Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:19:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068957.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_SRR6068957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:19:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,459,804
Mapped reads	2,025,127 / 82.33%
Unmapped reads	434,677 / 17.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,365 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	85,188 / 3.46%
Duplication rate	3.18%
Clipped reads	1,012,001 / 41.14%

2.2. ACGT Content

Number/percentage of A's	35,810,279 / 27.15%
Number/percentage of C's	22,675,080 / 17.19%
Number/percentage of T's	43,764,160 / 33.18%
Number/percentage of G's	29,334,079 / 22.24%
Number/percentage of N's	316,653 / 0.24%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.3806

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

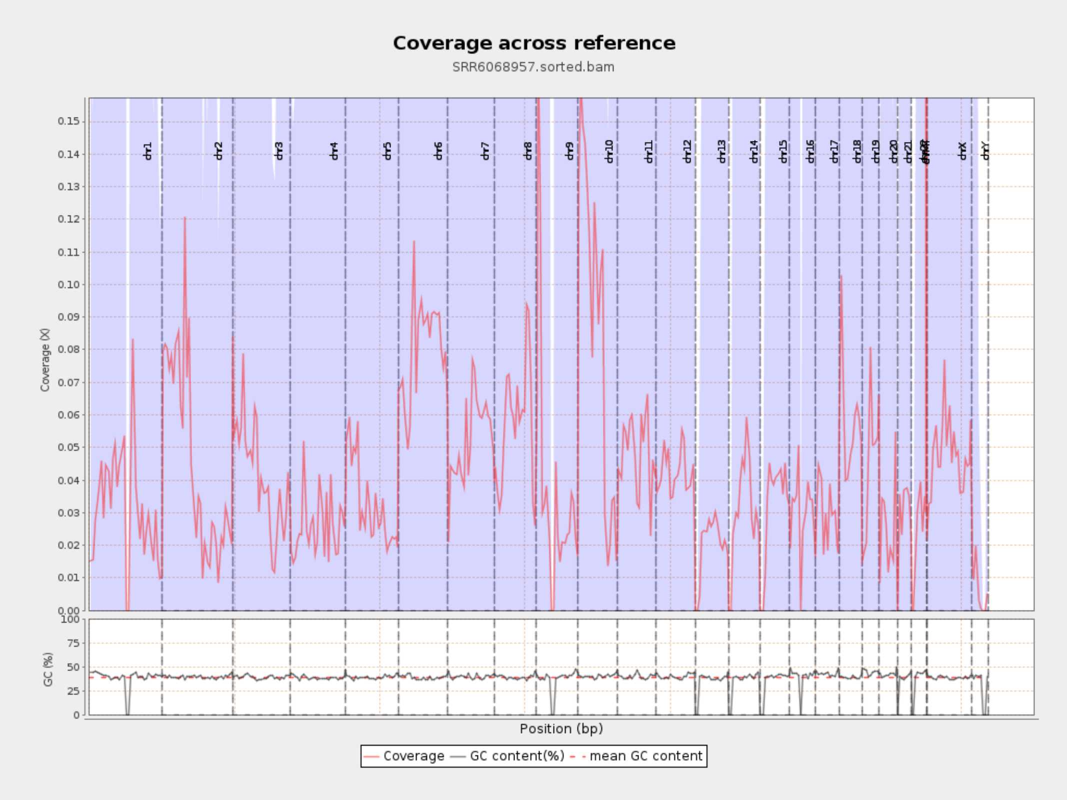
General error rate	0.98%
Mismatches	1,271,188
Insertions	11,764
Mapped reads with at least one insertion	0.58%
Deletions	33,533
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.09%

2.6. Chromosome stats

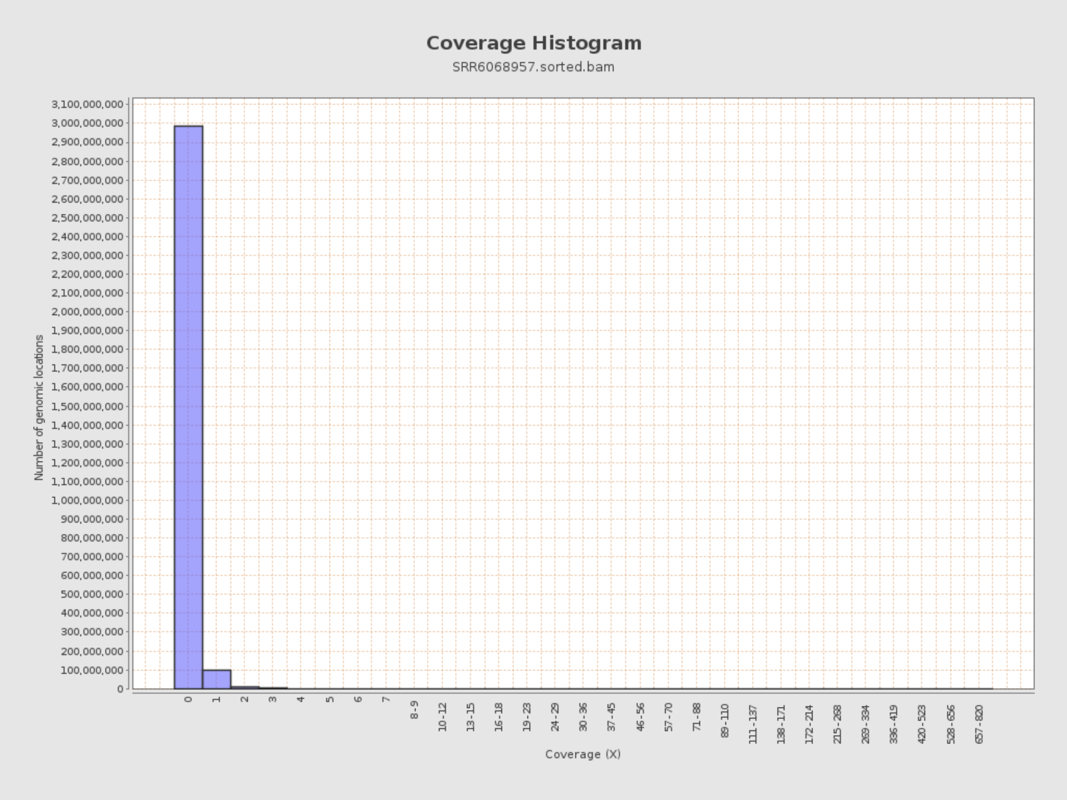
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7903632	0.0317	0.6596
chr2	243199373	11306545	0.0465	0.4282
chr3	198022430	8212007	0.0415	0.2293
chr4	191154276	4901198	0.0256	0.2142
chr5	180915260	5984787	0.0331	0.2074
chr6	171115067	13813498	0.0807	0.444
chr7	159138663	8462045	0.0532	0.4546

chr8	146364022	8369563	0.0572	0.5418
chr9	141213431	5401565	0.0383	0.3645
chr10	135534747	12179562	0.0899	0.4723
chr11	135006516	6474271	0.048	0.3826
chr12	133851895	5656451	0.0423	0.2349
chr13	115169878	2322444	0.0202	0.1591
chr14	107349540	3318720	0.0309	0.2087
chr15	102531392	3288638	0.0321	0.2008
chr16	90354753	2732787	0.0302	0.2255
chr17	81195210	2358897	0.0291	0.2246
chr18	78077248	4574673	0.0586	0.5867
chr19	59128983	2672442	0.0452	0.4589
chr20	63025520	1617582	0.0257	0.1937
chr21	48129895	1418060	0.0295	0.2285
chr22	51304566	1181042	0.023	0.172
chrMT	16571	120509	7.2723	4.4937
chrX	155270560	7326770	0.0472	0.2864
chrY	59373566	357548	0.006	0.1717

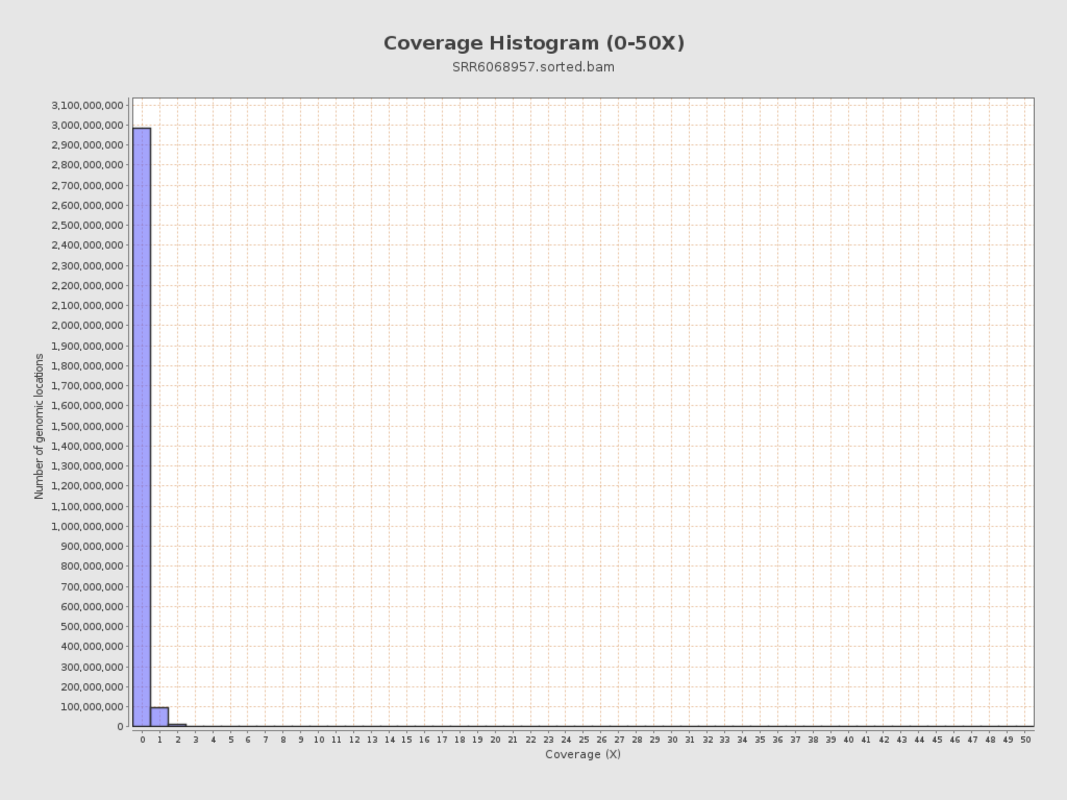
3. Results : Coverage across reference



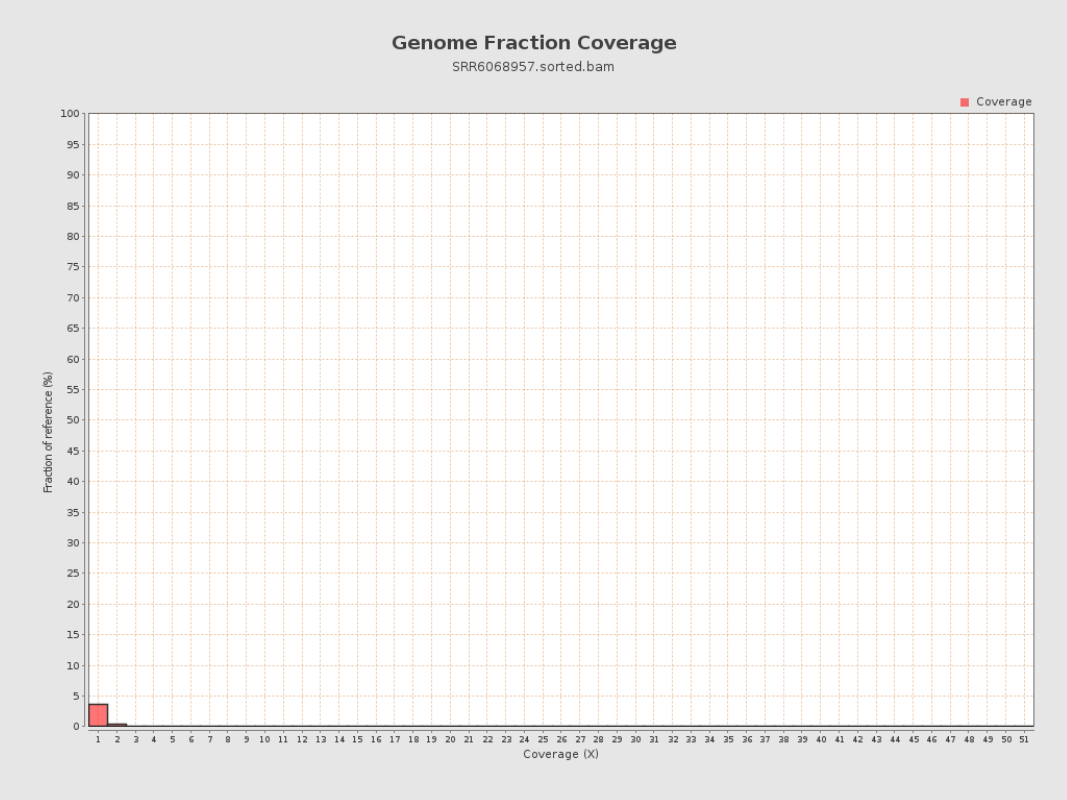
4. Results : Coverage Histogram



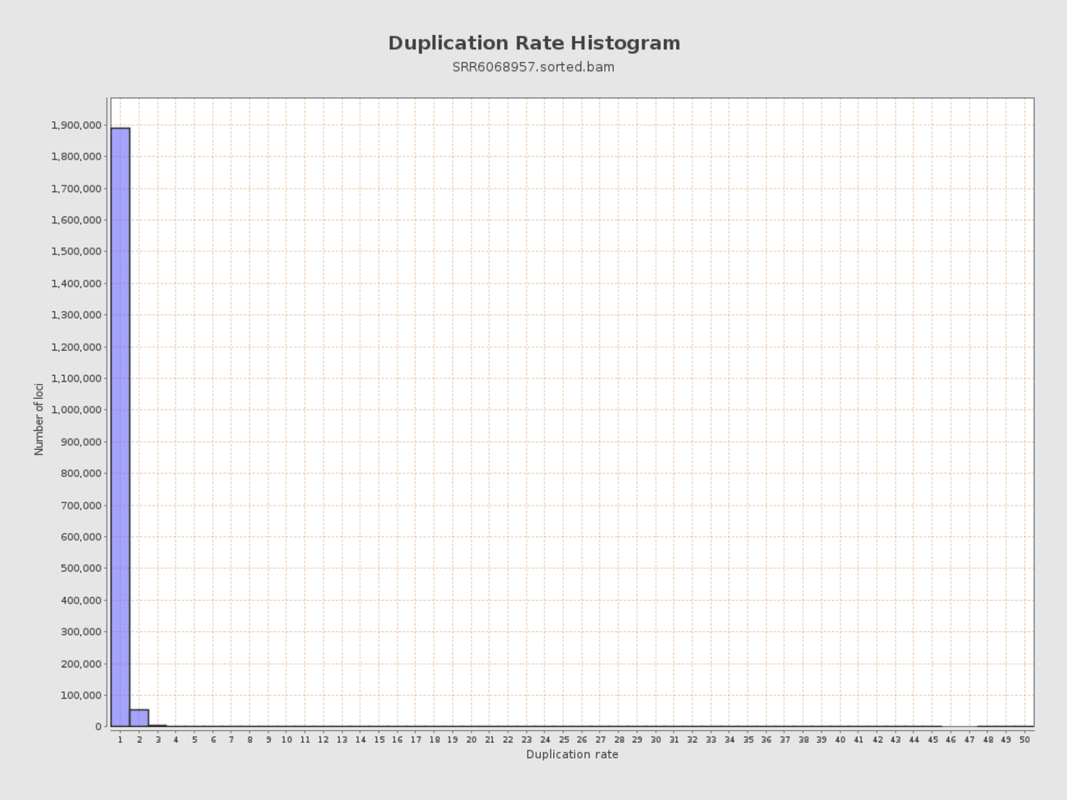
5. Results : Coverage Histogram (0-50X)



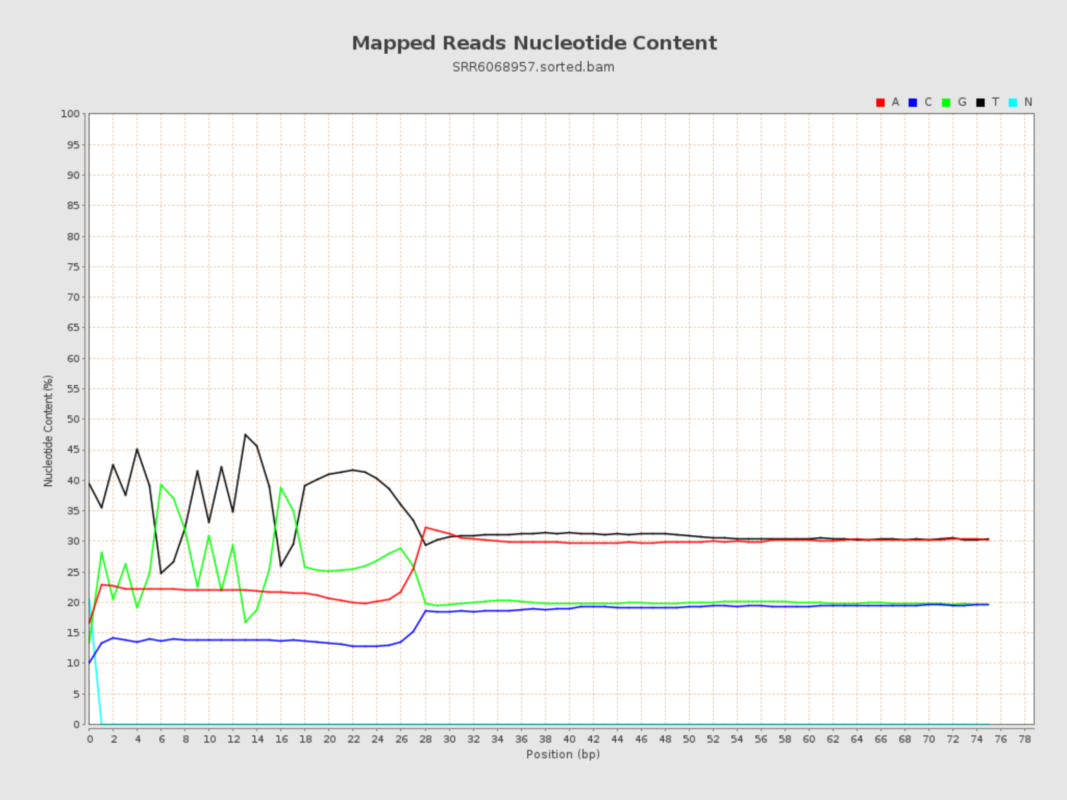
6. Results : Genome Fraction Coverage



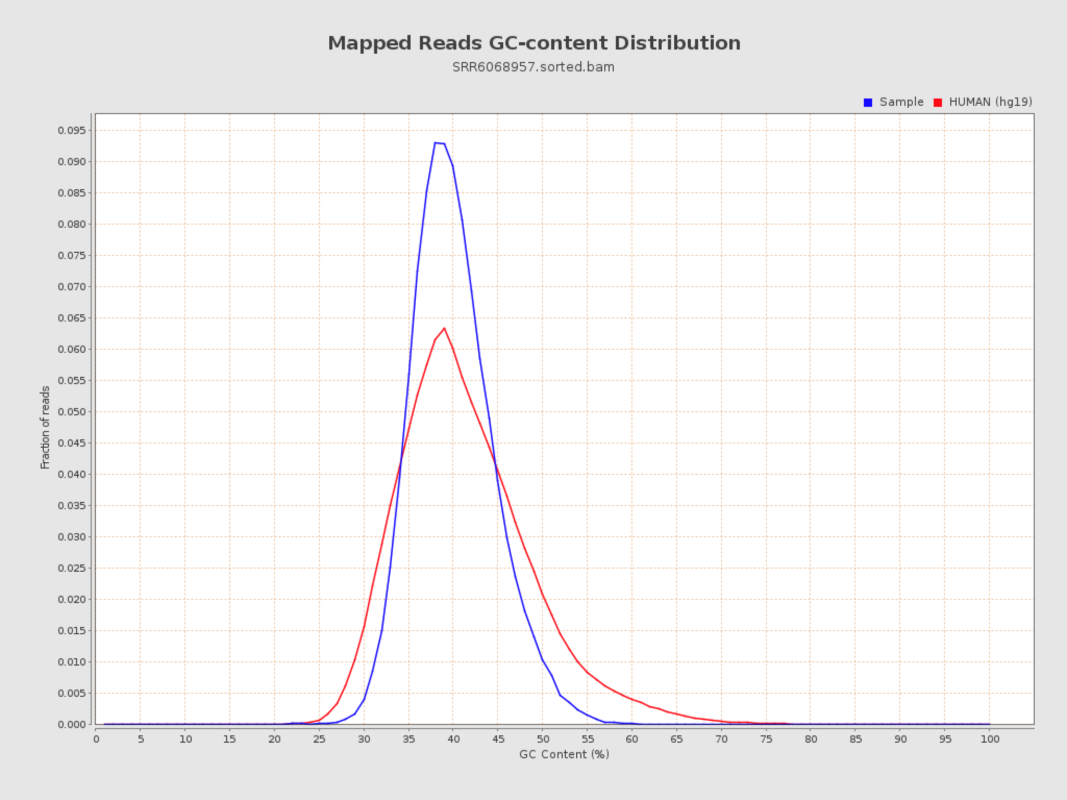
7. Results : Duplication Rate Histogram



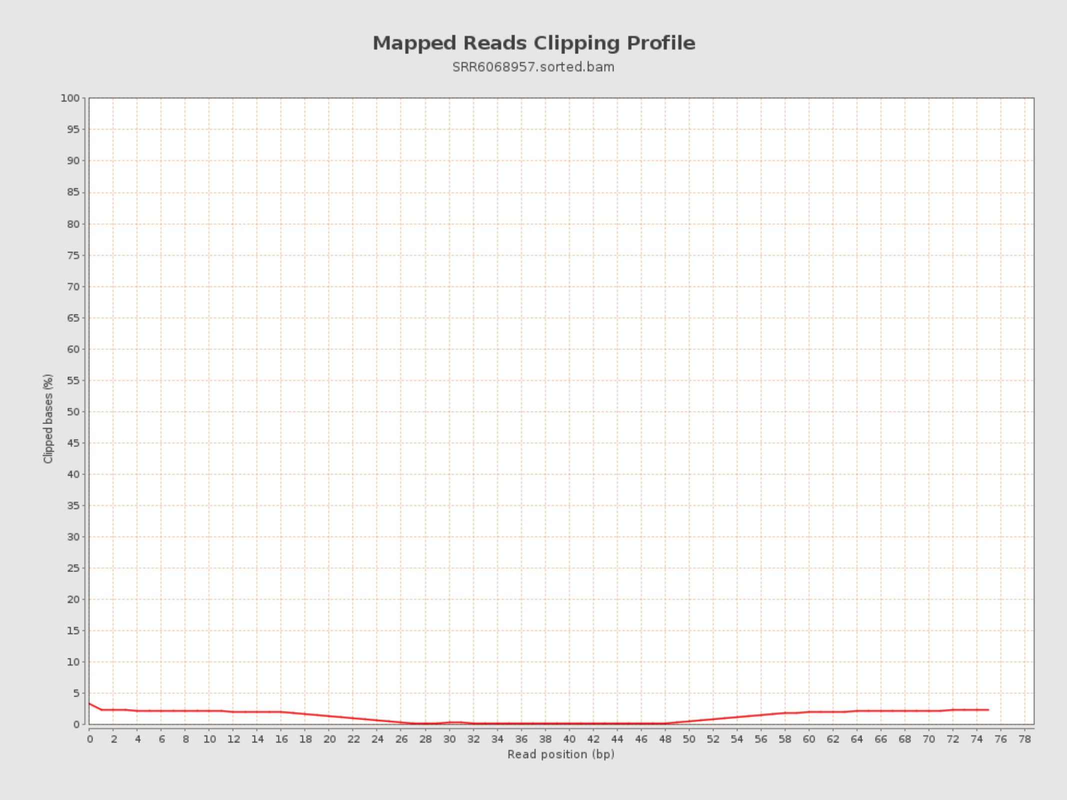
8. Results : Mapped Reads Nucleotide Content



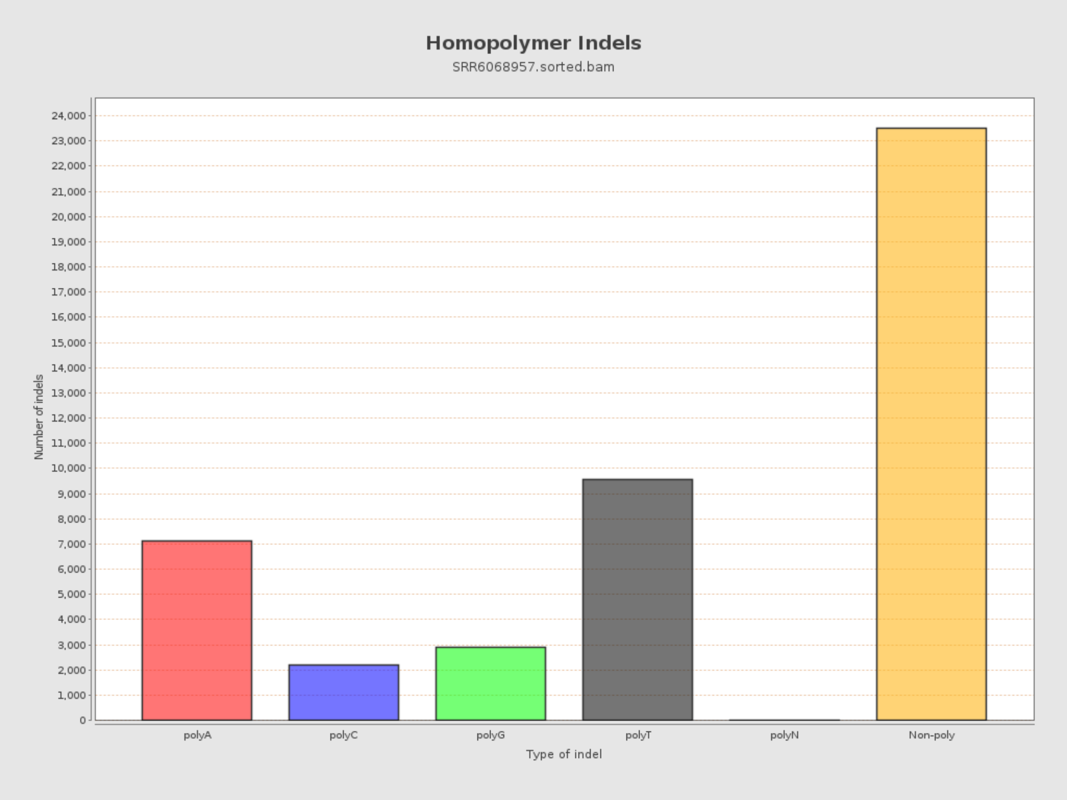
9. Results : Mapped Reads GC-content Distribution



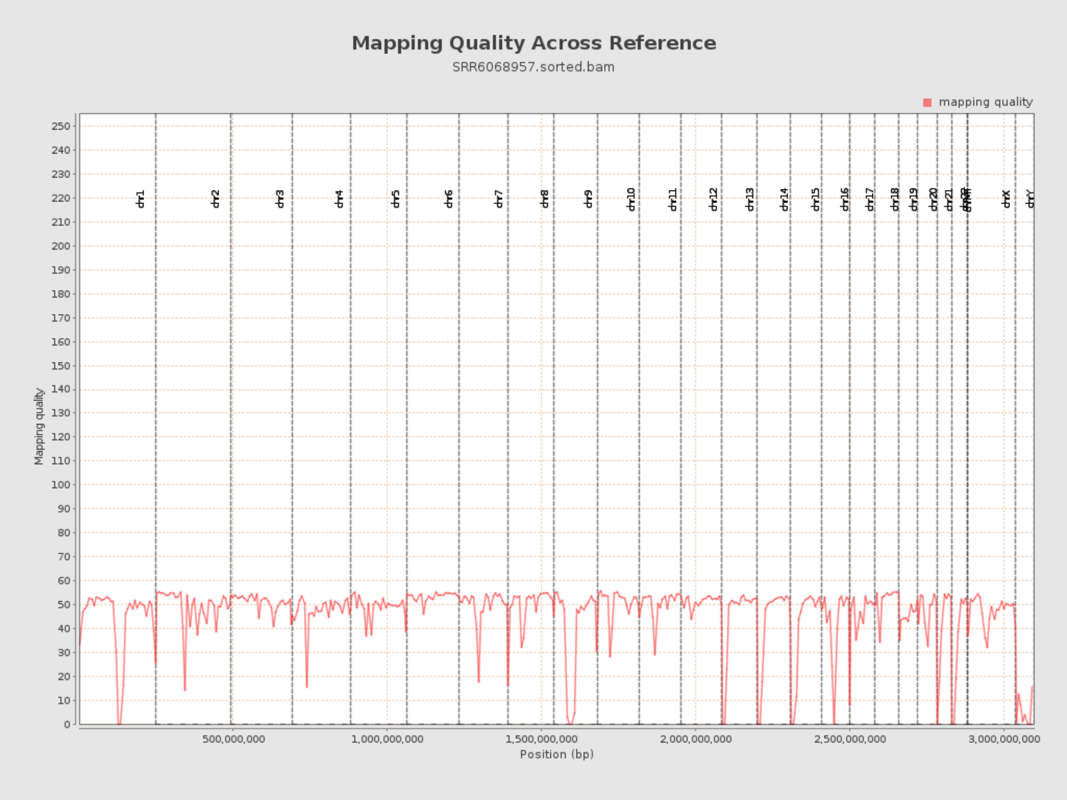
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram