Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:31:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717043.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_SRR9717043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:31:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,014,856
Mapped reads	905,333 / 89.21%
Unmapped reads	109,523 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,080 / 2.47%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	15,566 / 1.53%
Duplication rate	1.1%
Clipped reads	929,048 / 91.54%

2.2. ACGT Content

Number/percentage of A's	17,386,885 / 26.35%
Number/percentage of C's	13,763,370 / 20.86%
Number/percentage of T's	19,440,014 / 29.46%
Number/percentage of G's	15,395,765 / 23.33%
Number/percentage of N's	8,076 / 0.01%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2047

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

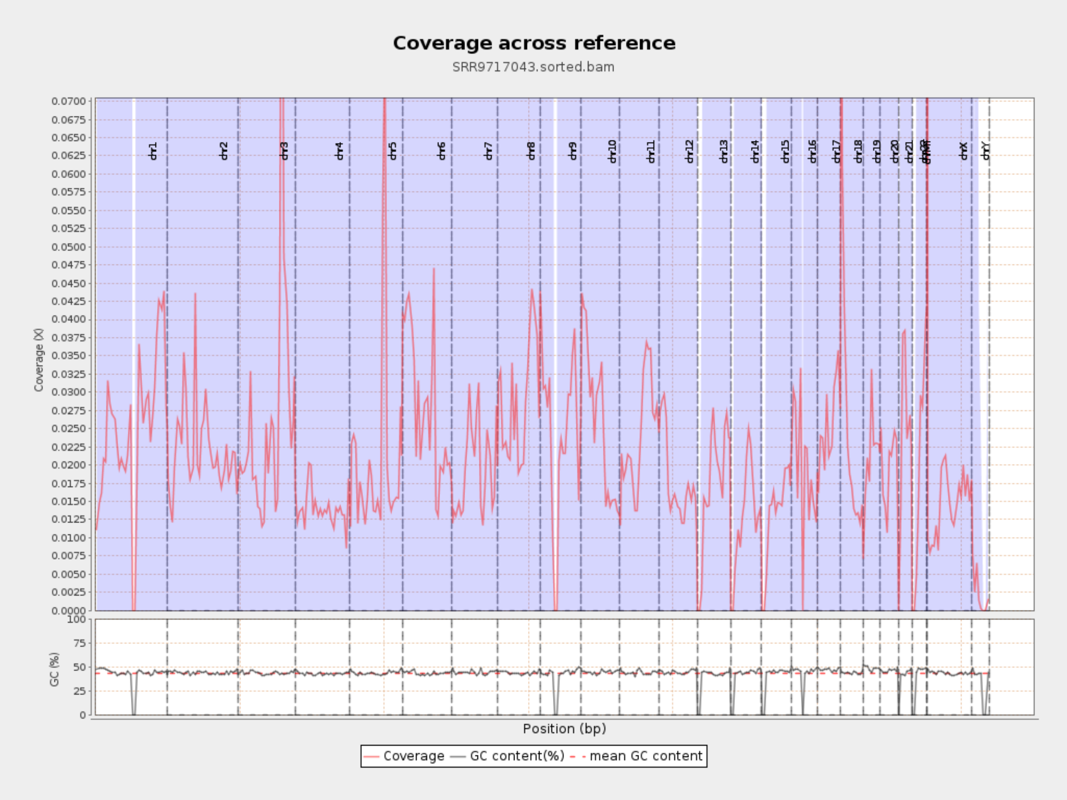
General error rate	0.75%
Mismatches	480,645
Insertions	5,757
Mapped reads with at least one insertion	0.63%
Deletions	12,682
Mapped reads with at least one deletion	1.38%
Homopolymer indels	39.66%

2.6. Chromosome stats

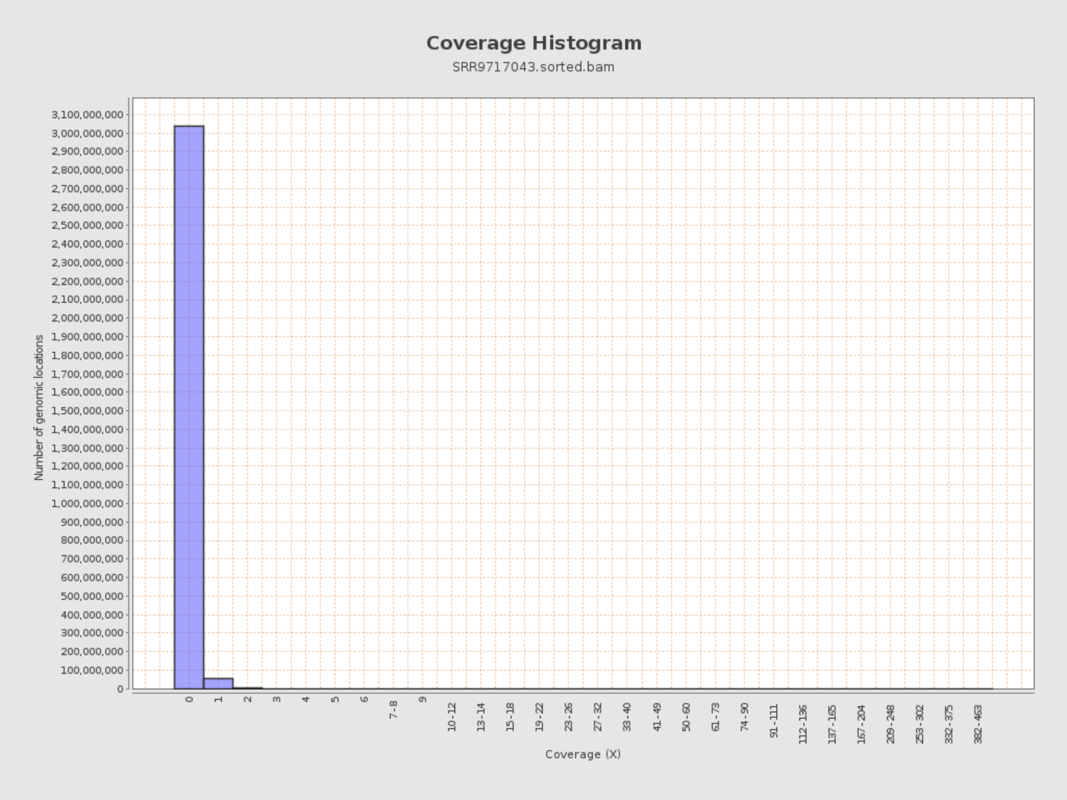
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6181717	0.0248	0.2256
chr2	243199373	5399851	0.0222	0.336
chr3	198022430	5344906	0.027	0.1779
chr4	191154276	2695642	0.0141	0.1309
chr5	180915260	3898149	0.0215	0.1576
chr6	171115067	4802679	0.0281	0.1888
chr7	159138663	3103139	0.0195	0.2468

chr8	146364022	4247677	0.029	0.2726
chr9	141213431	3435682	0.0243	0.2112
chr10	135534747	3536588	0.0261	0.2059
chr11	135006516	3265669	0.0242	0.1848
chr12	133851895	2388736	0.0178	0.1424
chr13	115169878	2002626	0.0174	0.1391
chr14	107349540	1372859	0.0128	0.1283
chr15	102531392	1337073	0.013	0.1213
chr16	90354753	1738602	0.0192	0.1539
chr17	81195210	2091822	0.0258	0.18
chr18	78077248	2060644	0.0264	0.3255
chr19	59128983	1277609	0.0216	0.2291
chr20	63025520	1213697	0.0193	0.1561
chr21	48129895	1200758	0.0249	0.1732
chr22	51304566	987865	0.0193	0.149
chrMT	16571	15913	0.9603	1.2672
chrX	155270560	2279469	0.0147	0.1453
chrY	59373566	136517	0.0023	0.0662

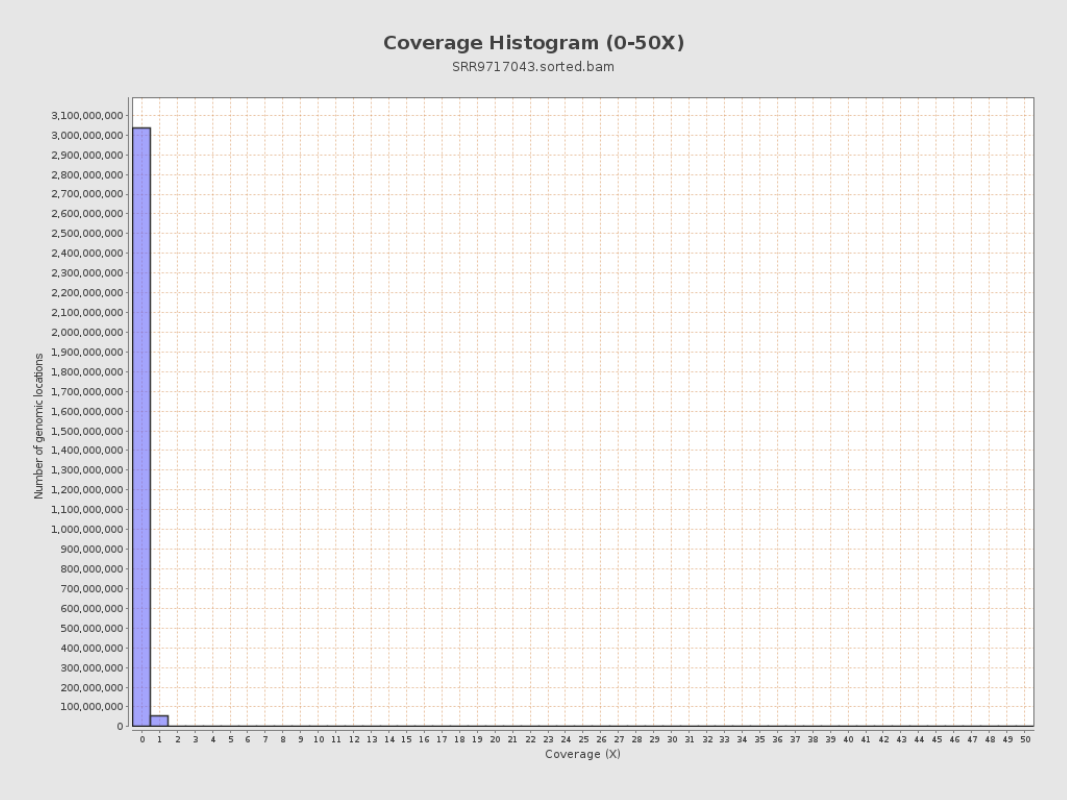
3. Results : Coverage across reference



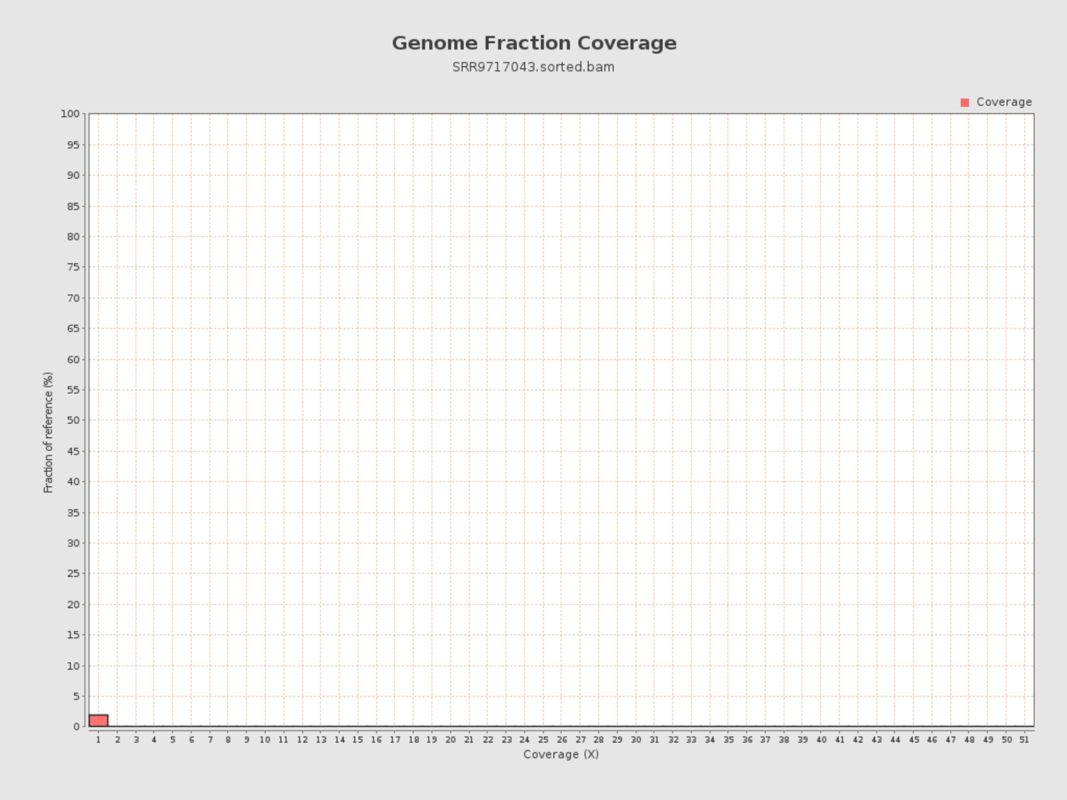
4. Results : Coverage Histogram



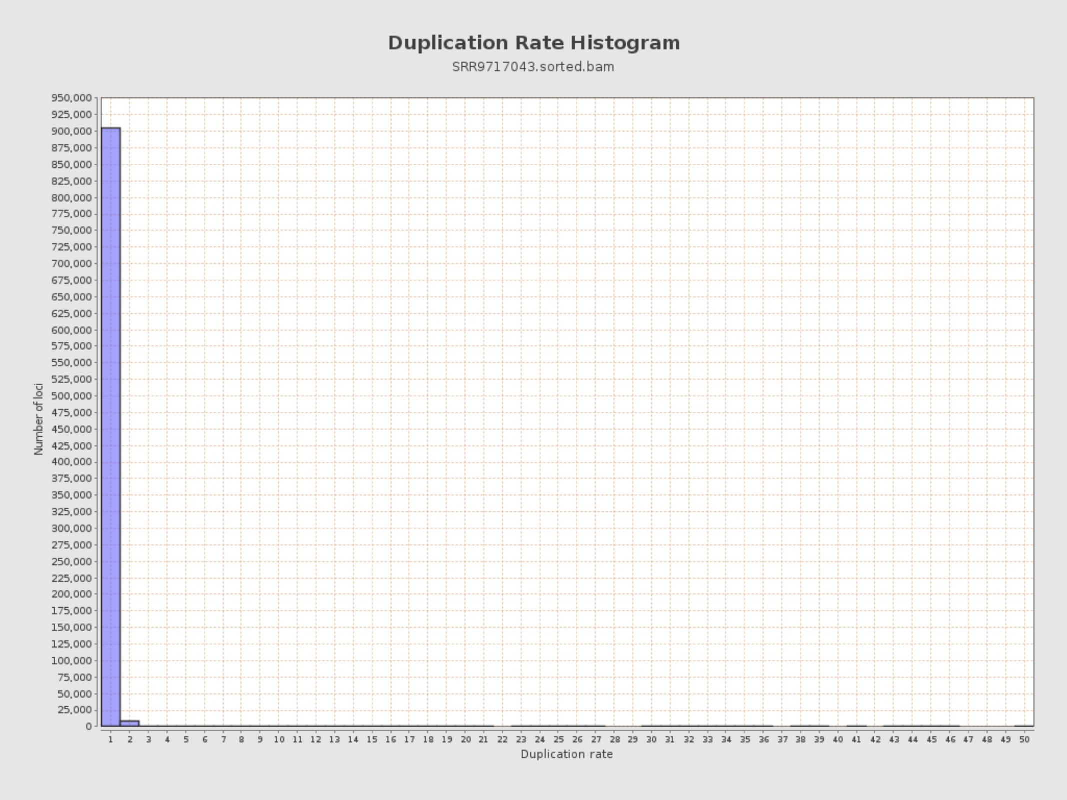
5. Results : Coverage Histogram (0-50X)



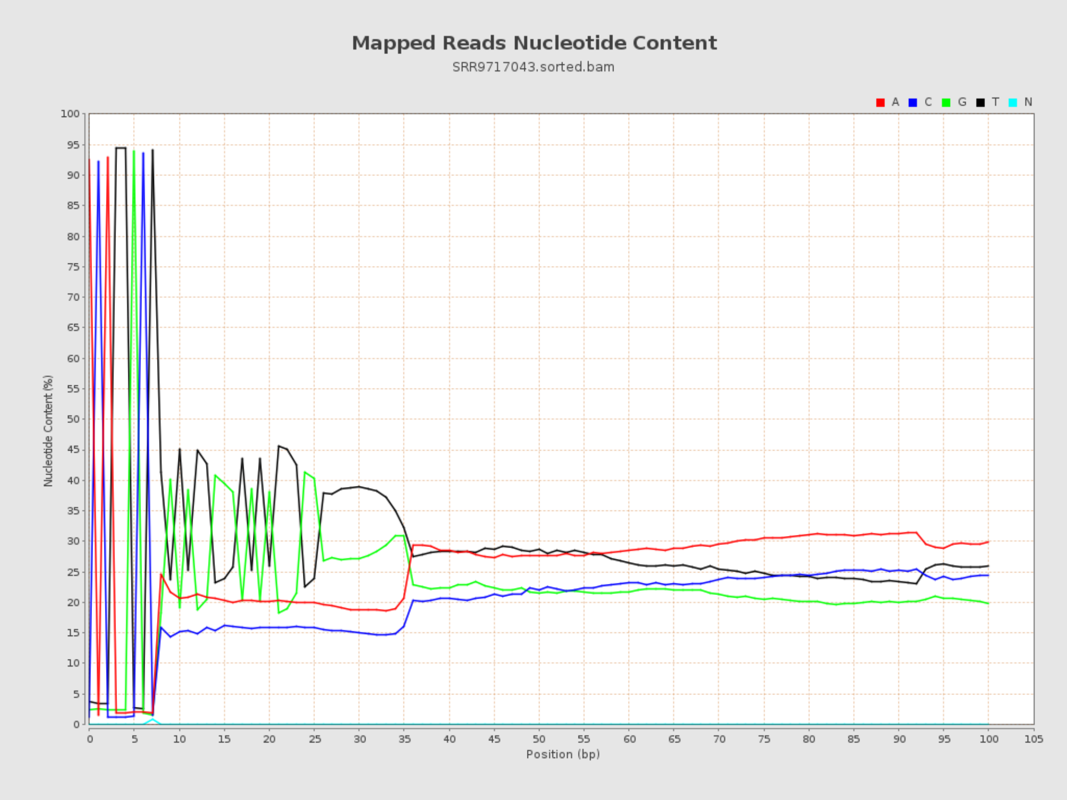
6. Results : Genome Fraction Coverage



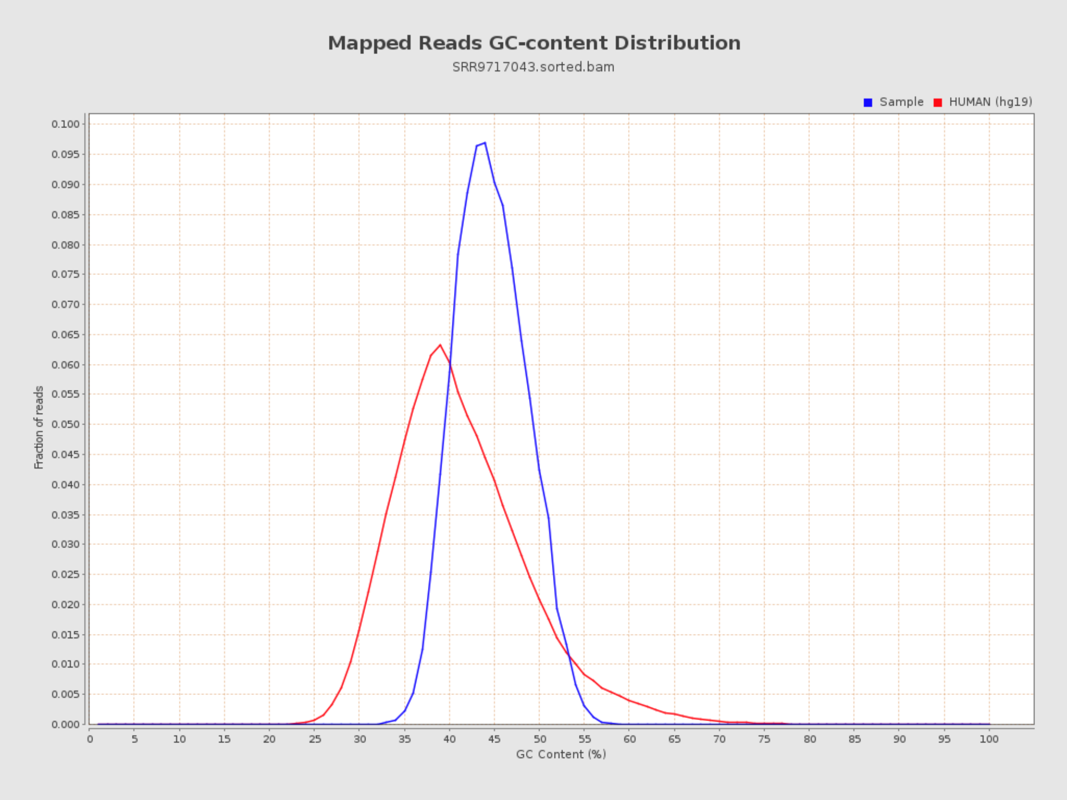
7. Results : Duplication Rate Histogram



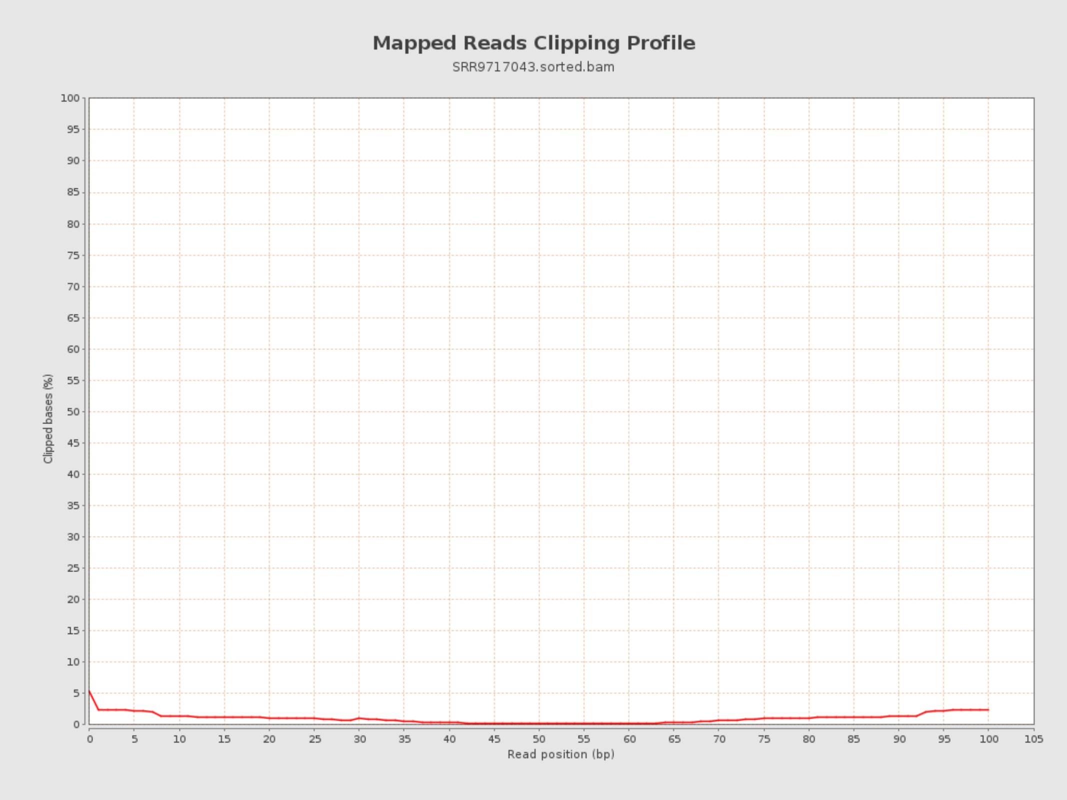
8. Results : Mapped Reads Nucleotide Content



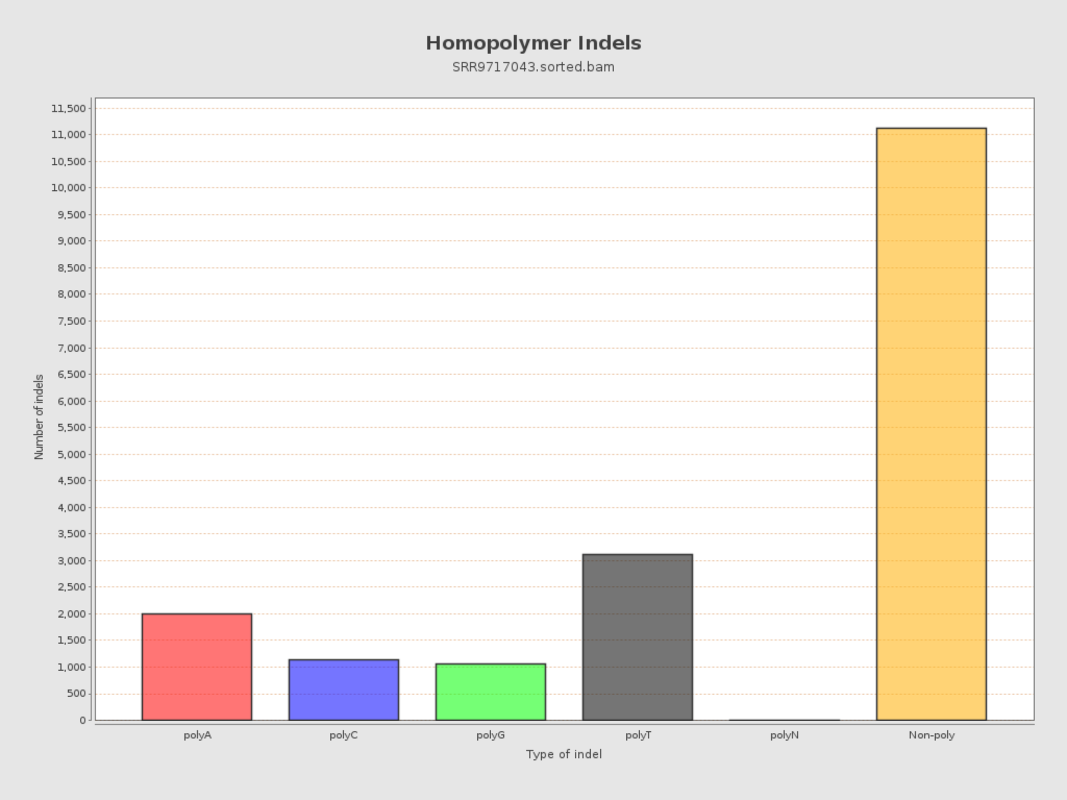
9. Results : Mapped Reads GC-content Distribution



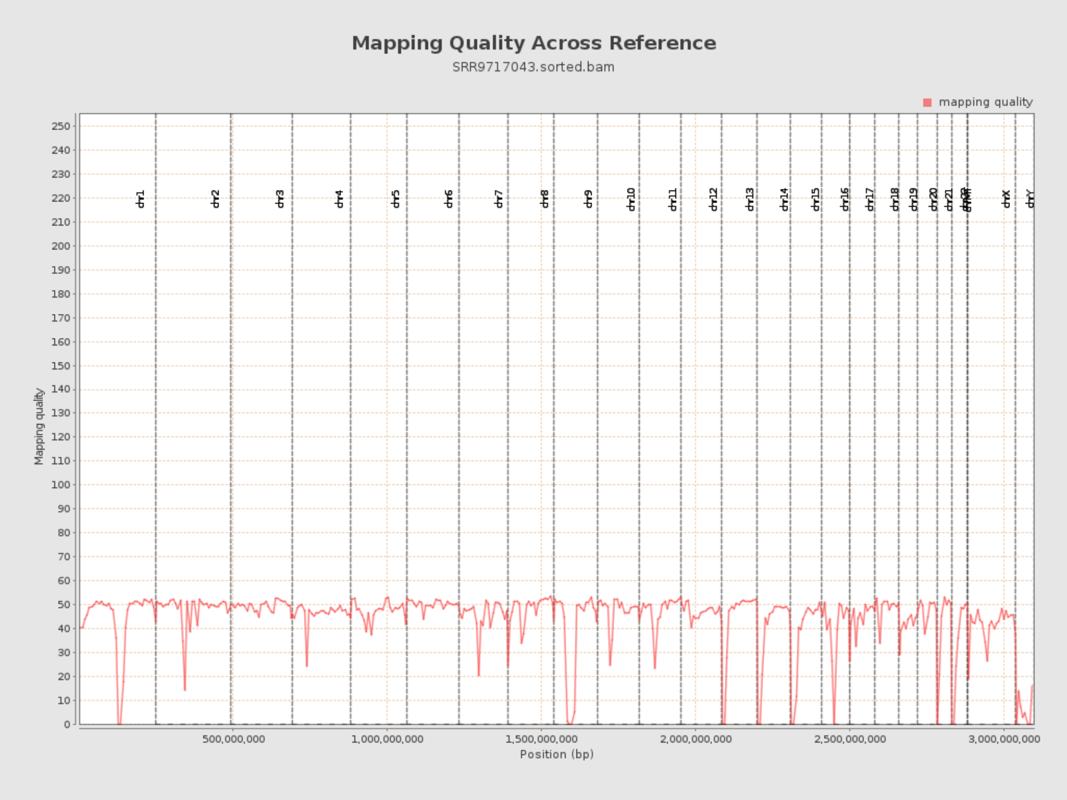
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram