Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:48:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080643.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_SRR3080643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:48:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,528,159
Mapped reads	1,396,153 / 91.36%
Unmapped reads	132,006 / 8.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,859 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	53,246 / 3.48%
Duplication rate	3.22%
Clipped reads	623,900 / 40.83%

2.2. ACGT Content

Number/percentage of A's	25,352,387 / 27.22%
Number/percentage of C's	17,370,236 / 18.65%
Number/percentage of T's	29,331,319 / 31.49%
Number/percentage of G's	21,092,160 / 22.64%
Number/percentage of N's	4,043 / 0%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2518

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

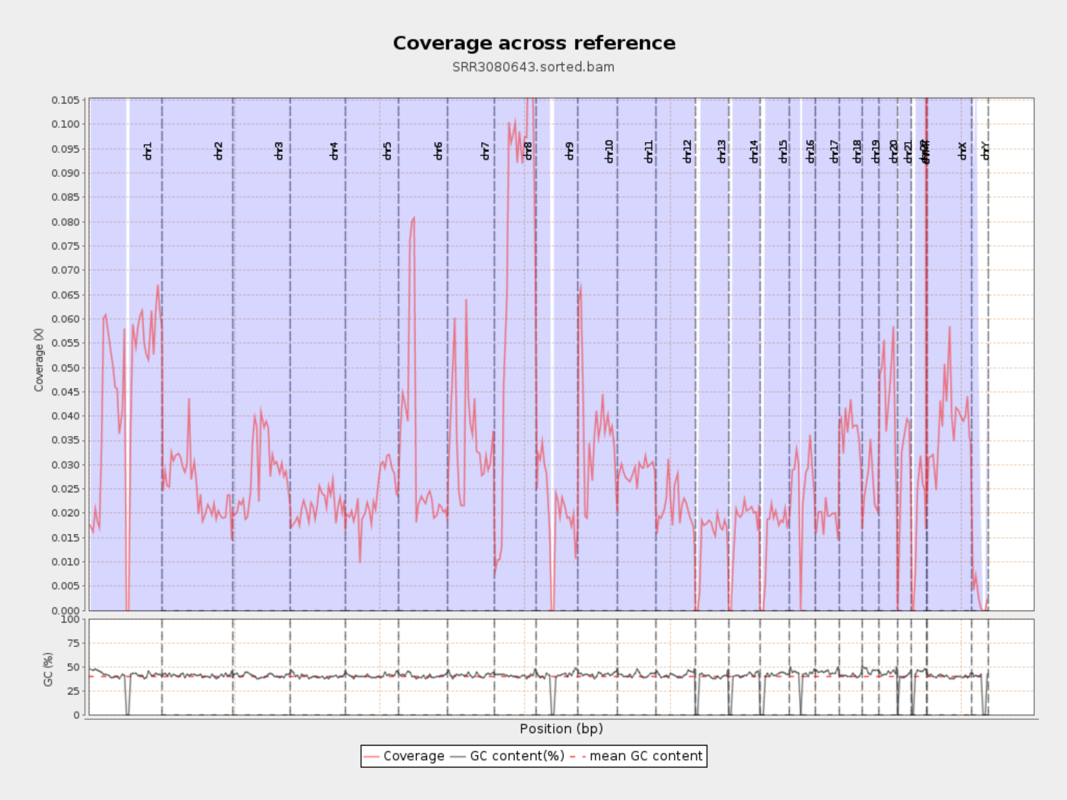
General error rate	0.7%
Mismatches	641,712
Insertions	6,957
Mapped reads with at least one insertion	0.49%
Deletions	21,625
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.44%

2.6. Chromosome stats

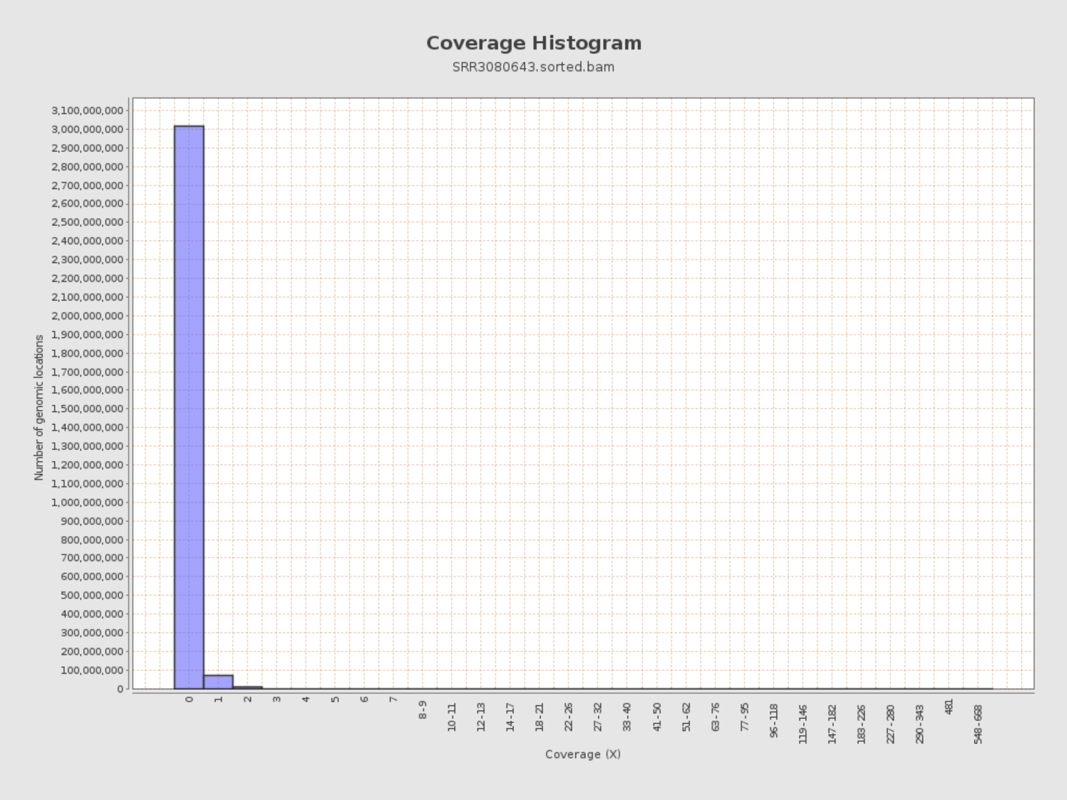
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11142192	0.0447	0.352
chr2	243199373	6143399	0.0253	0.3408
chr3	198022430	5668309	0.0286	0.1877
chr4	191154276	4078428	0.0213	0.1685
chr5	180915260	4217861	0.0233	0.169
chr6	171115067	5646784	0.033	0.2463
chr7	159138663	5755547	0.0362	0.4451

chr8	146364022	11034281	0.0754	0.3525
chr9	141213431	2905462	0.0206	0.1938
chr10	135534747	5134514	0.0379	0.2325
chr11	135006516	3857885	0.0286	0.2232
chr12	133851895	2859573	0.0214	0.1631
chr13	115169878	1695626	0.0147	0.1348
chr14	107349540	1814713	0.0169	0.1462
chr15	102531392	1583902	0.0154	0.1456
chr16	90354753	2361527	0.0261	0.1844
chr17	81195210	1531940	0.0189	0.1613
chr18	78077248	2927888	0.0375	0.2795
chr19	59128983	1536273	0.026	0.2323
chr20	63025520	2831241	0.0449	0.2385
chr21	48129895	1363442	0.0283	0.1898
chr22	51304566	927136	0.0181	0.1484
chrMT	16571	15795	0.9532	1.0375
chrX	155270560	5970182	0.0385	0.2299
chrY	59373566	181328	0.0031	0.0656

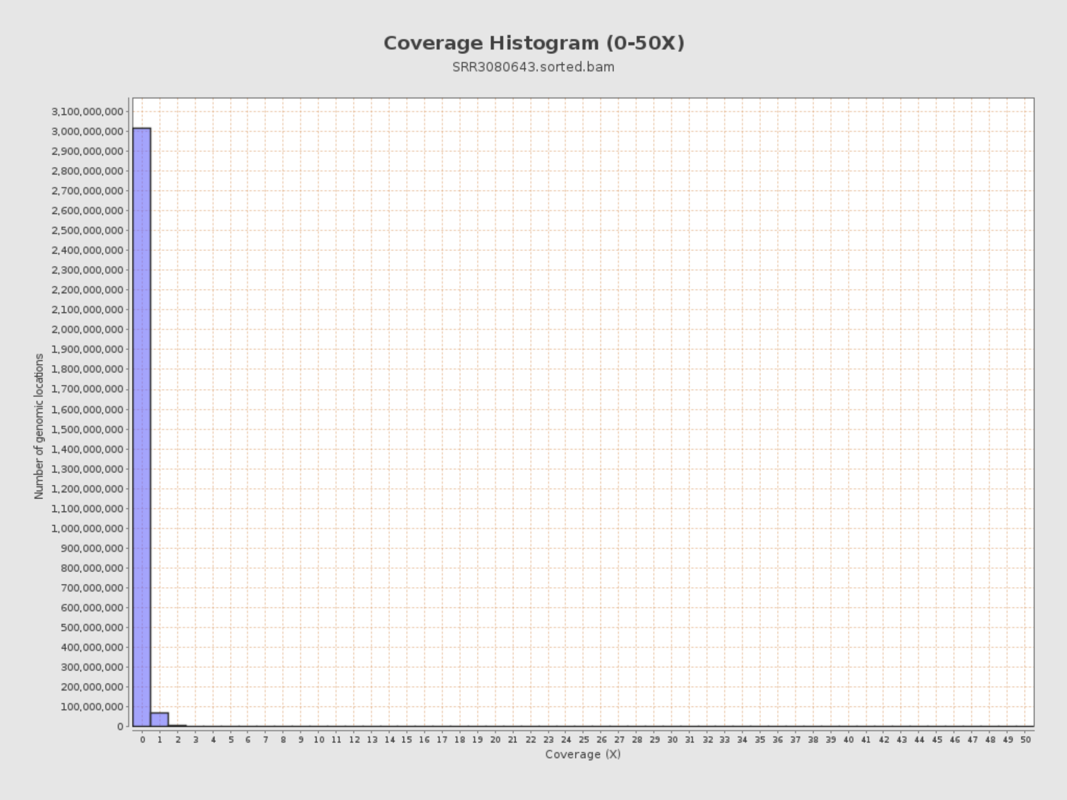
3. Results : Coverage across reference



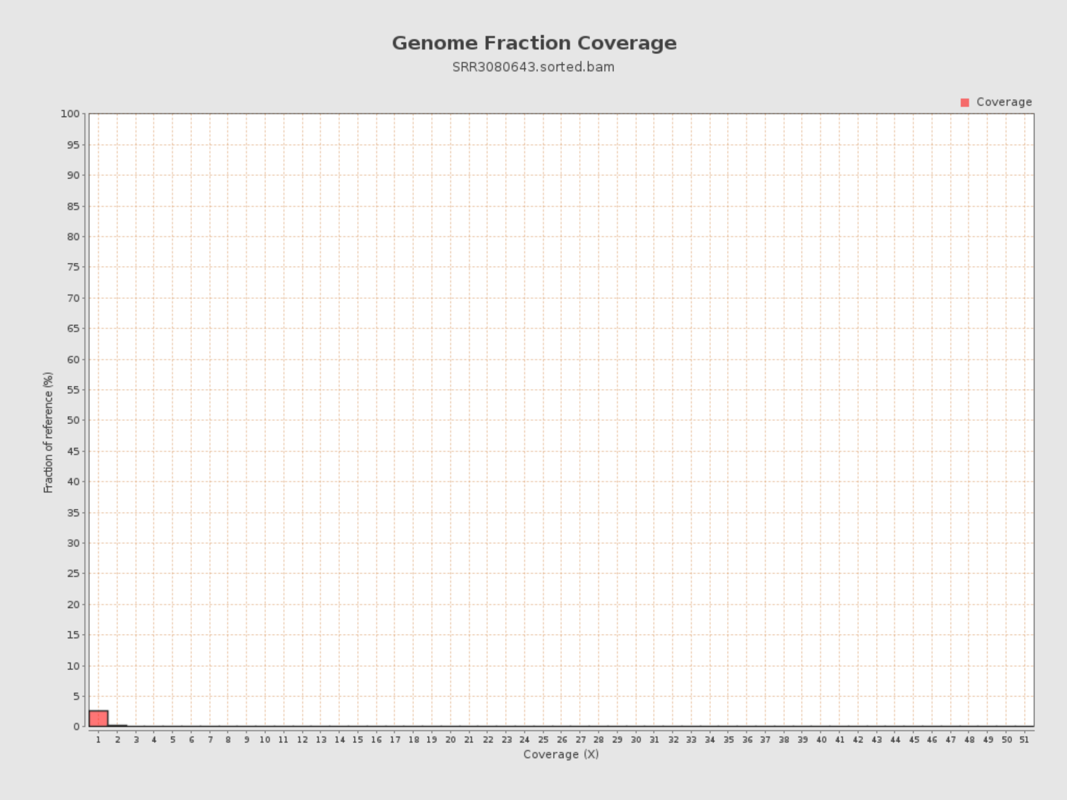
4. Results : Coverage Histogram



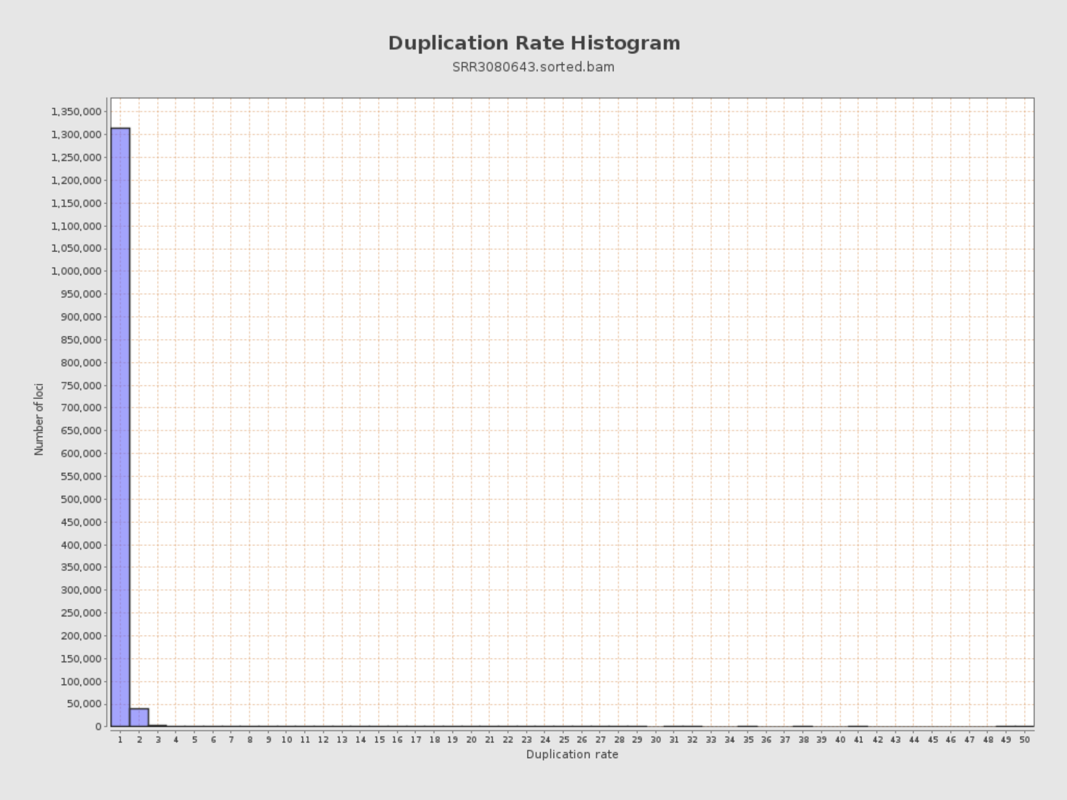
5. Results : Coverage Histogram (0-50X)



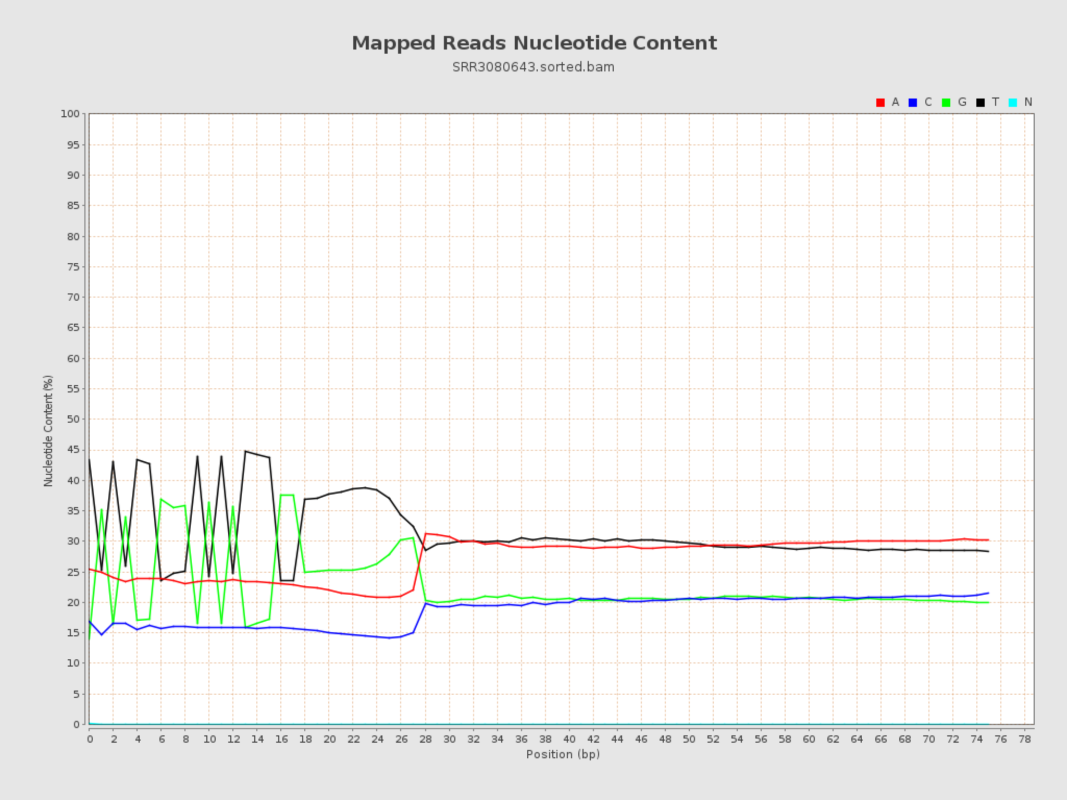
6. Results : Genome Fraction Coverage



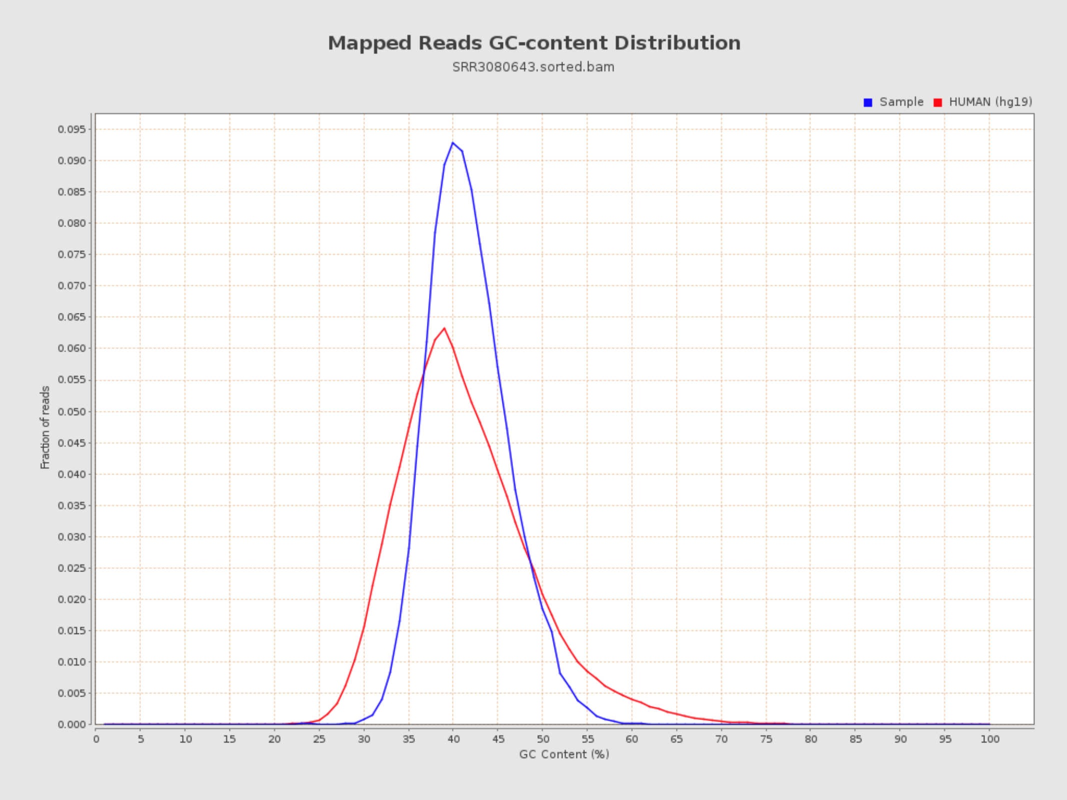
7. Results : Duplication Rate Histogram



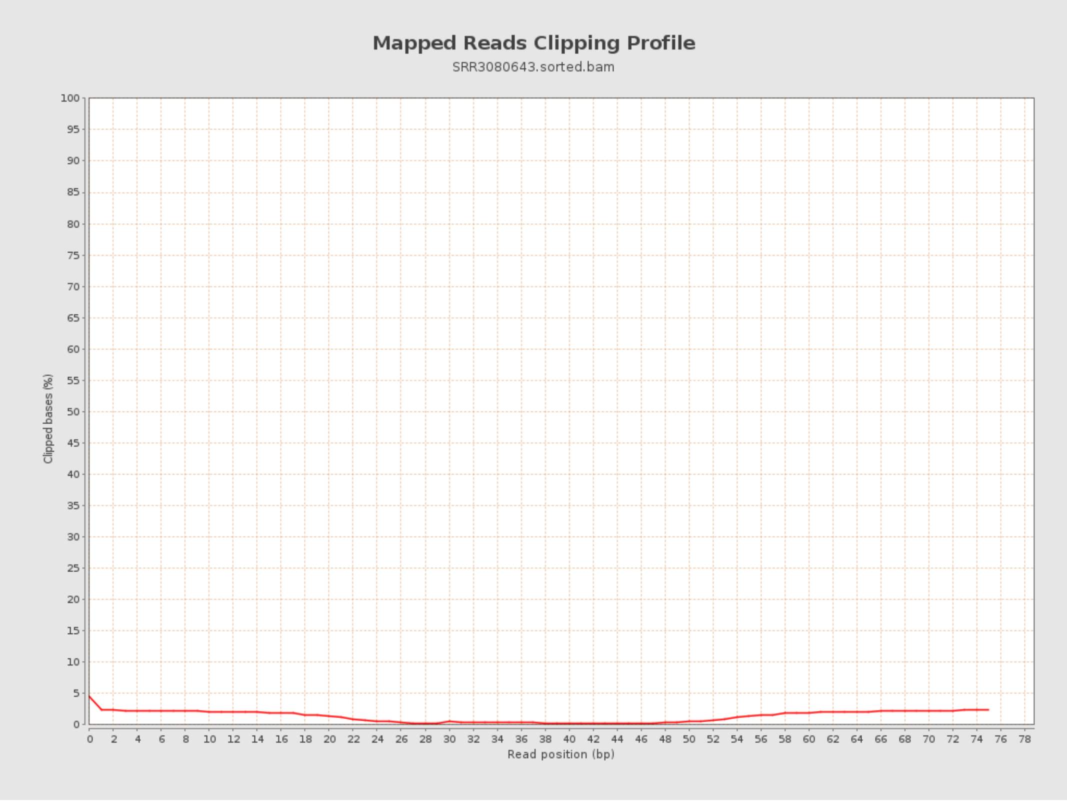
8. Results : Mapped Reads Nucleotide Content



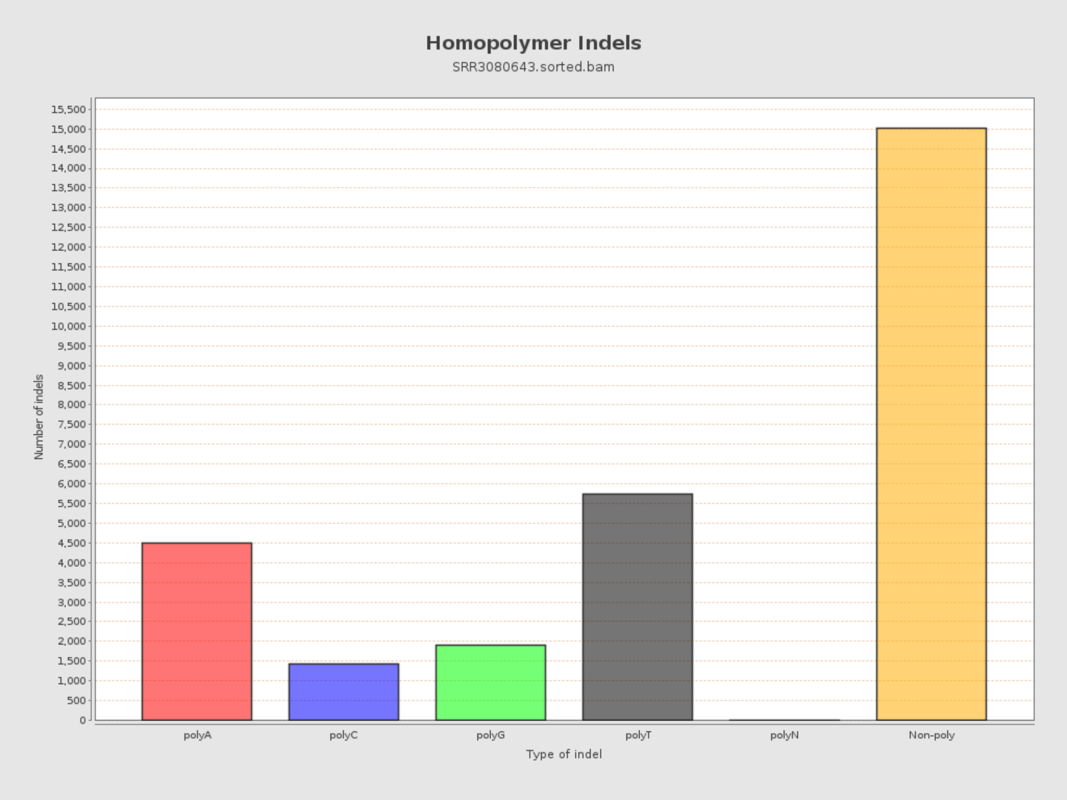
9. Results : Mapped Reads GC-content Distribution



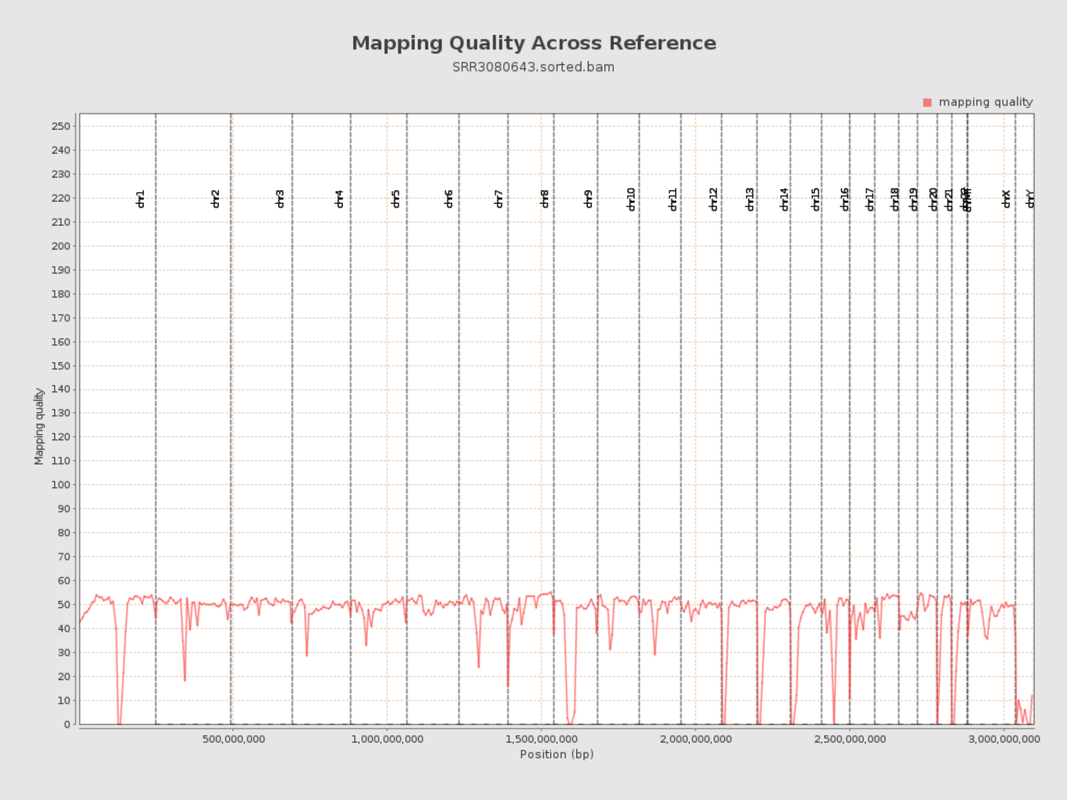
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram