Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:46:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717034.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_SRR9717034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:46:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,095,443
Mapped reads	1,586,868 / 75.73%
Unmapped reads	508,575 / 24.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,501 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	42,512 / 2.03%
Duplication rate	1.84%
Clipped reads	1,588,836 / 75.82%

2.2. ACGT Content

Number/percentage of A's	21,555,478 / 24.55%
Number/percentage of C's	15,973,908 / 18.19%
Number/percentage of T's	27,226,562 / 31%
Number/percentage of G's	23,060,324 / 26.26%
Number/percentage of N's	1,175 / 0%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2522

2.4. Mapping Quality

Mean Mapping Quality	41.23

2.5. Mismatches and indels

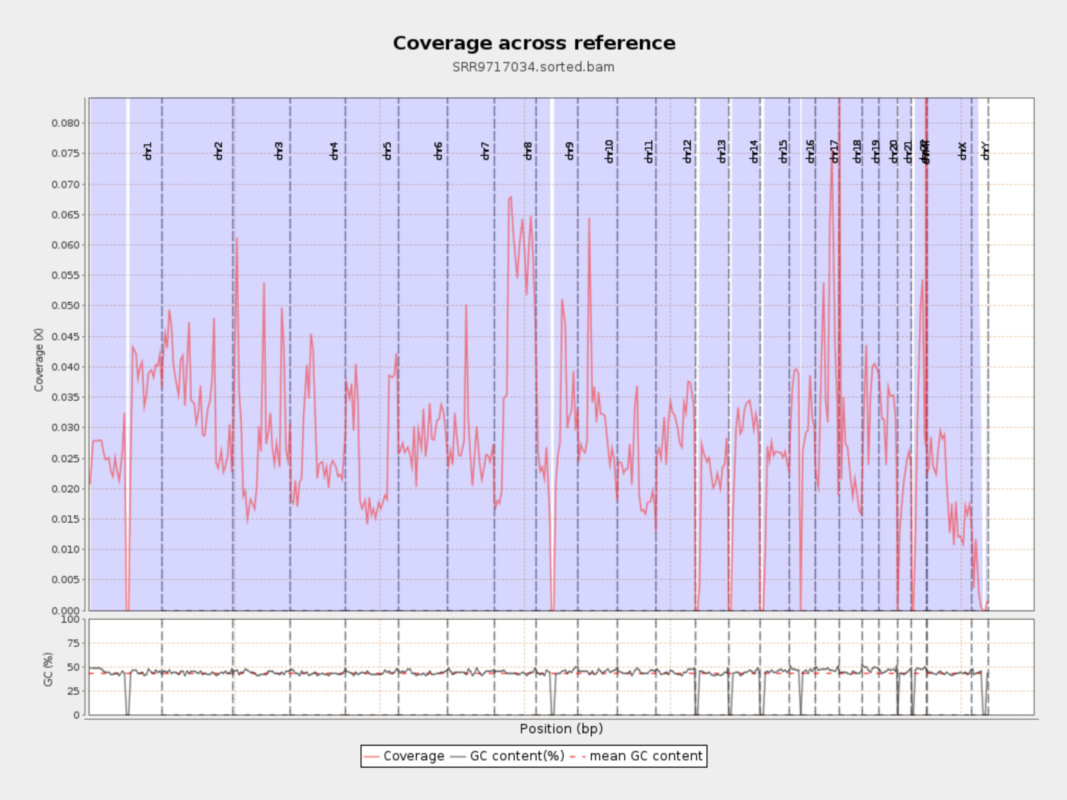
General error rate	0.53%
Mismatches	459,101
Insertions	6,045
Mapped reads with at least one insertion	0.38%
Deletions	16,188
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.16%

2.6. Chromosome stats

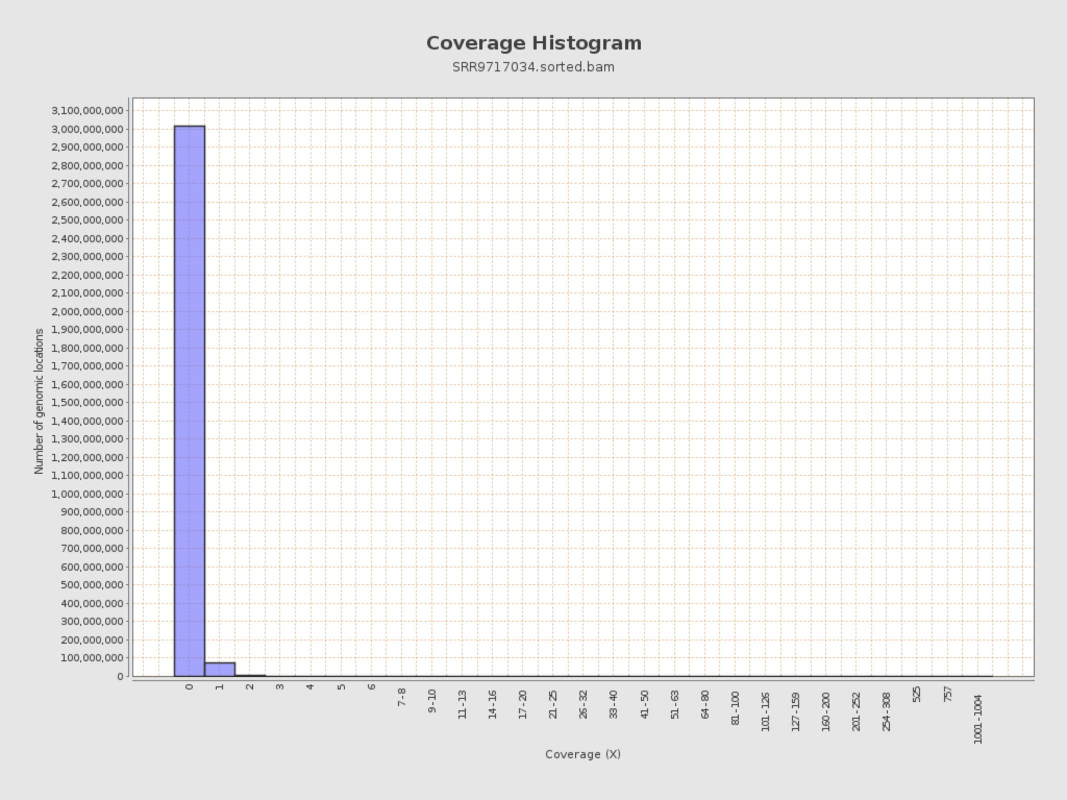
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7381113	0.0296	0.2972
chr2	243199373	8562132	0.0352	0.4506
chr3	198022430	5804589	0.0293	0.1931
chr4	191154276	4946391	0.0259	0.1887
chr5	180915260	4712490	0.026	0.1773
chr6	171115067	4856236	0.0284	0.2113
chr7	159138663	4321168	0.0272	0.3772

chr8	146364022	7080267	0.0484	0.2697
chr9	141213431	3718988	0.0263	0.1993
chr10	135534747	4197764	0.031	0.276
chr11	135006516	2972892	0.022	0.2003
chr12	133851895	4115051	0.0307	0.1942
chr13	115169878	2280871	0.0198	0.1585
chr14	107349540	2842364	0.0265	0.1846
chr15	102531392	2137490	0.0208	0.1621
chr16	90354753	2781242	0.0308	0.2025
chr17	81195210	3329614	0.041	0.2294
chr18	78077248	2003540	0.0257	0.2625
chr19	59128983	2138607	0.0362	0.2831
chr20	63025520	2030719	0.0322	0.1996
chr21	48129895	910465	0.0189	0.1554
chr22	51304566	1407308	0.0274	0.1836
chrMT	16571	13162	0.7943	1.049
chrX	155270560	3085905	0.0199	0.1766
chrY	59373566	212856	0.0036	0.0966

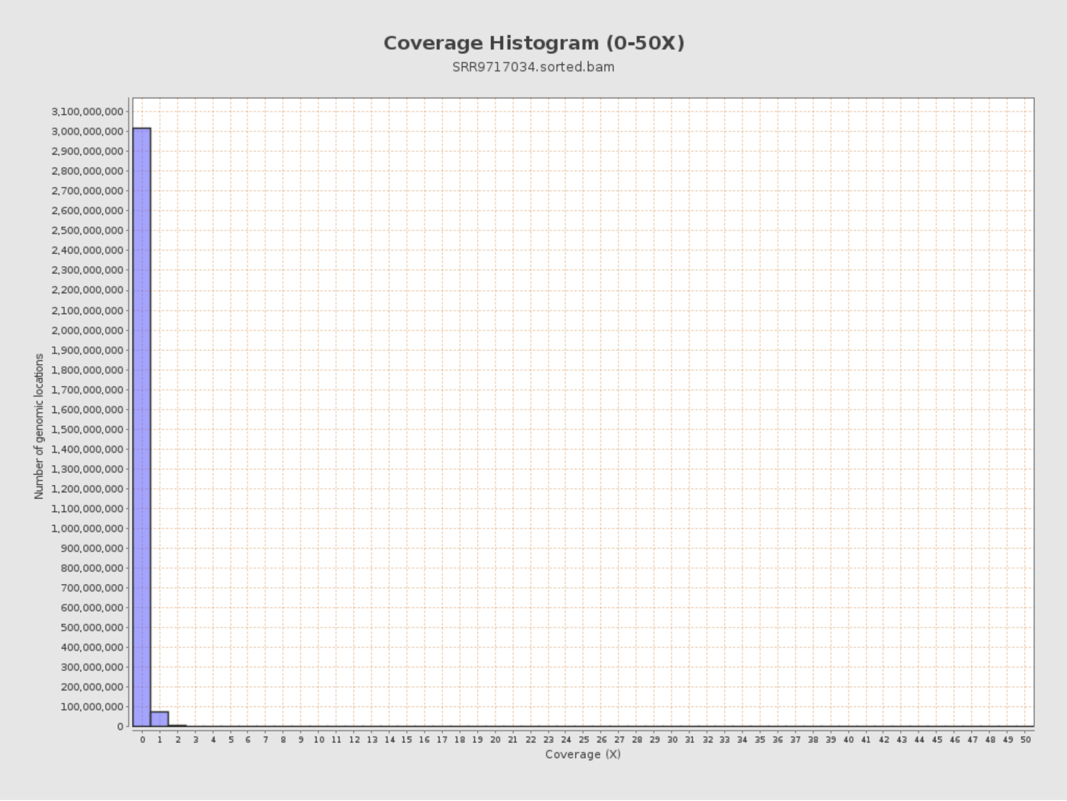
3. Results : Coverage across reference



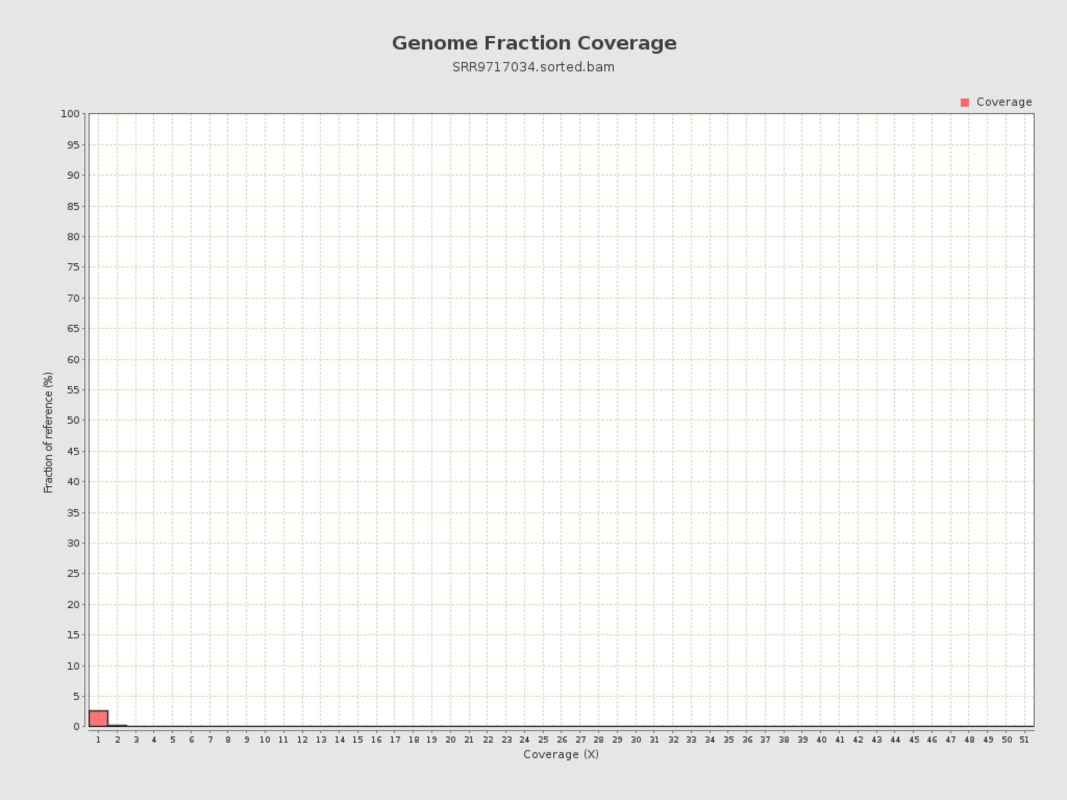
4. Results : Coverage Histogram



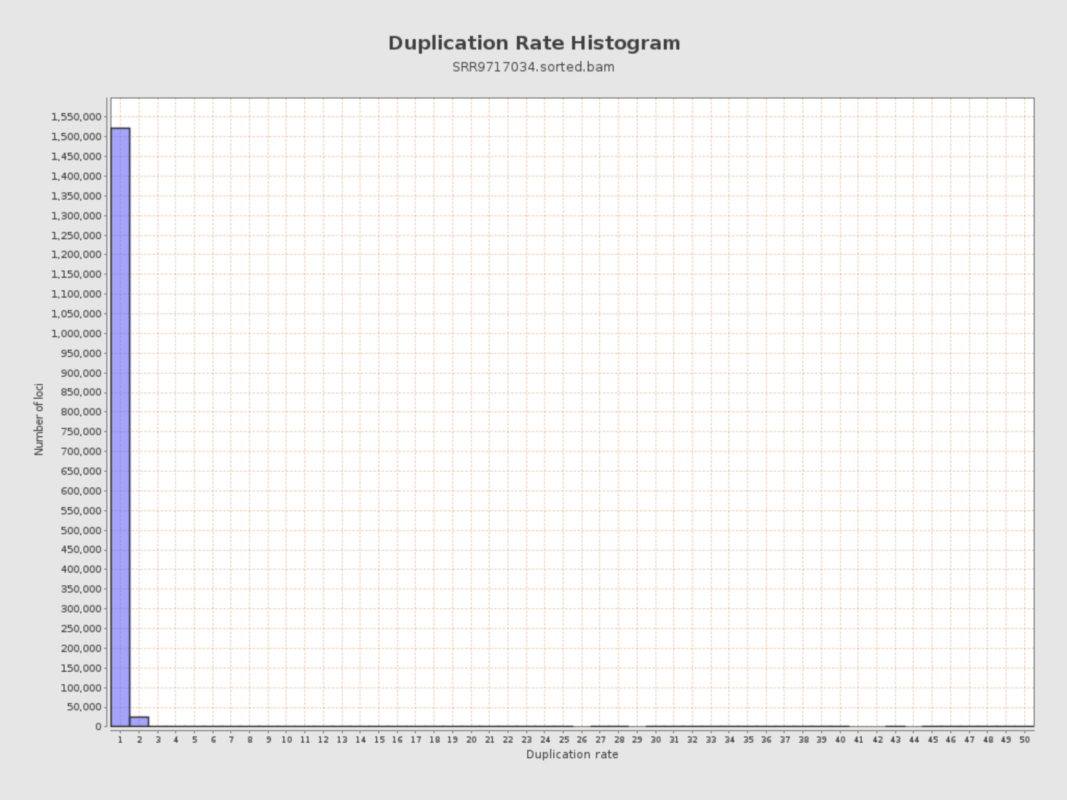
5. Results : Coverage Histogram (0-50X)



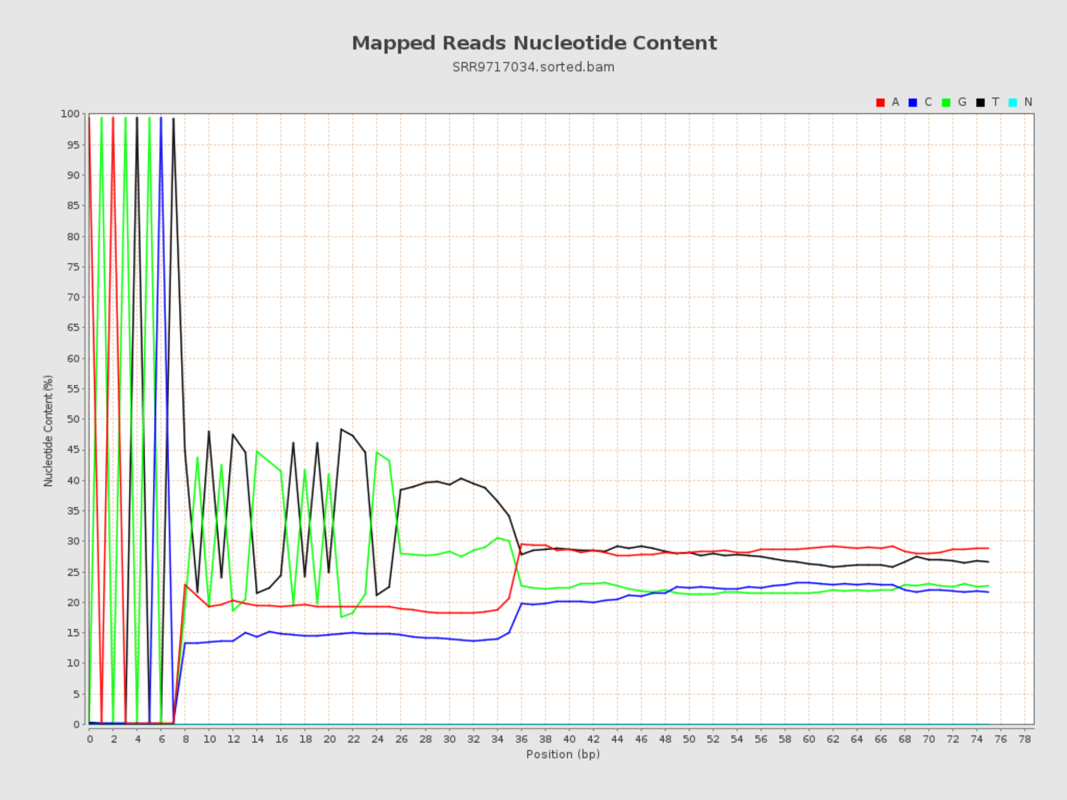
6. Results : Genome Fraction Coverage



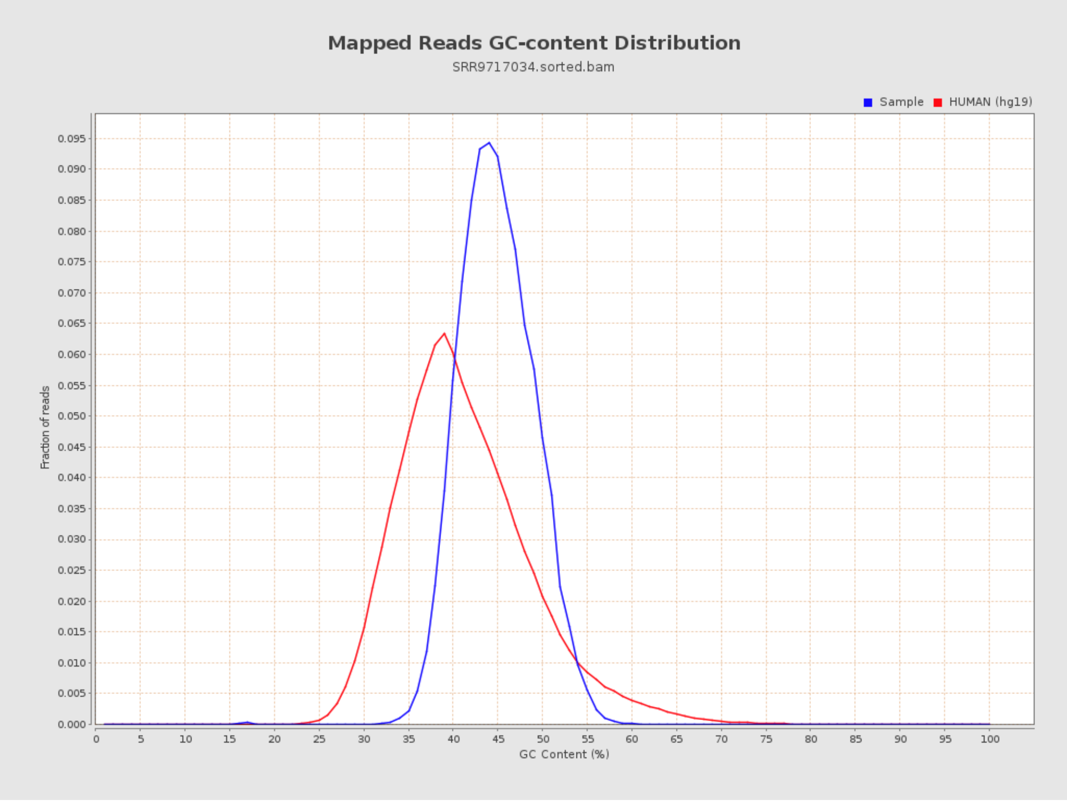
7. Results : Duplication Rate Histogram



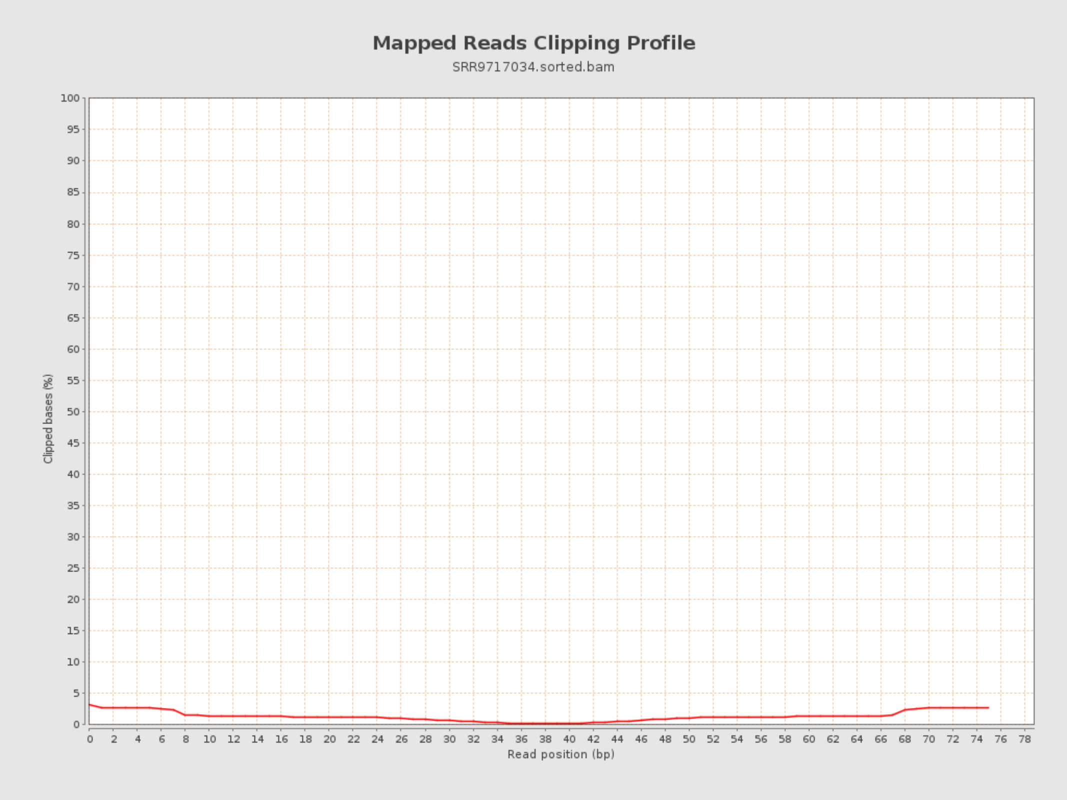
8. Results : Mapped Reads Nucleotide Content



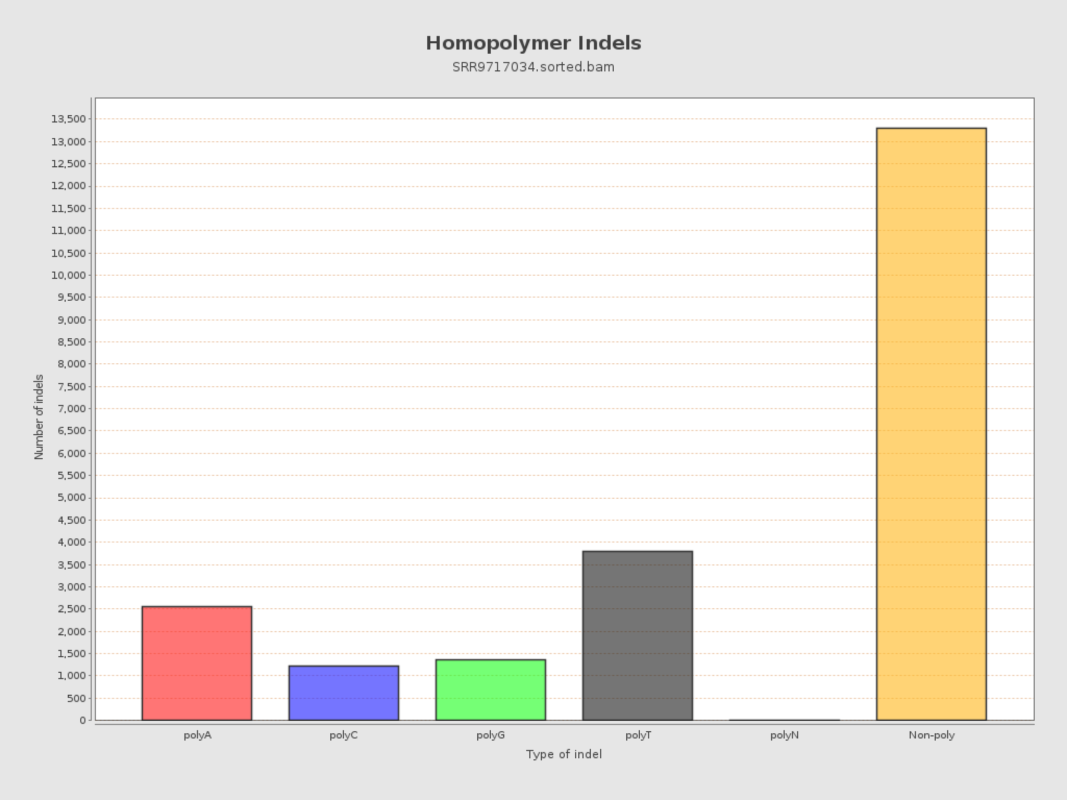
9. Results : Mapped Reads GC-content Distribution



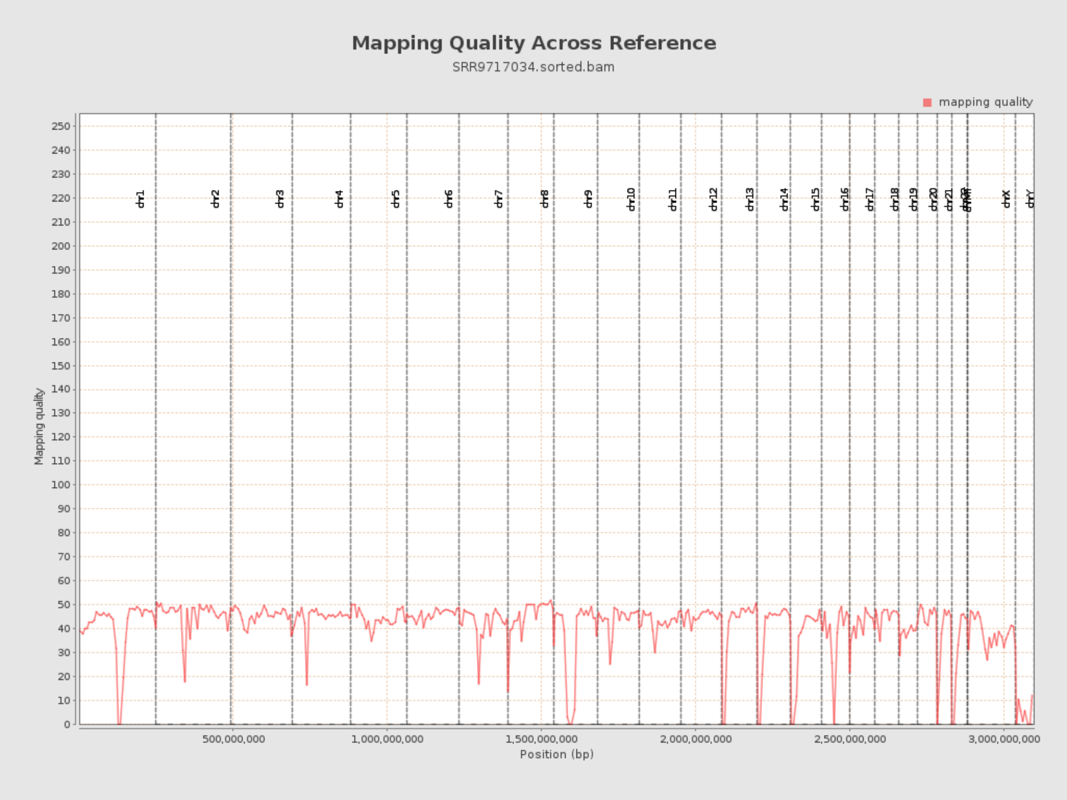
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram