Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:48:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085100.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_SRR3085100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:48:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,034,068
Mapped reads	1,634,090 / 80.34%
Unmapped reads	399,978 / 19.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,361 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	38,685 / 1.9%
Duplication rate	1.98%
Clipped reads	1,112,487 / 54.69%

2.2. ACGT Content

Number/percentage of A's	29,769,371 / 29.96%
Number/percentage of C's	19,314,627 / 19.44%
Number/percentage of T's	28,837,855 / 29.03%
Number/percentage of G's	21,428,304 / 21.57%
Number/percentage of N's	1,924 / 0%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.2461

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

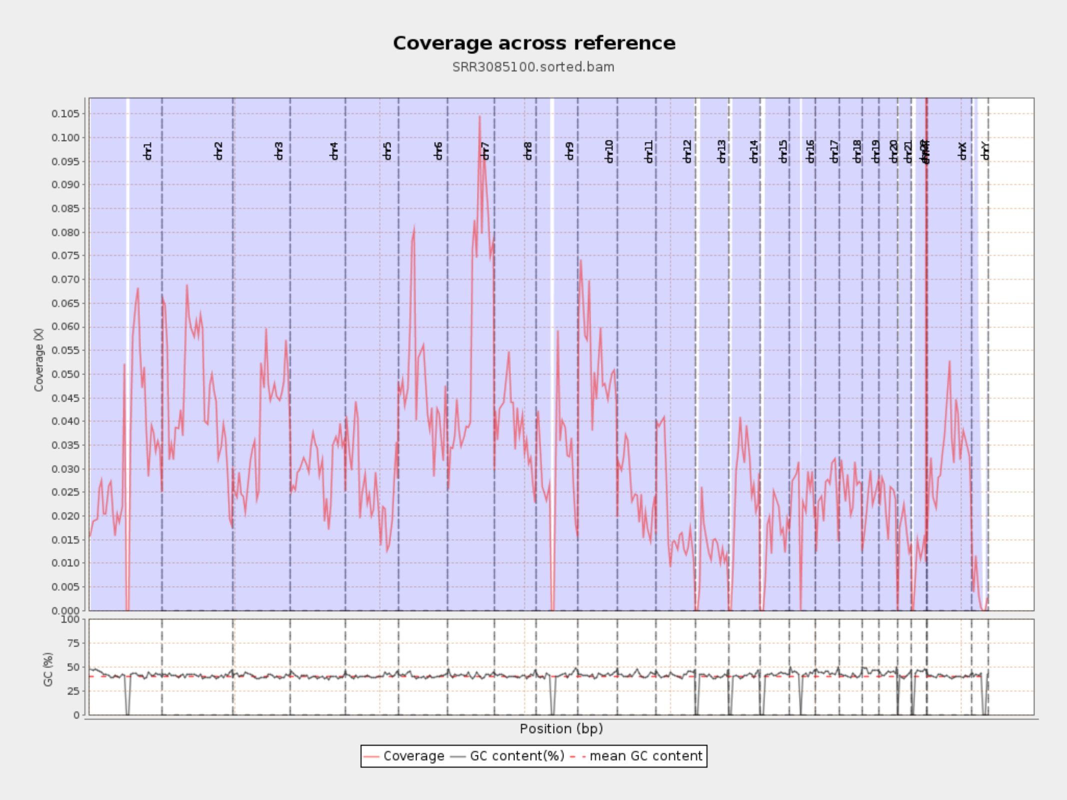
General error rate	0.88%
Mismatches	860,258
Insertions	7,213
Mapped reads with at least one insertion	0.44%
Deletions	19,015
Mapped reads with at least one deletion	1.15%
Homopolymer indels	45.73%

2.6. Chromosome stats

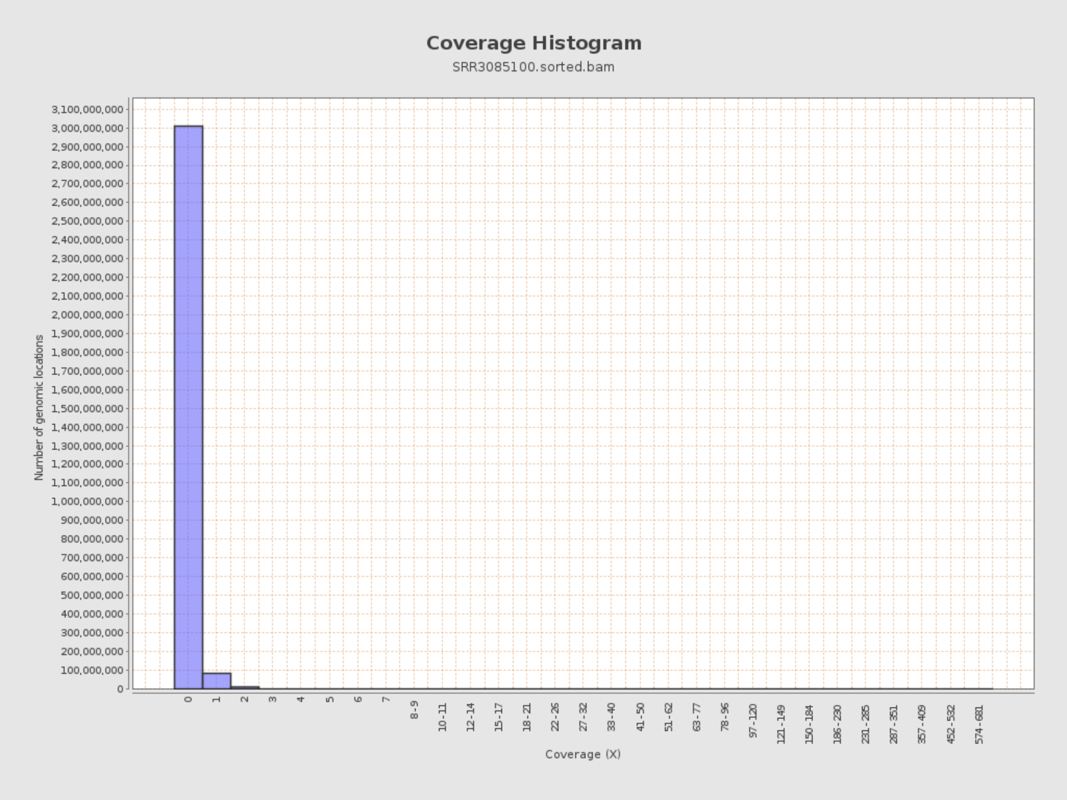
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7783608	0.0312	0.3322
chr2	243199373	11162240	0.0459	0.2702
chr3	198022430	7594800	0.0384	0.2163
chr4	191154276	5821336	0.0305	0.1945
chr5	180915260	4763376	0.0263	0.1763
chr6	171115067	8162384	0.0477	0.2893
chr7	159138663	9558484	0.0601	0.2927

chr8	146364022	5710033	0.039	0.4365
chr9	141213431	4154209	0.0294	0.2134
chr10	135534747	7308647	0.0539	0.3551
chr11	135006516	3367308	0.0249	0.1866
chr12	133851895	2723360	0.0203	0.1569
chr13	115169878	1376949	0.012	0.1174
chr14	107349540	2700551	0.0252	0.1787
chr15	102531392	1542410	0.015	0.1331
chr16	90354753	2147034	0.0238	0.1765
chr17	81195210	1960022	0.0241	0.1778
chr18	78077248	2067287	0.0265	0.2761
chr19	59128983	1373295	0.0232	0.2465
chr20	63025520	1435937	0.0228	0.1663
chr21	48129895	748412	0.0155	0.1438
chr22	51304566	500413	0.0098	0.1062
chrMT	16571	8465	0.5108	0.8304
chrX	155270560	5204719	0.0335	0.2077
chrY	59373566	207029	0.0035	0.082

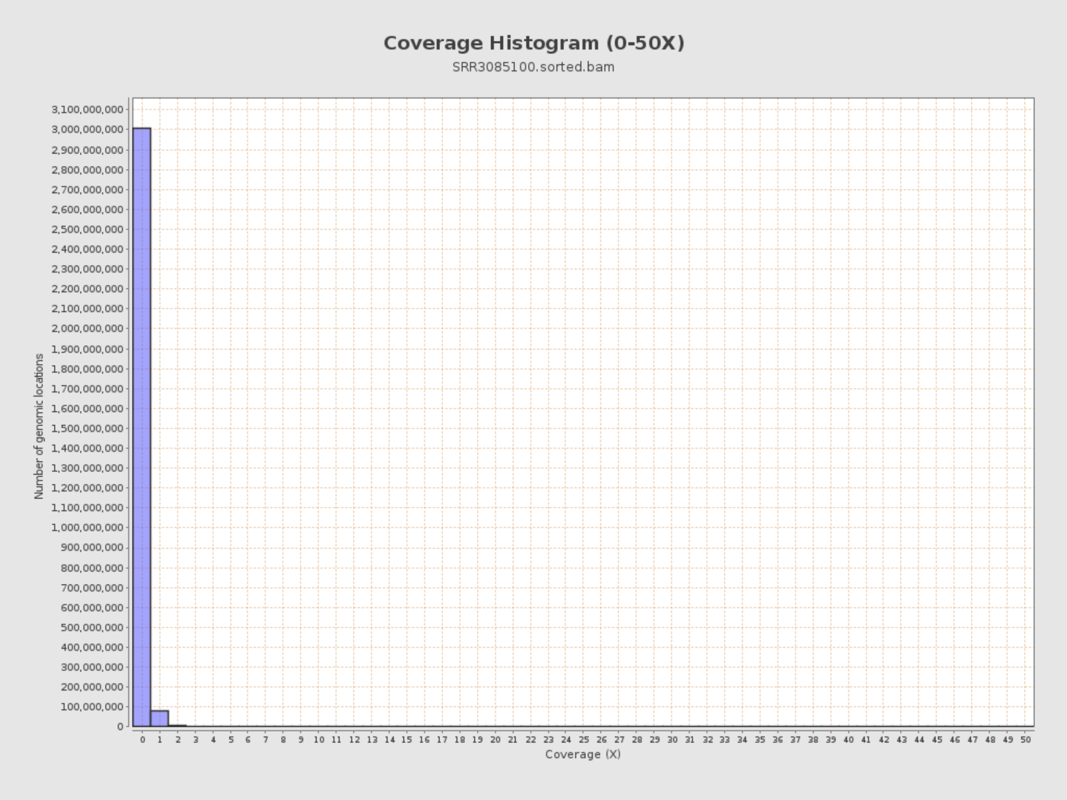
3. Results : Coverage across reference



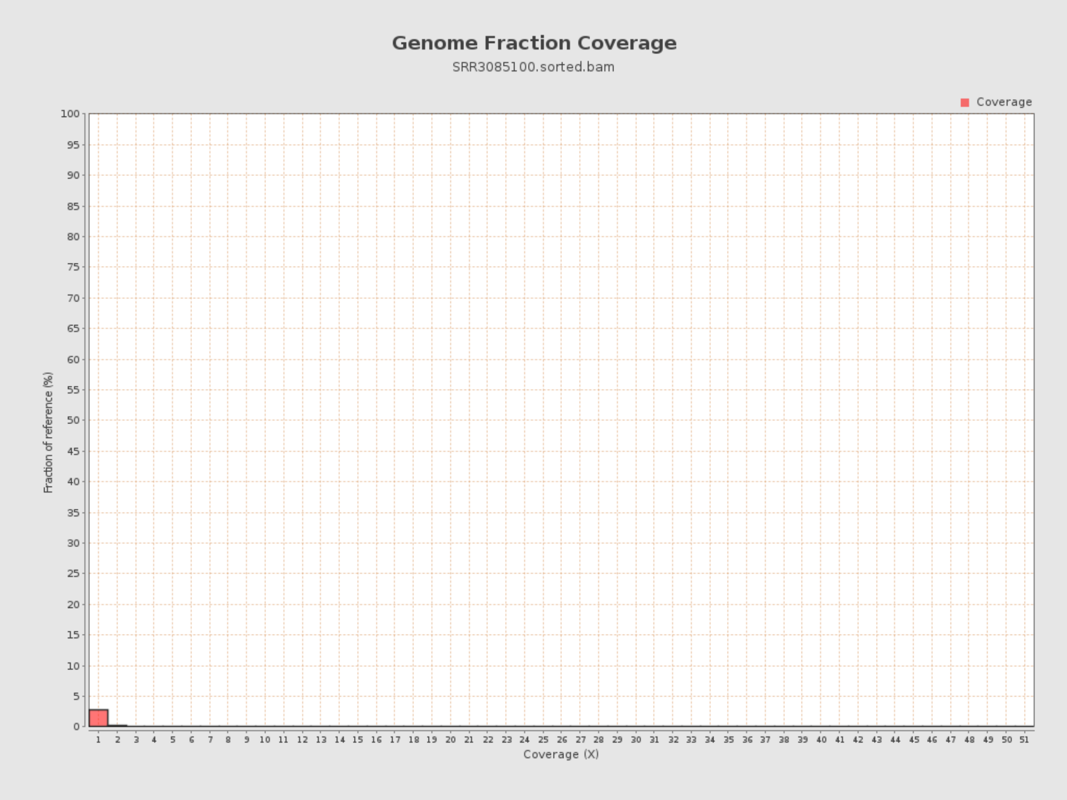
4. Results : Coverage Histogram



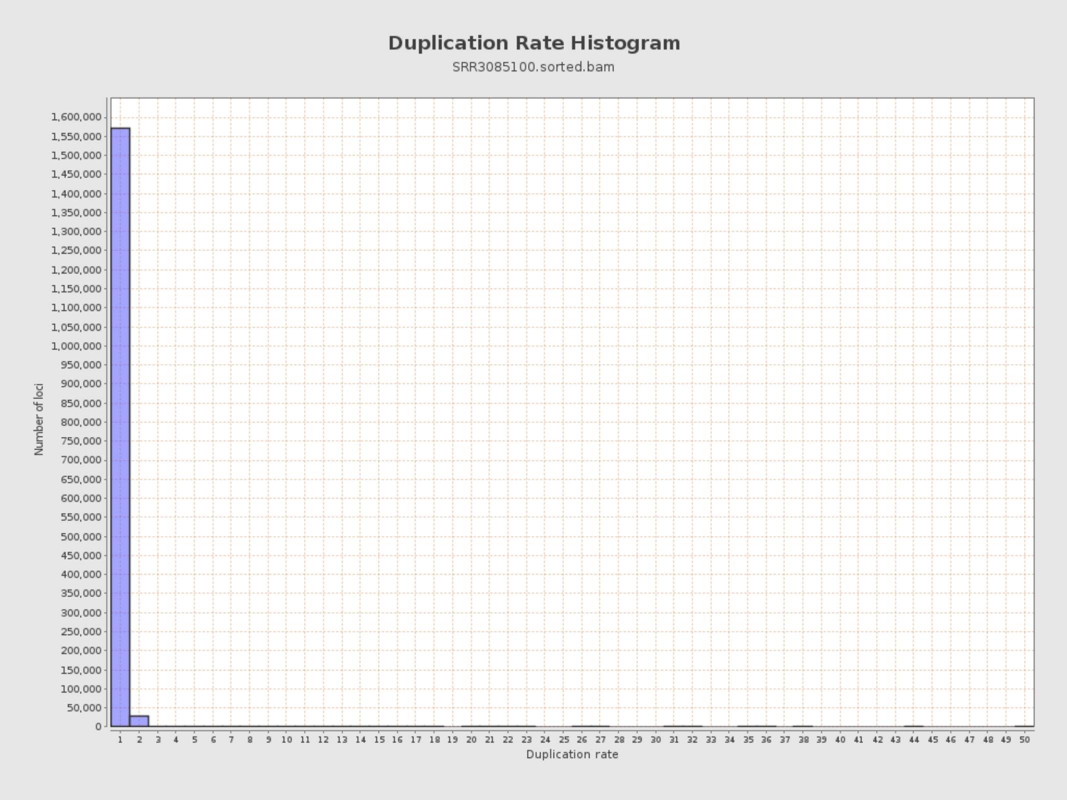
5. Results : Coverage Histogram (0-50X)



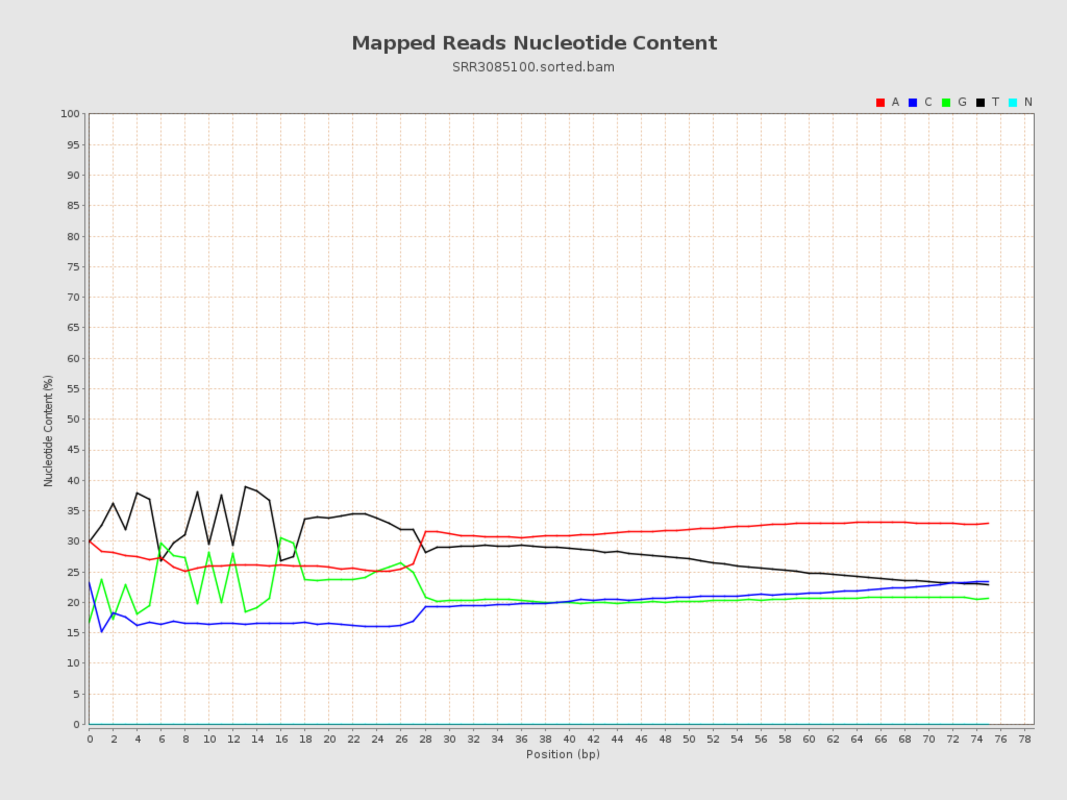
6. Results : Genome Fraction Coverage



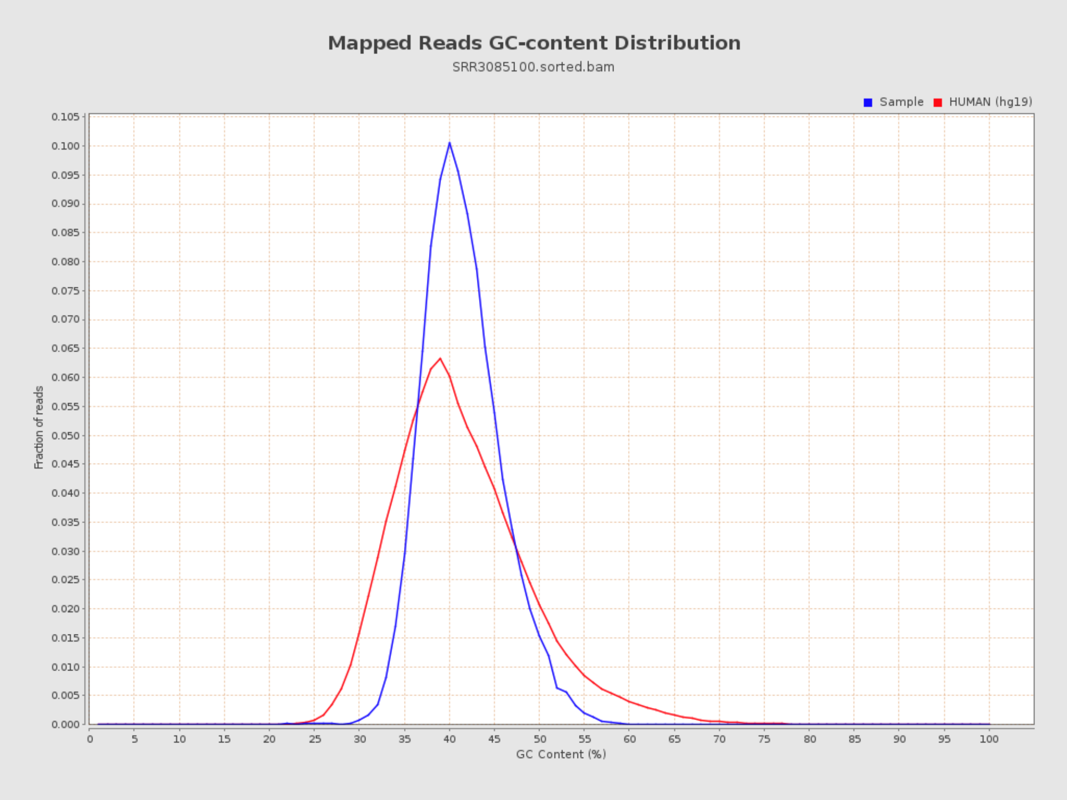
7. Results : Duplication Rate Histogram



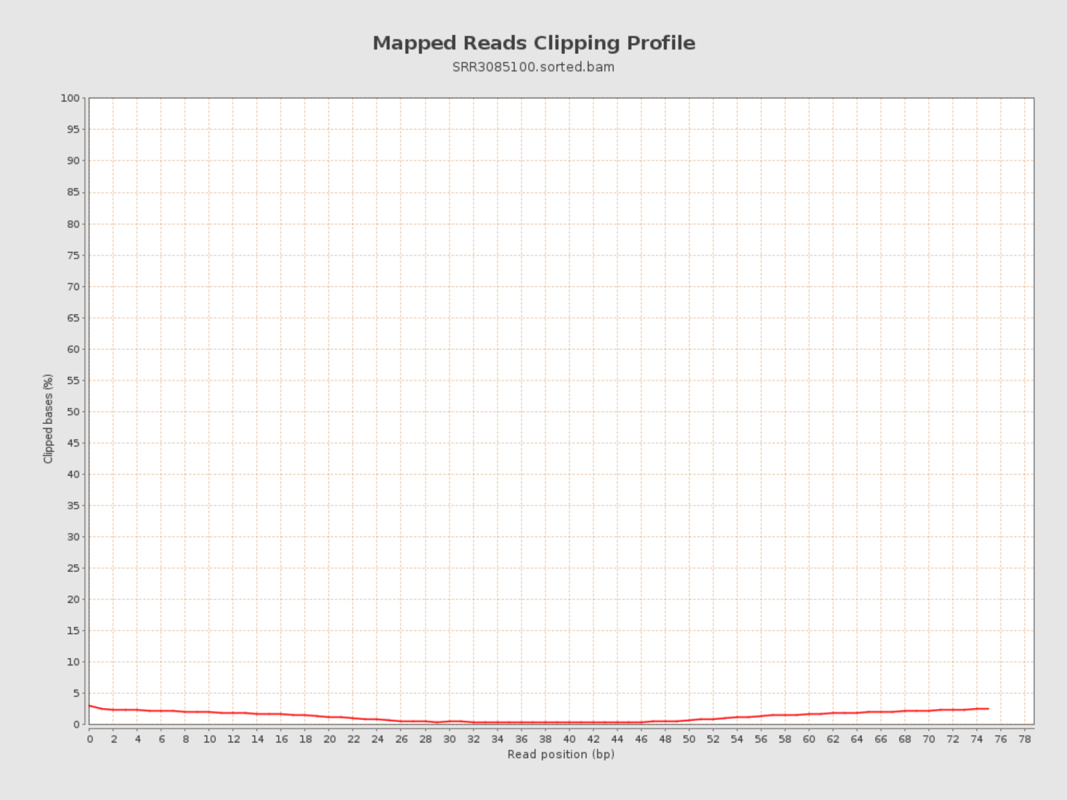
8. Results : Mapped Reads Nucleotide Content



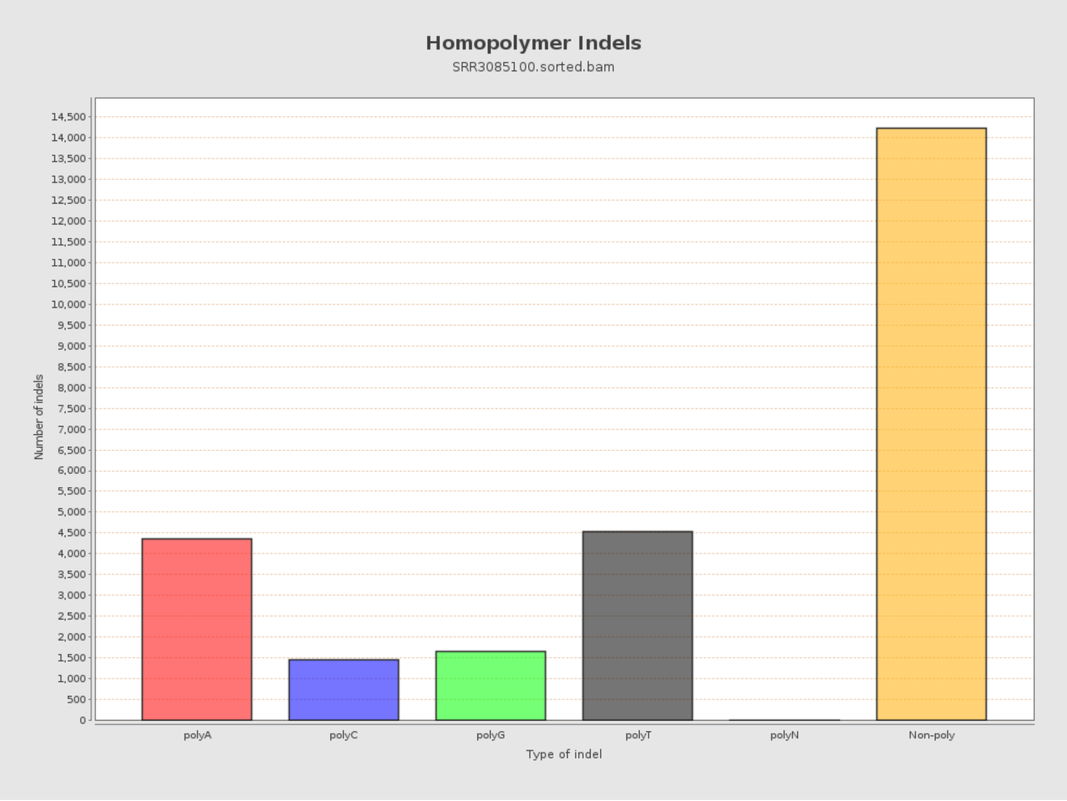
9. Results : Mapped Reads GC-content Distribution



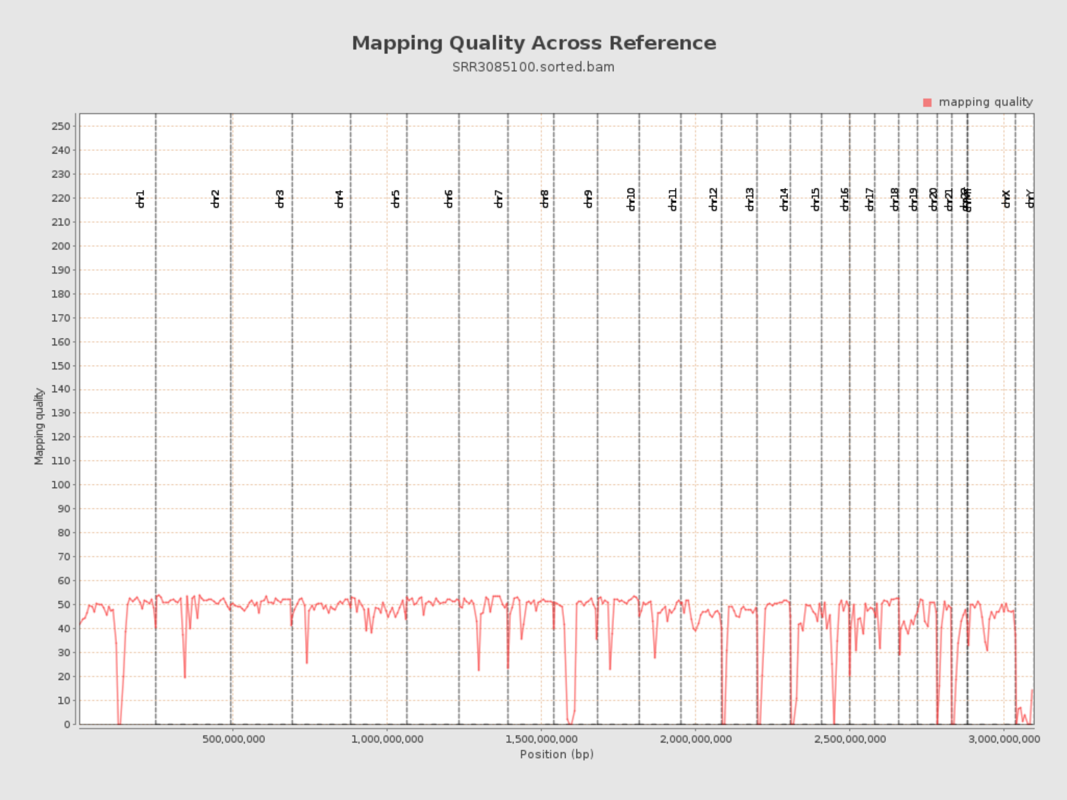
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram