Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:55:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717037.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_SRR9717037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:55:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	739,235
Mapped reads	536,612 / 72.59%
Unmapped reads	202,623 / 27.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,560 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	9,638 / 1.3%
Duplication rate	1.29%
Clipped reads	536,990 / 72.64%

2.2. ACGT Content

Number/percentage of A's	7,667,367 / 25.32%
Number/percentage of C's	5,959,186 / 19.68%
Number/percentage of T's	9,462,740 / 31.25%
Number/percentage of G's	7,188,719 / 23.74%
Number/percentage of N's	424 / 0%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1238

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

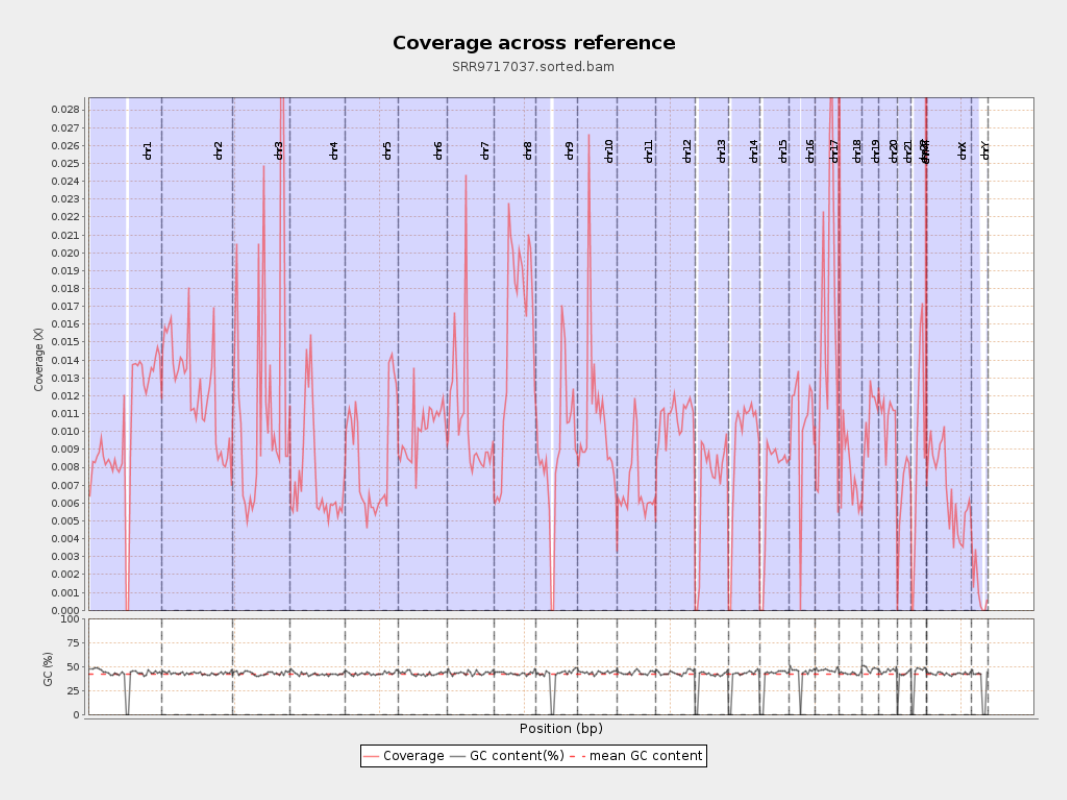
General error rate	0.52%
Mismatches	152,522
Insertions	2,041
Mapped reads with at least one insertion	0.38%
Deletions	5,645
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.66%

2.6. Chromosome stats

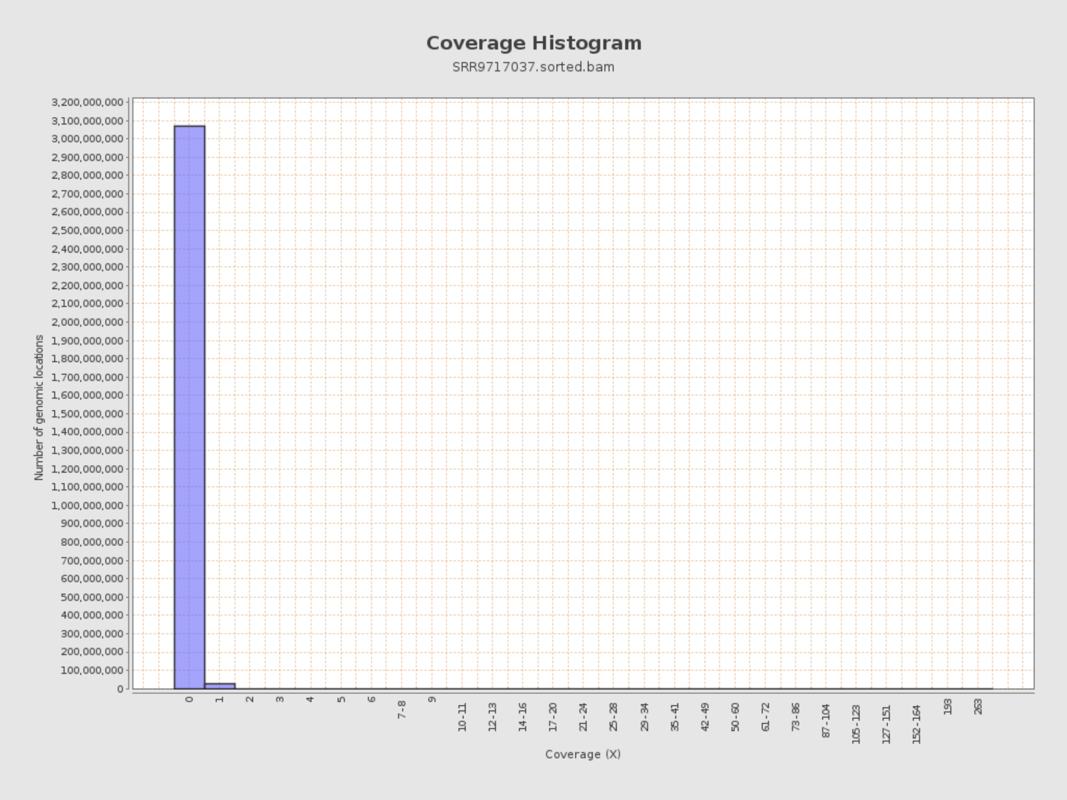
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2500658	0.01	0.1331
chr2	243199373	3001356	0.0123	0.1585
chr3	198022430	2453077	0.0124	0.1209
chr4	191154276	1426989	0.0075	0.0914
chr5	180915260	1543757	0.0085	0.0955
chr6	171115067	1722128	0.0101	0.1087
chr7	159138663	1703143	0.0107	0.2176

chr8	146364022	2248120	0.0154	0.1358
chr9	141213431	1241713	0.0088	0.103
chr10	135534747	1455814	0.0107	0.1653
chr11	135006516	913202	0.0068	0.093
chr12	133851895	1431412	0.0107	0.1109
chr13	115169878	807529	0.007	0.0865
chr14	107349540	976882	0.0091	0.0987
chr15	102531392	723948	0.0071	0.0874
chr16	90354753	941241	0.0104	0.1098
chr17	81195210	1287207	0.0159	0.1322
chr18	78077248	712773	0.0091	0.1212
chr19	59128983	627010	0.0106	0.1386
chr20	63025520	675355	0.0107	0.1089
chr21	48129895	307668	0.0064	0.0837
chr22	51304566	444972	0.0087	0.0968
chrMT	16571	16707	1.0082	1.2207
chrX	155270560	1057610	0.0068	0.0914
chrY	59373566	67119	0.0011	0.0383

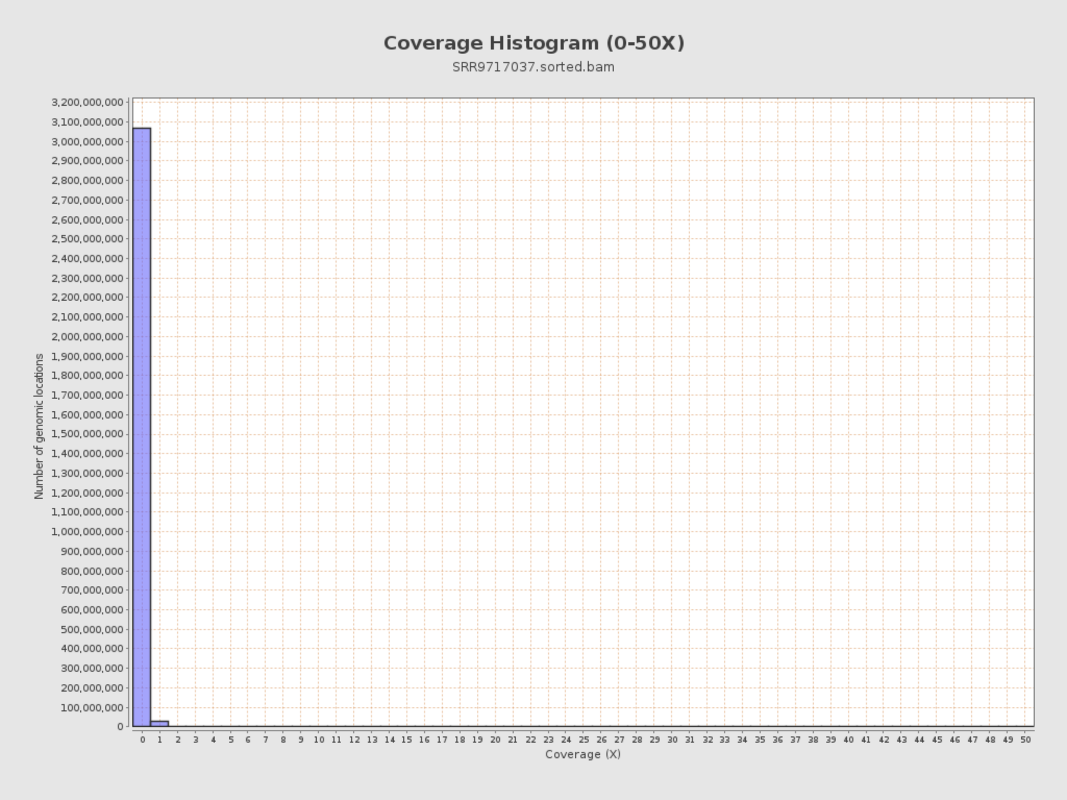
3. Results : Coverage across reference



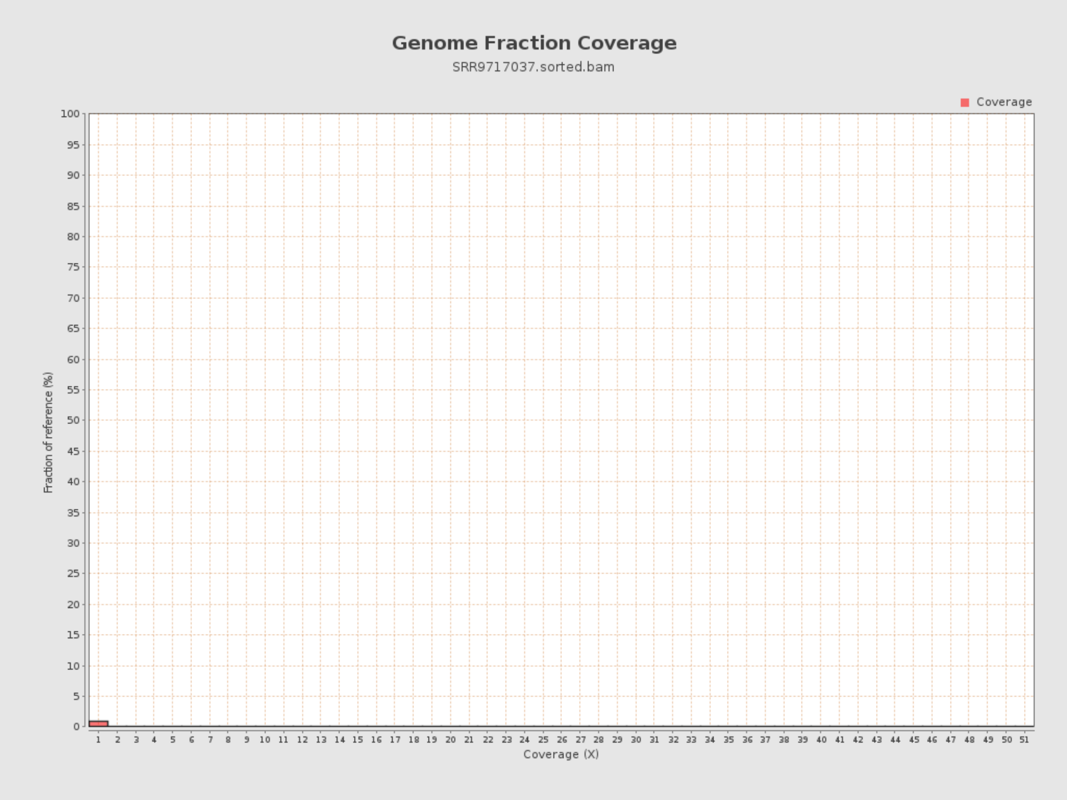
4. Results : Coverage Histogram



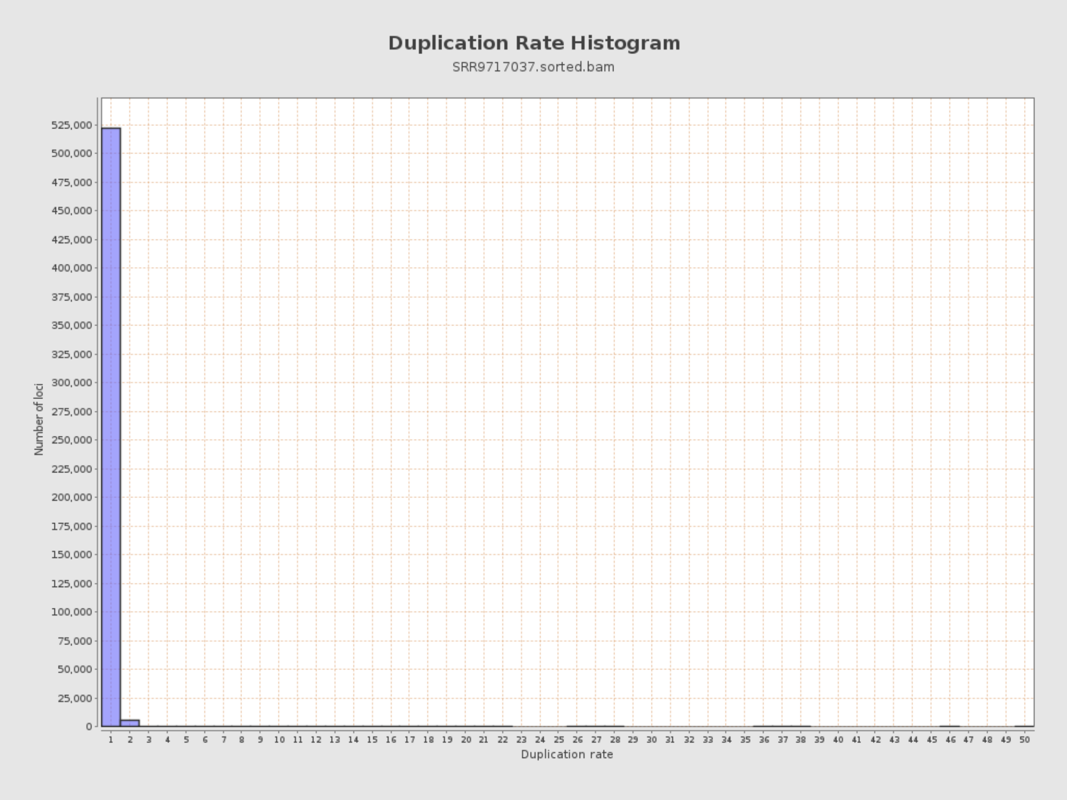
5. Results : Coverage Histogram (0-50X)



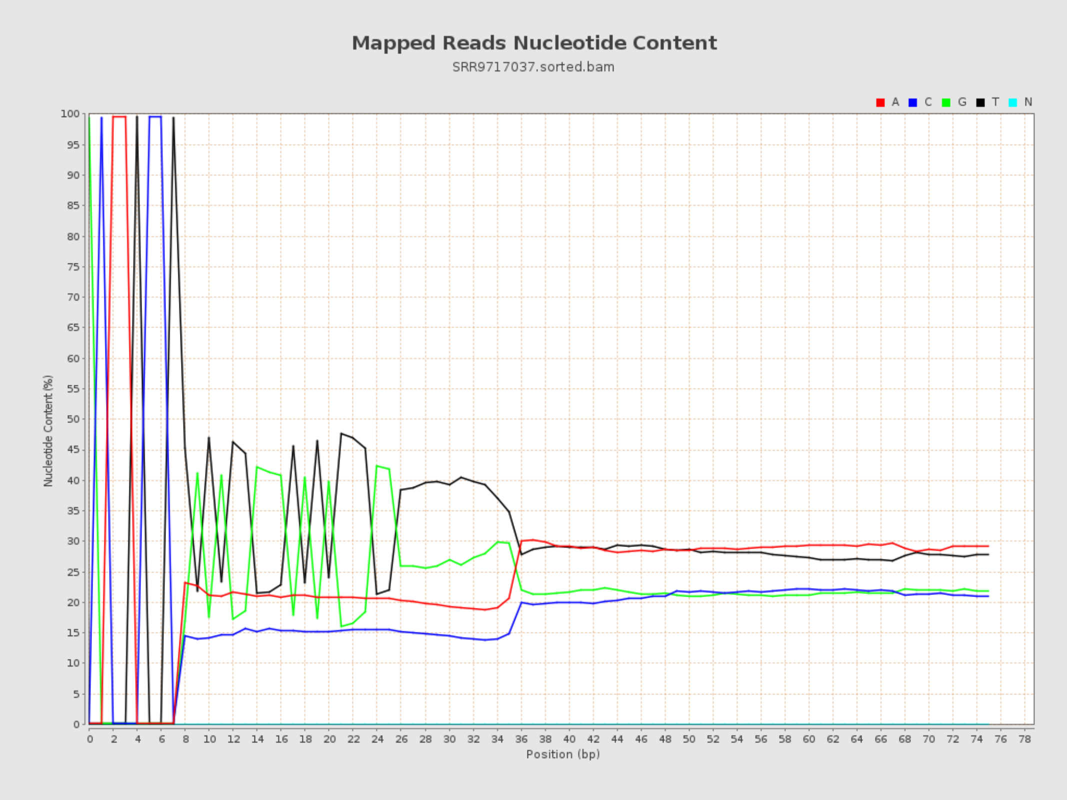
6. Results : Genome Fraction Coverage



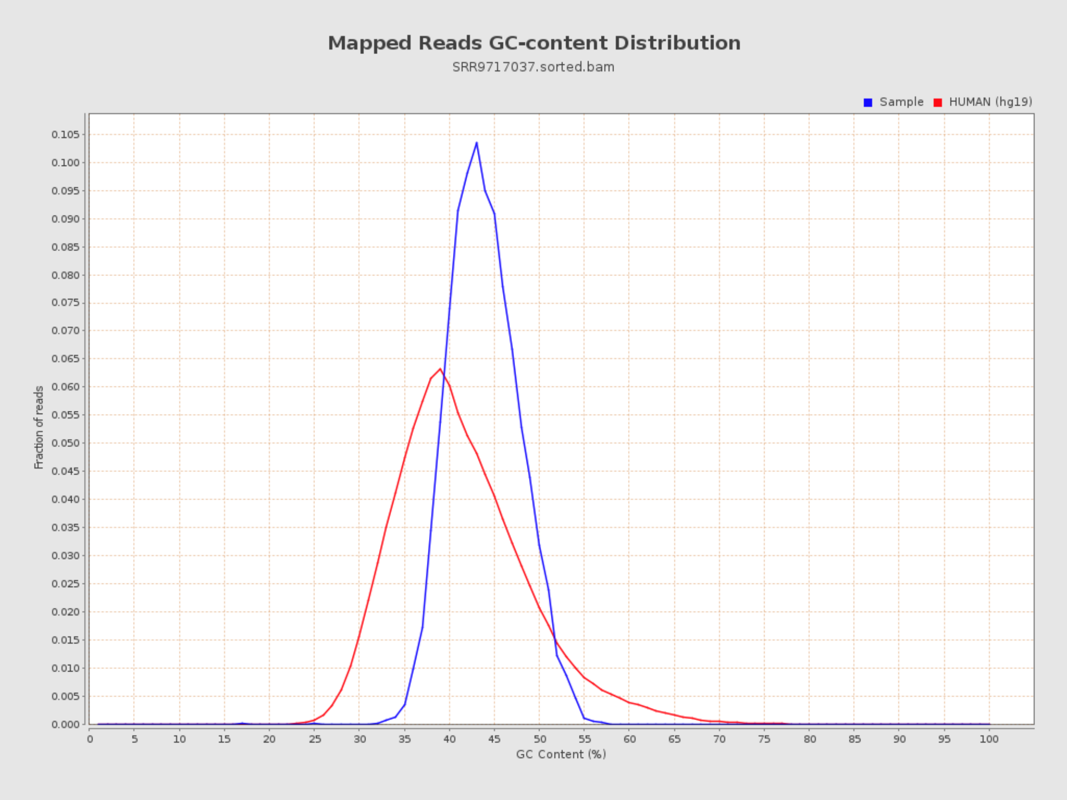
7. Results : Duplication Rate Histogram



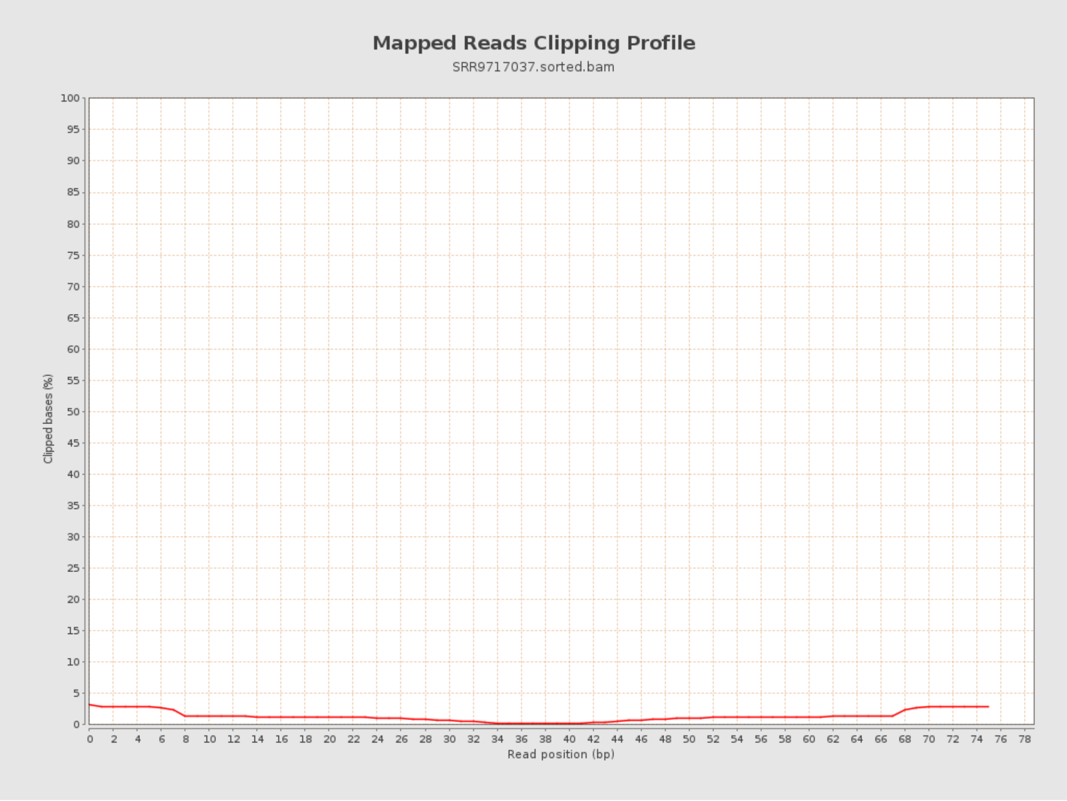
8. Results : Mapped Reads Nucleotide Content



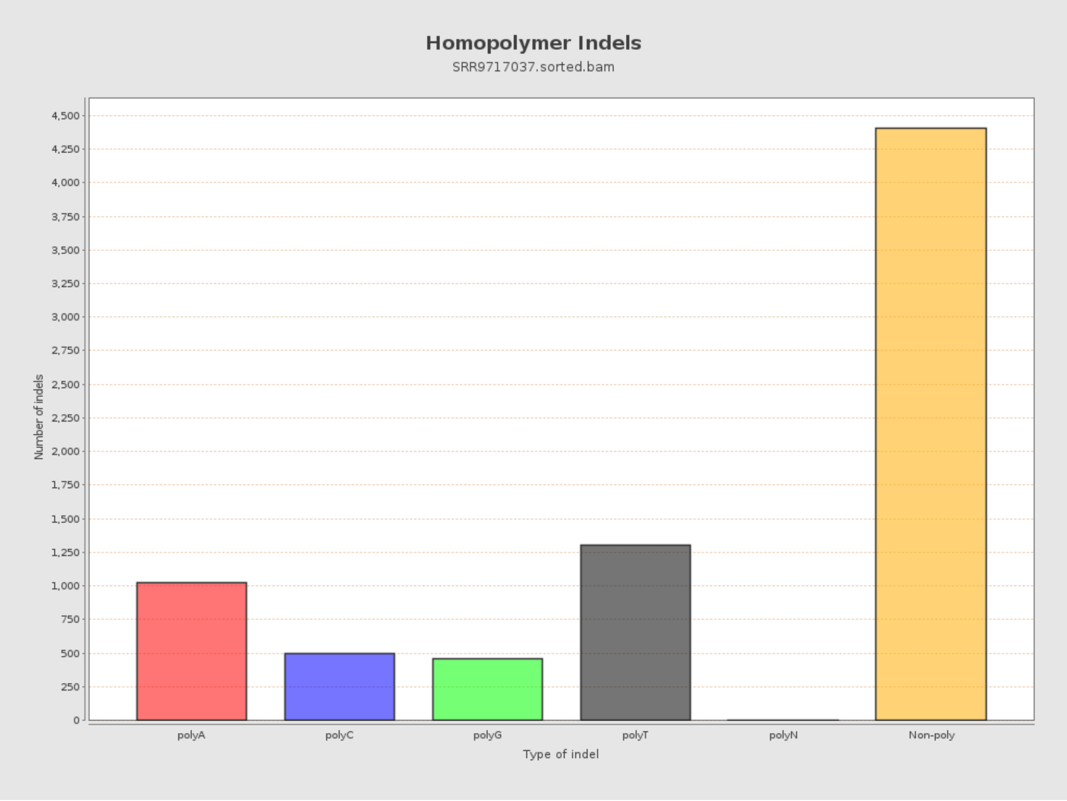
9. Results : Mapped Reads GC-content Distribution



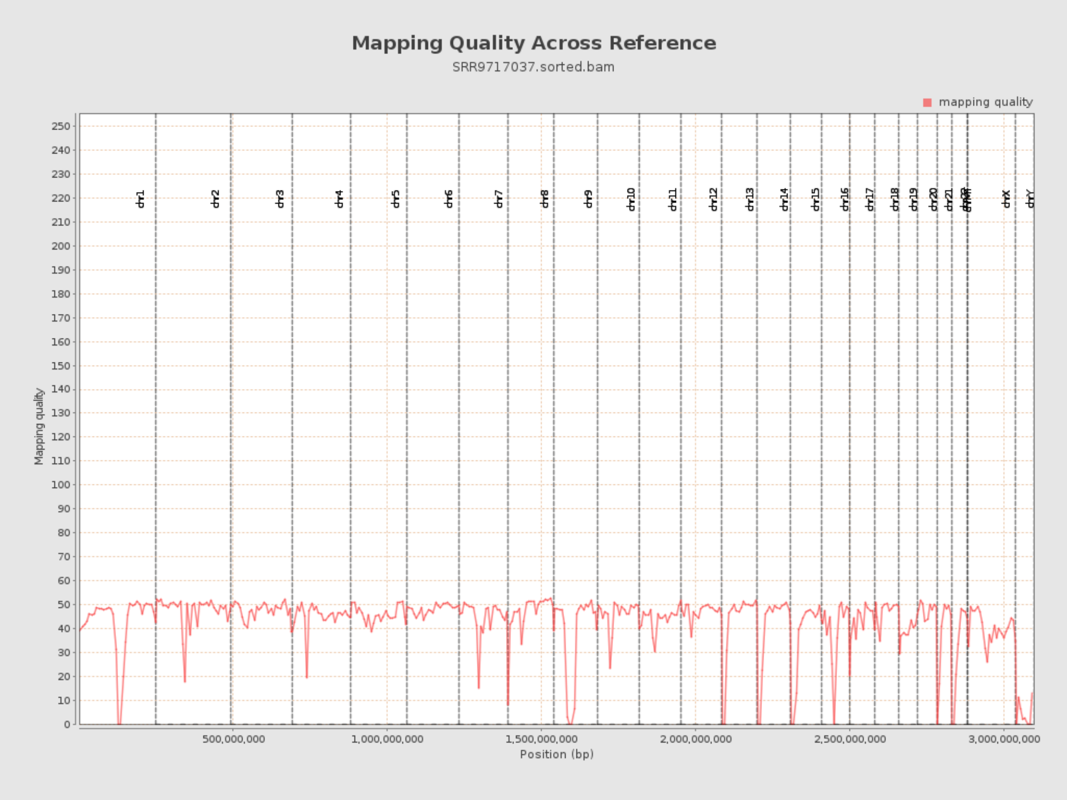
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram