Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:06:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717055.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_SRR9717055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:06:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	757,209
Mapped reads	583,964 / 77.12%
Unmapped reads	173,245 / 22.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,357 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,562 / 1.26%
Duplication rate	1.15%
Clipped reads	585,289 / 77.3%

2.2. ACGT Content

Number/percentage of A's	7,730,012 / 23.96%
Number/percentage of C's	6,725,272 / 20.85%
Number/percentage of T's	9,678,834 / 30%
Number/percentage of G's	8,124,259 / 25.18%
Number/percentage of N's	864 / 0%
GC Percentage	46.03%

2.3. Coverage

Mean	0.0104

Standard Deviation	0.1202

2.4. Mapping Quality

Mean Mapping Quality	38.75

2.5. Mismatches and indels

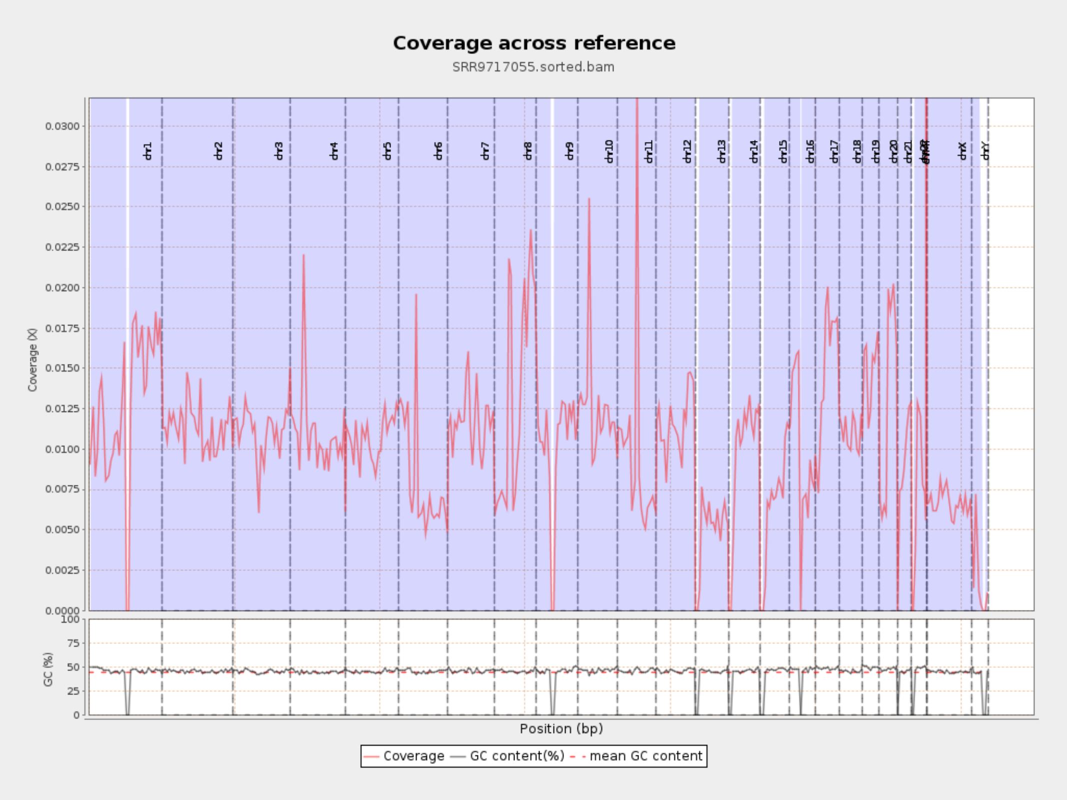
General error rate	0.56%
Mismatches	173,984
Insertions	2,555
Mapped reads with at least one insertion	0.43%
Deletions	5,431
Mapped reads with at least one deletion	0.92%
Homopolymer indels	33.47%

2.6. Chromosome stats

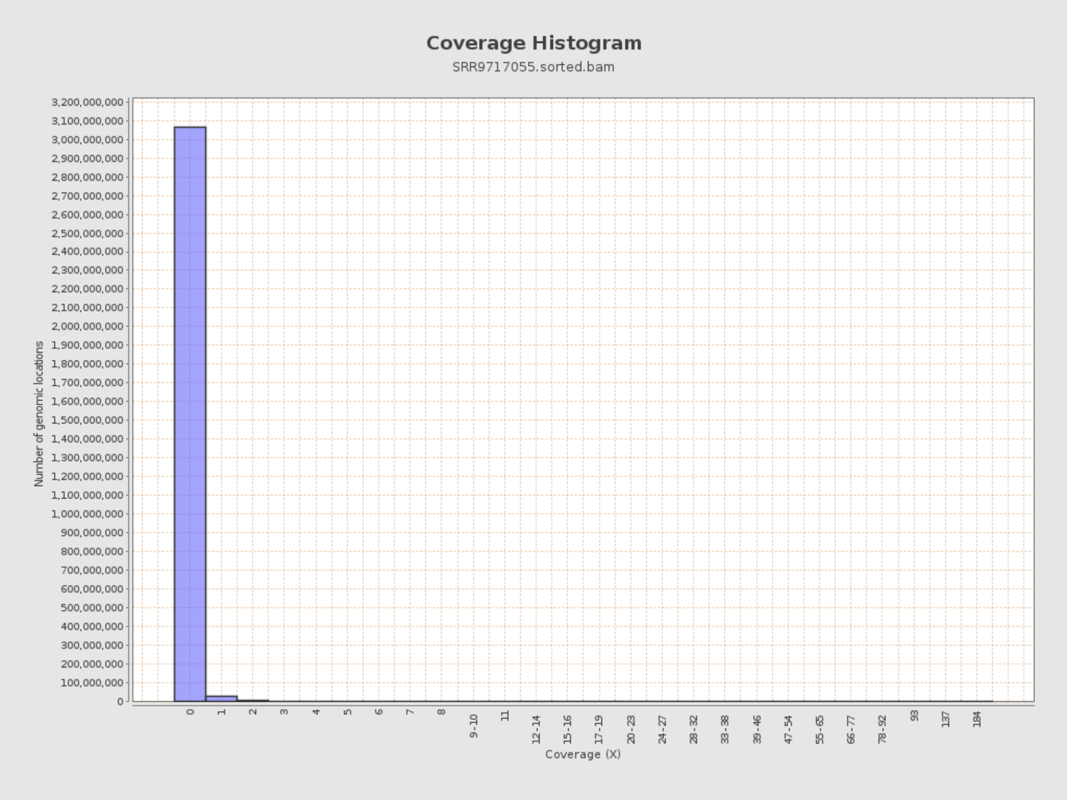
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3165641	0.0127	0.1395
chr2	243199373	2769705	0.0114	0.1455
chr3	198022430	2186224	0.011	0.114
chr4	191154276	2100390	0.011	0.1206
chr5	180915260	1931762	0.0107	0.1085
chr6	171115067	1400359	0.0082	0.0982
chr7	159138663	1870580	0.0118	0.1283

chr8	146364022	1974637	0.0135	0.1288
chr9	141213431	1412655	0.01	0.1106
chr10	135534747	1703693	0.0126	0.1677
chr11	135006516	1317737	0.0098	0.1146
chr12	133851895	1553767	0.0116	0.1149
chr13	115169878	571241	0.005	0.0756
chr14	107349540	1031236	0.0096	0.1066
chr15	102531392	660252	0.0064	0.0865
chr16	90354753	885305	0.0098	0.1096
chr17	81195210	1234281	0.0152	0.1378
chr18	78077248	859218	0.011	0.1248
chr19	59128983	872969	0.0148	0.1444
chr20	63025520	825087	0.0131	0.1277
chr21	48129895	431789	0.009	0.1128
chr22	51304566	349922	0.0068	0.0883
chrMT	16571	16228	0.9793	1.264
chrX	155270560	1036835	0.0067	0.0927
chrY	59373566	107031	0.0018	0.0713

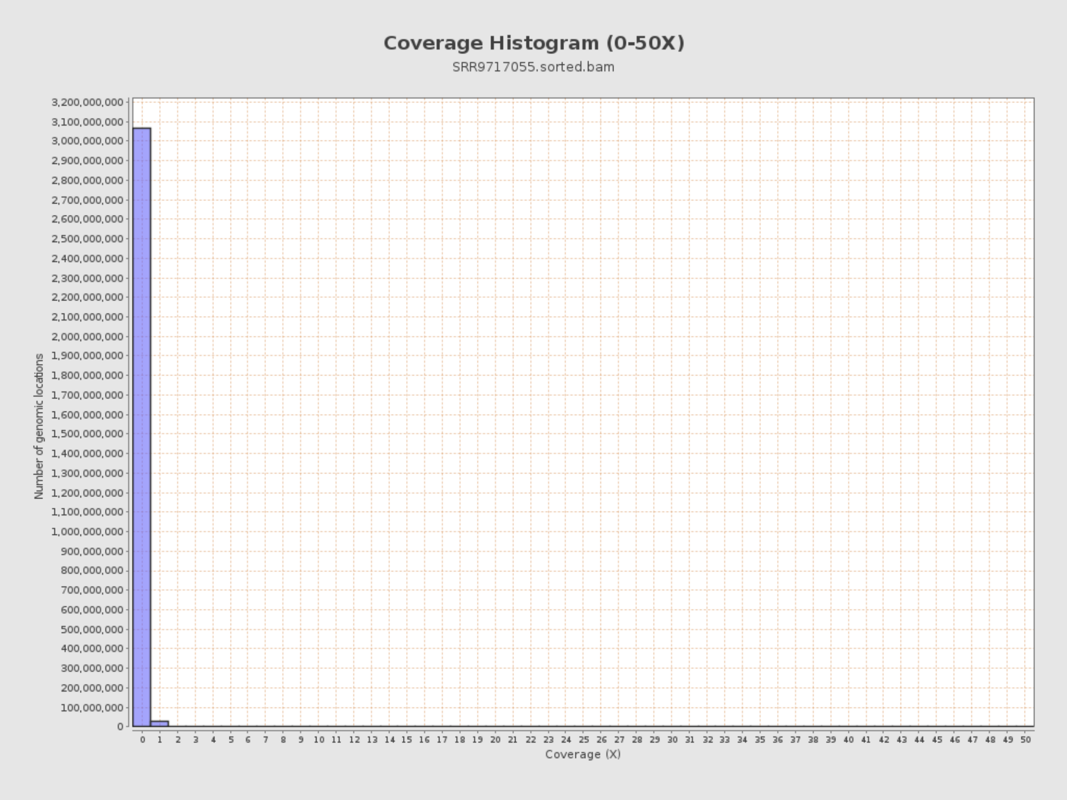
3. Results : Coverage across reference



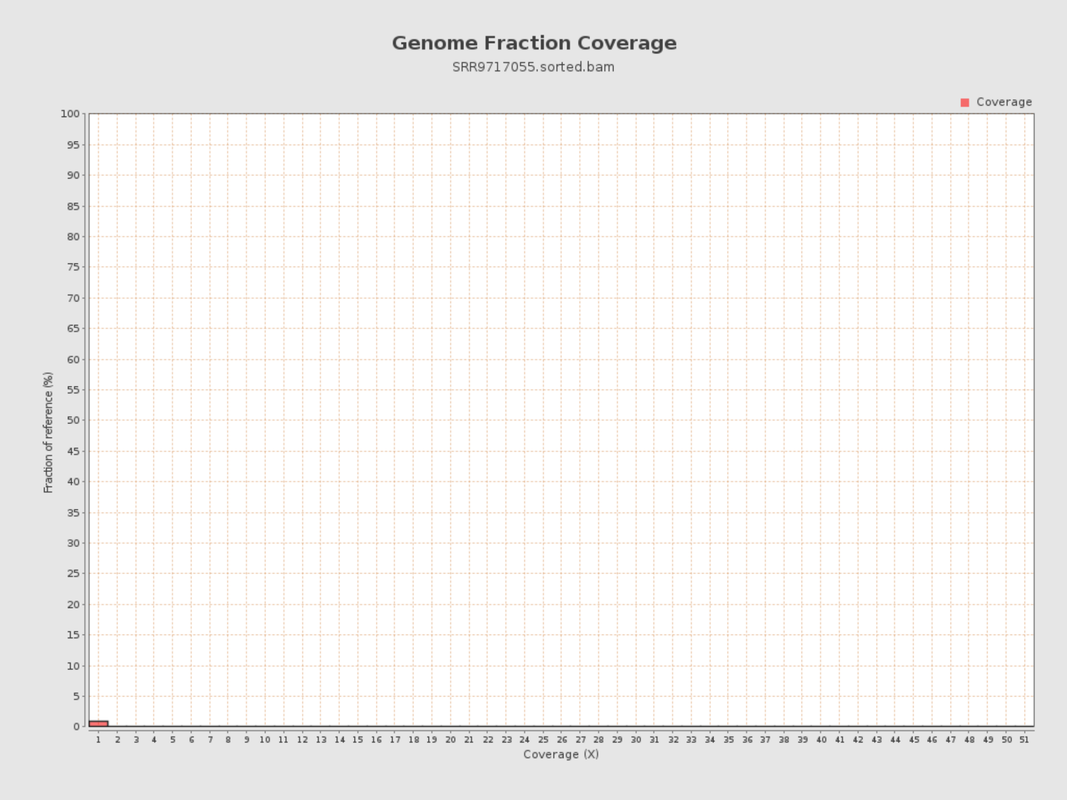
4. Results : Coverage Histogram



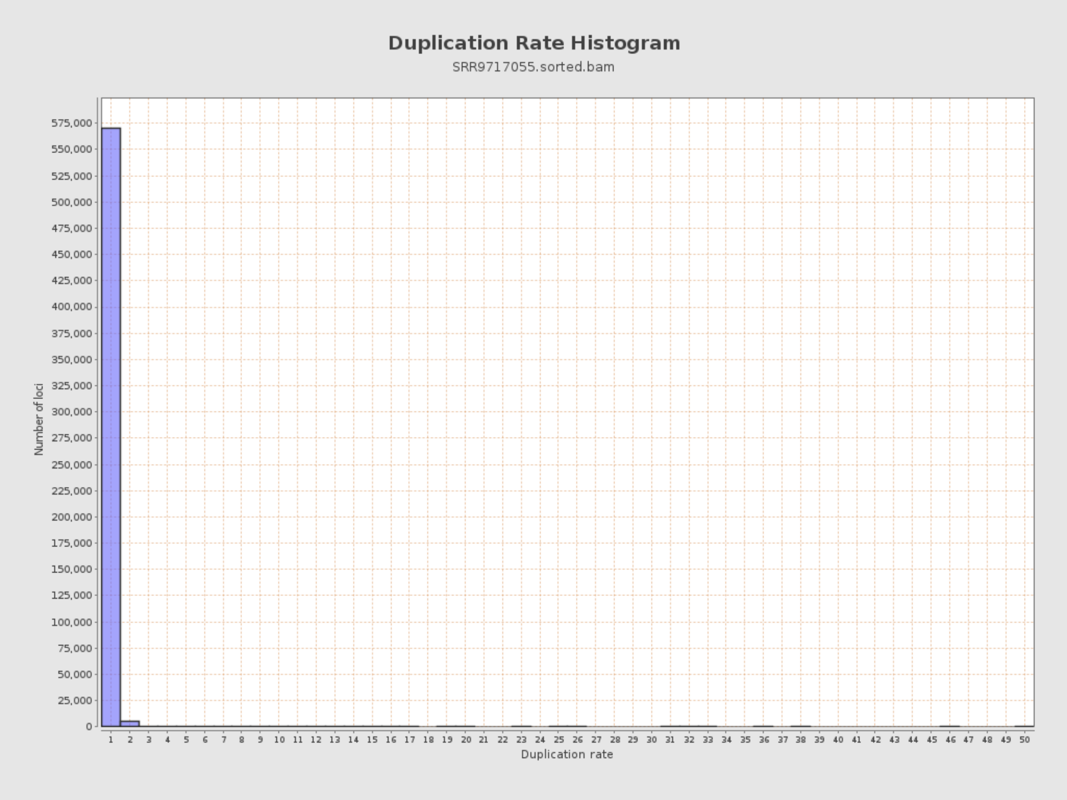
5. Results : Coverage Histogram (0-50X)



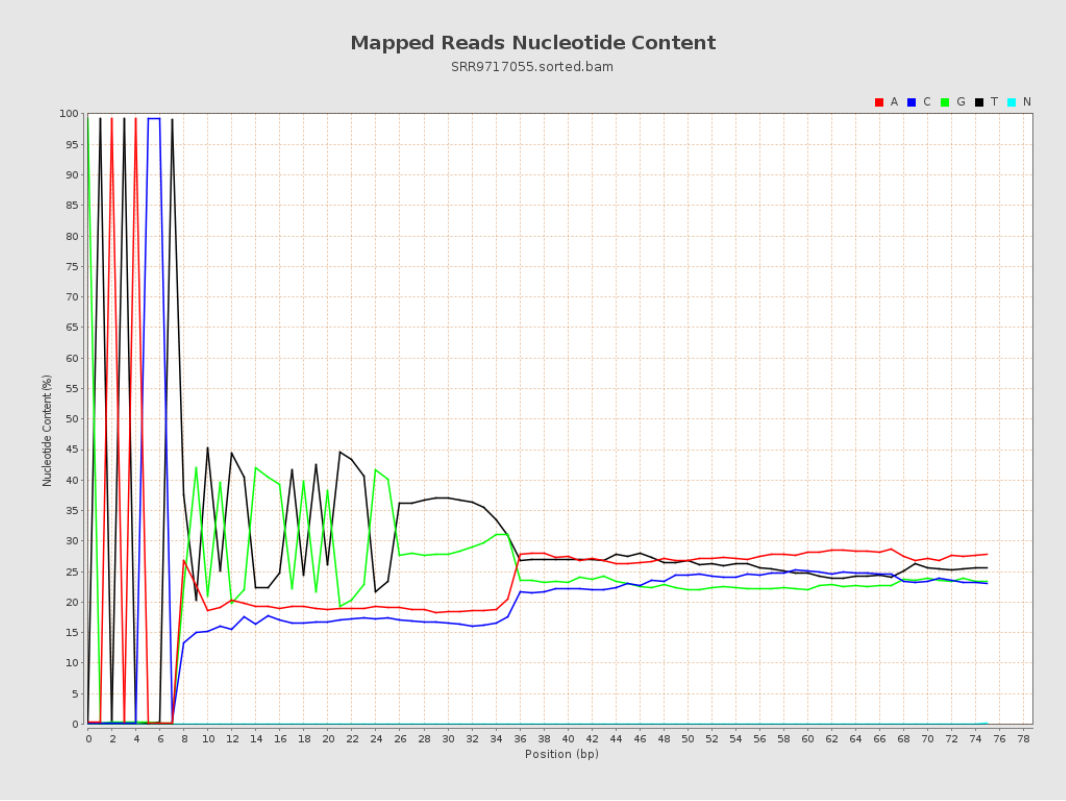
6. Results : Genome Fraction Coverage



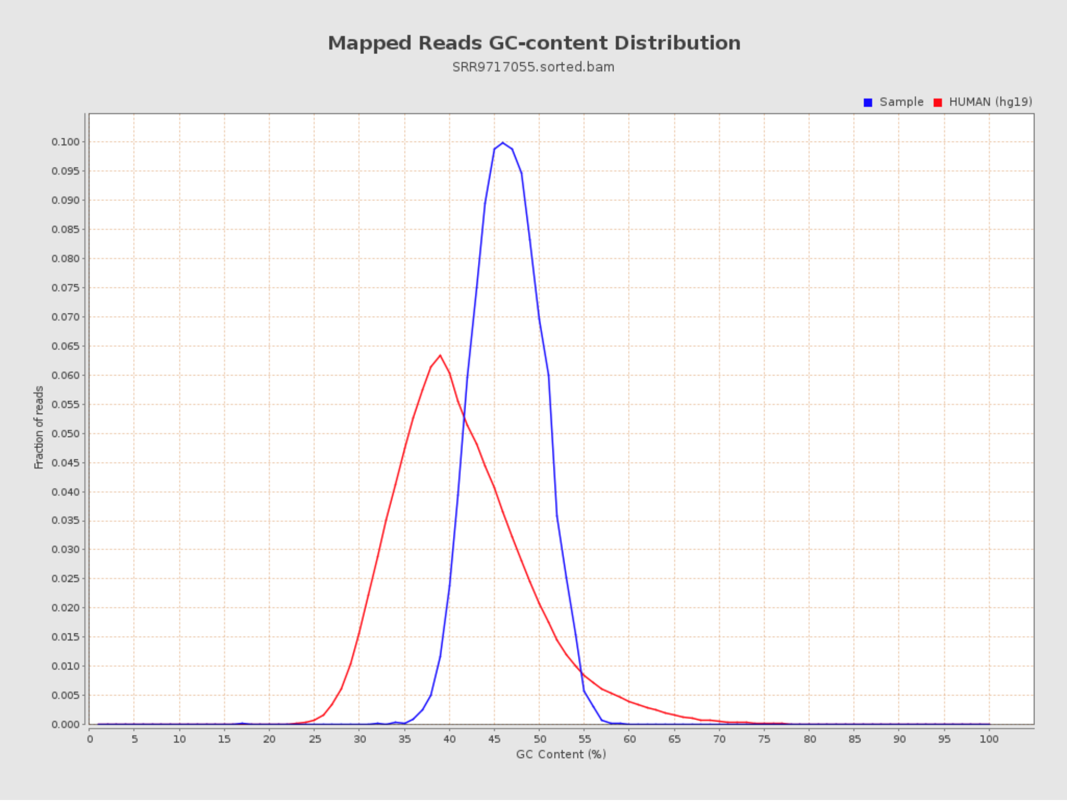
7. Results : Duplication Rate Histogram



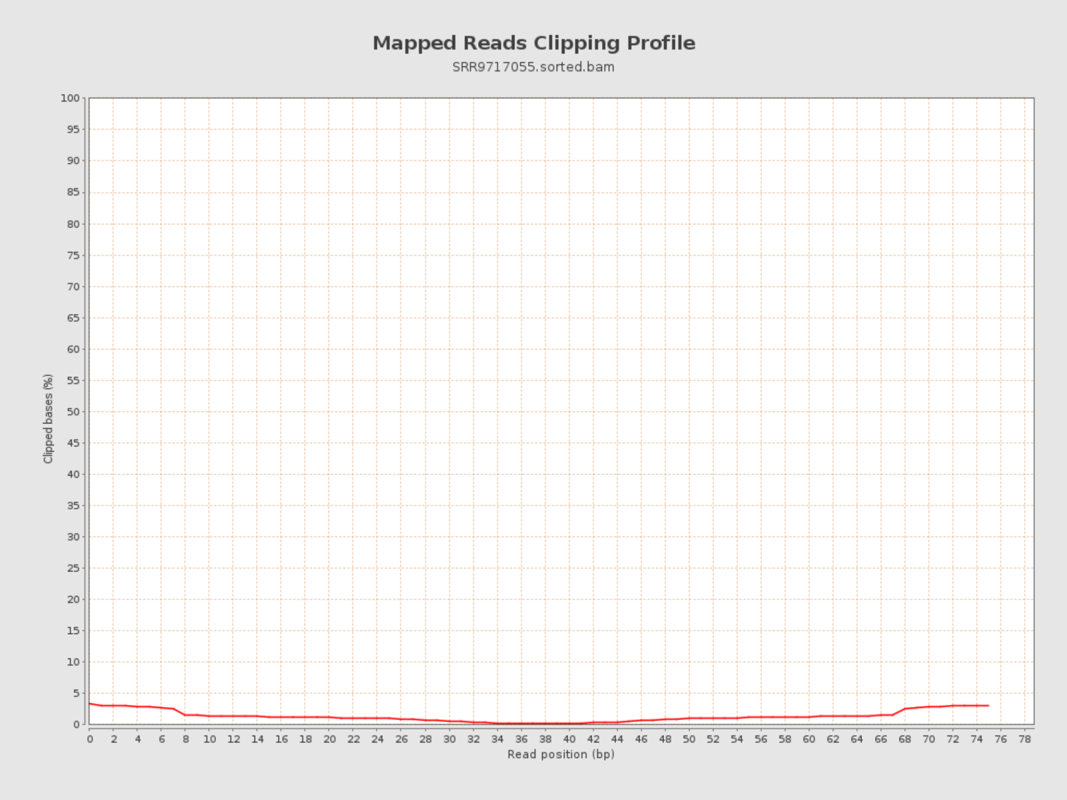
8. Results : Mapped Reads Nucleotide Content



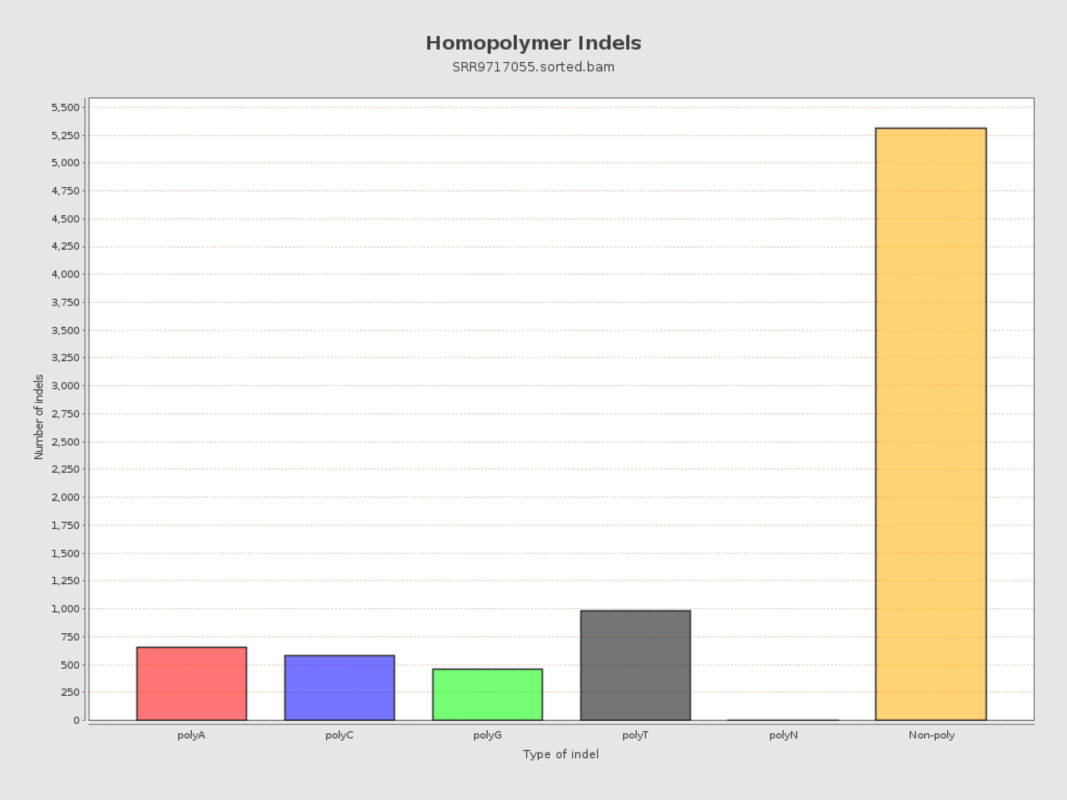
9. Results : Mapped Reads GC-content Distribution



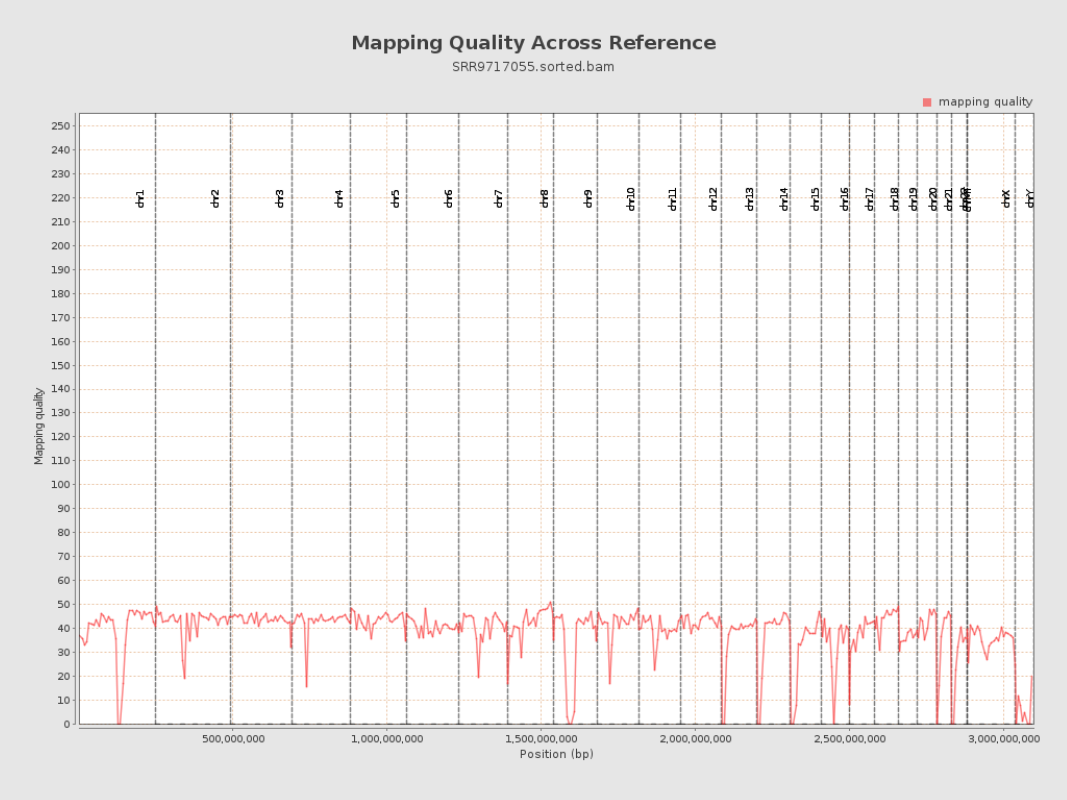
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram