Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:56:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081232.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_SRR3081232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:56:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,014,587
Mapped reads	1,773,130 / 88.01%
Unmapped reads	241,457 / 11.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,260 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	75,388 / 3.74%
Duplication rate	3.69%
Clipped reads	901,114 / 44.73%

2.2. ACGT Content

Number/percentage of A's	33,102,510 / 28.44%
Number/percentage of C's	22,456,830 / 19.29%
Number/percentage of T's	35,687,755 / 30.66%
Number/percentage of G's	25,142,186 / 21.6%
Number/percentage of N's	8,562 / 0.01%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.2675

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

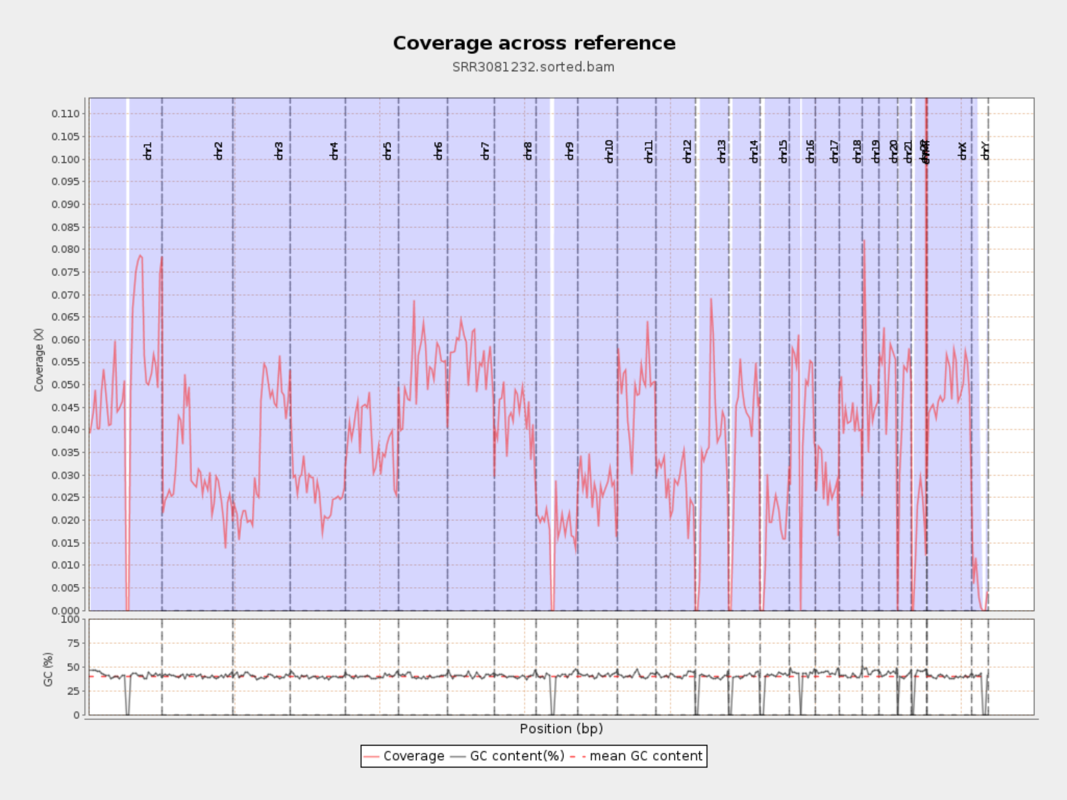
General error rate	0.87%
Mismatches	994,091
Insertions	8,469
Mapped reads with at least one insertion	0.47%
Deletions	26,582
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.29%

2.6. Chromosome stats

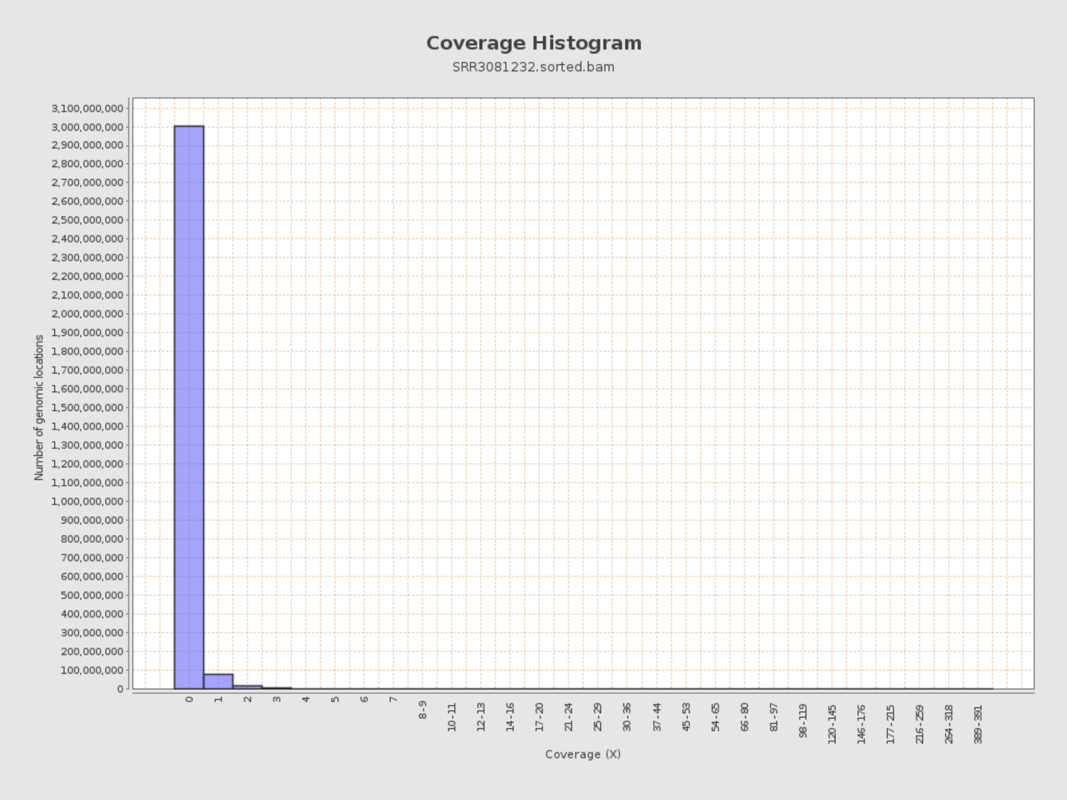
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12618807	0.0506	0.3631
chr2	243199373	7185189	0.0295	0.2947
chr3	198022430	7096870	0.0358	0.2269
chr4	191154276	5074430	0.0265	0.194
chr5	180915260	6811131	0.0376	0.2298
chr6	171115067	9085313	0.0531	0.2984
chr7	159138663	8954503	0.0563	0.3697

chr8	146364022	6268274	0.0428	0.3135
chr9	141213431	2450886	0.0174	0.1806
chr10	135534747	3709321	0.0274	0.2287
chr11	135006516	6567587	0.0486	0.2897
chr12	133851895	3690843	0.0276	0.1974
chr13	115169878	4056129	0.0352	0.2252
chr14	107349540	4162526	0.0388	0.2404
chr15	102531392	1814030	0.0177	0.1649
chr16	90354753	4141022	0.0458	0.2582
chr17	81195210	2285582	0.0281	0.2087
chr18	78077248	3376916	0.0433	0.3159
chr19	59128983	2921375	0.0494	0.3273
chr20	63025520	3341832	0.053	0.279
chr21	48129895	2075820	0.0431	0.2526
chr22	51304566	850023	0.0166	0.1528
chrMT	16571	107510	6.4878	4.7318
chrX	155270560	7526477	0.0485	0.2694
chrY	59373566	269116	0.0045	0.0885

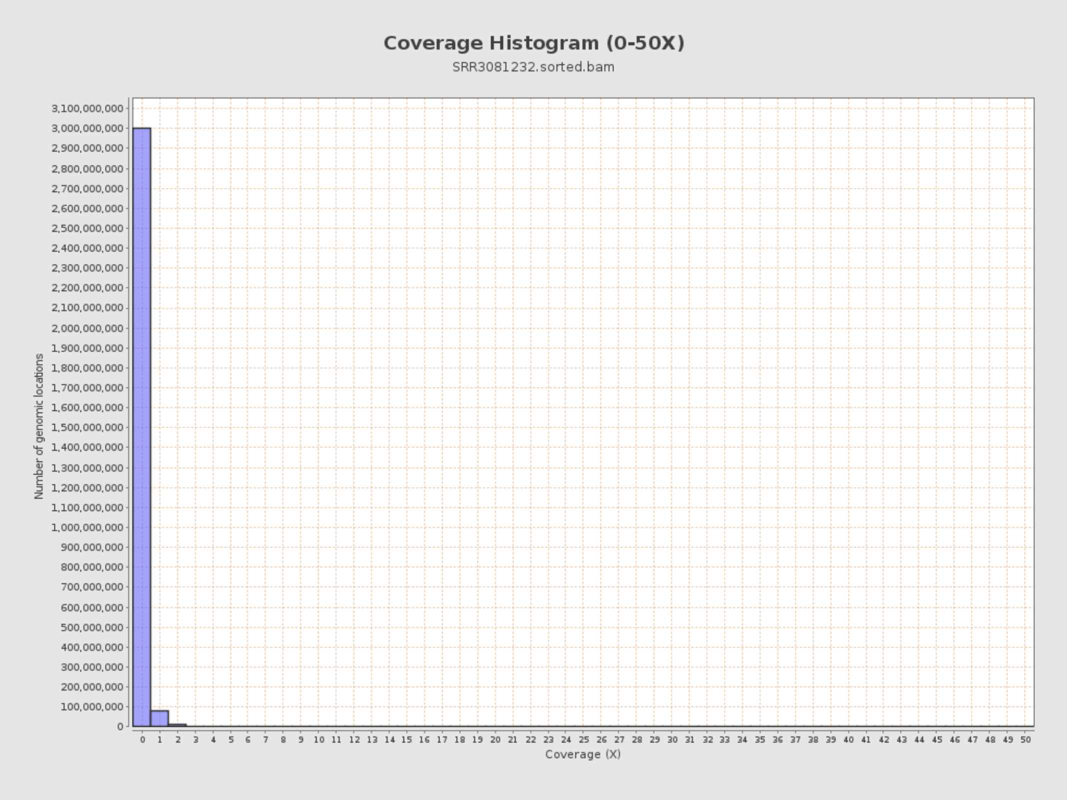
3. Results : Coverage across reference



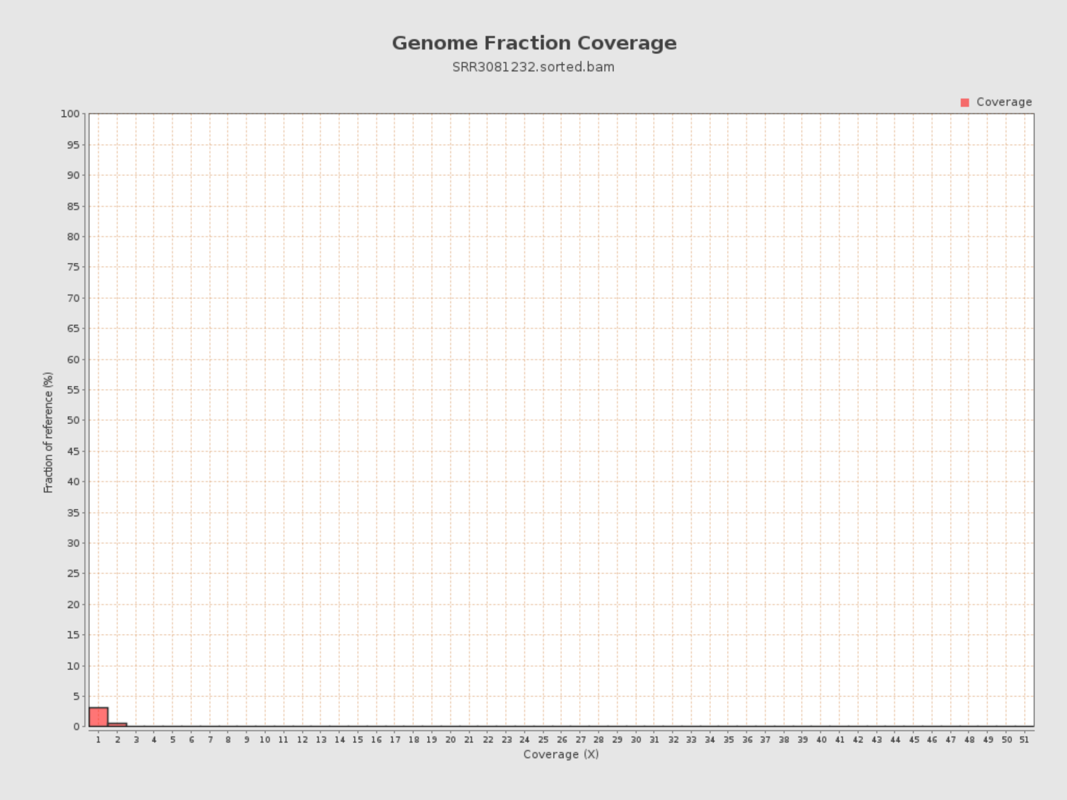
4. Results : Coverage Histogram



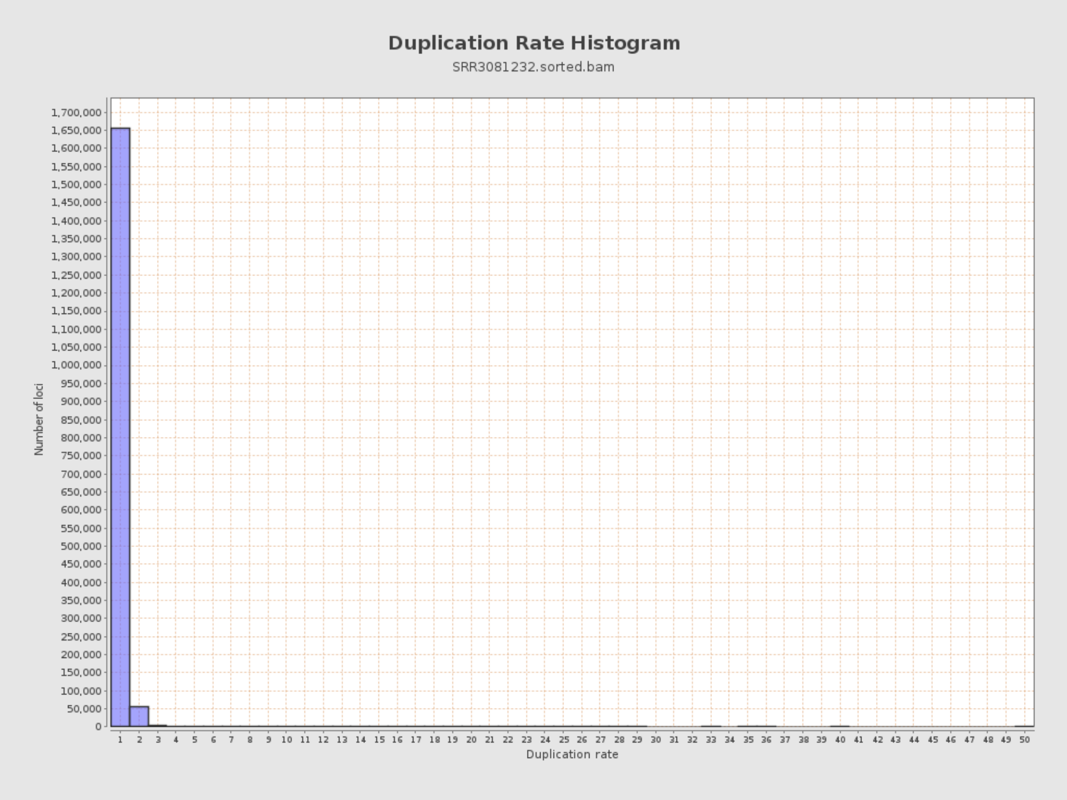
5. Results : Coverage Histogram (0-50X)



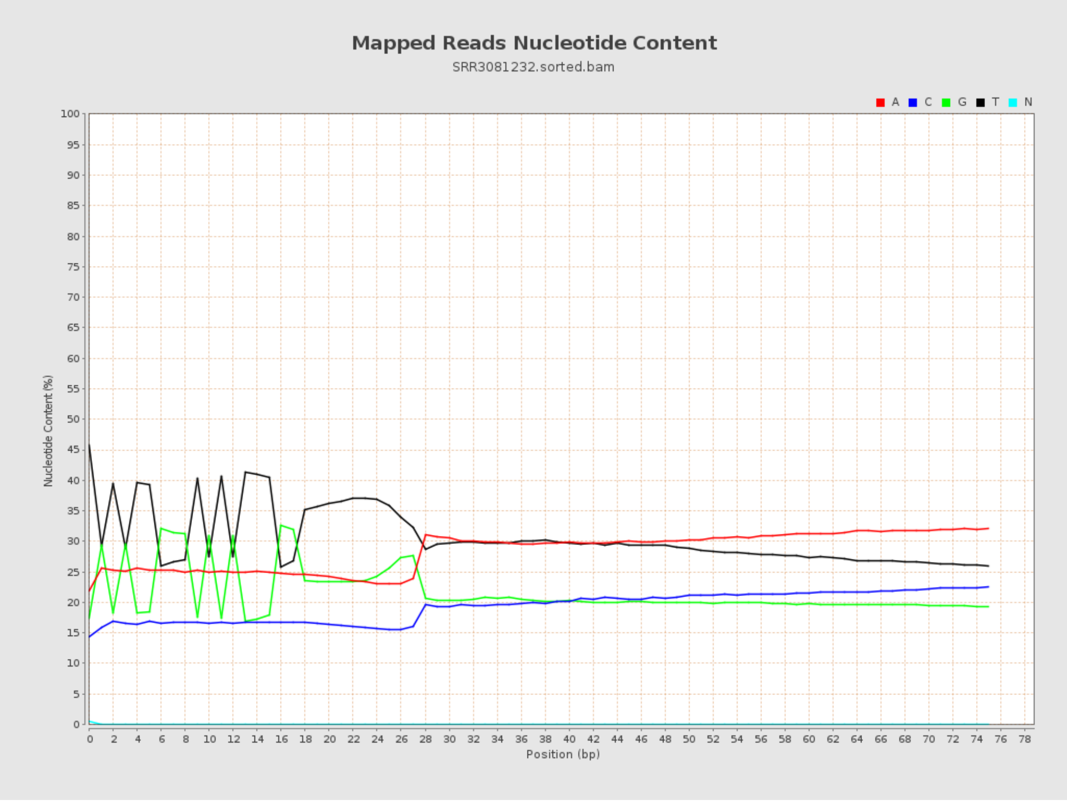
6. Results : Genome Fraction Coverage



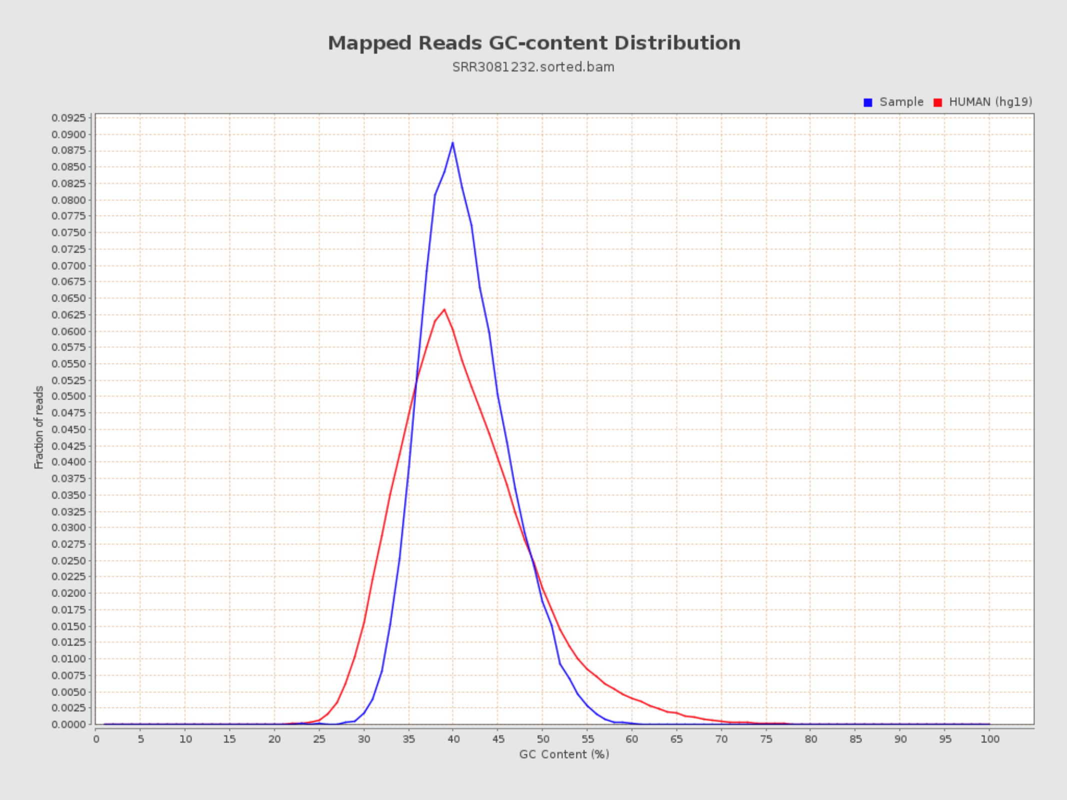
7. Results : Duplication Rate Histogram



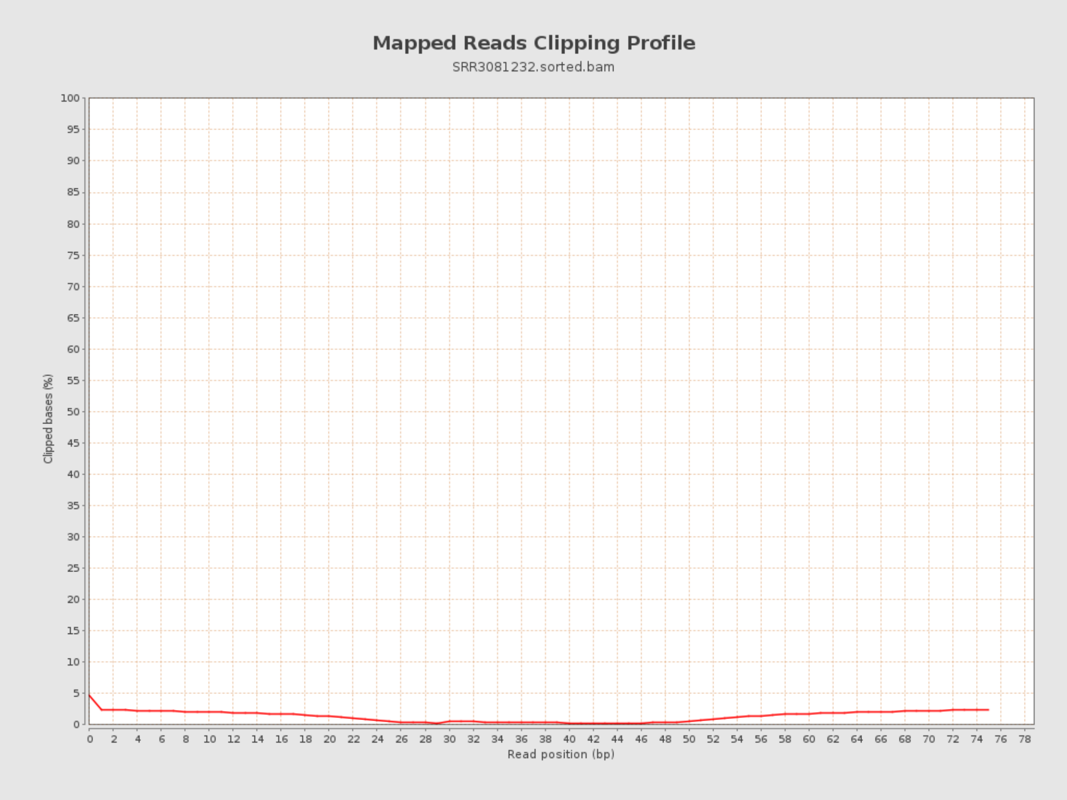
8. Results : Mapped Reads Nucleotide Content



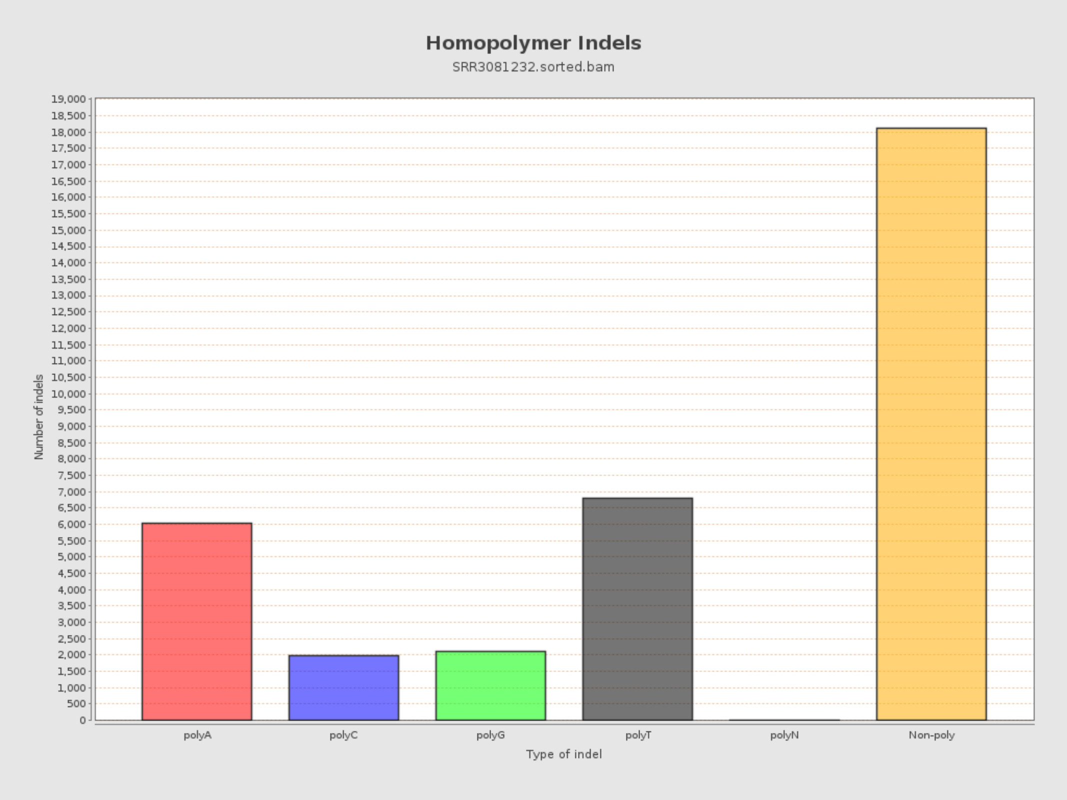
9. Results : Mapped Reads GC-content Distribution



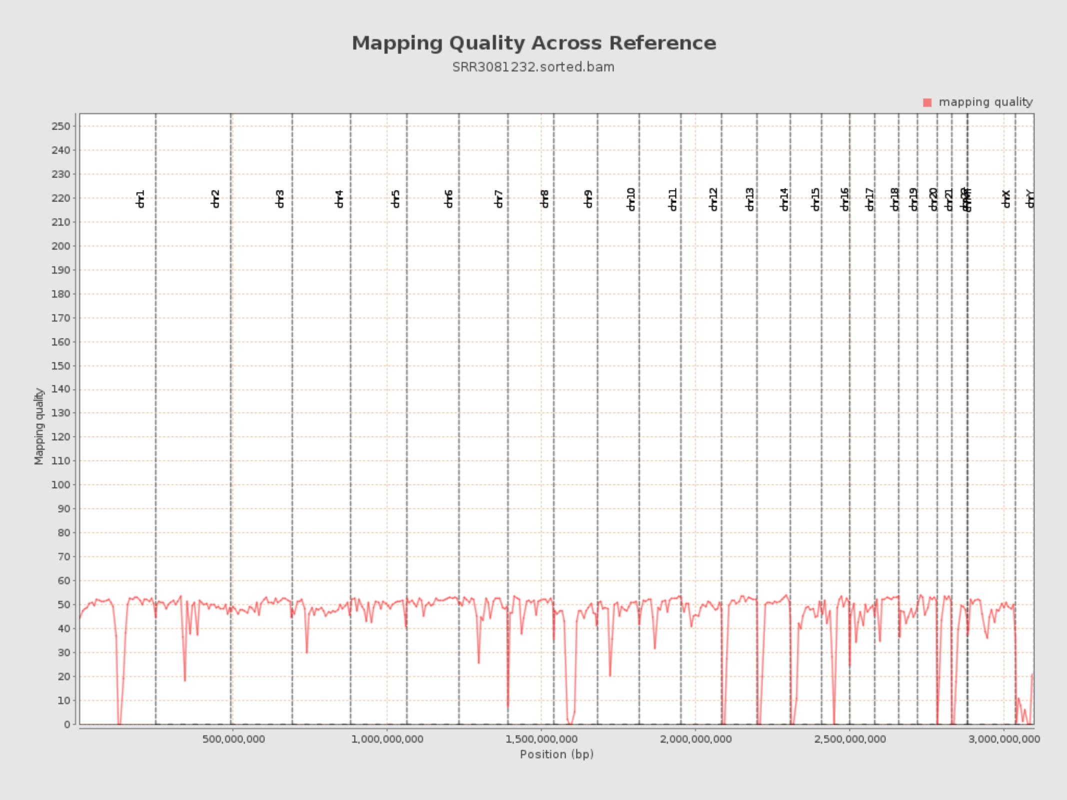
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram