Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:54:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080662.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_SRR3080662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:54:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,384,530
Mapped reads	1,256,253 / 90.73%
Unmapped reads	128,277 / 9.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,544 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	42,581 / 3.08%
Duplication rate	2.92%
Clipped reads	597,374 / 43.15%

2.2. ACGT Content

Number/percentage of A's	21,419,940 / 25.83%
Number/percentage of C's	16,221,374 / 19.56%
Number/percentage of T's	25,311,195 / 30.52%
Number/percentage of G's	19,977,607 / 24.09%
Number/percentage of N's	3,526 / 0%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2274

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

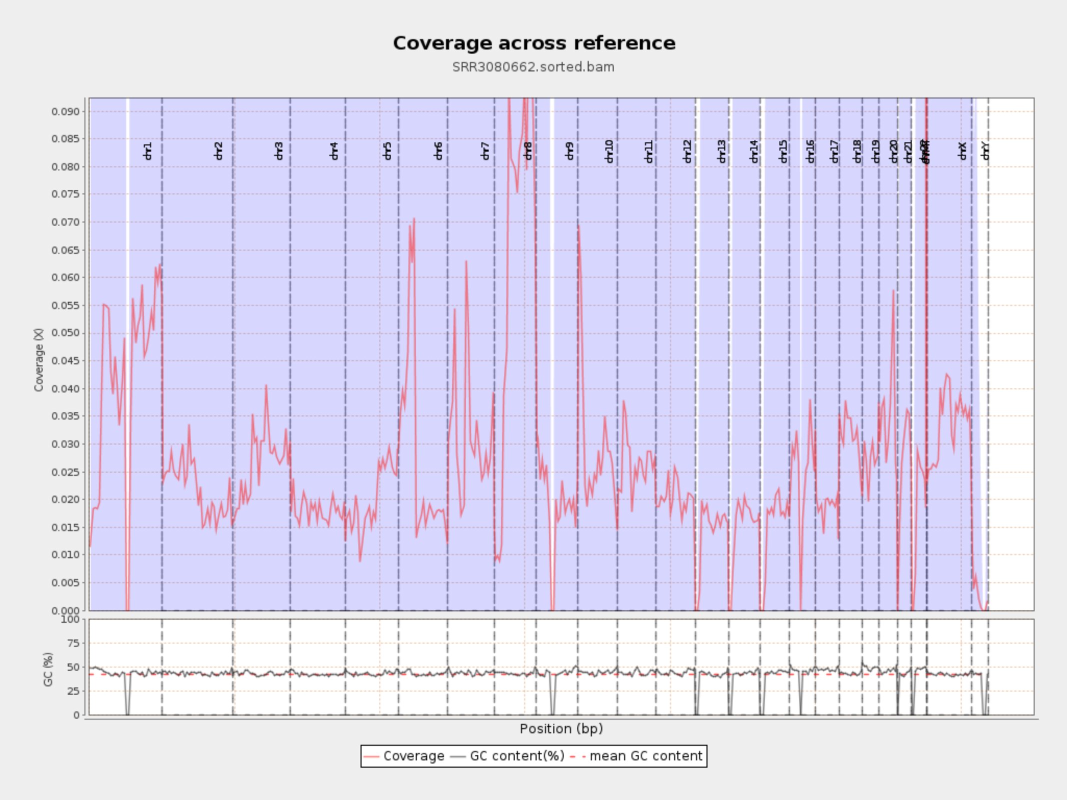
General error rate	0.7%
Mismatches	573,053
Insertions	5,715
Mapped reads with at least one insertion	0.45%
Deletions	17,262
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.39%

2.6. Chromosome stats

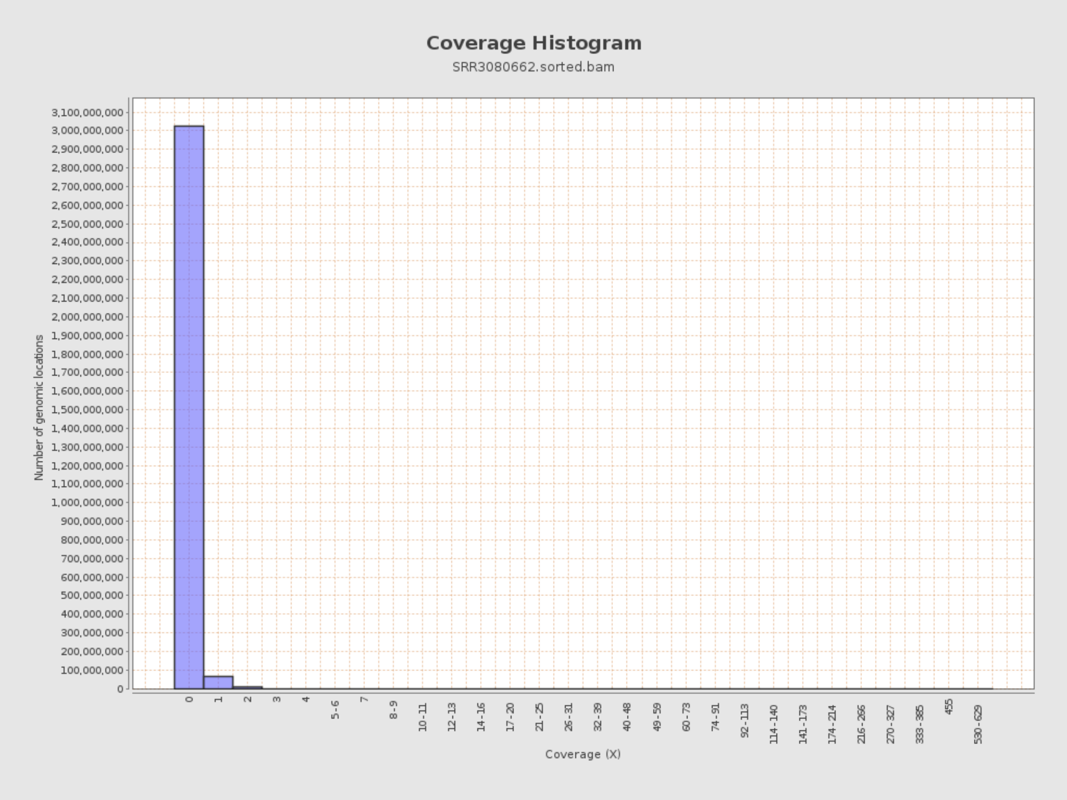
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10255414	0.0411	0.2676
chr2	243199373	5345403	0.022	0.3142
chr3	198022430	5274648	0.0266	0.1805
chr4	191154276	3457874	0.0181	0.1506
chr5	180915260	3657393	0.0202	0.1566
chr6	171115067	4844465	0.0283	0.2215
chr7	159138663	5139753	0.0323	0.4488

chr8	146364022	9664320	0.066	0.3075
chr9	141213431	2629508	0.0186	0.1693
chr10	135534747	4088340	0.0302	0.1983
chr11	135006516	3578625	0.0265	0.1904
chr12	133851895	2703721	0.0202	0.1585
chr13	115169878	1610119	0.014	0.1307
chr14	107349540	1583101	0.0147	0.1373
chr15	102531392	1523151	0.0149	0.1424
chr16	90354753	2271106	0.0251	0.1812
chr17	81195210	1513467	0.0186	0.1534
chr18	78077248	2489235	0.0319	0.2465
chr19	59128983	1603332	0.0271	0.2035
chr20	63025520	2209837	0.0351	0.2118
chr21	48129895	1252617	0.026	0.1832
chr22	51304566	889531	0.0173	0.1467
chrMT	16571	14344	0.8656	1.1296
chrX	155270560	5203084	0.0335	0.208
chrY	59373566	159024	0.0027	0.0602

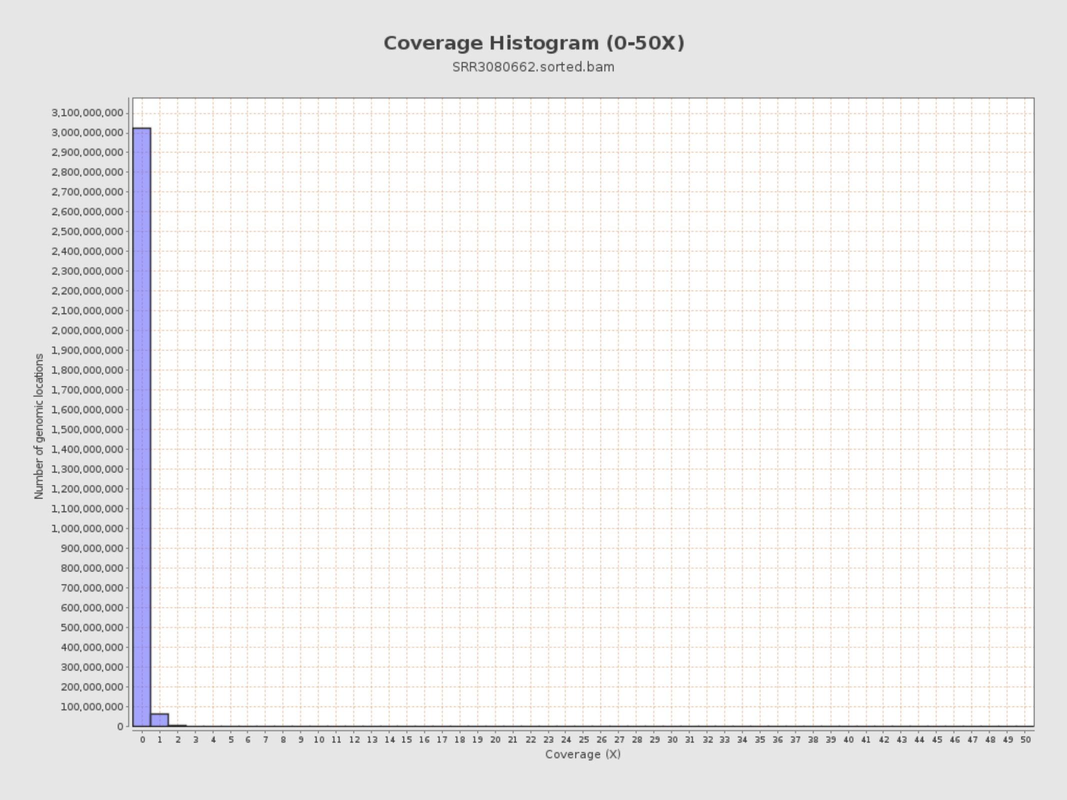
3. Results : Coverage across reference



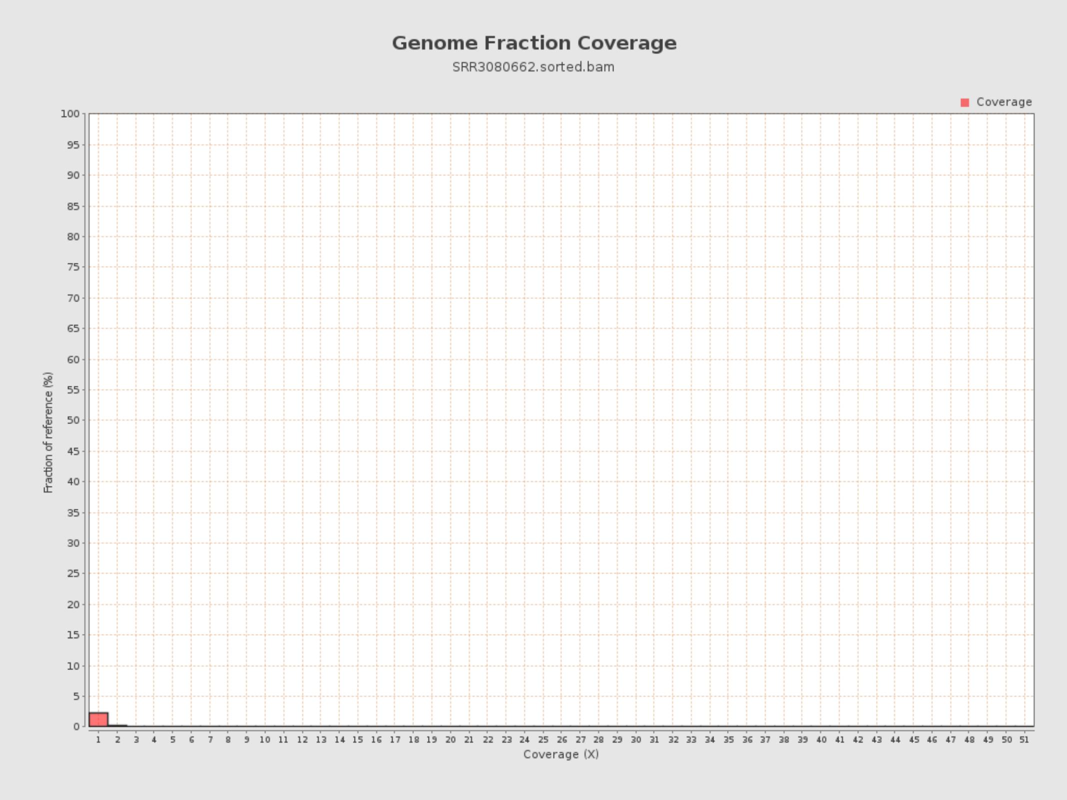
4. Results : Coverage Histogram



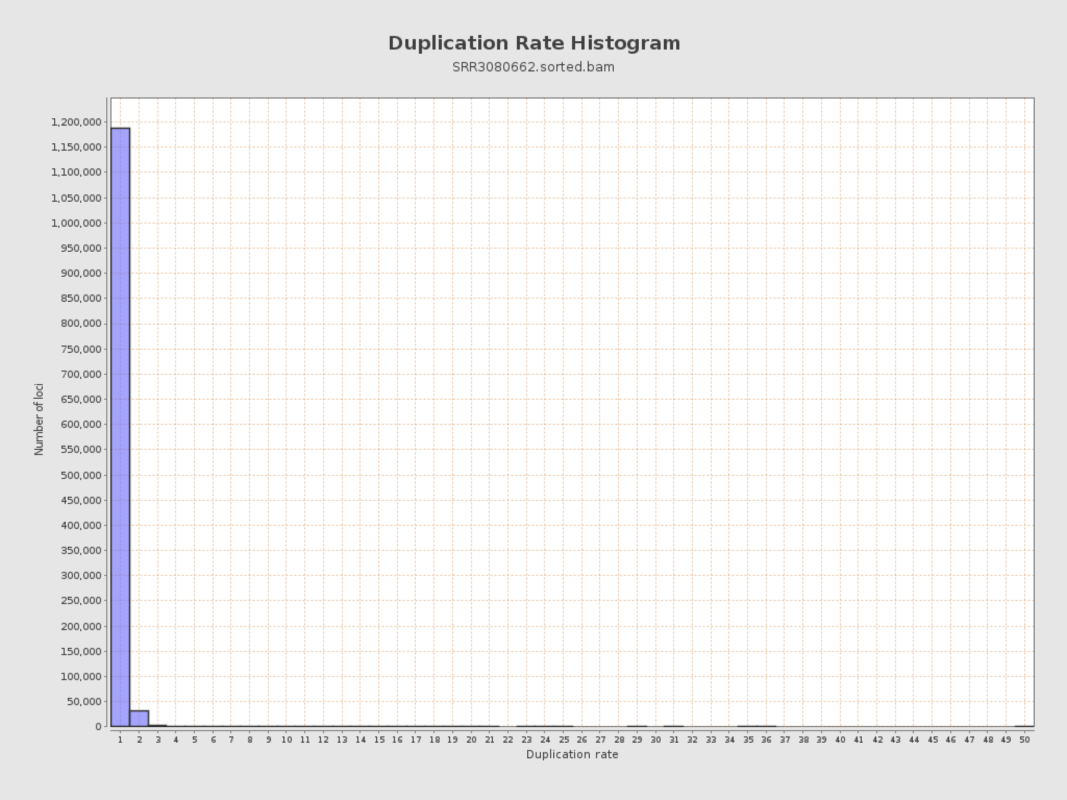
5. Results : Coverage Histogram (0-50X)



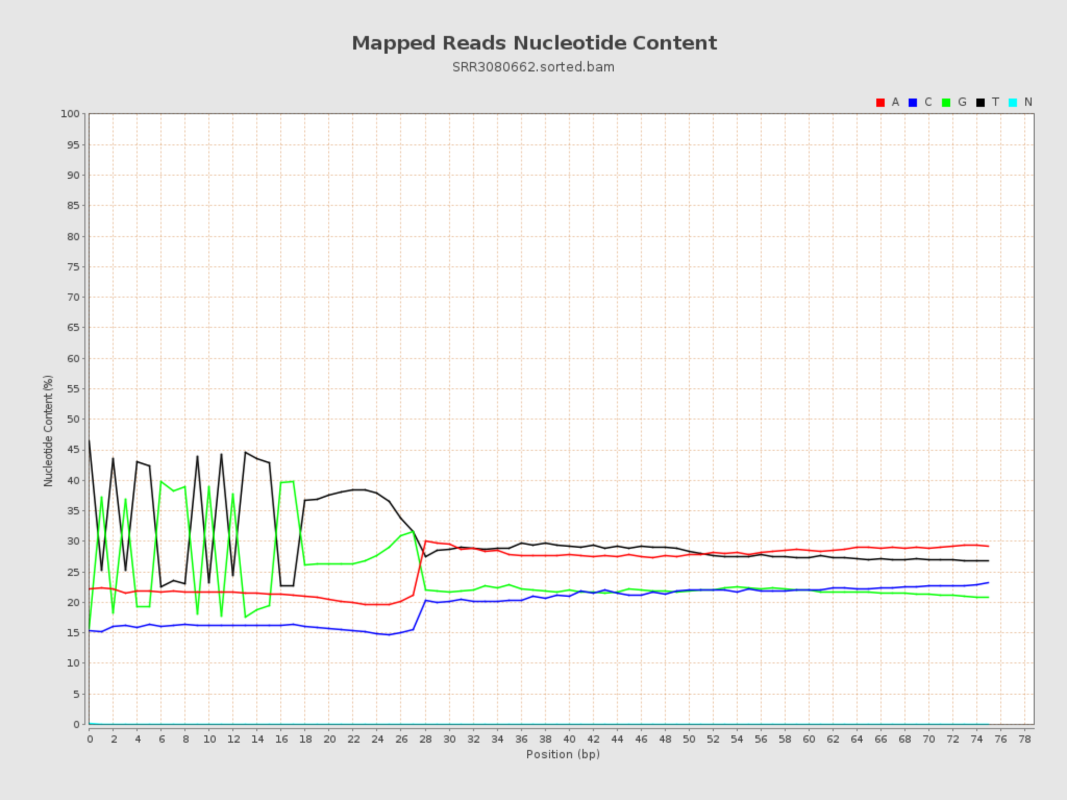
6. Results : Genome Fraction Coverage



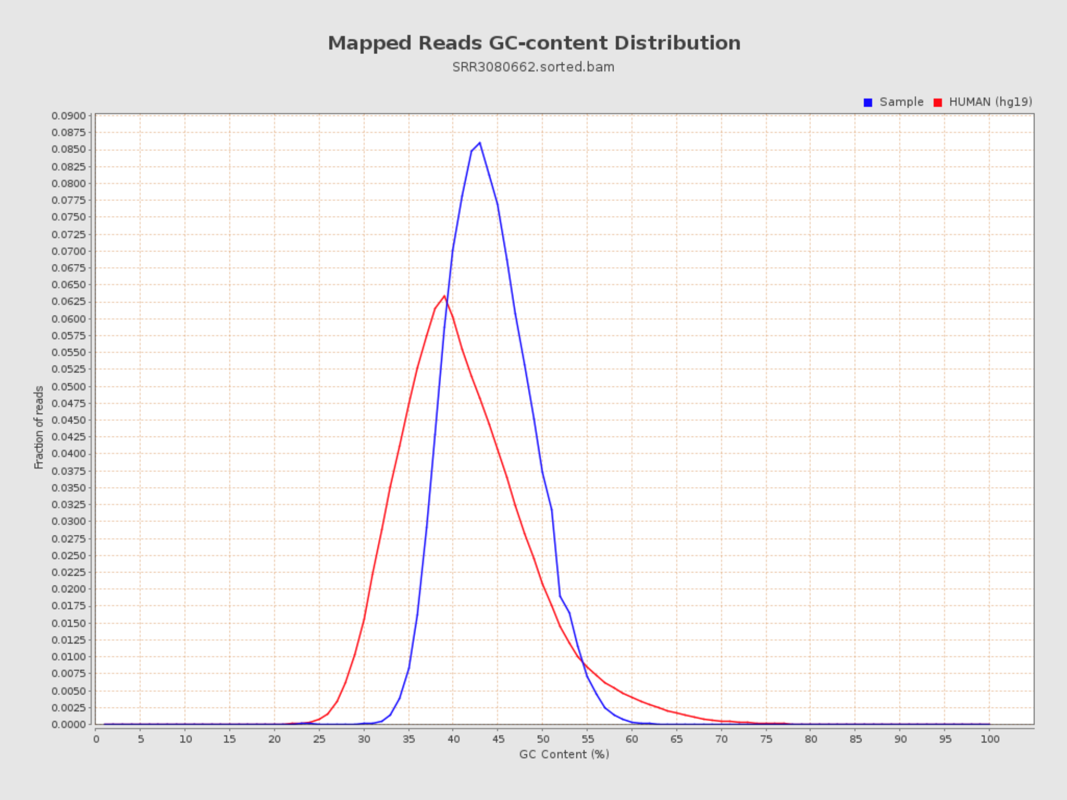
7. Results : Duplication Rate Histogram



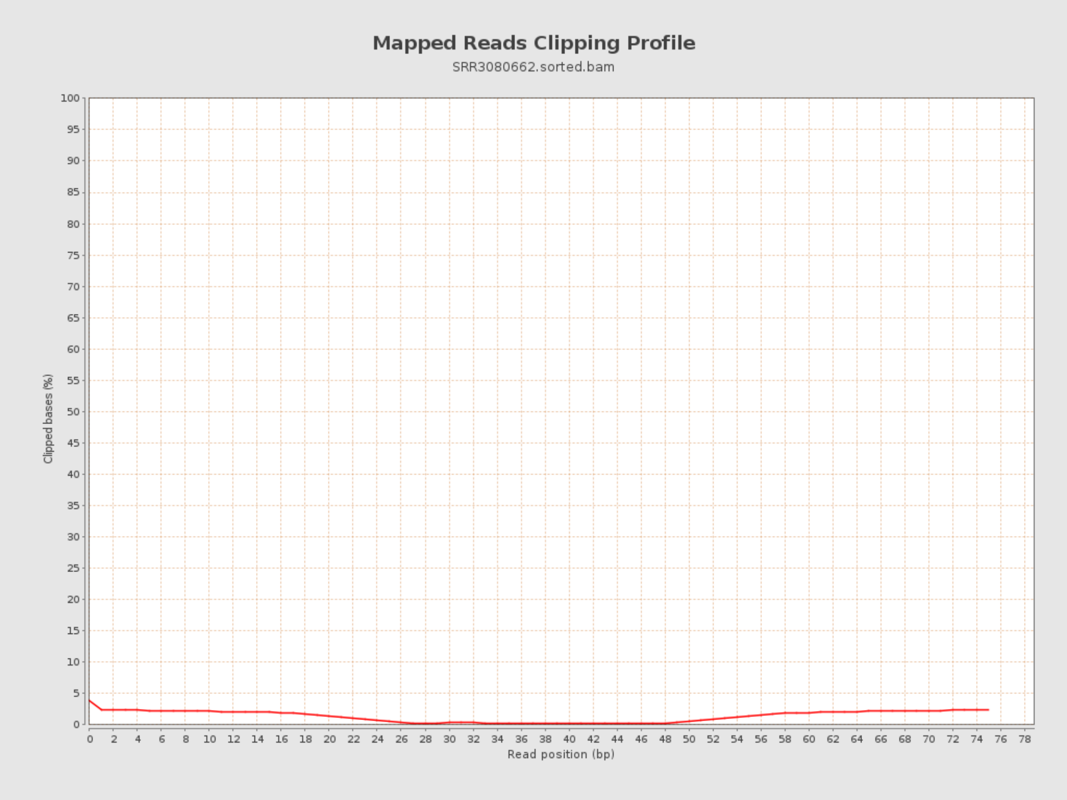
8. Results : Mapped Reads Nucleotide Content



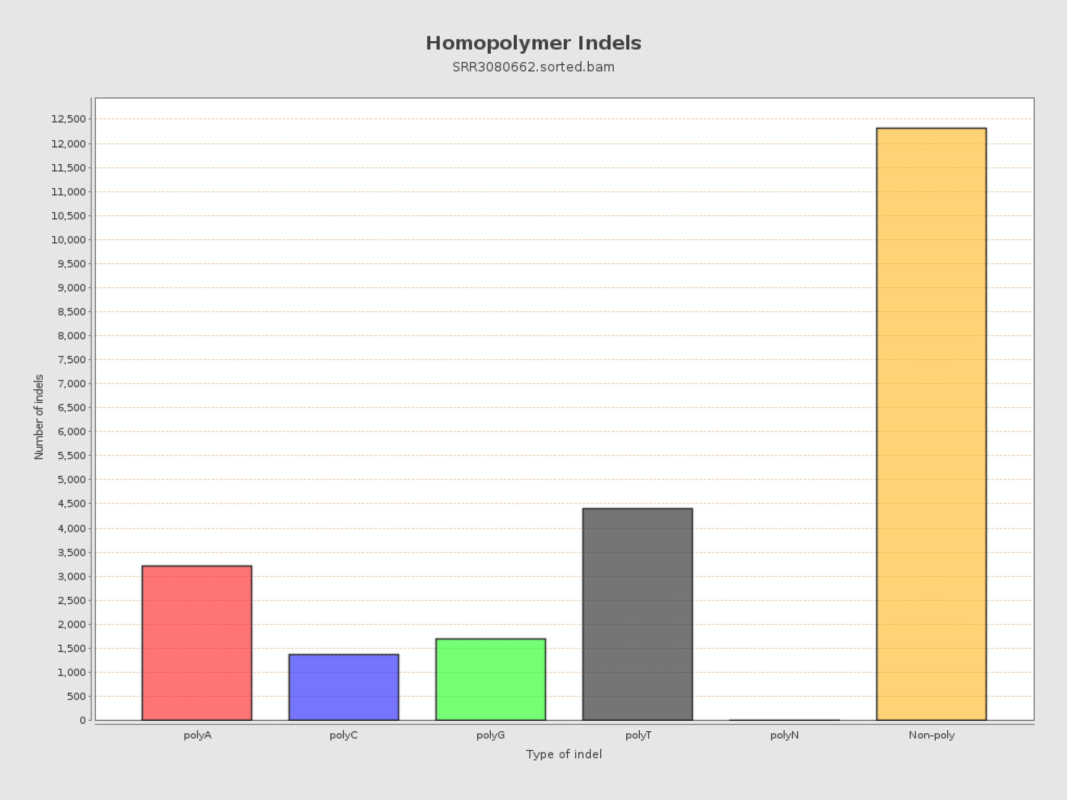
9. Results : Mapped Reads GC-content Distribution



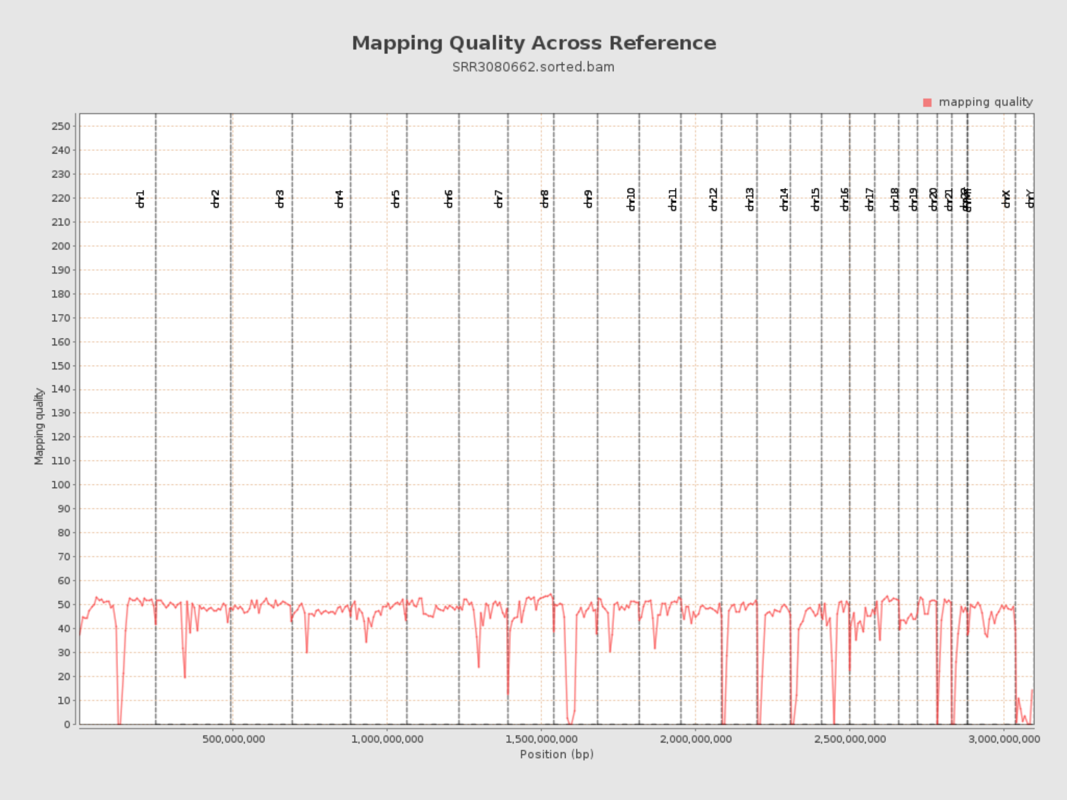
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram