Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:41:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082944.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_SRR3082944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,189,904
Mapped reads	5,456,310 / 88.15%
Unmapped reads	733,594 / 11.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,317 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	573,671 / 9.27%
Duplication rate	6.33%
Clipped reads	2,300,757 / 37.17%

2.2. ACGT Content

Number/percentage of A's	103,727,268 / 28.2%
Number/percentage of C's	64,889,739 / 17.64%
Number/percentage of T's	120,411,530 / 32.73%
Number/percentage of G's	78,759,620 / 21.41%
Number/percentage of N's	102,845 / 0.03%
GC Percentage	39.05%

2.3. Coverage

Mean	0.1189

Standard Deviation	0.8446

2.4. Mapping Quality

Mean Mapping Quality	46.81

2.5. Mismatches and indels

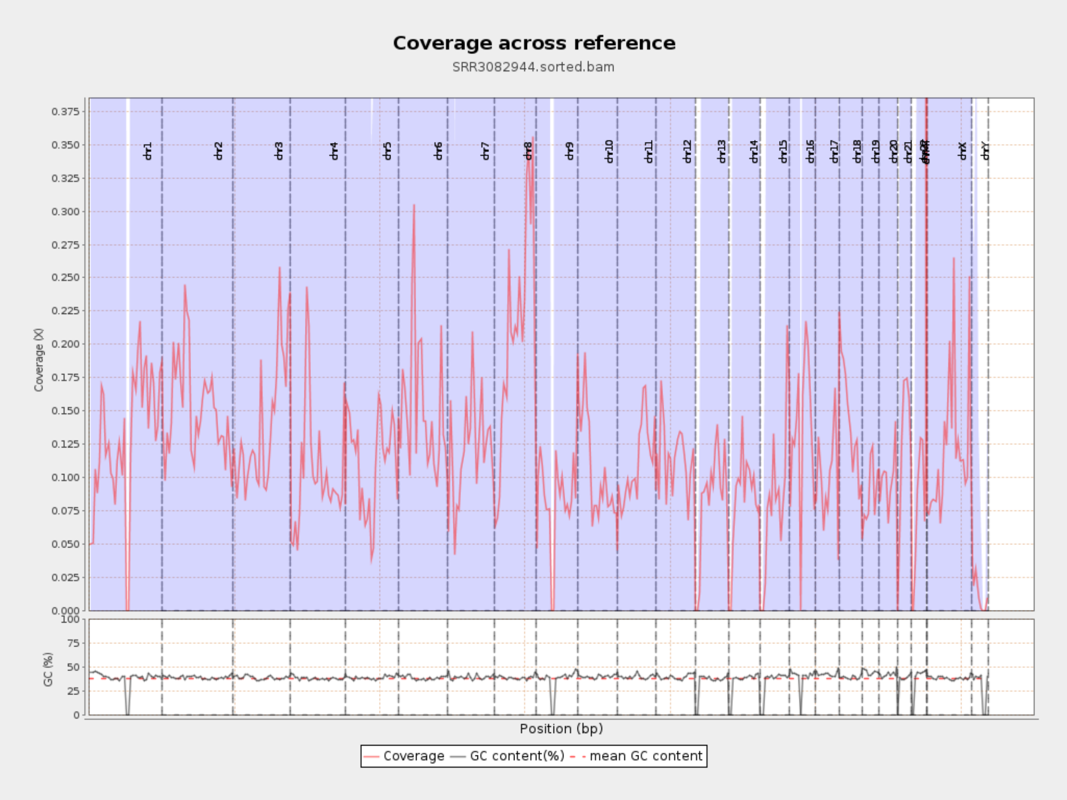
General error rate	0.96%
Mismatches	3,468,617
Insertions	32,757
Mapped reads with at least one insertion	0.6%
Deletions	86,701
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.66%

2.6. Chromosome stats

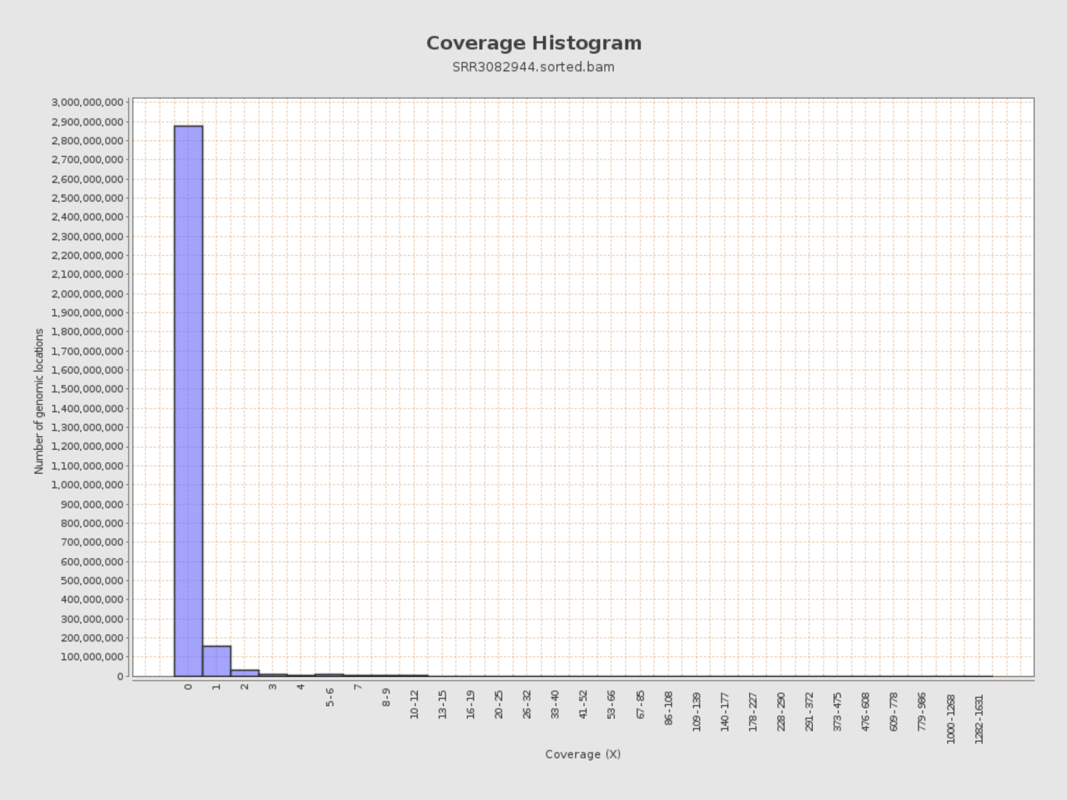
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31984050	0.1283	1.0376
chr2	243199373	37098066	0.1525	1.2326
chr3	198022430	27146559	0.1371	0.667
chr4	191154276	19726852	0.1032	0.5532
chr5	180915260	20131985	0.1113	0.6034
chr6	171115067	26081750	0.1524	0.8873
chr7	159138663	19519417	0.1227	0.9654

chr8	146364022	30644847	0.2094	1.3255
chr9	141213431	11764127	0.0833	0.8396
chr10	135534747	14381608	0.1061	0.7193
chr11	135006516	14982459	0.111	0.6814
chr12	133851895	15167871	0.1133	0.6511
chr13	115169878	9532675	0.0828	0.4972
chr14	107349540	8844635	0.0824	0.5627
chr15	102531392	8313856	0.0811	0.5347
chr16	90354753	12156741	0.1345	0.6263
chr17	81195210	8003198	0.0986	0.6476
chr18	78077248	11237574	0.1439	1.5432
chr19	59128983	5274540	0.0892	0.7948
chr20	63025520	6231323	0.0989	0.5484
chr21	48129895	5911763	0.1228	0.5351
chr22	51304566	3744874	0.073	0.4046
chrMT	16571	391500	23.6256	16.4846
chrX	155270560	19043211	0.1226	0.7321
chrY	59373566	715455	0.0121	0.2111

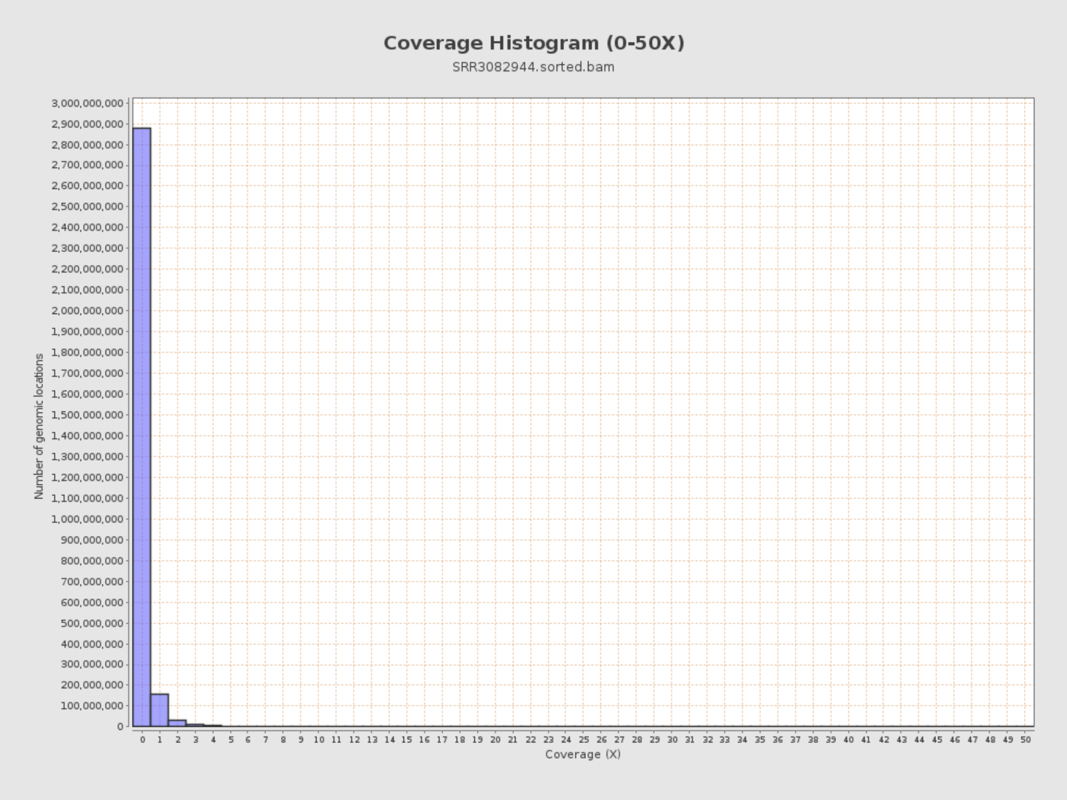
3. Results : Coverage across reference



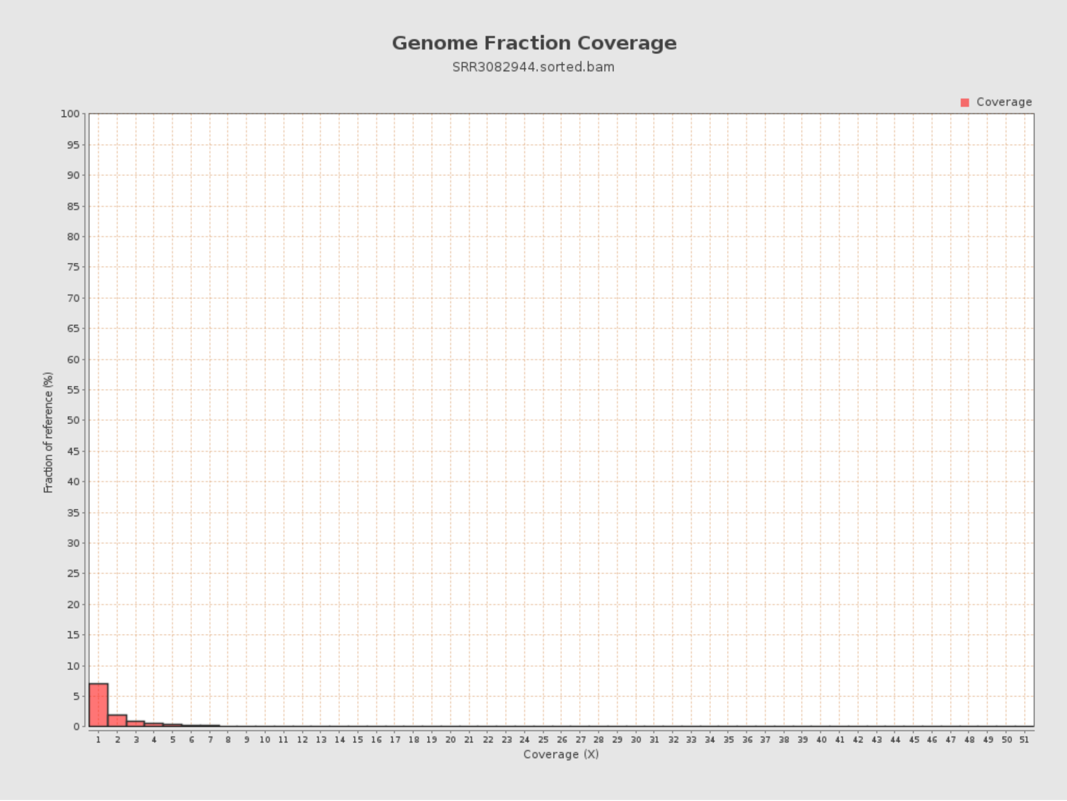
4. Results : Coverage Histogram



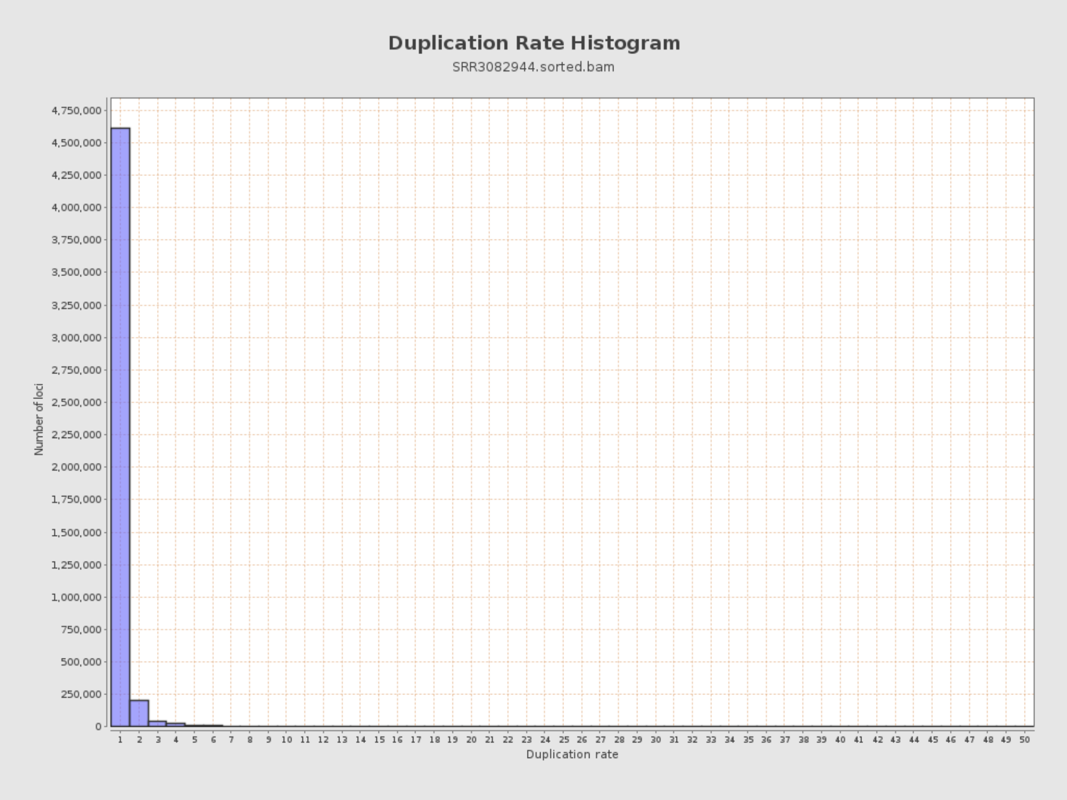
5. Results : Coverage Histogram (0-50X)



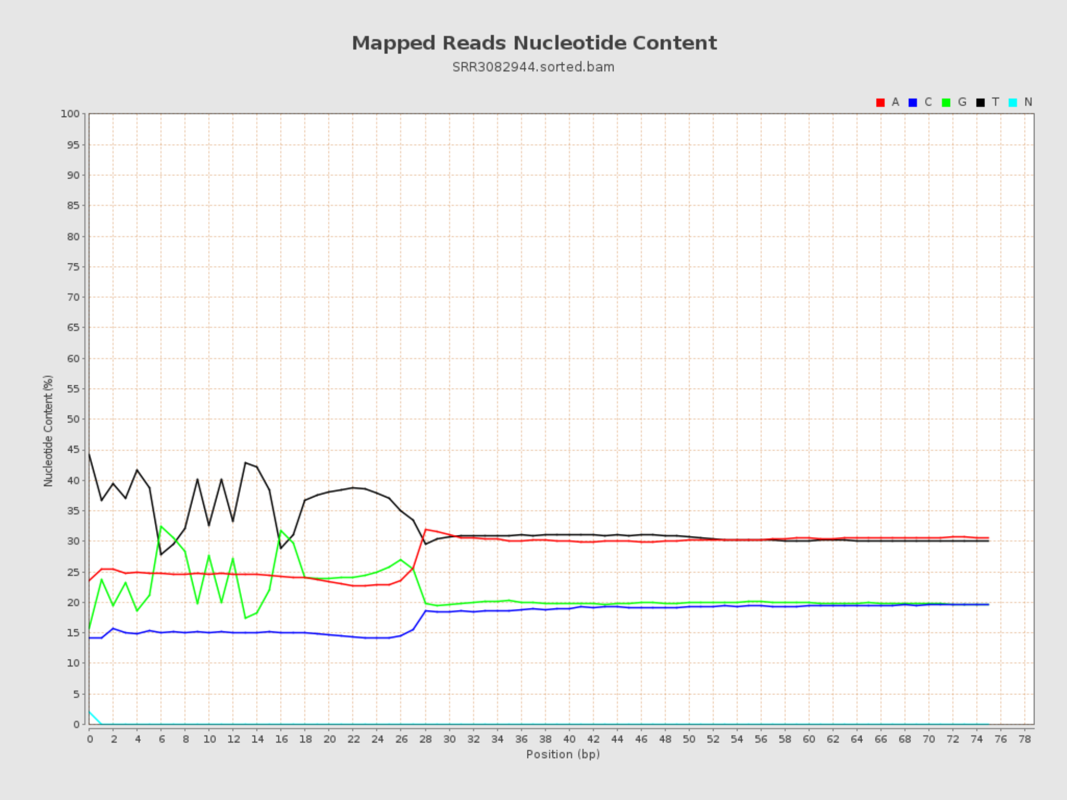
6. Results : Genome Fraction Coverage



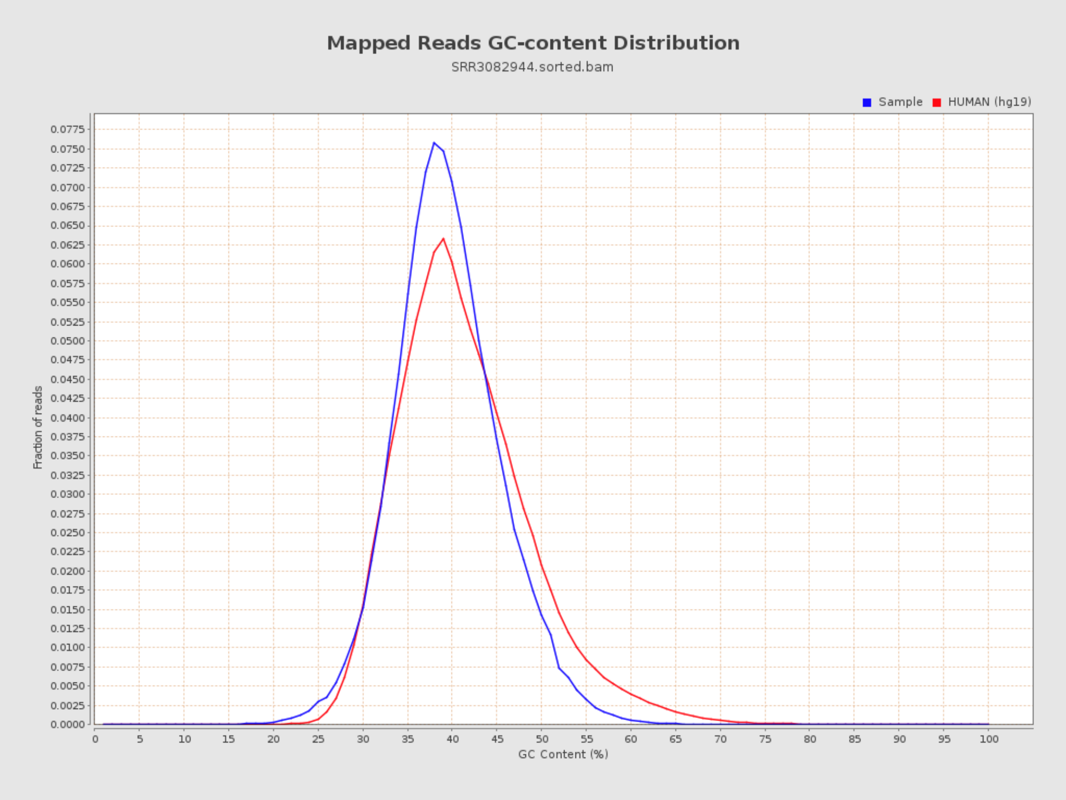
7. Results : Duplication Rate Histogram



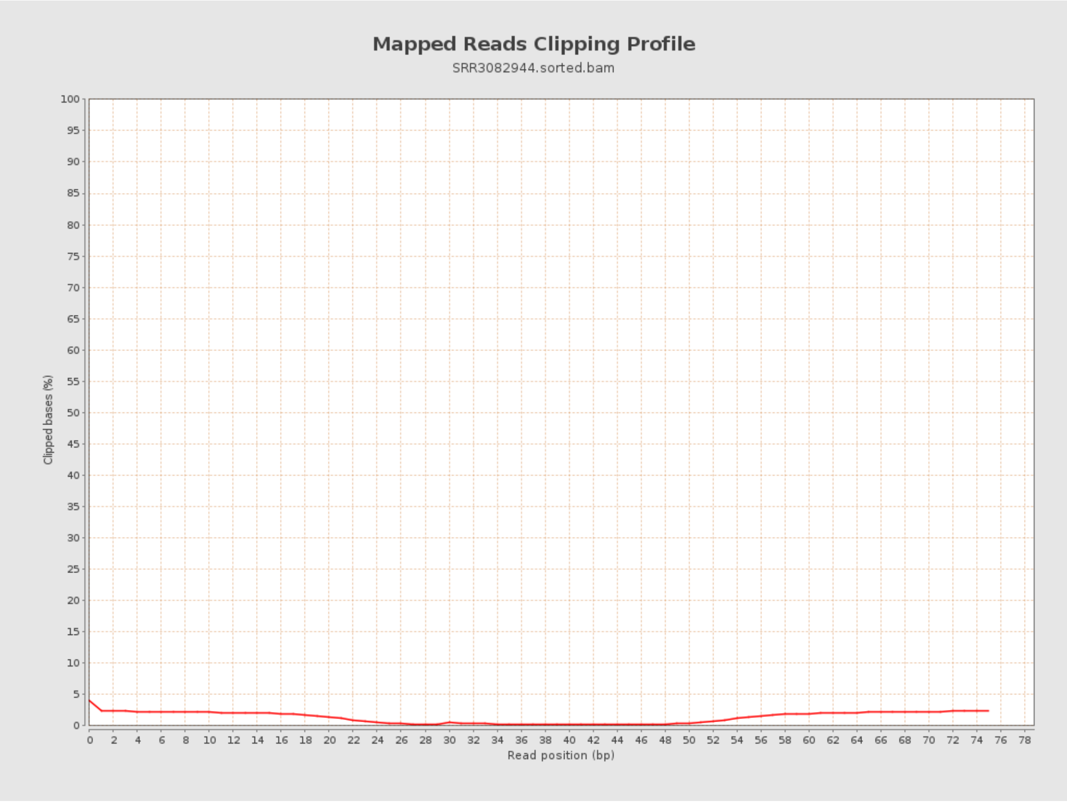
8. Results : Mapped Reads Nucleotide Content



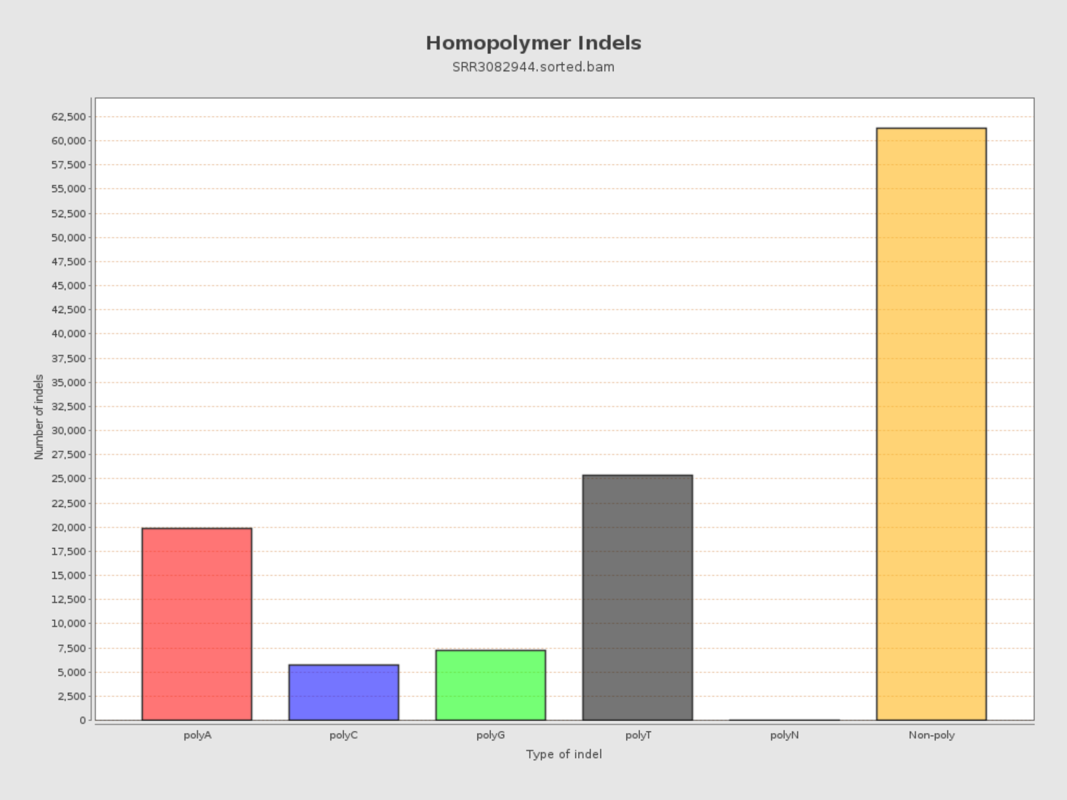
9. Results : Mapped Reads GC-content Distribution



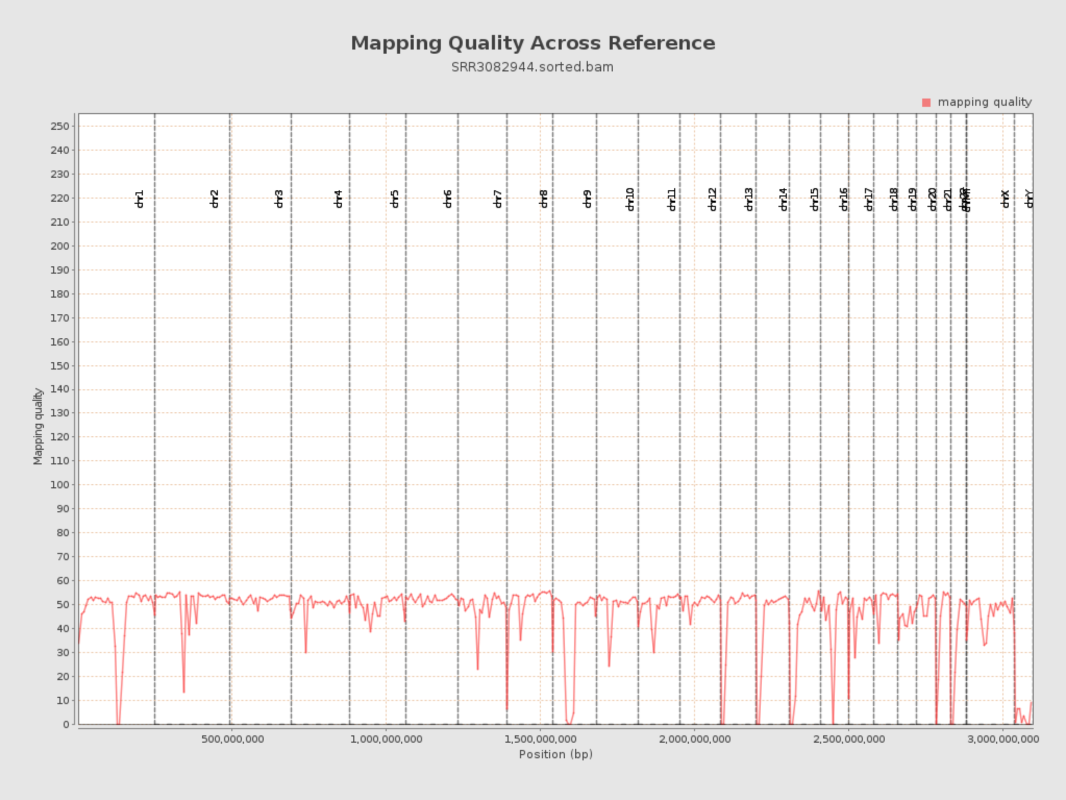
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram