Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:27:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082935.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_SRR3082935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:27:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	891,213
Mapped reads	806,941 / 90.54%
Unmapped reads	84,272 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,134 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	27,569 / 3.09%
Duplication rate	3.11%
Clipped reads	300,628 / 33.73%

2.2. ACGT Content

Number/percentage of A's	15,672,110 / 28.42%
Number/percentage of C's	9,967,406 / 18.07%
Number/percentage of T's	17,893,364 / 32.44%
Number/percentage of G's	11,615,359 / 21.06%
Number/percentage of N's	2,564 / 0%
GC Percentage	39.13%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1636

2.4. Mapping Quality

Mean Mapping Quality	46.95

2.5. Mismatches and indels

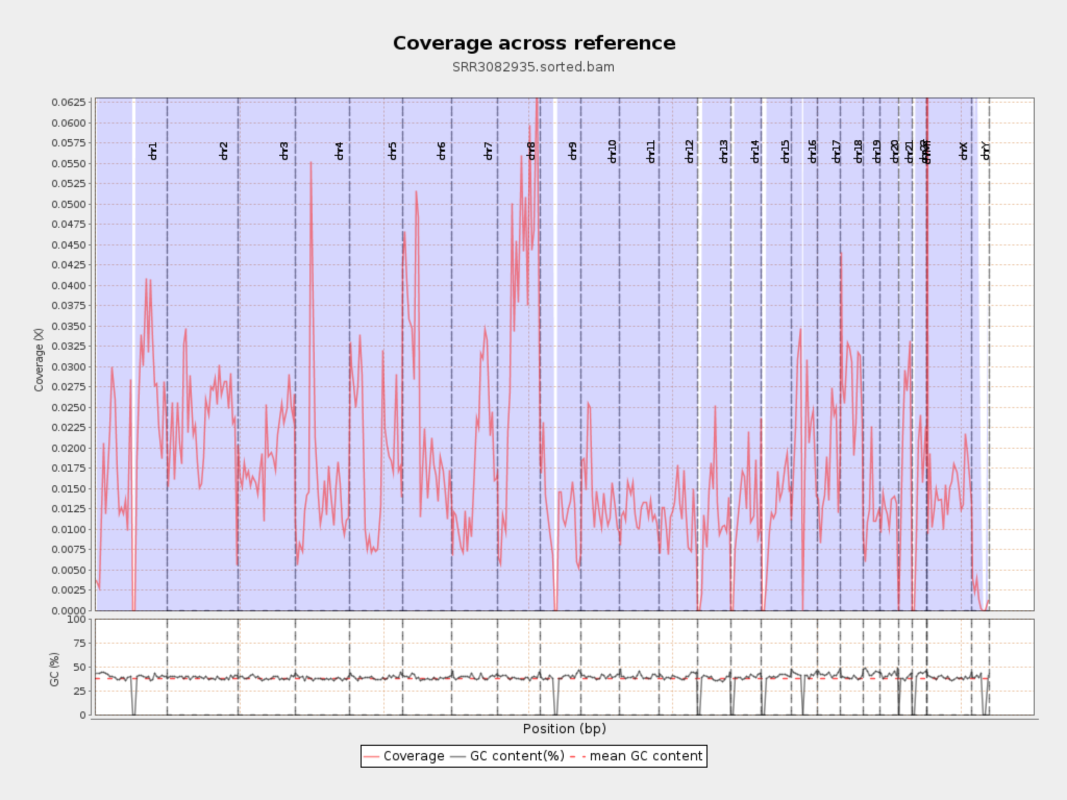
General error rate	0.75%
Mismatches	404,719
Insertions	4,623
Mapped reads with at least one insertion	0.57%
Deletions	12,600
Mapped reads with at least one deletion	1.55%
Homopolymer indels	49.08%

2.6. Chromosome stats

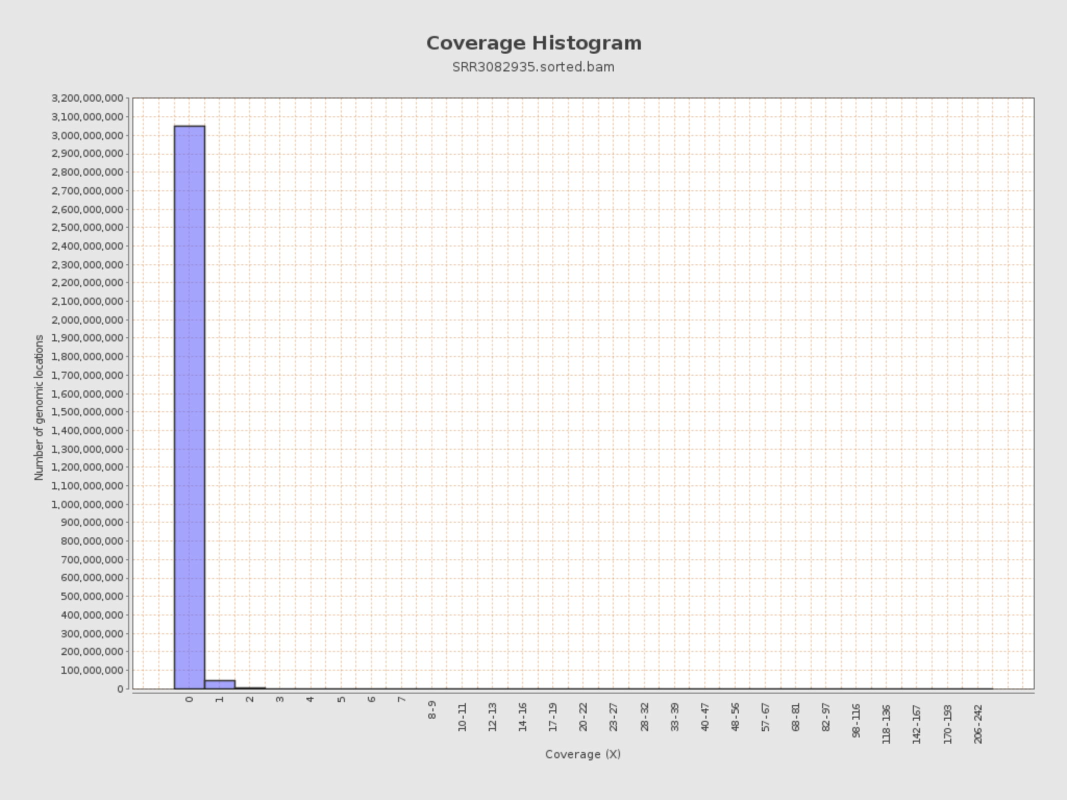
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5112967	0.0205	0.1975
chr2	243199373	5764534	0.0237	0.1987
chr3	198022430	3883880	0.0196	0.1574
chr4	191154276	2970412	0.0155	0.1414
chr5	180915260	3423259	0.0189	0.1548
chr6	171115067	4273823	0.025	0.1855
chr7	159138663	2818484	0.0177	0.1555

chr8	146364022	5319293	0.0363	0.2652
chr9	141213431	1570040	0.0111	0.1317
chr10	135534747	1964338	0.0145	0.1417
chr11	135006516	1658749	0.0123	0.1292
chr12	133851895	1543605	0.0115	0.1197
chr13	115169878	1269214	0.011	0.1185
chr14	107349540	1275688	0.0119	0.1244
chr15	102531392	1172881	0.0114	0.1215
chr16	90354753	1877635	0.0208	0.1647
chr17	81195210	1388209	0.0171	0.1509
chr18	78077248	2236929	0.0287	0.2366
chr19	59128983	718112	0.0121	0.1413
chr20	63025520	770684	0.0122	0.1259
chr21	48129895	1018544	0.0212	0.1647
chr22	51304566	748144	0.0146	0.1356
chrMT	16571	8137	0.491	0.7892
chrX	155270560	2294251	0.0148	0.1375
chrY	59373566	89442	0.0015	0.0439

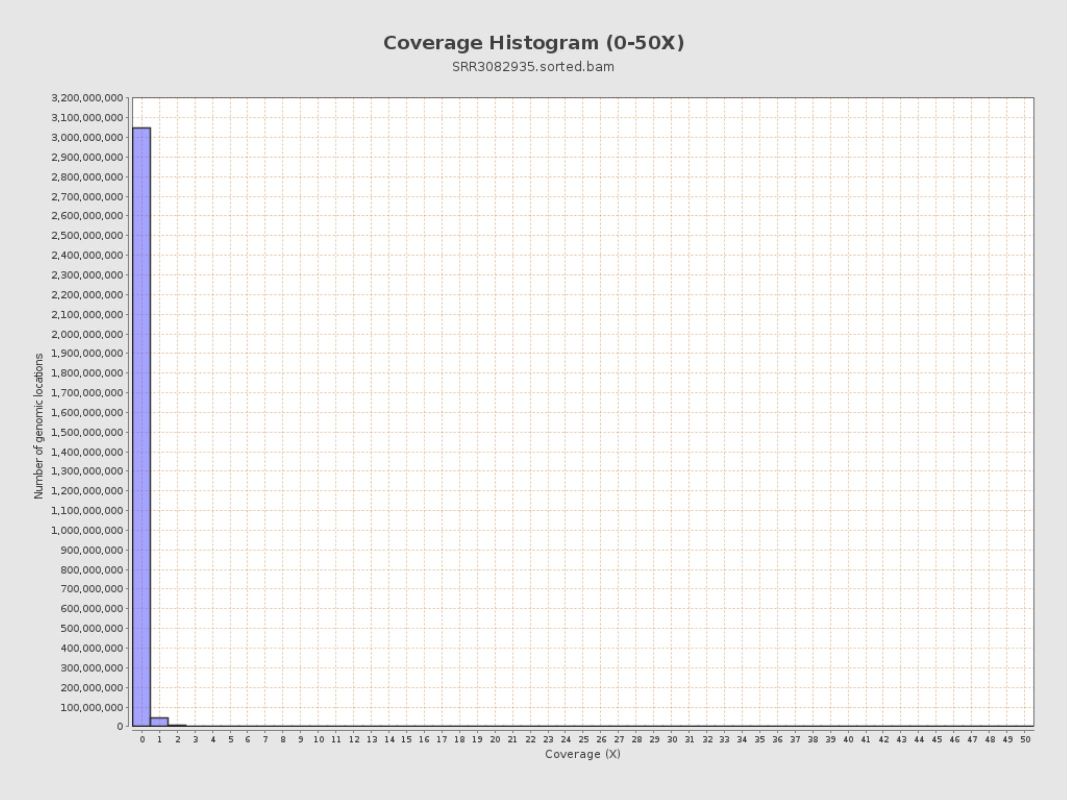
3. Results : Coverage across reference



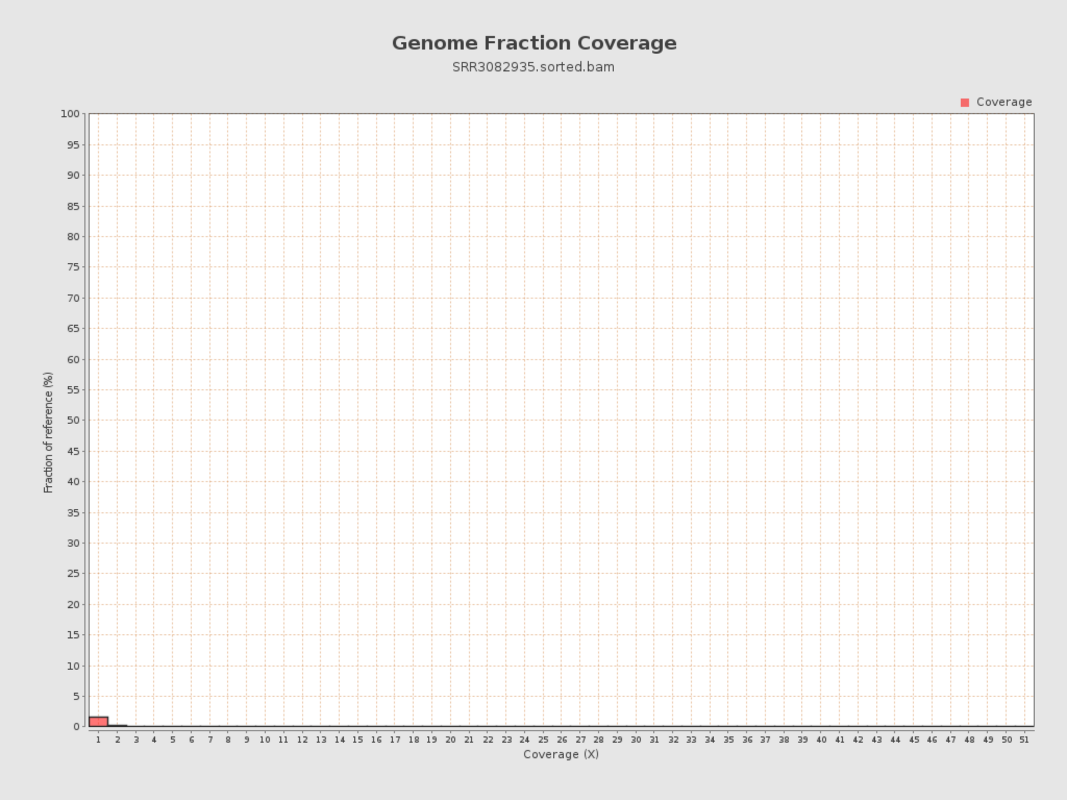
4. Results : Coverage Histogram



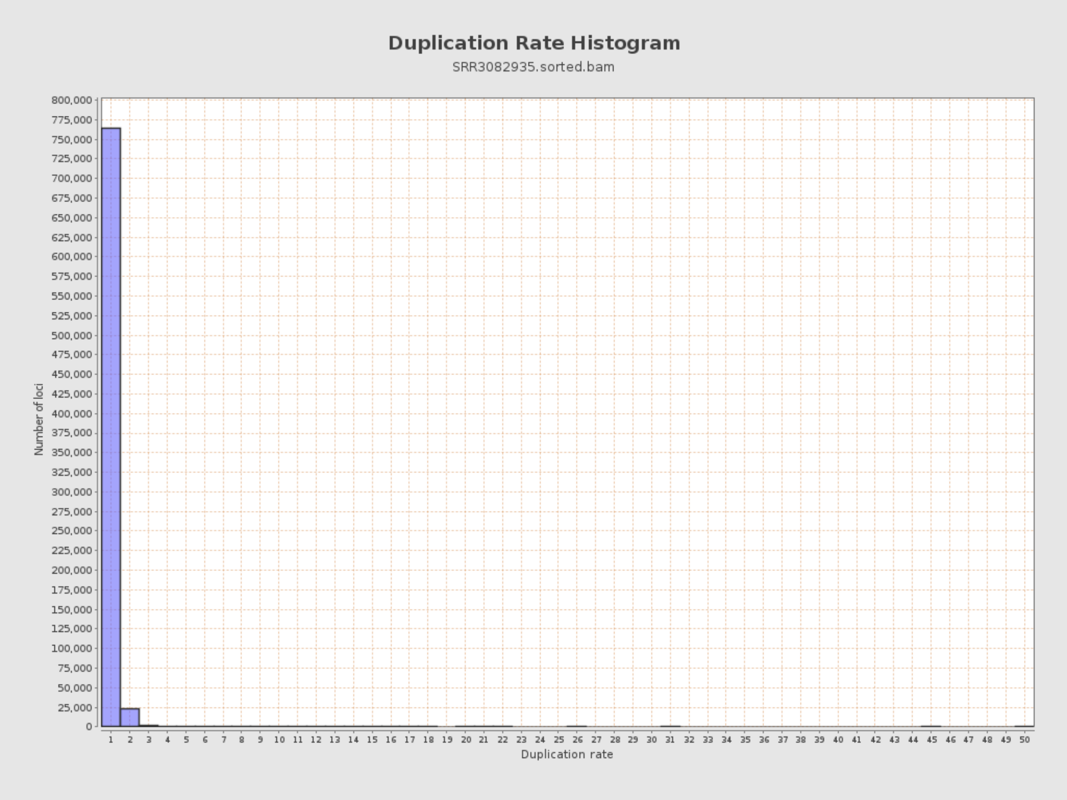
5. Results : Coverage Histogram (0-50X)



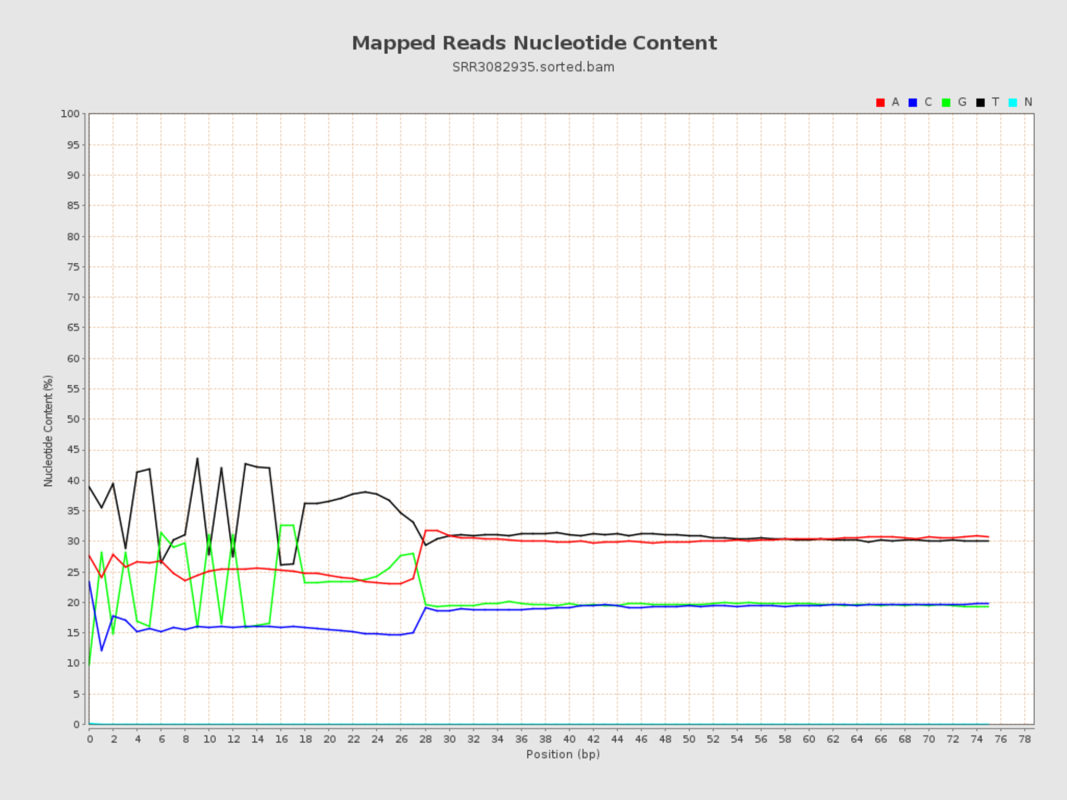
6. Results : Genome Fraction Coverage



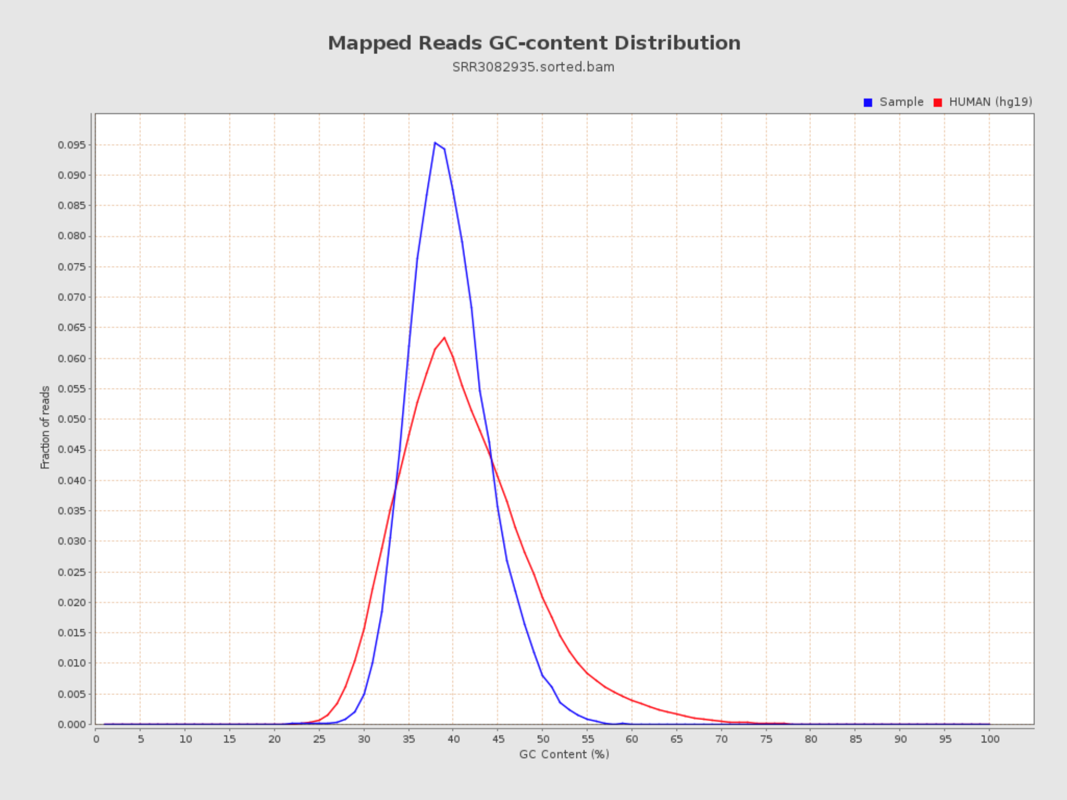
7. Results : Duplication Rate Histogram



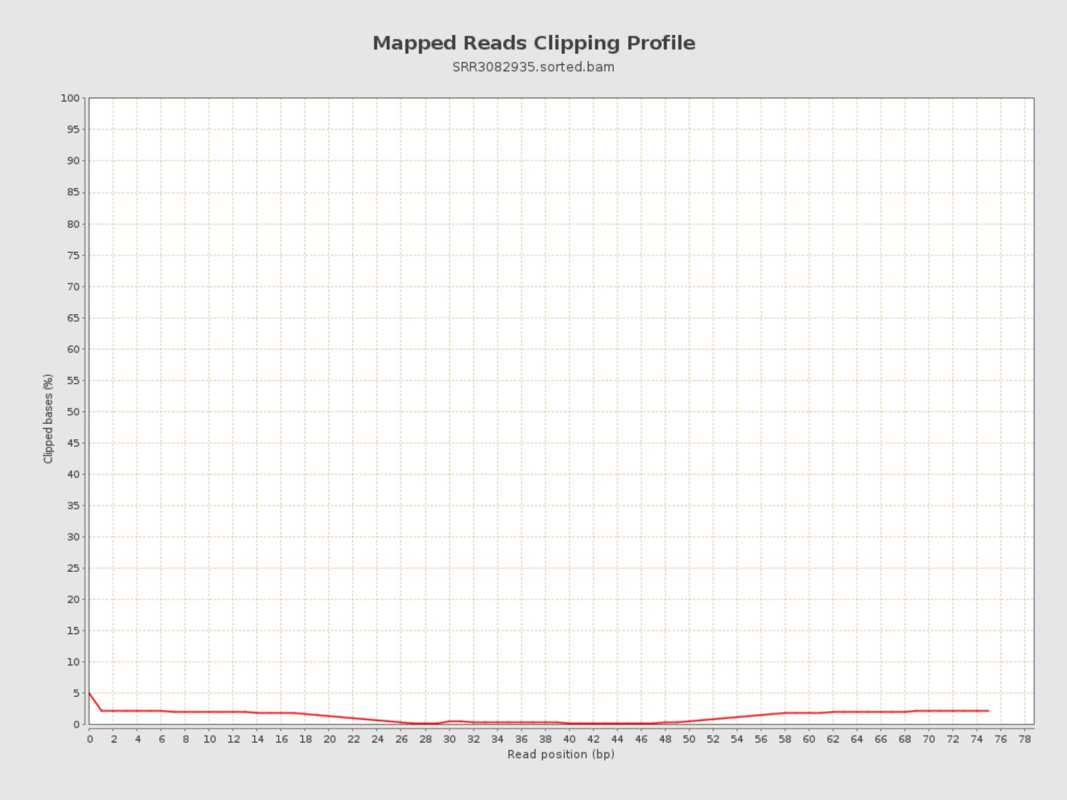
8. Results : Mapped Reads Nucleotide Content



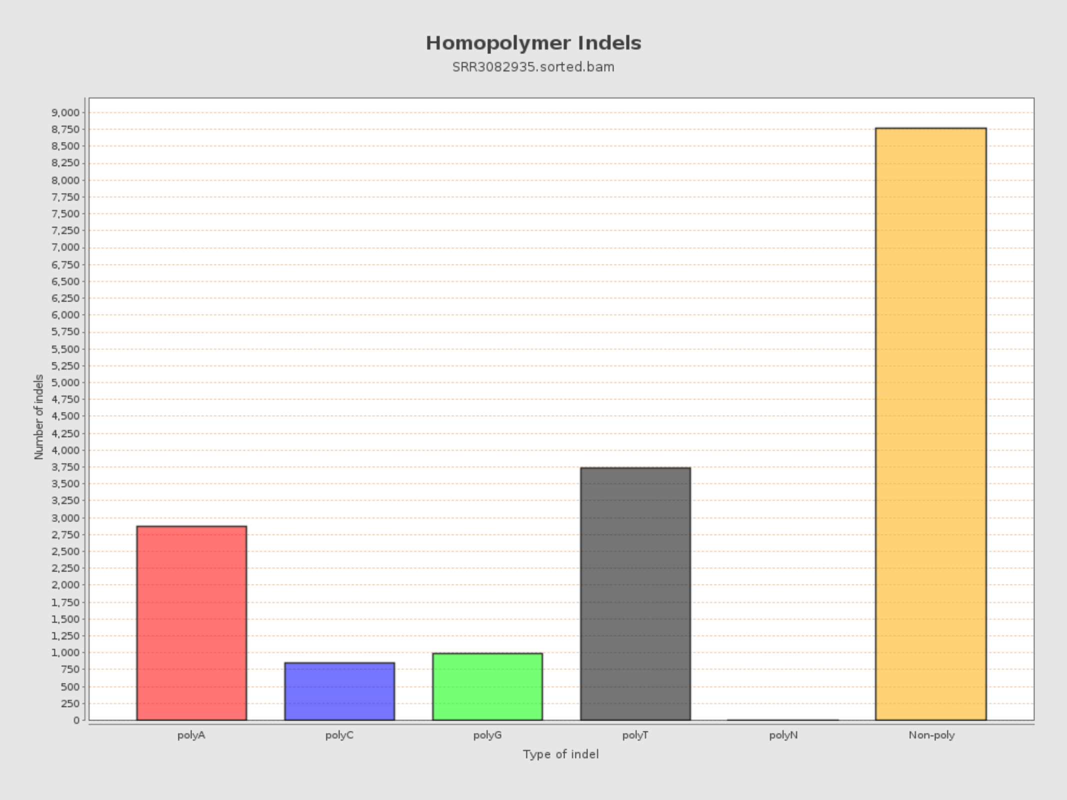
9. Results : Mapped Reads GC-content Distribution



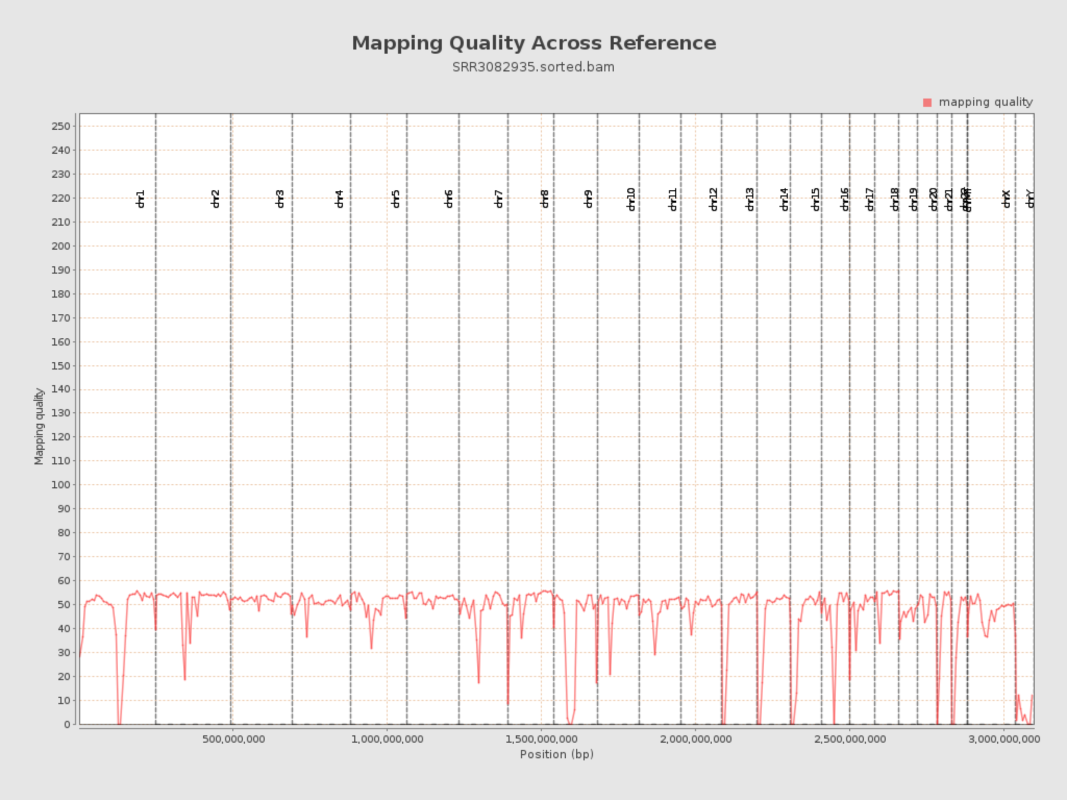
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram