Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:59:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717053.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_SRR9717053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:59:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,084,000
Mapped reads	928,668 / 85.67%
Unmapped reads	155,332 / 14.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,646 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	18,823 / 1.74%
Duplication rate	1.46%
Clipped reads	929,469 / 85.74%

2.2. ACGT Content

Number/percentage of A's	12,403,075 / 23.77%
Number/percentage of C's	11,739,774 / 22.5%
Number/percentage of T's	14,737,893 / 28.24%
Number/percentage of G's	13,305,081 / 25.49%
Number/percentage of N's	1,438 / 0%
GC Percentage	47.99%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1597

2.4. Mapping Quality

Mean Mapping Quality	38.46

2.5. Mismatches and indels

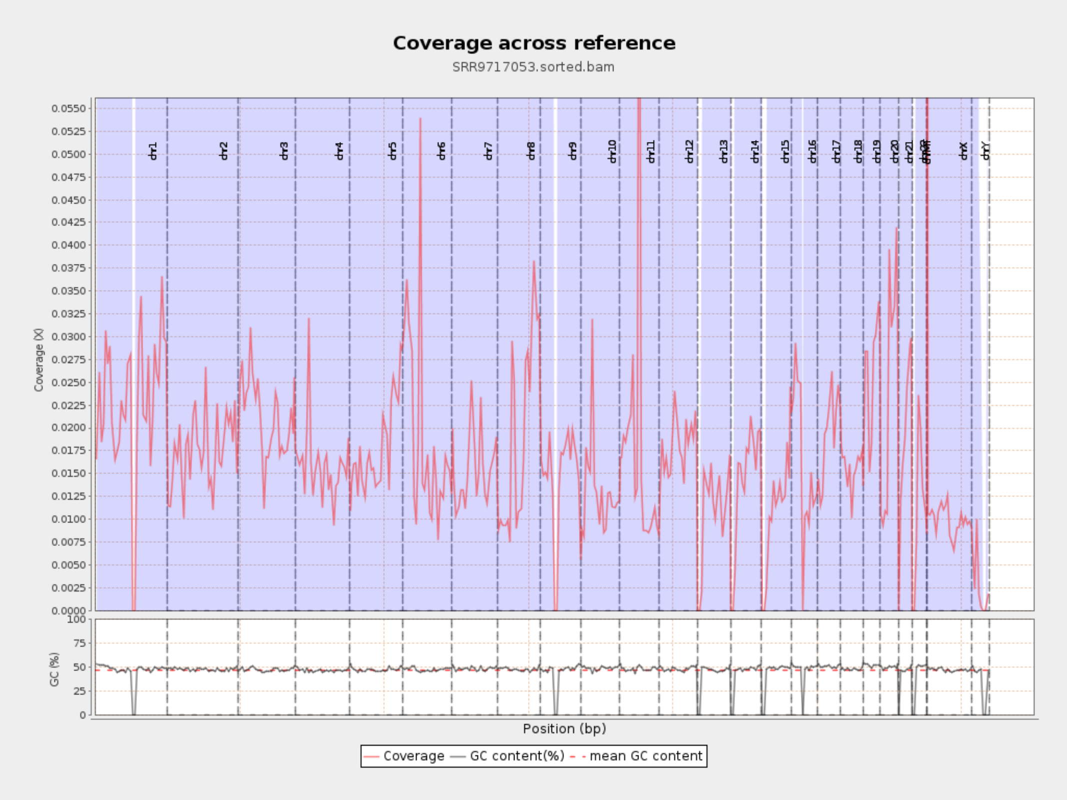
General error rate	0.54%
Mismatches	270,198
Insertions	4,587
Mapped reads with at least one insertion	0.49%
Deletions	8,786
Mapped reads with at least one deletion	0.94%
Homopolymer indels	33.27%

2.6. Chromosome stats

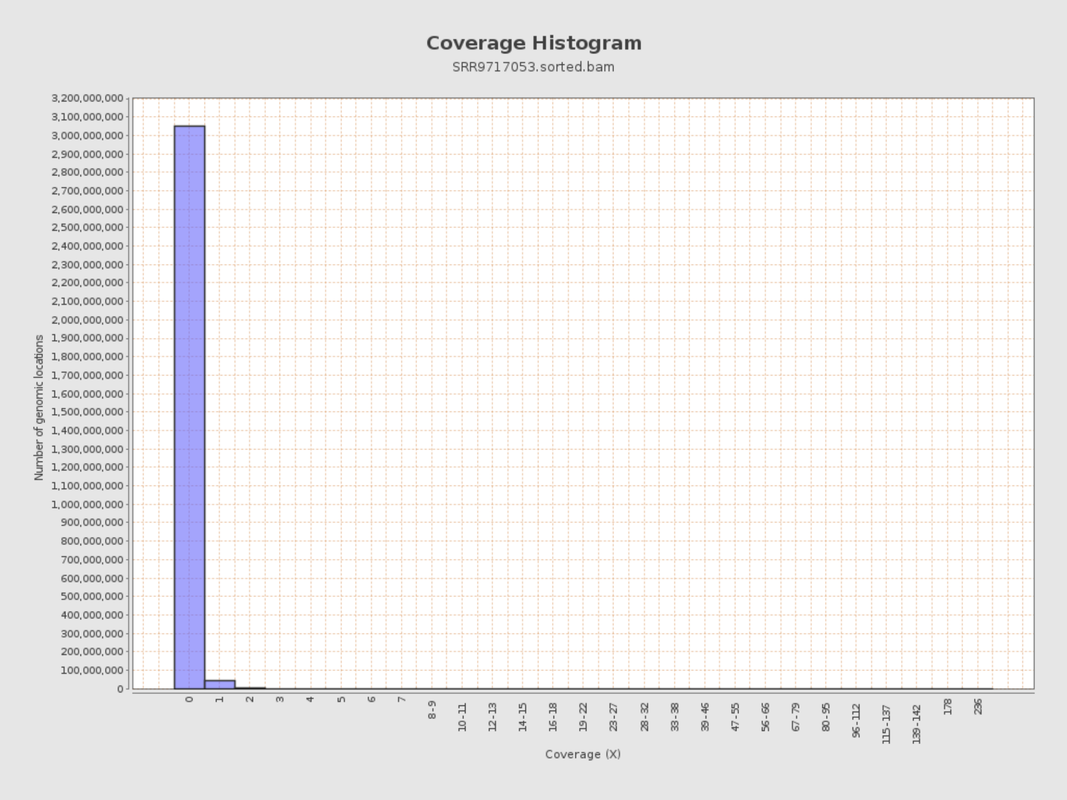
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5659186	0.0227	0.1996
chr2	243199373	4271174	0.0176	0.1928
chr3	198022430	4193669	0.0212	0.1622
chr4	191154276	3058145	0.016	0.1532
chr5	180915260	3229795	0.0179	0.1455
chr6	171115067	3302441	0.0193	0.1561
chr7	159138663	2488018	0.0156	0.1523

chr8	146364022	2844628	0.0194	0.1574
chr9	141213431	2072597	0.0147	0.1402
chr10	135534747	1794353	0.0132	0.1854
chr11	135006516	2536015	0.0188	0.1852
chr12	133851895	2409912	0.018	0.1459
chr13	115169878	1241585	0.0108	0.1122
chr14	107349540	1509037	0.0141	0.1333
chr15	102531392	1092191	0.0107	0.112
chr16	90354753	1443457	0.016	0.1457
chr17	81195210	1561856	0.0192	0.1596
chr18	78077248	1209957	0.0155	0.1736
chr19	59128983	1525559	0.0258	0.202
chr20	63025520	1524738	0.0242	0.1763
chr21	48129895	927442	0.0193	0.1628
chr22	51304566	594875	0.0116	0.1212
chrMT	16571	7296	0.4403	0.7328
chrX	155270560	1543198	0.0099	0.1157
chrY	59373566	160765	0.0027	0.091

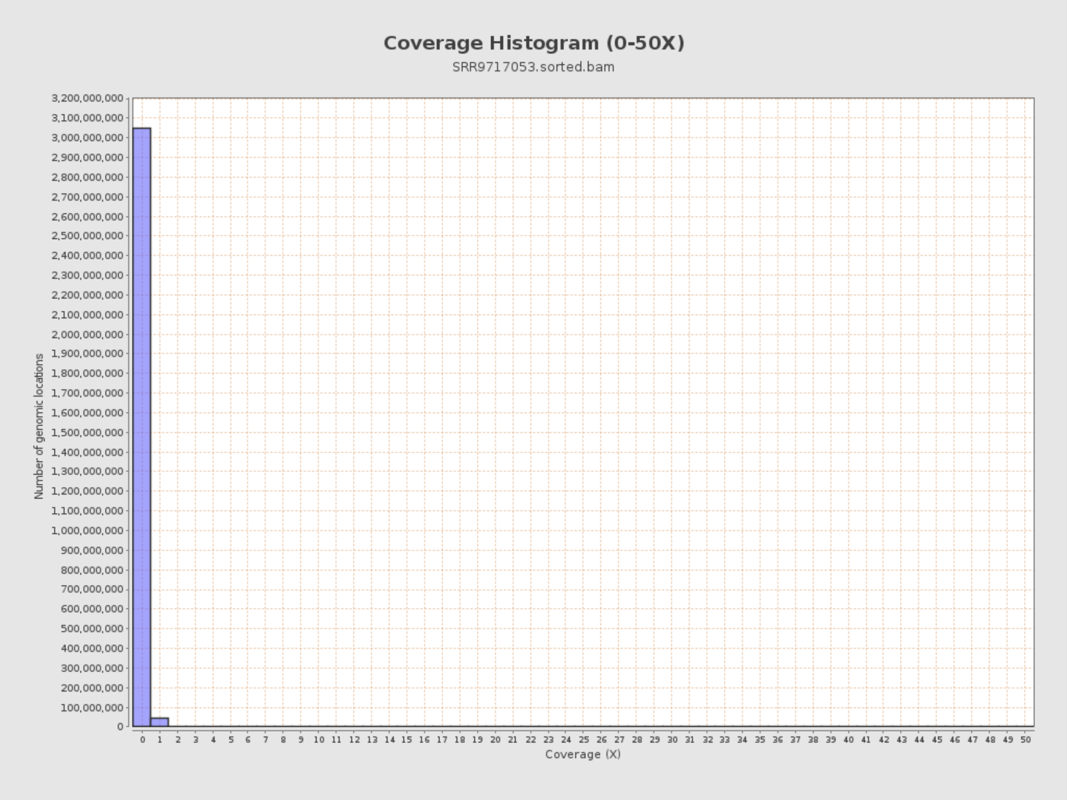
3. Results : Coverage across reference



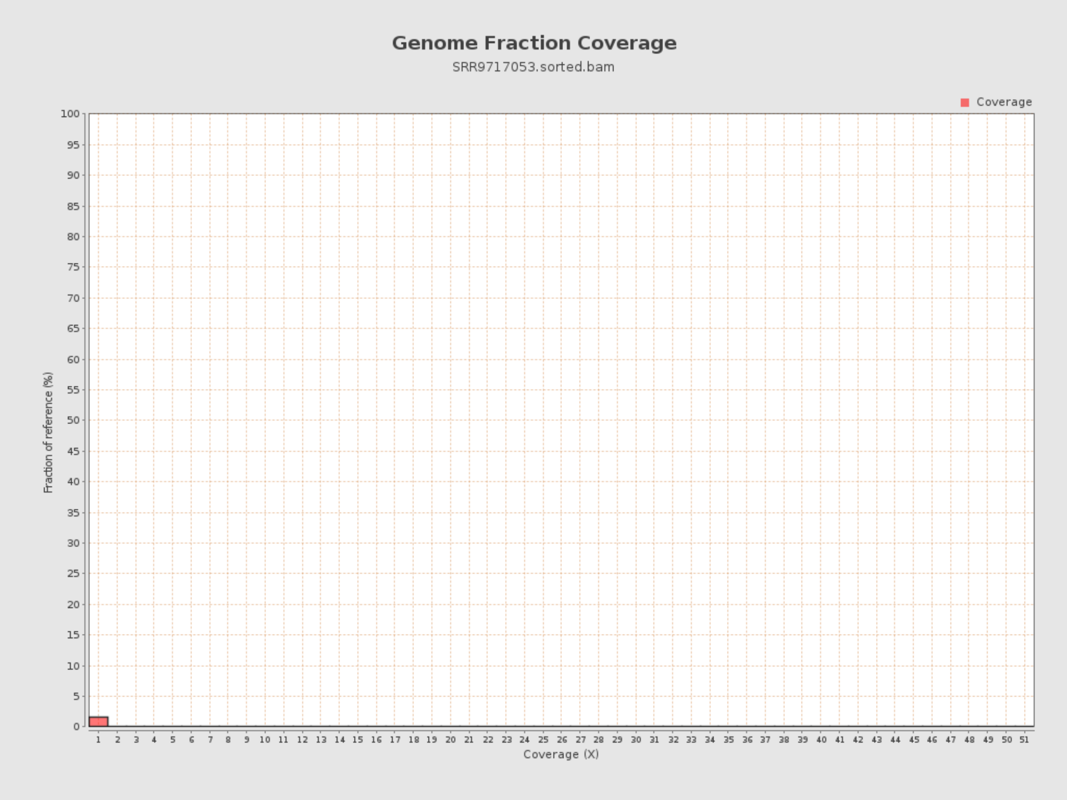
4. Results : Coverage Histogram



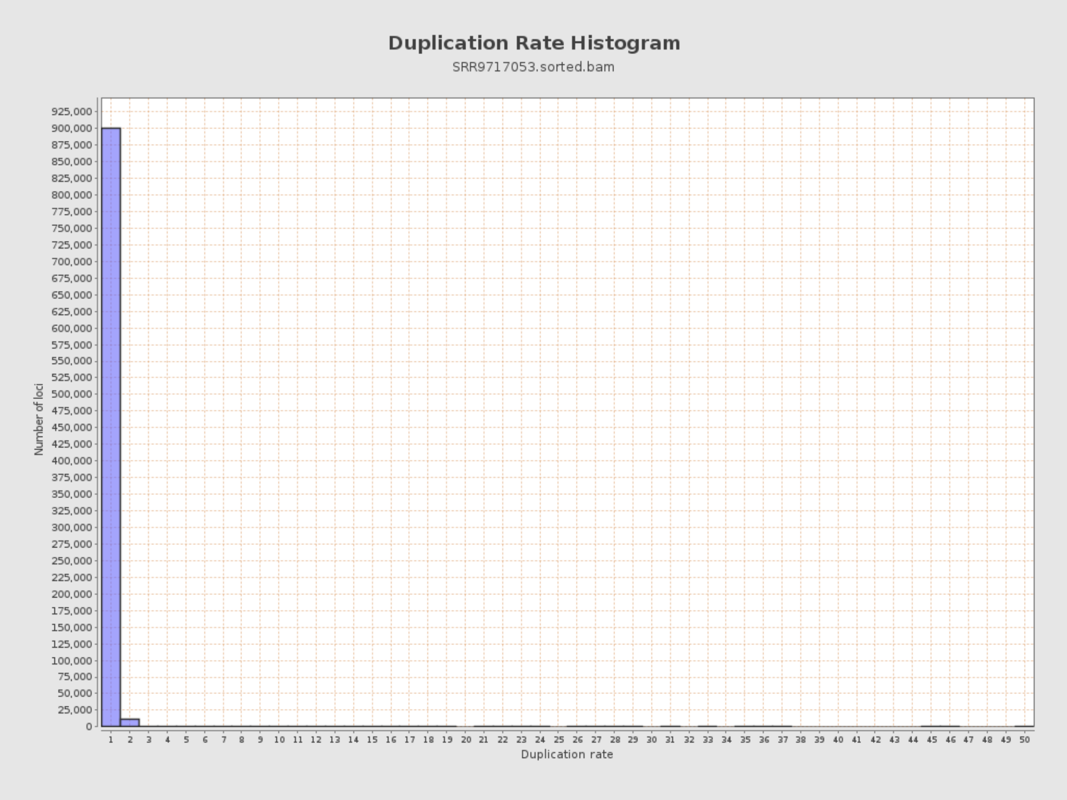
5. Results : Coverage Histogram (0-50X)



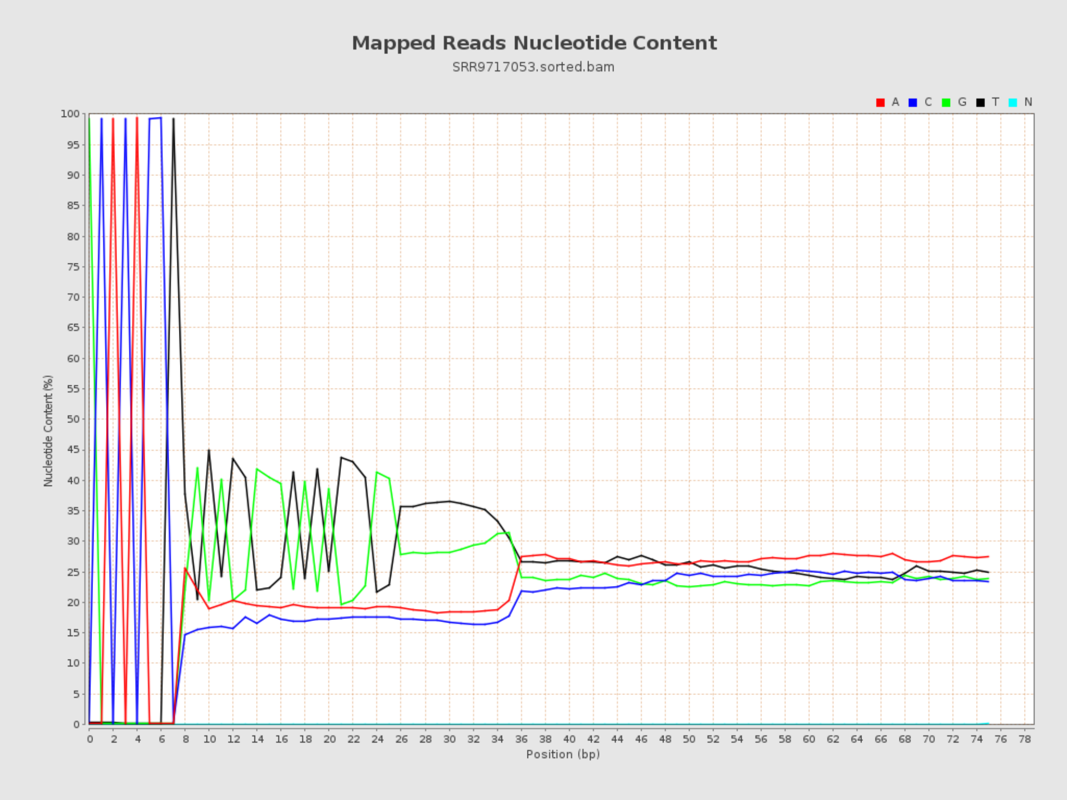
6. Results : Genome Fraction Coverage



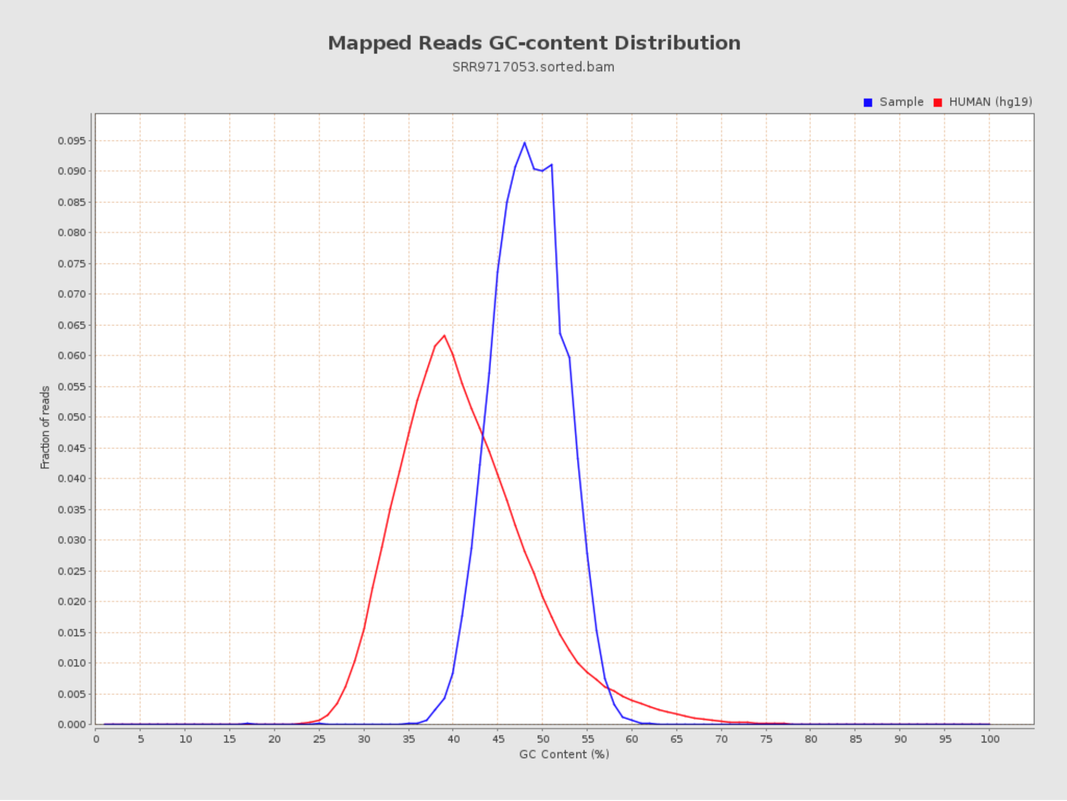
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



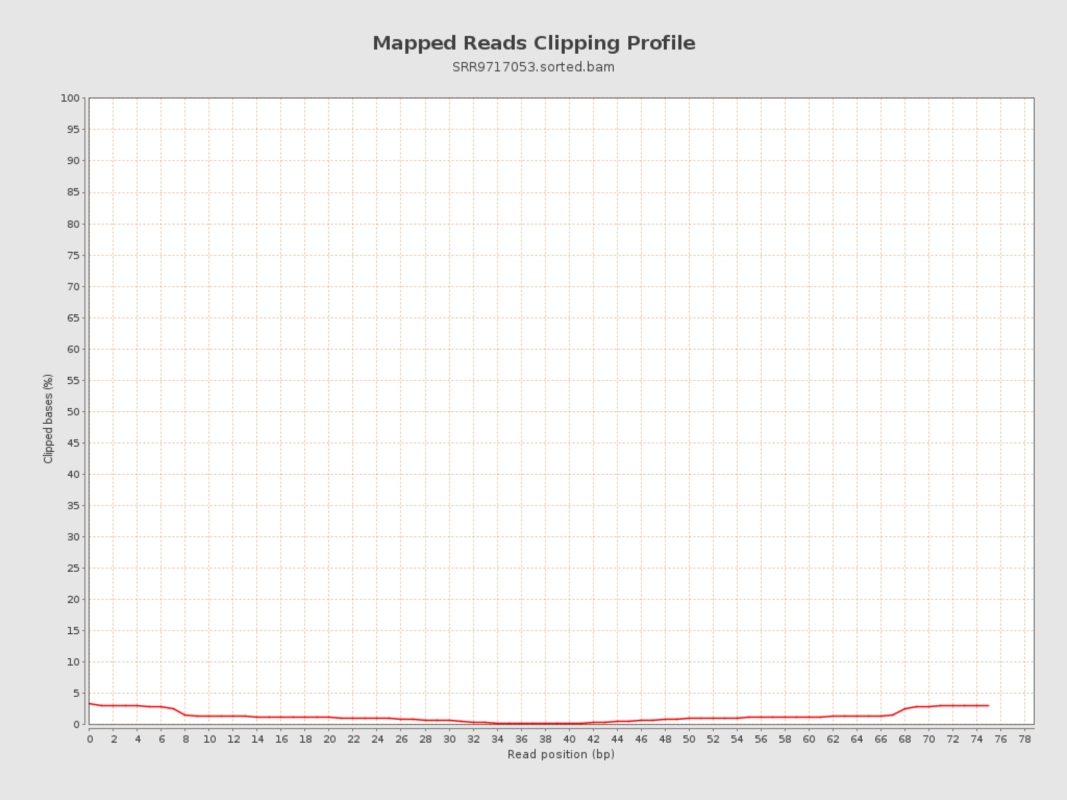
9. Results : Mapped Reads GC-content Distribution



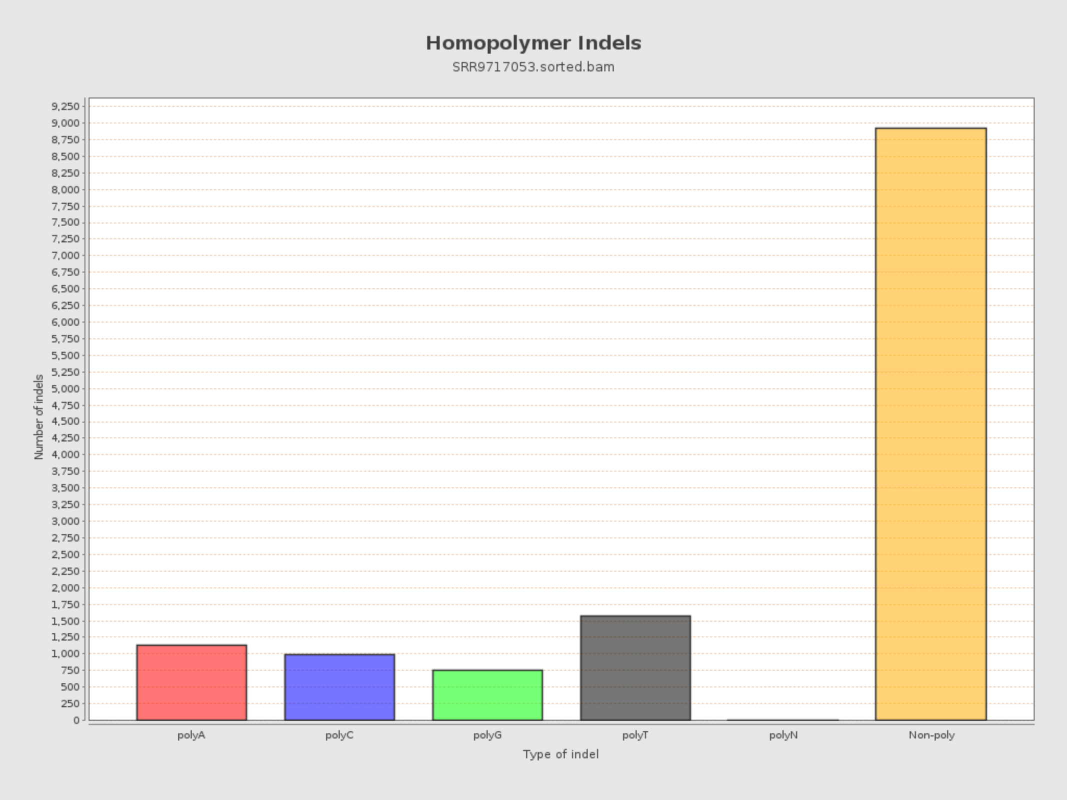
Mapped Reads GC-content Distribution

SRR9717053.sorted.bam

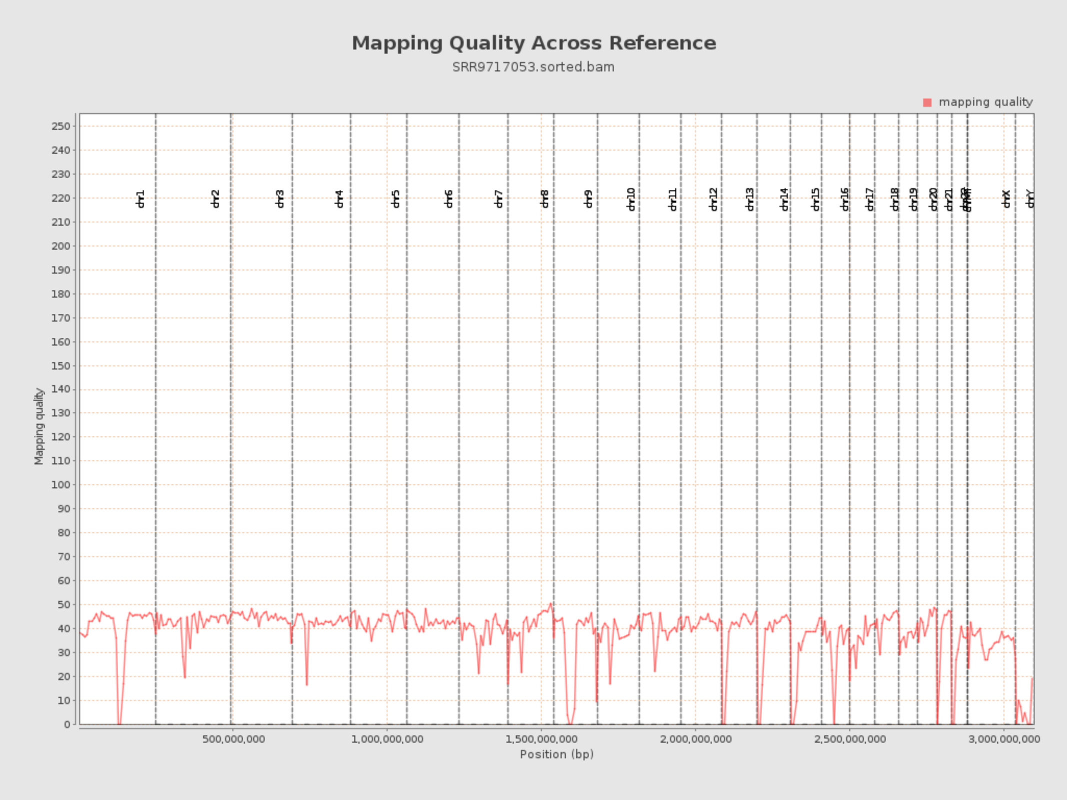
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram