Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:13:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085037.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_SRR3085037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:12:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,951,053
Mapped reads	2,647,672 / 89.72%
Unmapped reads	303,381 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,577 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	95,439 / 3.23%
Duplication rate	2.82%
Clipped reads	1,297,098 / 43.95%

2.2. ACGT Content

Number/percentage of A's	48,635,267 / 27.8%
Number/percentage of C's	34,220,015 / 19.56%
Number/percentage of T's	52,872,000 / 30.22%
Number/percentage of G's	39,205,083 / 22.41%
Number/percentage of N's	18,486 / 0.01%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.3993

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

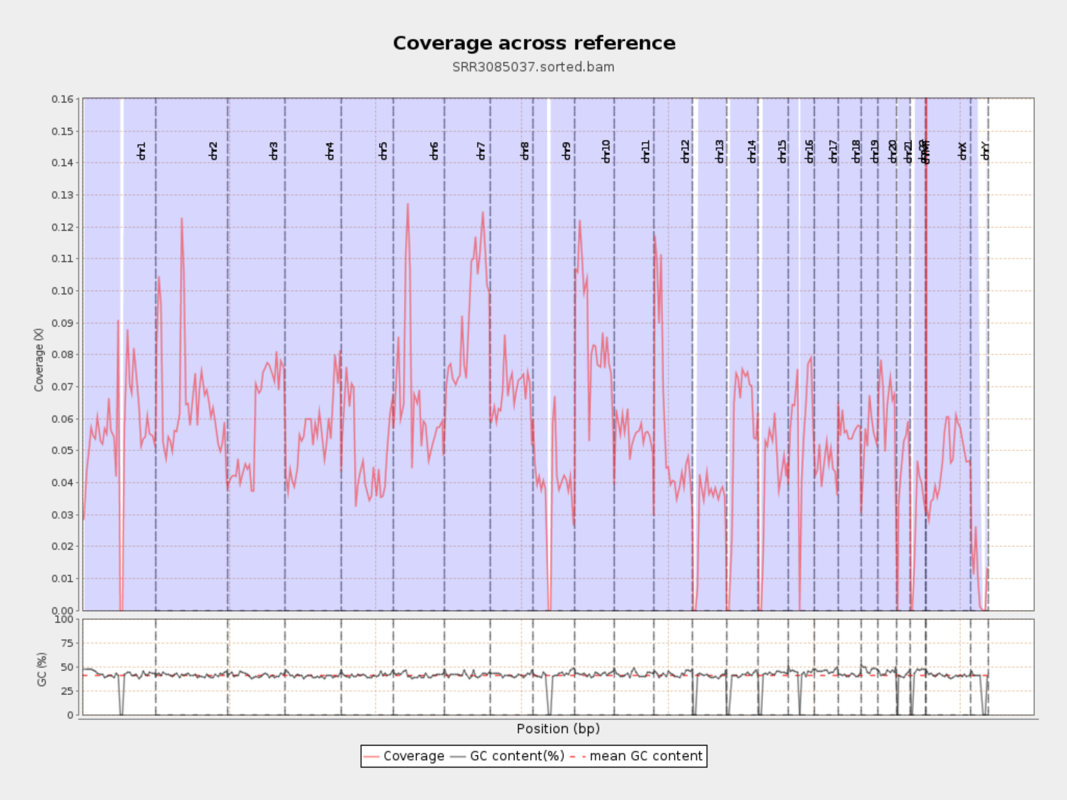
General error rate	0.93%
Mismatches	1,604,857
Insertions	13,227
Mapped reads with at least one insertion	0.5%
Deletions	36,508
Mapped reads with at least one deletion	1.37%
Homopolymer indels	45.19%

2.6. Chromosome stats

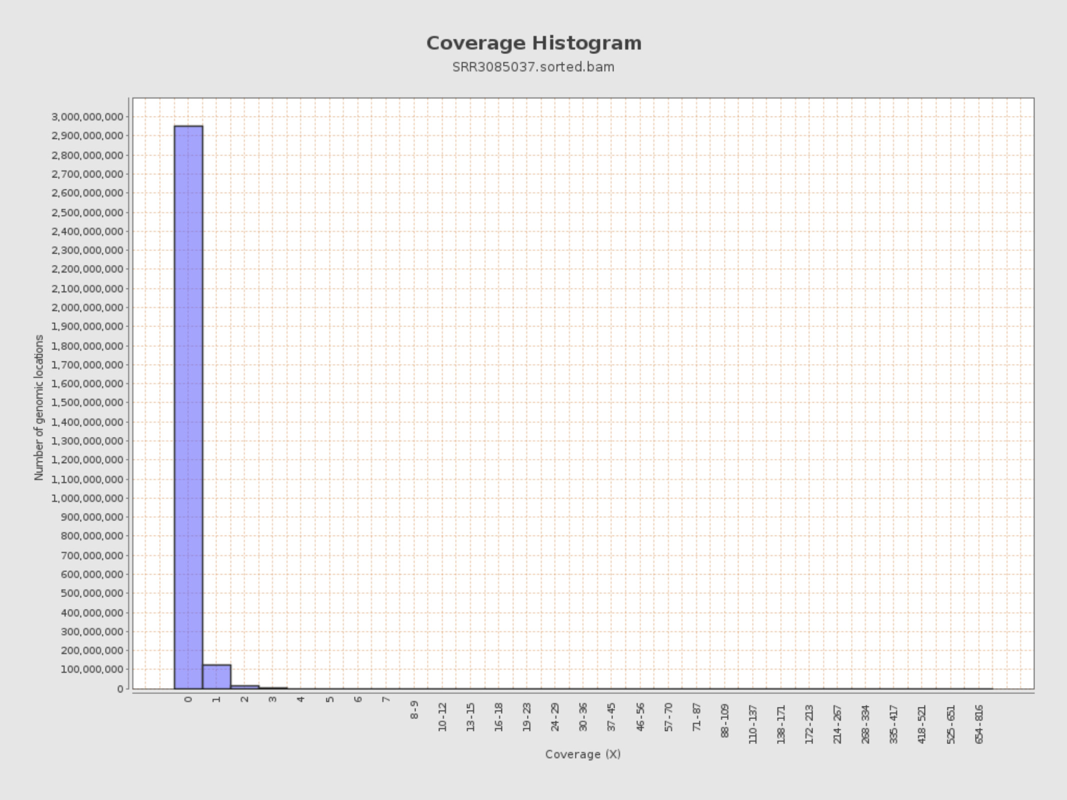
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13746317	0.0552	0.5568
chr2	243199373	16131499	0.0663	0.5552
chr3	198022430	11577808	0.0585	0.281
chr4	191154276	10594422	0.0554	0.282
chr5	180915260	8825803	0.0488	0.2545
chr6	171115067	11488489	0.0671	0.405
chr7	159138663	14492375	0.0911	0.5154

chr8	146364022	9962818	0.0681	0.5896
chr9	141213431	5339787	0.0378	0.3488
chr10	135534747	11796317	0.087	0.4921
chr11	135006516	7477891	0.0554	0.3782
chr12	133851895	7739077	0.0578	0.2838
chr13	115169878	3621229	0.0314	0.2039
chr14	107349540	6046230	0.0563	0.2879
chr15	102531392	4104650	0.04	0.2422
chr16	90354753	5115463	0.0566	0.2949
chr17	81195210	3712362	0.0457	0.2743
chr18	78077248	4440721	0.0569	0.5814
chr19	59128983	3208096	0.0543	0.4519
chr20	63025520	4138829	0.0657	0.3022
chr21	48129895	2082687	0.0433	0.2532
chr22	51304566	1432080	0.0279	0.194
chrMT	16571	74756	4.5113	3.9698
chrX	155270560	7266405	0.0468	0.2775
chrY	59373566	597320	0.0101	0.1494

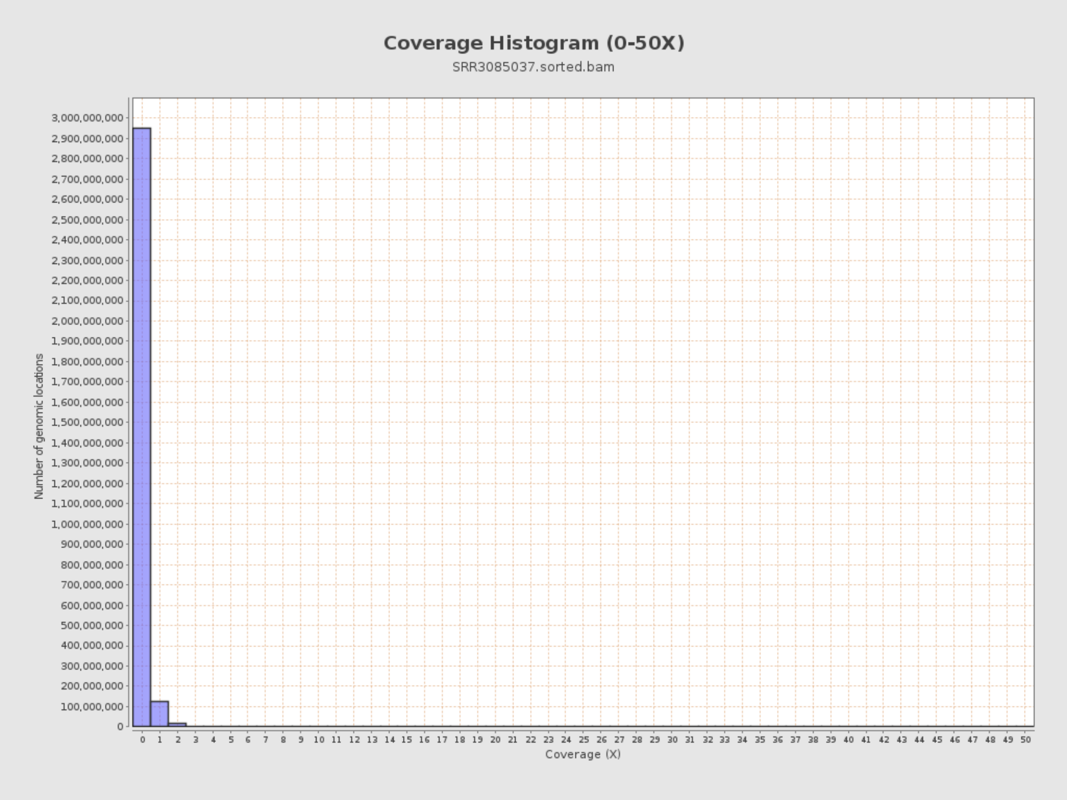
3. Results : Coverage across reference



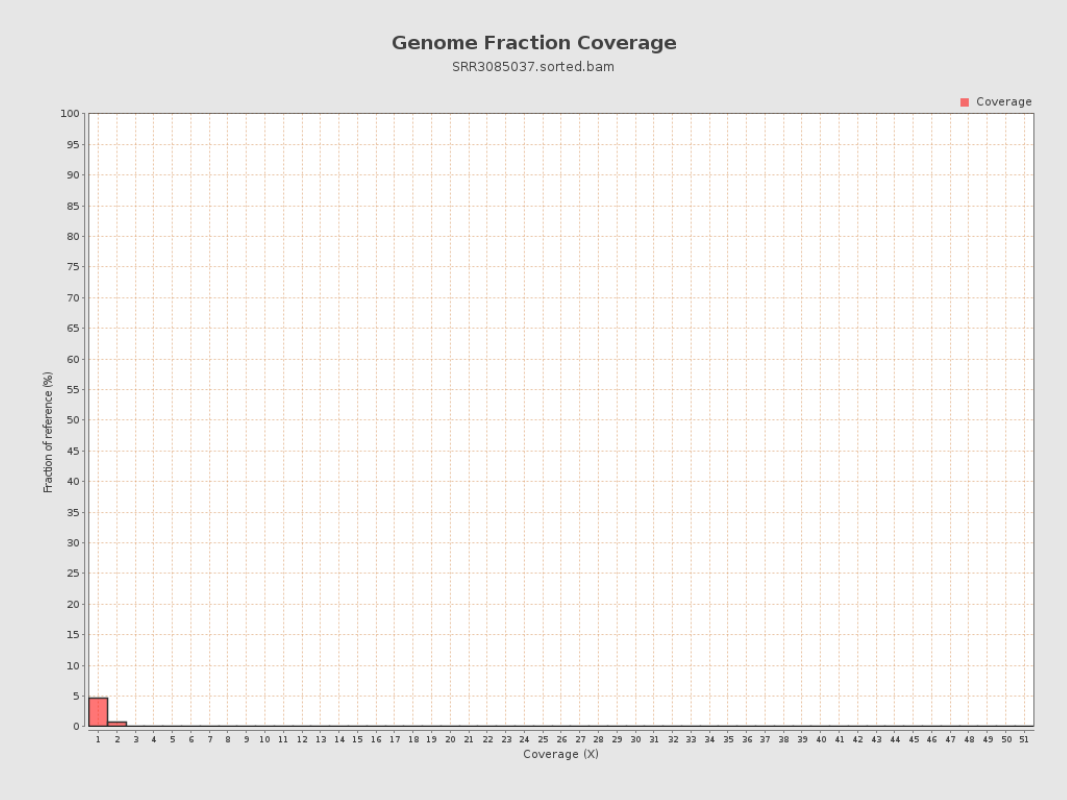
4. Results : Coverage Histogram



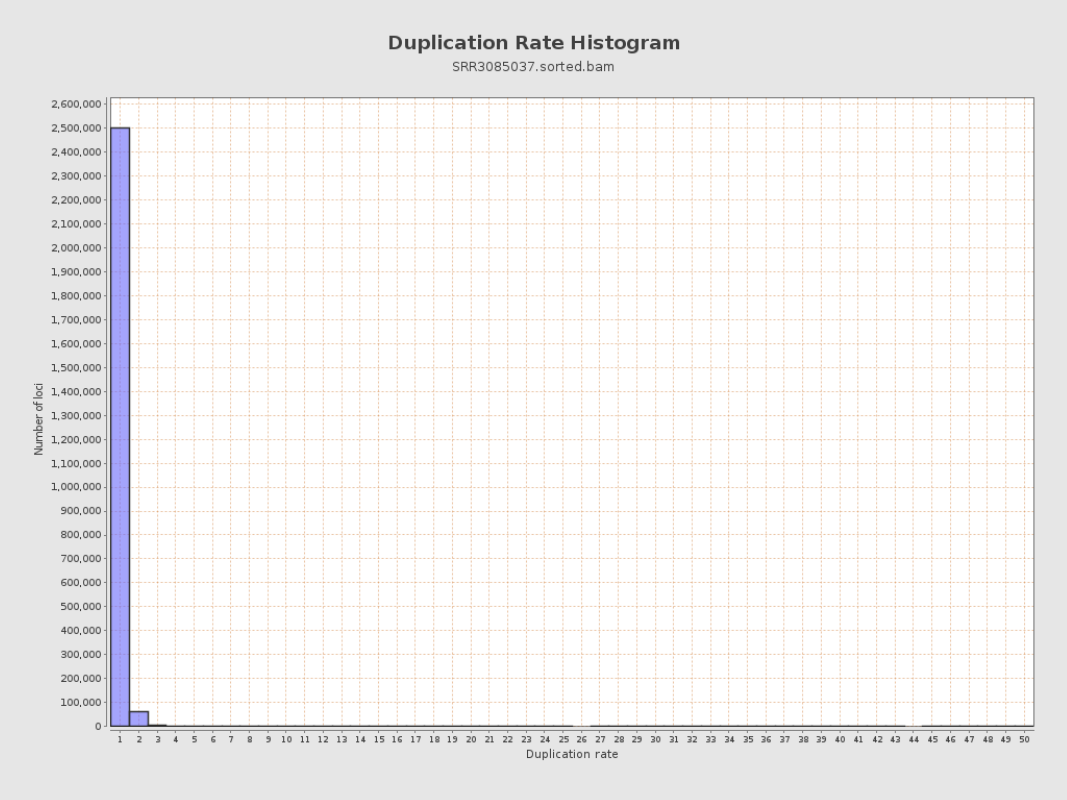
5. Results : Coverage Histogram (0-50X)



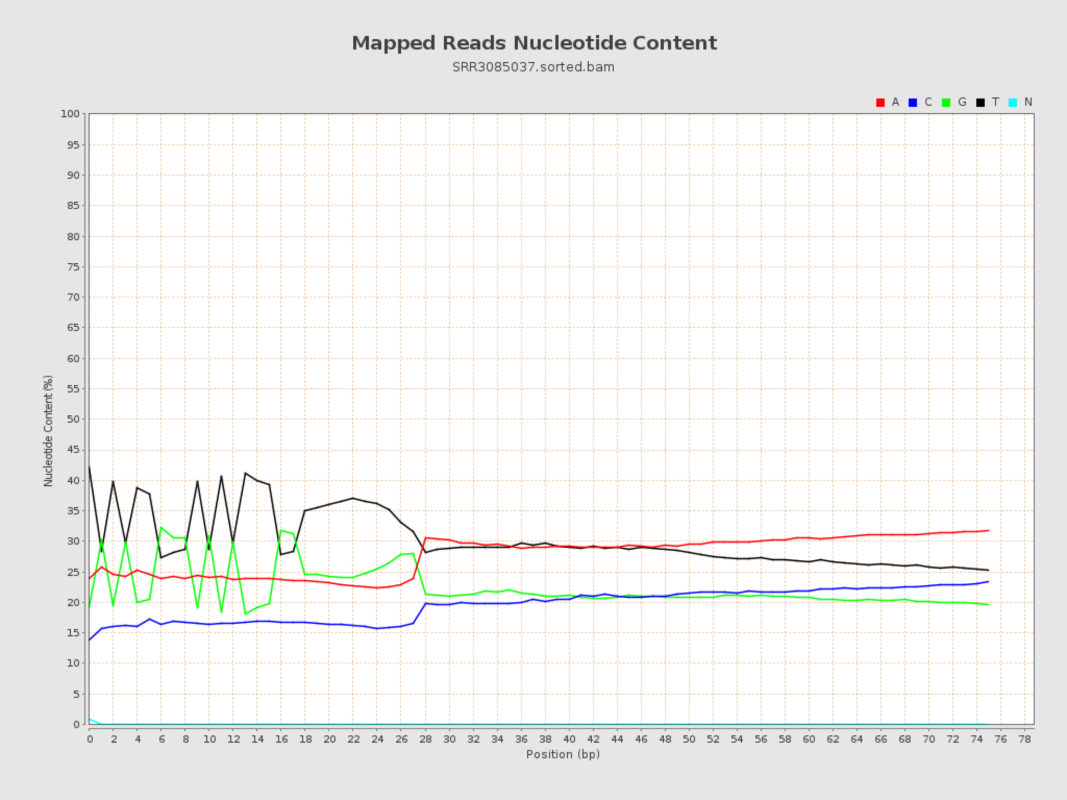
6. Results : Genome Fraction Coverage



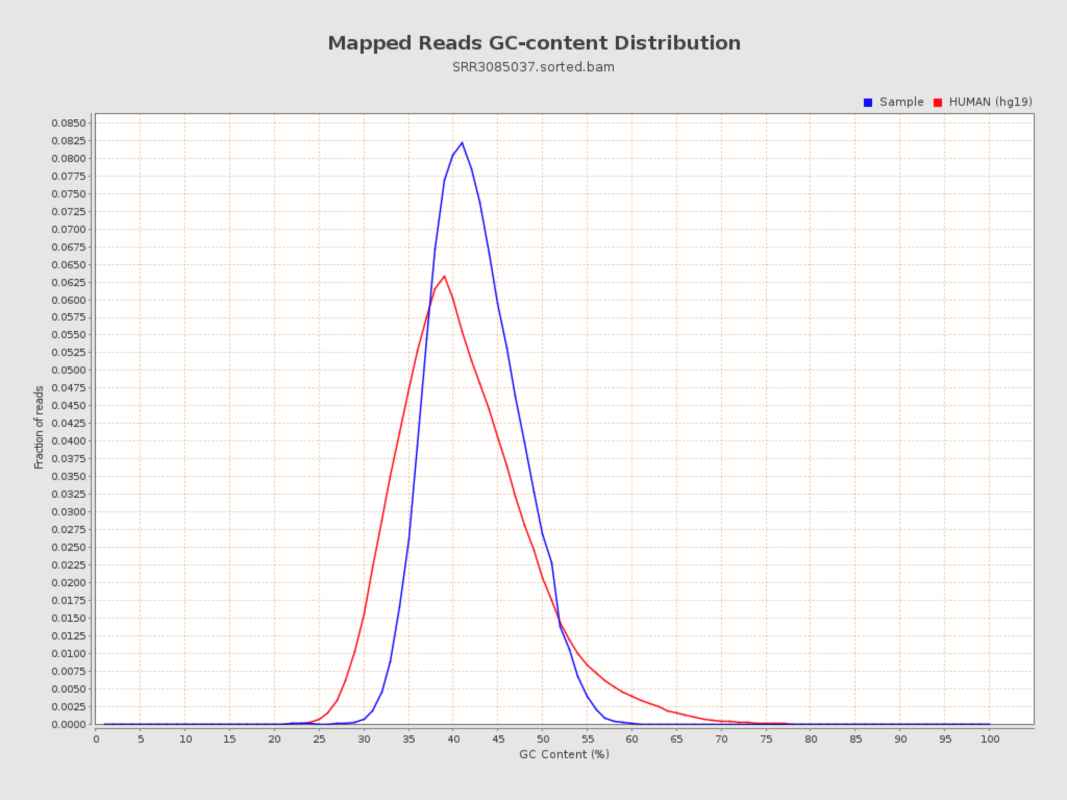
7. Results : Duplication Rate Histogram



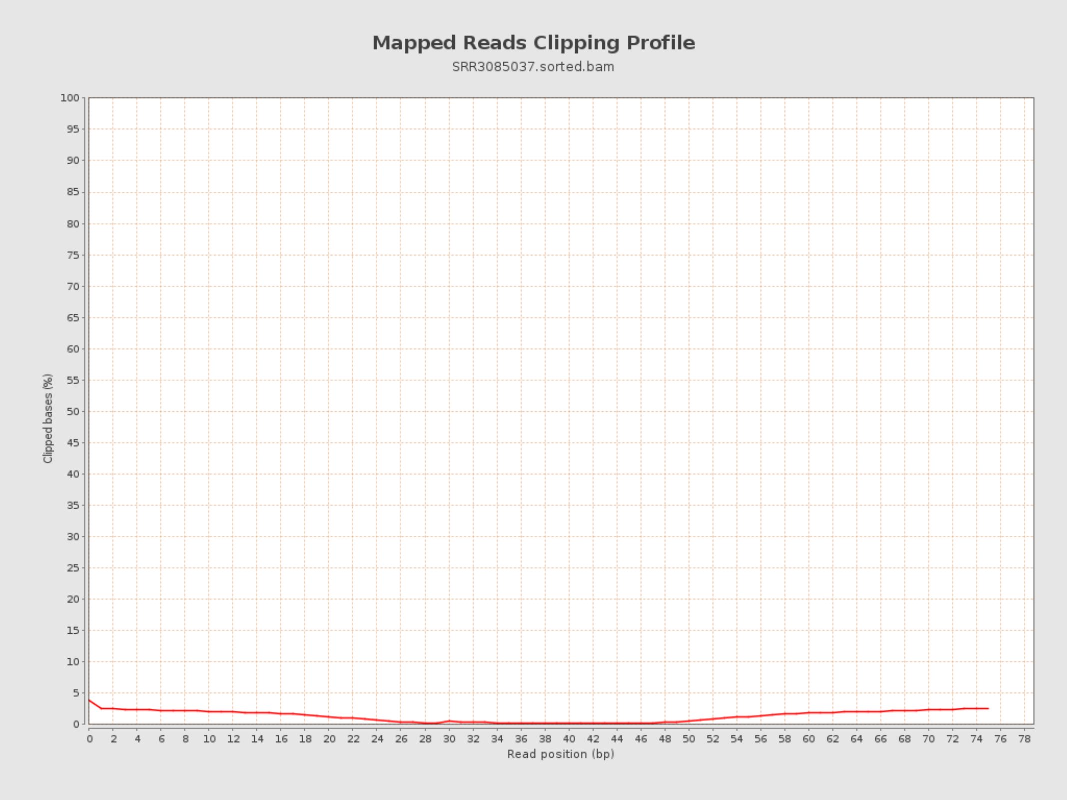
8. Results : Mapped Reads Nucleotide Content



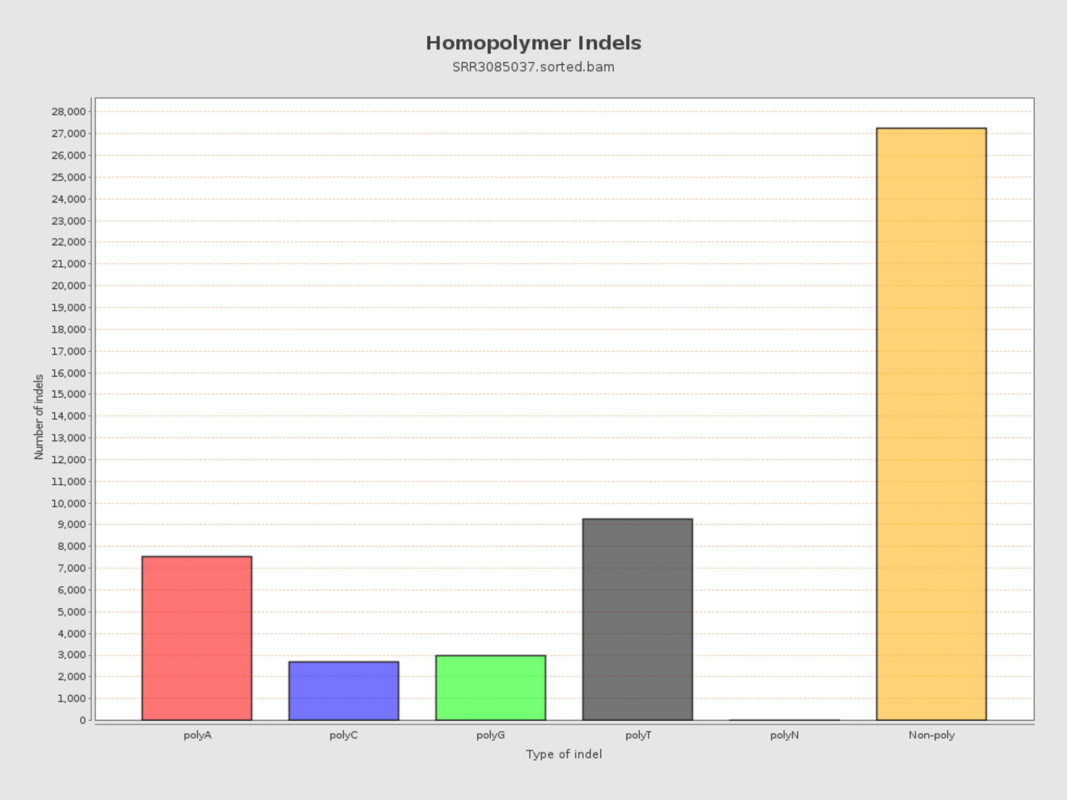
9. Results : Mapped Reads GC-content Distribution



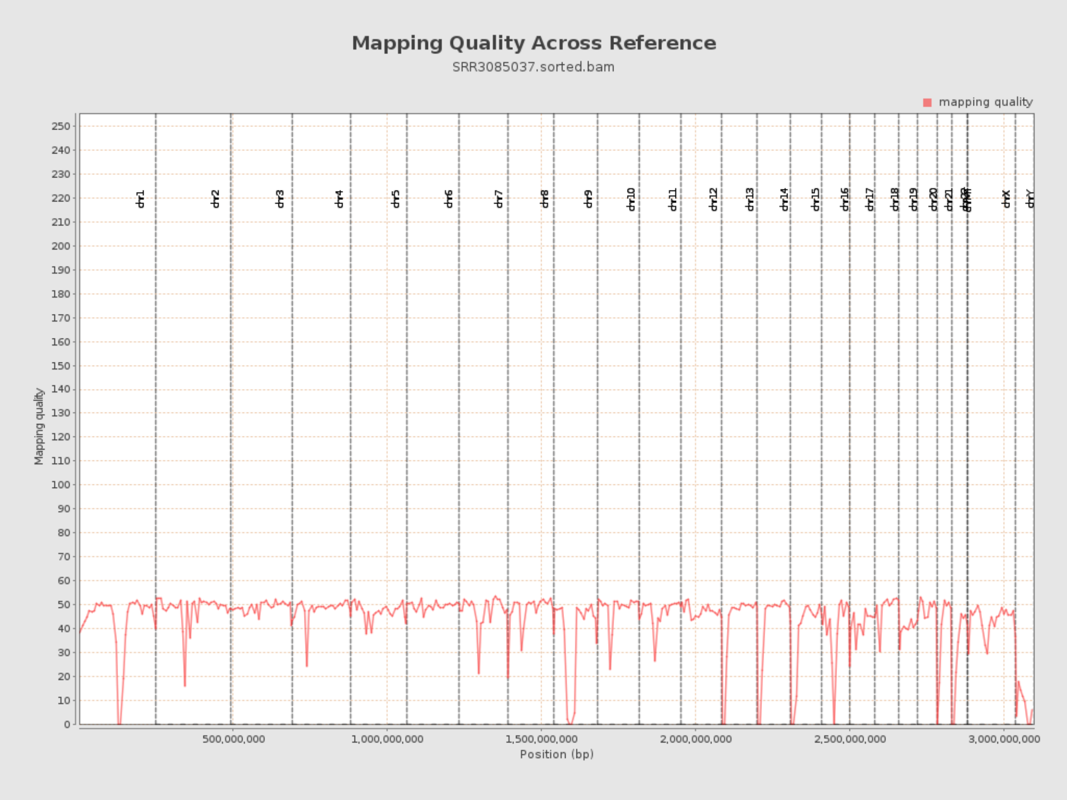
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram