Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:37:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084763.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_SRR3084763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:37:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,128,560
Mapped reads	1,948,558 / 91.54%
Unmapped reads	180,002 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,298 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	72,456 / 3.4%
Duplication rate	2.83%
Clipped reads	717,056 / 33.69%

2.2. ACGT Content

Number/percentage of A's	37,995,323 / 28.45%
Number/percentage of C's	24,887,996 / 18.64%
Number/percentage of T's	41,858,225 / 31.35%
Number/percentage of G's	28,759,883 / 21.54%
Number/percentage of N's	37,039 / 0.03%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.3639

2.4. Mapping Quality

Mean Mapping Quality	47.41

2.5. Mismatches and indels

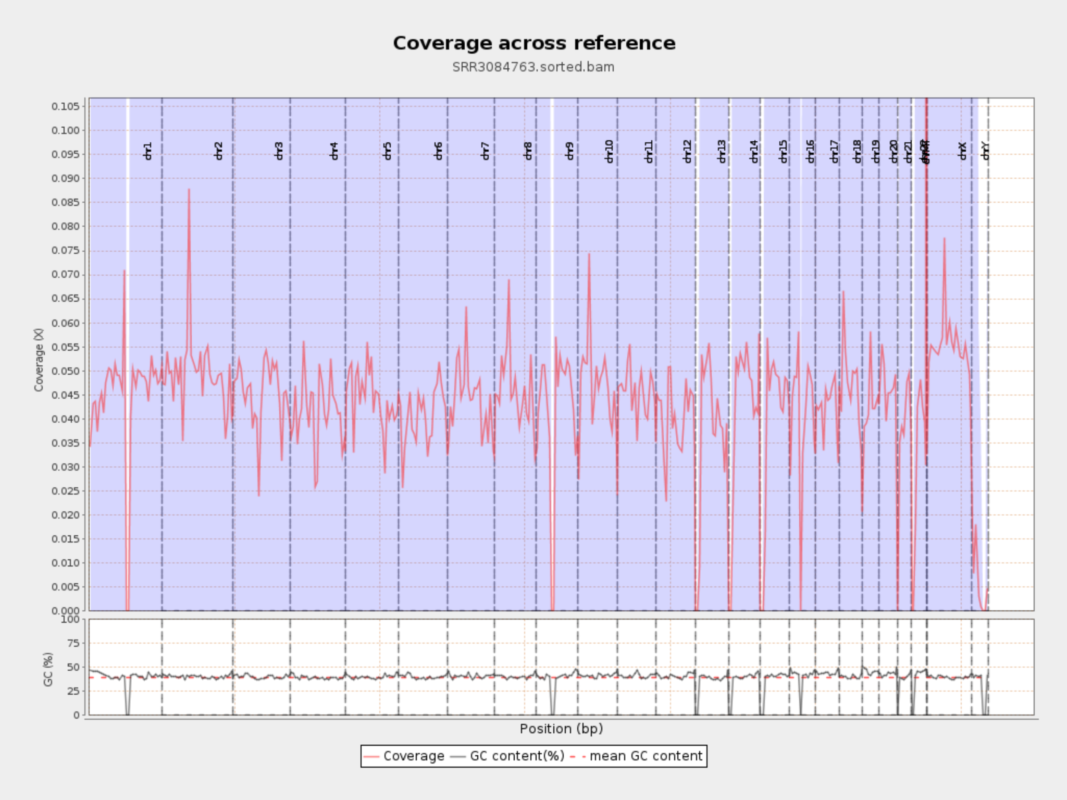
General error rate	0.86%
Mismatches	1,130,921
Insertions	10,833
Mapped reads with at least one insertion	0.55%
Deletions	35,502
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.91%

2.6. Chromosome stats

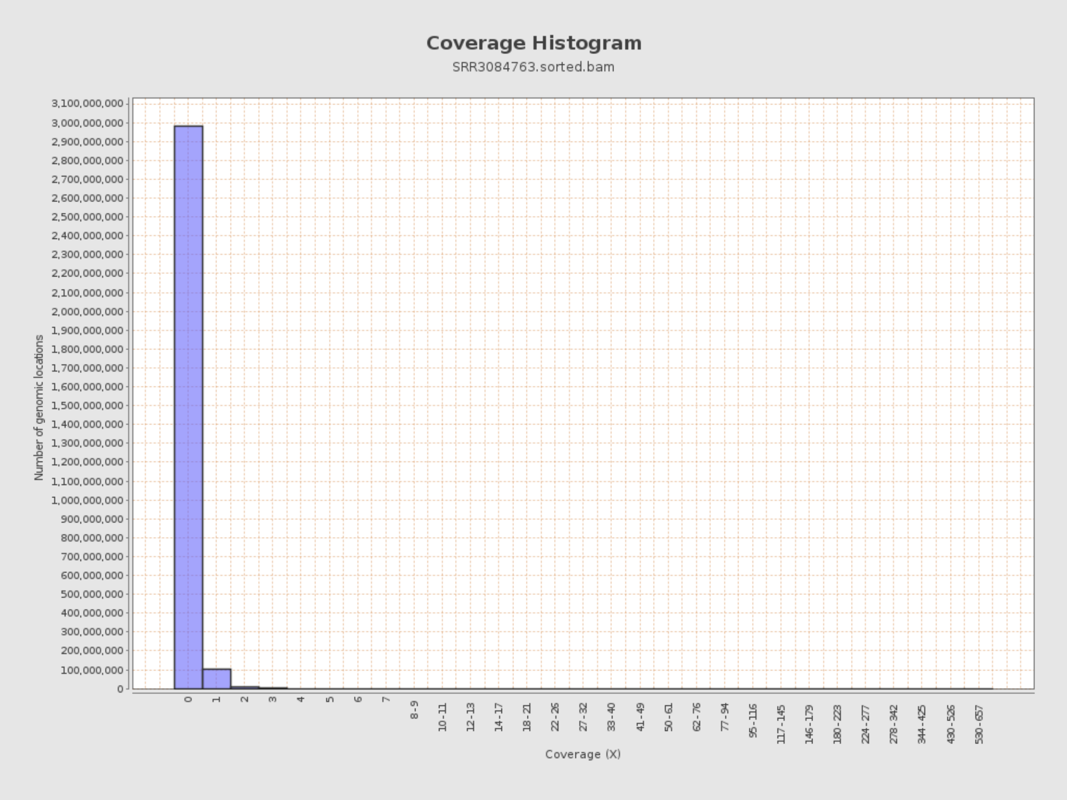
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11101235	0.0445	0.6002
chr2	243199373	12098254	0.0497	0.4388
chr3	198022430	8950706	0.0452	0.2362
chr4	191154276	7883576	0.0412	0.246
chr5	180915260	8002477	0.0442	0.2349
chr6	171115067	6953620	0.0406	0.2336
chr7	159138663	7035036	0.0442	0.4009

chr8	146364022	6762666	0.0462	0.479
chr9	141213431	5882564	0.0417	0.3634
chr10	135534747	6419459	0.0474	0.3466
chr11	135006516	6135998	0.0454	0.3302
chr12	133851895	5403906	0.0404	0.2271
chr13	115169878	4138027	0.0359	0.2108
chr14	107349540	4368952	0.0407	0.2416
chr15	102531392	3987613	0.0389	0.2209
chr16	90354753	3694593	0.0409	0.261
chr17	81195210	3418058	0.0421	0.2493
chr18	78077248	3748079	0.048	0.8158
chr19	59128983	2511326	0.0425	0.4626
chr20	63025520	2921229	0.0463	0.2577
chr21	48129895	1784807	0.0371	0.2334
chr22	51304566	1525549	0.0297	0.1898
chrMT	16571	12942	0.781	1.0301
chrX	155270560	8510618	0.0548	0.2945
chrY	59373566	345657	0.0058	0.1409

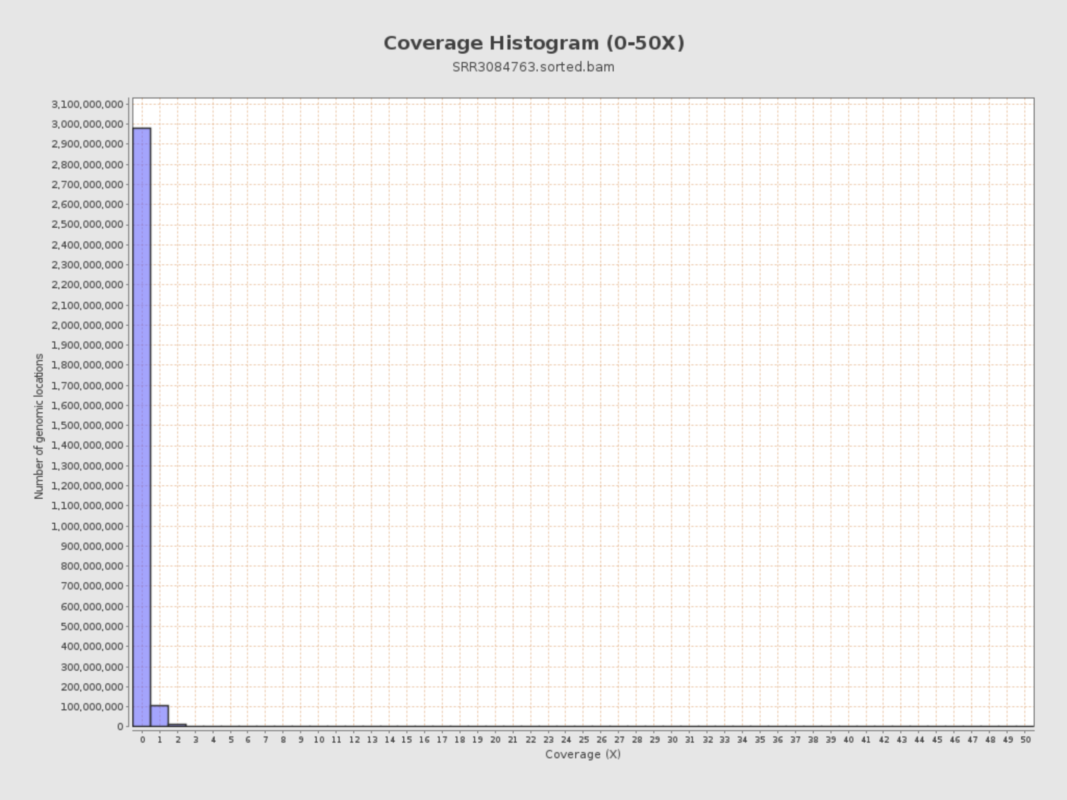
3. Results : Coverage across reference



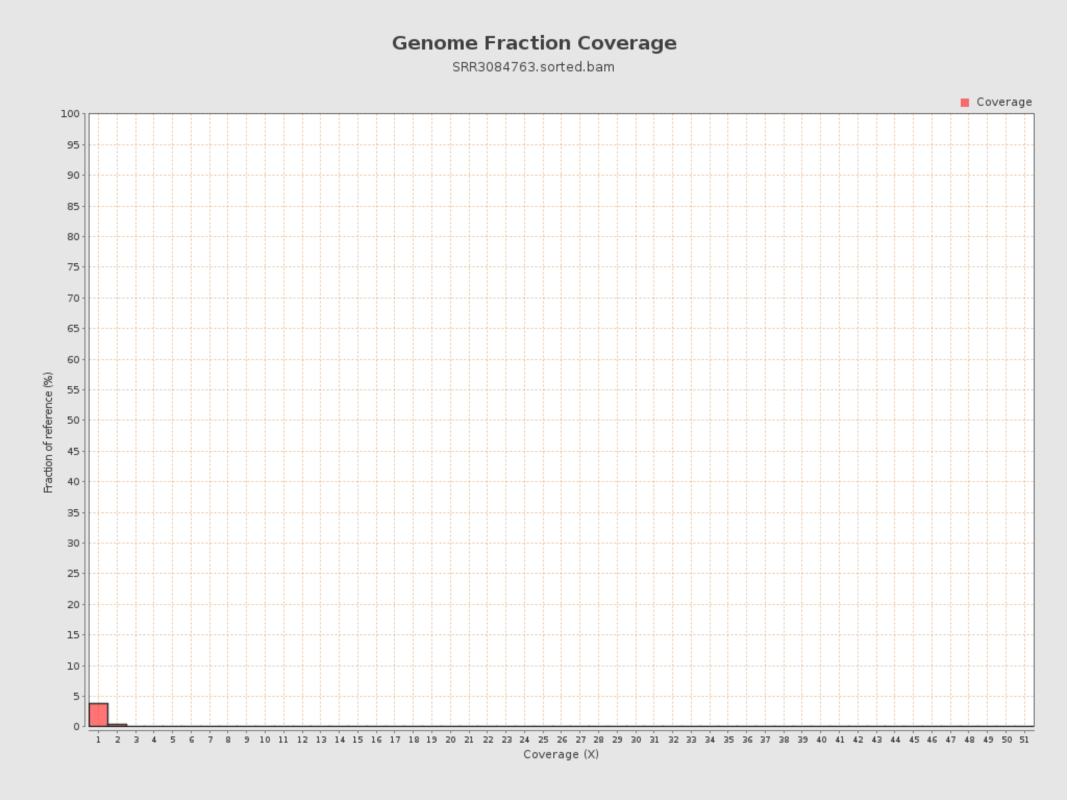
4. Results : Coverage Histogram



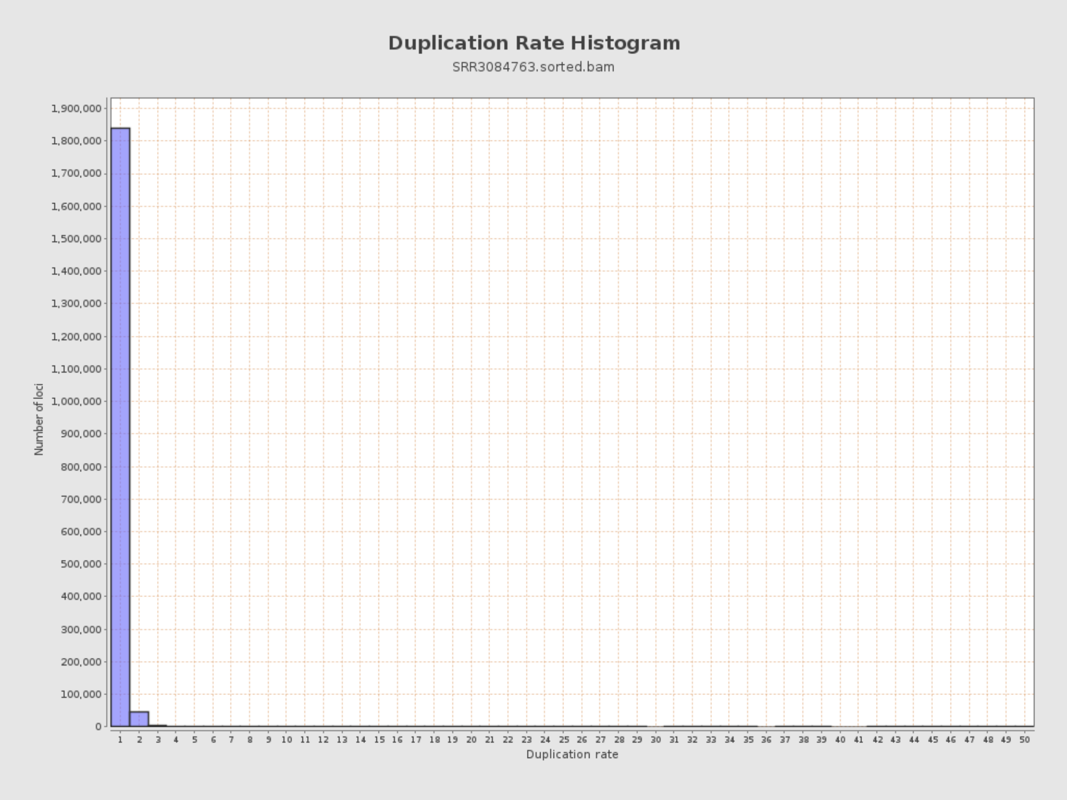
5. Results : Coverage Histogram (0-50X)



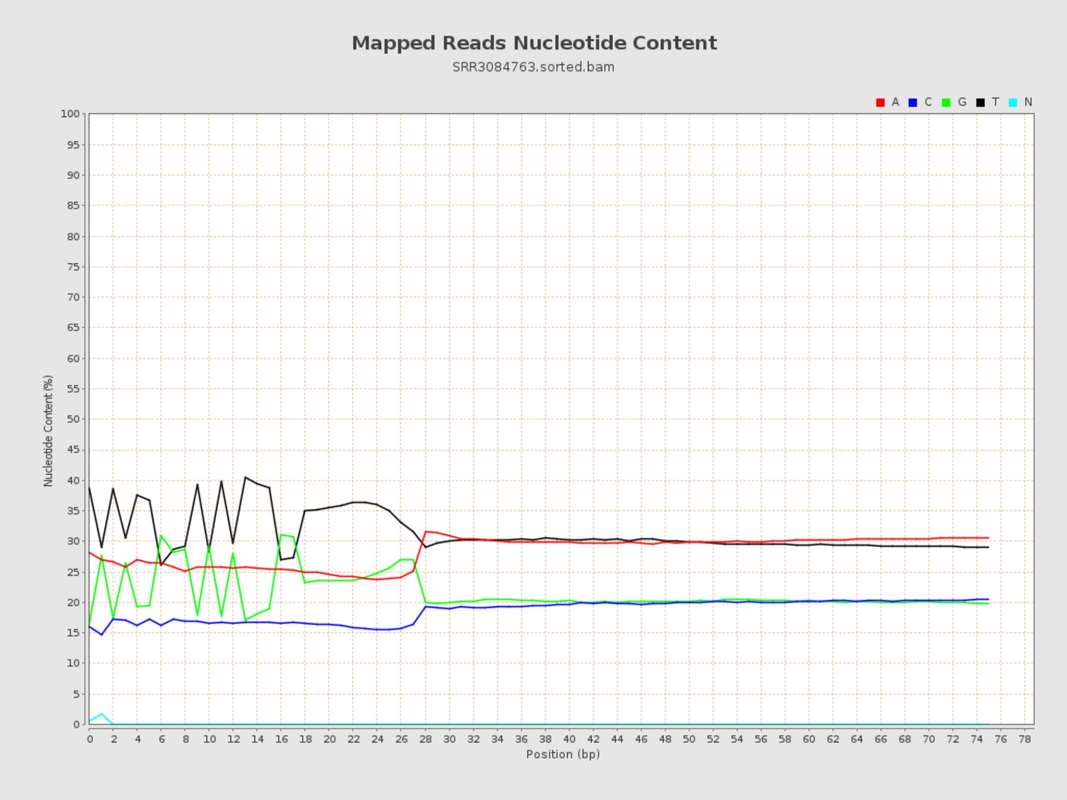
6. Results : Genome Fraction Coverage



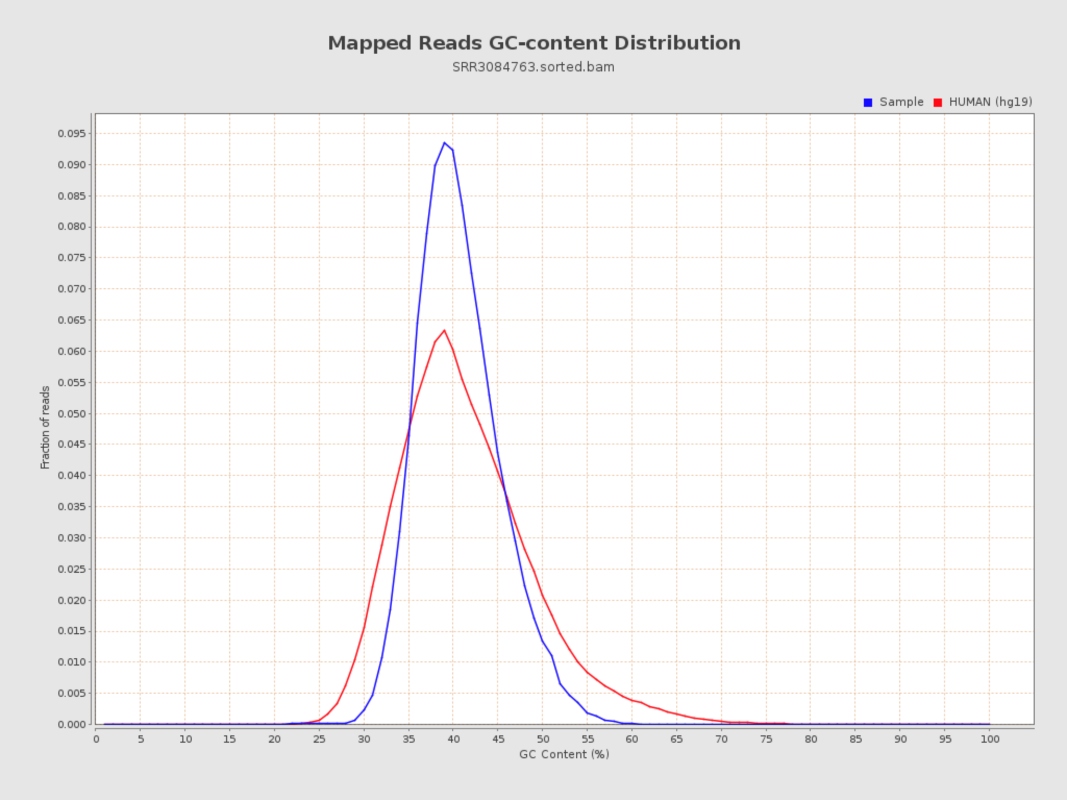
7. Results : Duplication Rate Histogram



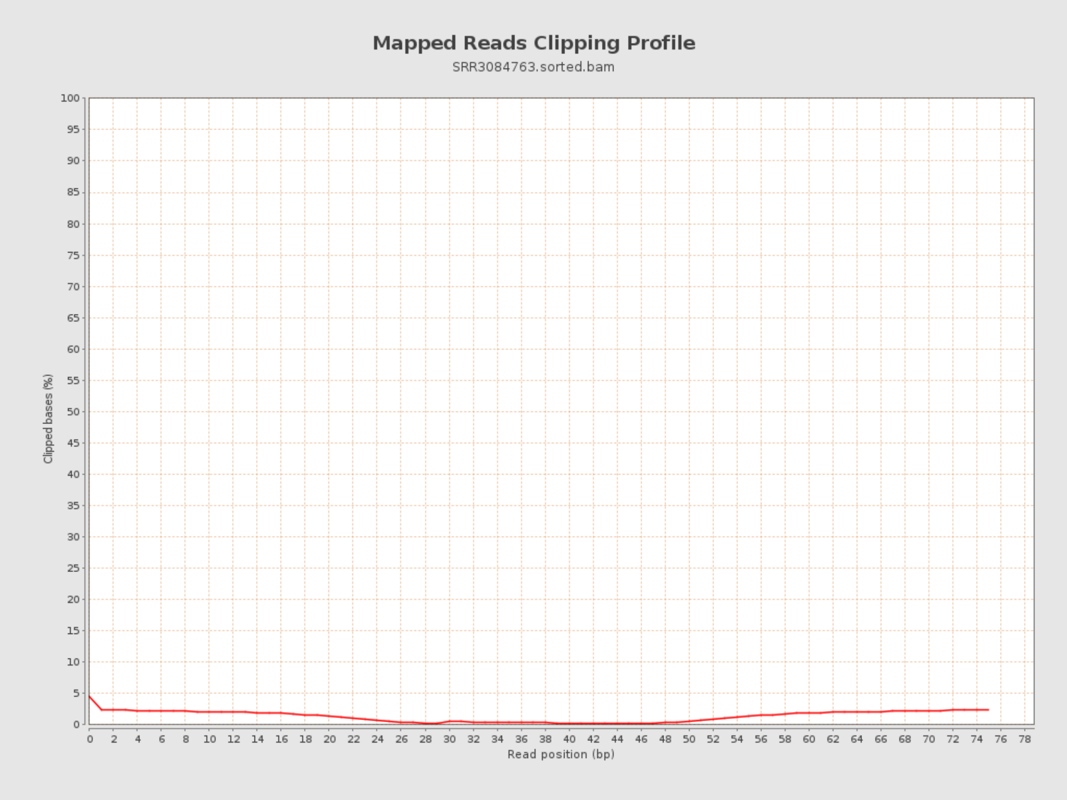
8. Results : Mapped Reads Nucleotide Content



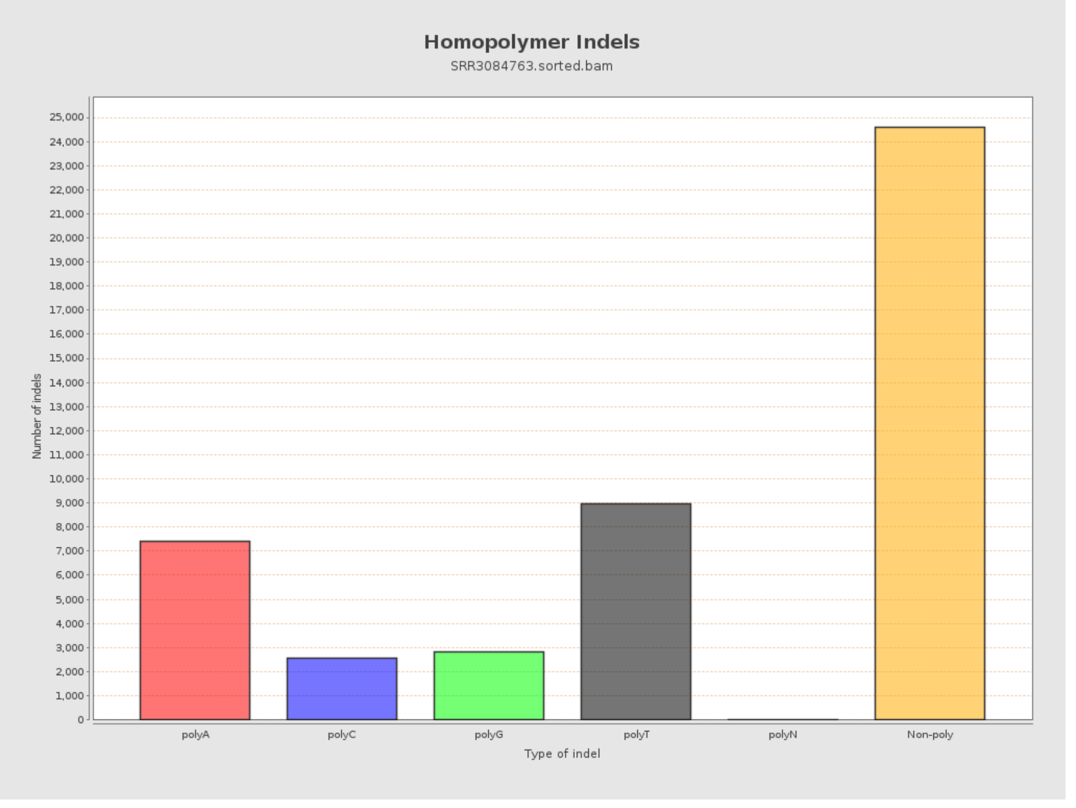
9. Results : Mapped Reads GC-content Distribution



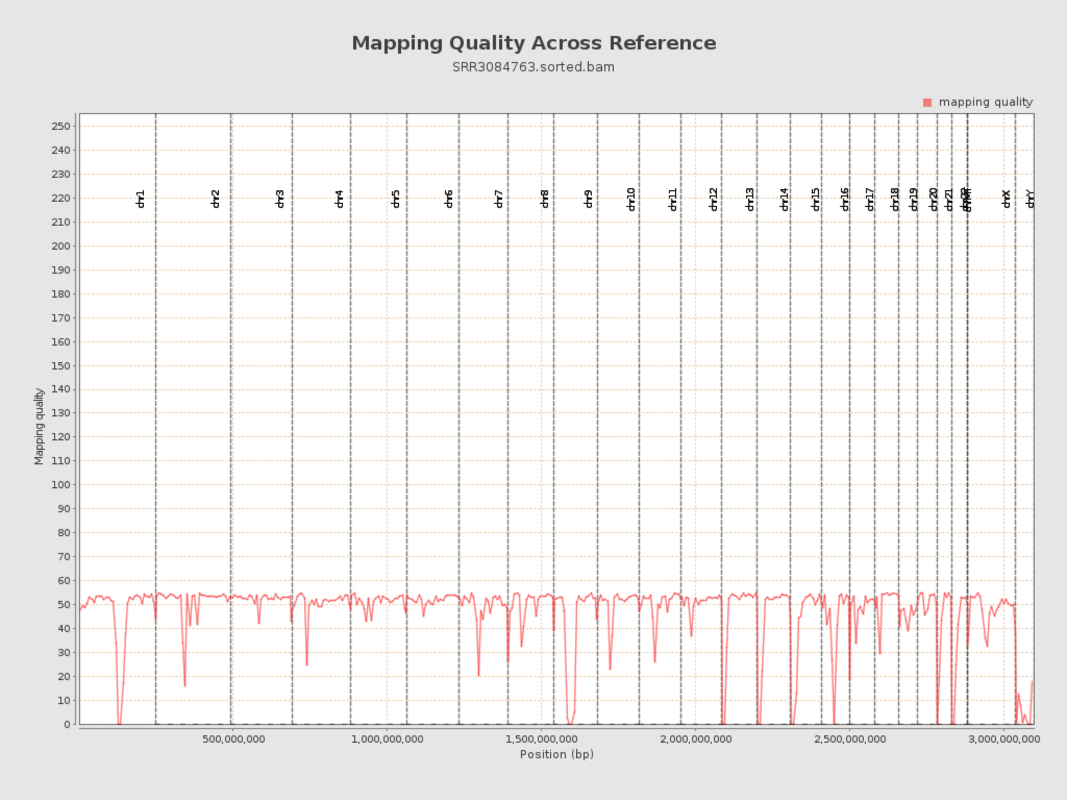
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram