Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:02:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082770.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_SRR3082770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:02:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,208,336
Mapped reads	4,661,905 / 89.51%
Unmapped reads	546,431 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,208 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	244,469 / 4.69%
Duplication rate	4.05%
Clipped reads	1,802,132 / 34.6%

2.2. ACGT Content

Number/percentage of A's	92,260,640 / 28.8%
Number/percentage of C's	60,013,371 / 18.73%
Number/percentage of T's	101,718,092 / 31.75%
Number/percentage of G's	66,345,114 / 20.71%
Number/percentage of N's	17,196 / 0.01%
GC Percentage	39.44%

2.3. Coverage

Mean	0.1035

Standard Deviation	0.7549

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

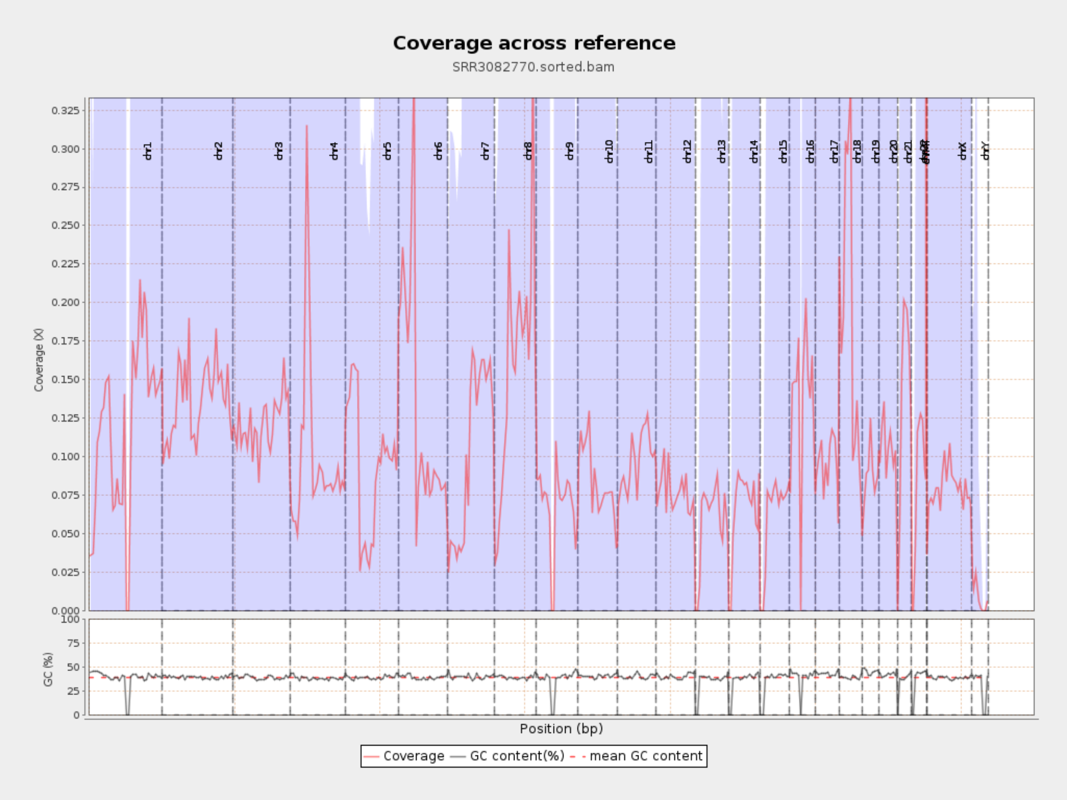
General error rate	0.9%
Mismatches	2,830,947
Insertions	25,065
Mapped reads with at least one insertion	0.53%
Deletions	69,660
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.59%

2.6. Chromosome stats

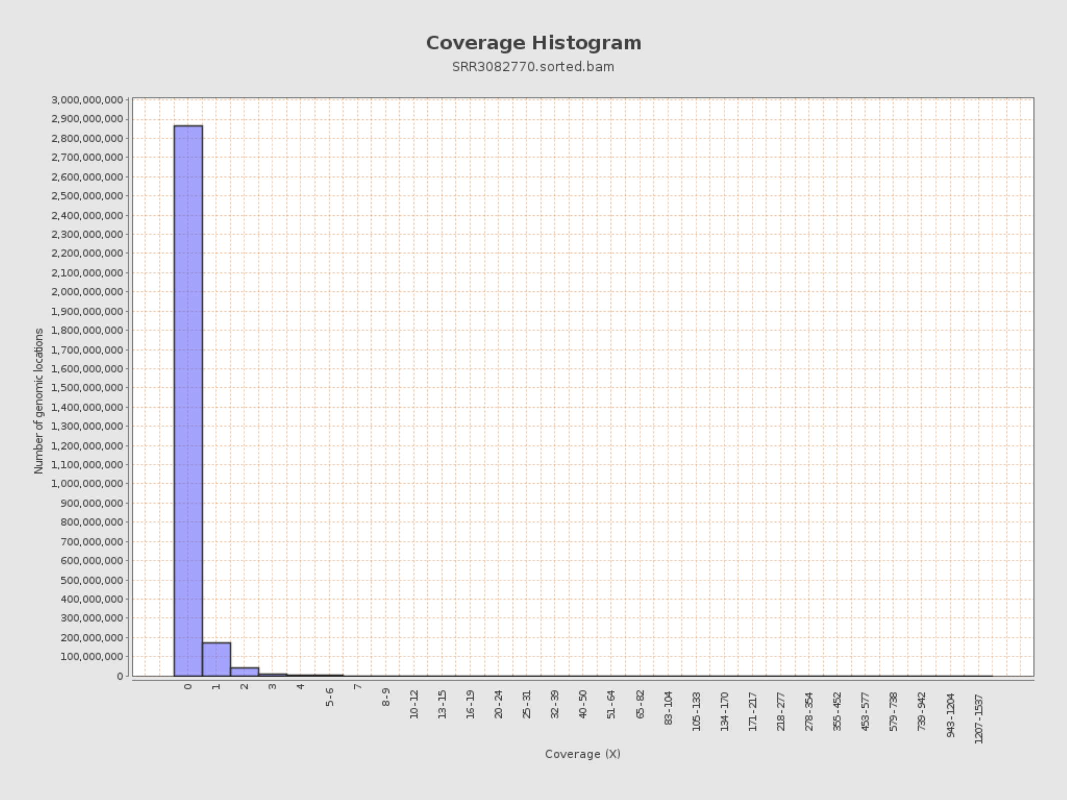
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29694534	0.1191	1.4649
chr2	243199373	33227421	0.1366	0.9375
chr3	198022430	23972963	0.1211	0.4527
chr4	191154276	18965527	0.0992	0.4298
chr5	180915260	16997176	0.094	0.4031
chr6	171115067	22870146	0.1337	0.7852
chr7	159138663	16636290	0.1045	0.6337

chr8	146364022	23516700	0.1607	1.027
chr9	141213431	9570198	0.0678	0.6871
chr10	135534747	11585317	0.0855	0.5261
chr11	135006516	12979993	0.0961	0.6406
chr12	133851895	10241854	0.0765	0.3721
chr13	115169878	6614373	0.0574	0.3093
chr14	107349540	6929868	0.0646	0.4042
chr15	102531392	6254217	0.061	0.3158
chr16	90354753	12253126	0.1356	0.5477
chr17	81195210	7702401	0.0949	0.4847
chr18	78077248	14636473	0.1875	1.5359
chr19	59128983	5242013	0.0887	0.9289
chr20	63025520	6619809	0.105	0.445
chr21	48129895	6626922	0.1377	0.5076
chr22	51304566	4045605	0.0789	0.3611
chrMT	16571	494384	29.8343	18.2563
chrX	155270560	12281620	0.0791	0.4482
chrY	59373566	514619	0.0087	0.1723

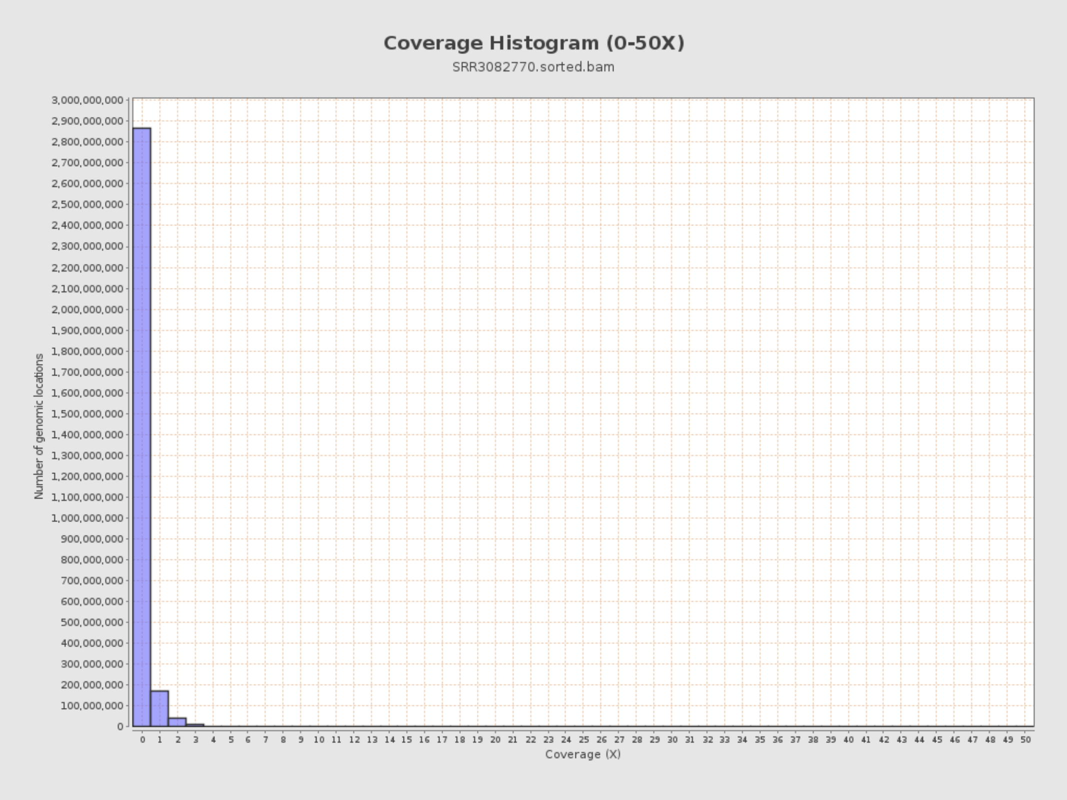
3. Results : Coverage across reference



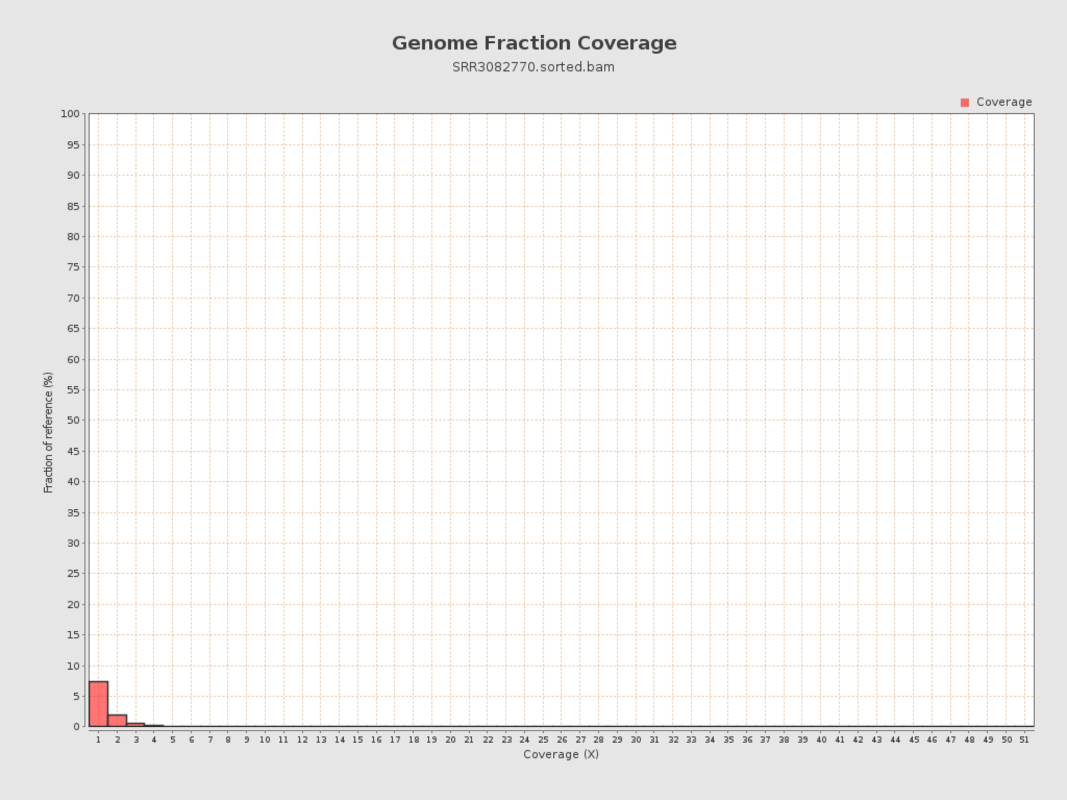
4. Results : Coverage Histogram



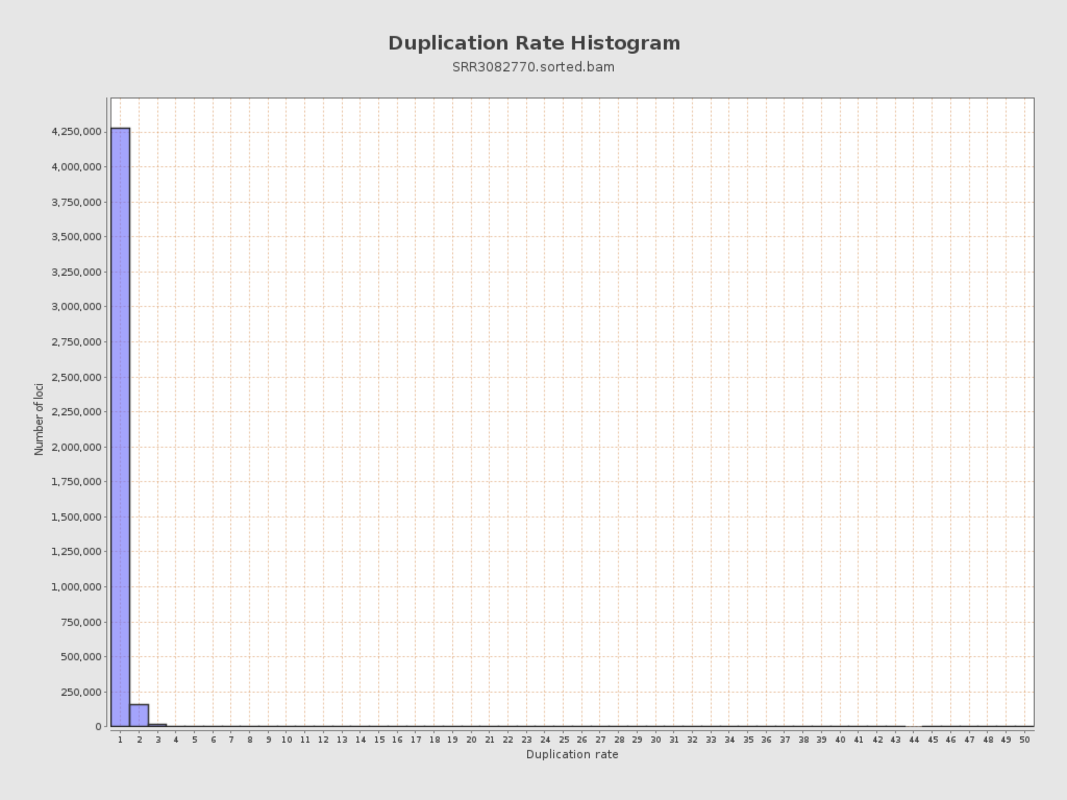
5. Results : Coverage Histogram (0-50X)



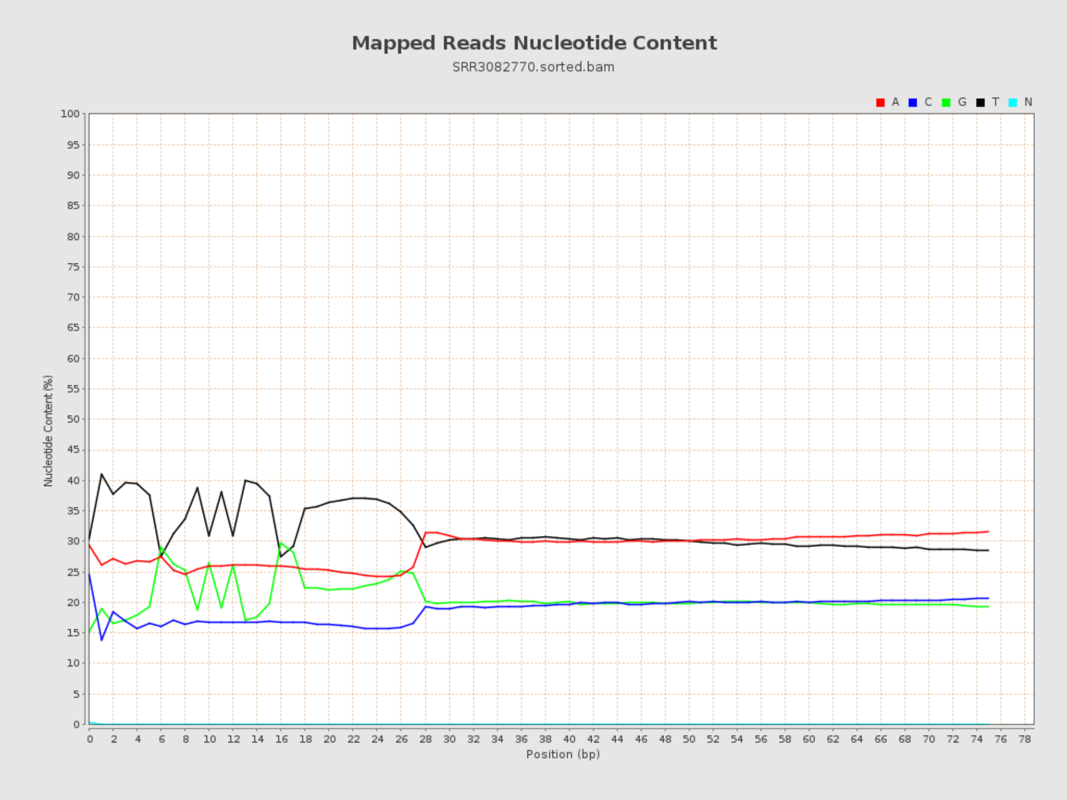
6. Results : Genome Fraction Coverage



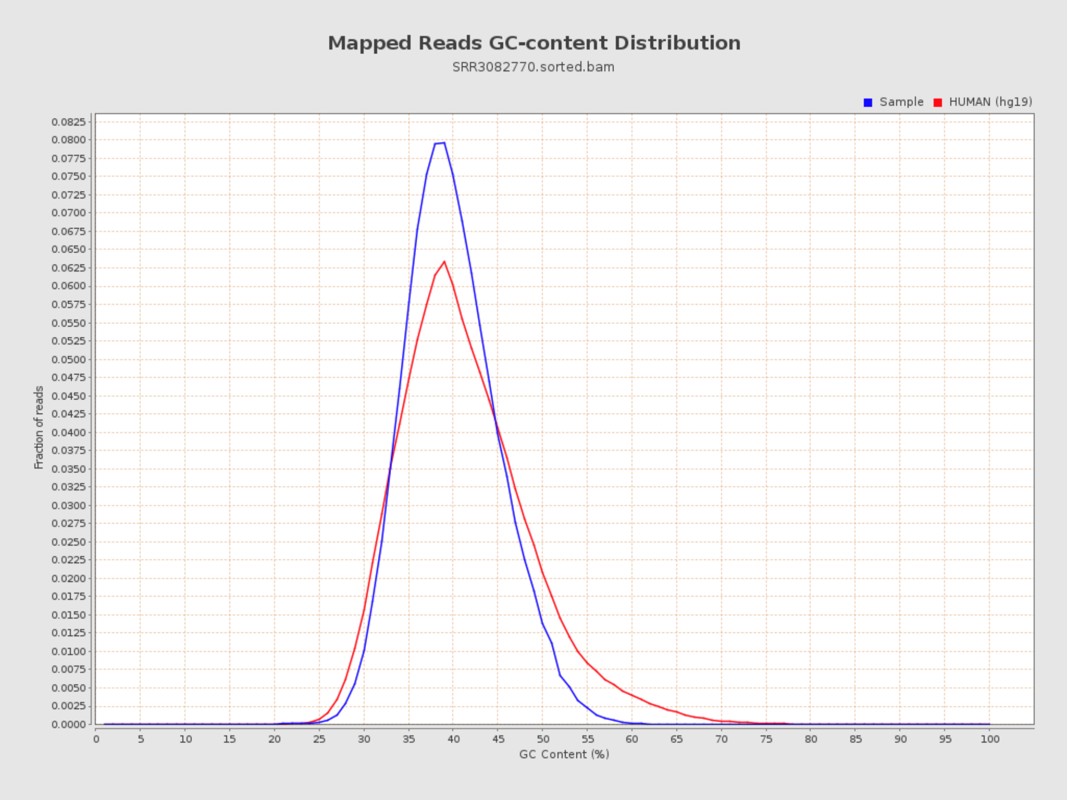
7. Results : Duplication Rate Histogram



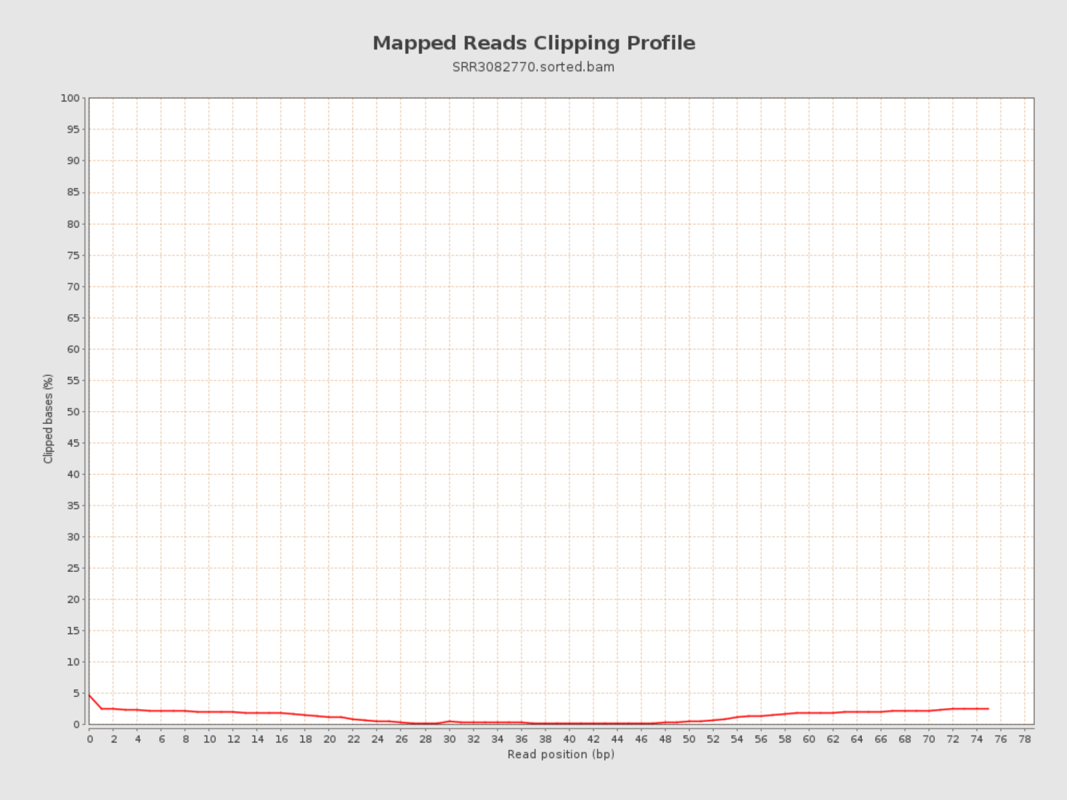
8. Results : Mapped Reads Nucleotide Content



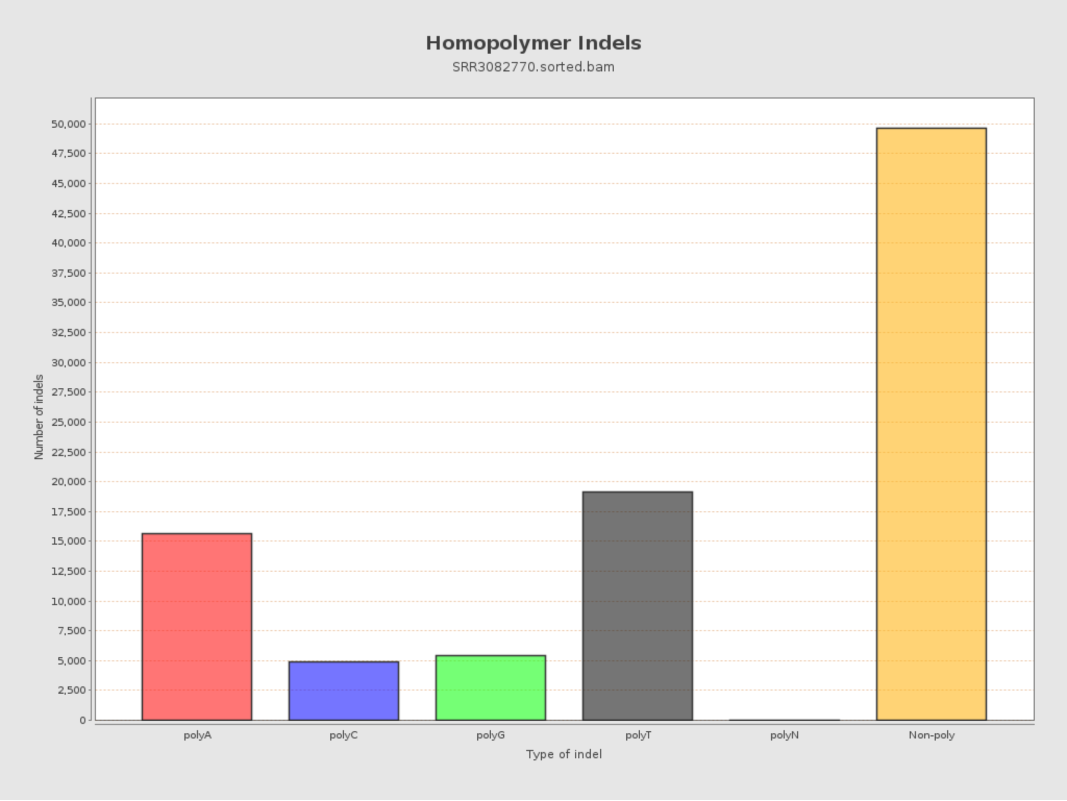
9. Results : Mapped Reads GC-content Distribution



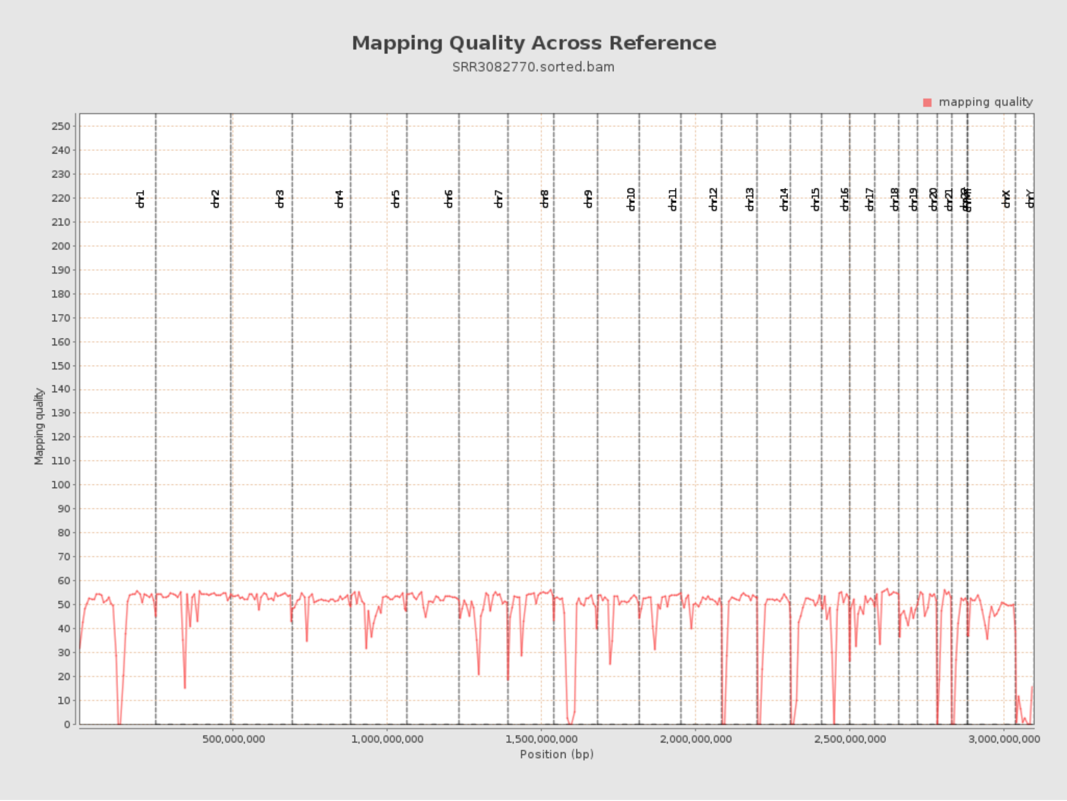
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram