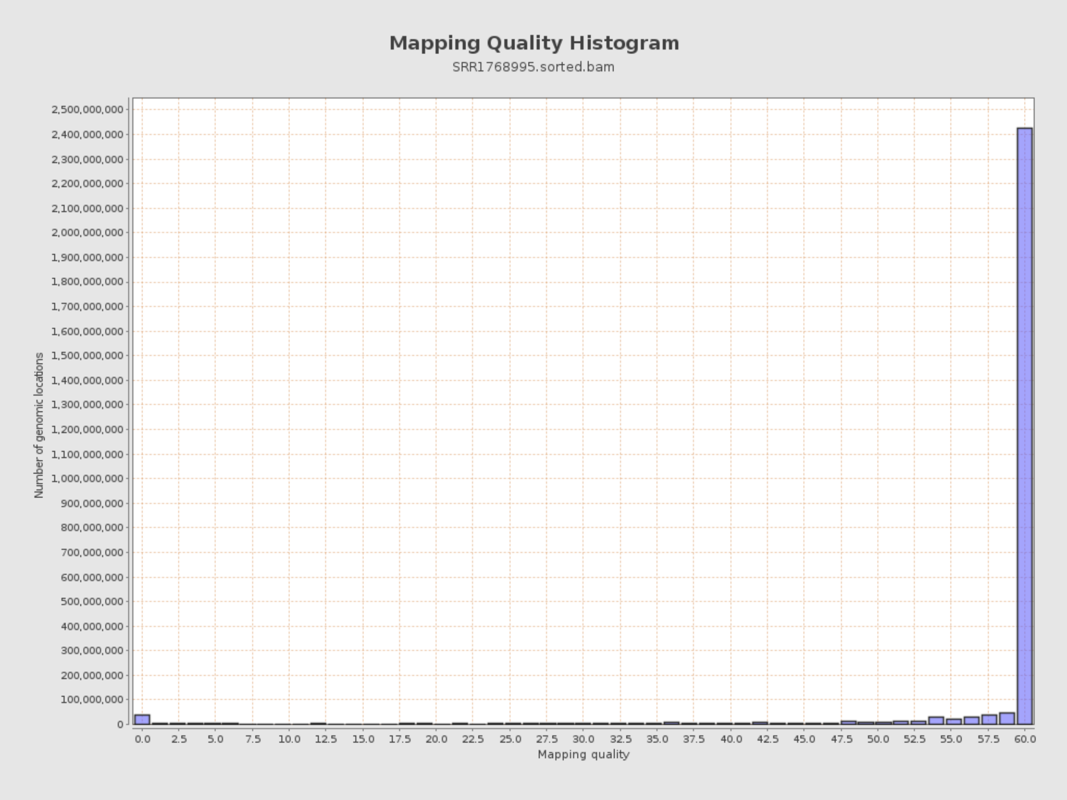
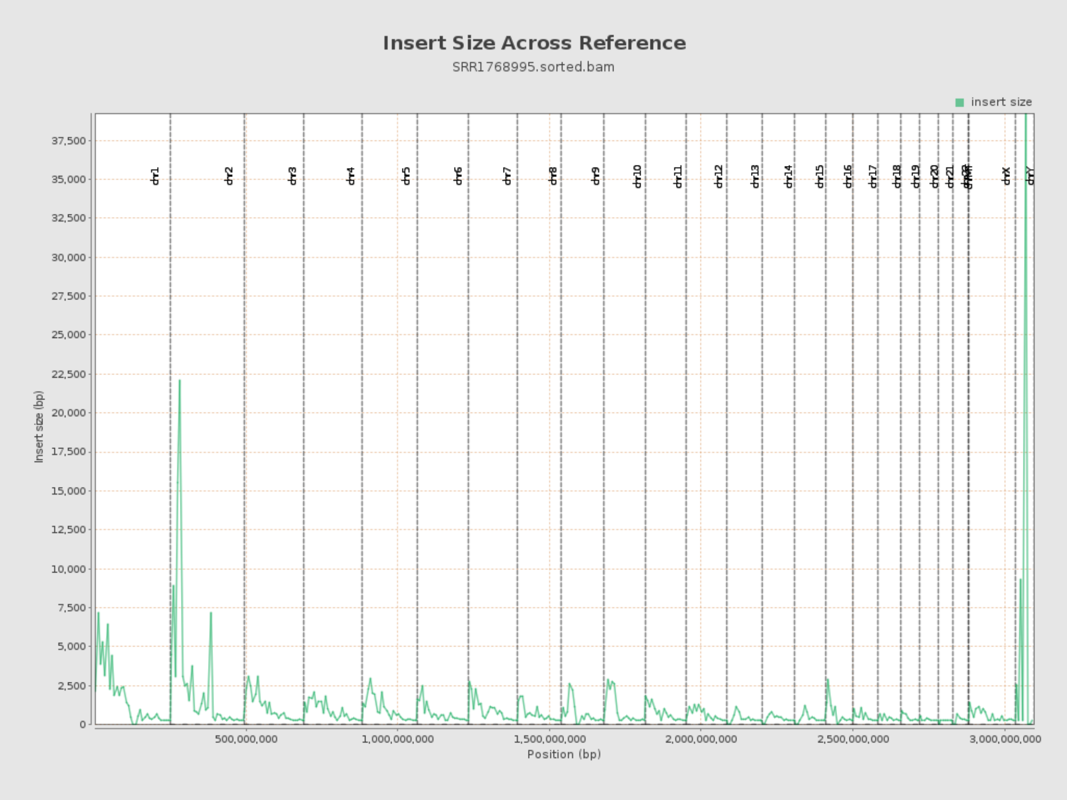
13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram