Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:47:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819045.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_SRR1819045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:47:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	555,476
Mapped reads	485,479 / 87.4%
Unmapped reads	69,997 / 12.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,073 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	7,321 / 1.32%
Duplication rate	1.16%
Clipped reads	486,545 / 87.59%

2.2. ACGT Content

Number/percentage of A's	6,895,865 / 25.15%
Number/percentage of C's	5,256,087 / 19.17%
Number/percentage of T's	8,646,553 / 31.54%
Number/percentage of G's	6,615,705 / 24.13%
Number/percentage of N's	622 / 0%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.107

2.4. Mapping Quality

Mean Mapping Quality	43.42

2.5. Mismatches and indels

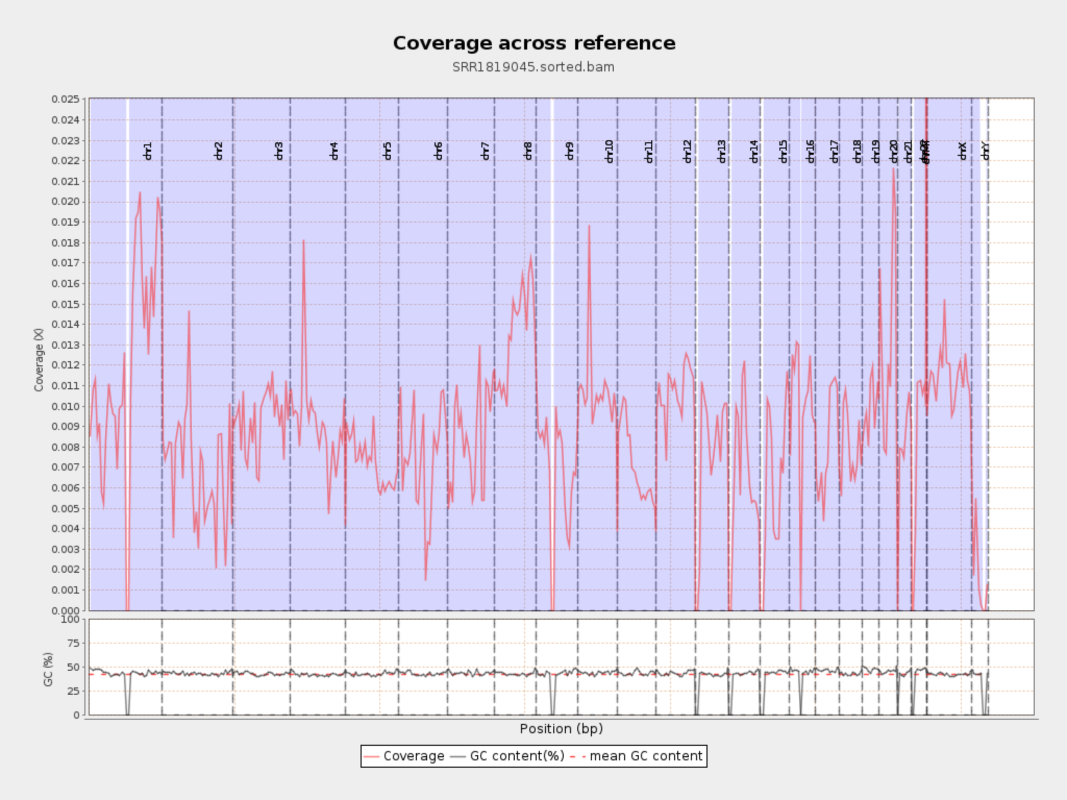
General error rate	0.51%
Mismatches	136,163
Insertions	1,905
Mapped reads with at least one insertion	0.39%
Deletions	4,264
Mapped reads with at least one deletion	0.87%
Homopolymer indels	41.09%

2.6. Chromosome stats

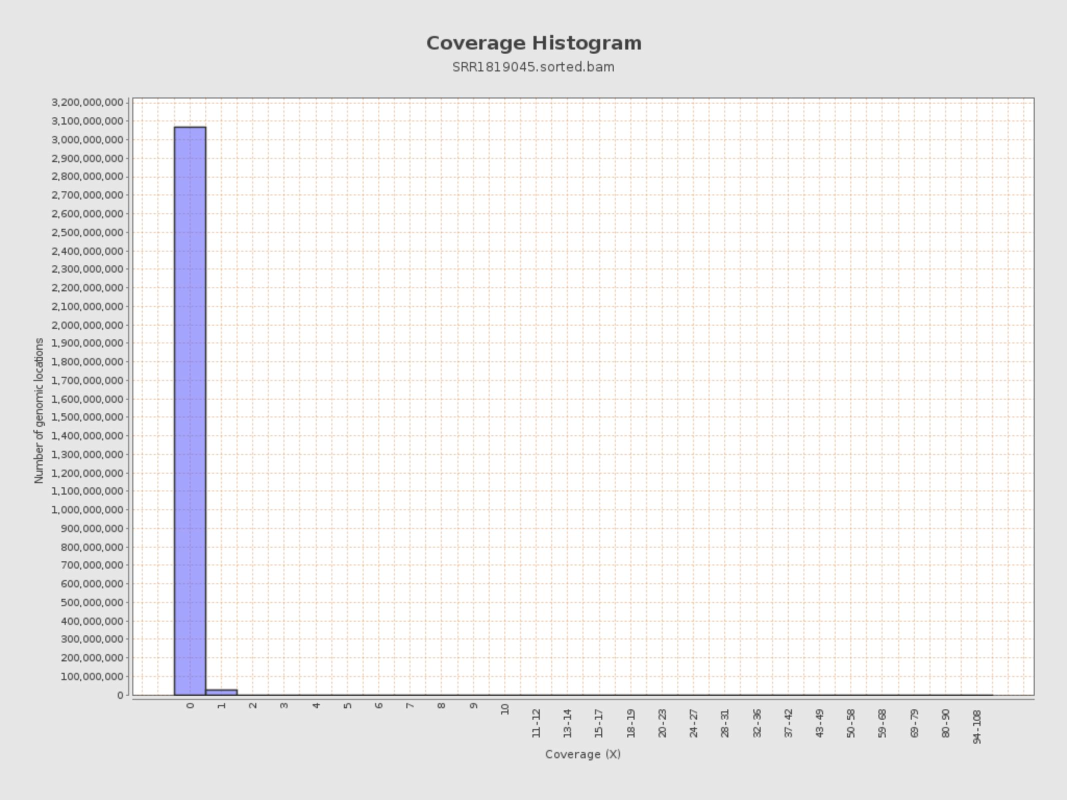
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2970964	0.0119	0.1374
chr2	243199373	1660264	0.0068	0.1072
chr3	198022430	1855815	0.0094	0.1004
chr4	191154276	1751652	0.0092	0.1043
chr5	180915260	1311504	0.0072	0.0884
chr6	171115067	1294087	0.0076	0.0921
chr7	159138663	1337324	0.0084	0.1016

chr8	146364022	1994208	0.0136	0.1253
chr9	141213431	923084	0.0065	0.0975
chr10	135534747	1463739	0.0108	0.1276
chr11	135006516	949003	0.007	0.0951
chr12	133851895	1440756	0.0108	0.107
chr13	115169878	874529	0.0076	0.0898
chr14	107349540	688613	0.0064	0.0861
chr15	102531392	641854	0.0063	0.0816
chr16	90354753	909000	0.0101	0.1083
chr17	81195210	664036	0.0082	0.0943
chr18	78077248	619769	0.0079	0.1468
chr19	59128983	588170	0.0099	0.1217
chr20	63025520	832184	0.0132	0.1219
chr21	48129895	382803	0.008	0.0972
chr22	51304566	389673	0.0076	0.09
chrMT	16571	2373	0.1432	0.369
chrX	155270560	1778680	0.0115	0.1149
chrY	59373566	98201	0.0017	0.0525

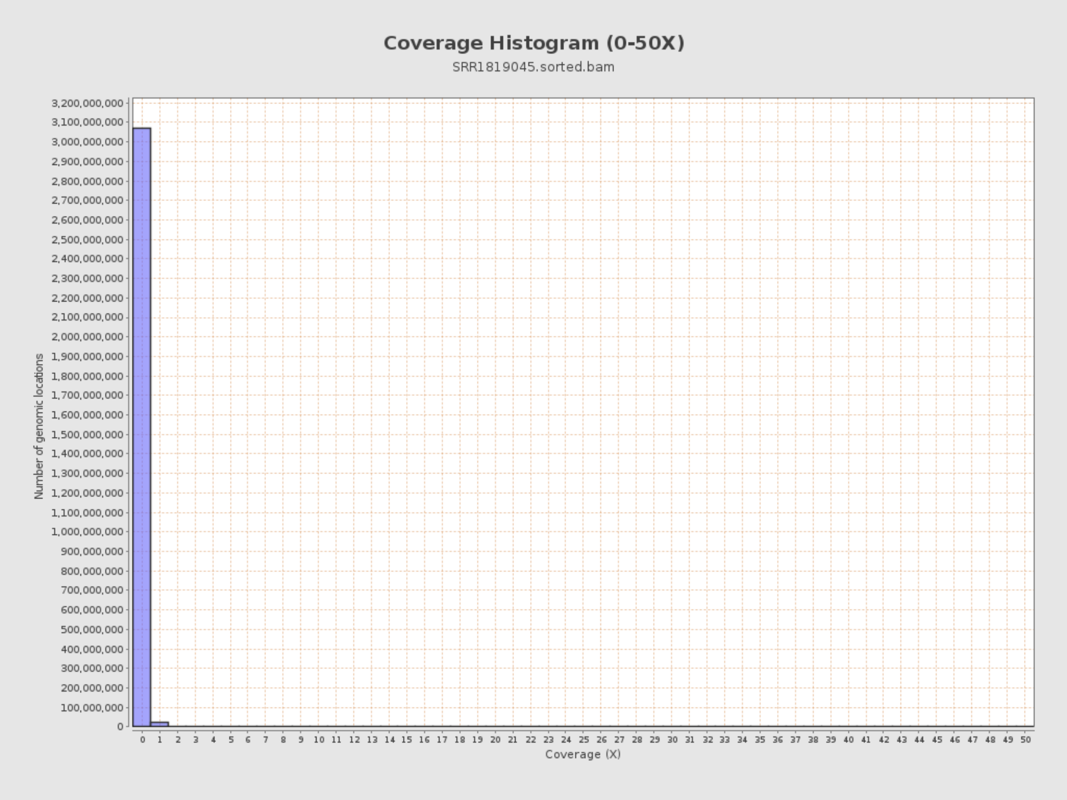
3. Results : Coverage across reference



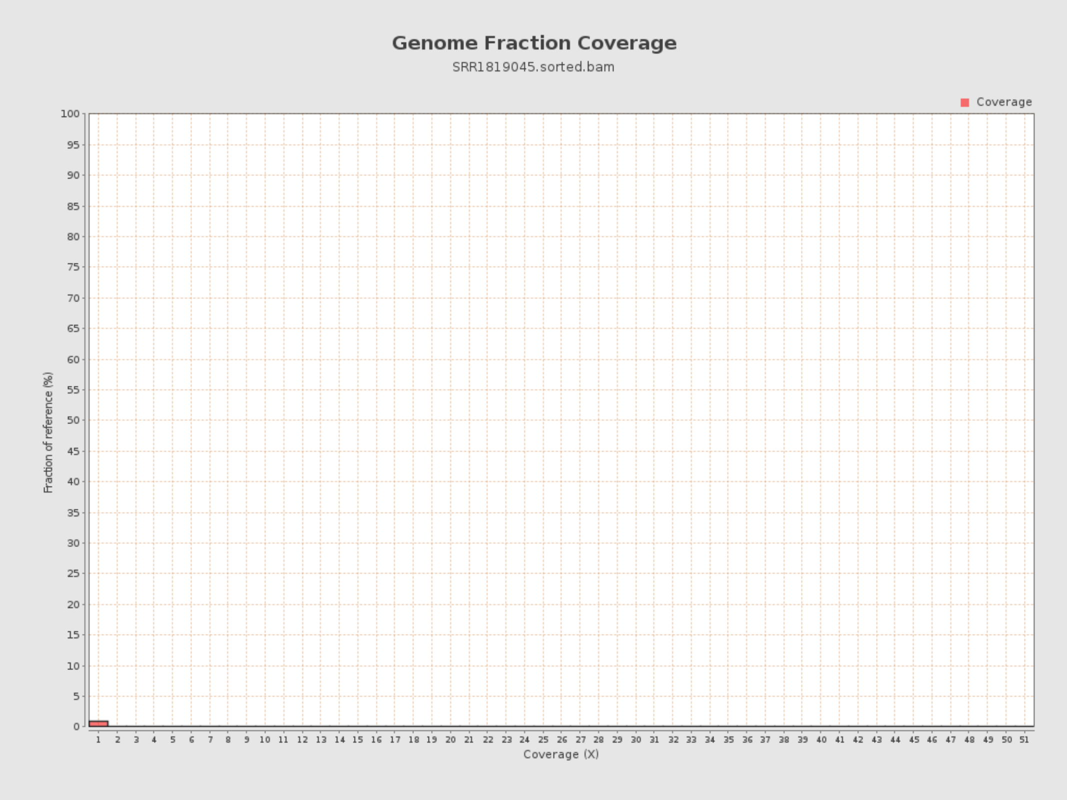
4. Results : Coverage Histogram



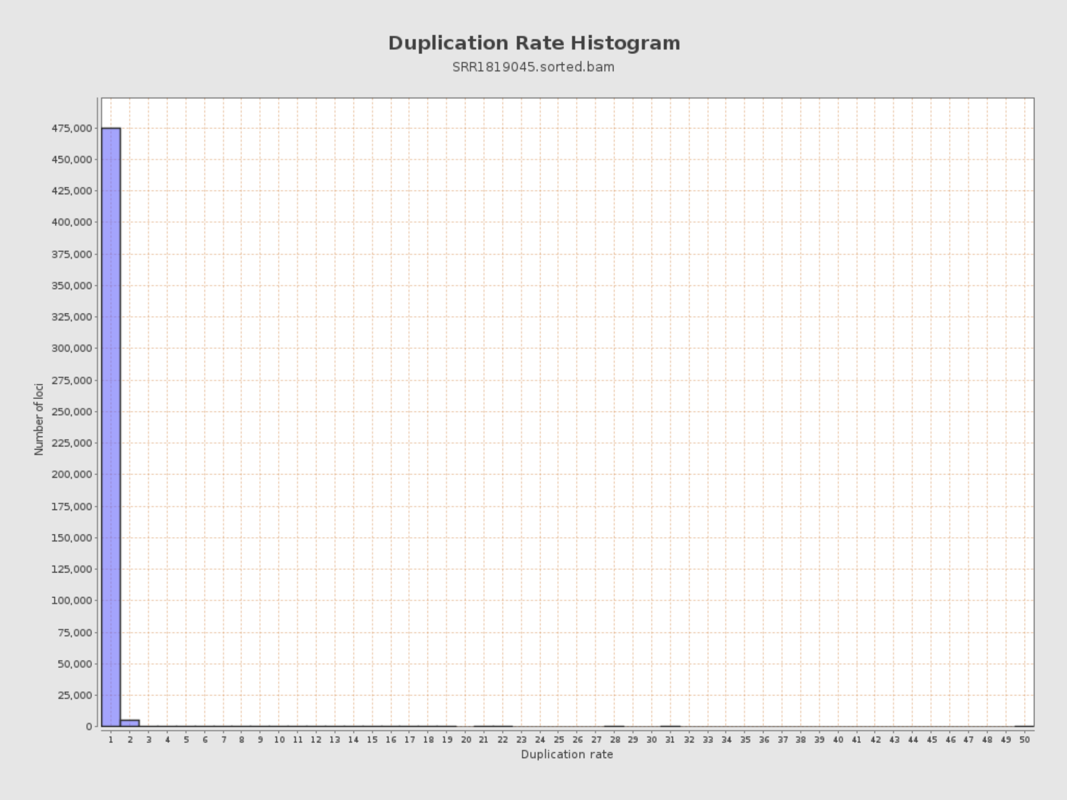
5. Results : Coverage Histogram (0-50X)



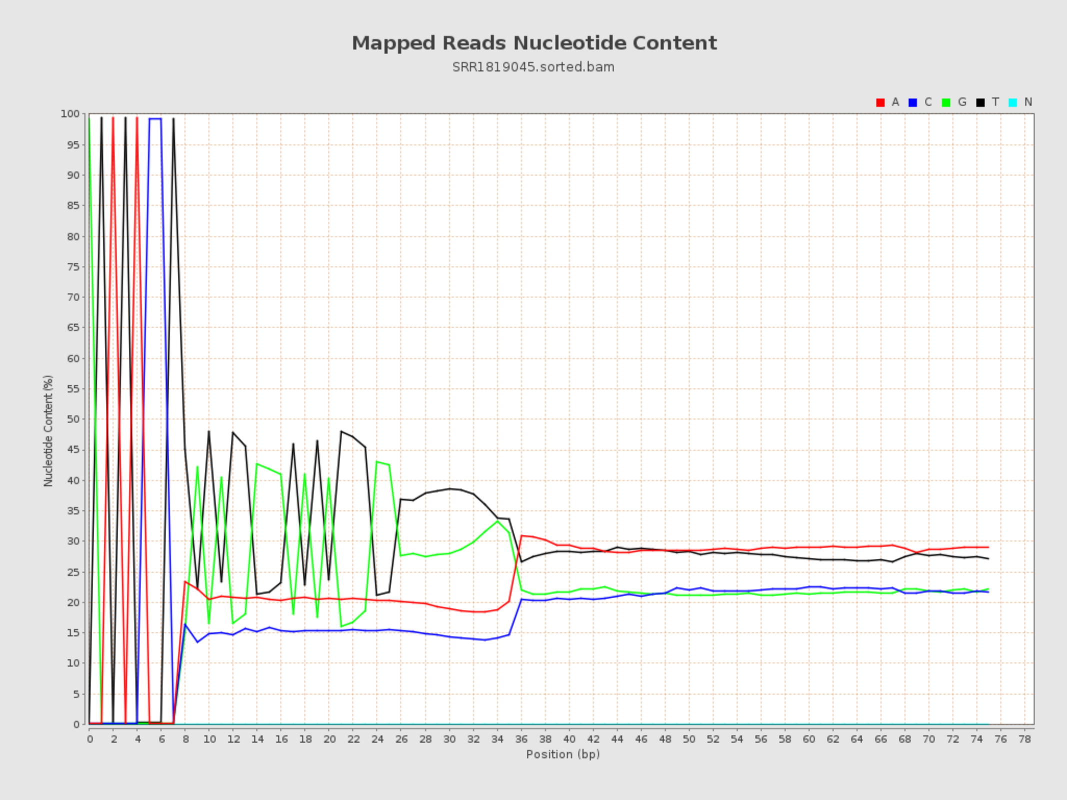
6. Results : Genome Fraction Coverage



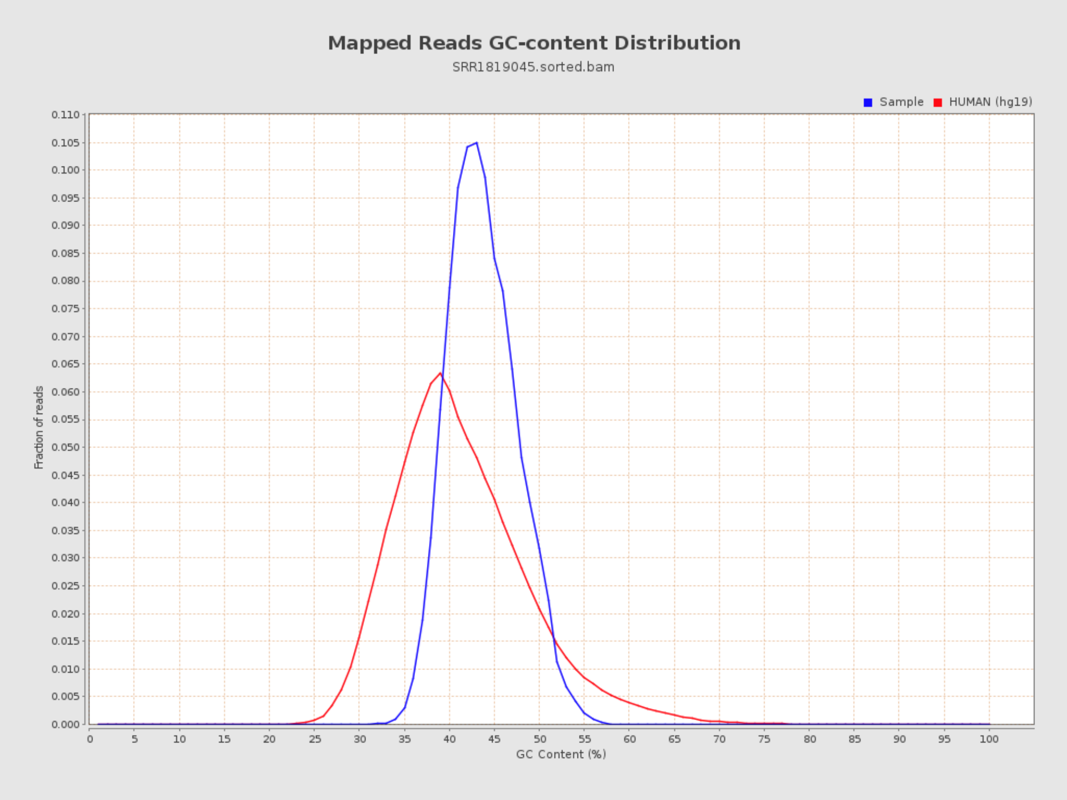
7. Results : Duplication Rate Histogram



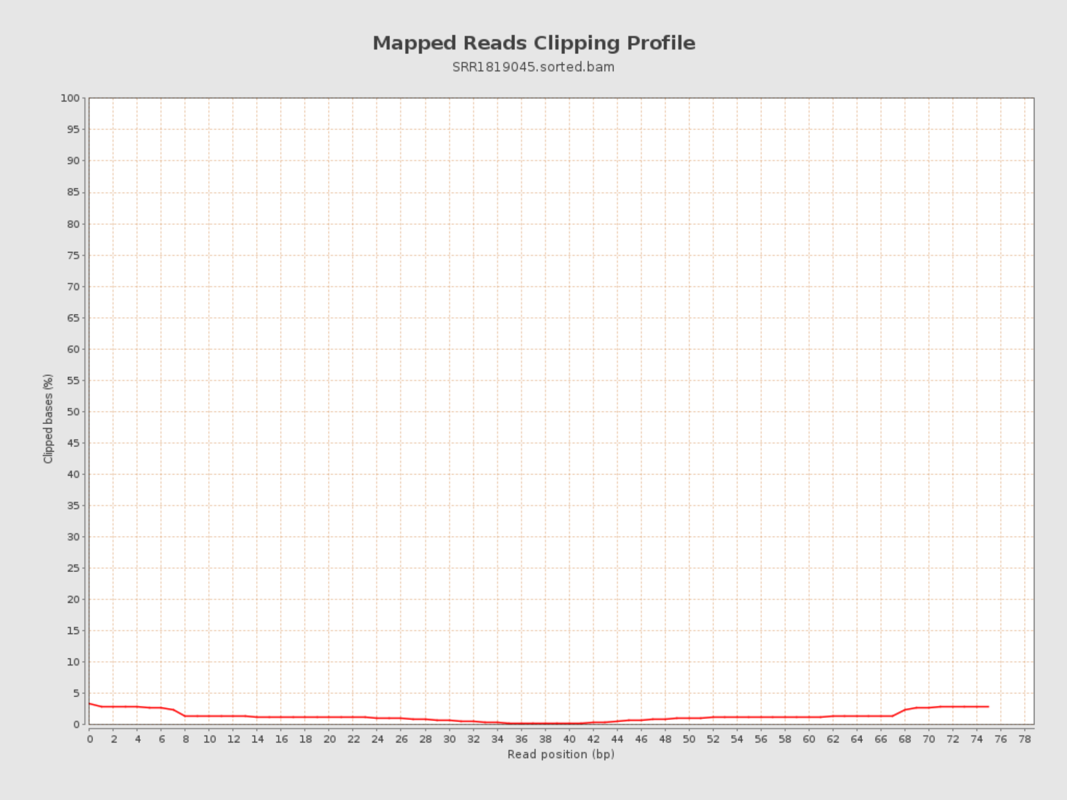
8. Results : Mapped Reads Nucleotide Content



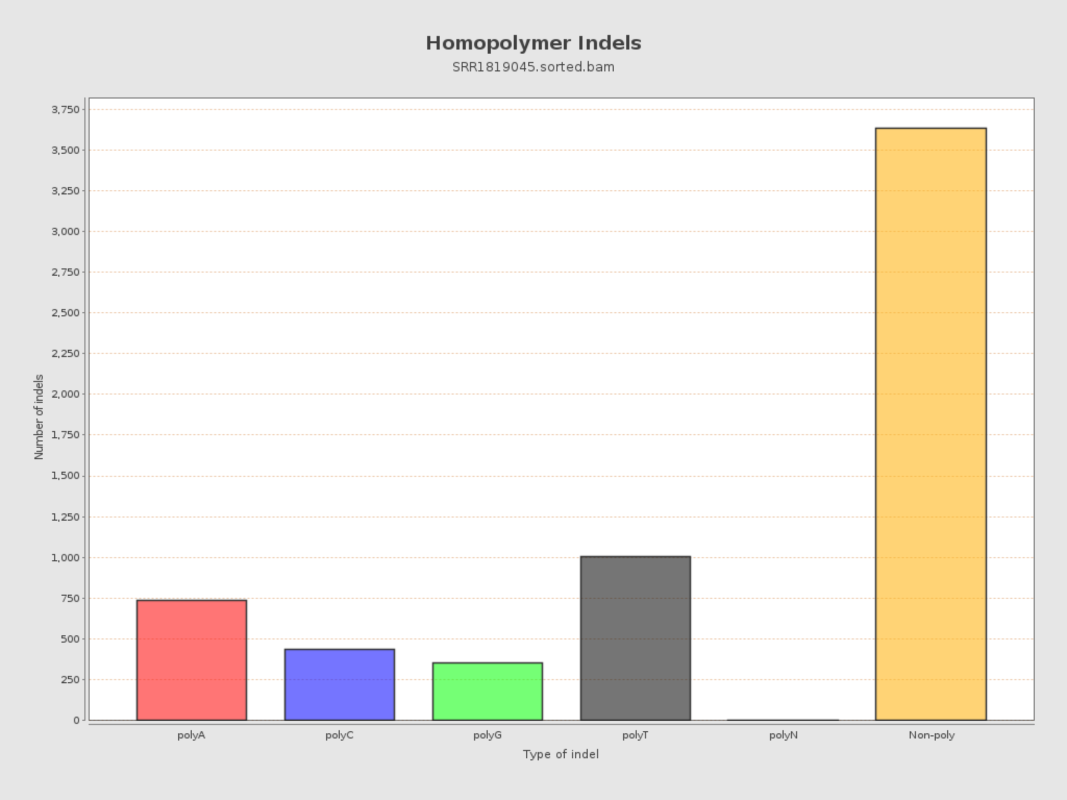
9. Results : Mapped Reads GC-content Distribution



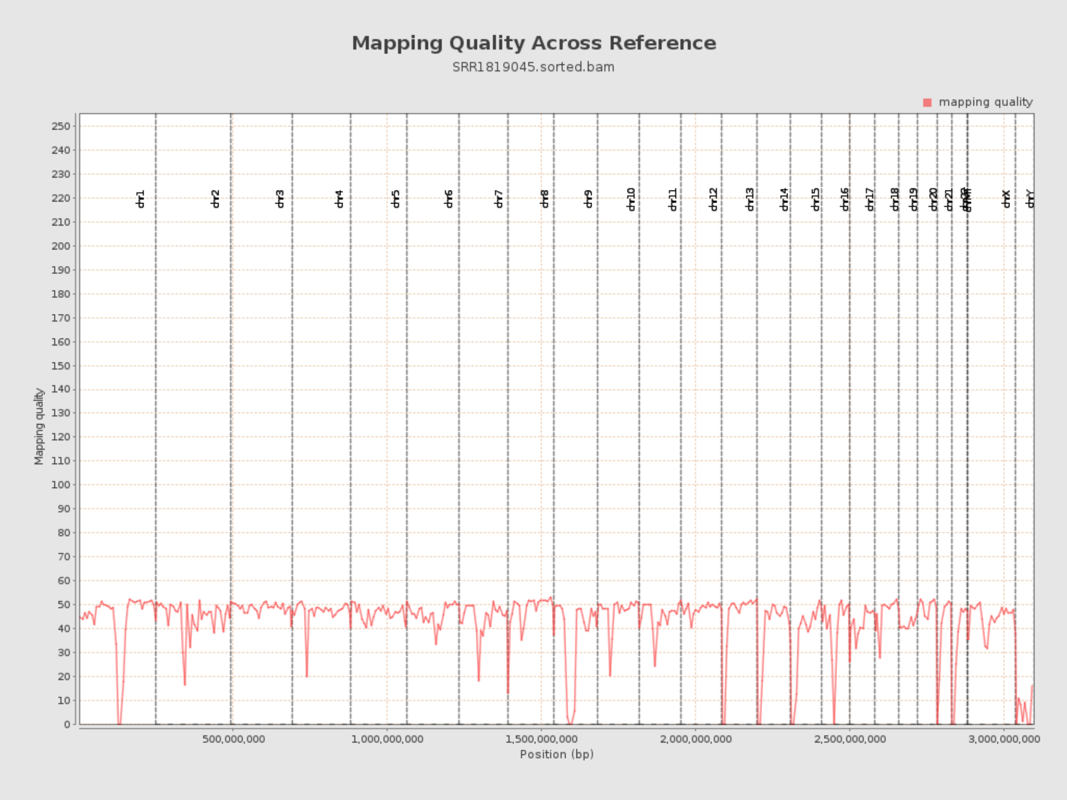
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram