Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:43:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717033.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_SRR9717033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:43:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	484,922
Mapped reads	411,680 / 84.9%
Unmapped reads	73,242 / 15.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,751 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	5,642 / 1.16%
Duplication rate	1.02%
Clipped reads	412,382 / 85.04%

2.2. ACGT Content

Number/percentage of A's	5,514,152 / 23.75%
Number/percentage of C's	4,264,312 / 18.36%
Number/percentage of T's	7,511,709 / 32.35%
Number/percentage of G's	5,930,631 / 25.54%
Number/percentage of N's	274 / 0%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.1005

2.4. Mapping Quality

Mean Mapping Quality	41.92

2.5. Mismatches and indels

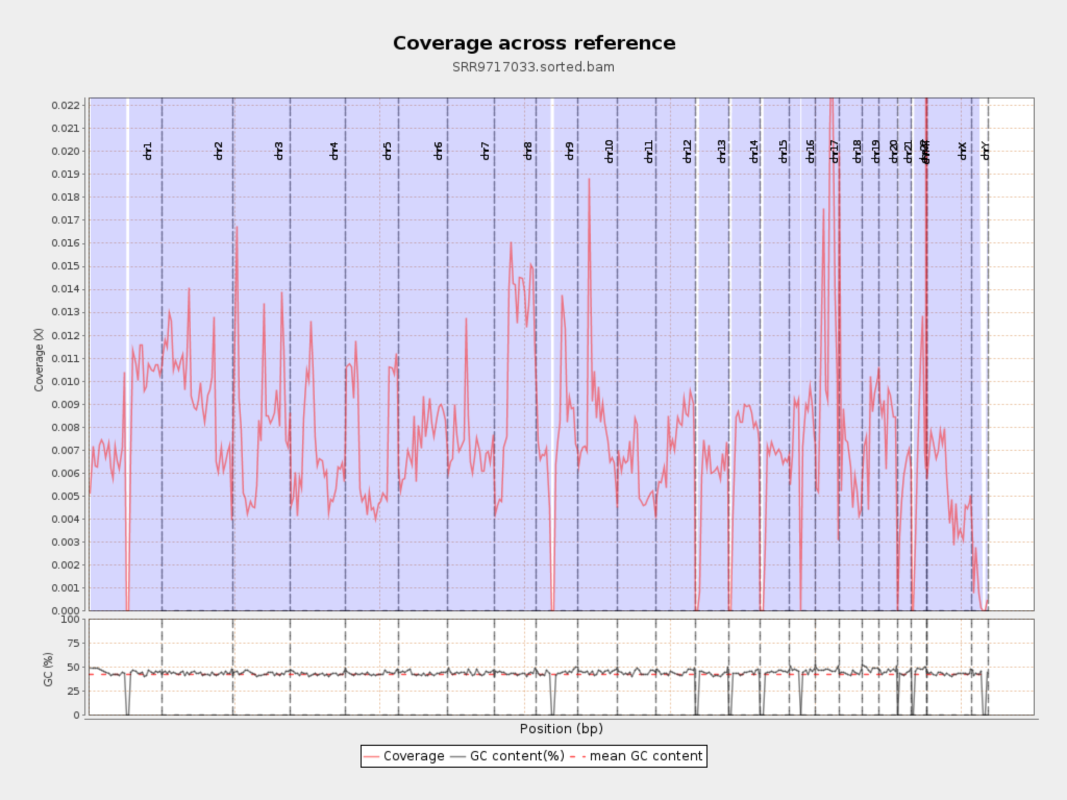
General error rate	0.54%
Mismatches	121,613
Insertions	1,770
Mapped reads with at least one insertion	0.43%
Deletions	4,265
Mapped reads with at least one deletion	1.03%
Homopolymer indels	38.84%

2.6. Chromosome stats

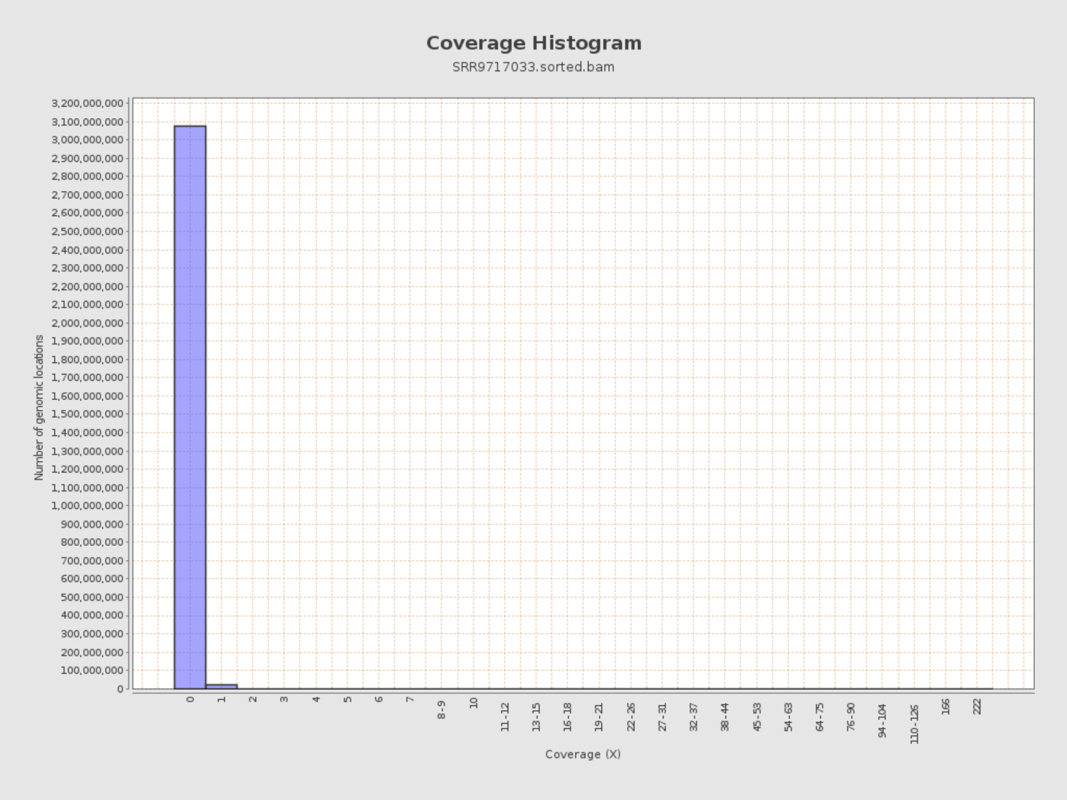
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1989374	0.008	0.1271
chr2	243199373	2323203	0.0096	0.1366
chr3	198022430	1625119	0.0082	0.0933
chr4	191154276	1268386	0.0066	0.0857
chr5	180915260	1322000	0.0073	0.0878
chr6	171115067	1289919	0.0075	0.0923
chr7	159138663	1157576	0.0073	0.1195

chr8	146364022	1646903	0.0113	0.1151
chr9	141213431	1018148	0.0072	0.0912
chr10	135534747	1129880	0.0083	0.1107
chr11	135006516	797136	0.0059	0.083
chr12	133851895	1001211	0.0075	0.0894
chr13	115169878	616252	0.0054	0.0749
chr14	107349540	759457	0.0071	0.0871
chr15	102531392	571992	0.0056	0.0767
chr16	90354753	688562	0.0076	0.0914
chr17	81195210	1017565	0.0125	0.1172
chr18	78077248	516093	0.0066	0.0986
chr19	59128983	484880	0.0082	0.1109
chr20	63025520	530494	0.0084	0.0944
chr21	48129895	244395	0.0051	0.0738
chr22	51304566	321791	0.0063	0.0817
chrMT	16571	3434	0.2072	0.4733
chrX	155270560	850267	0.0055	0.0799
chrY	59373566	53838	0.0009	0.0342

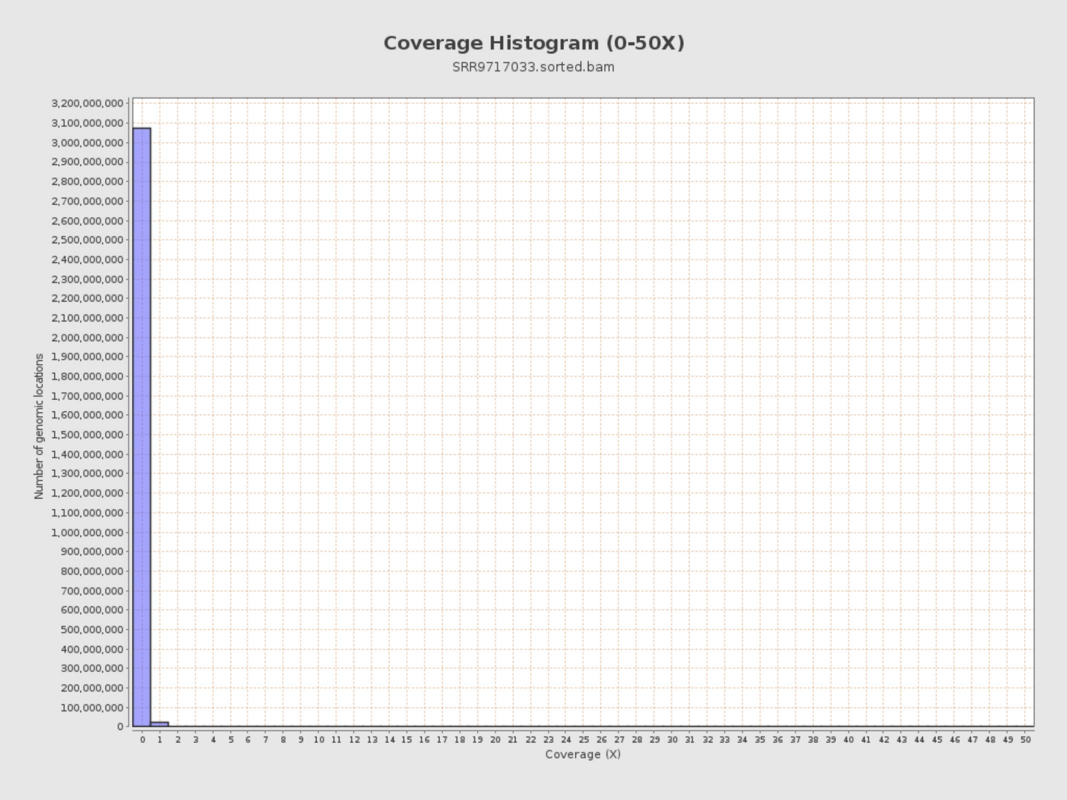
3. Results : Coverage across reference



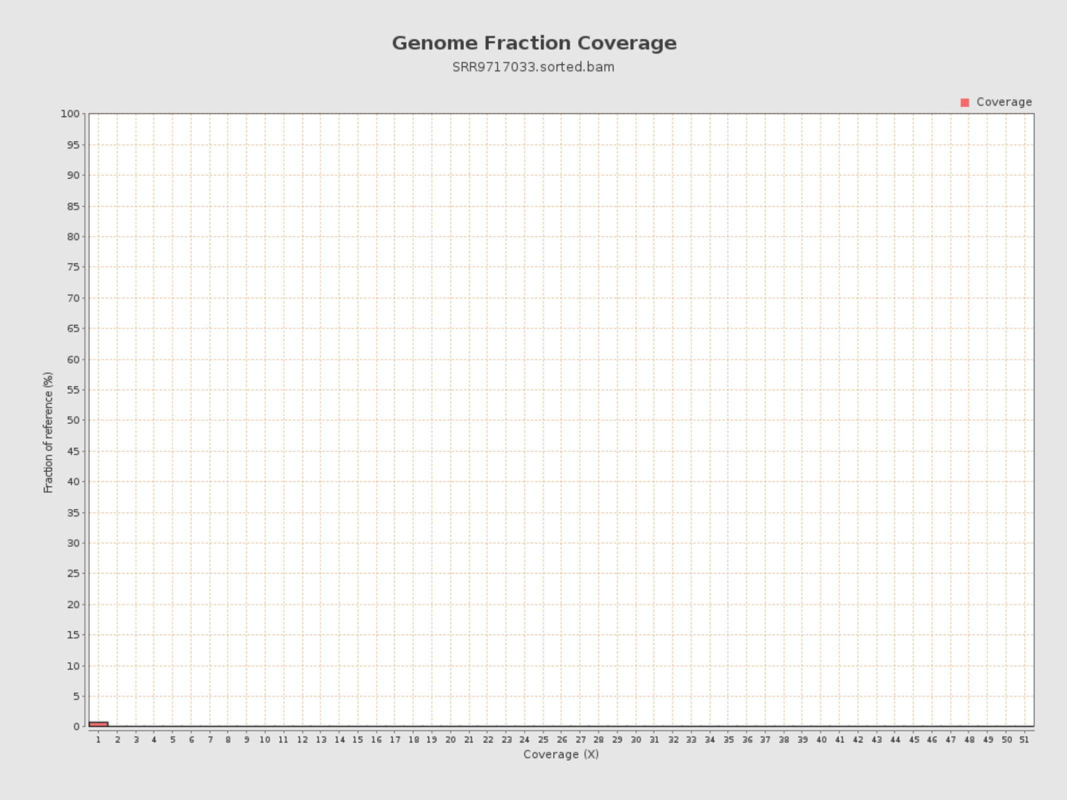
4. Results : Coverage Histogram



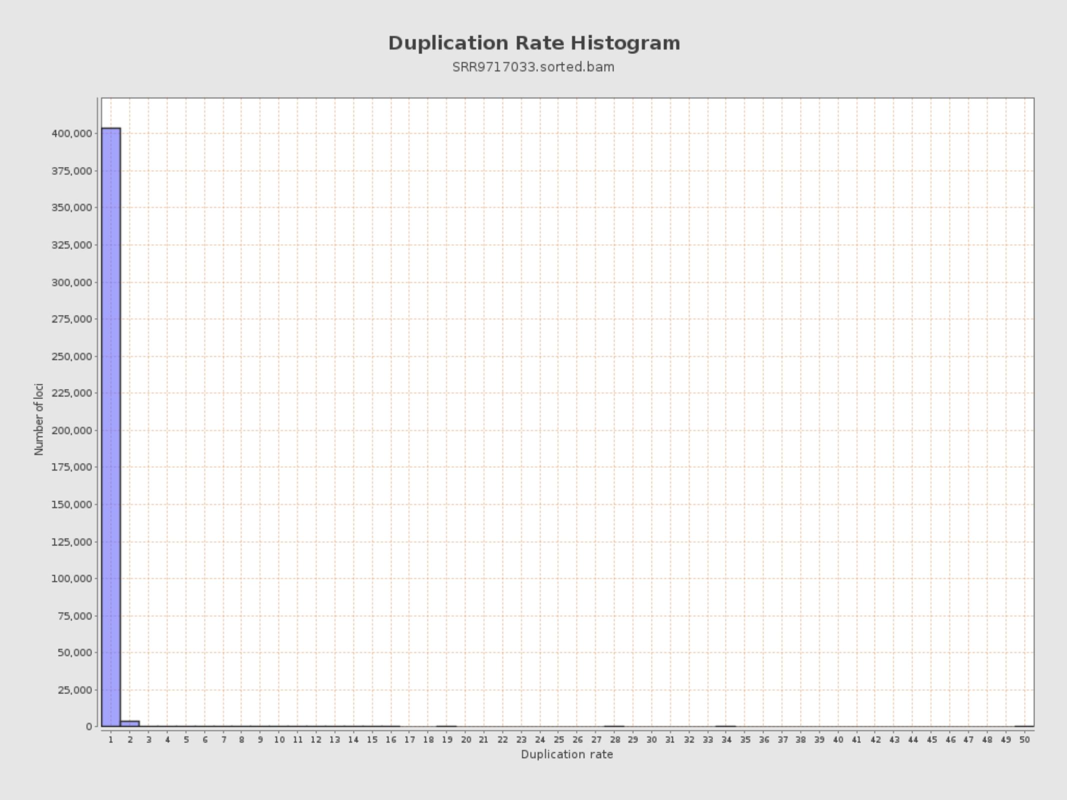
5. Results : Coverage Histogram (0-50X)



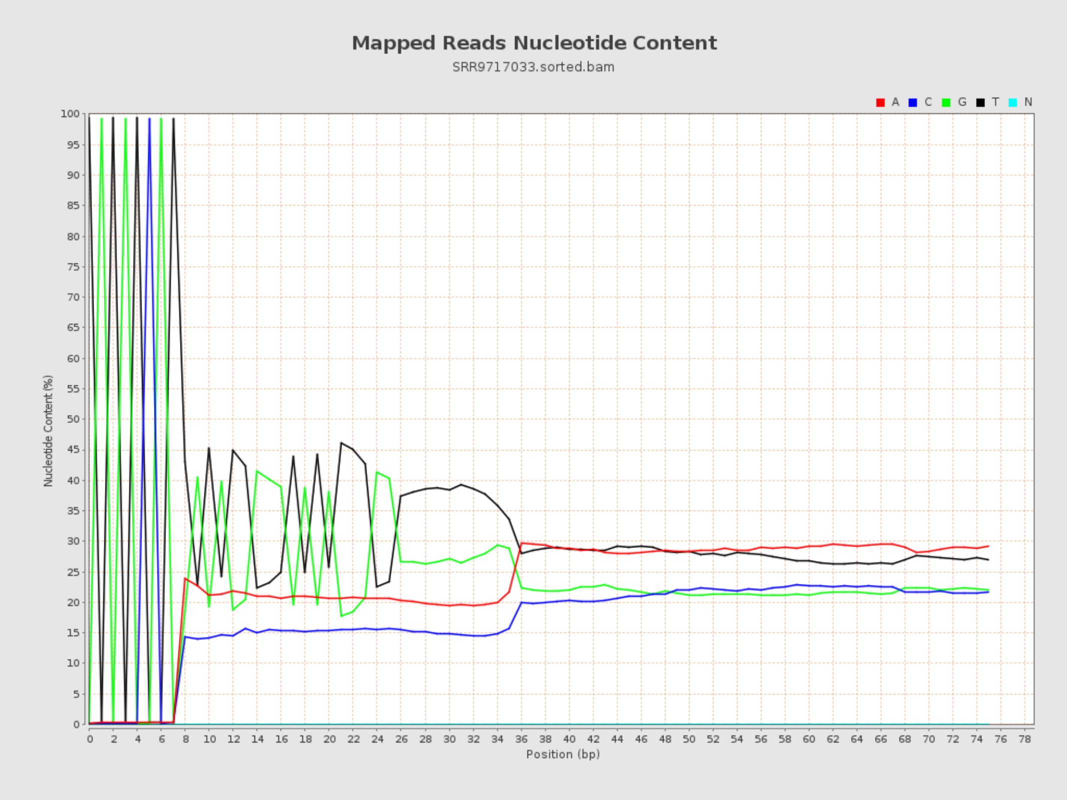
6. Results : Genome Fraction Coverage



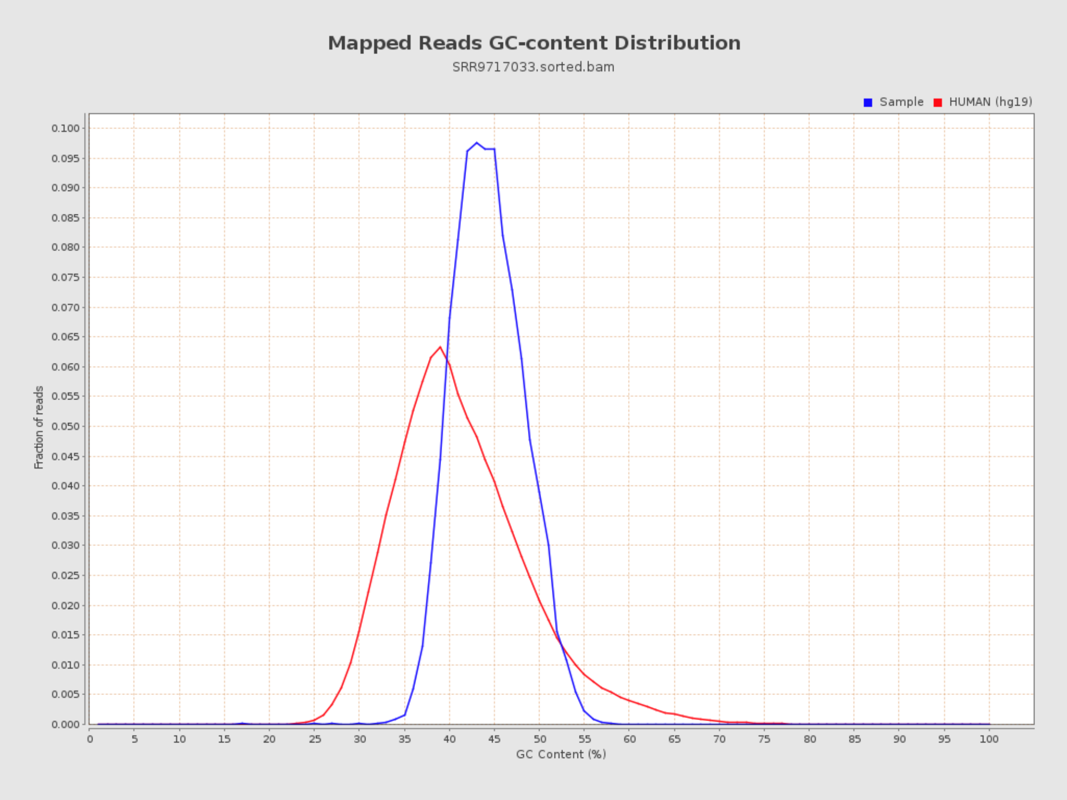
7. Results : Duplication Rate Histogram



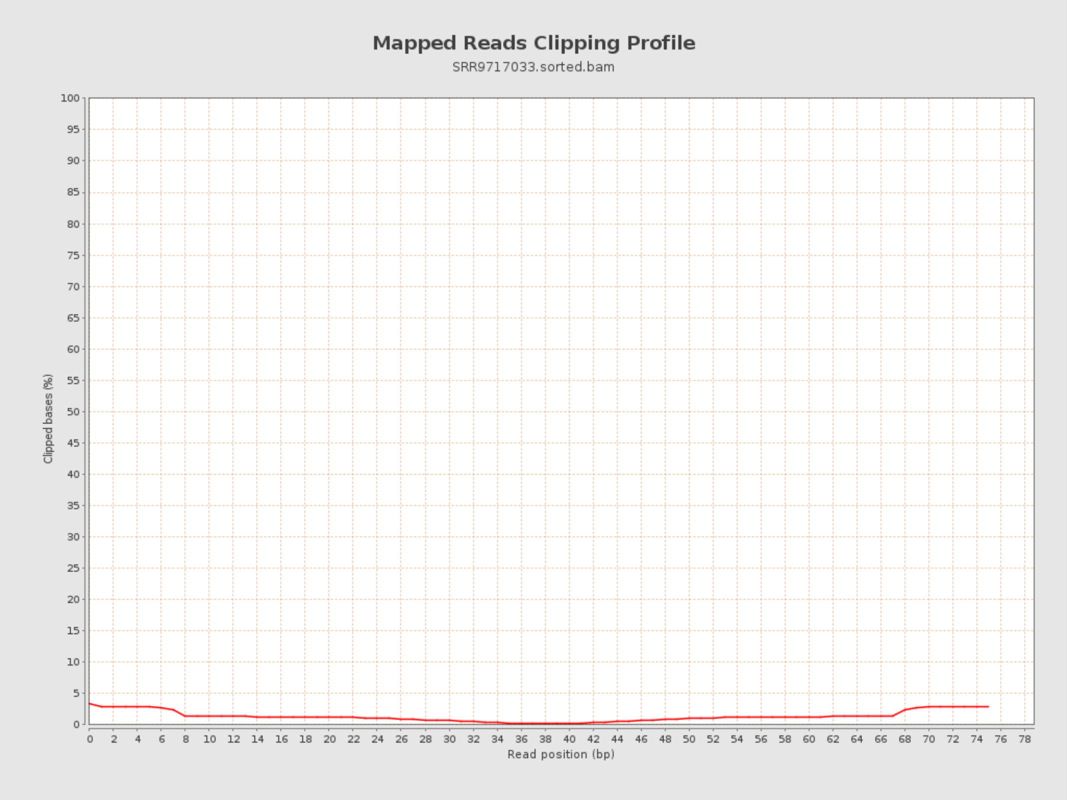
8. Results : Mapped Reads Nucleotide Content



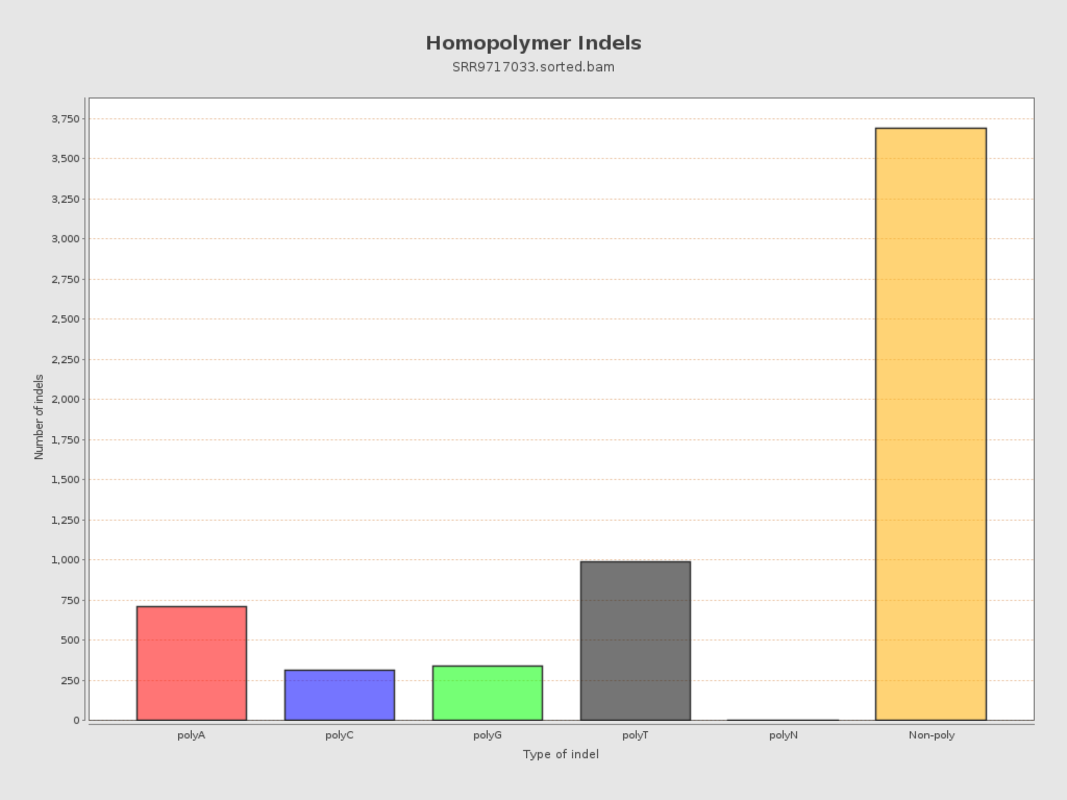
9. Results : Mapped Reads GC-content Distribution



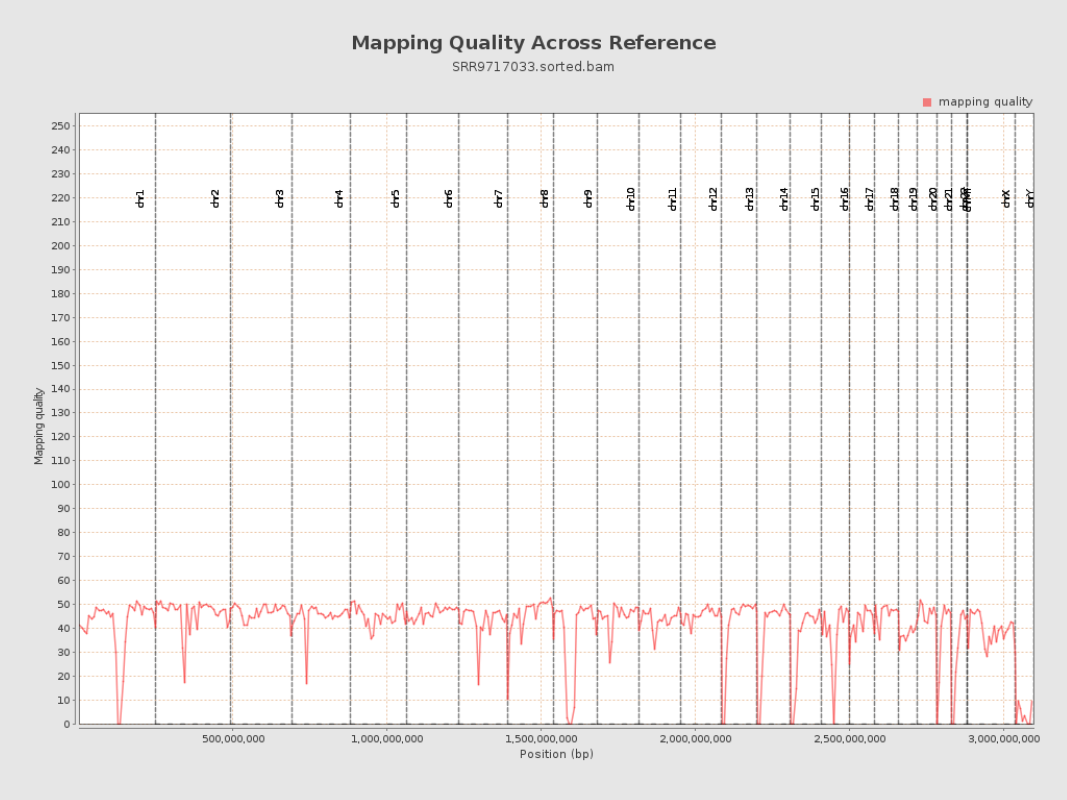
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram