Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:28:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717068.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_SRR9717068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:28:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,075,835
Mapped reads	896,735 / 83.35%
Unmapped reads	179,100 / 16.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,264 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	41,830 / 3.89%
Duplication rate	4.11%
Clipped reads	897,062 / 83.38%

2.2. ACGT Content

Number/percentage of A's	11,562,908 / 23.43%
Number/percentage of C's	10,080,154 / 20.43%
Number/percentage of T's	15,105,369 / 30.61%
Number/percentage of G's	12,596,725 / 25.53%
Number/percentage of N's	928 / 0%
GC Percentage	45.95%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.1578

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Mismatches and indels

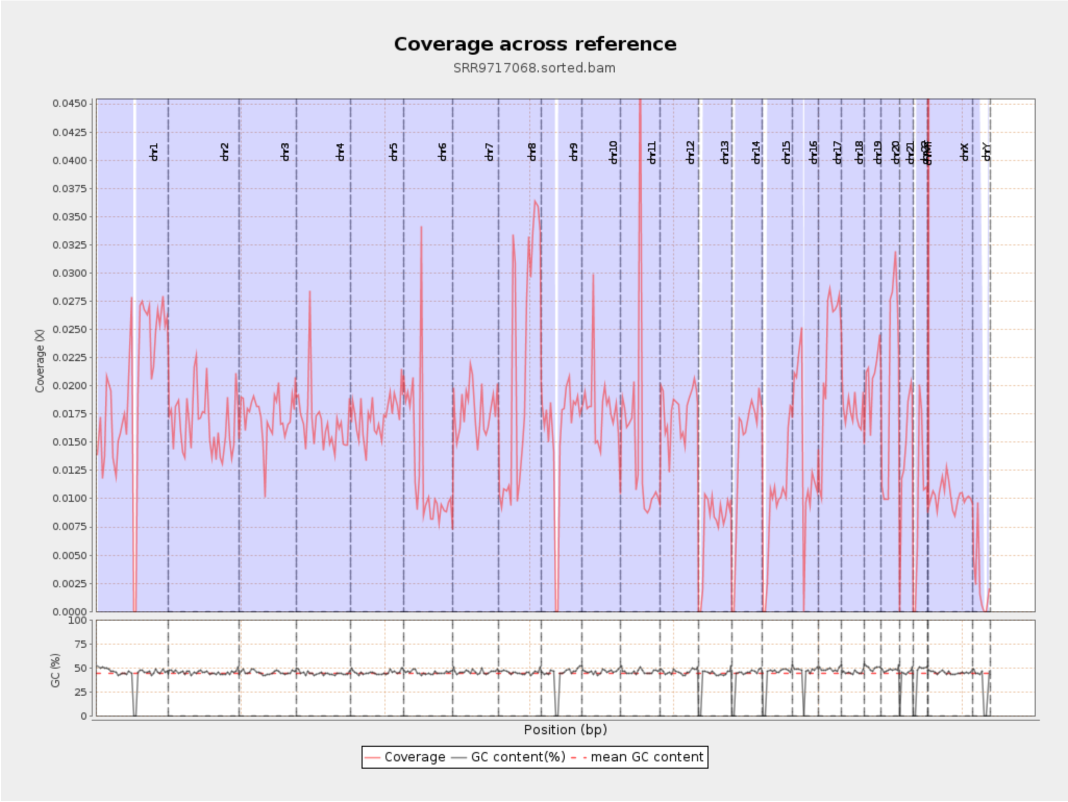
General error rate	0.67%
Mismatches	324,207
Insertions	2,865
Mapped reads with at least one insertion	0.32%
Deletions	7,638
Mapped reads with at least one deletion	0.84%
Homopolymer indels	41.67%

2.6. Chromosome stats

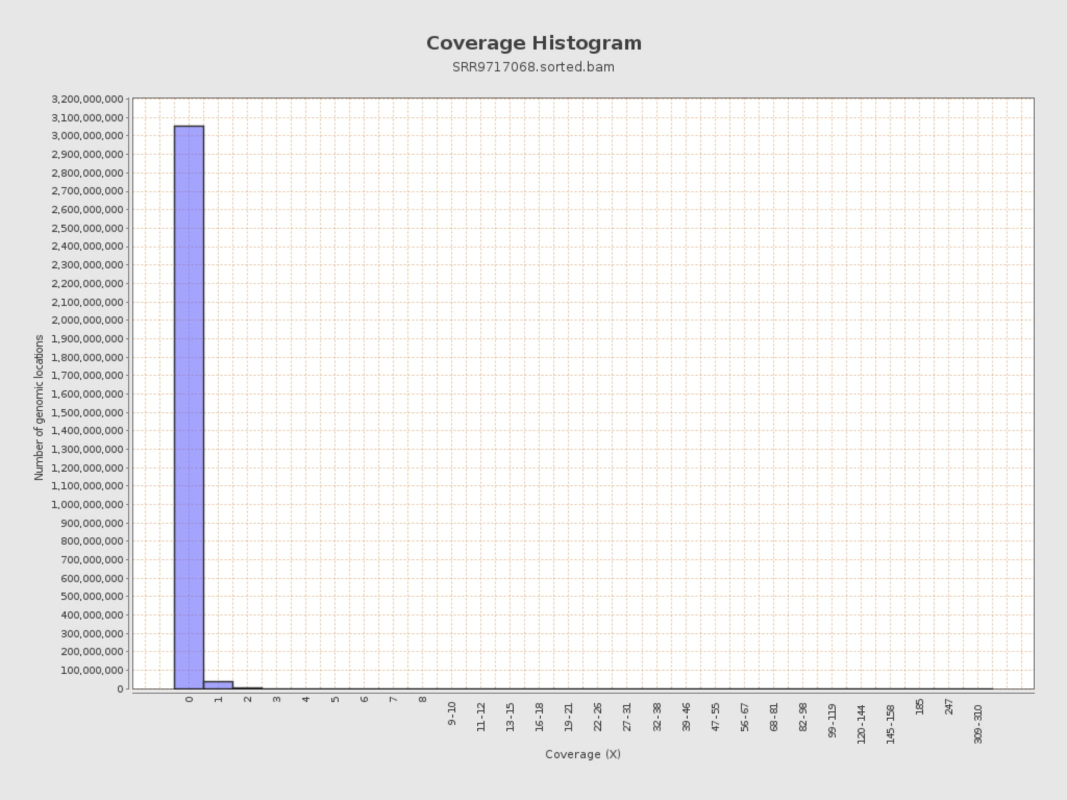
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4873374	0.0196	0.2
chr2	243199373	4049440	0.0167	0.2016
chr3	198022430	3424910	0.0173	0.1456
chr4	191154276	3220249	0.0168	0.1513
chr5	180915260	3139823	0.0174	0.1447
chr6	171115067	2167771	0.0127	0.1331
chr7	159138663	2844486	0.0179	0.1789

chr8	146364022	3138846	0.0214	0.1683
chr9	141213431	2217440	0.0157	0.1488
chr10	135534747	2436785	0.018	0.1791
chr11	135006516	2102700	0.0156	0.1565
chr12	133851895	2371062	0.0177	0.1455
chr13	115169878	868051	0.0075	0.0948
chr14	107349540	1550900	0.0144	0.1326
chr15	102531392	979970	0.0096	0.1068
chr16	90354753	1281747	0.0142	0.1402
chr17	81195210	1839574	0.0227	0.1724
chr18	78077248	1384244	0.0177	0.186
chr19	59128983	1223194	0.0207	0.1904
chr20	63025520	1257075	0.0199	0.1595
chr21	48129895	698260	0.0145	0.1417
chr22	51304566	524110	0.0102	0.1121
chrMT	16571	21344	1.288	1.3789
chrX	155270560	1595989	0.0103	0.1167
chrY	59373566	147890	0.0025	0.0798

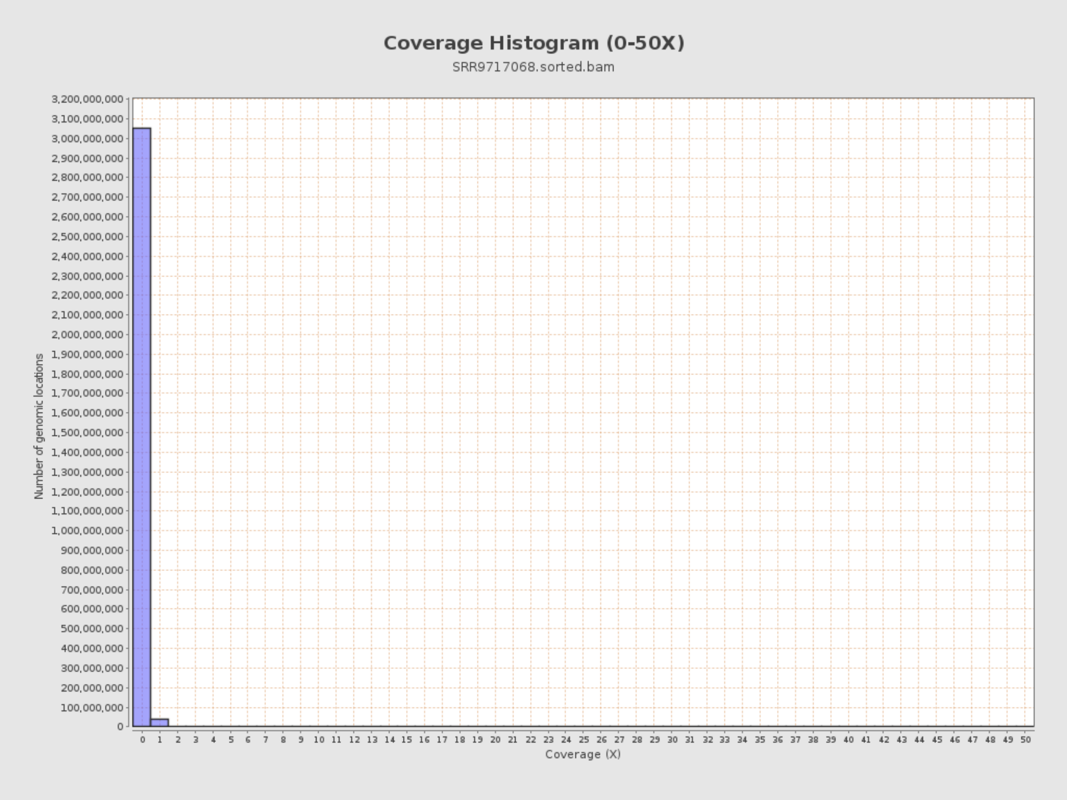
3. Results : Coverage across reference



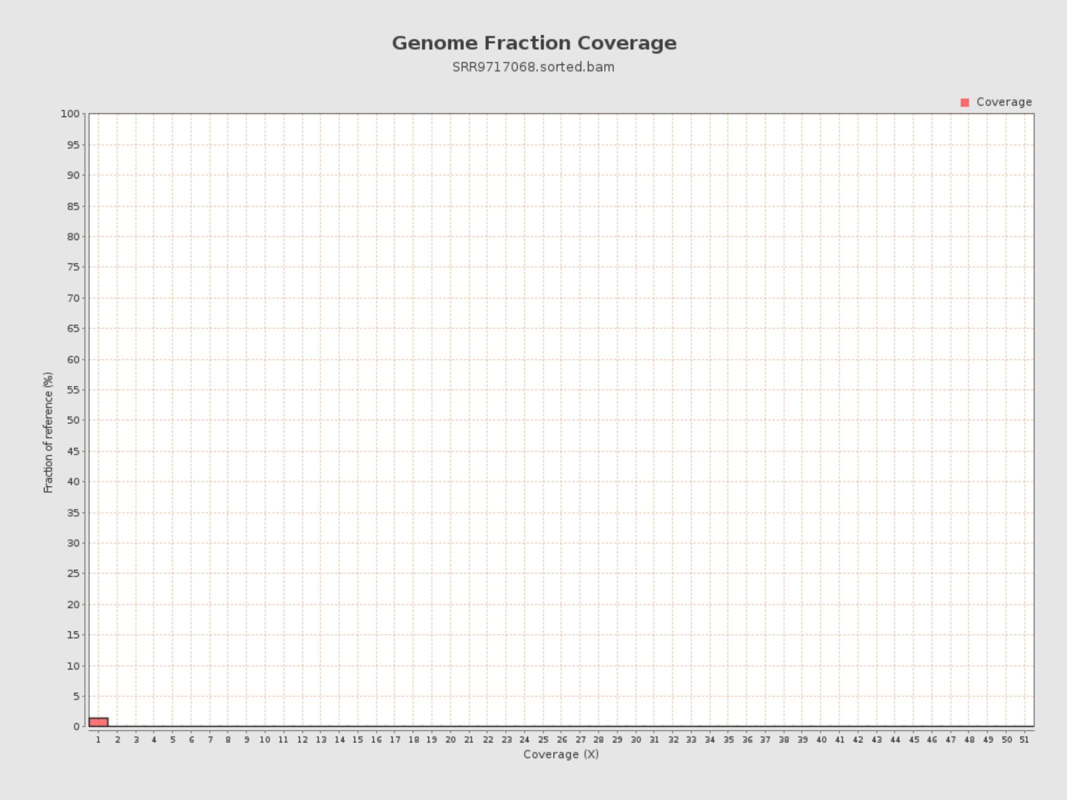
4. Results : Coverage Histogram



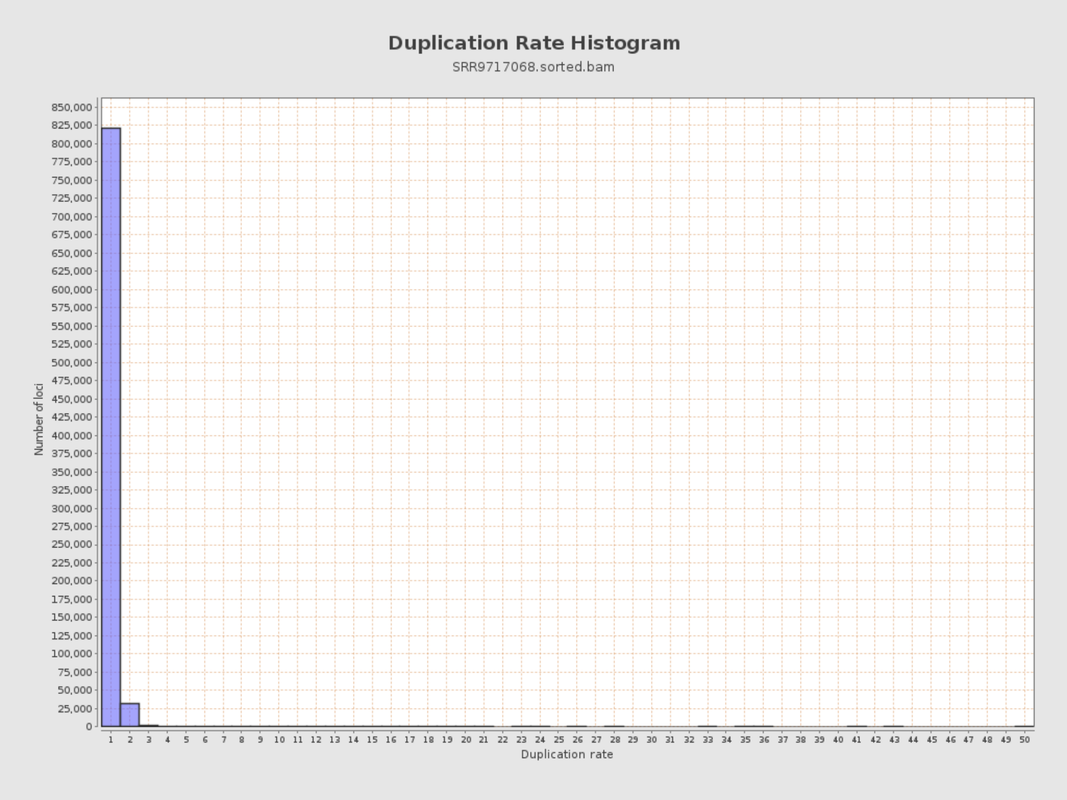
5. Results : Coverage Histogram (0-50X)



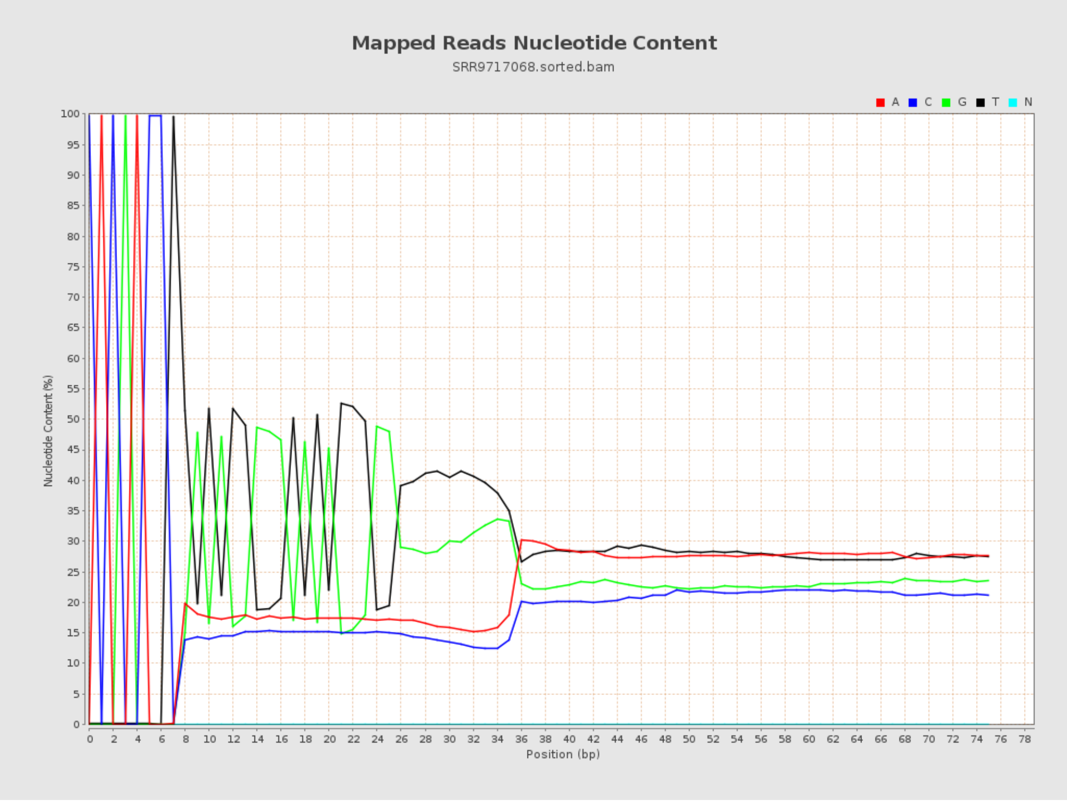
6. Results : Genome Fraction Coverage



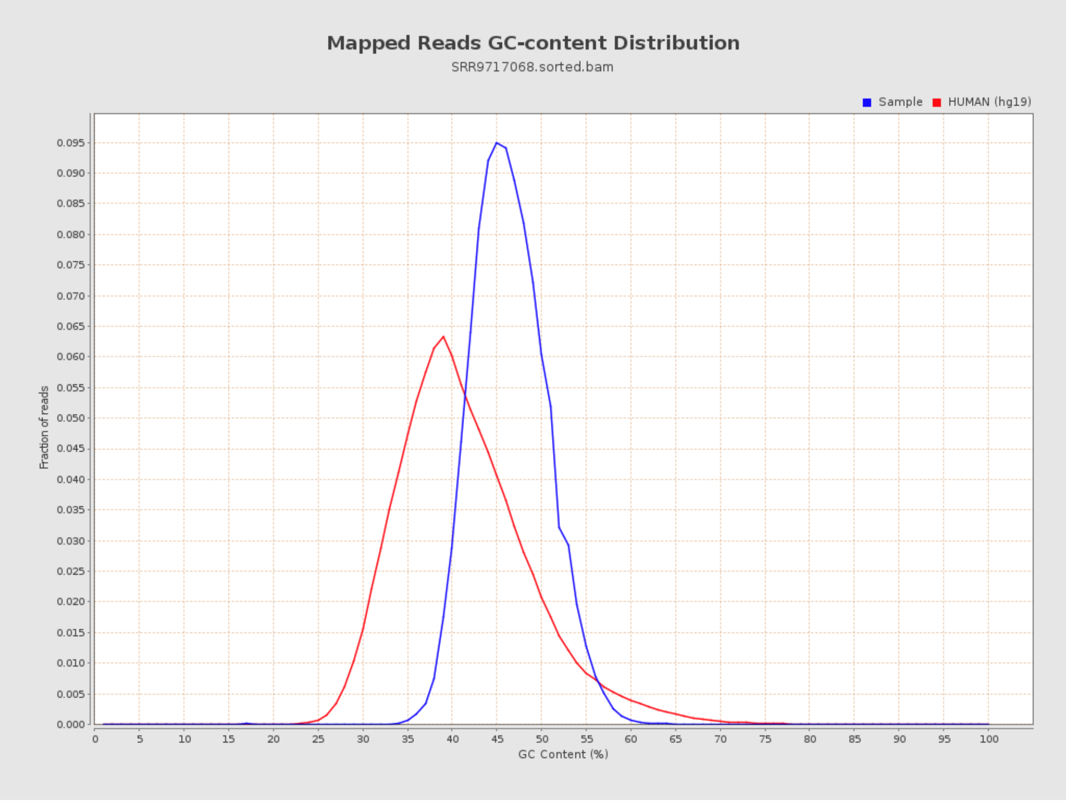
7. Results : Duplication Rate Histogram



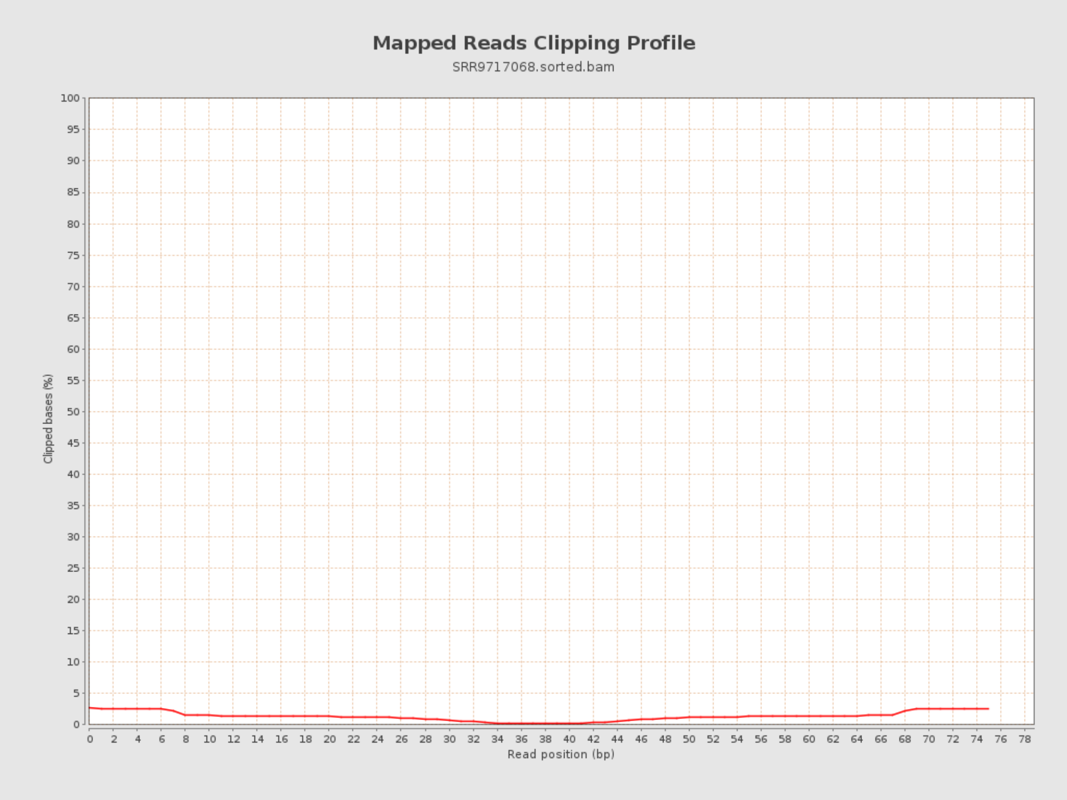
8. Results : Mapped Reads Nucleotide Content



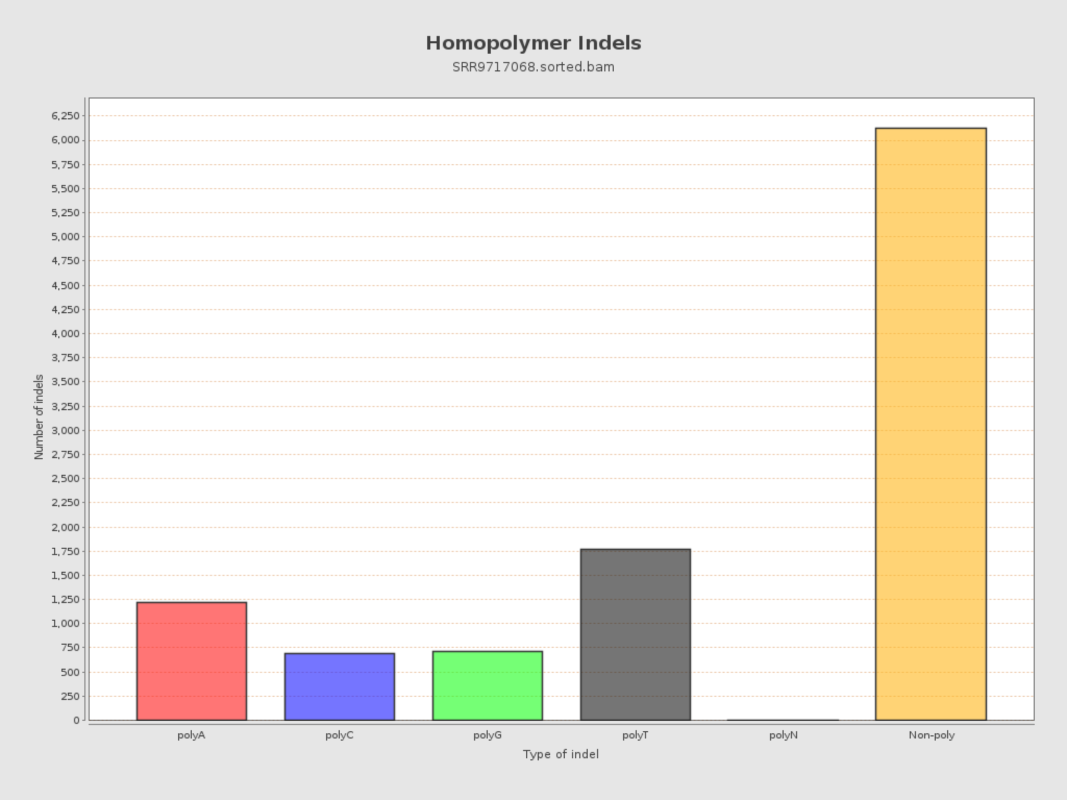
9. Results : Mapped Reads GC-content Distribution



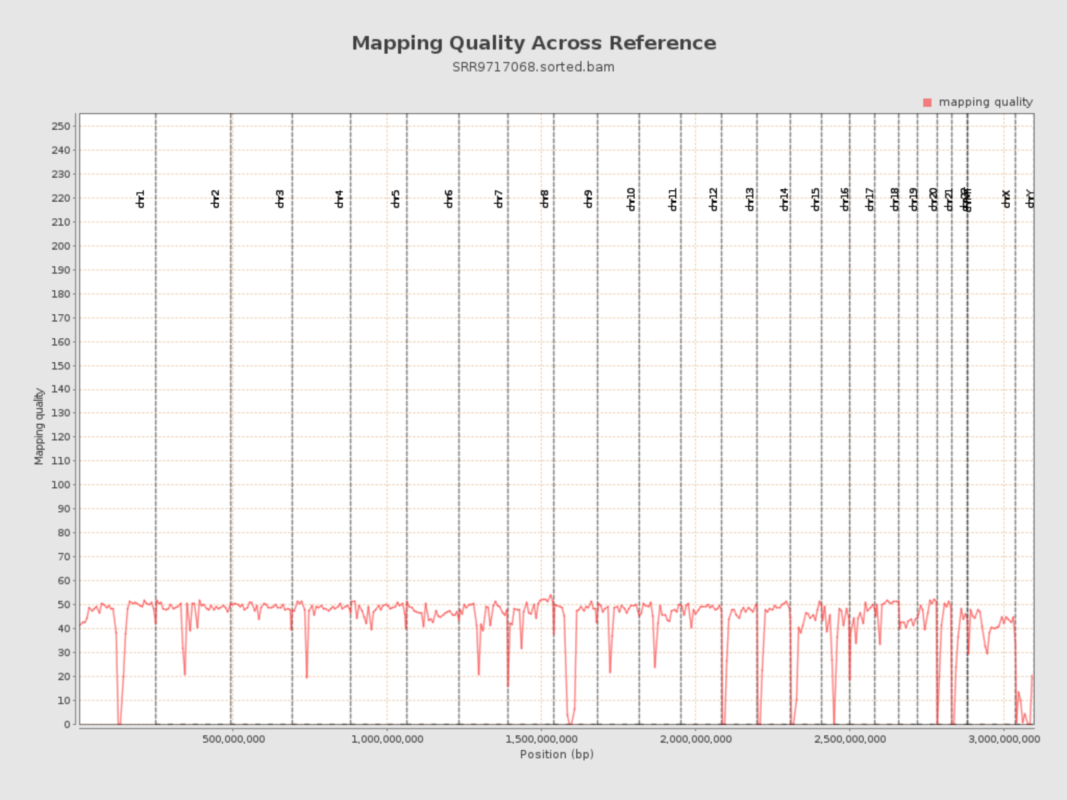
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram