Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:20:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085039.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_SRR3085039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:20:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,400,610
Mapped reads	3,119,370 / 91.73%
Unmapped reads	281,240 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,585 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	123,629 / 3.64%
Duplication rate	3.19%
Clipped reads	1,408,045 / 41.41%

2.2. ACGT Content

Number/percentage of A's	57,699,830 / 27.66%
Number/percentage of C's	40,900,989 / 19.61%
Number/percentage of T's	63,229,878 / 30.31%
Number/percentage of G's	46,727,856 / 22.4%
Number/percentage of N's	22,080 / 0.01%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0674

Standard Deviation	0.4418

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

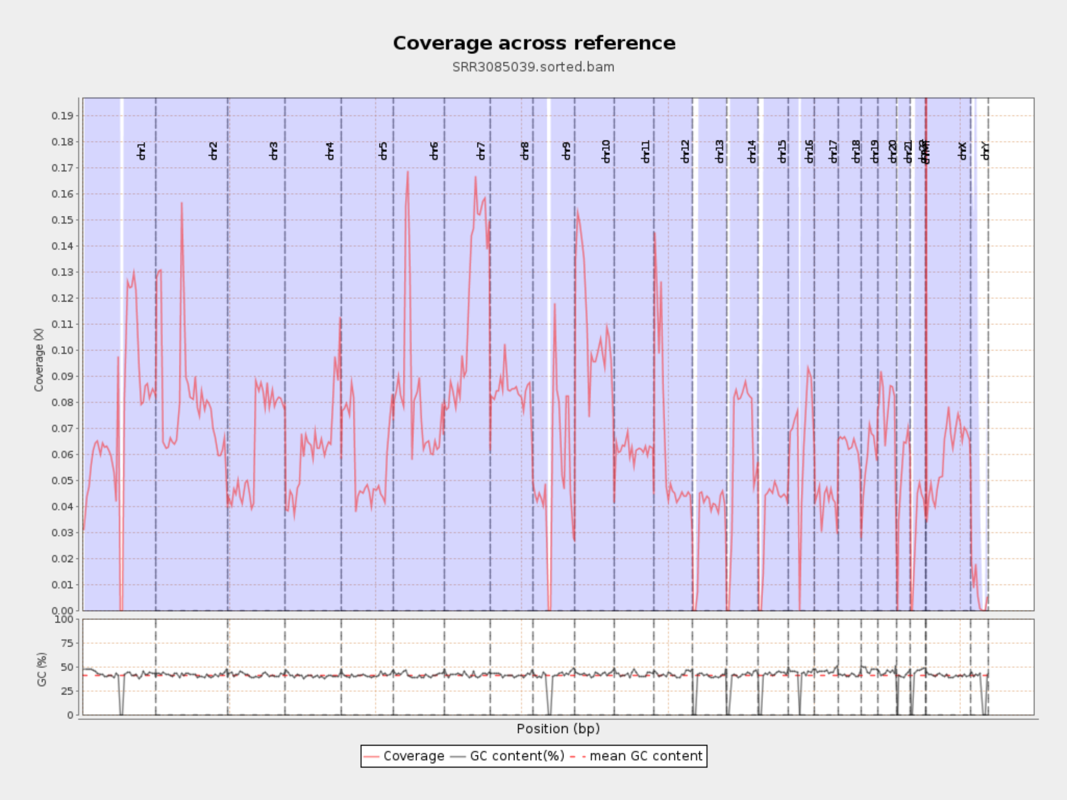
General error rate	0.86%
Mismatches	1,761,290
Insertions	13,838
Mapped reads with at least one insertion	0.44%
Deletions	37,034
Mapped reads with at least one deletion	1.18%
Homopolymer indels	46.41%

2.6. Chromosome stats

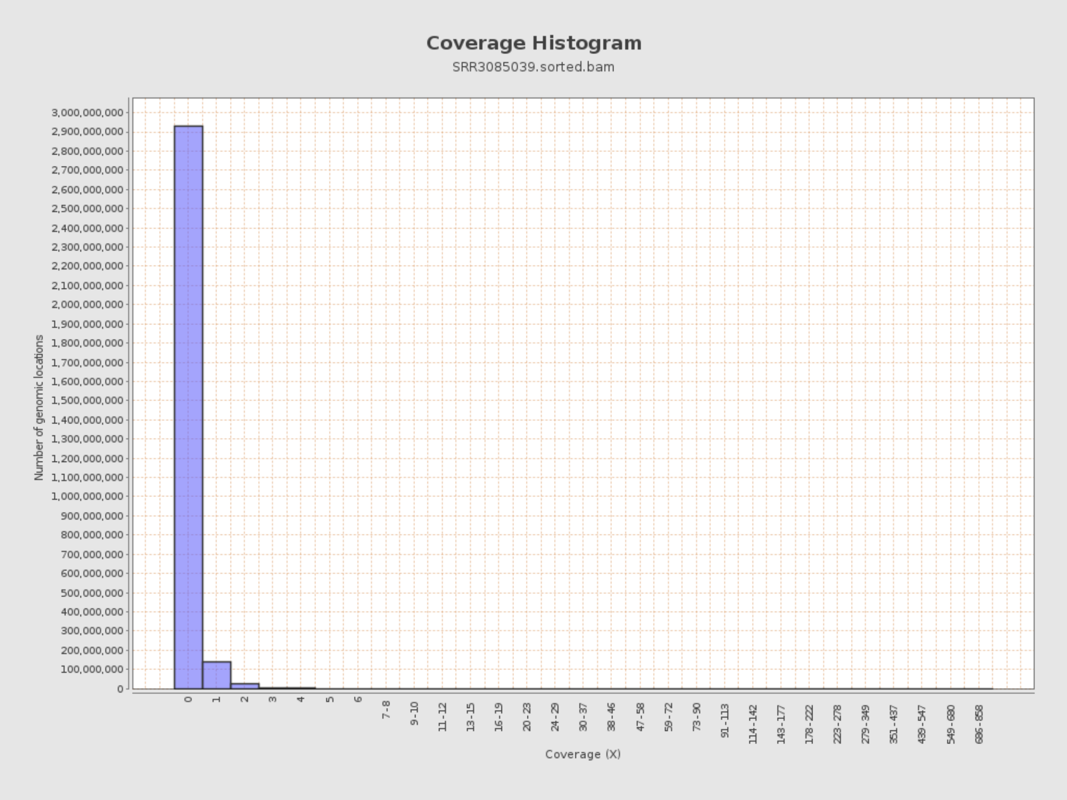
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18079865	0.0725	0.5771
chr2	243199373	19874570	0.0817	0.6132
chr3	198022430	12682311	0.064	0.3029
chr4	191154276	12009023	0.0628	0.3044
chr5	180915260	10432234	0.0577	0.2862
chr6	171115067	14240693	0.0832	0.4564
chr7	159138663	18479790	0.1161	0.5726

chr8	146364022	12339221	0.0843	0.6378
chr9	141213431	7499281	0.0531	0.4503
chr10	135534747	14884584	0.1098	0.5085
chr11	135006516	8298324	0.0615	0.4469
chr12	133851895	8633280	0.0645	0.3157
chr13	115169878	4046995	0.0351	0.2197
chr14	107349540	6851376	0.0638	0.3333
chr15	102531392	3745068	0.0365	0.2481
chr16	90354753	5881688	0.0651	0.3244
chr17	81195210	3431720	0.0423	0.2738
chr18	78077248	4971635	0.0637	0.7376
chr19	59128983	3491095	0.059	0.4561
chr20	63025520	4991061	0.0792	0.3401
chr21	48129895	2474283	0.0514	0.2878
chr22	51304566	1614554	0.0315	0.2084
chrMT	16571	9330	0.563	0.8547
chrX	155270560	9297073	0.0599	0.3379
chrY	59373566	386531	0.0065	0.117

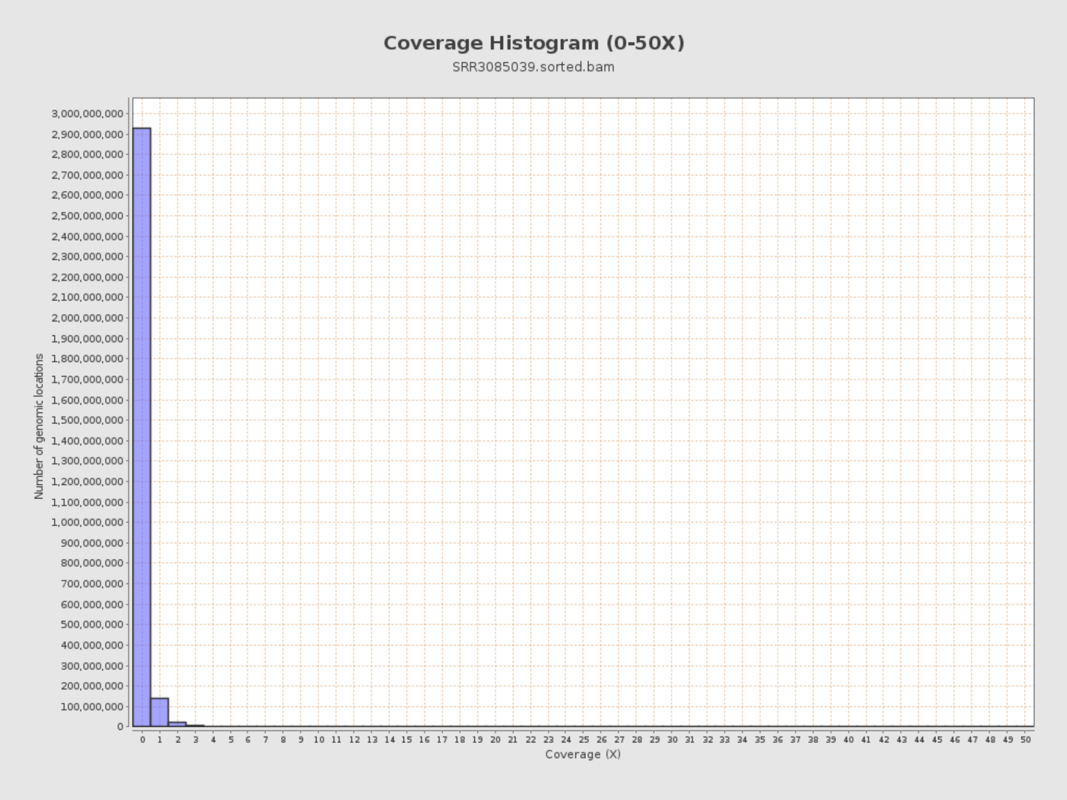
3. Results : Coverage across reference



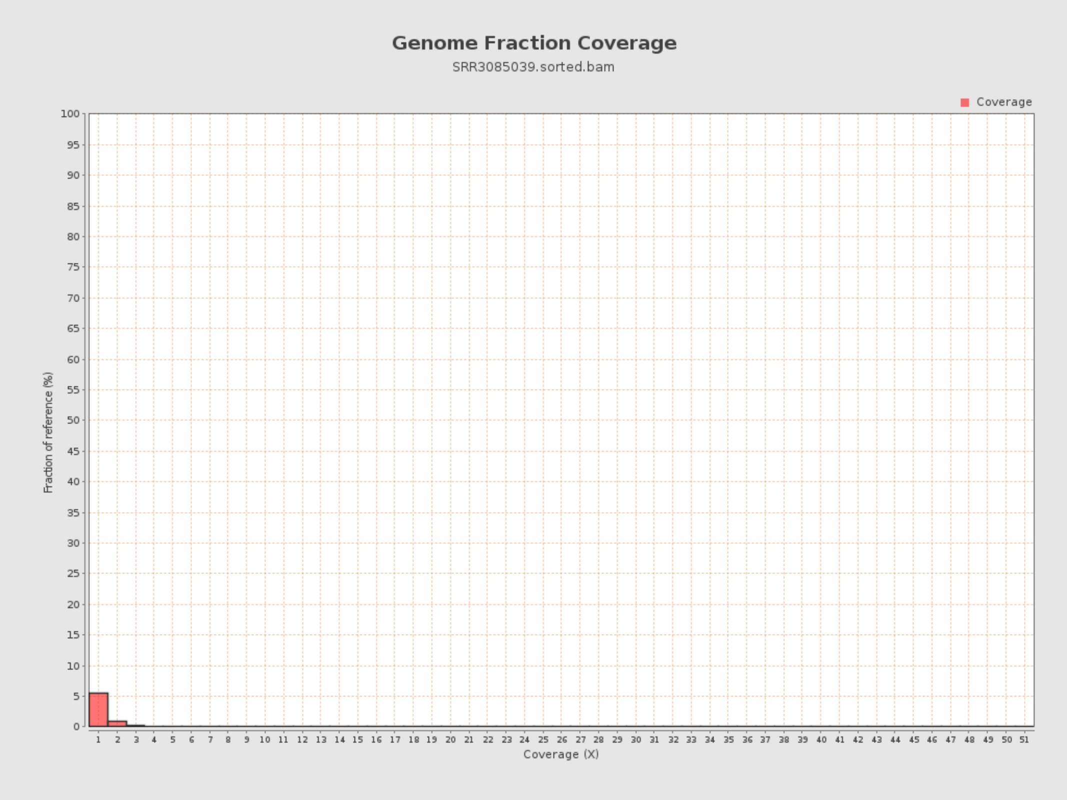
4. Results : Coverage Histogram



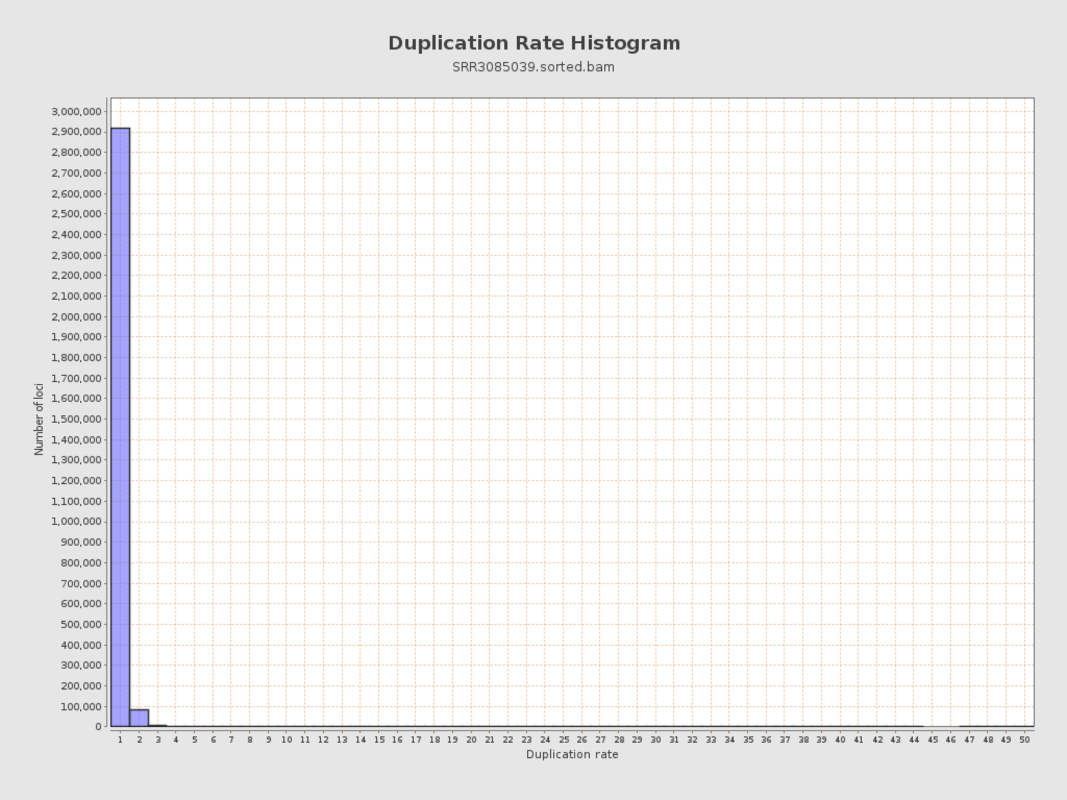
5. Results : Coverage Histogram (0-50X)



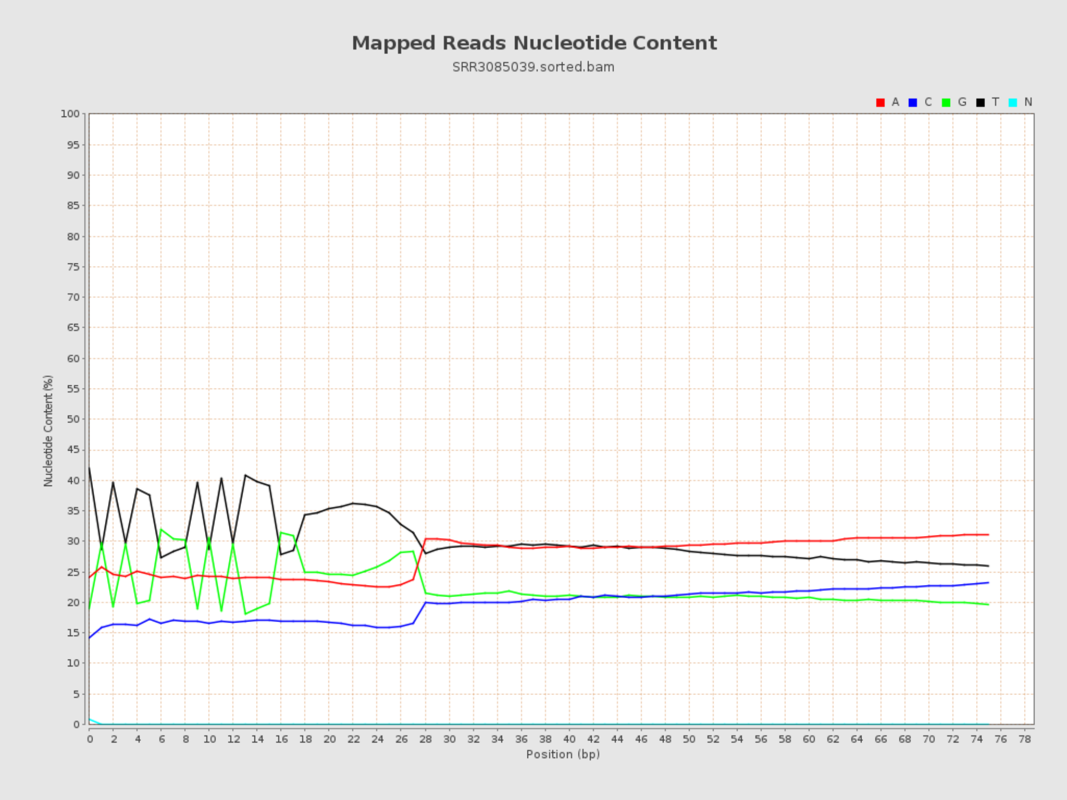
6. Results : Genome Fraction Coverage



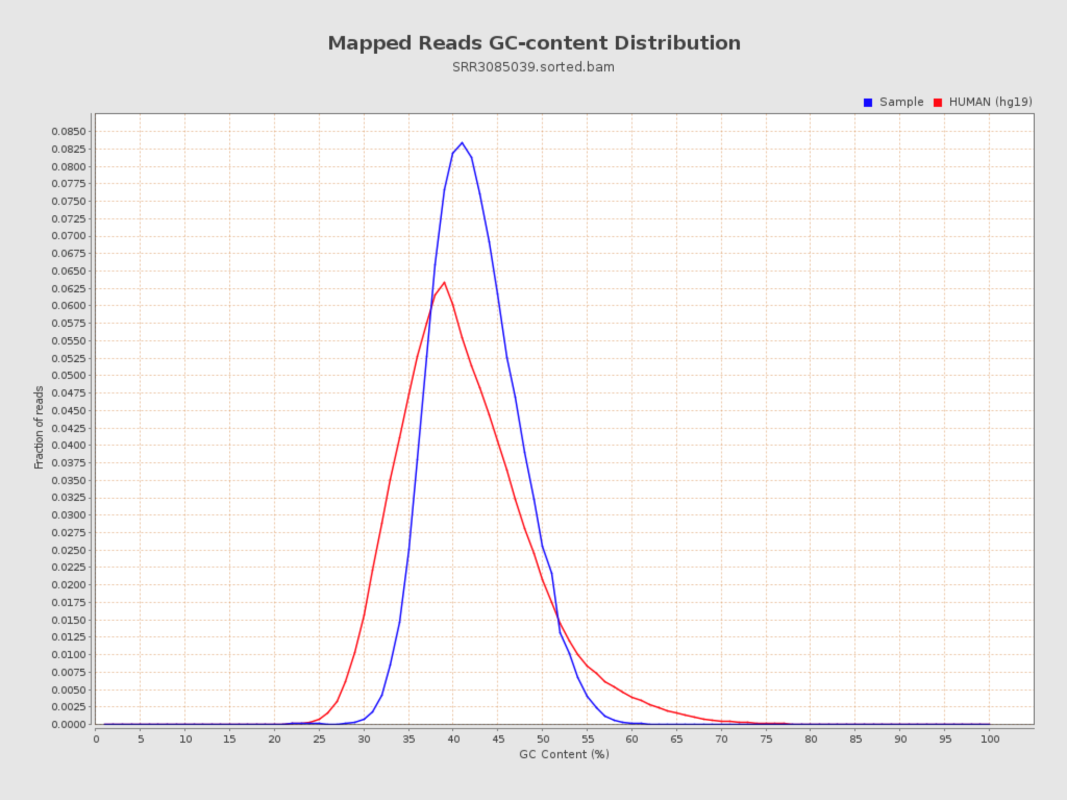
7. Results : Duplication Rate Histogram



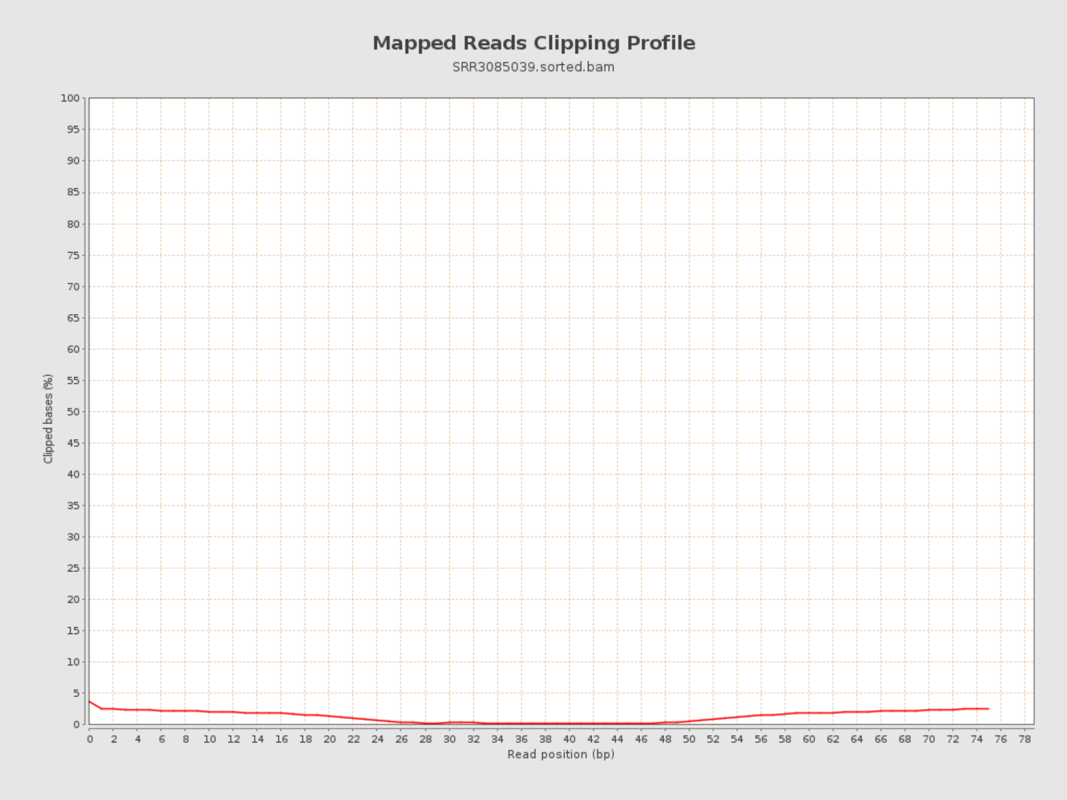
8. Results : Mapped Reads Nucleotide Content



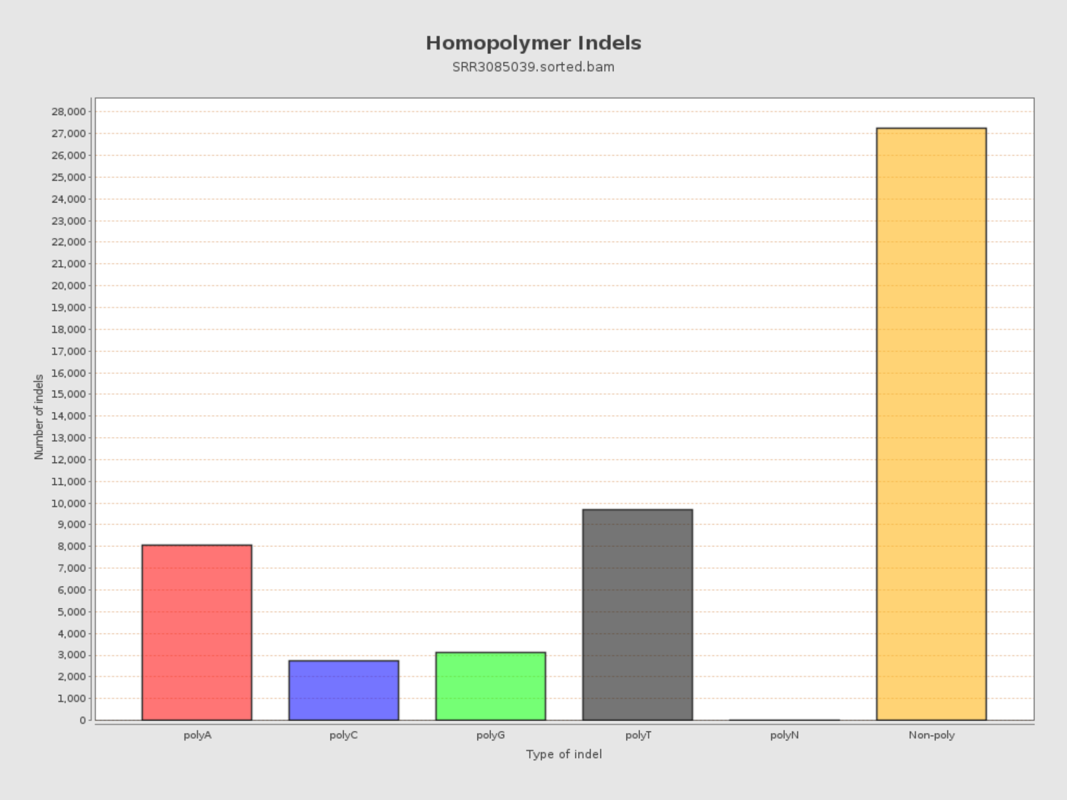
9. Results : Mapped Reads GC-content Distribution



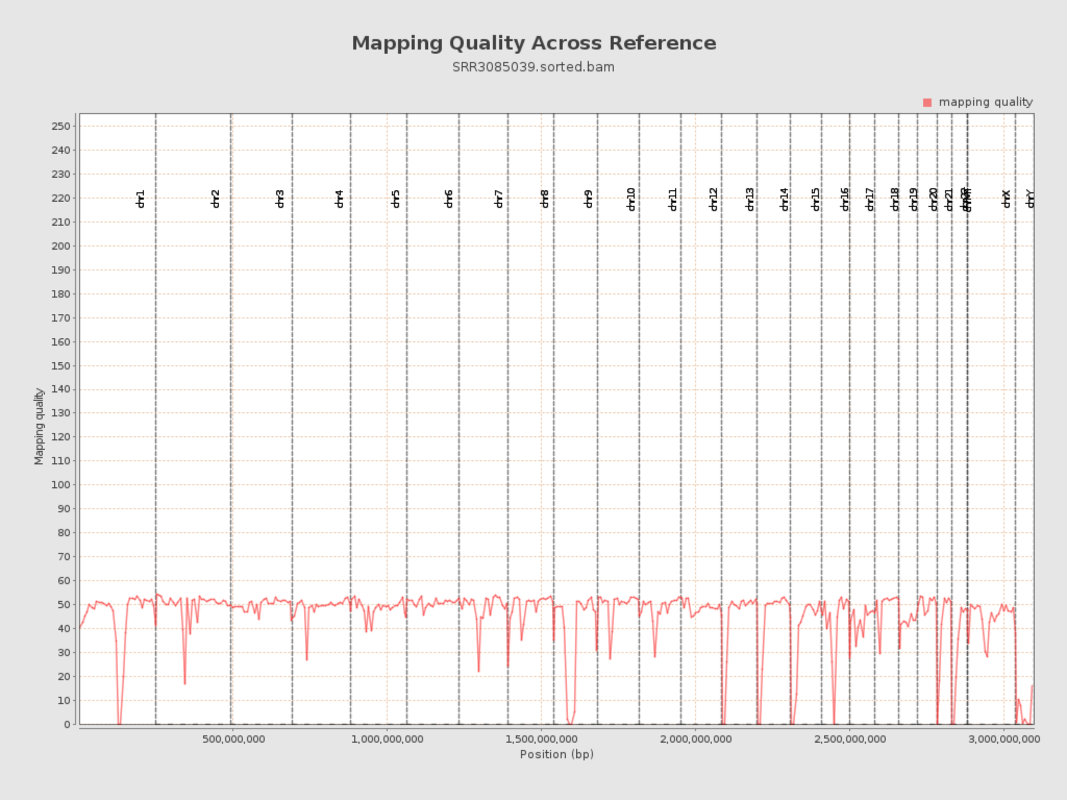
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram