Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:10:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068954.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_SRR6068954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:10:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,061,288
Mapped reads	1,538,613 / 74.64%
Unmapped reads	522,675 / 25.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,350 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	90,780 / 4.4%
Duplication rate	5.06%
Clipped reads	692,916 / 33.62%

2.2. ACGT Content

Number/percentage of A's	28,161,770 / 27.57%
Number/percentage of C's	17,943,372 / 17.57%
Number/percentage of T's	33,739,571 / 33.03%
Number/percentage of G's	22,049,595 / 21.59%
Number/percentage of N's	249,711 / 0.24%
GC Percentage	39.15%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2847

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Mismatches and indels

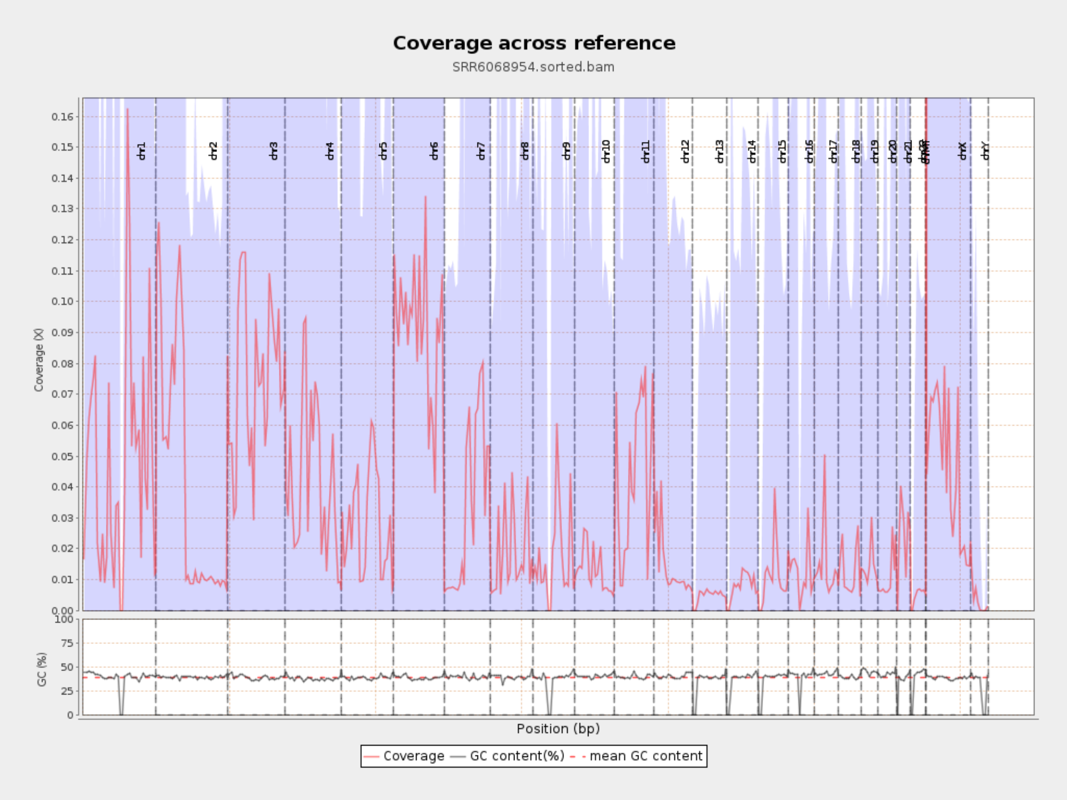
General error rate	1.04%
Mismatches	1,045,815
Insertions	8,690
Mapped reads with at least one insertion	0.56%
Deletions	27,684
Mapped reads with at least one deletion	1.78%
Homopolymer indels	48.73%

2.6. Chromosome stats

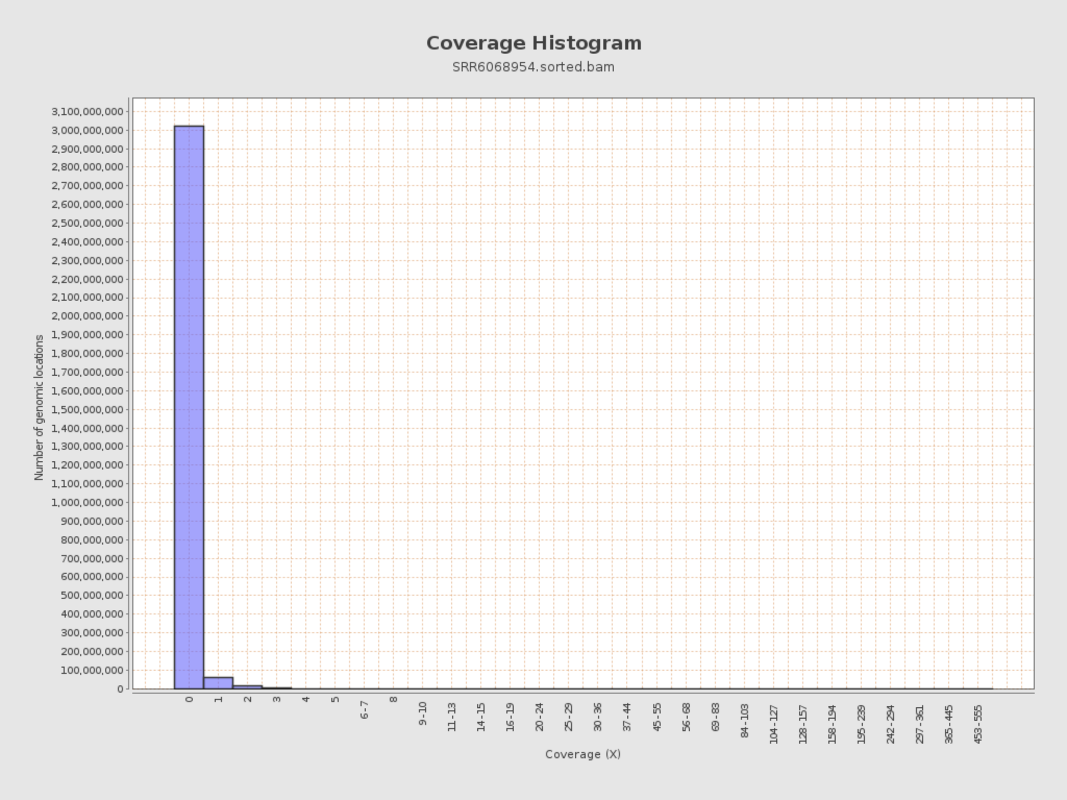
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11743717	0.0471	0.3346
chr2	243199373	10073973	0.0414	0.3491
chr3	198022430	14794365	0.0747	0.3474
chr4	191154276	8268519	0.0433	0.2667
chr5	180915260	5170248	0.0286	0.2149
chr6	171115067	15495923	0.0906	0.4164
chr7	159138663	5228653	0.0329	0.2432

chr8	146364022	2816452	0.0192	0.3672
chr9	141213431	2489434	0.0176	0.1826
chr10	135534747	1747526	0.0129	0.1582
chr11	135006516	5934110	0.044	0.4662
chr12	133851895	1910961	0.0143	0.1532
chr13	115169878	553995	0.0048	0.0856
chr14	107349540	871047	0.0081	0.1195
chr15	102531392	1143705	0.0112	0.1333
chr16	90354753	1104105	0.0122	0.1401
chr17	81195210	1159655	0.0143	0.2044
chr18	78077248	1026133	0.0131	0.3256
chr19	59128983	860263	0.0145	0.2402
chr20	63025520	677400	0.0107	0.1455
chr21	48129895	1121095	0.0233	0.1944
chr22	51304566	242245	0.0047	0.0838
chrMT	16571	318916	19.2454	10.1326
chrX	155270560	7248325	0.0467	0.2982
chrY	59373566	188639	0.0032	0.0709

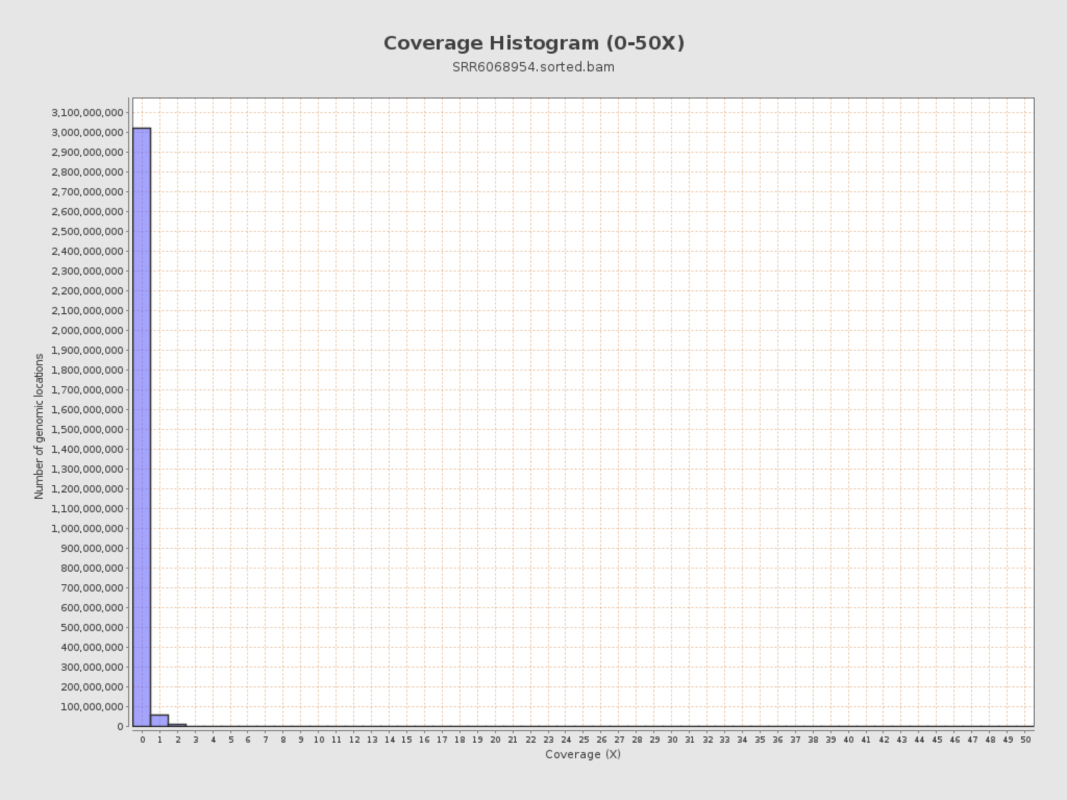
3. Results : Coverage across reference



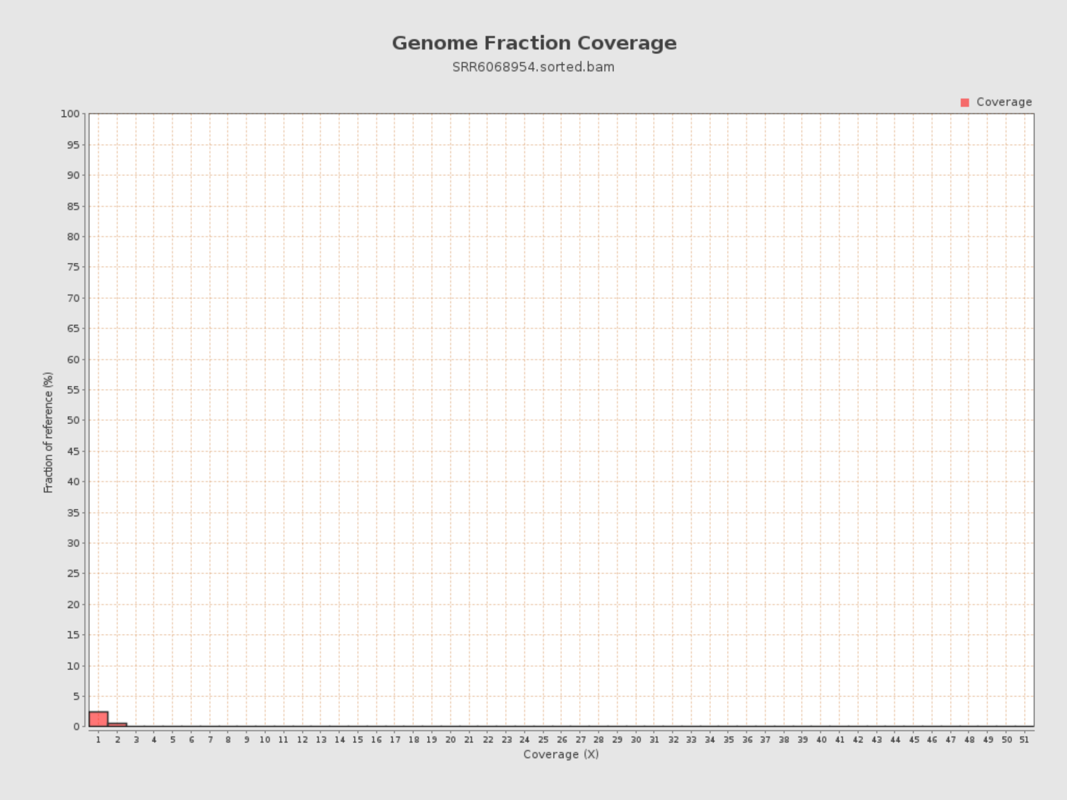
4. Results : Coverage Histogram



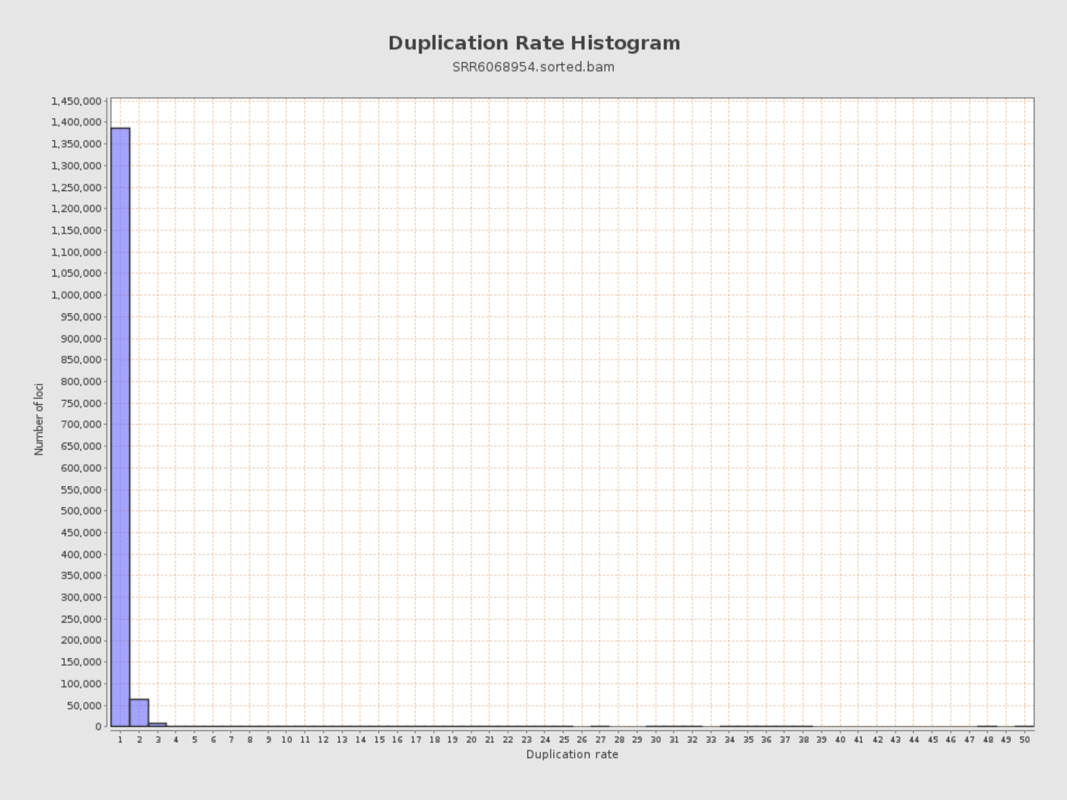
5. Results : Coverage Histogram (0-50X)



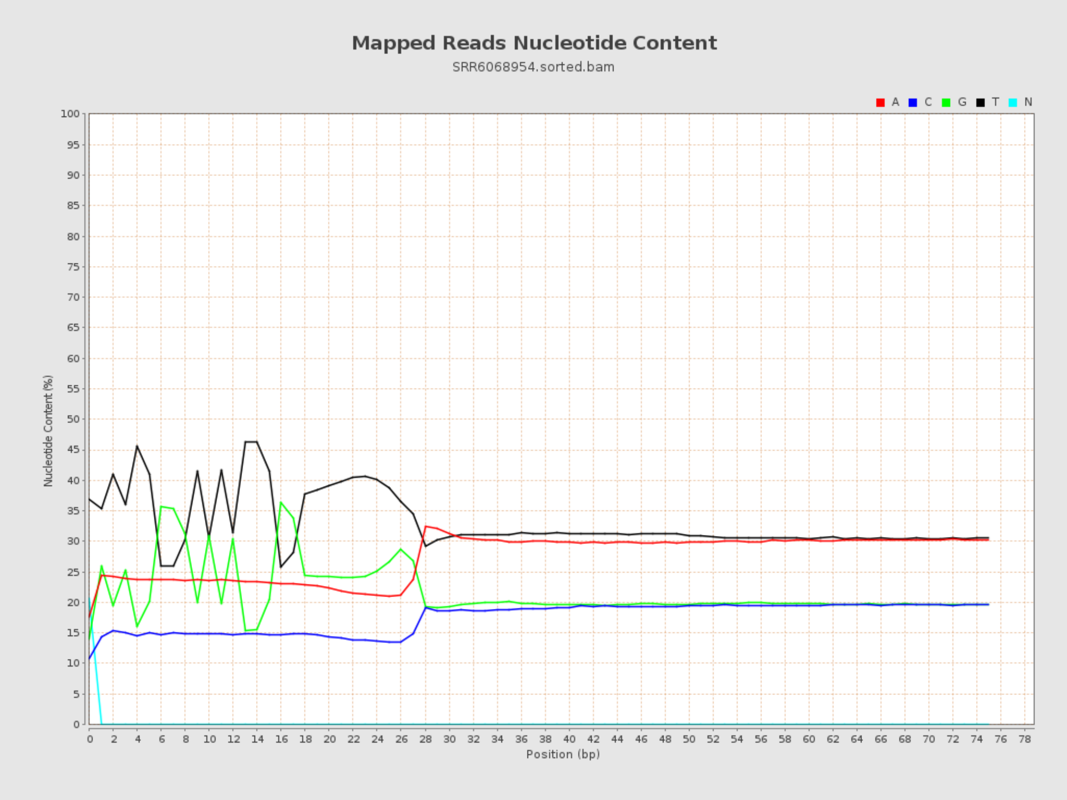
6. Results : Genome Fraction Coverage



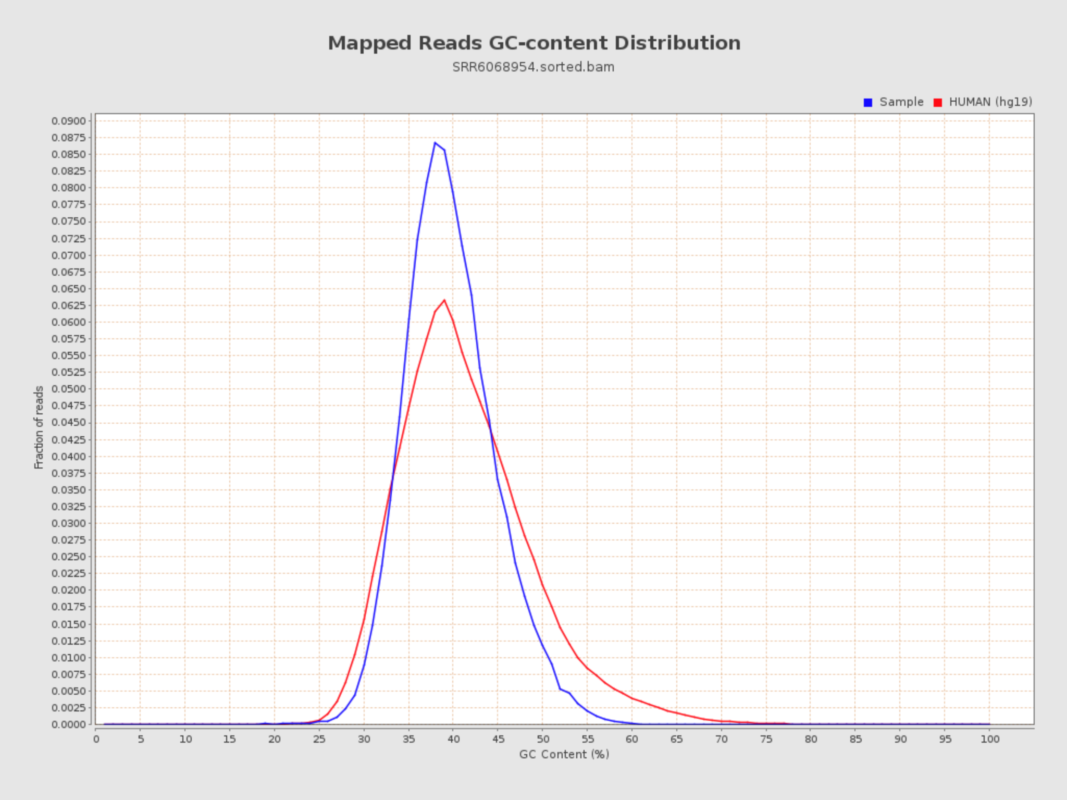
7. Results : Duplication Rate Histogram



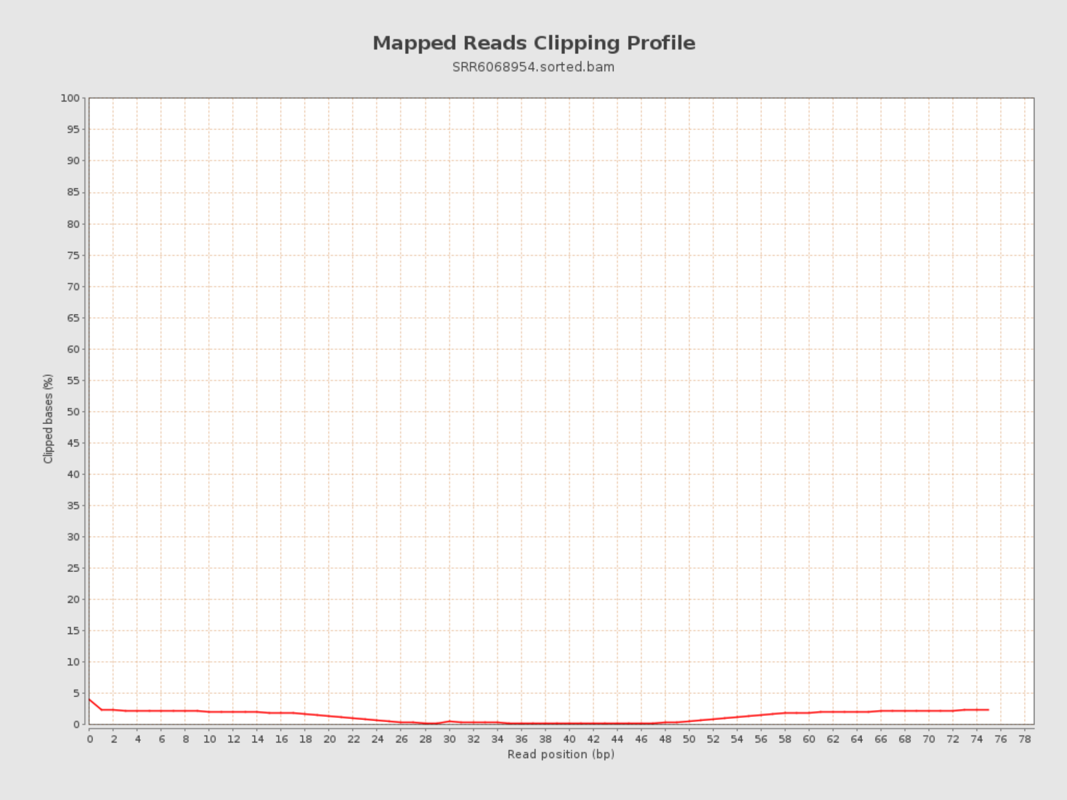
8. Results : Mapped Reads Nucleotide Content



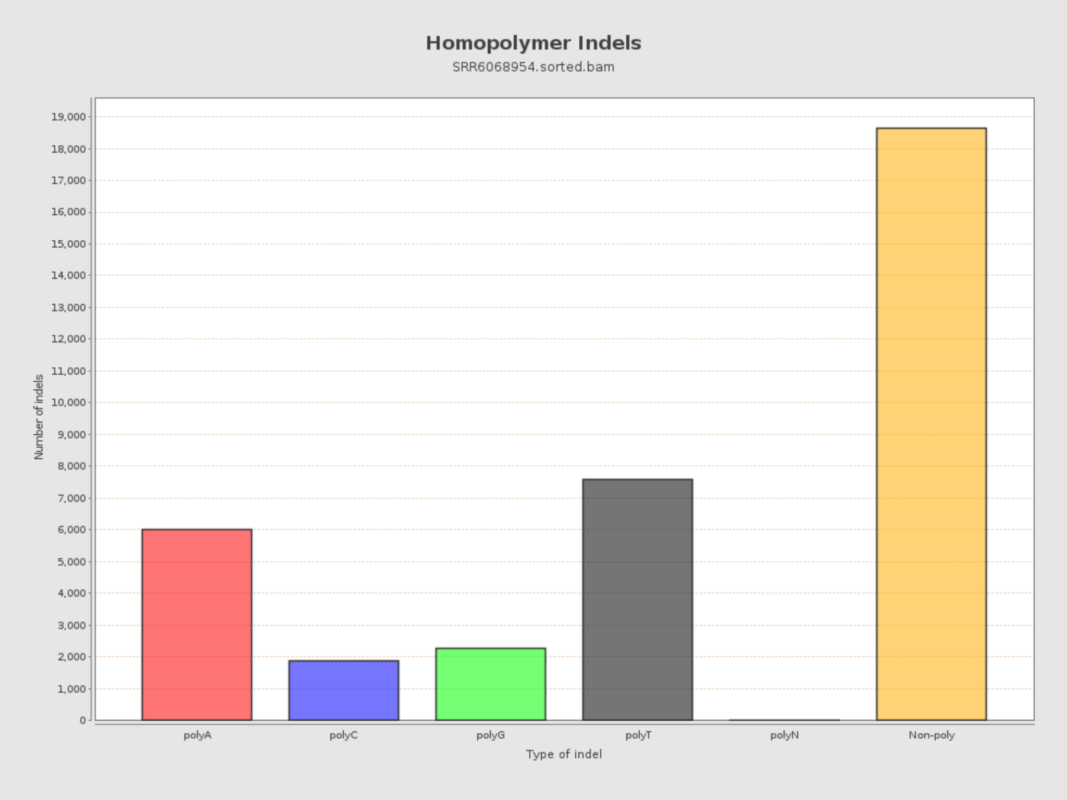
9. Results : Mapped Reads GC-content Distribution



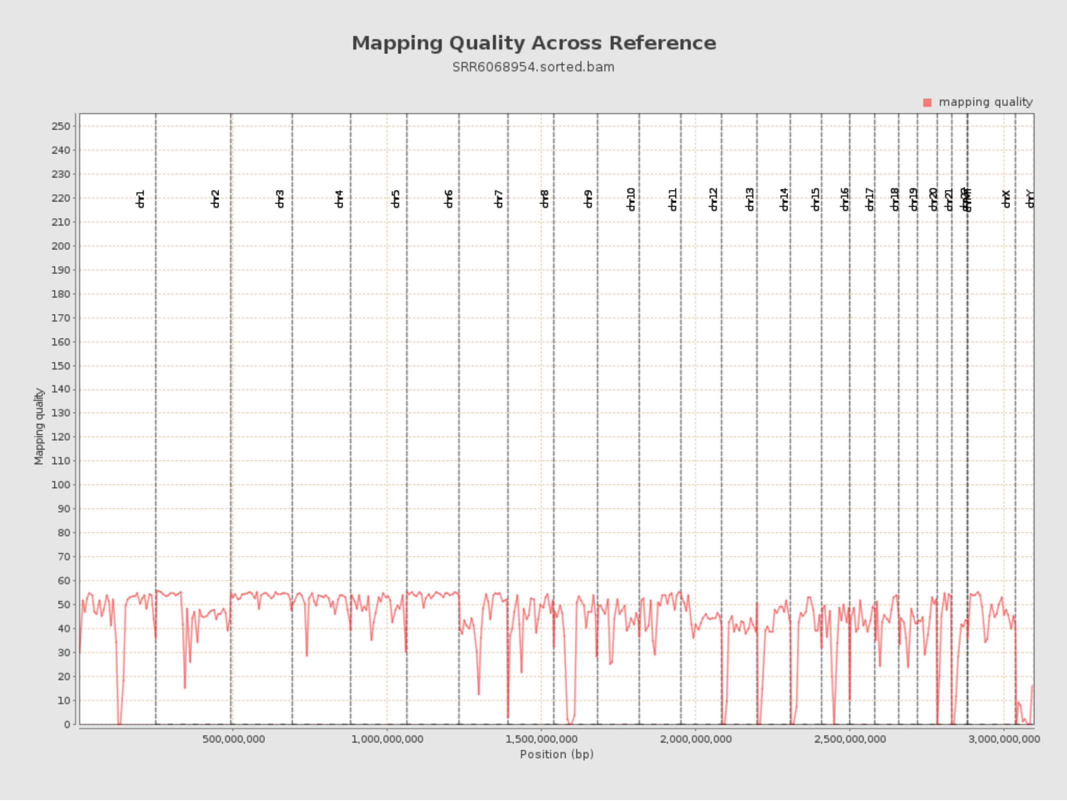
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram