Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717070.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_SRR9717070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717070.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:35:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	640,898
Mapped reads	562,287 / 87.73%
Unmapped reads	78,611 / 12.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,296 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	13,613 / 2.12%
Duplication rate	1.77%
Clipped reads	563,190 / 87.88%

2.2. ACGT Content

Number/percentage of A's	8,146,897 / 24.86%
Number/percentage of C's	5,828,213 / 17.78%
Number/percentage of T's	10,836,966 / 33.06%
Number/percentage of G's	7,963,280 / 24.3%
Number/percentage of N's	706 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.1306

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

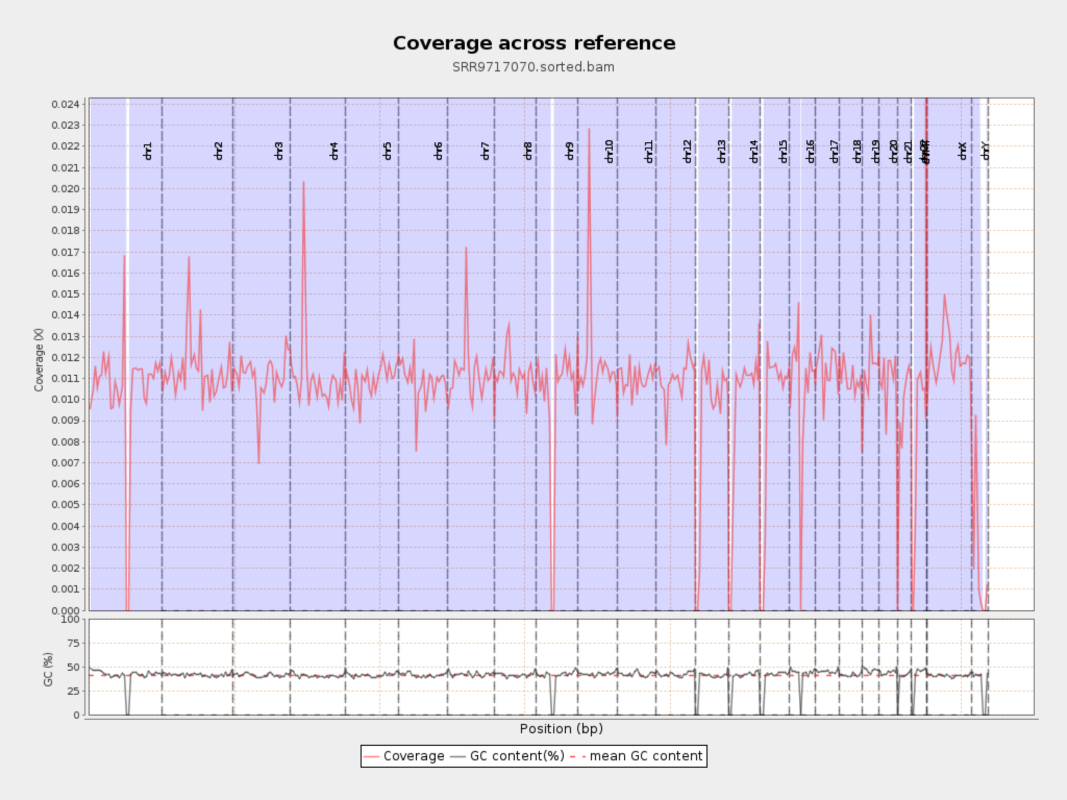
General error rate	0.53%
Mismatches	167,439
Insertions	2,291
Mapped reads with at least one insertion	0.4%
Deletions	6,634
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.54%

2.6. Chromosome stats

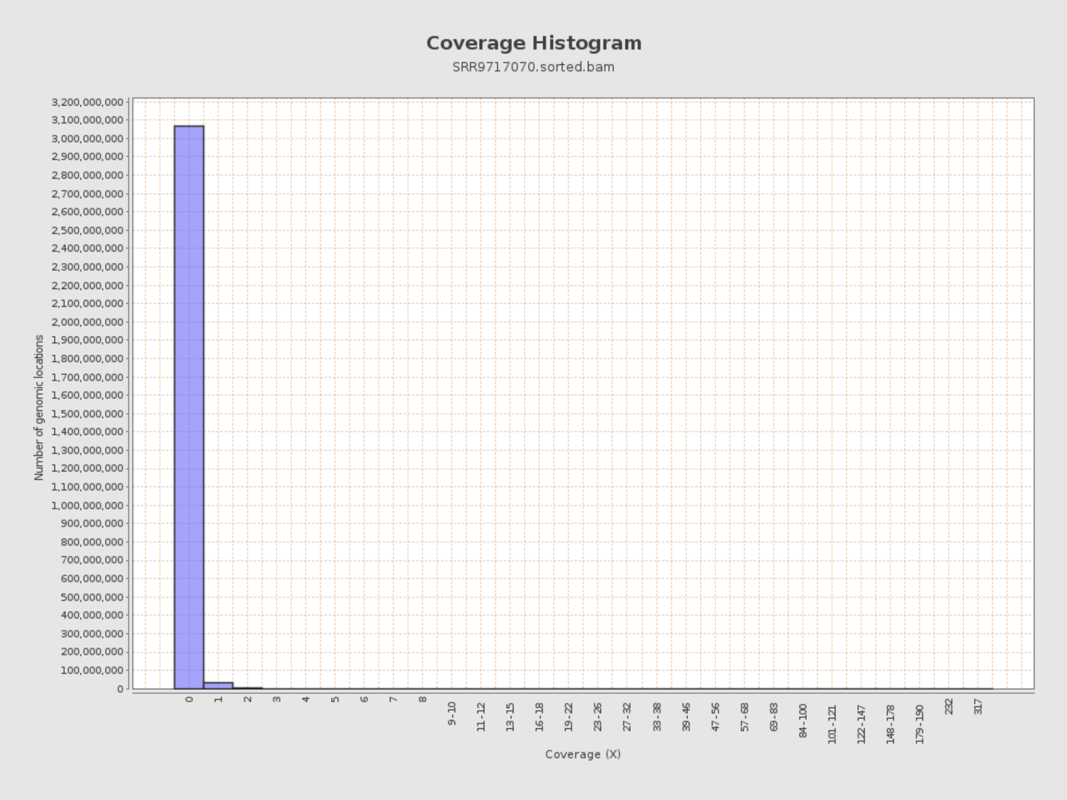
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2590958	0.0104	0.1718
chr2	243199373	2778820	0.0114	0.1752
chr3	198022430	2187245	0.011	0.1097
chr4	191154276	2113248	0.0111	0.1188
chr5	180915260	1975763	0.0109	0.1088
chr6	171115067	1858305	0.0109	0.1158
chr7	159138663	1810367	0.0114	0.1444

chr8	146364022	1642572	0.0112	0.1545
chr9	141213431	1387426	0.0098	0.1167
chr10	135534747	1587036	0.0117	0.1431
chr11	135006516	1482126	0.011	0.1208
chr12	133851895	1470573	0.011	0.1102
chr13	115169878	1029919	0.0089	0.0989
chr14	107349540	994778	0.0093	0.1009
chr15	102531392	942984	0.0092	0.1003
chr16	90354753	946140	0.0105	0.1102
chr17	81195210	929215	0.0114	0.1141
chr18	78077248	861250	0.011	0.1577
chr19	59128983	677222	0.0115	0.1528
chr20	63025520	690814	0.011	0.1111
chr21	48129895	437566	0.0091	0.1106
chr22	51304566	383634	0.0075	0.0903
chrMT	16571	6633	0.4003	0.675
chrX	155270560	1869173	0.012	0.1187
chrY	59373566	133048	0.0022	0.1023

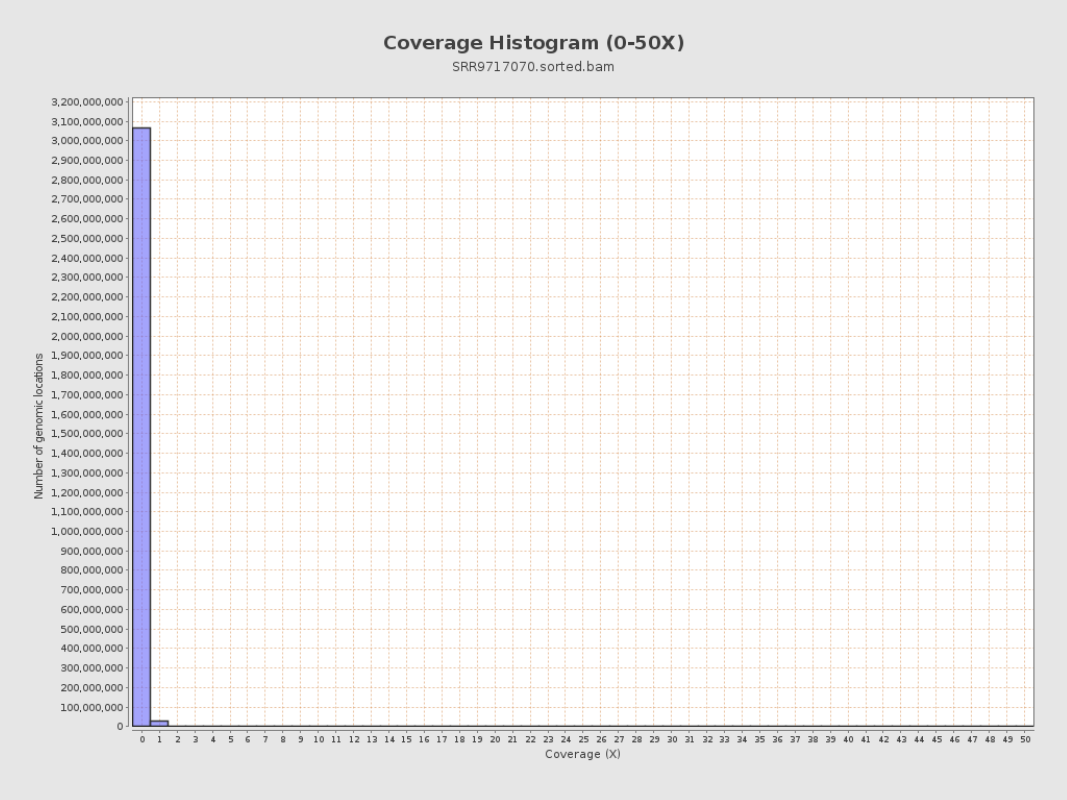
3. Results : Coverage across reference



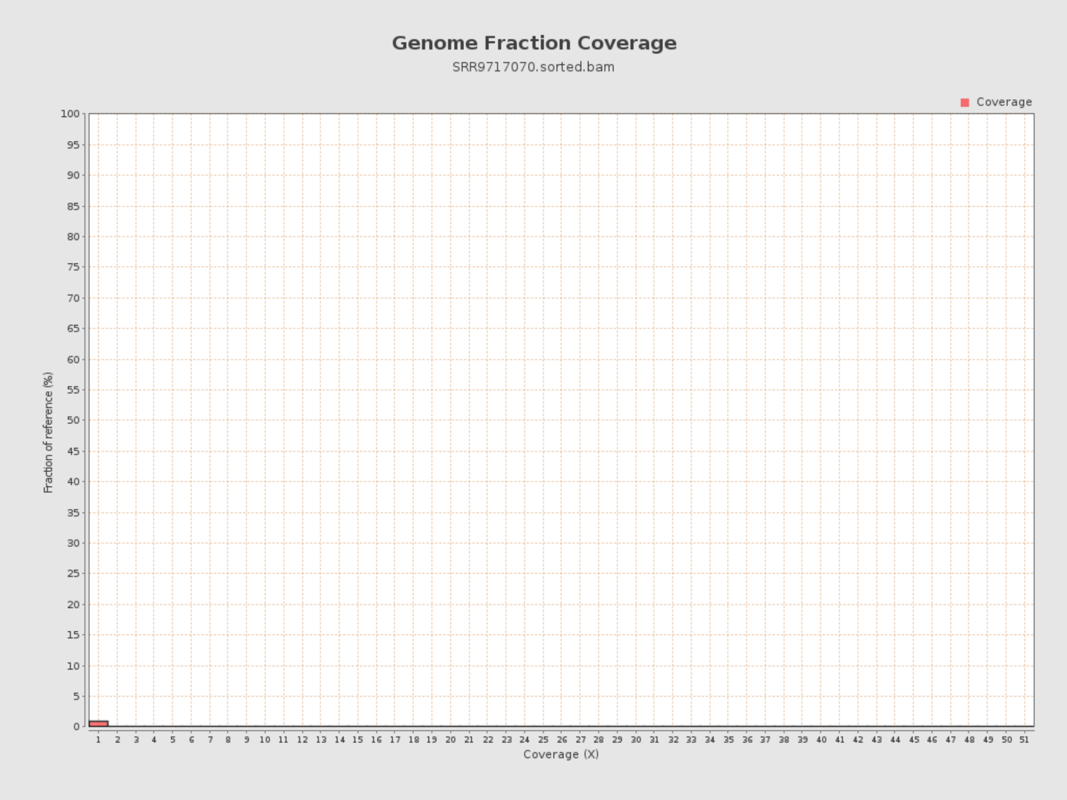
4. Results : Coverage Histogram



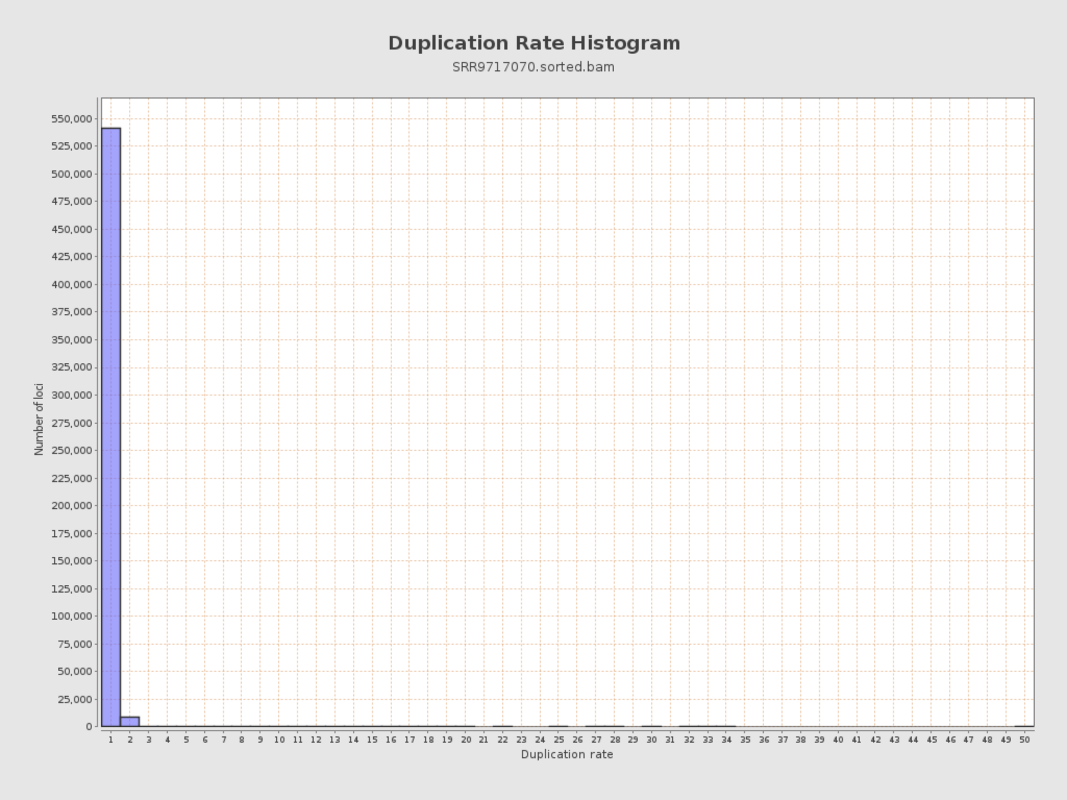
5. Results : Coverage Histogram (0-50X)



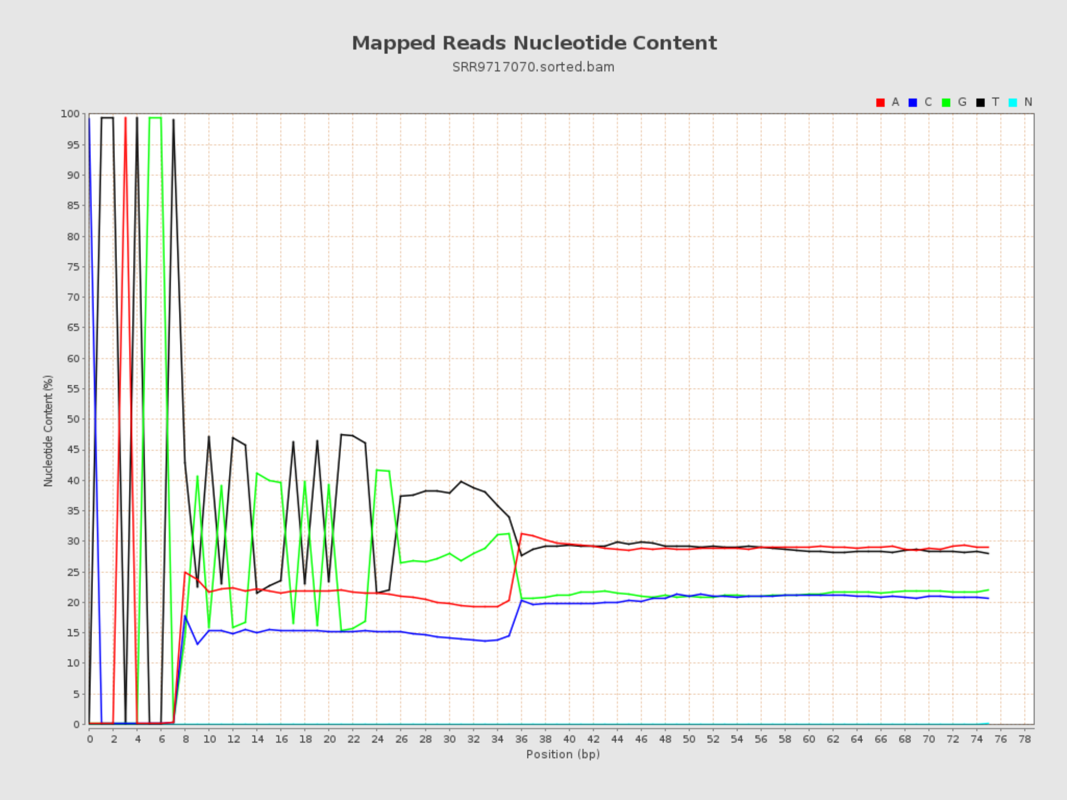
6. Results : Genome Fraction Coverage



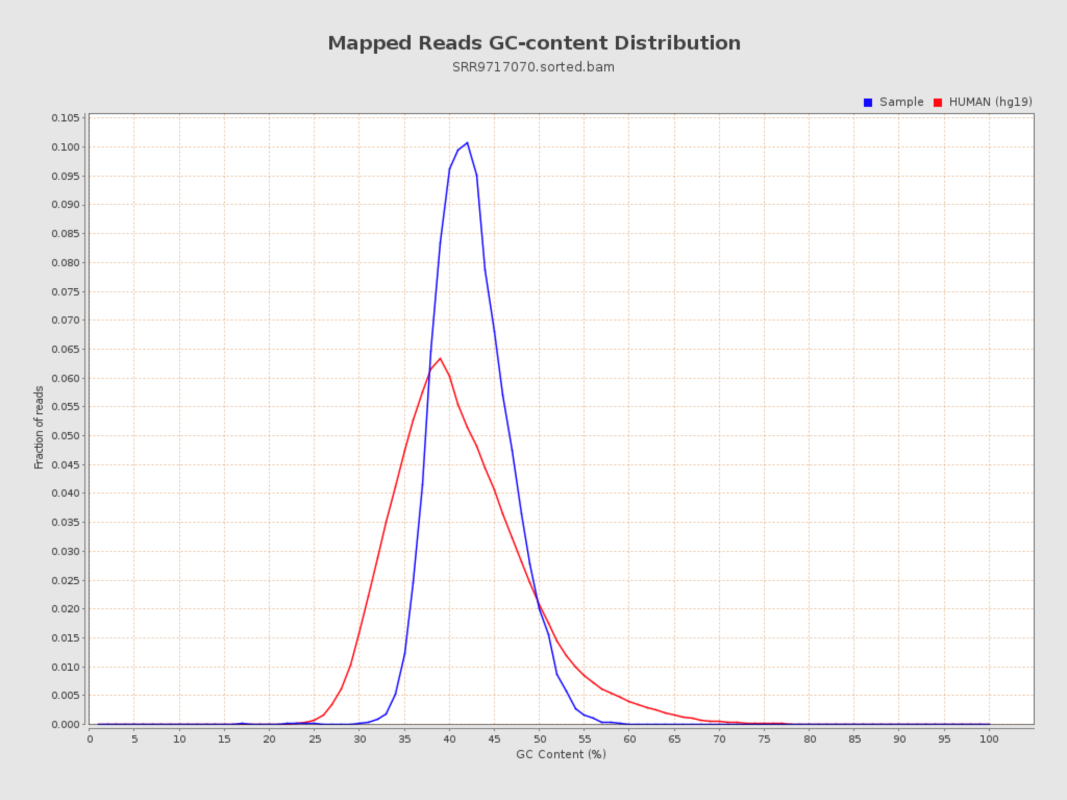
7. Results : Duplication Rate Histogram



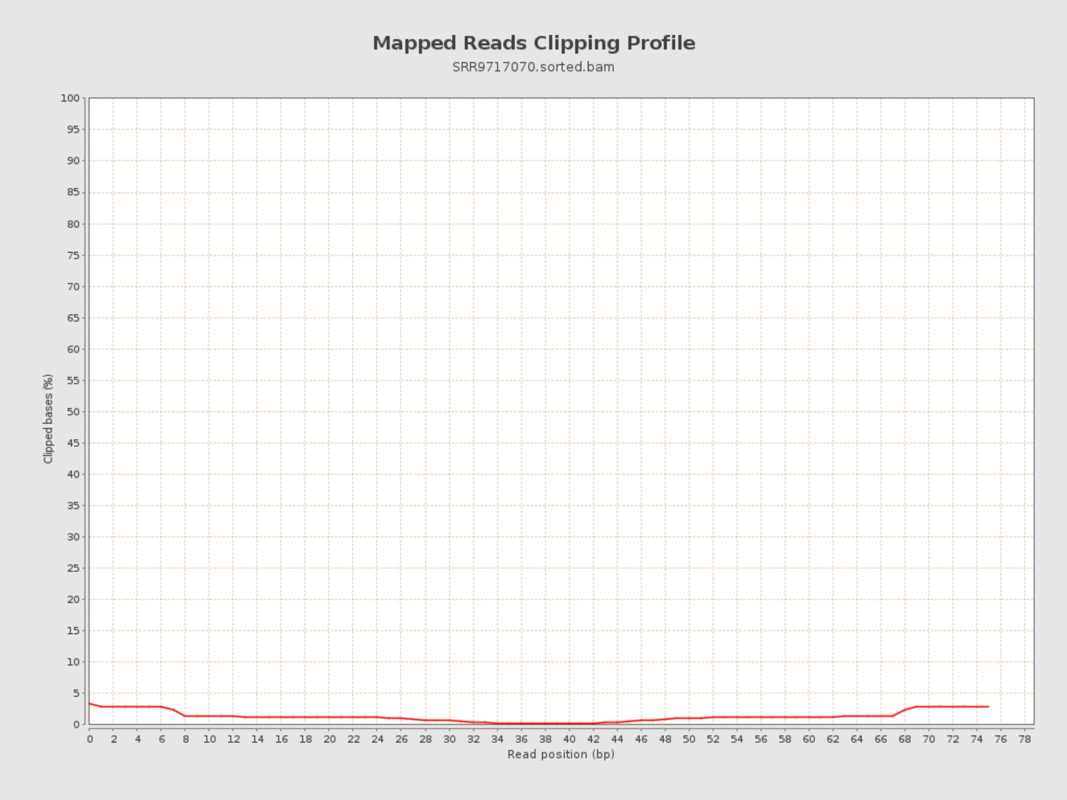
8. Results : Mapped Reads Nucleotide Content



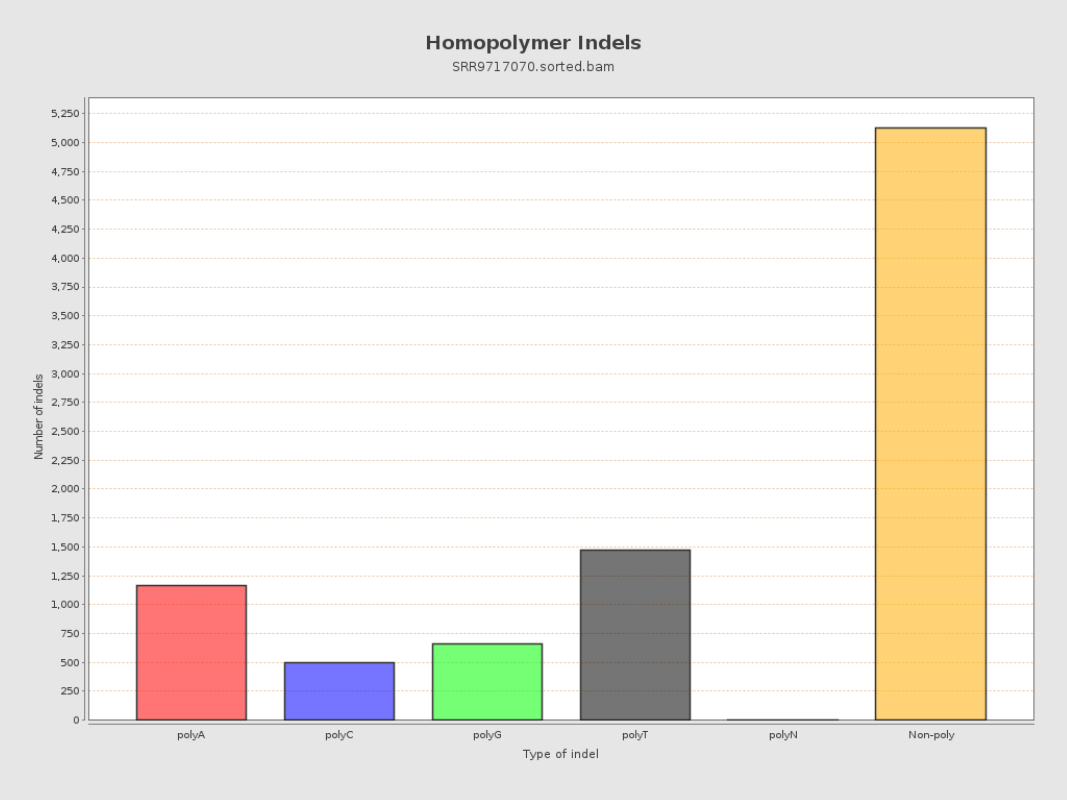
9. Results : Mapped Reads GC-content Distribution



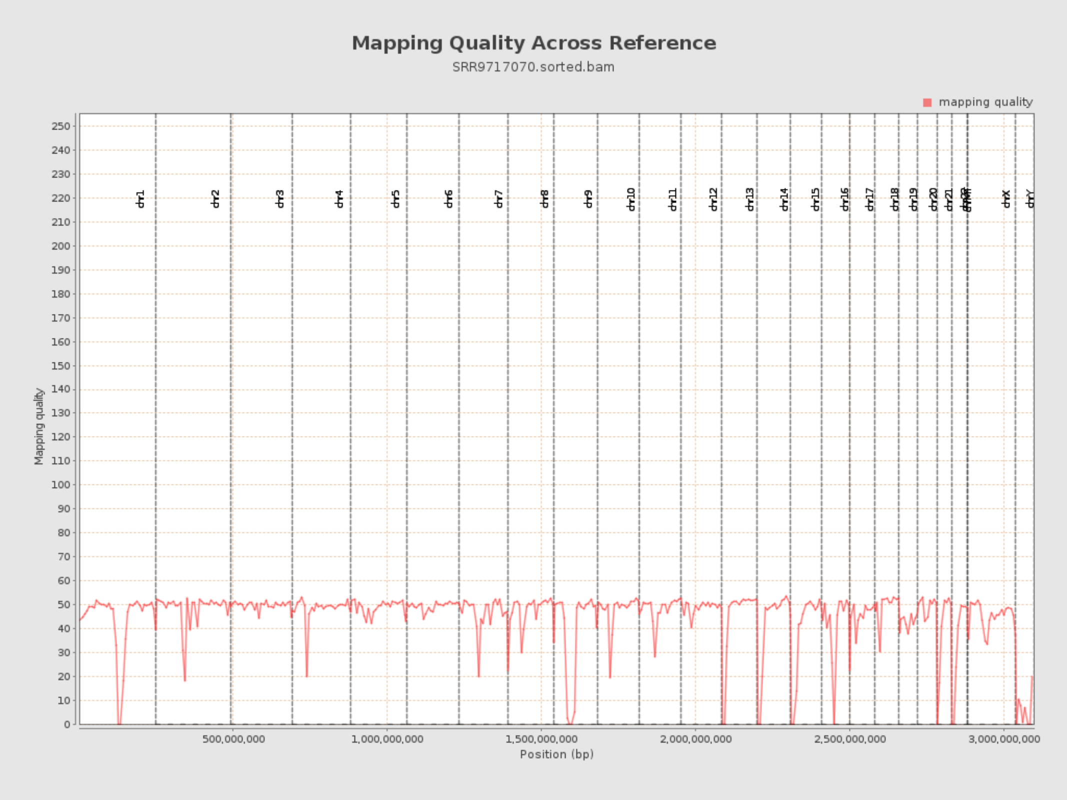
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram