Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:15:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082975.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_SRR3082975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:15:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,678,238
Mapped reads	4,970,802 / 87.54%
Unmapped reads	707,436 / 12.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,683 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	464,965 / 8.19%
Duplication rate	6%
Clipped reads	2,185,618 / 38.49%

2.2. ACGT Content

Number/percentage of A's	93,003,356 / 27.91%
Number/percentage of C's	58,560,534 / 17.58%
Number/percentage of T's	109,589,455 / 32.89%
Number/percentage of G's	71,936,111 / 21.59%
Number/percentage of N's	91,223 / 0.03%
GC Percentage	39.17%

2.3. Coverage

Mean	0.1077

Standard Deviation	0.8542

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

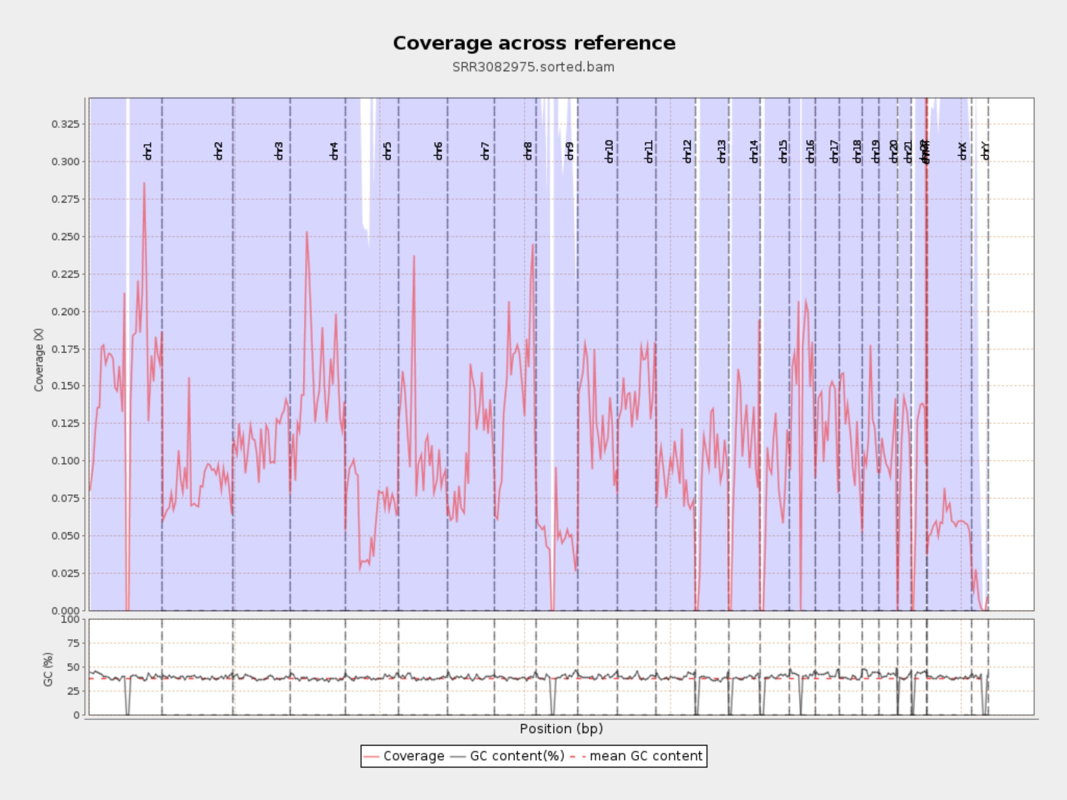
General error rate	0.98%
Mismatches	3,198,979
Insertions	30,367
Mapped reads with at least one insertion	0.61%
Deletions	80,368
Mapped reads with at least one deletion	1.6%
Homopolymer indels	49.28%

2.6. Chromosome stats

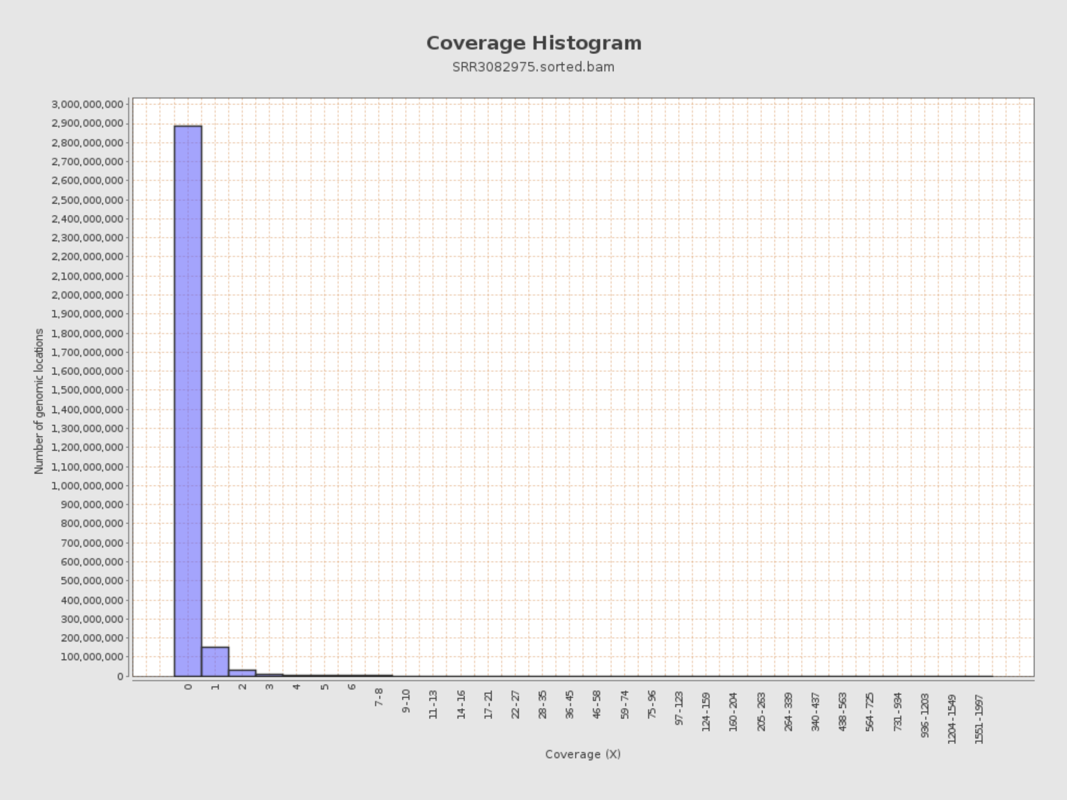
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39100354	0.1569	1.5174
chr2	243199373	20568227	0.0846	0.8836
chr3	198022430	22562422	0.1139	0.5459
chr4	191154276	28867352	0.151	0.7151
chr5	180915260	11969334	0.0662	0.3173
chr6	171115067	19501168	0.114	0.8504
chr7	159138663	17109726	0.1075	0.8

chr8	146364022	21867176	0.1494	1.4094
chr9	141213431	6433314	0.0456	0.6953
chr10	135534747	17848914	0.1317	0.7707
chr11	135006516	19825328	0.1468	0.832
chr12	133851895	11819032	0.0883	0.5143
chr13	115169878	10236880	0.0889	0.5229
chr14	107349540	10953768	0.102	0.6144
chr15	102531392	8042521	0.0784	0.4748
chr16	90354753	13841476	0.1532	0.6846
chr17	81195210	10193840	0.1255	0.6966
chr18	78077248	9301113	0.1191	1.4985
chr19	59128983	6820208	0.1153	1.0681
chr20	63025520	6602925	0.1048	0.5487
chr21	48129895	4893206	0.1017	0.4977
chr22	51304566	4727936	0.0922	0.4999
chrMT	16571	645395	38.9473	21.7147
chrX	155270560	9036447	0.0582	0.394
chrY	59373566	541267	0.0091	0.1733

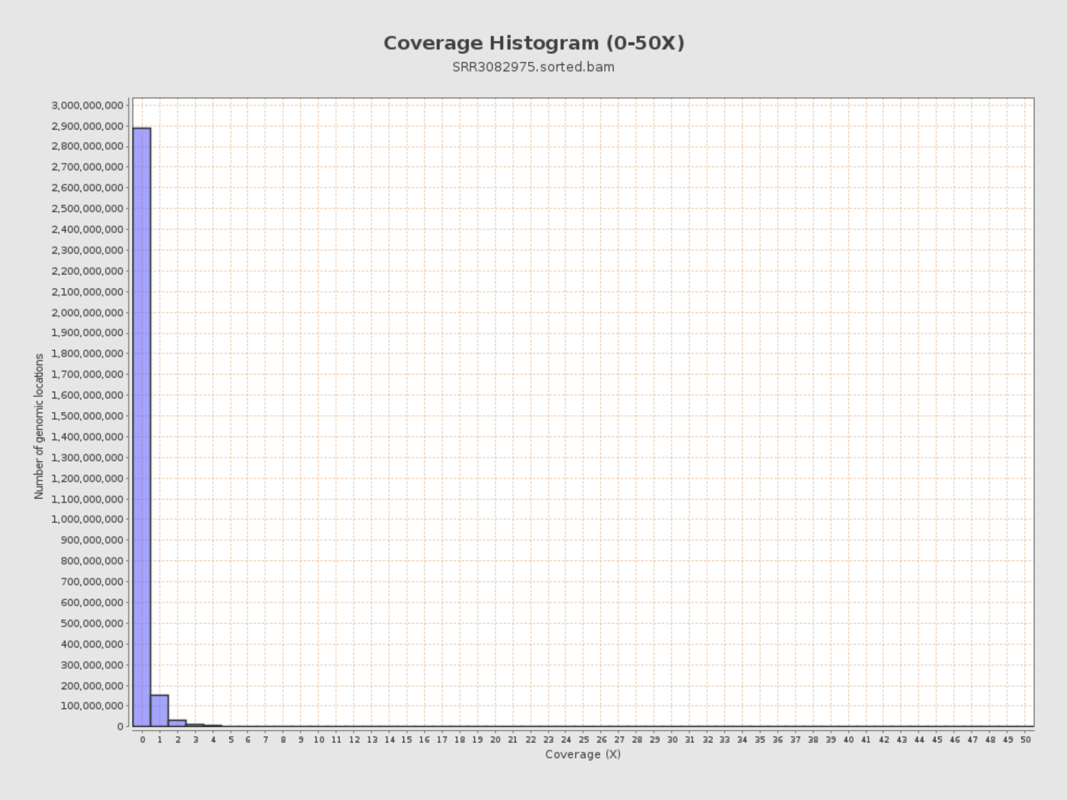
3. Results : Coverage across reference



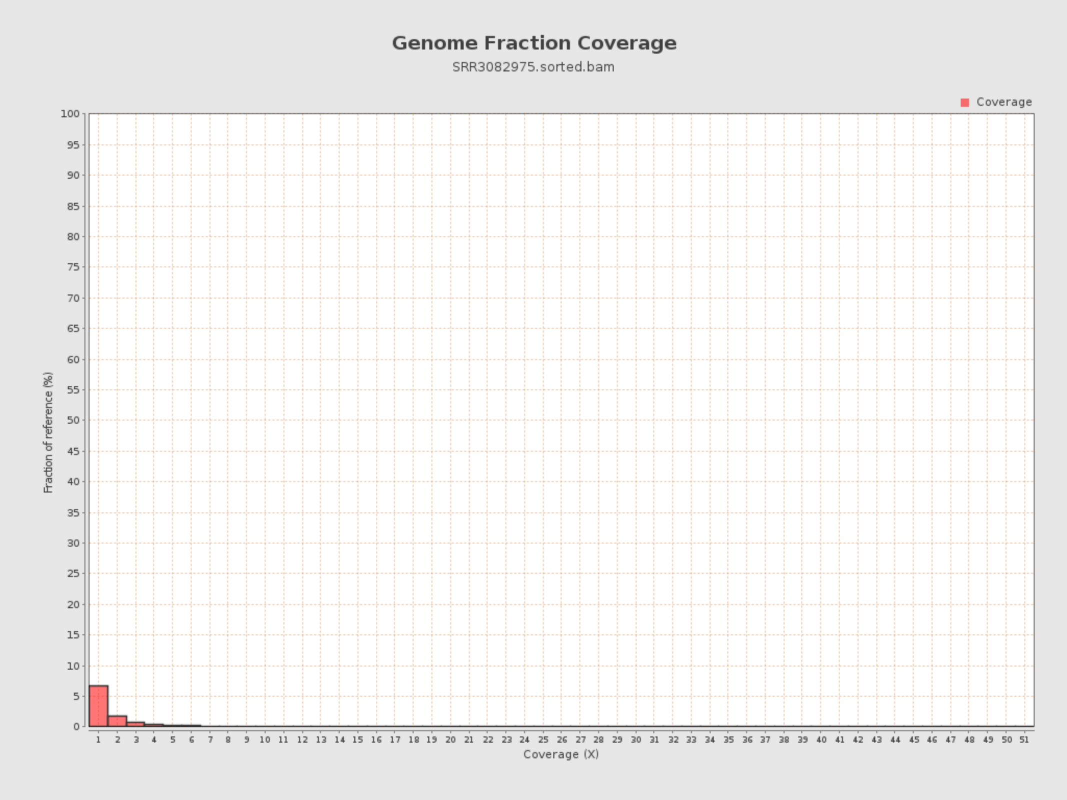
4. Results : Coverage Histogram



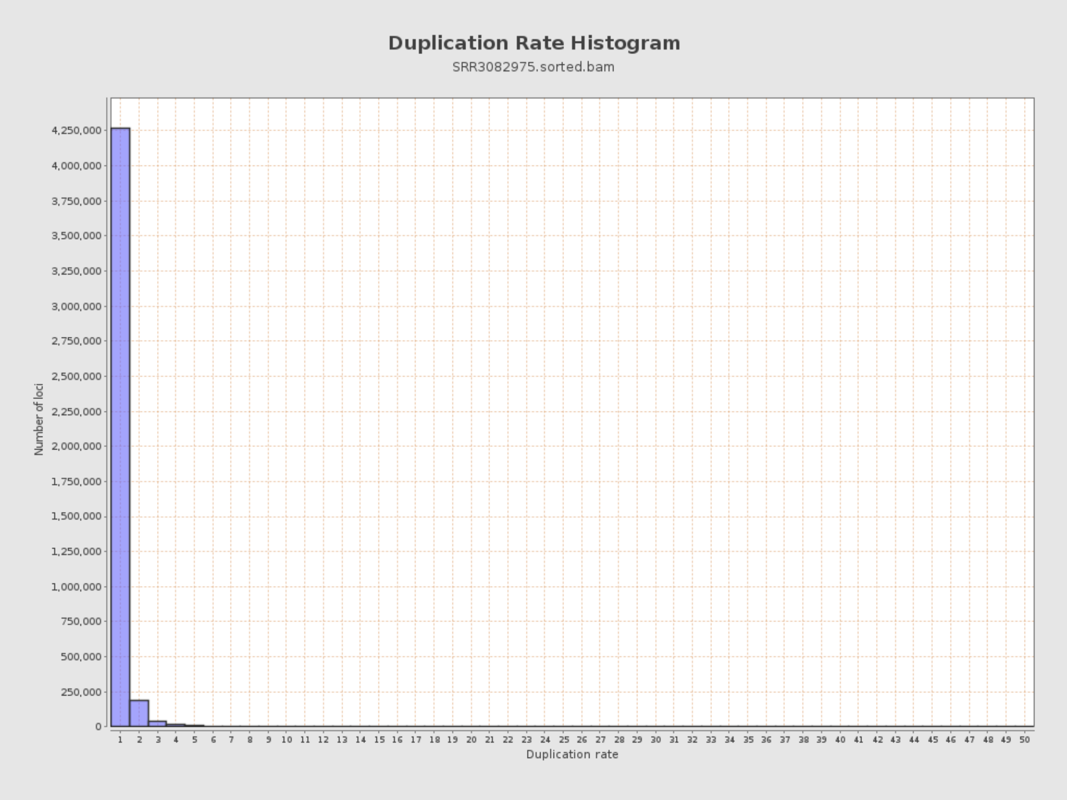
5. Results : Coverage Histogram (0-50X)



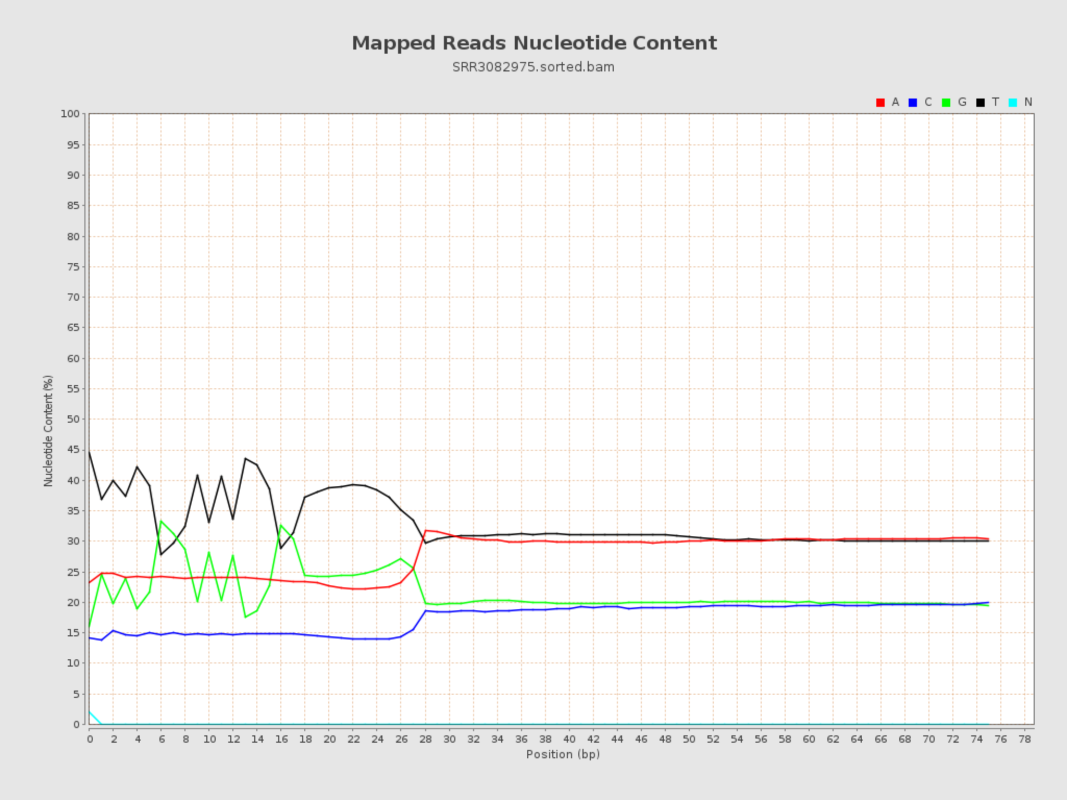
6. Results : Genome Fraction Coverage



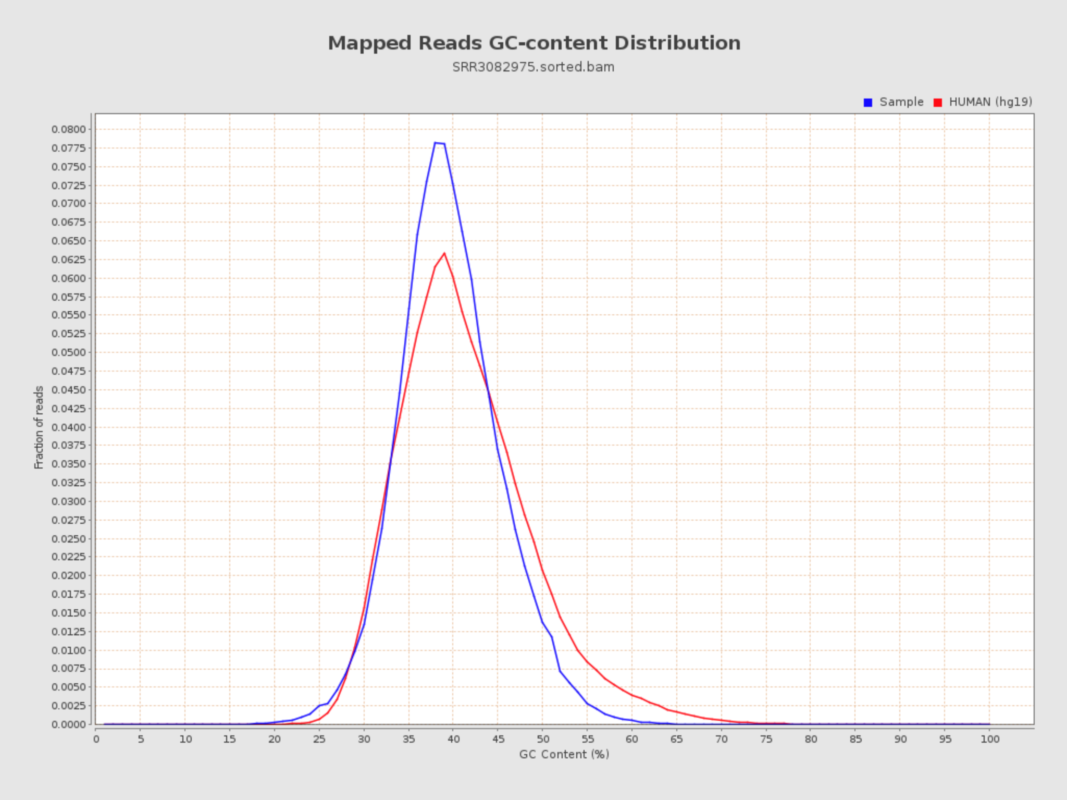
7. Results : Duplication Rate Histogram



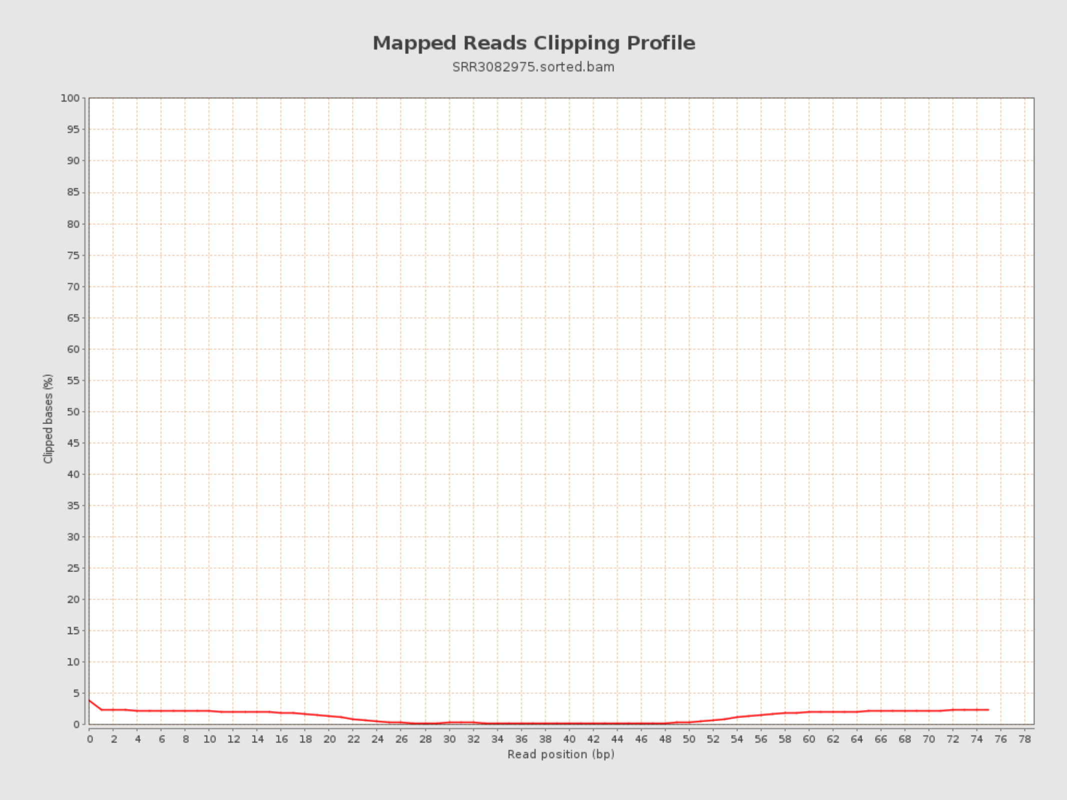
8. Results : Mapped Reads Nucleotide Content



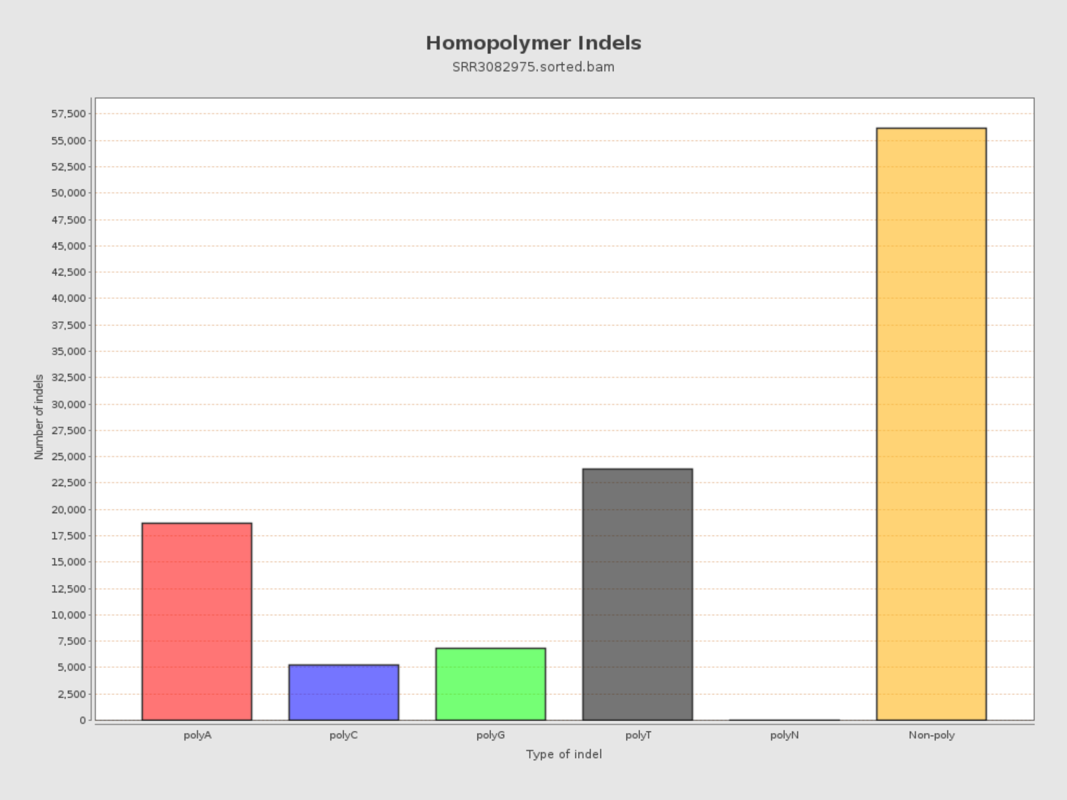
9. Results : Mapped Reads GC-content Distribution



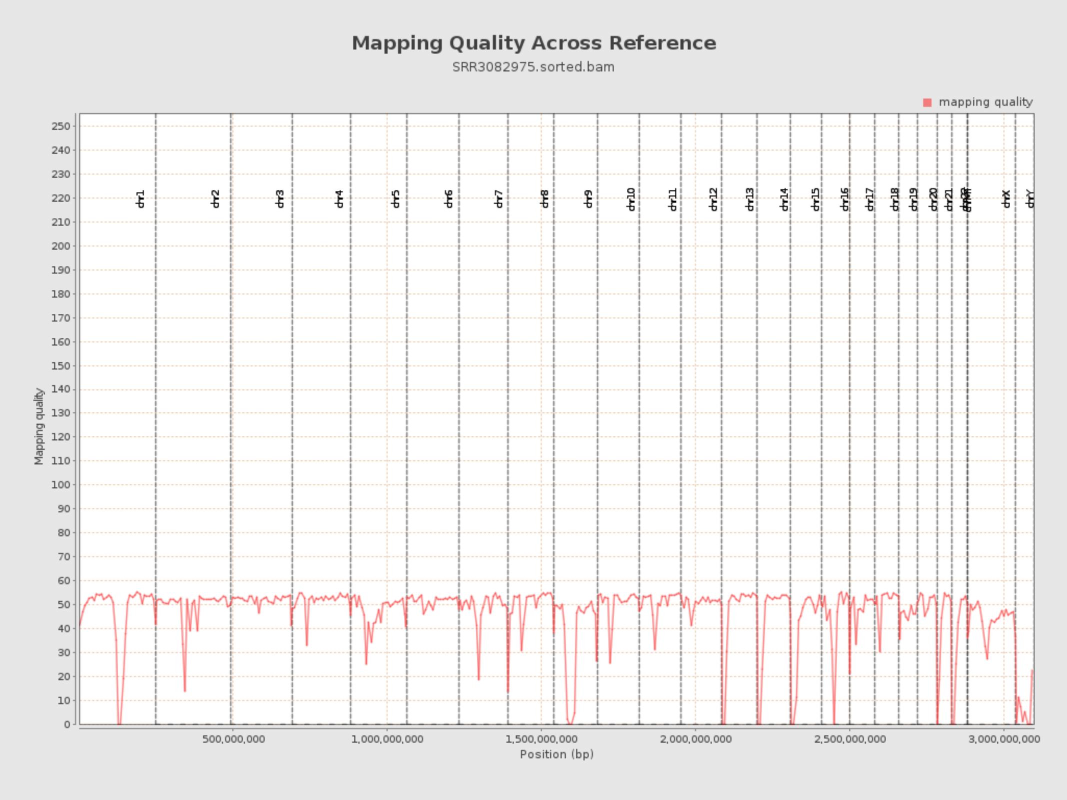
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram