Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:17:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085057.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_SRR3085057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:17:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,756,628
Mapped reads	1,422,471 / 80.98%
Unmapped reads	334,157 / 19.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,772 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	29,941 / 1.7%
Duplication rate	1.63%
Clipped reads	945,454 / 53.82%

2.2. ACGT Content

Number/percentage of A's	26,392,719 / 30.21%
Number/percentage of C's	17,037,039 / 19.5%
Number/percentage of T's	25,221,148 / 28.87%
Number/percentage of G's	18,713,016 / 21.42%
Number/percentage of N's	1,958 / 0%
GC Percentage	40.92%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2401

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

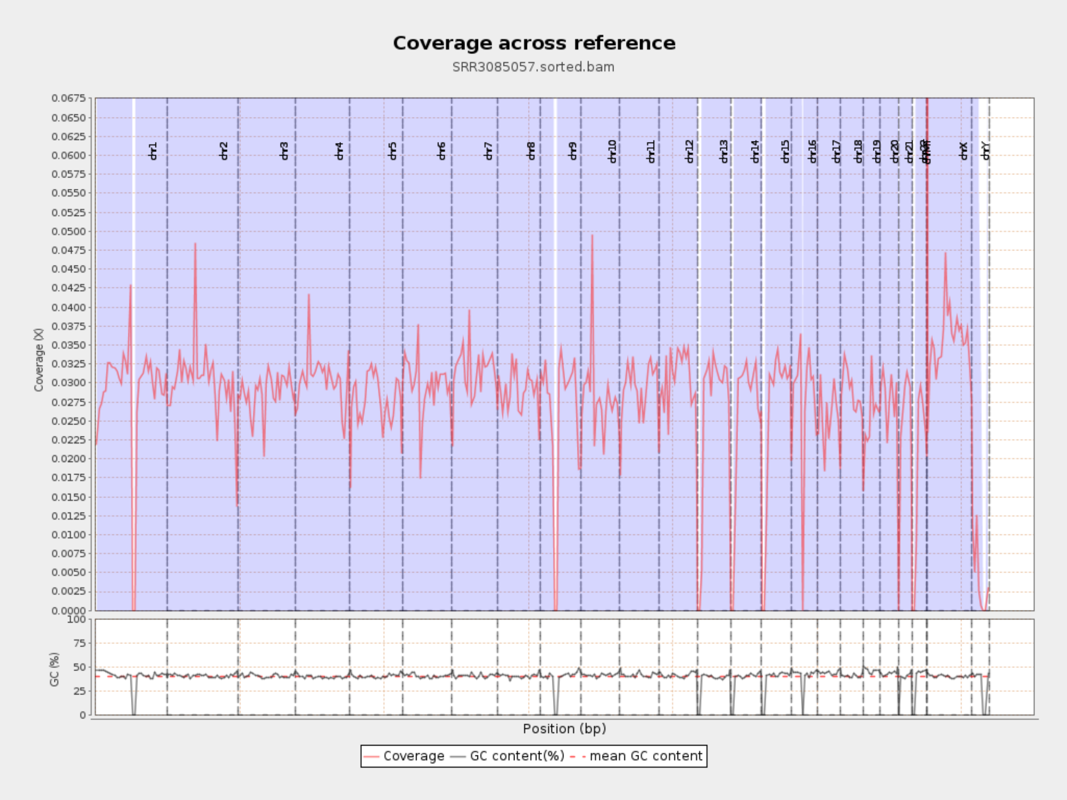
General error rate	0.9%
Mismatches	777,485
Insertions	6,918
Mapped reads with at least one insertion	0.48%
Deletions	18,327
Mapped reads with at least one deletion	1.28%
Homopolymer indels	44.9%

2.6. Chromosome stats

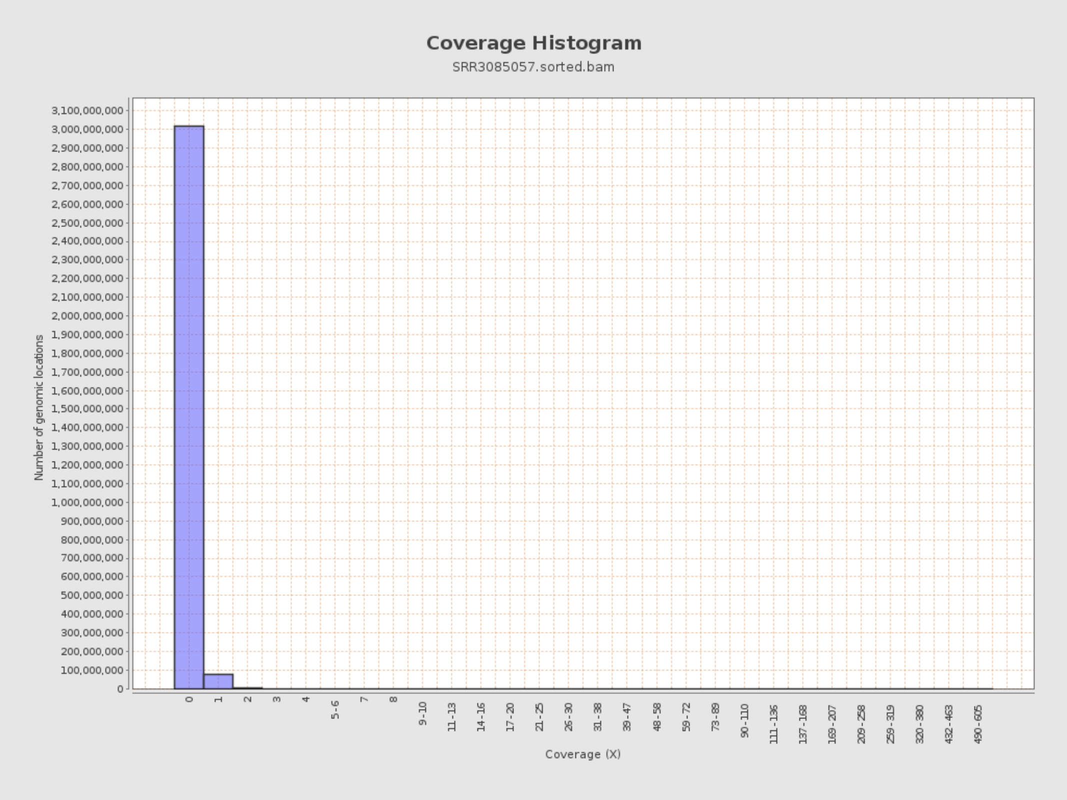
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7182026	0.0288	0.3678
chr2	243199373	7372600	0.0303	0.2456
chr3	198022430	5695609	0.0288	0.1817
chr4	191154276	5820505	0.0304	0.1945
chr5	180915260	5064529	0.028	0.1783
chr6	171115067	5091136	0.0298	0.2088
chr7	159138663	5037071	0.0317	0.2429

chr8	146364022	4262940	0.0291	0.3922
chr9	141213431	3693524	0.0262	0.22
chr10	135534747	3842034	0.0283	0.2539
chr11	135006516	3998057	0.0296	0.2272
chr12	133851895	4104807	0.0307	0.1877
chr13	115169878	2962247	0.0257	0.1703
chr14	107349540	2689740	0.0251	0.1779
chr15	102531392	2618443	0.0255	0.1697
chr16	90354753	2468927	0.0273	0.191
chr17	81195210	2063826	0.0254	0.1809
chr18	78077248	2262709	0.029	0.3833
chr19	59128983	1502846	0.0254	0.264
chr20	63025520	1744840	0.0277	0.1813
chr21	48129895	1185064	0.0246	0.1781
chr22	51304566	948545	0.0185	0.1446
chrMT	16571	6301	0.3802	0.6759
chrX	155270560	5534948	0.0356	0.2183
chrY	59373566	242059	0.0041	0.0904

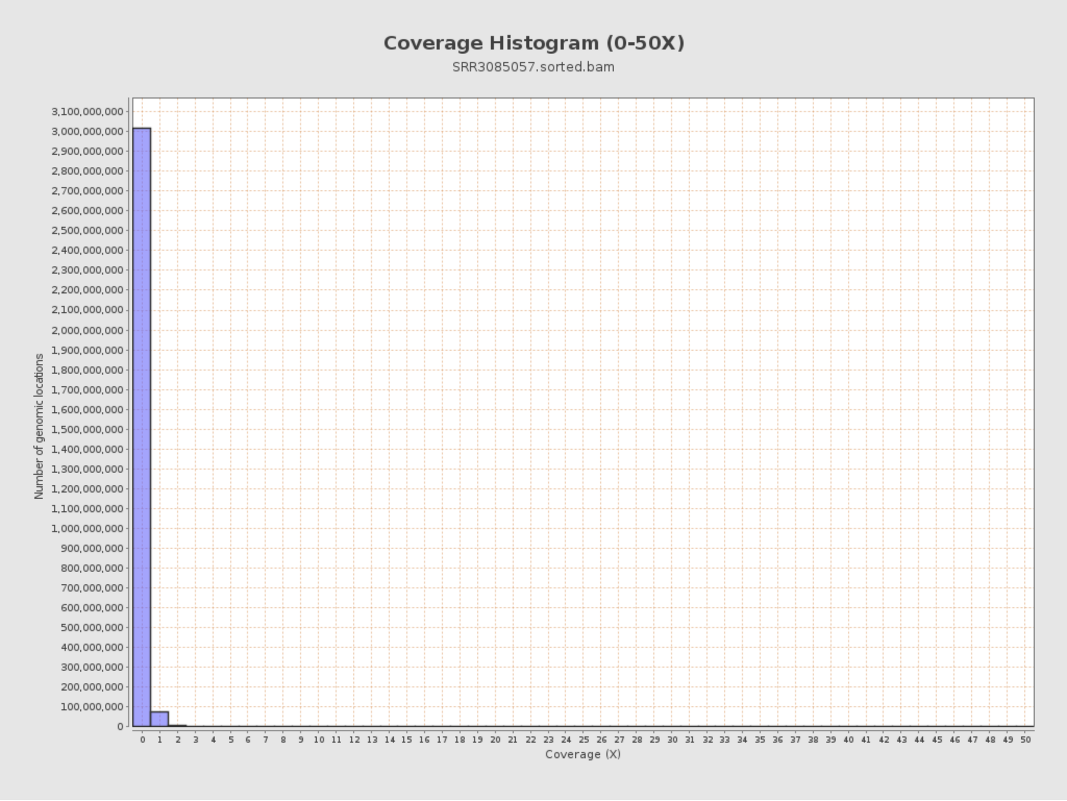
3. Results : Coverage across reference



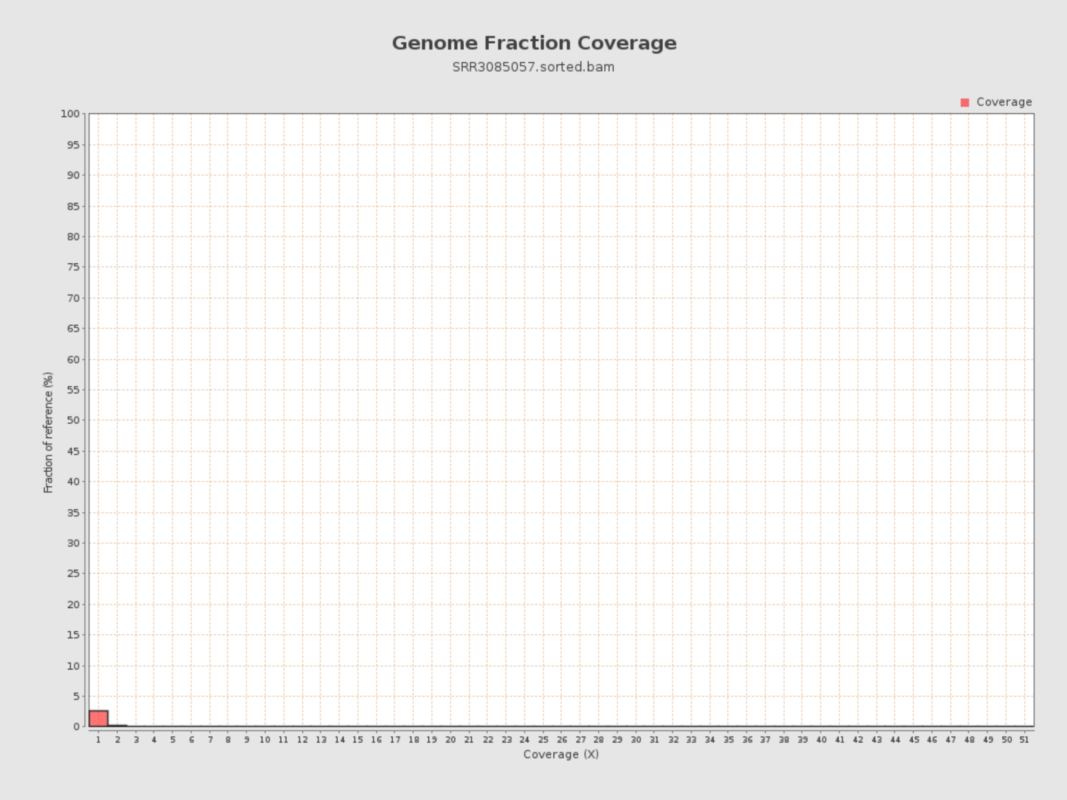
4. Results : Coverage Histogram



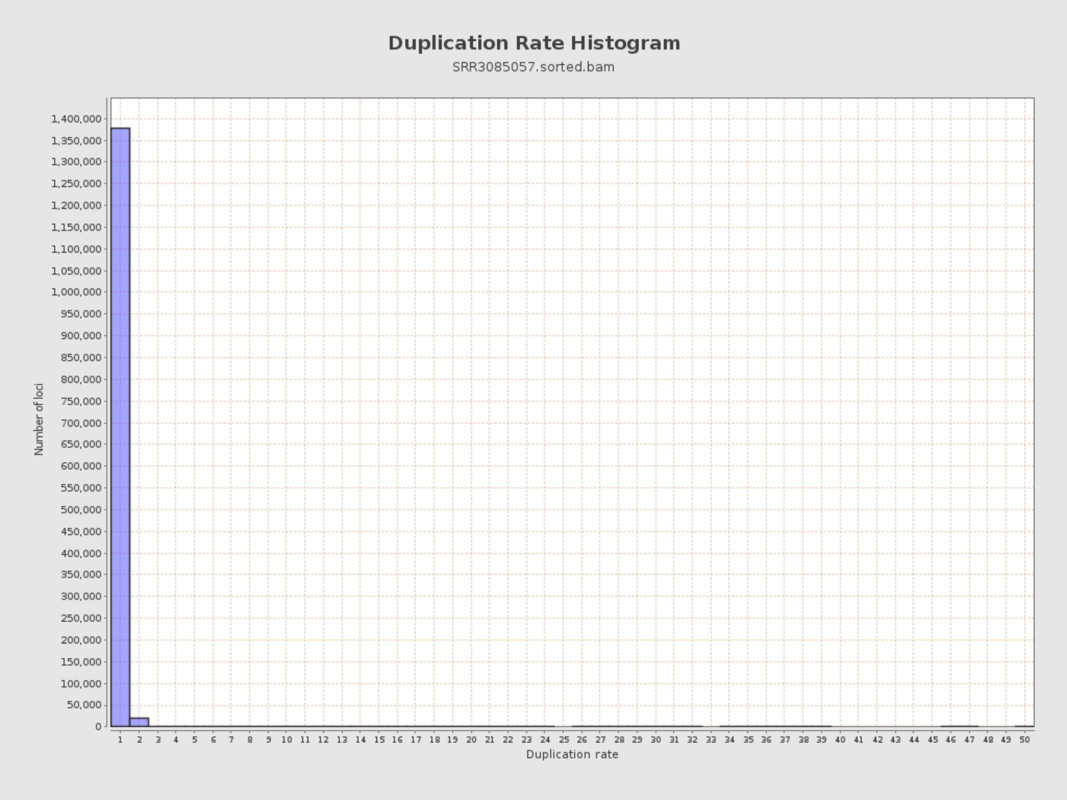
5. Results : Coverage Histogram (0-50X)



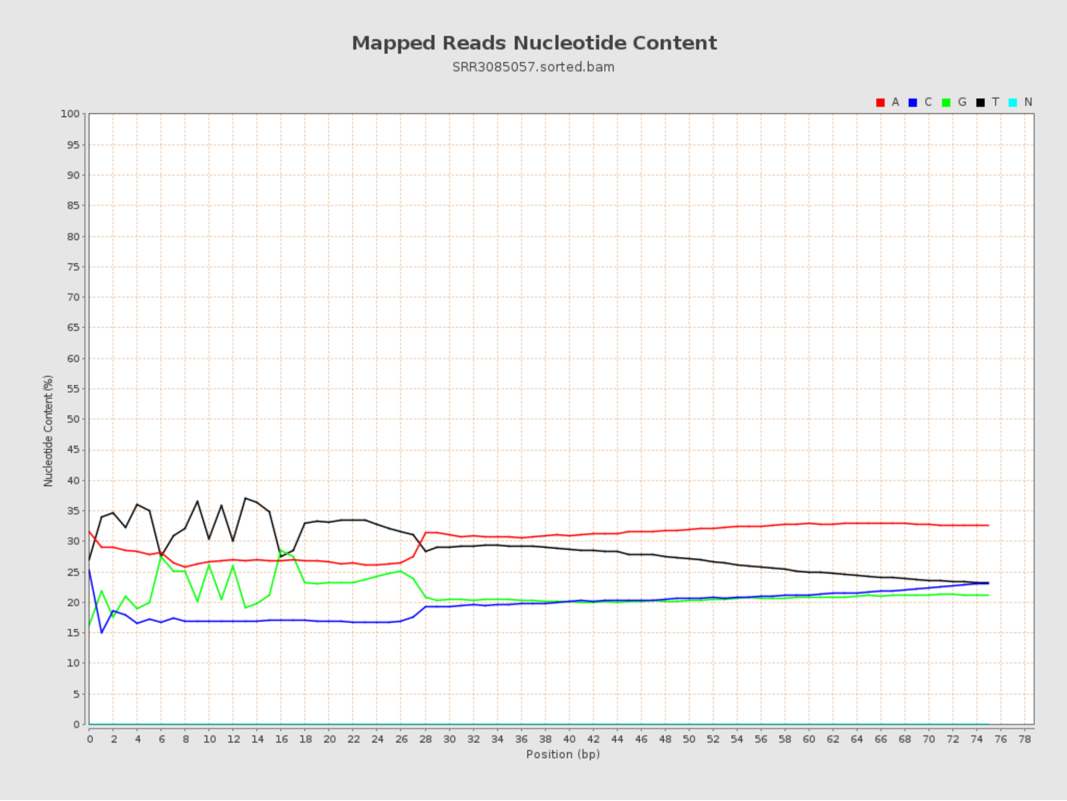
6. Results : Genome Fraction Coverage



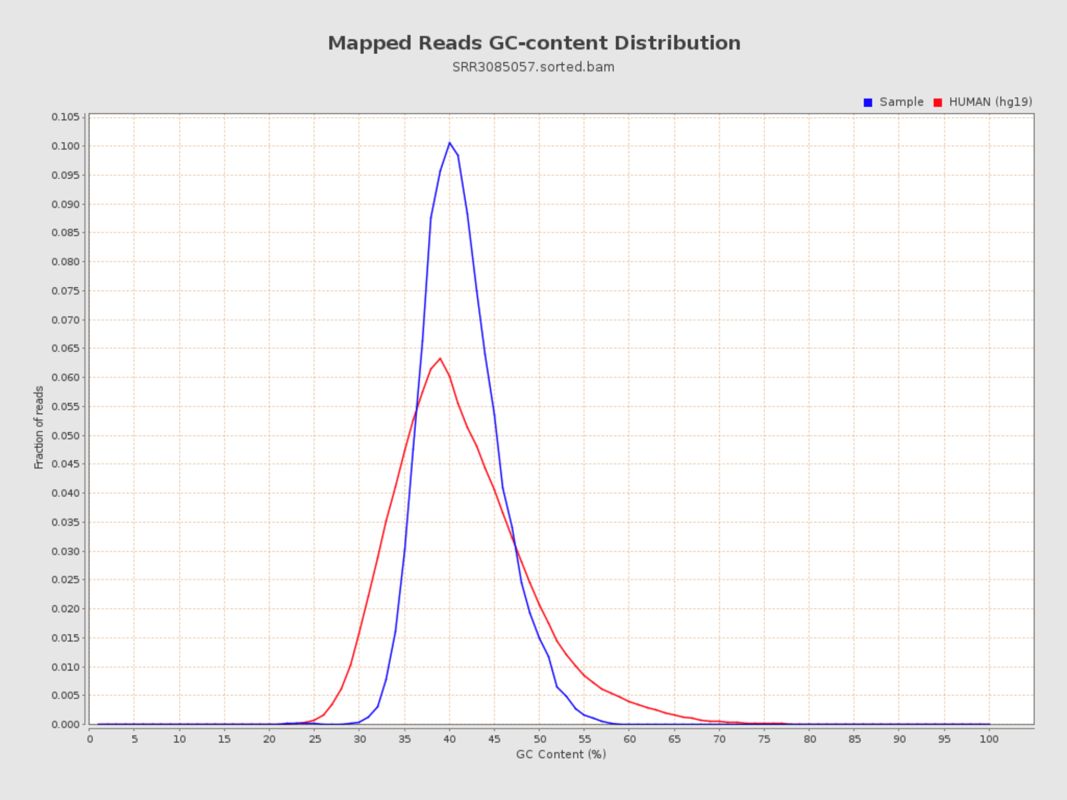
7. Results : Duplication Rate Histogram



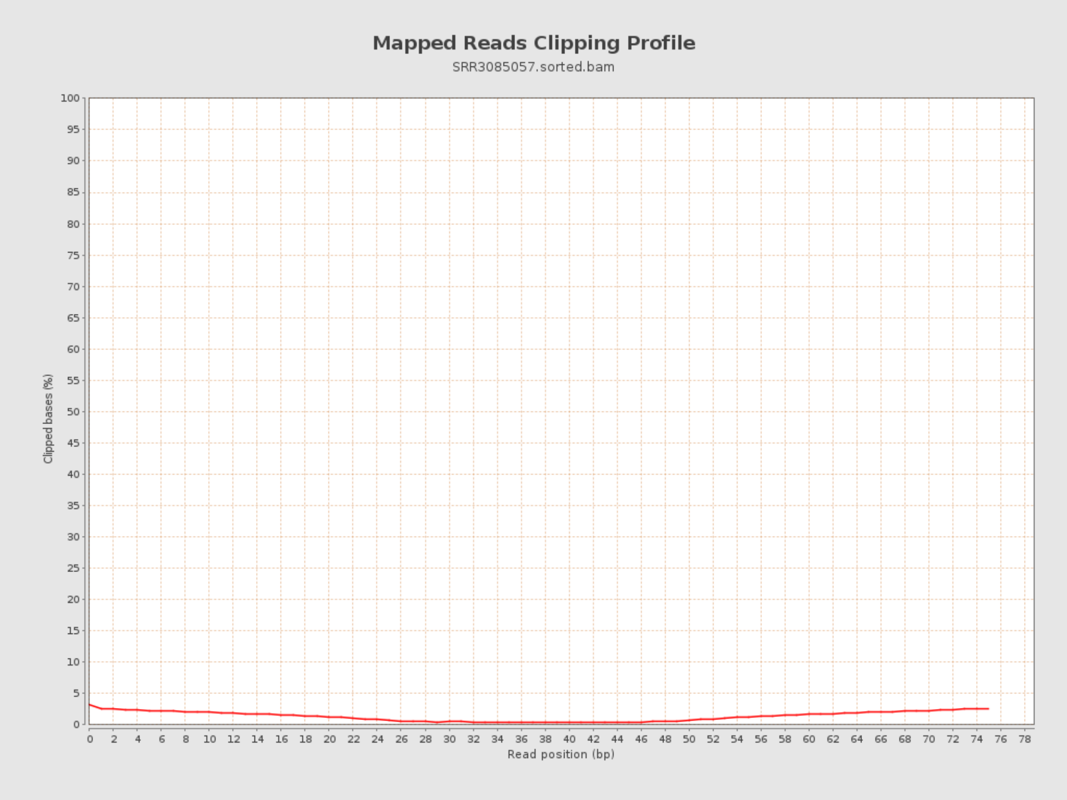
8. Results : Mapped Reads Nucleotide Content



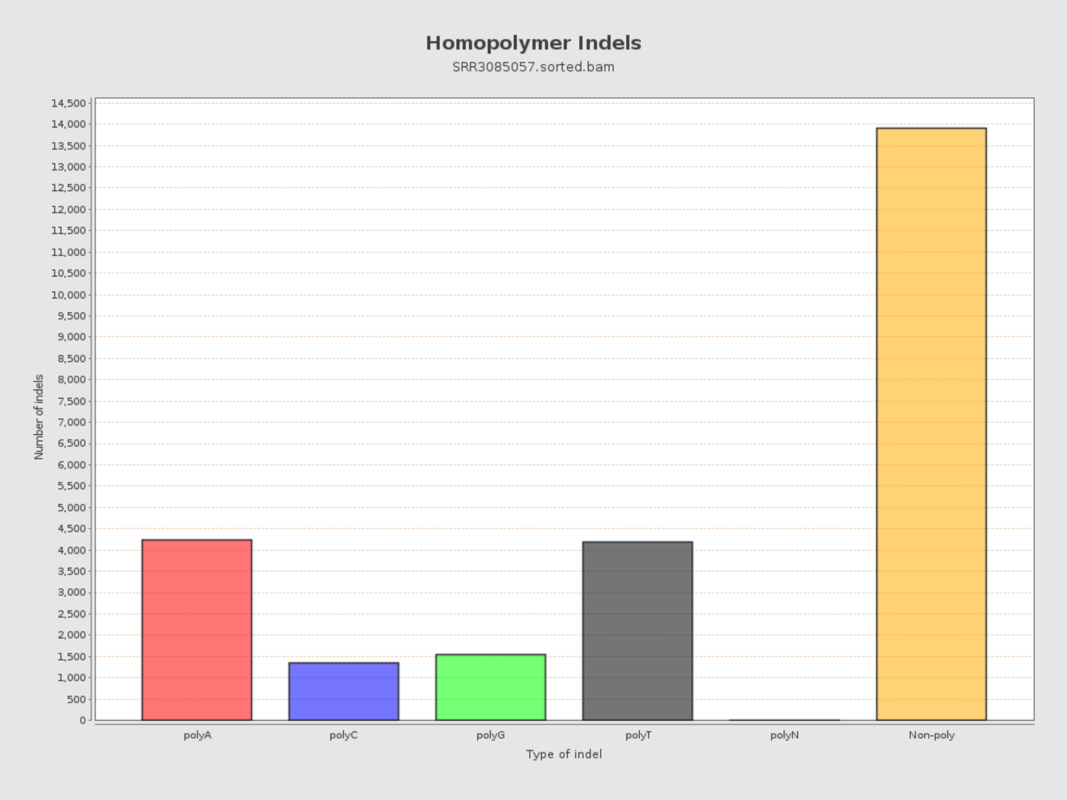
9. Results : Mapped Reads GC-content Distribution



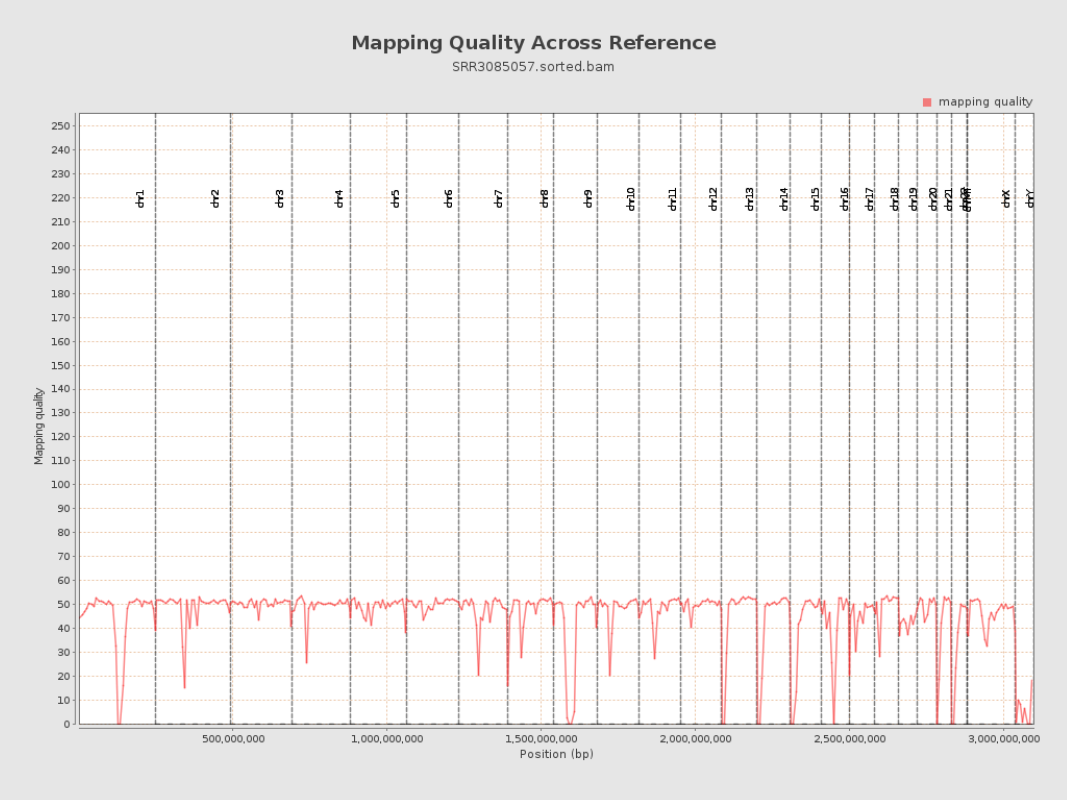
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram