Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:30:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085025.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_SRR3085025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085025.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:30:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,613,553
Mapped reads	2,336,128 / 89.39%
Unmapped reads	277,425 / 10.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,476 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	84,611 / 3.24%
Duplication rate	2.52%
Clipped reads	1,064,150 / 40.72%

2.2. ACGT Content

Number/percentage of A's	43,210,483 / 27.72%
Number/percentage of C's	30,149,531 / 19.34%
Number/percentage of T's	47,365,664 / 30.38%
Number/percentage of G's	35,157,744 / 22.55%
Number/percentage of N's	7,517 / 0%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0504

Standard Deviation	0.4612

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Mismatches and indels

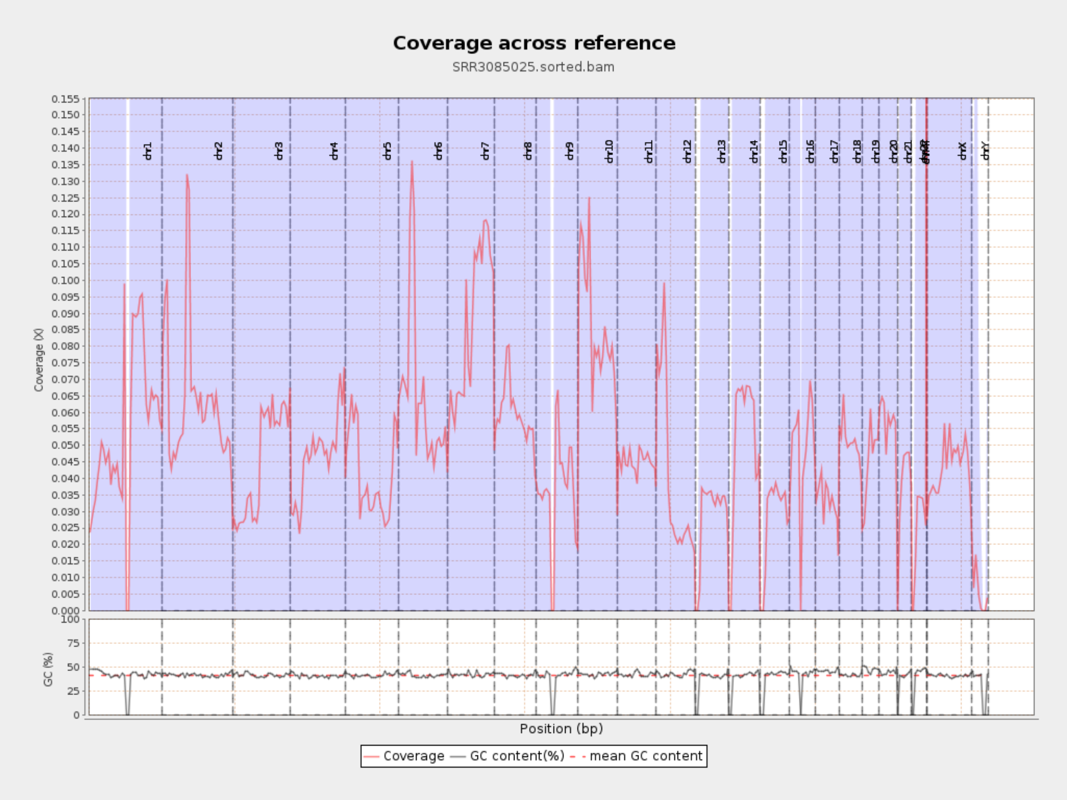
General error rate	0.91%
Mismatches	1,397,247
Insertions	11,588
Mapped reads with at least one insertion	0.49%
Deletions	34,670
Mapped reads with at least one deletion	1.47%
Homopolymer indels	45.35%

2.6. Chromosome stats

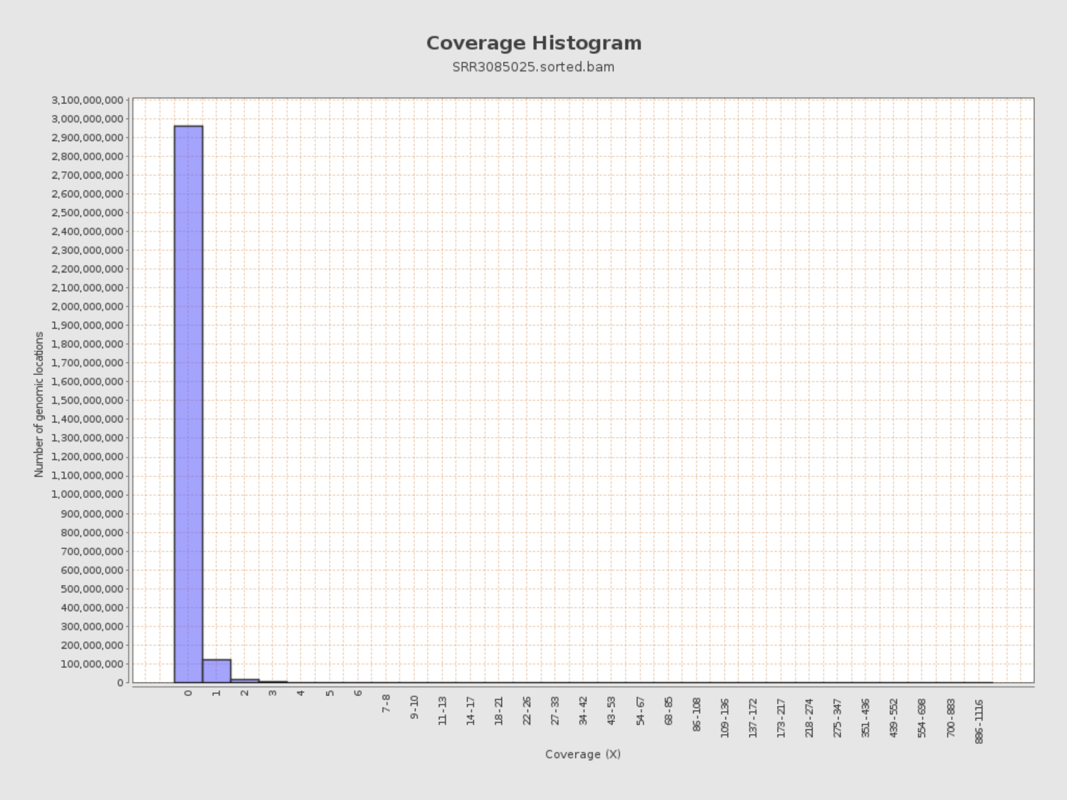
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13550064	0.0544	0.7533
chr2	243199373	15640375	0.0643	0.6267
chr3	198022430	8833013	0.0446	0.2516
chr4	191154276	8969435	0.0469	0.2532
chr5	180915260	7464447	0.0413	0.229
chr6	171115067	11272804	0.0659	0.4396
chr7	159138663	13926562	0.0875	0.5855

chr8	146364022	8721355	0.0596	0.7429
chr9	141213431	5175751	0.0367	0.447
chr10	135534747	11752847	0.0867	0.5919
chr11	135006516	6078358	0.045	0.391
chr12	133851895	5352147	0.04	0.2364
chr13	115169878	3285409	0.0285	0.188
chr14	107349540	5475391	0.051	0.2764
chr15	102531392	2848084	0.0278	0.1998
chr16	90354753	4502556	0.0498	0.2783
chr17	81195210	2670576	0.0329	0.2406
chr18	78077248	4029579	0.0516	0.7799
chr19	59128983	2686248	0.0454	0.5072
chr20	63025520	3599516	0.0571	0.275
chr21	48129895	1823636	0.0379	0.2372
chr22	51304566	1179892	0.023	0.1669
chrMT	16571	7938	0.479	0.7482
chrX	155270560	6776791	0.0436	0.2961
chrY	59373566	327381	0.0055	0.1135

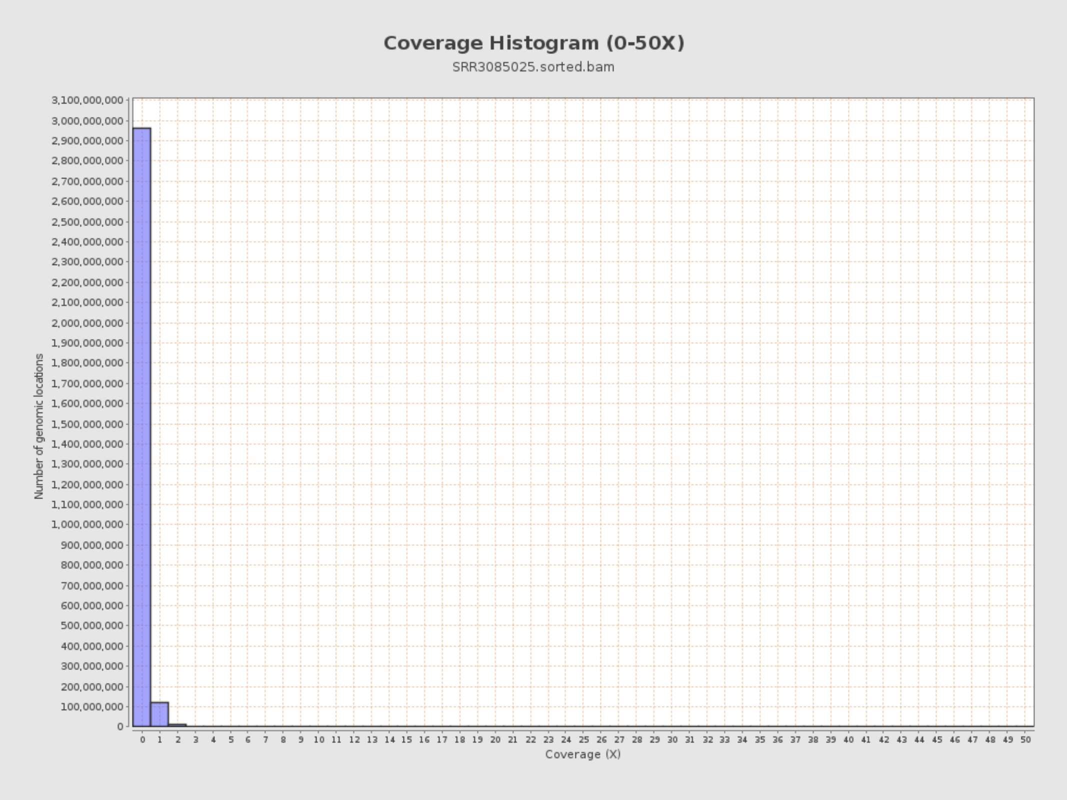
3. Results : Coverage across reference



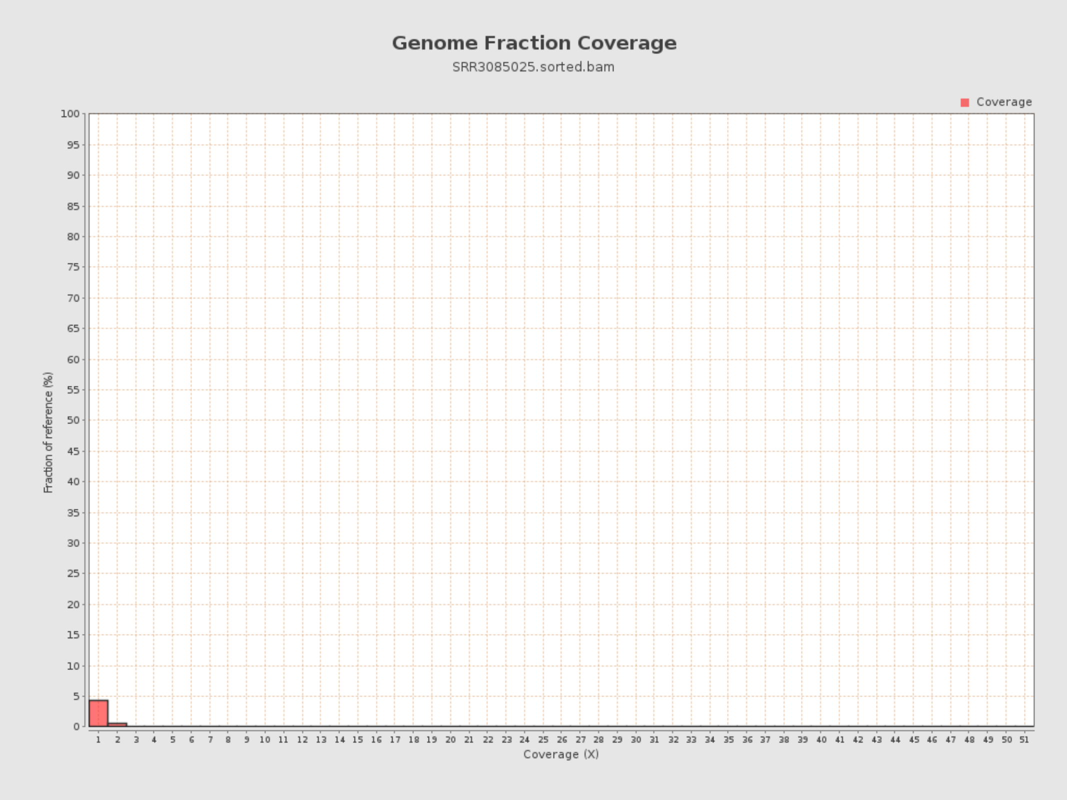
4. Results : Coverage Histogram



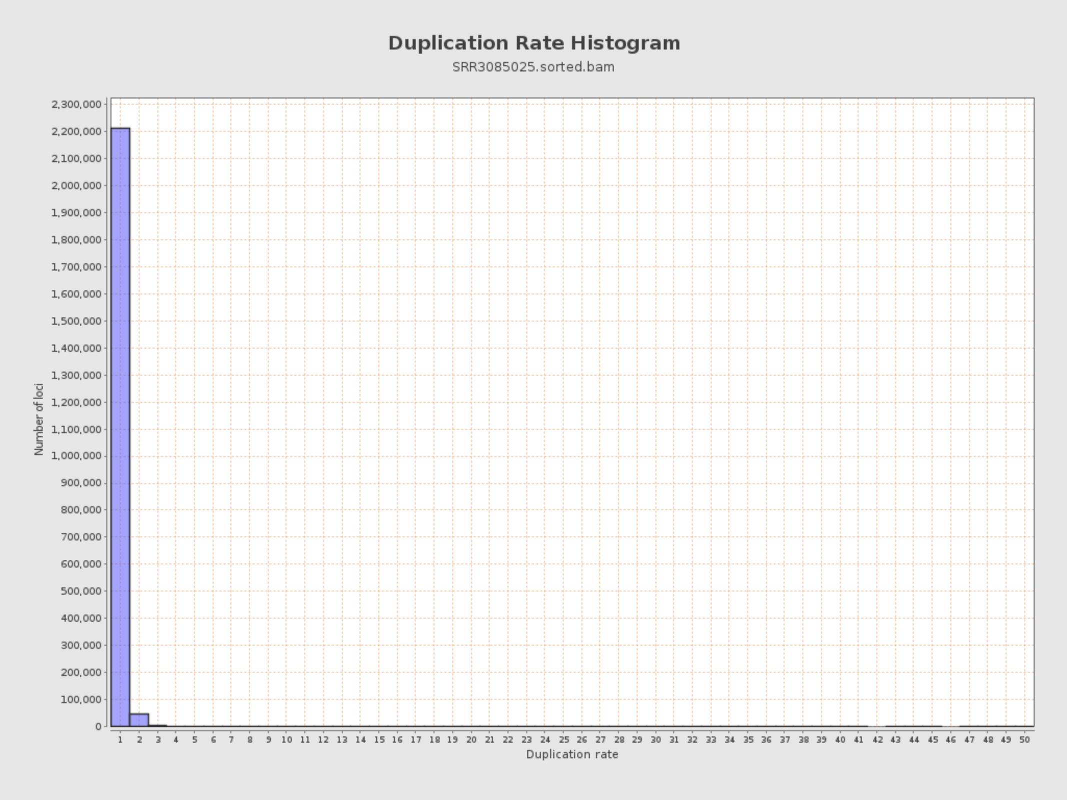
5. Results : Coverage Histogram (0-50X)



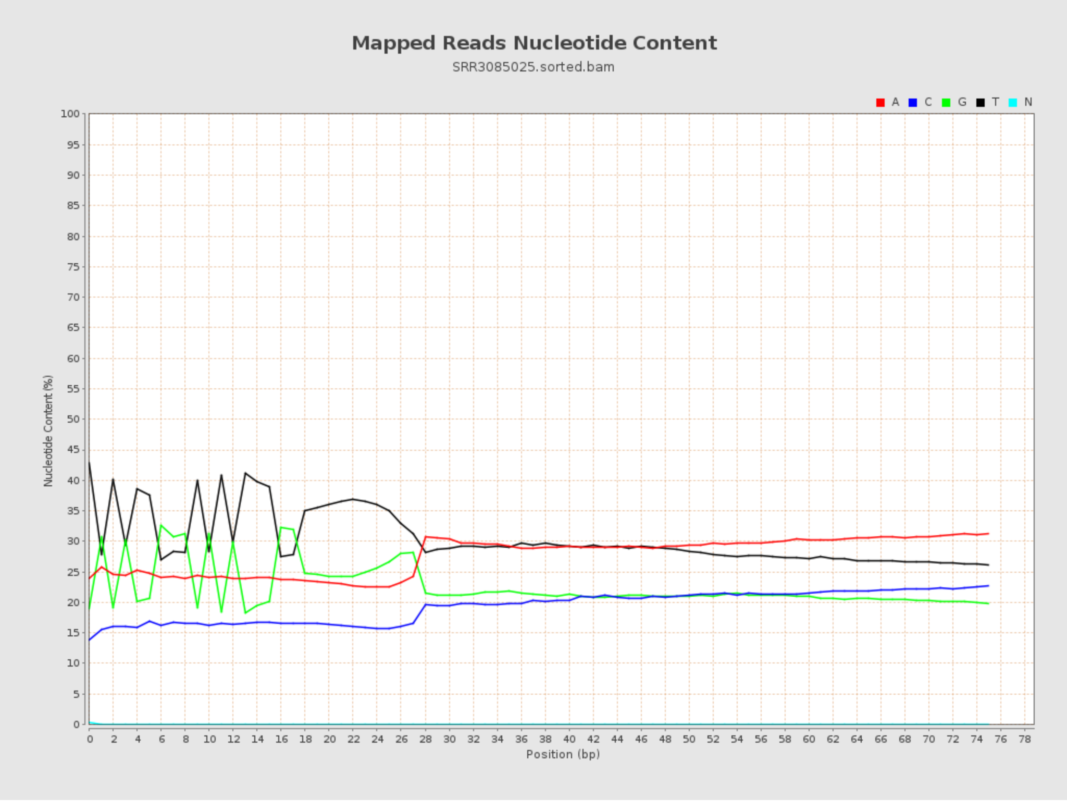
6. Results : Genome Fraction Coverage



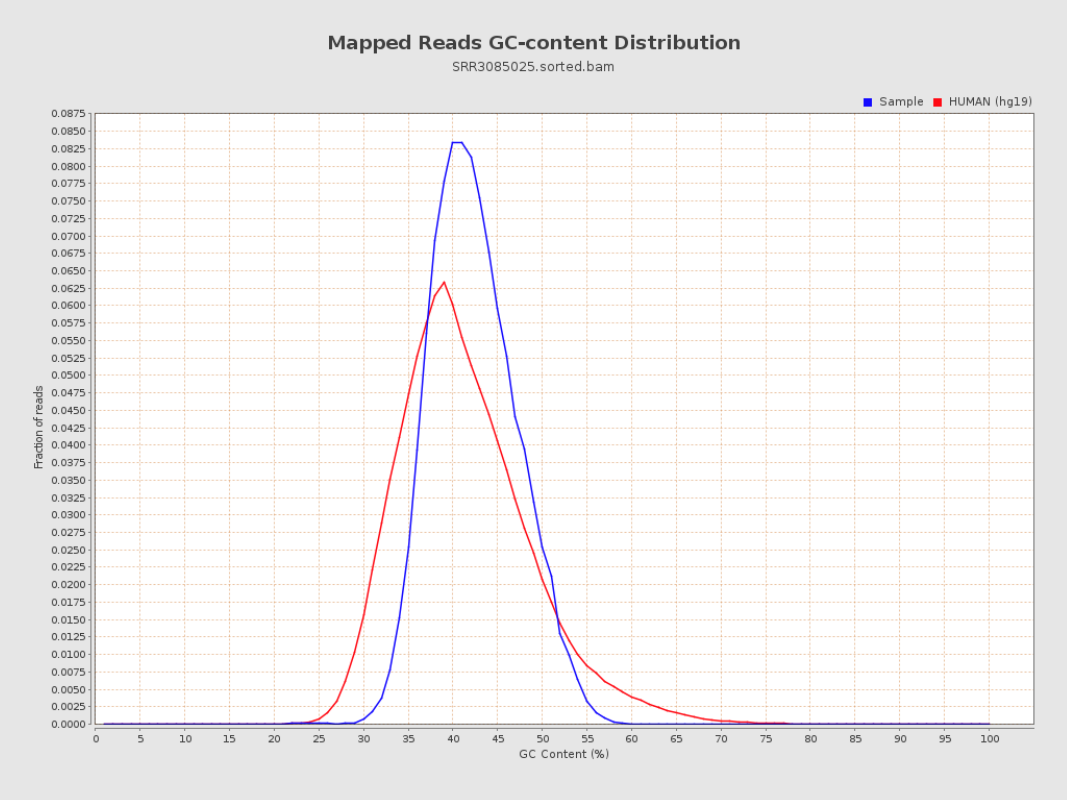
7. Results : Duplication Rate Histogram



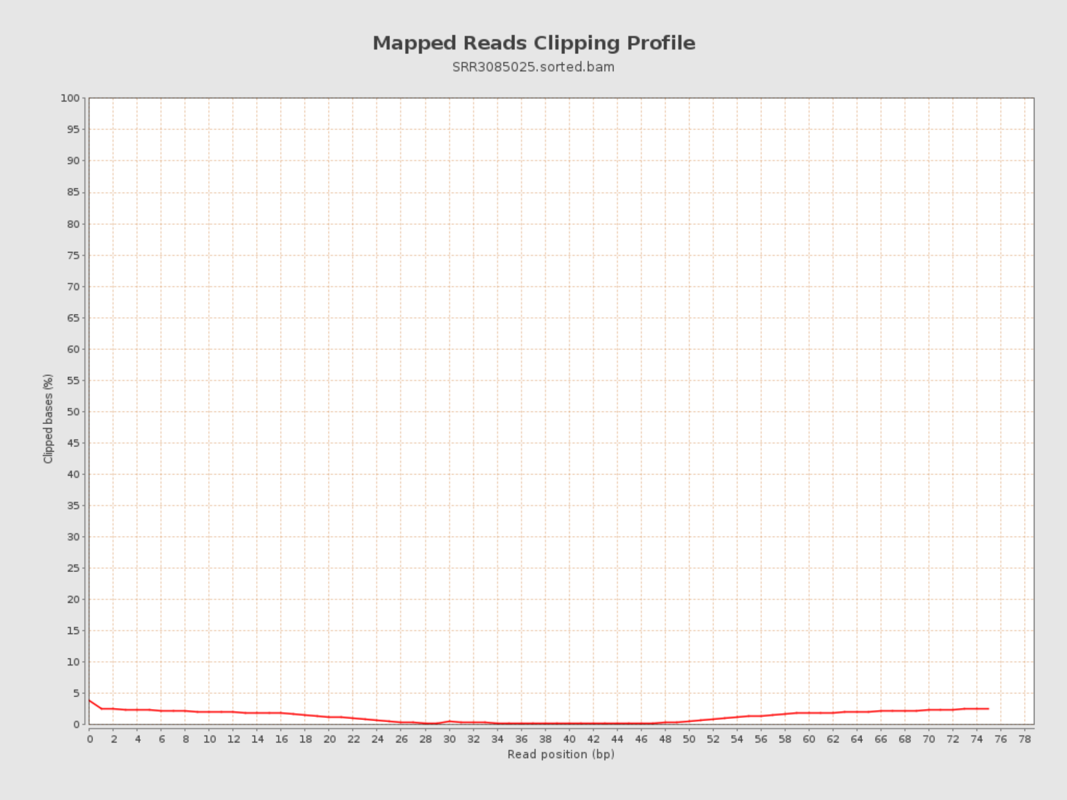
8. Results : Mapped Reads Nucleotide Content



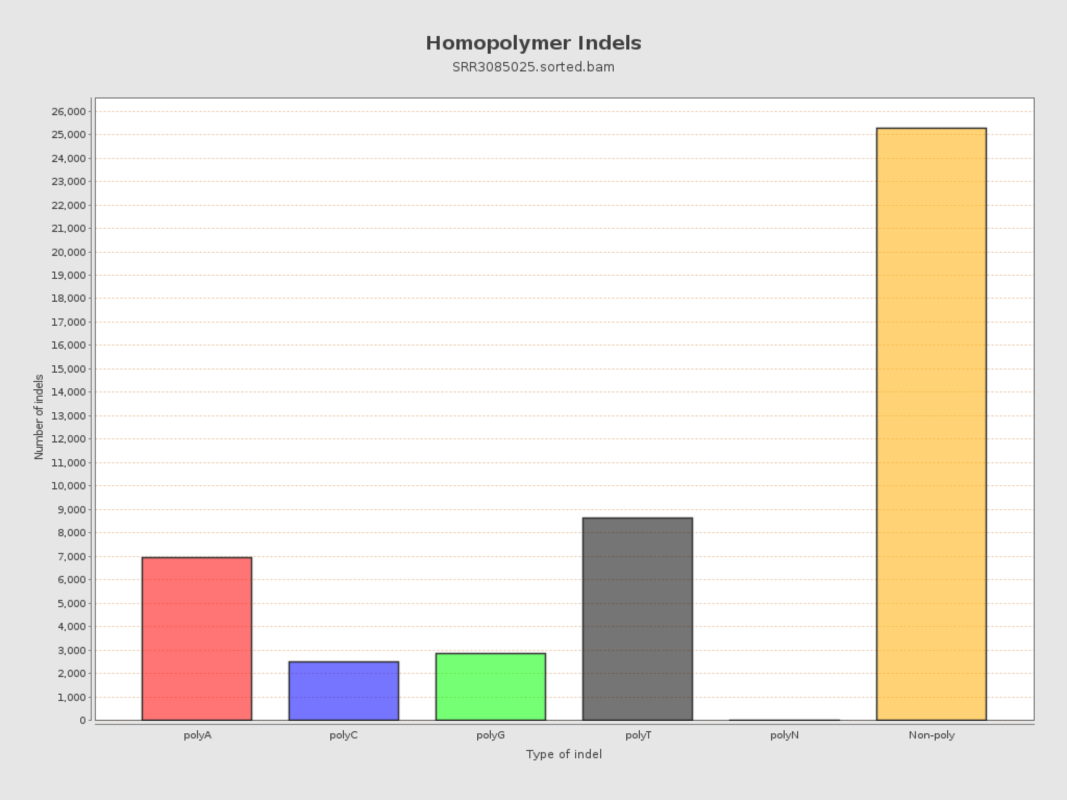
9. Results : Mapped Reads GC-content Distribution



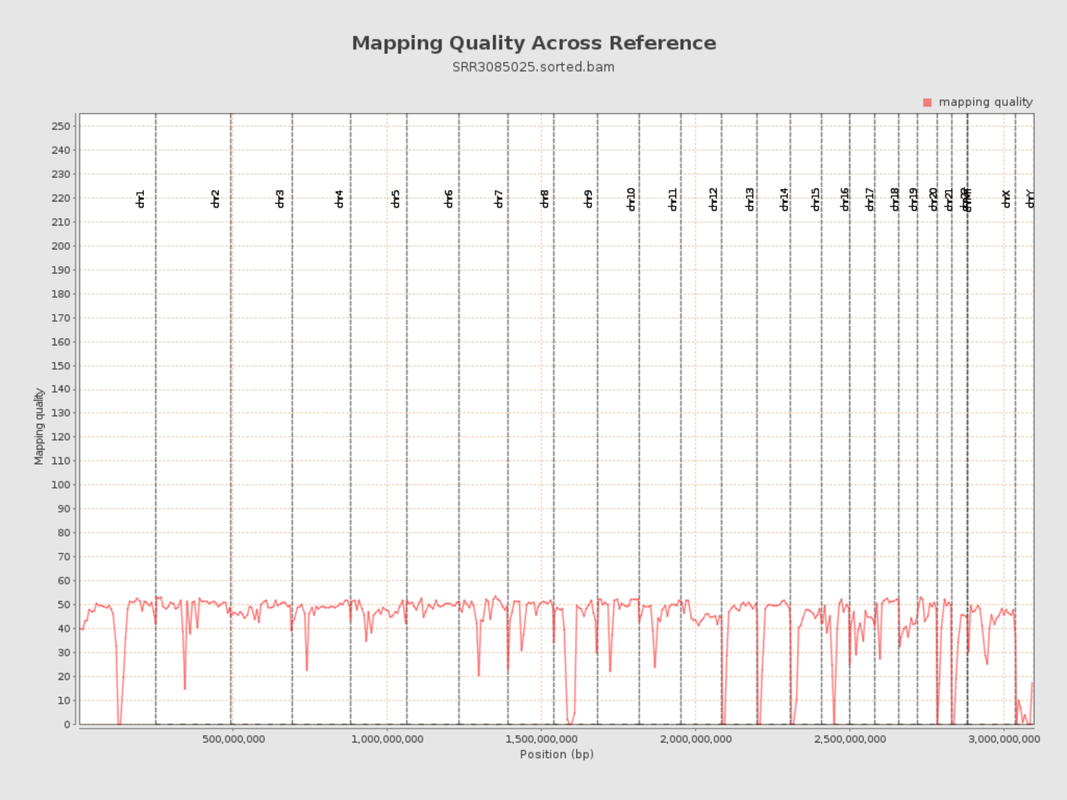
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram