Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:23:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080725.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_SRR3080725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080725.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,360,324
Mapped reads	1,184,220 / 87.05%
Unmapped reads	176,104 / 12.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,957 / 1.39%
Read min/max/mean length	30 / 76 / 76.49
Duplicated reads (estimated)	56,025 / 4.12%
Duplication rate	2.82%
Clipped reads	495,297 / 36.41%

2.2. ACGT Content

Number/percentage of A's	23,700,089 / 29.39%
Number/percentage of C's	15,326,817 / 19%
Number/percentage of T's	23,754,118 / 29.45%
Number/percentage of G's	17,867,289 / 22.15%
Number/percentage of N's	1,185 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.5019

2.4. Mapping Quality

Mean Mapping Quality	42.21

2.5. Mismatches and indels

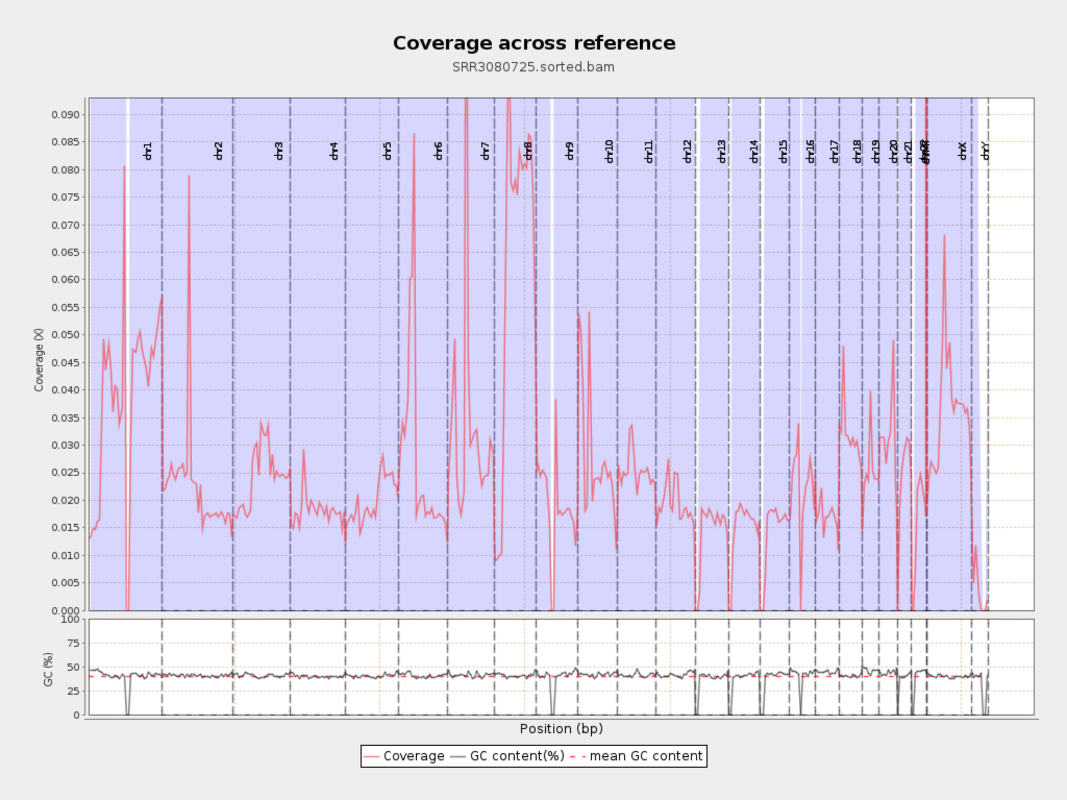
General error rate	0.92%
Mismatches	730,395
Insertions	7,434
Mapped reads with at least one insertion	0.62%
Deletions	16,141
Mapped reads with at least one deletion	1.35%
Homopolymer indels	44.3%

2.6. Chromosome stats

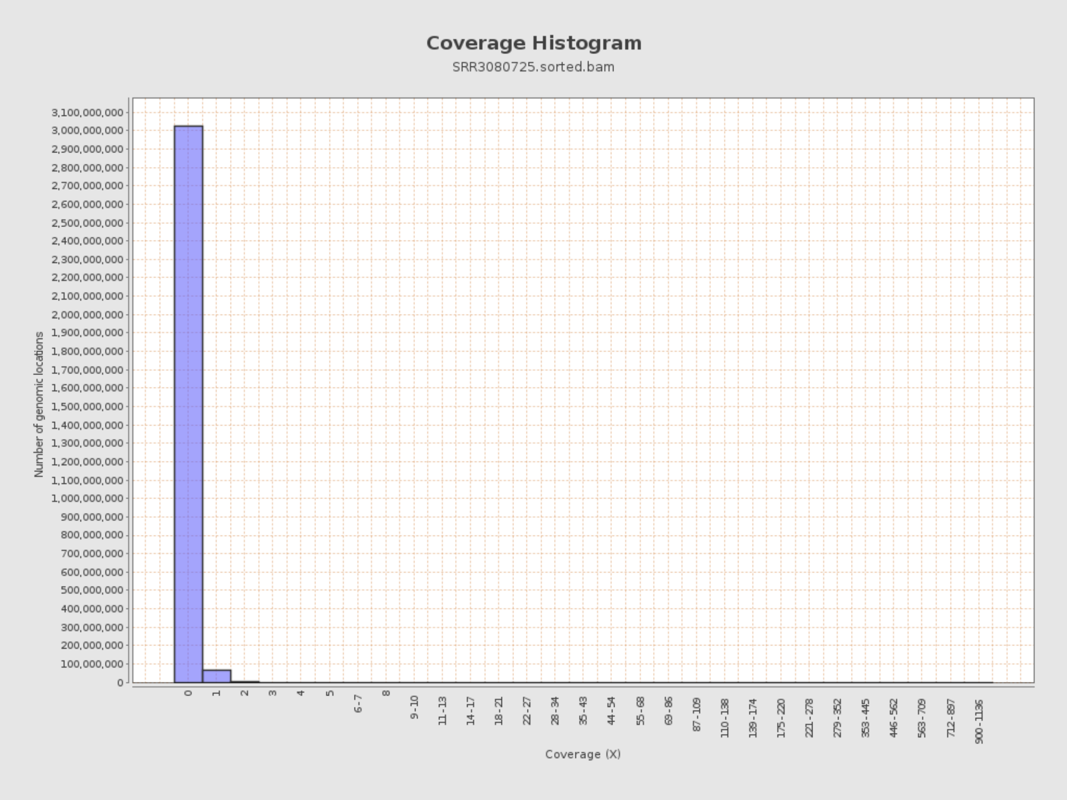
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9484634	0.0381	0.8593
chr2	243199373	5495674	0.0226	0.3887
chr3	198022430	4816575	0.0243	0.1669
chr4	191154276	3474651	0.0182	0.1543
chr5	180915260	3636417	0.0201	0.1562
chr6	171115067	4737158	0.0277	0.3259
chr7	159138663	5505326	0.0346	1.4642

chr8	146364022	9218320	0.063	0.6811
chr9	141213431	2609552	0.0185	0.3356
chr10	135534747	3837056	0.0283	0.3424
chr11	135006516	3410566	0.0253	0.2967
chr12	133851895	2594099	0.0194	0.156
chr13	115169878	1627376	0.0141	0.1243
chr14	107349540	1572210	0.0146	0.1762
chr15	102531392	1434126	0.014	0.1278
chr16	90354753	2017874	0.0223	0.1967
chr17	81195210	1365247	0.0168	0.1751
chr18	78077248	2521248	0.0323	0.5885
chr19	59128983	1514322	0.0256	0.4928
chr20	63025520	1976651	0.0314	0.2027
chr21	48129895	1162020	0.0241	0.1807
chr22	51304566	774968	0.0151	0.1291
chrMT	16571	44093	2.6609	2.26
chrX	155270560	5623401	0.0362	0.2532
chrY	59373566	224242	0.0038	0.1038

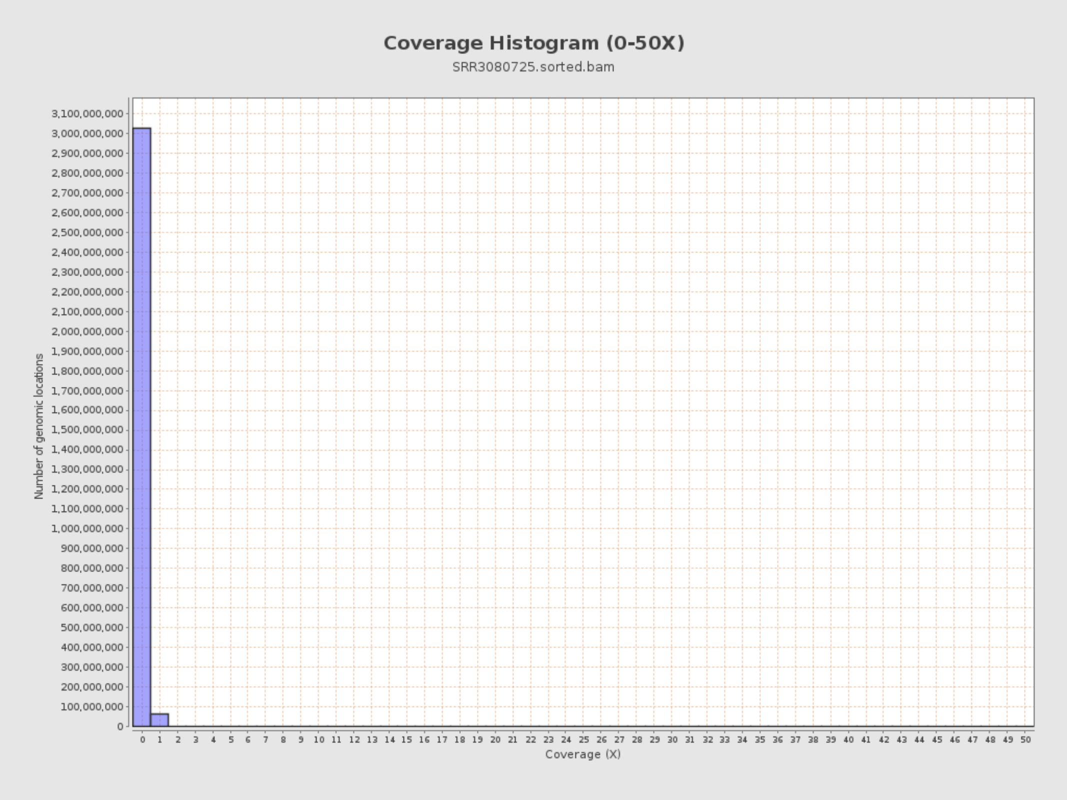
3. Results : Coverage across reference



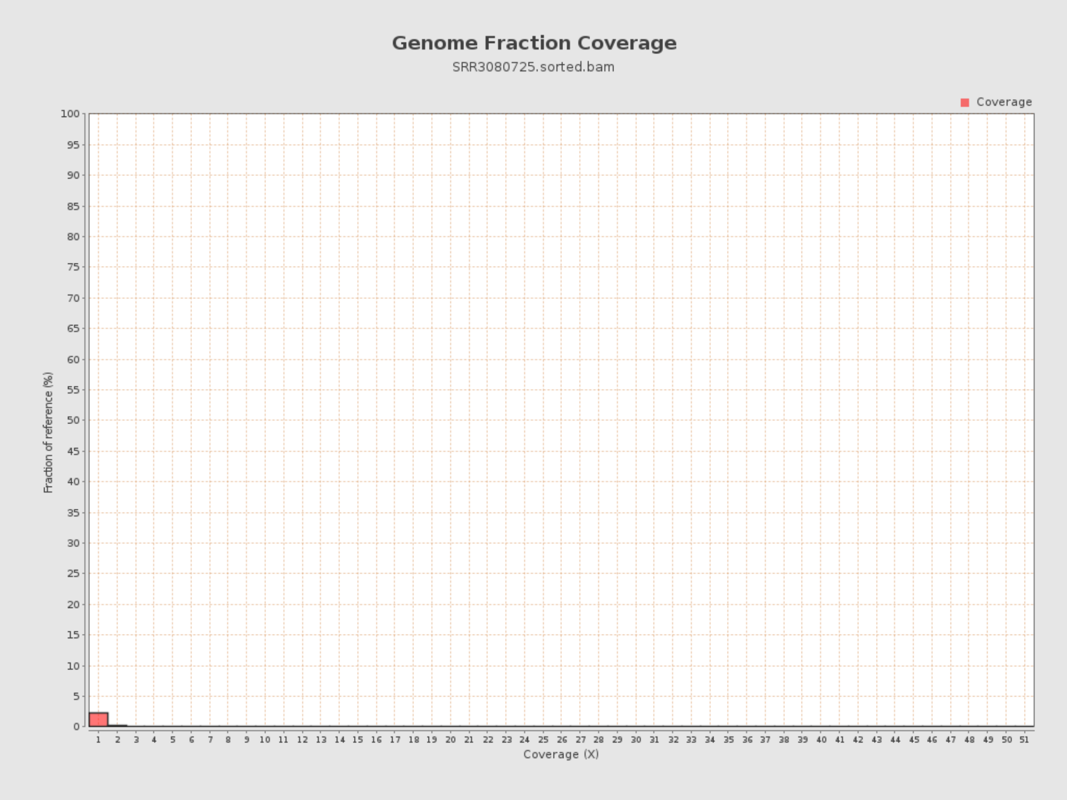
4. Results : Coverage Histogram



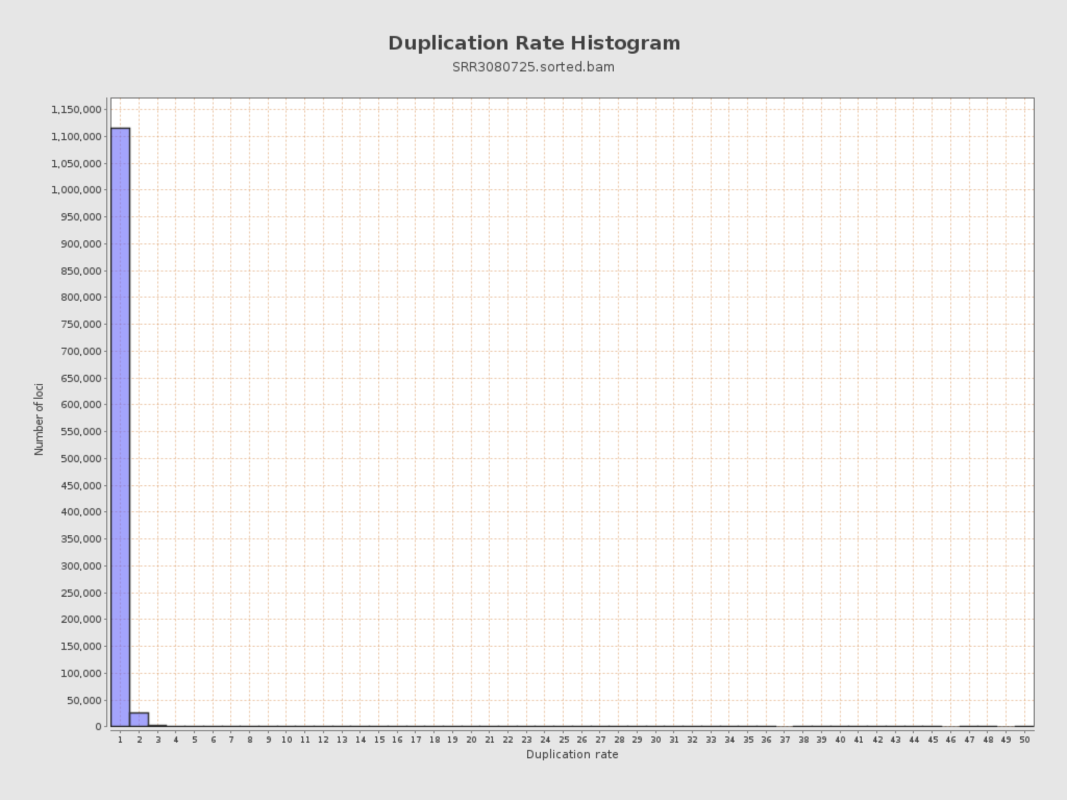
5. Results : Coverage Histogram (0-50X)



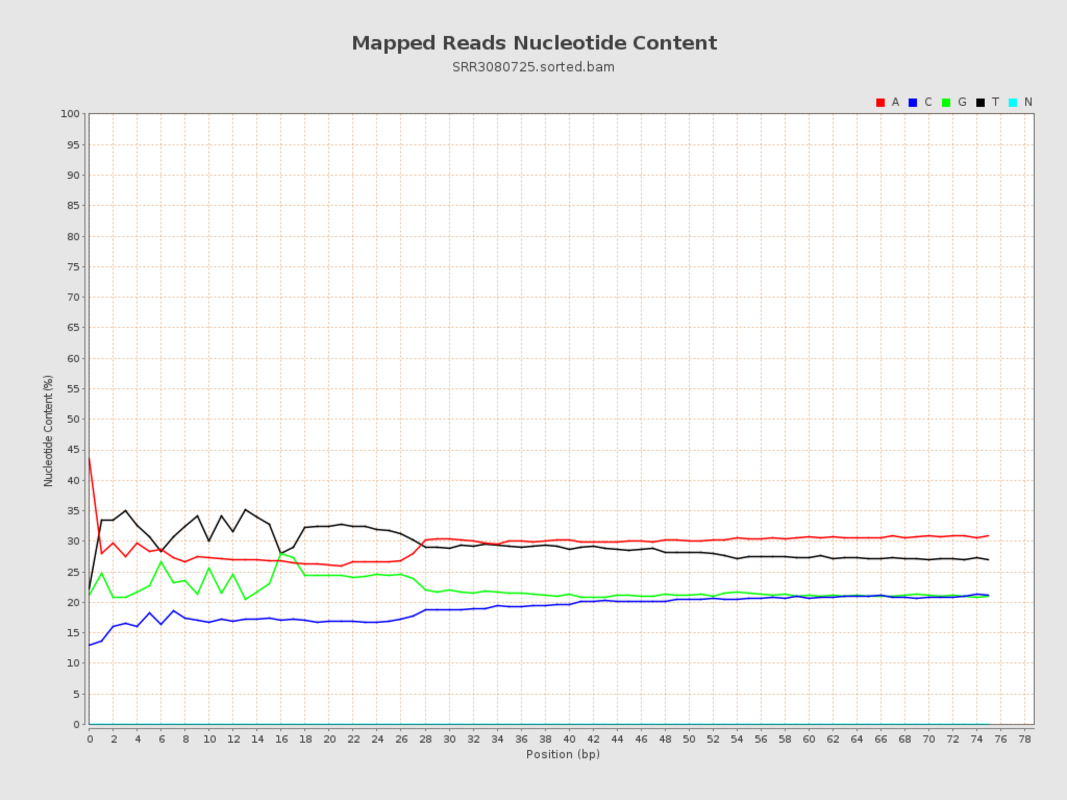
6. Results : Genome Fraction Coverage



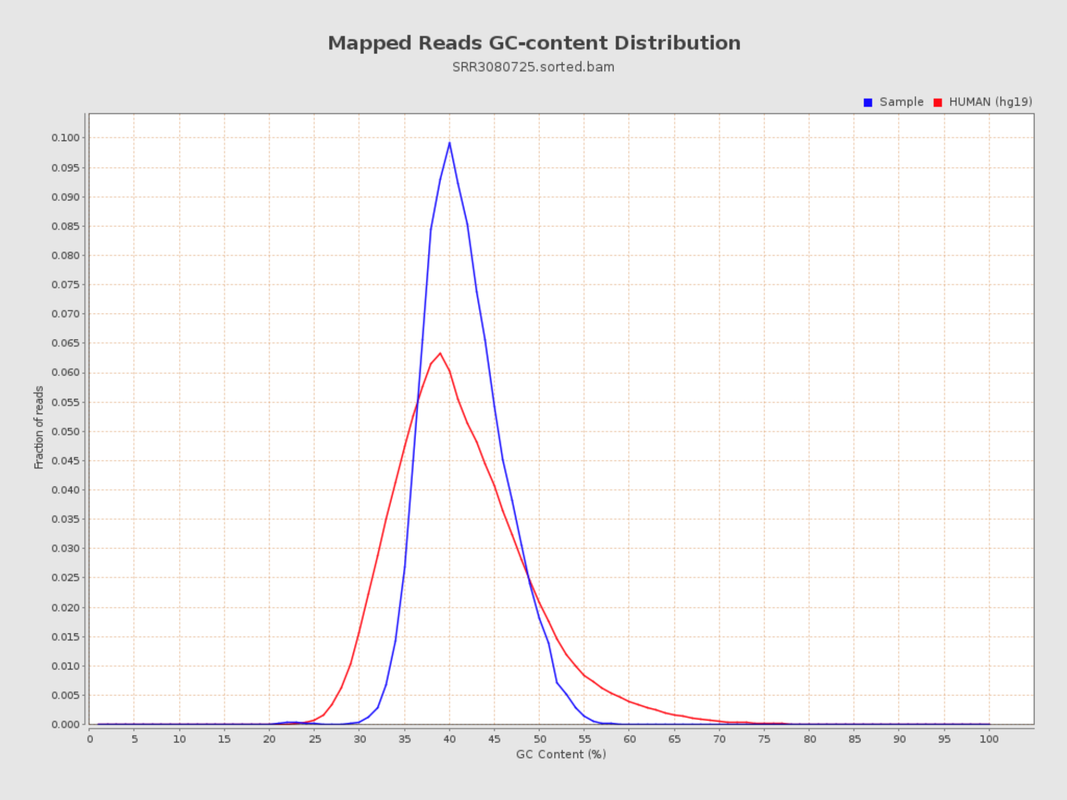
7. Results : Duplication Rate Histogram



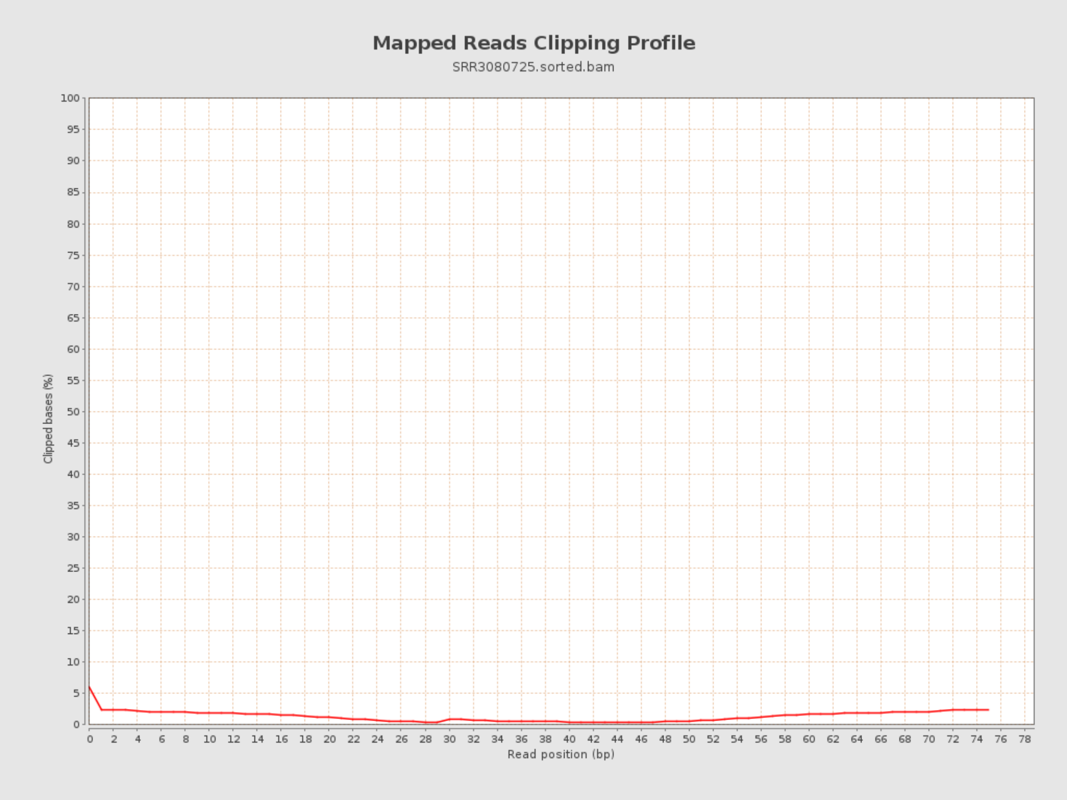
8. Results : Mapped Reads Nucleotide Content



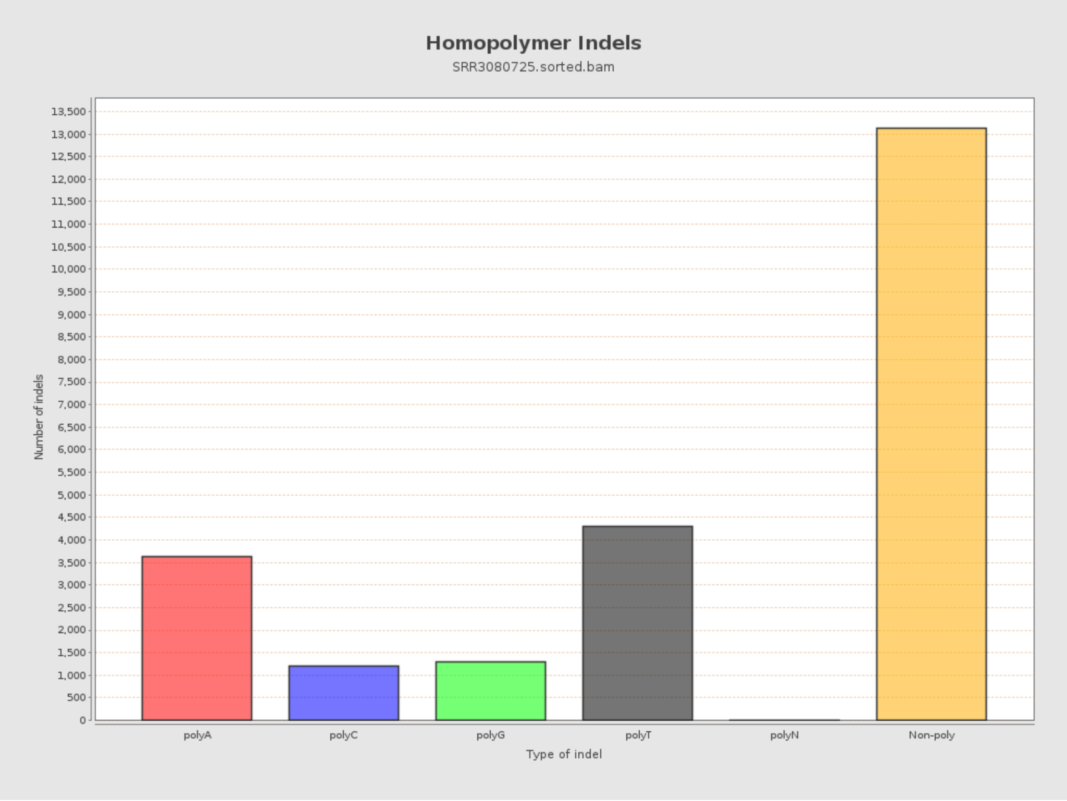
9. Results : Mapped Reads GC-content Distribution



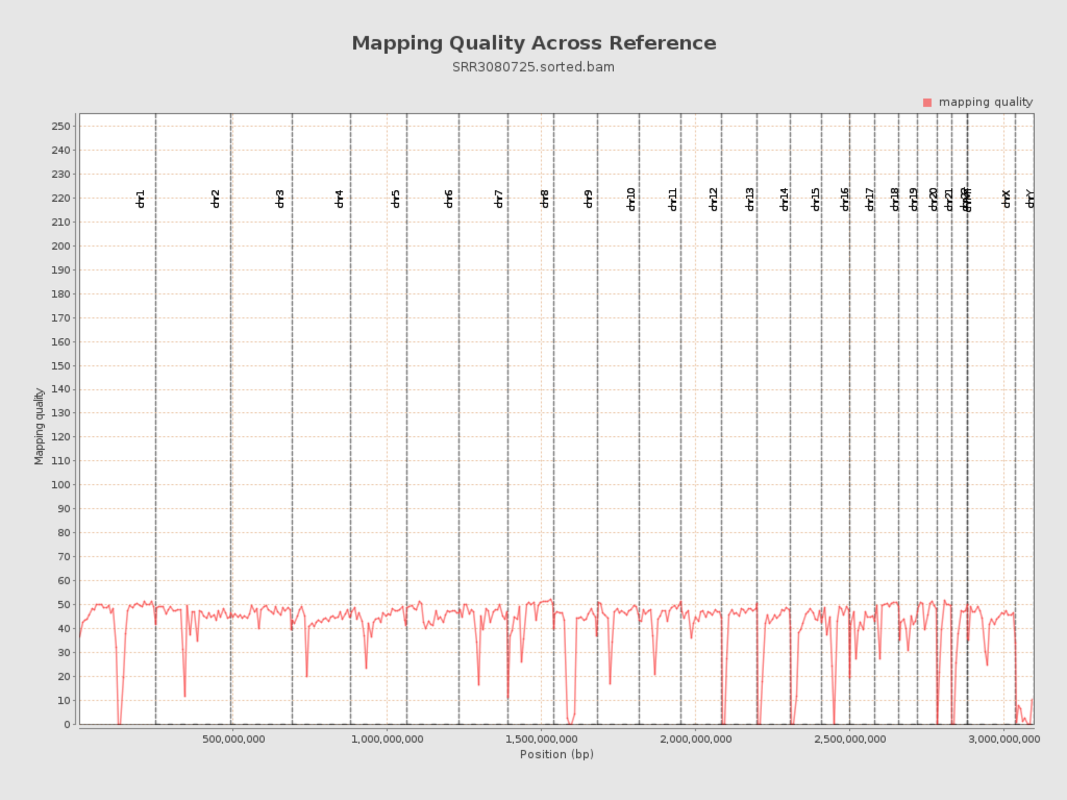
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram