Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:15:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080686.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_SRR3080686 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080686.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:15:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080686.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,107,910
Mapped reads	992,737 / 89.6%
Unmapped reads	115,173 / 10.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,745 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	31,713 / 2.86%
Duplication rate	2%
Clipped reads	491,762 / 44.39%

2.2. ACGT Content

Number/percentage of A's	17,936,600 / 27.49%
Number/percentage of C's	12,363,671 / 18.95%
Number/percentage of T's	19,593,955 / 30.03%
Number/percentage of G's	15,349,480 / 23.53%
Number/percentage of N's	2,637 / 0%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.3125

2.4. Mapping Quality

Mean Mapping Quality	41.96

2.5. Mismatches and indels

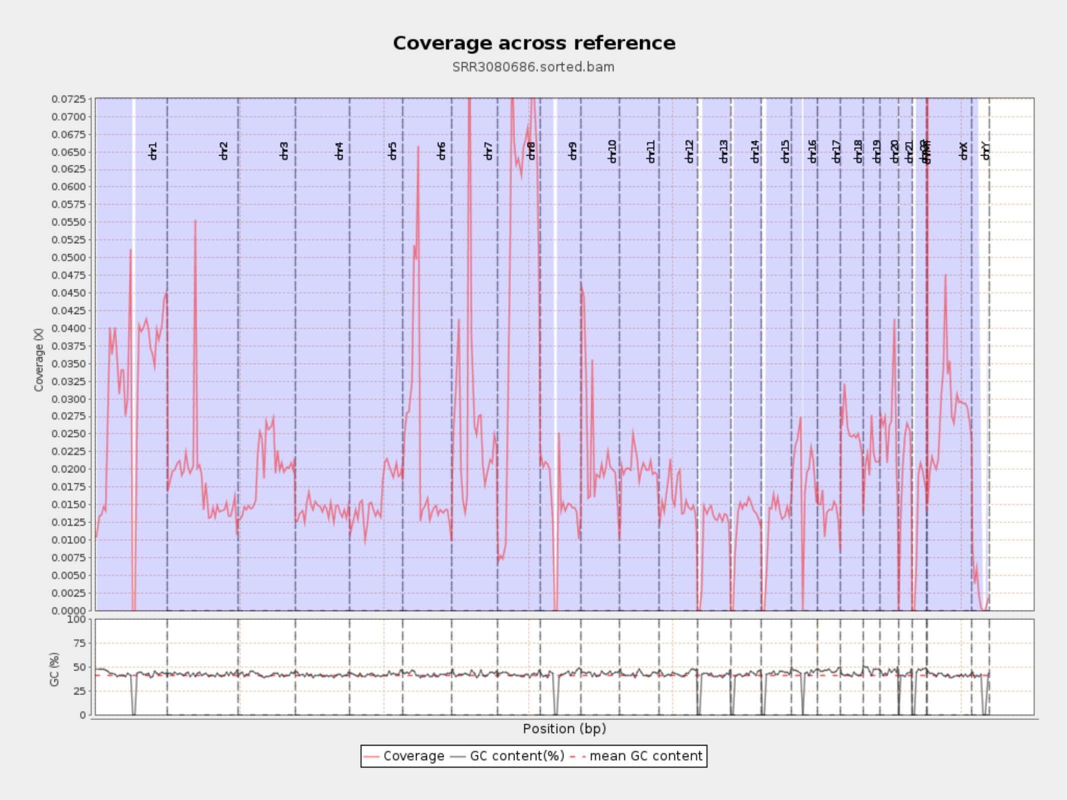
General error rate	0.75%
Mismatches	476,589
Insertions	5,606
Mapped reads with at least one insertion	0.56%
Deletions	13,421
Mapped reads with at least one deletion	1.34%
Homopolymer indels	42.74%

2.6. Chromosome stats

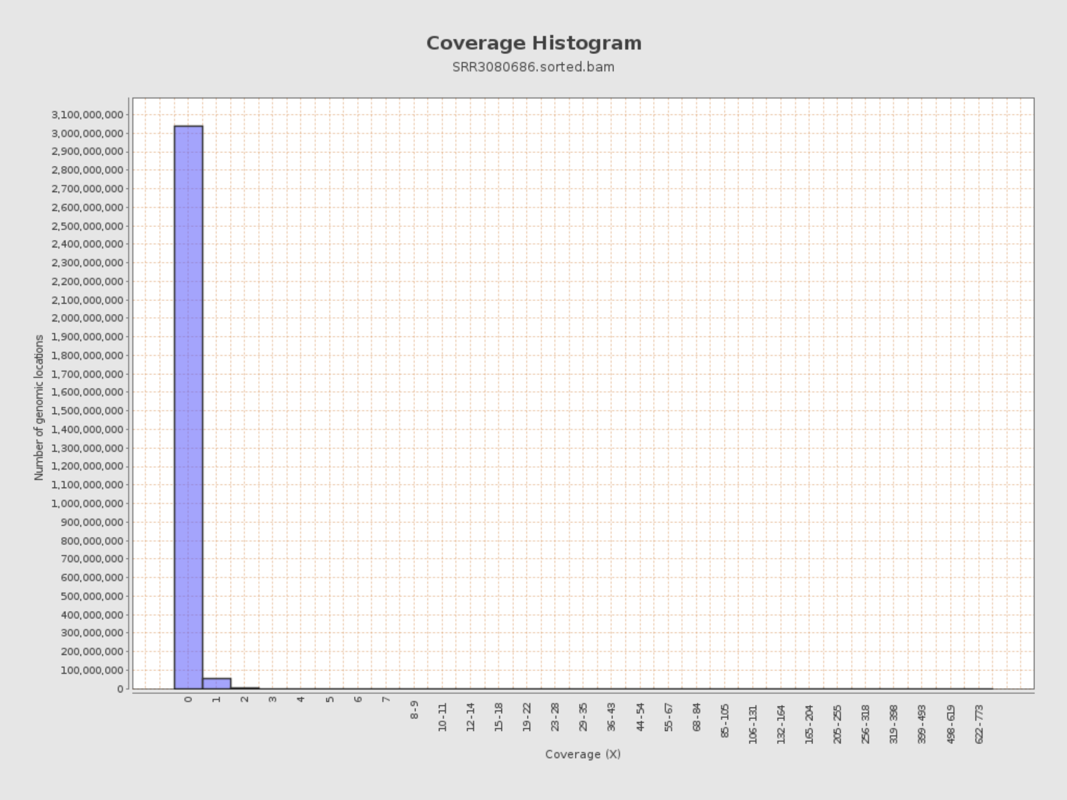
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7780382	0.0312	0.4484
chr2	243199373	4447230	0.0183	0.3248
chr3	198022430	3906751	0.0197	0.1491
chr4	191154276	2720750	0.0142	0.1303
chr5	180915260	2916312	0.0161	0.1343
chr6	171115067	3826745	0.0224	0.2472
chr7	159138663	4360449	0.0274	0.9063

chr8	146364022	7438203	0.0508	0.3279
chr9	141213431	2117045	0.015	0.2213
chr10	135534747	3131918	0.0231	0.2344
chr11	135006516	2738199	0.0203	0.2079
chr12	133851895	2110818	0.0158	0.1366
chr13	115169878	1303245	0.0113	0.1102
chr14	107349540	1306732	0.0122	0.131
chr15	102531392	1200353	0.0117	0.12
chr16	90354753	1729379	0.0191	0.1639
chr17	81195210	1136830	0.014	0.1397
chr18	78077248	2007150	0.0257	0.3688
chr19	59128983	1276177	0.0216	0.3117
chr20	63025520	1663529	0.0264	0.1771
chr21	48129895	950151	0.0197	0.1553
chr22	51304566	675412	0.0132	0.1192
chrMT	16571	14534	0.8771	1.0886
chrX	155270560	4354794	0.028	0.2072
chrY	59373566	155455	0.0026	0.0602

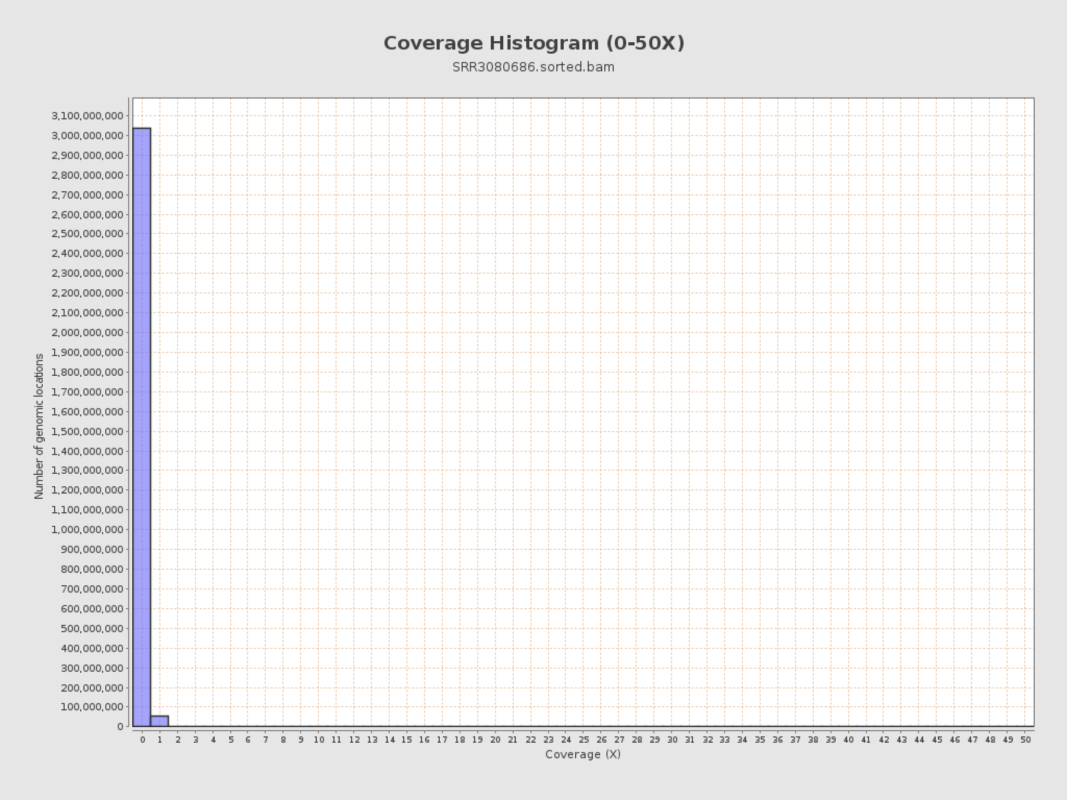
3. Results : Coverage across reference



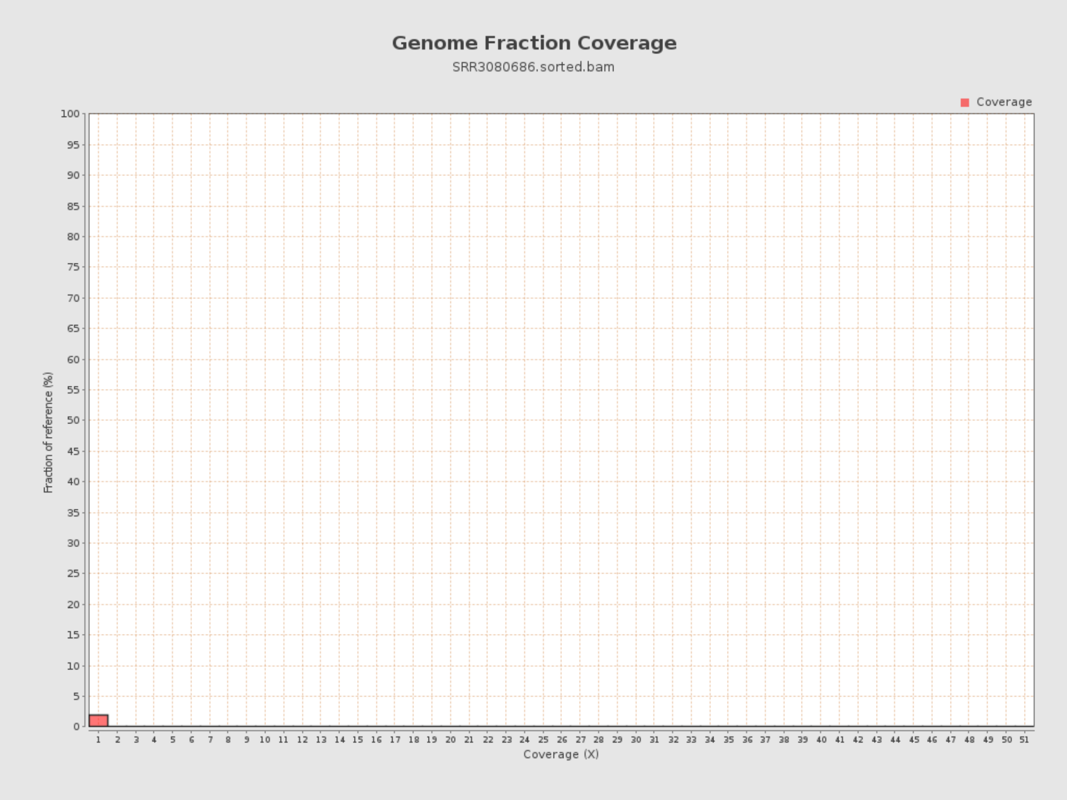
4. Results : Coverage Histogram



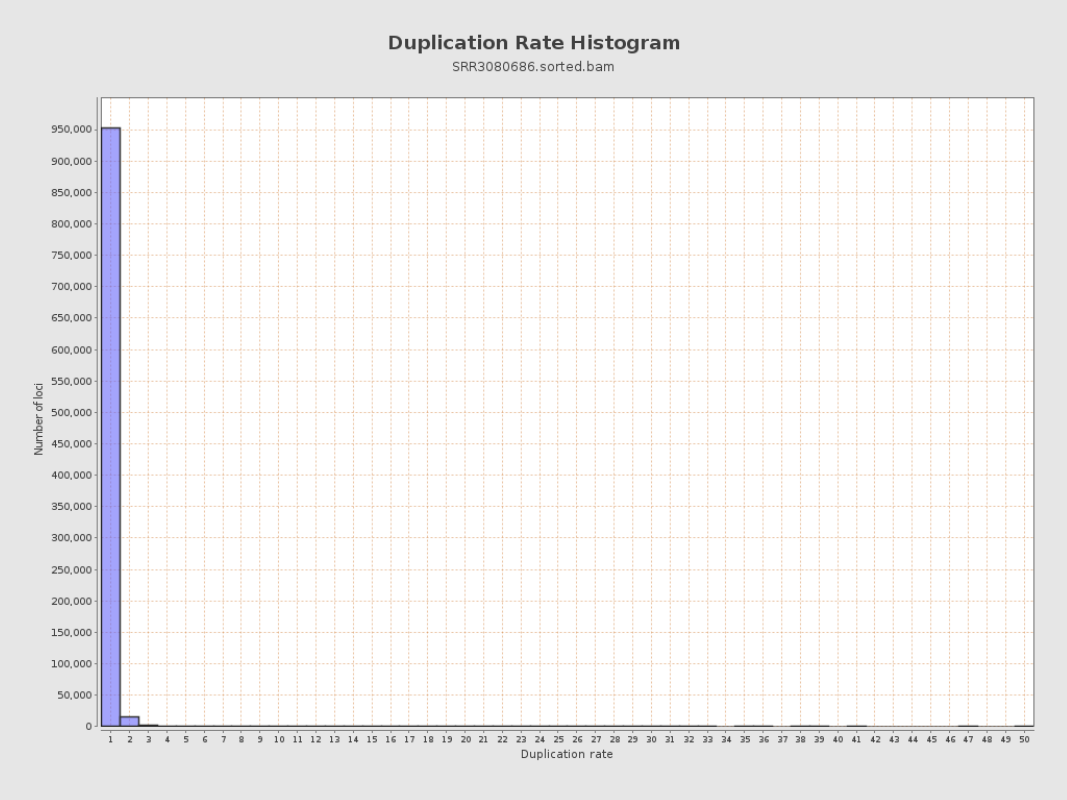
5. Results : Coverage Histogram (0-50X)



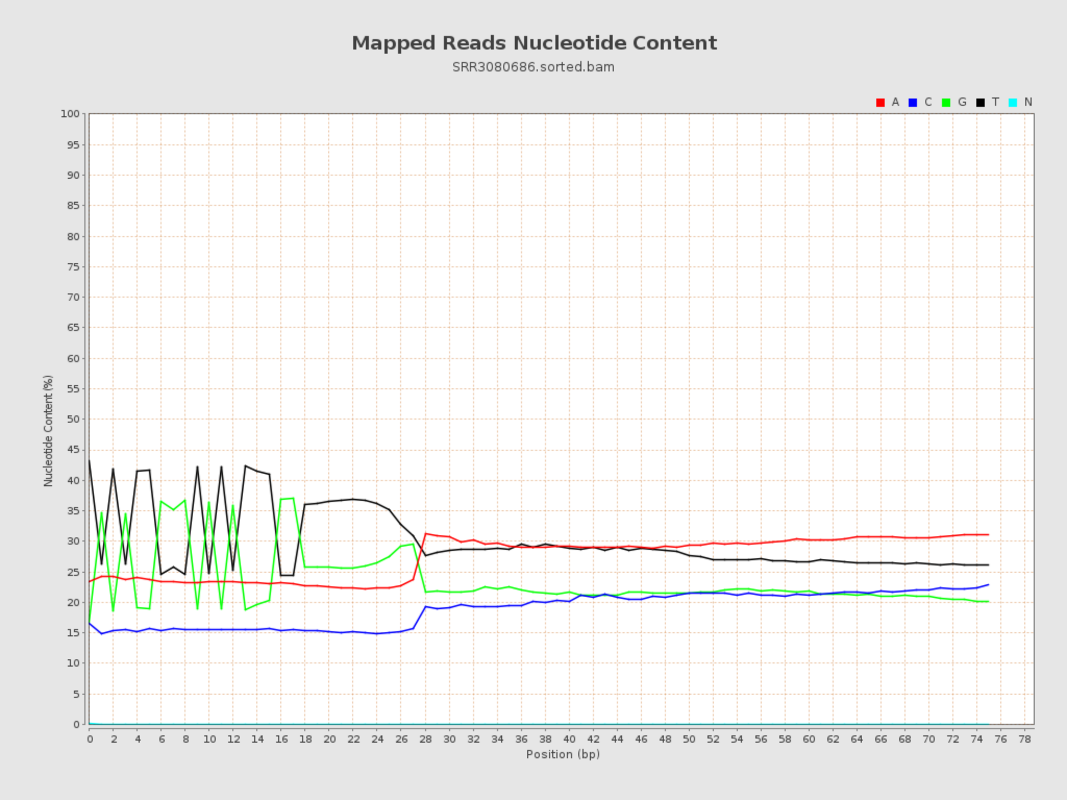
6. Results : Genome Fraction Coverage



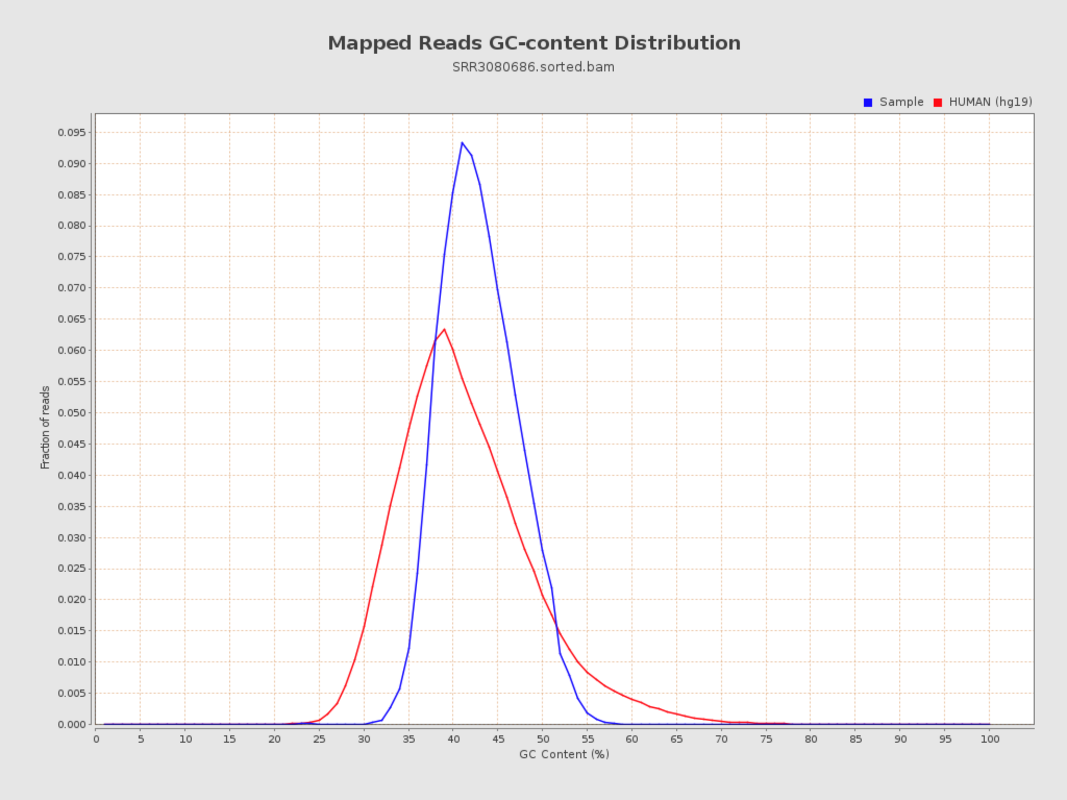
7. Results : Duplication Rate Histogram



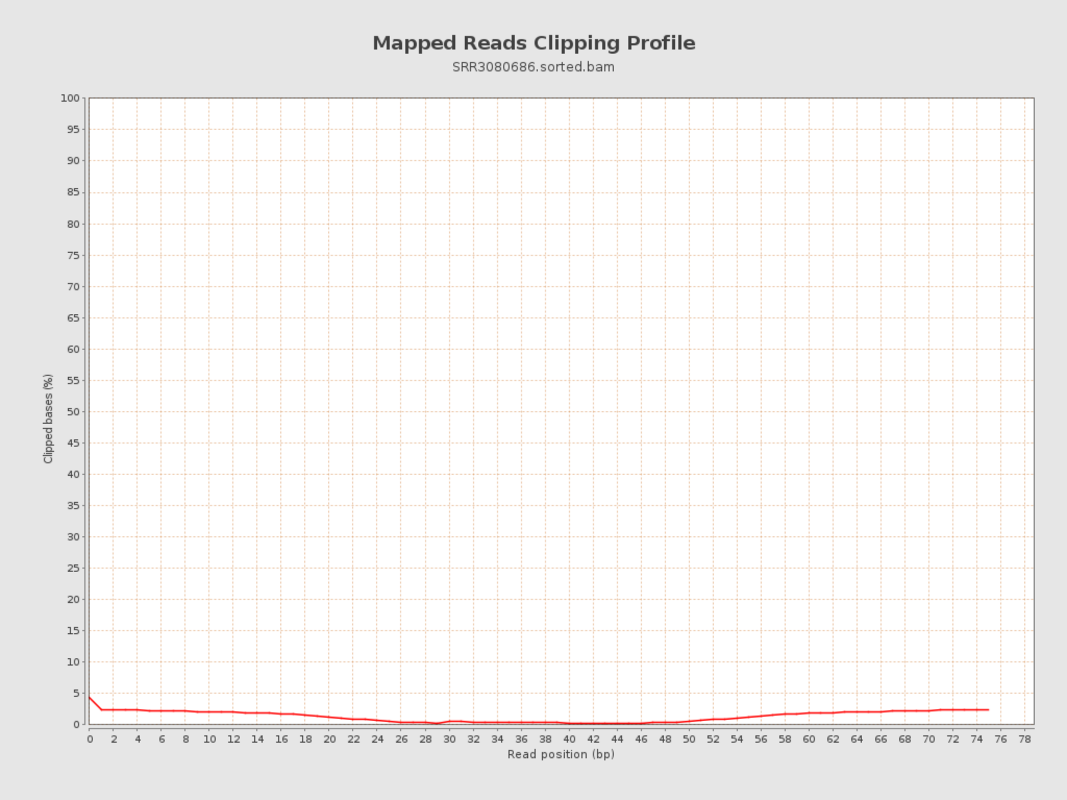
8. Results : Mapped Reads Nucleotide Content



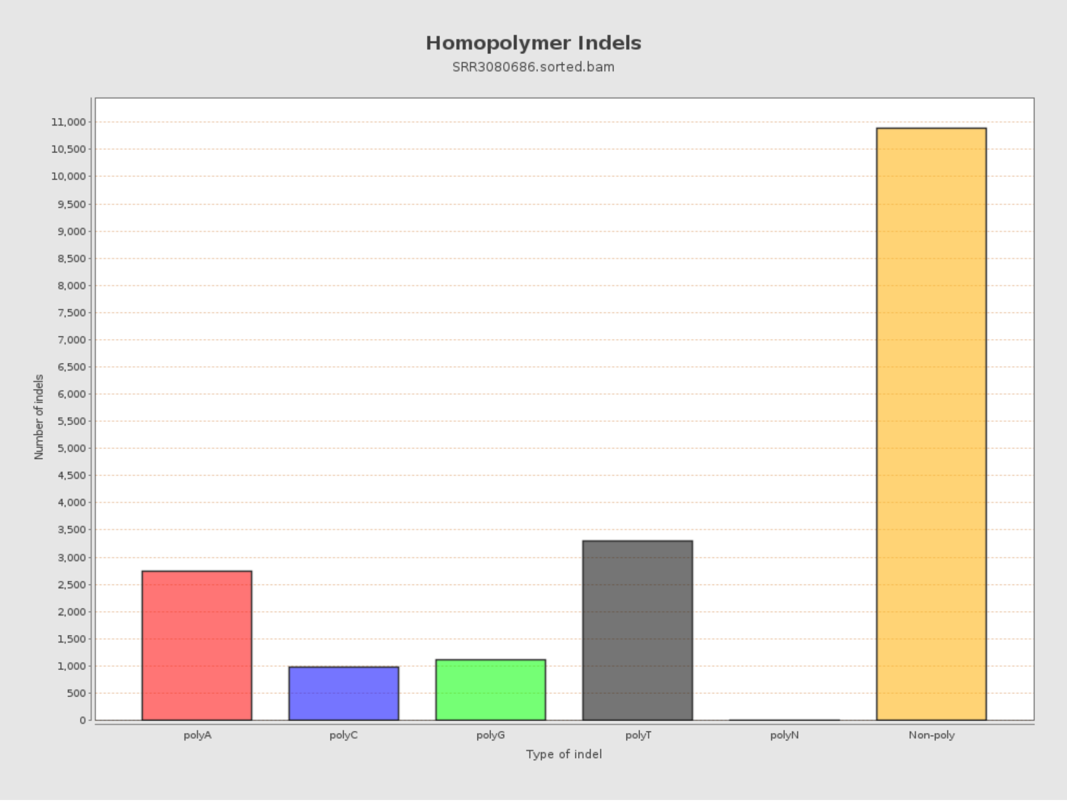
9. Results : Mapped Reads GC-content Distribution



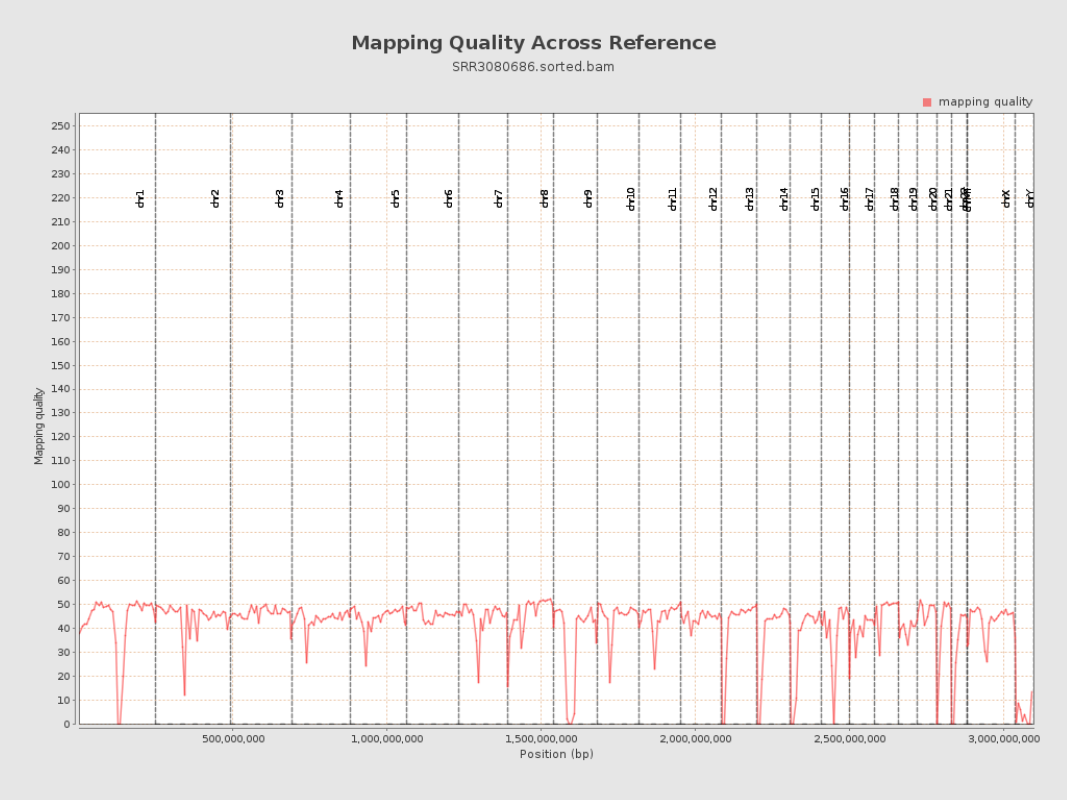
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram