Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:49:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085030.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_SRR3085030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:49:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,871,102
Mapped reads	1,708,643 / 91.32%
Unmapped reads	162,459 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,475 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	50,377 / 2.69%
Duplication rate	2.32%
Clipped reads	733,921 / 39.22%

2.2. ACGT Content

Number/percentage of A's	31,884,770 / 27.77%
Number/percentage of C's	22,124,862 / 19.27%
Number/percentage of T's	35,251,870 / 30.7%
Number/percentage of G's	25,568,120 / 22.27%
Number/percentage of N's	4,475 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0371

Standard Deviation	0.2892

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

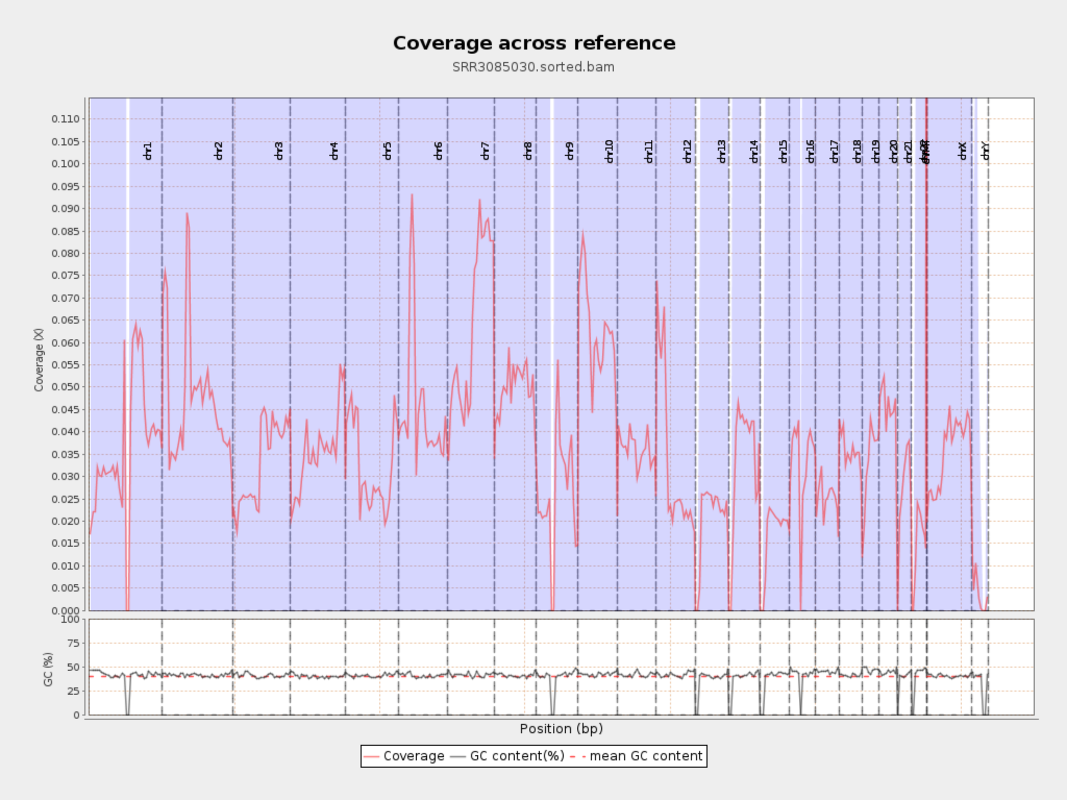
General error rate	0.84%
Mismatches	954,341
Insertions	8,012
Mapped reads with at least one insertion	0.47%
Deletions	23,404
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.92%

2.6. Chromosome stats

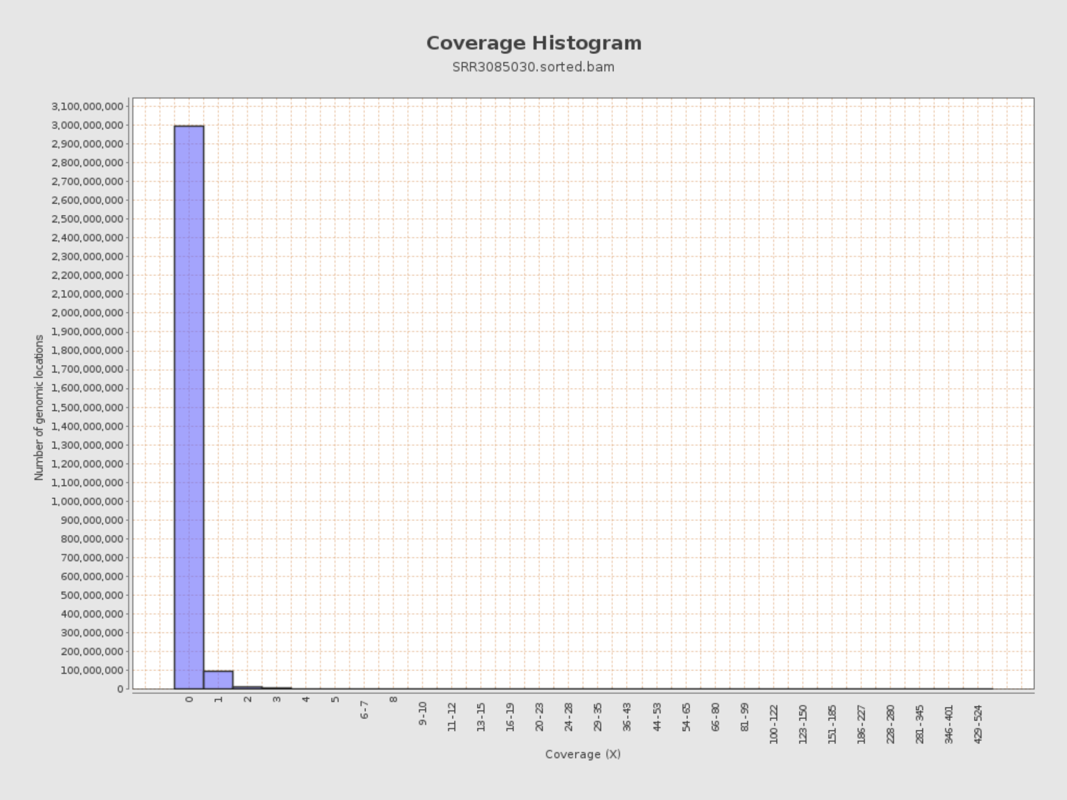
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9061067	0.0364	0.3813
chr2	243199373	11721121	0.0482	0.4172
chr3	198022430	6503603	0.0328	0.2002
chr4	191154276	6818692	0.0357	0.2109
chr5	180915260	5840848	0.0323	0.1977
chr6	171115067	7818914	0.0457	0.2847
chr7	159138663	10196623	0.0641	0.3388

chr8	146364022	7290706	0.0498	0.4128
chr9	141213431	3717603	0.0263	0.2779
chr10	135534747	8607981	0.0635	0.3495
chr11	135006516	4832010	0.0358	0.3096
chr12	133851895	4430821	0.0331	0.2037
chr13	115169878	2355386	0.0205	0.1557
chr14	107349540	3533822	0.0329	0.2085
chr15	102531392	1715777	0.0167	0.1503
chr16	90354753	3014734	0.0334	0.2121
chr17	81195210	2014643	0.0248	0.1973
chr18	78077248	2802321	0.0359	0.448
chr19	59128983	1988873	0.0336	0.3095
chr20	63025520	2866219	0.0455	0.2387
chr21	48129895	1292710	0.0269	0.1885
chr22	51304566	726109	0.0142	0.1293
chrMT	16571	8670	0.5232	0.8491
chrX	155270560	5493141	0.0354	0.2337
chrY	59373566	221870	0.0037	0.0779

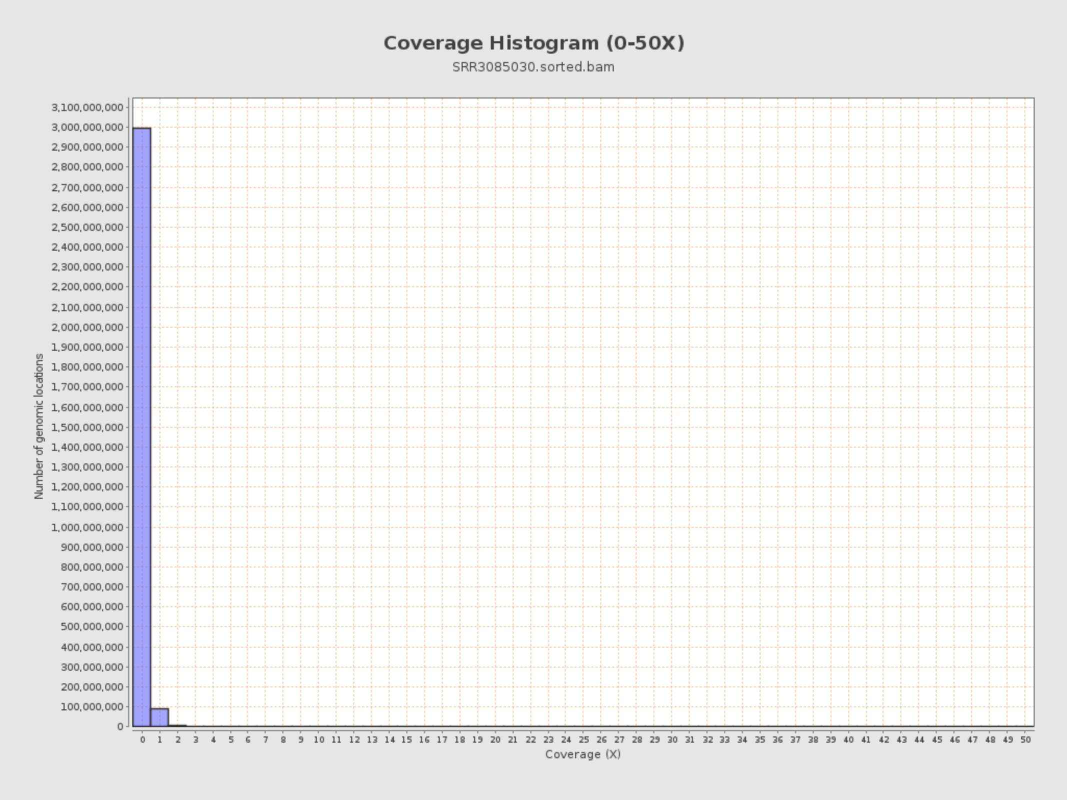
3. Results : Coverage across reference



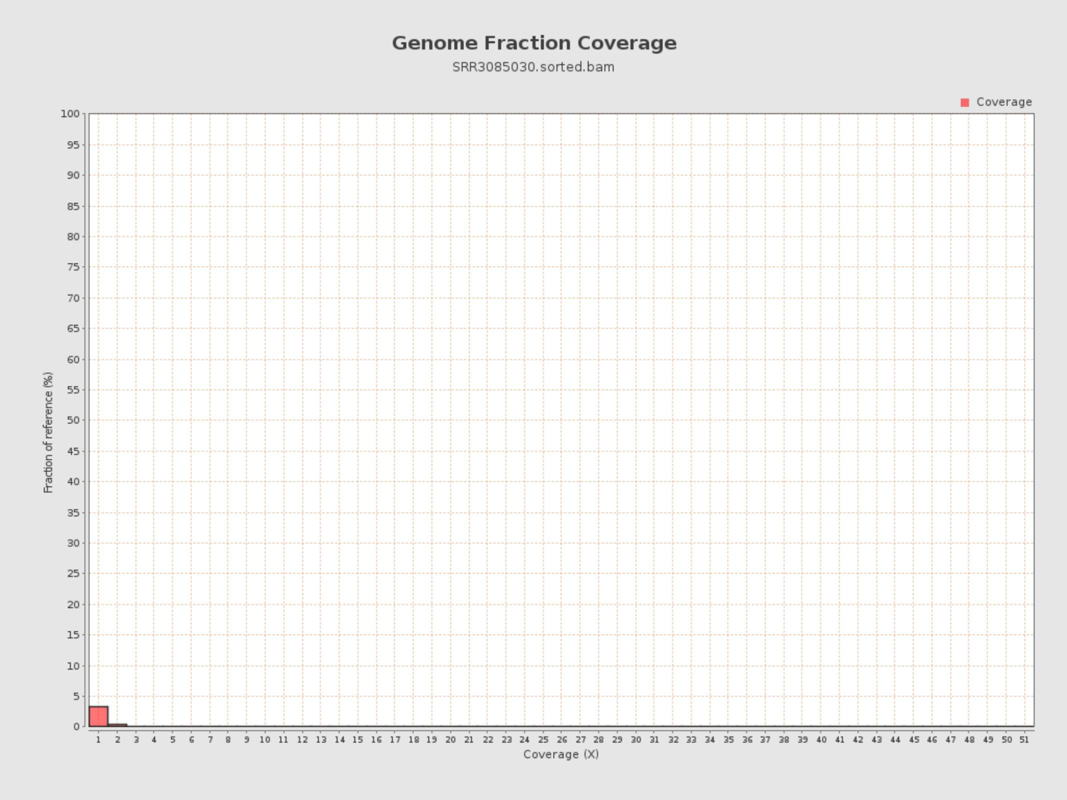
4. Results : Coverage Histogram



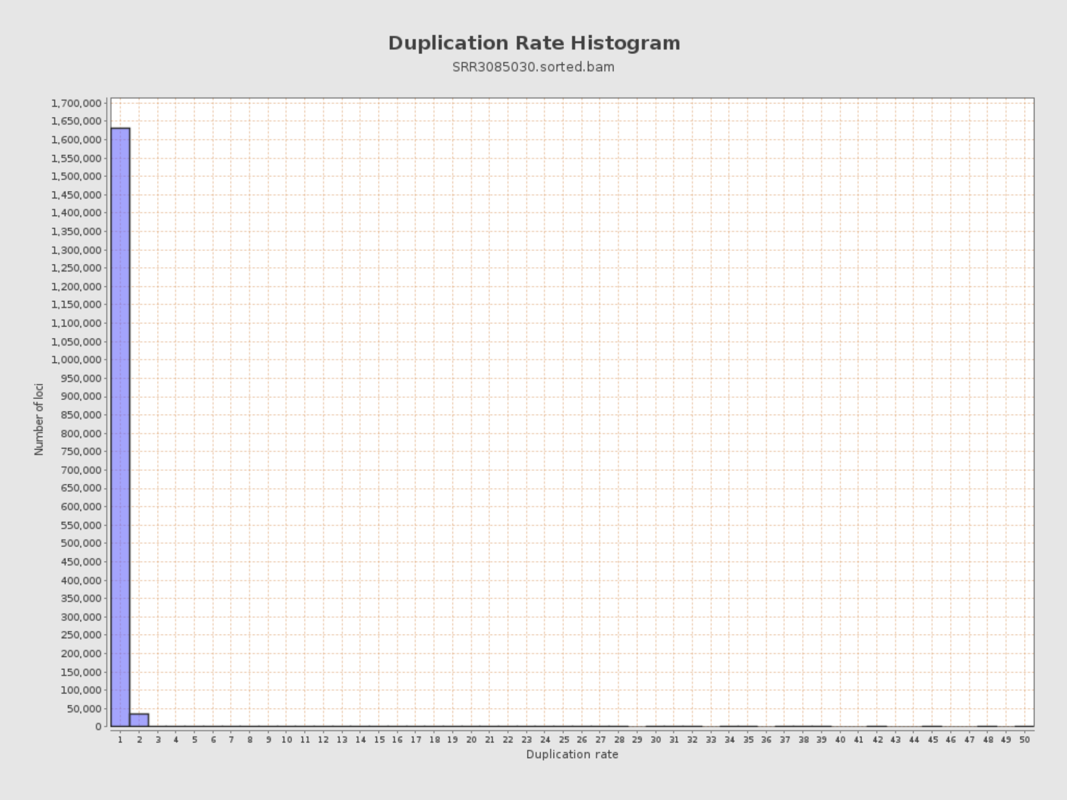
5. Results : Coverage Histogram (0-50X)



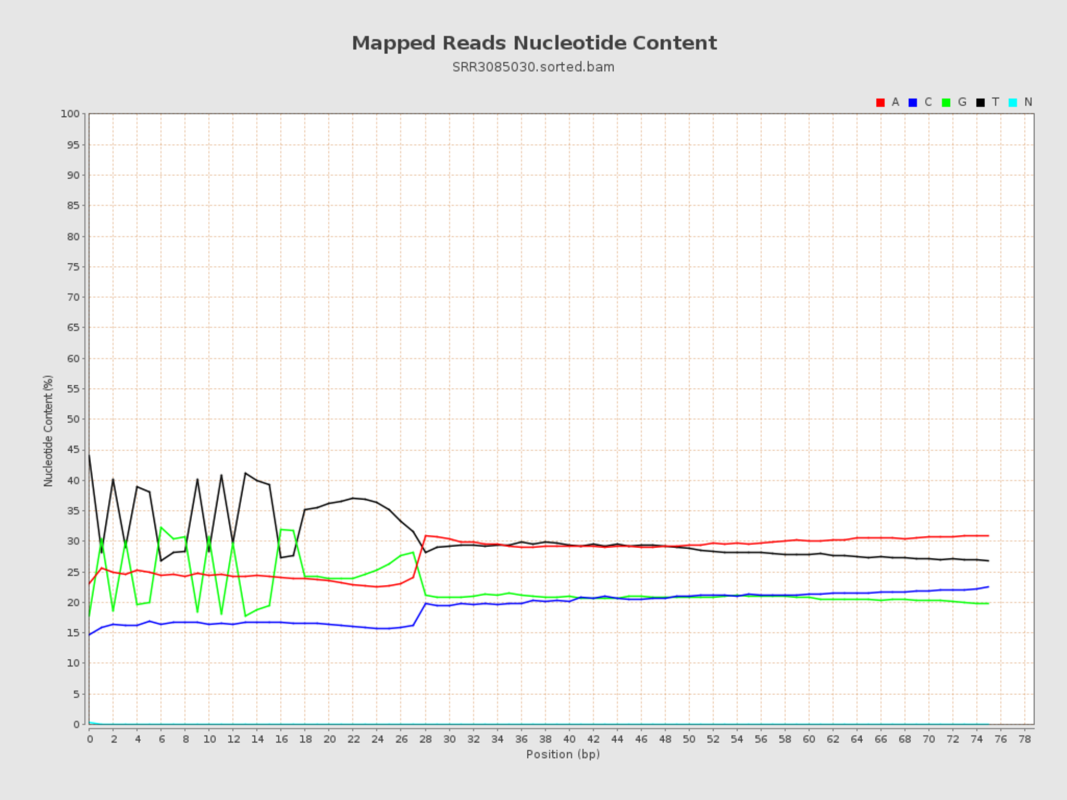
6. Results : Genome Fraction Coverage



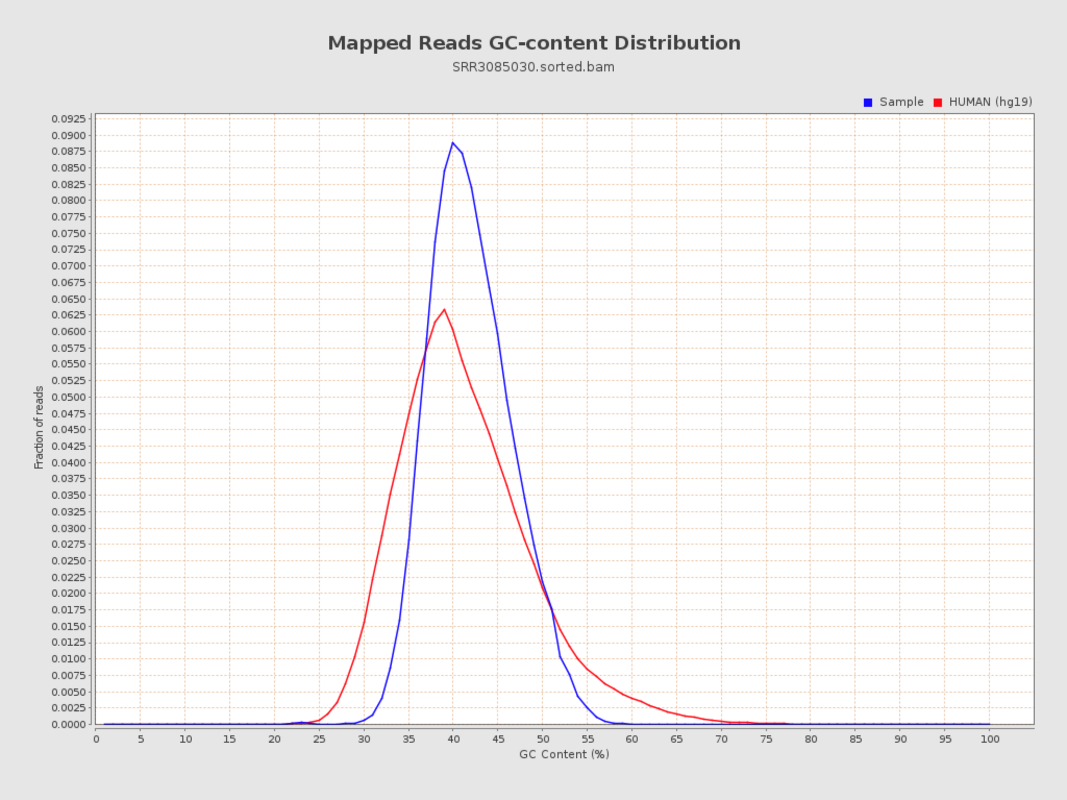
7. Results : Duplication Rate Histogram



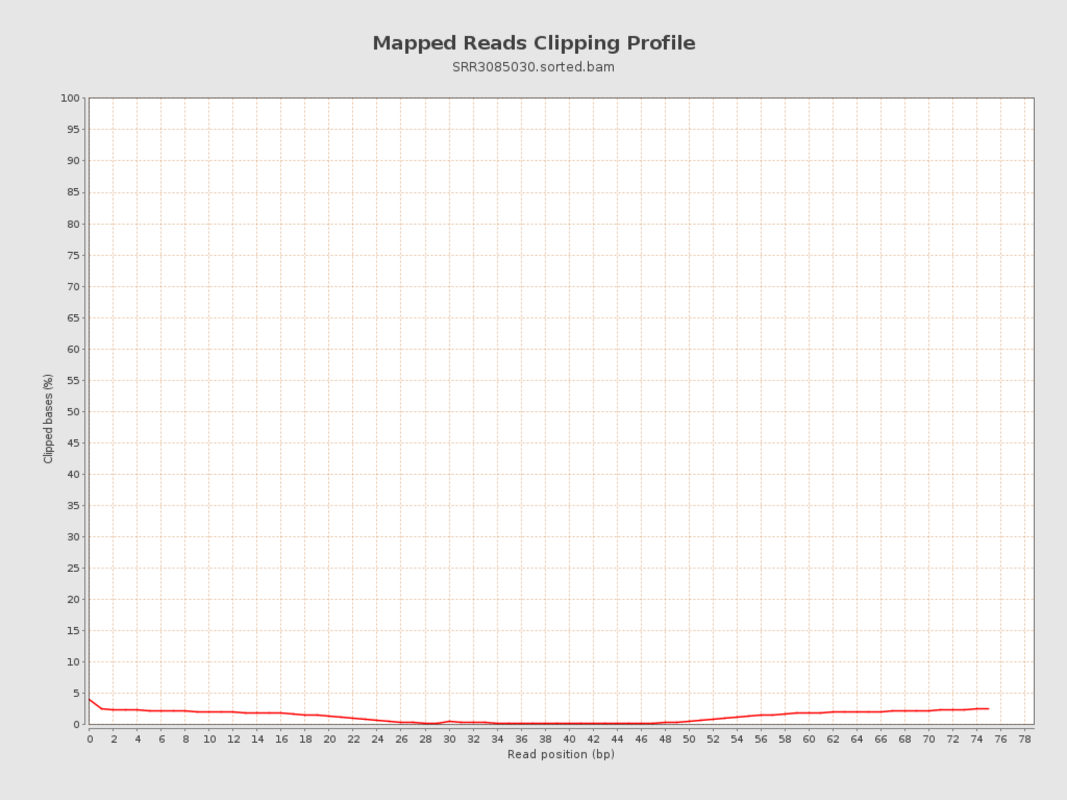
8. Results : Mapped Reads Nucleotide Content



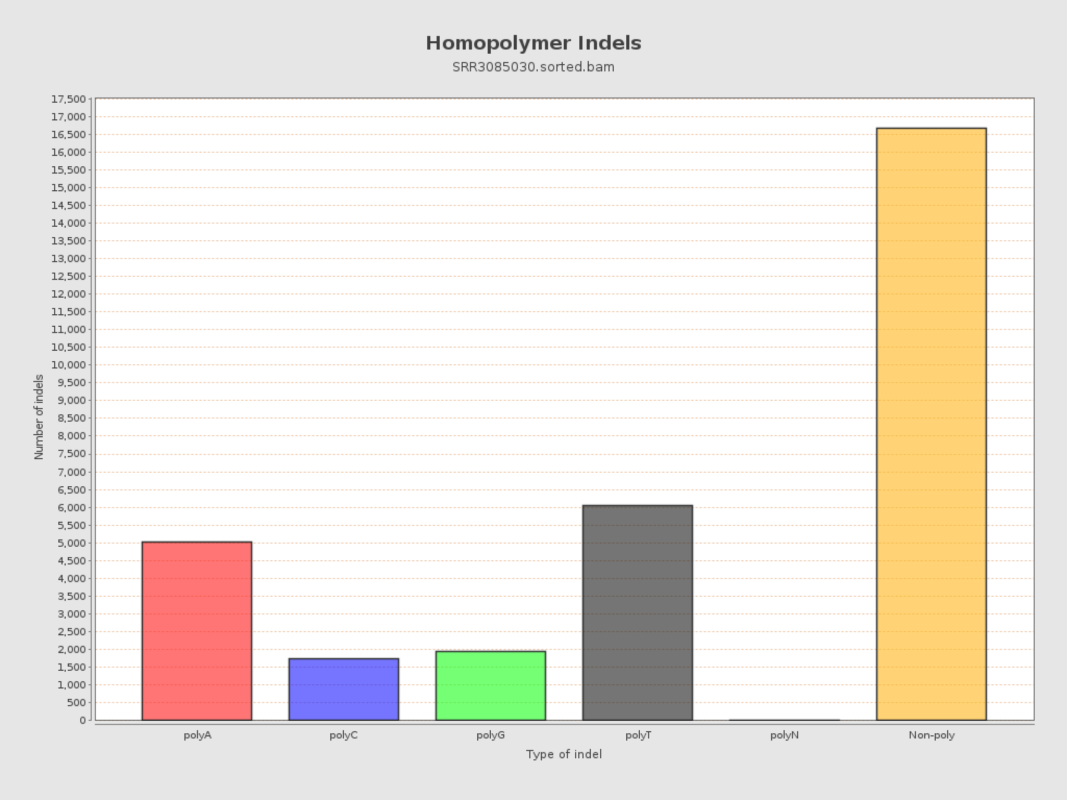
9. Results : Mapped Reads GC-content Distribution



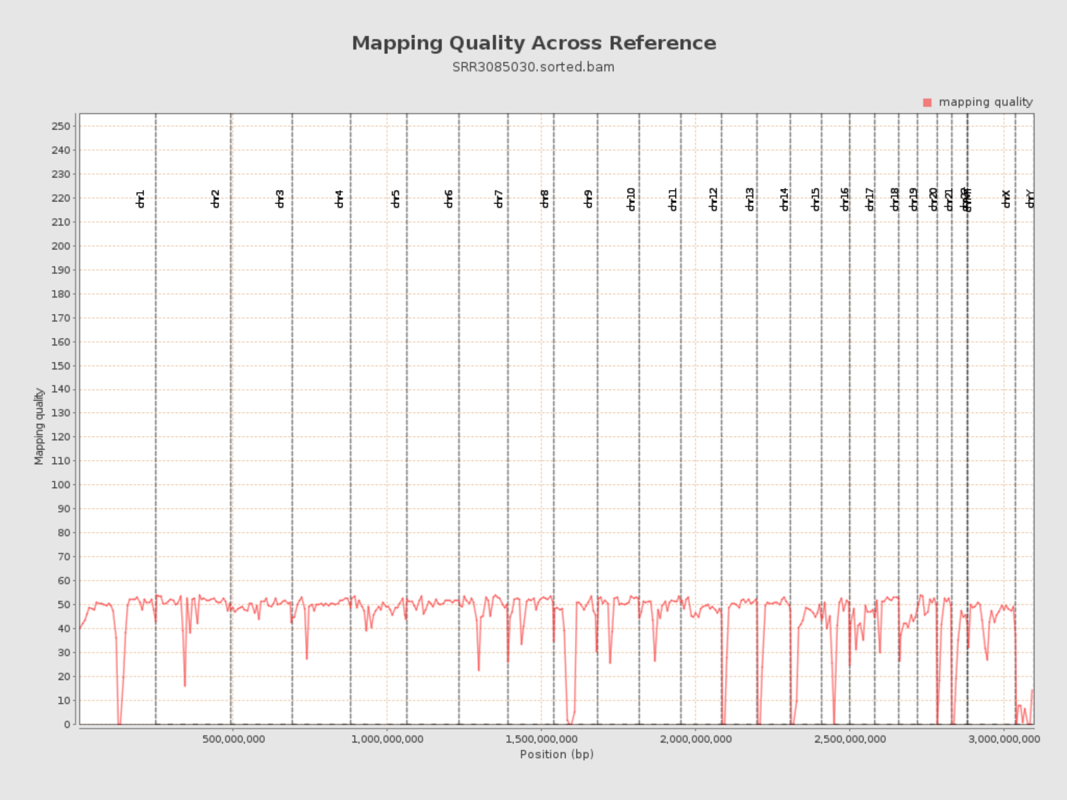
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram