Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:31:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085087.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_SRR3085087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:31:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,369,219
Mapped reads	1,050,694 / 76.74%
Unmapped reads	318,525 / 23.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,276 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	21,403 / 1.56%
Duplication rate	1.66%
Clipped reads	531,080 / 38.79%

2.2. ACGT Content

Number/percentage of A's	20,387,882 / 29.76%
Number/percentage of C's	12,605,860 / 18.4%
Number/percentage of T's	20,390,934 / 29.76%
Number/percentage of G's	15,131,228 / 22.08%
Number/percentage of N's	1,436 / 0%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.1956

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

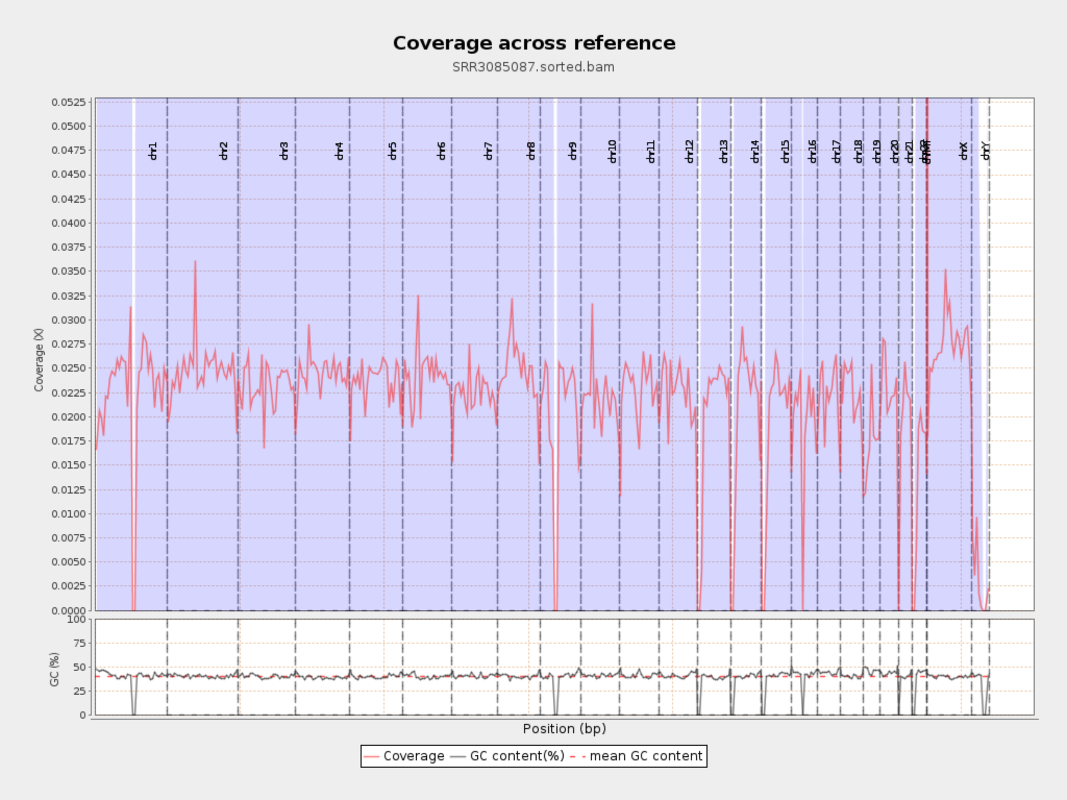
General error rate	0.94%
Mismatches	635,097
Insertions	5,687
Mapped reads with at least one insertion	0.54%
Deletions	14,250
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.32%

2.6. Chromosome stats

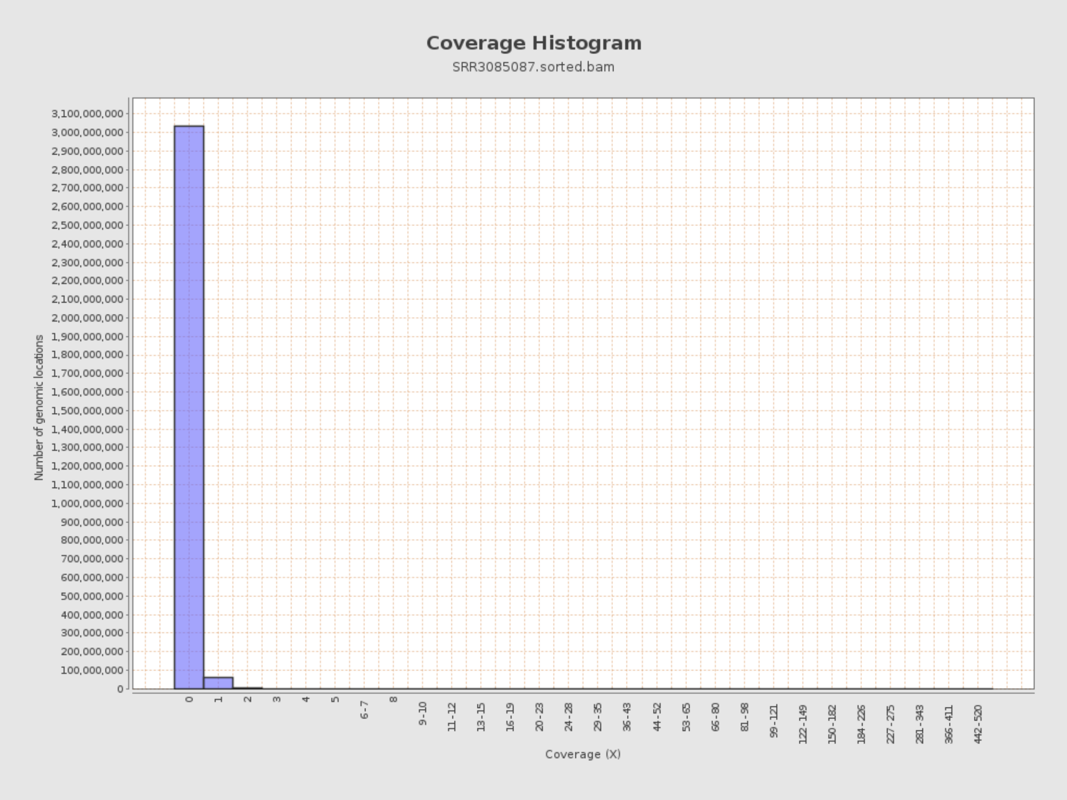
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5572346	0.0224	0.2612
chr2	243199373	6010246	0.0247	0.2094
chr3	198022430	4598057	0.0232	0.1602
chr4	191154276	4673558	0.0244	0.1676
chr5	180915260	4318064	0.0239	0.1623
chr6	171115067	4151660	0.0243	0.1801
chr7	159138663	3553337	0.0223	0.1834

chr8	146364022	3635869	0.0248	0.3485
chr9	141213431	2817024	0.0199	0.1808
chr10	135534747	2970843	0.0219	0.1907
chr11	135006516	3094707	0.0229	0.1845
chr12	133851895	3025405	0.0226	0.158
chr13	115169878	2245392	0.0195	0.1462
chr14	107349540	2150988	0.02	0.1531
chr15	102531392	1940207	0.0189	0.1445
chr16	90354753	1710747	0.0189	0.1517
chr17	81195210	1801734	0.0222	0.1674
chr18	78077248	1765392	0.0226	0.294
chr19	59128983	1023164	0.0173	0.1892
chr20	63025520	1442684	0.0229	0.1618
chr21	48129895	925883	0.0192	0.1526
chr22	51304566	667467	0.013	0.1192
chrMT	16571	10897	0.6576	0.9138
chrX	155270560	4258579	0.0274	0.1834
chrY	59373566	176263	0.003	0.0739

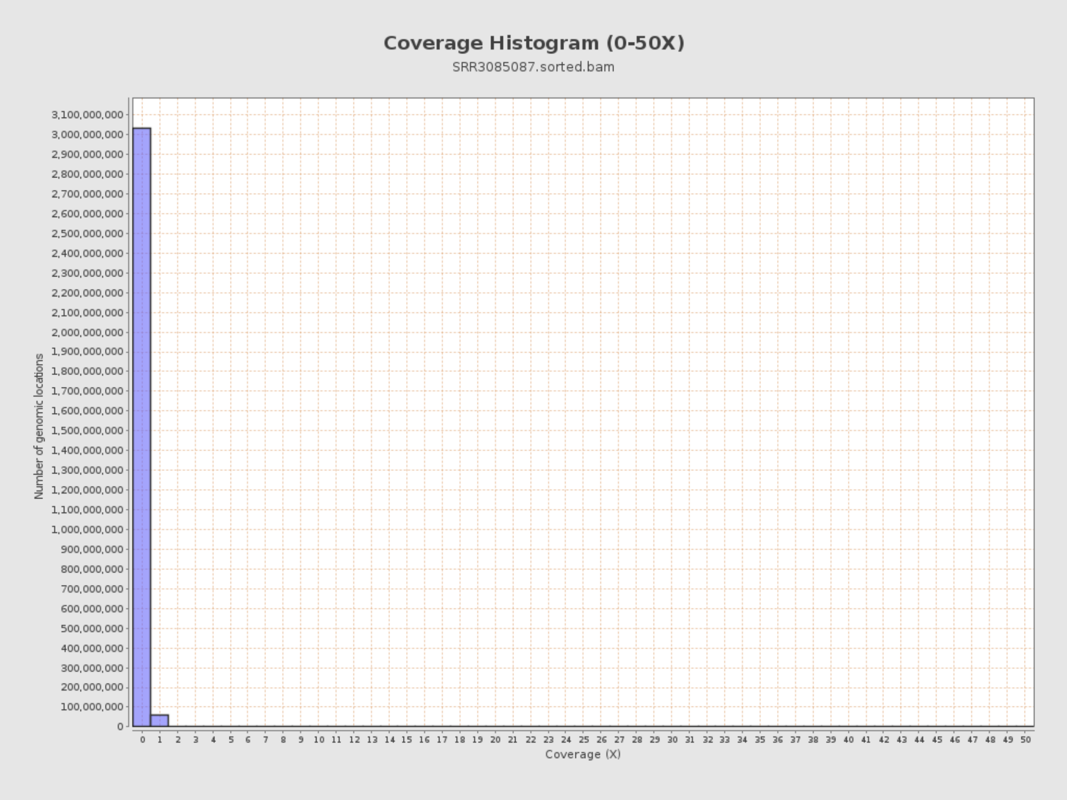
3. Results : Coverage across reference



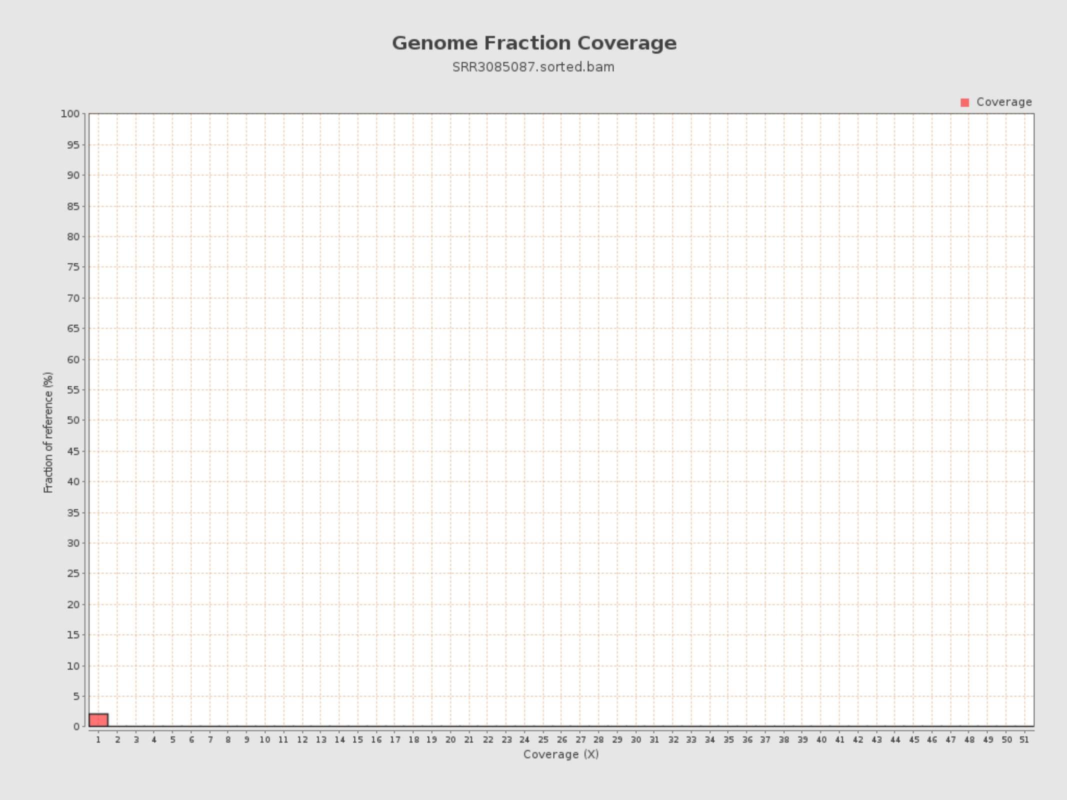
4. Results : Coverage Histogram



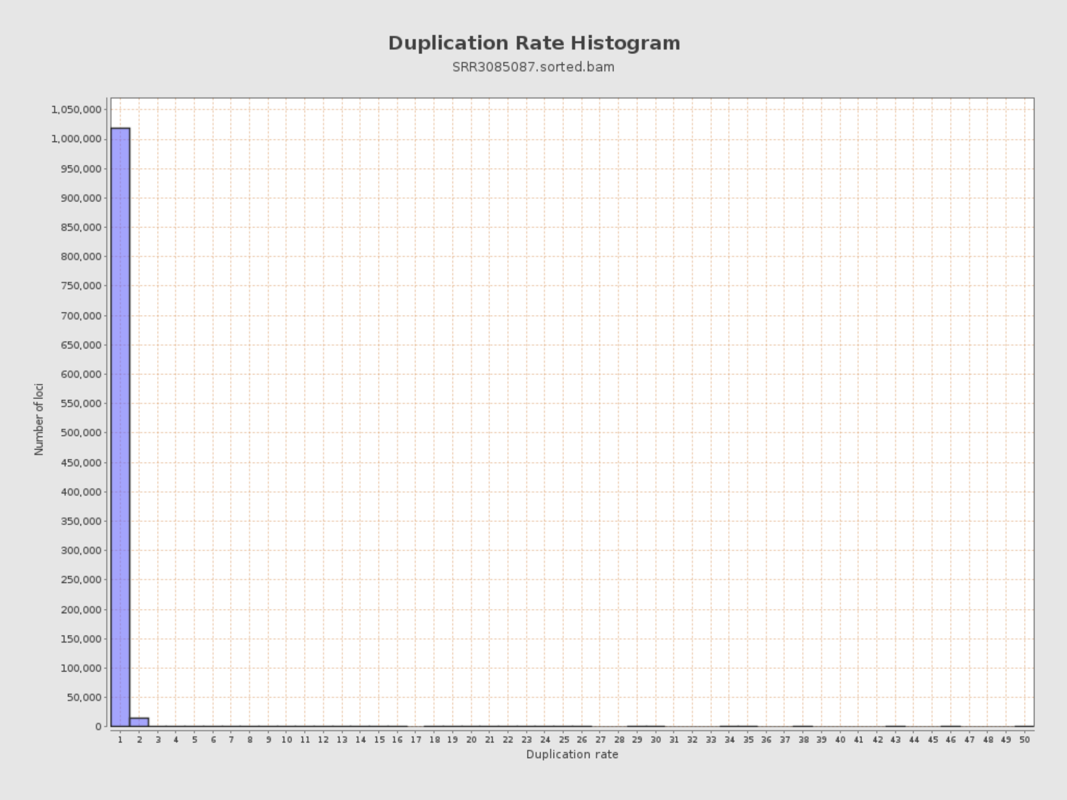
5. Results : Coverage Histogram (0-50X)



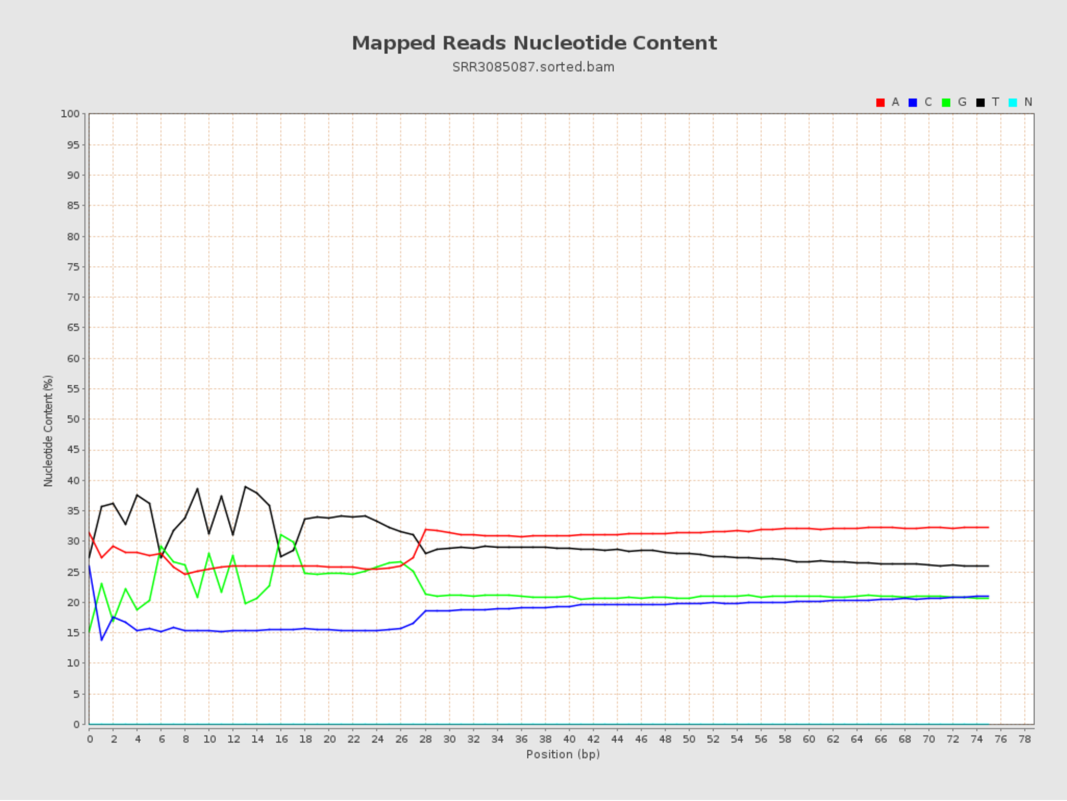
6. Results : Genome Fraction Coverage



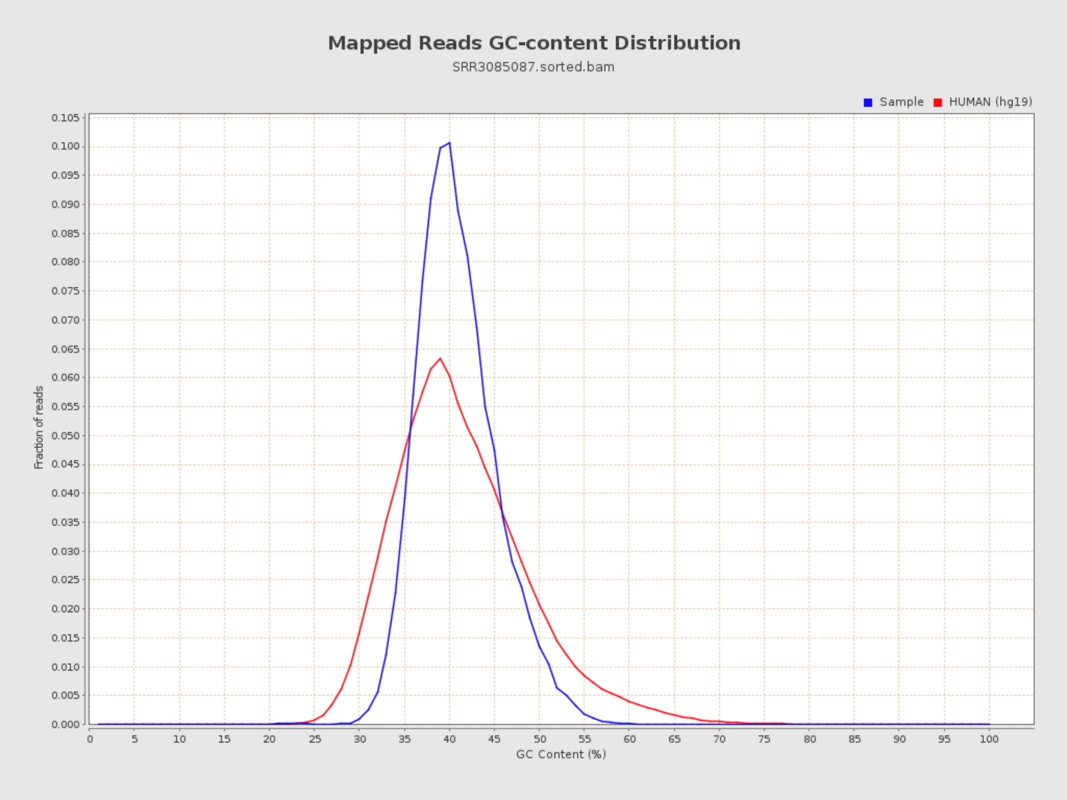
7. Results : Duplication Rate Histogram



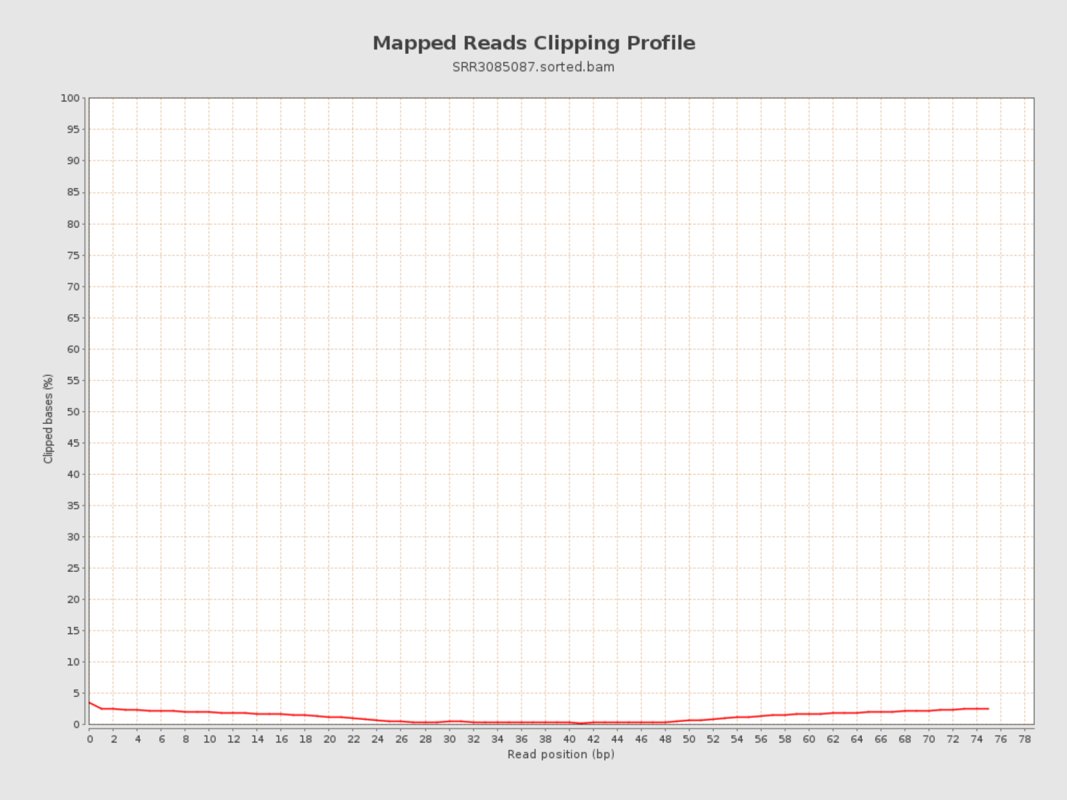
8. Results : Mapped Reads Nucleotide Content



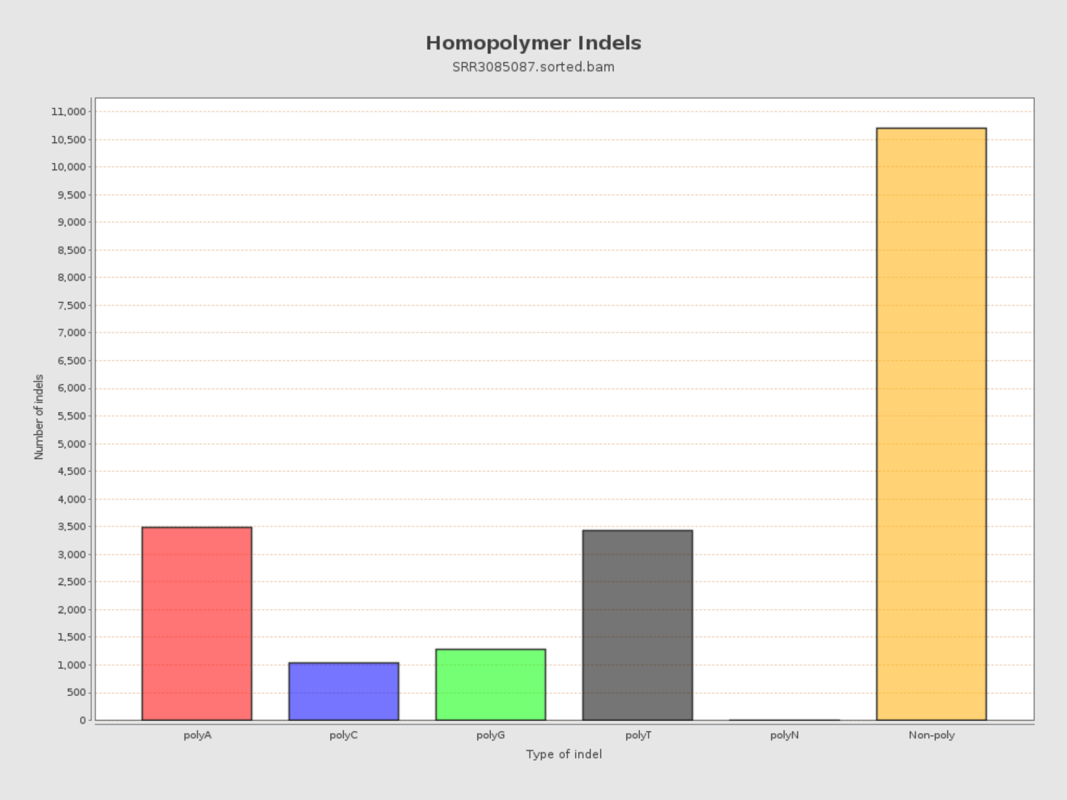
9. Results : Mapped Reads GC-content Distribution



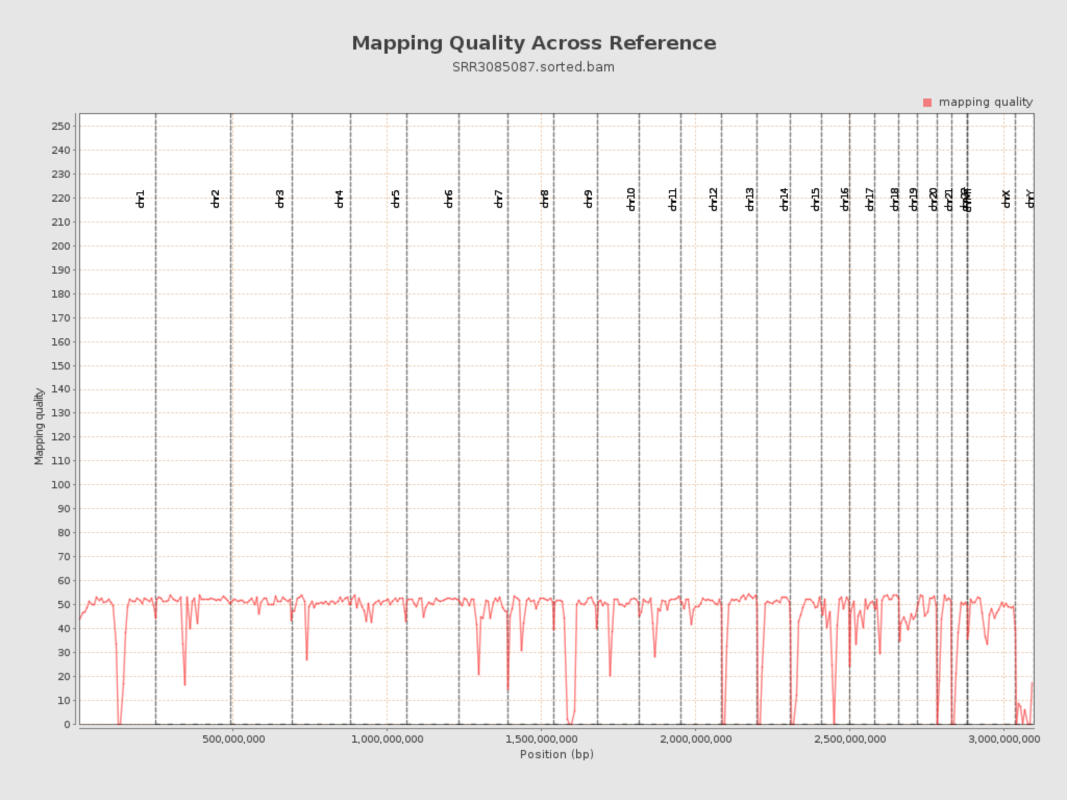
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram