Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:00:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080633.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_SRR3080633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:00:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,893,007
Mapped reads	4,829,840 / 81.96%
Unmapped reads	1,063,167 / 18.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,307 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	271,485 / 4.61%
Duplication rate	4.36%
Clipped reads	2,348,329 / 39.85%

2.2. ACGT Content

Number/percentage of A's	86,799,372 / 27.2%
Number/percentage of C's	56,509,940 / 17.71%
Number/percentage of T's	104,032,398 / 32.6%
Number/percentage of G's	71,515,502 / 22.41%
Number/percentage of N's	259,063 / 0.08%
GC Percentage	40.12%

2.3. Coverage

Mean	0.1031

Standard Deviation	0.7928

2.4. Mapping Quality

Mean Mapping Quality	46.82

2.5. Mismatches and indels

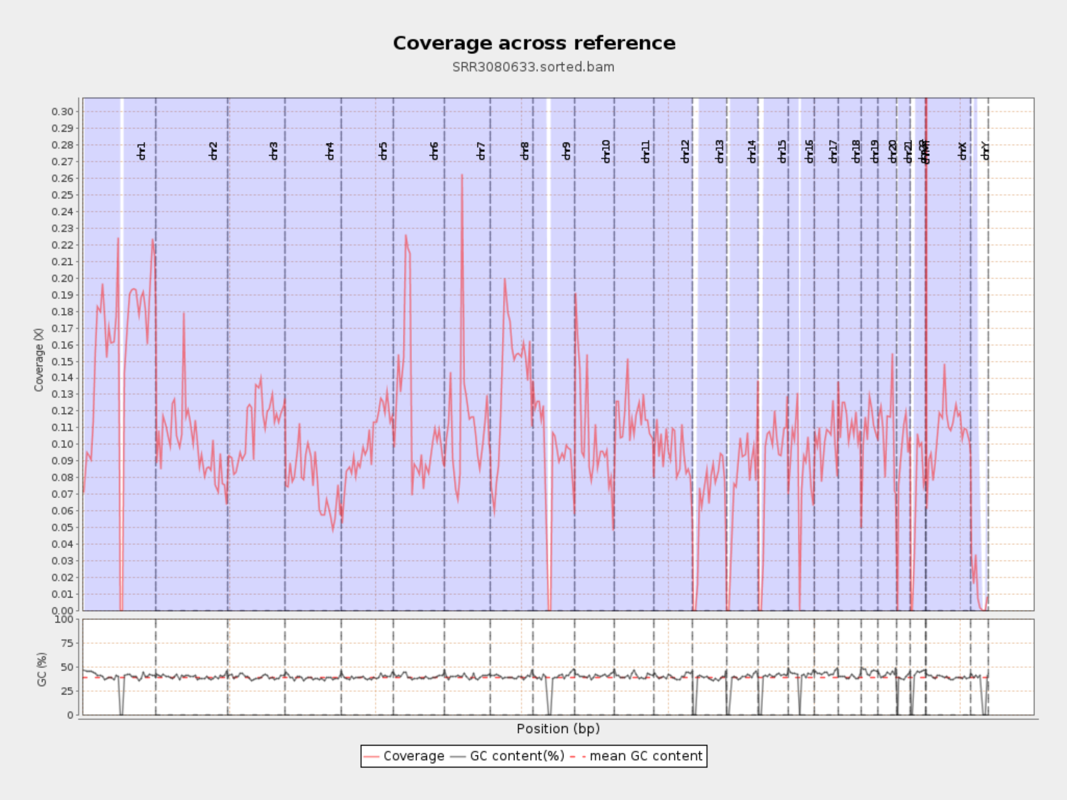
General error rate	0.93%
Mismatches	2,905,857
Insertions	27,381
Mapped reads with at least one insertion	0.56%
Deletions	82,312
Mapped reads with at least one deletion	1.69%
Homopolymer indels	48.14%

2.6. Chromosome stats

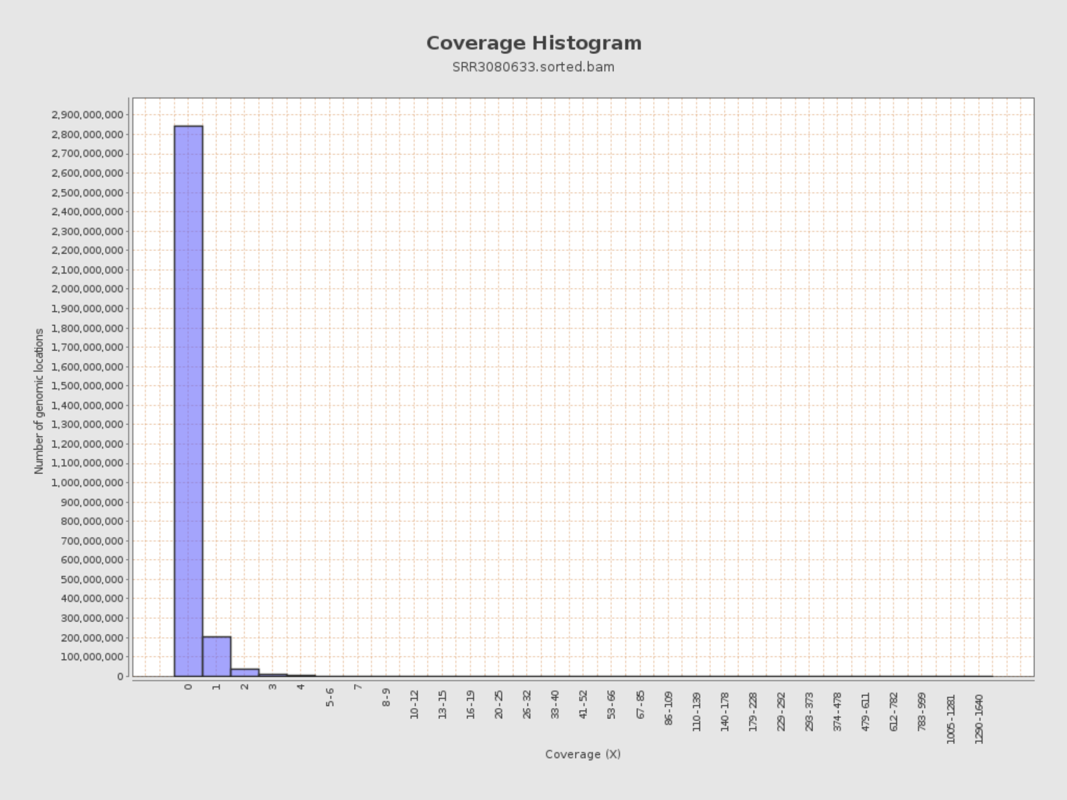
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39122220	0.157	1.2938
chr2	243199373	24436162	0.1005	0.7149
chr3	198022430	21902714	0.1106	0.4112
chr4	191154276	14542090	0.0761	0.3632
chr5	180915260	18003935	0.0995	0.3844
chr6	171115067	20109441	0.1175	0.6225
chr7	159138663	18005190	0.1131	1.9834

chr8	146364022	20207286	0.1381	0.9848
chr9	141213431	12815203	0.0908	0.6316
chr10	135534747	14195427	0.1047	0.7606
chr11	135006516	15575852	0.1154	0.5943
chr12	133851895	12736698	0.0952	0.3852
chr13	115169878	7594786	0.0659	0.3036
chr14	107349540	8108129	0.0755	0.3984
chr15	102531392	8675226	0.0846	0.3511
chr16	90354753	7554674	0.0836	0.4212
chr17	81195210	8369884	0.1031	0.4672
chr18	78077248	8871762	0.1136	1.1407
chr19	59128983	6443641	0.109	0.8479
chr20	63025520	6860517	0.1089	0.4216
chr21	48129895	4332779	0.09	0.422
chr22	51304566	3360362	0.0655	0.3062
chrMT	16571	119123	7.1886	6.8175
chrX	155270560	16626179	0.1071	0.4577
chrY	59373566	682673	0.0115	0.2301

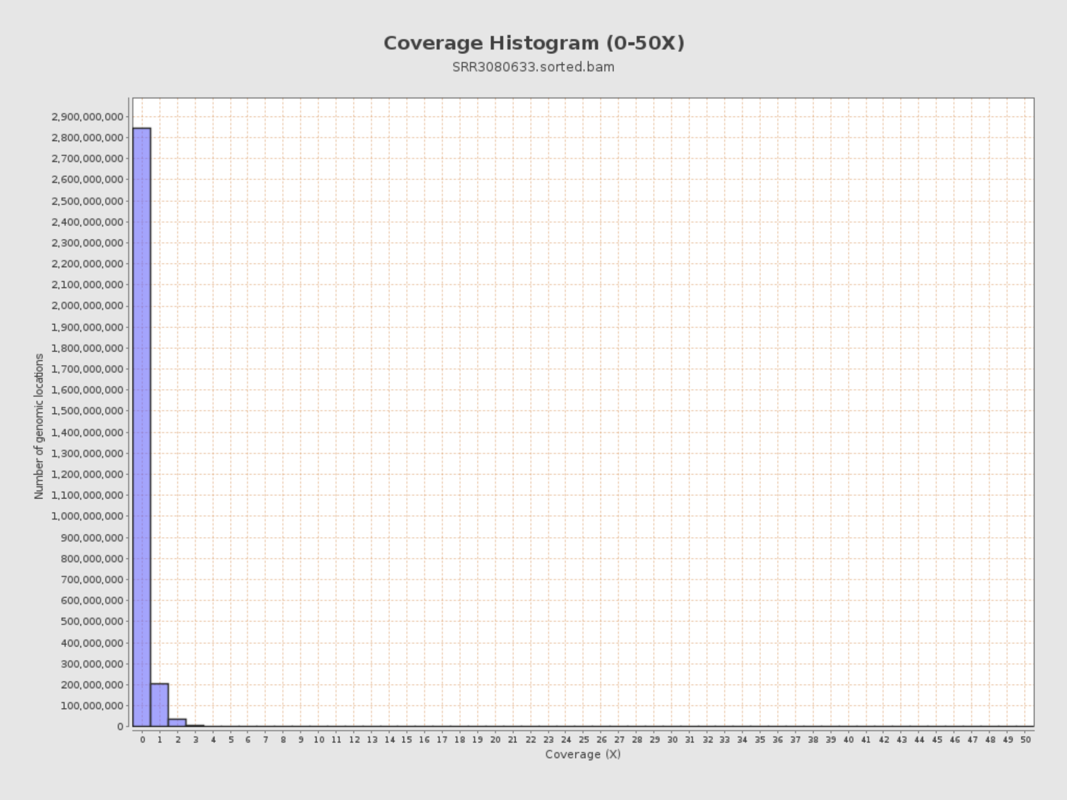
3. Results : Coverage across reference



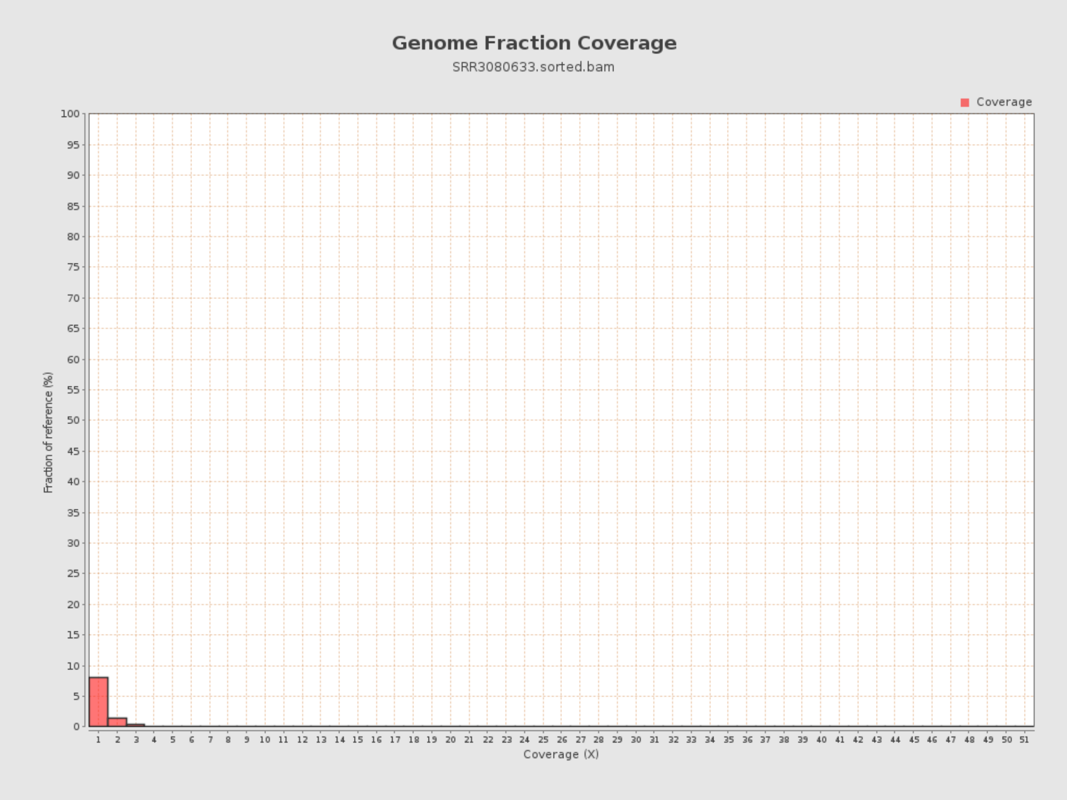
4. Results : Coverage Histogram



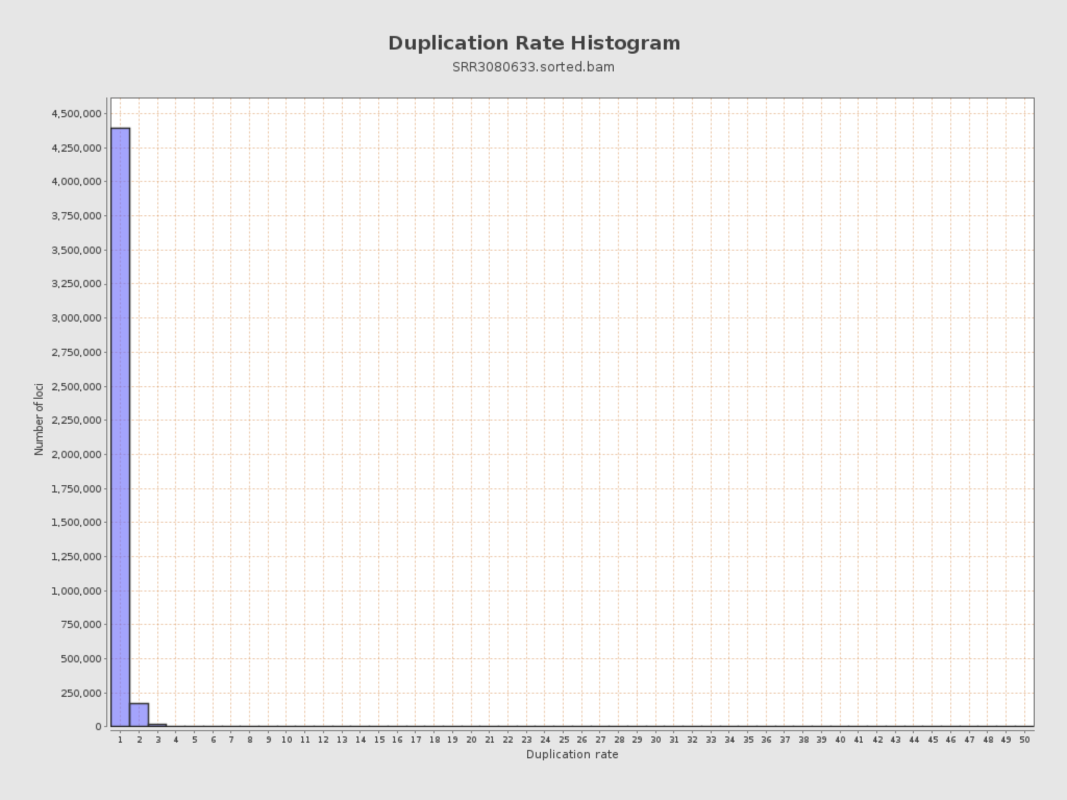
5. Results : Coverage Histogram (0-50X)



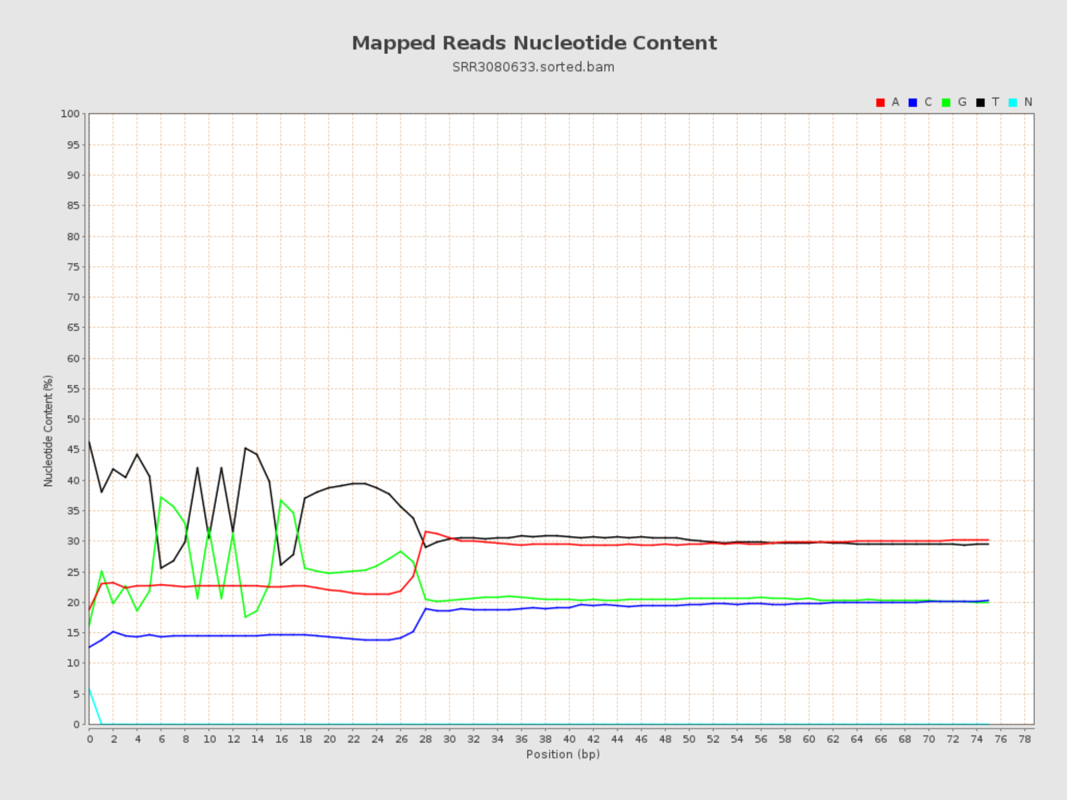
6. Results : Genome Fraction Coverage



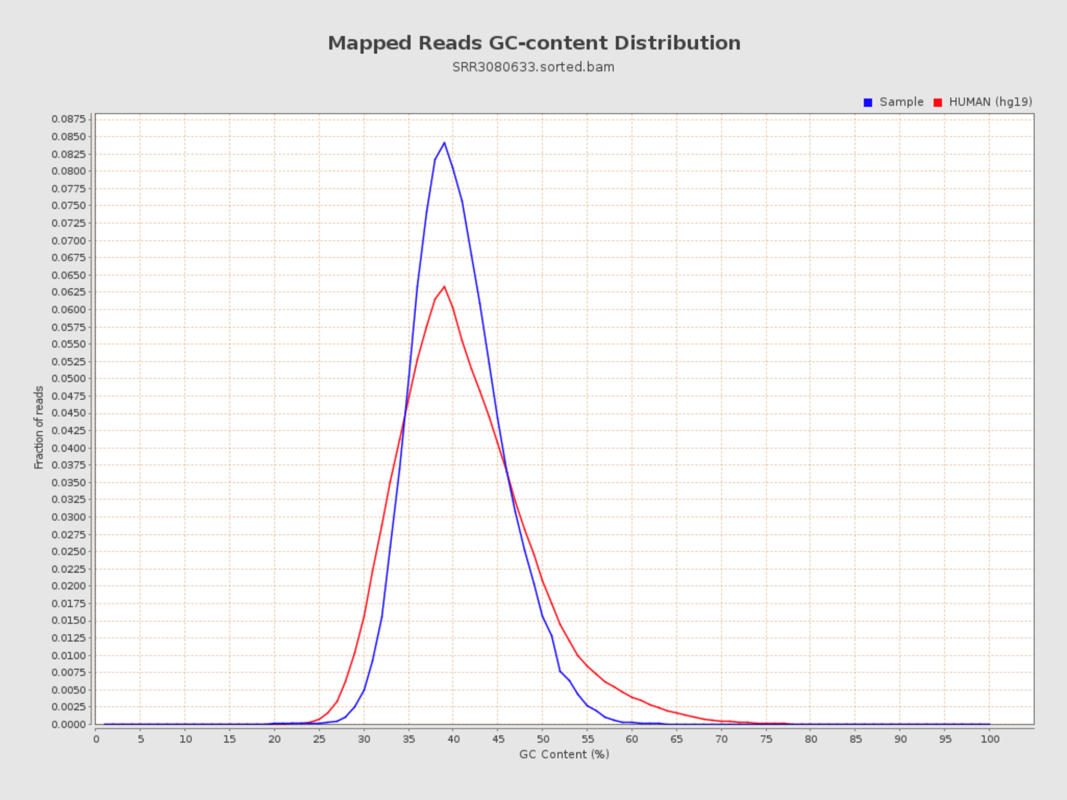
7. Results : Duplication Rate Histogram



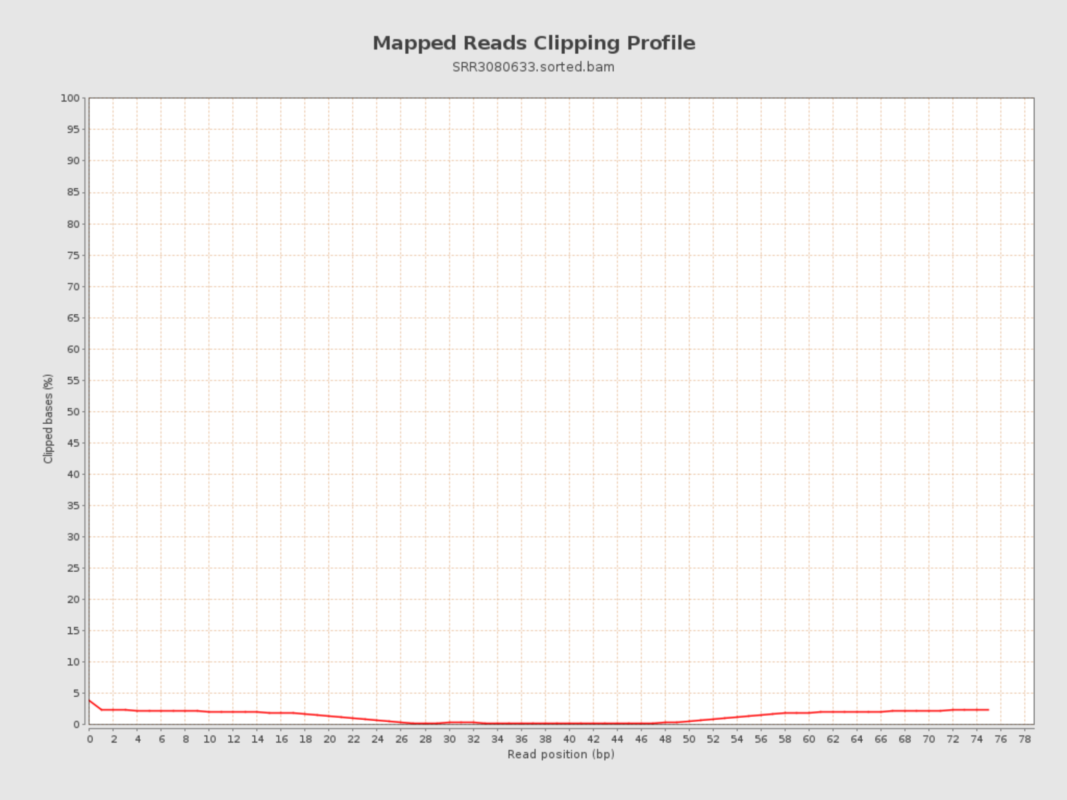
8. Results : Mapped Reads Nucleotide Content



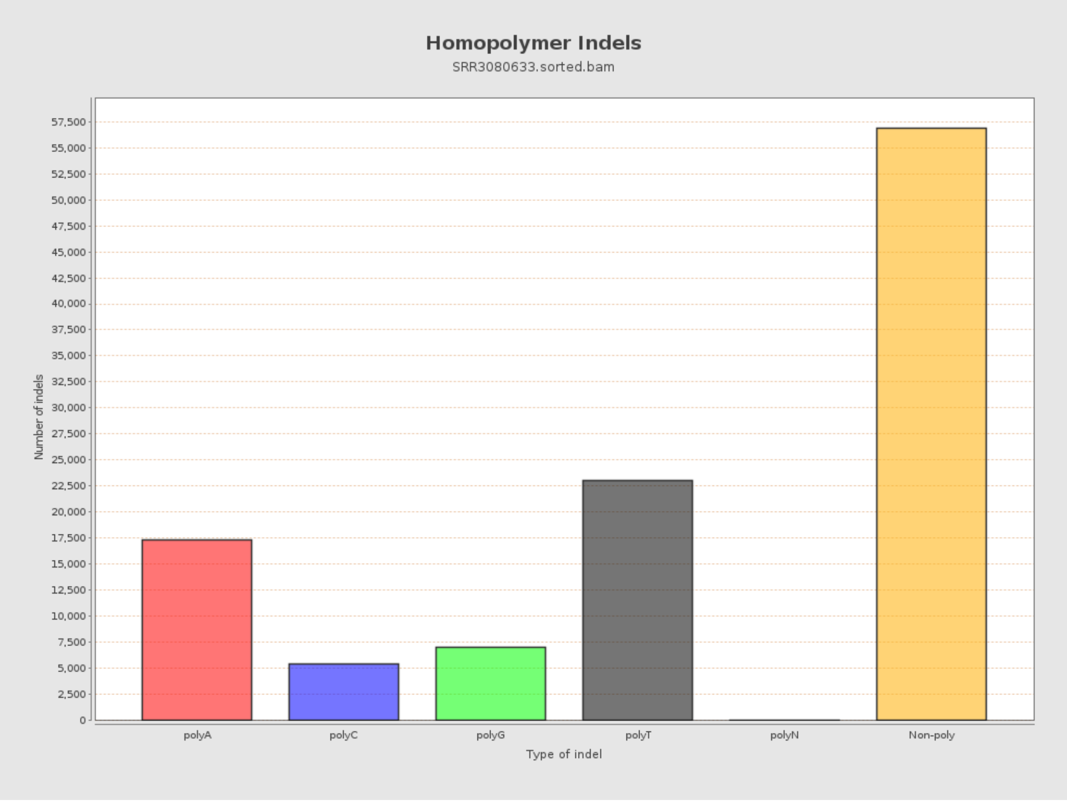
9. Results : Mapped Reads GC-content Distribution



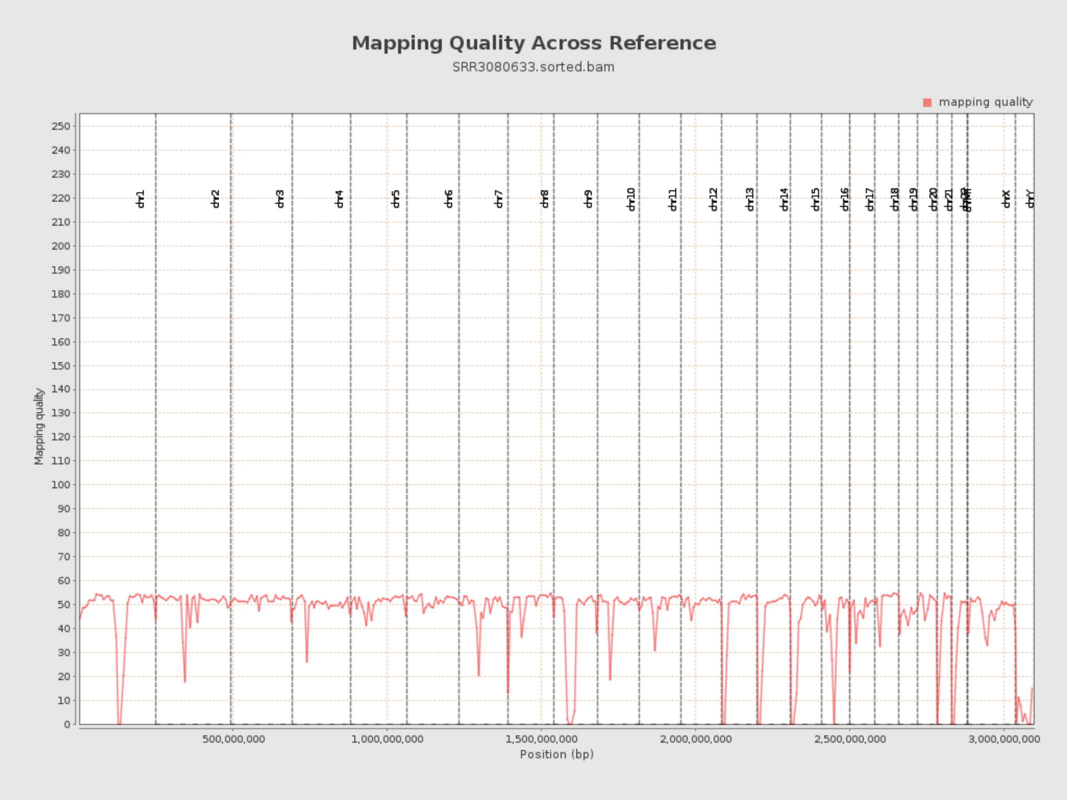
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram