Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:18:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717058.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_SRR9717058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:18:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	669,750
Mapped reads	600,794 / 89.7%
Unmapped reads	68,956 / 10.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,227 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,468 / 2.61%
Duplication rate	2.19%
Clipped reads	600,827 / 89.71%

2.2. ACGT Content

Number/percentage of A's	7,857,265 / 23.01%
Number/percentage of C's	6,551,970 / 19.19%
Number/percentage of T's	11,425,274 / 33.47%
Number/percentage of G's	8,305,025 / 24.33%
Number/percentage of N's	694 / 0%
GC Percentage	43.52%

2.3. Coverage

Mean	0.011

Standard Deviation	0.1342

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

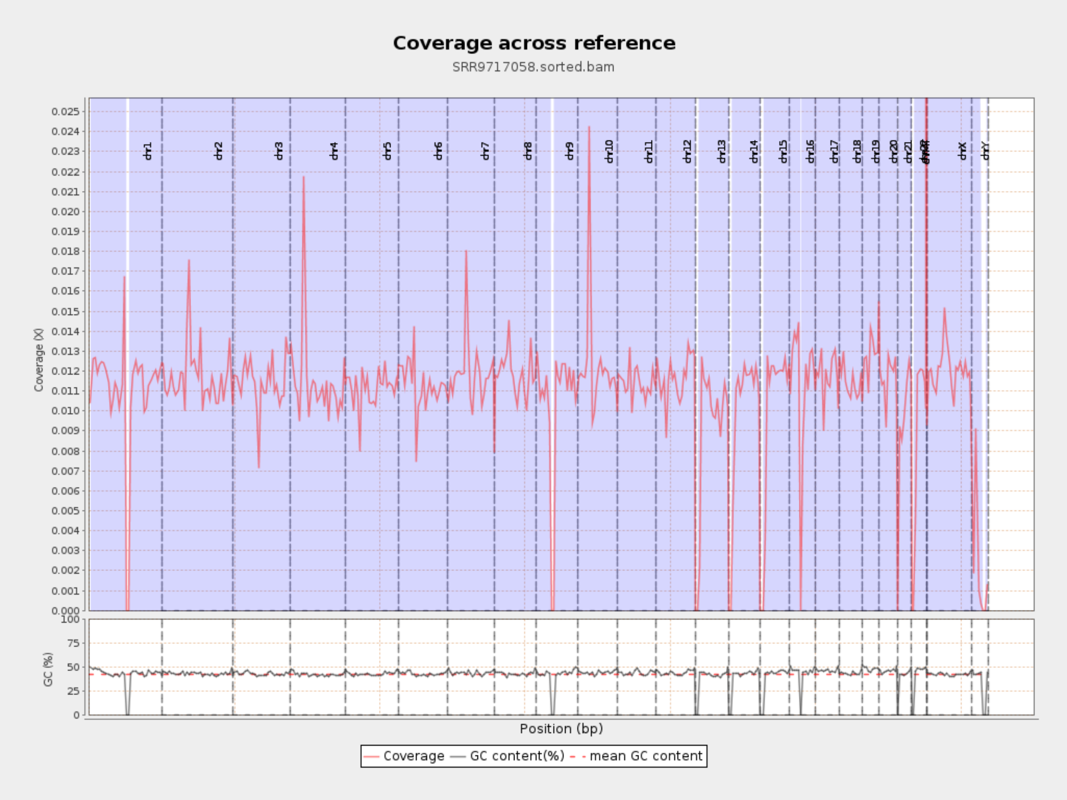
General error rate	0.54%
Mismatches	177,980
Insertions	2,750
Mapped reads with at least one insertion	0.46%
Deletions	6,762
Mapped reads with at least one deletion	1.12%
Homopolymer indels	39.84%

2.6. Chromosome stats

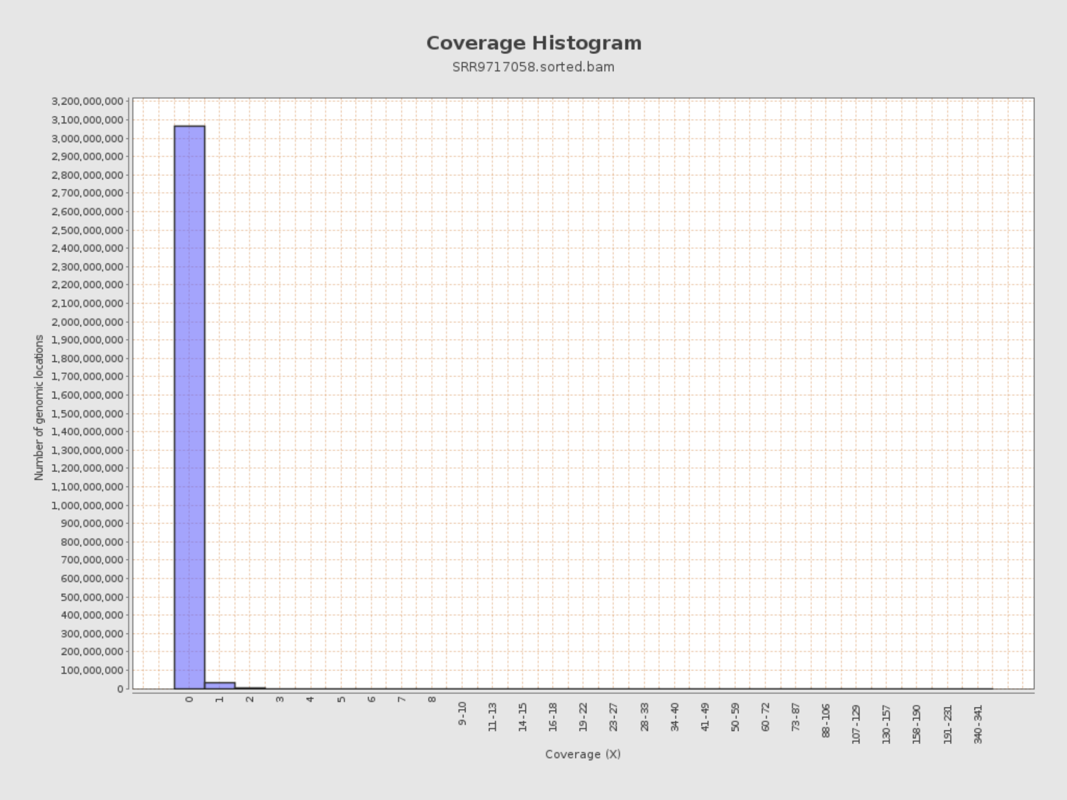
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2737861	0.011	0.1778
chr2	243199373	2858092	0.0118	0.1845
chr3	198022430	2267642	0.0115	0.1126
chr4	191154276	2187438	0.0114	0.1252
chr5	180915260	2008806	0.0111	0.1107
chr6	171115067	1937234	0.0113	0.1174
chr7	159138663	1897018	0.0119	0.1496

chr8	146364022	1735611	0.0119	0.1508
chr9	141213431	1439516	0.0102	0.1193
chr10	135534747	1666807	0.0123	0.1478
chr11	135006516	1538133	0.0114	0.1238
chr12	133851895	1560314	0.0117	0.1146
chr13	115169878	1031888	0.009	0.0999
chr14	107349540	1043486	0.0097	0.1043
chr15	102531392	1000371	0.0098	0.1047
chr16	90354753	1021449	0.0113	0.1162
chr17	81195210	951053	0.0117	0.117
chr18	78077248	896250	0.0115	0.1588
chr19	59128983	758284	0.0128	0.1529
chr20	63025520	735206	0.0117	0.1148
chr21	48129895	454934	0.0095	0.1114
chr22	51304566	421440	0.0082	0.0956
chrMT	16571	5347	0.3227	0.6345
chrX	155270560	1866900	0.012	0.1195
chrY	59373566	129984	0.0022	0.0993

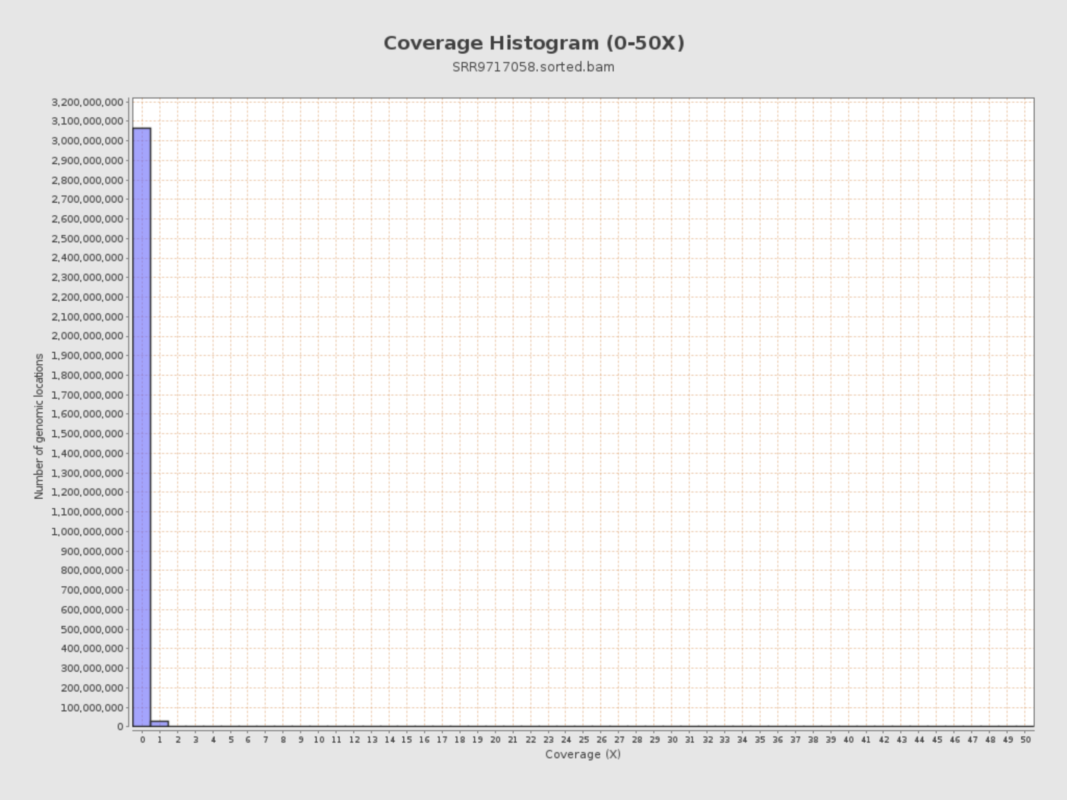
3. Results : Coverage across reference



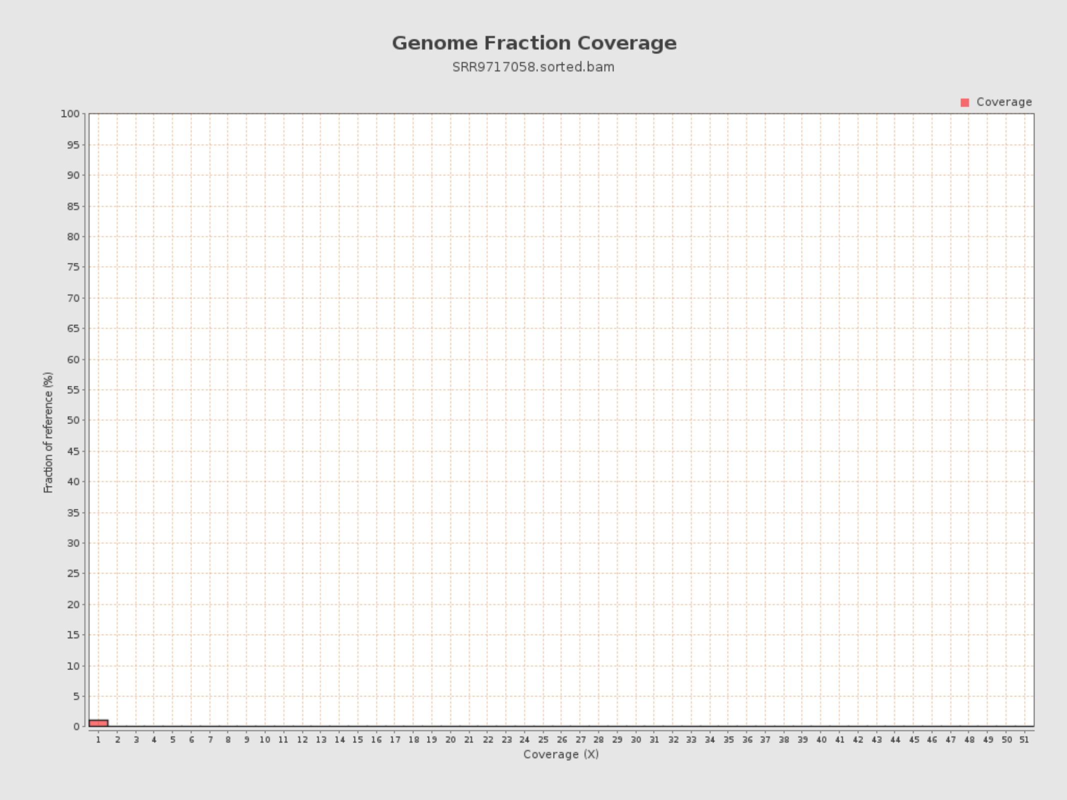
4. Results : Coverage Histogram



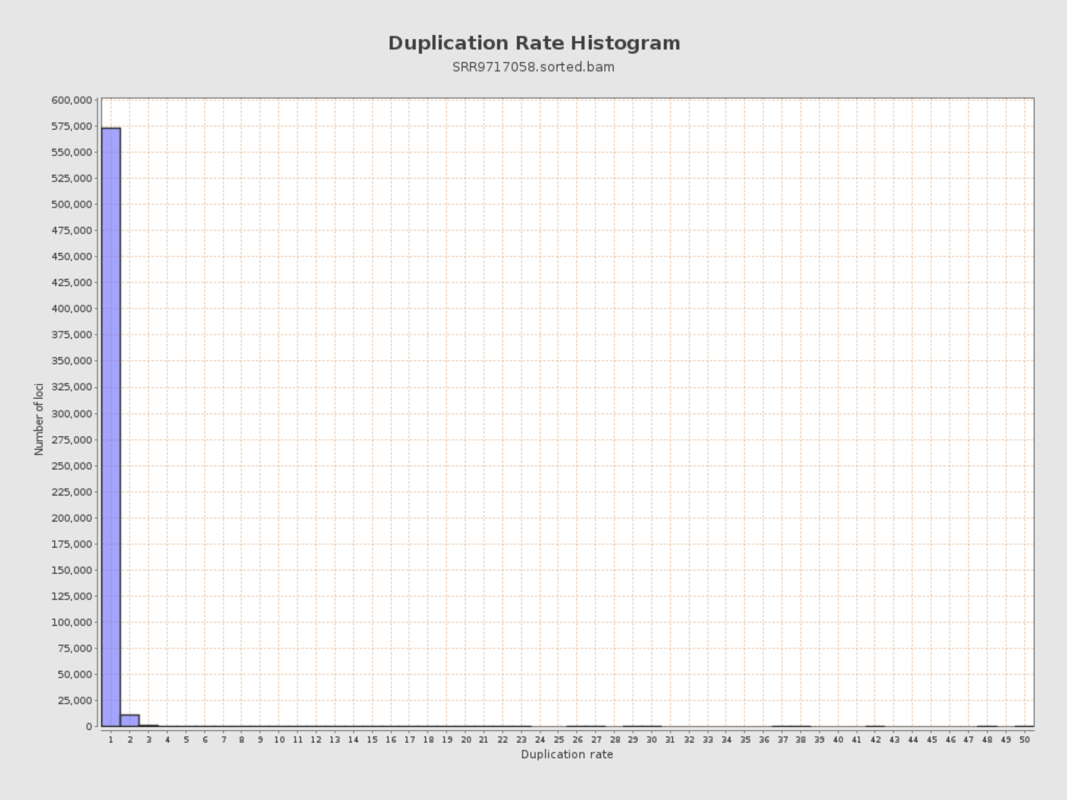
5. Results : Coverage Histogram (0-50X)



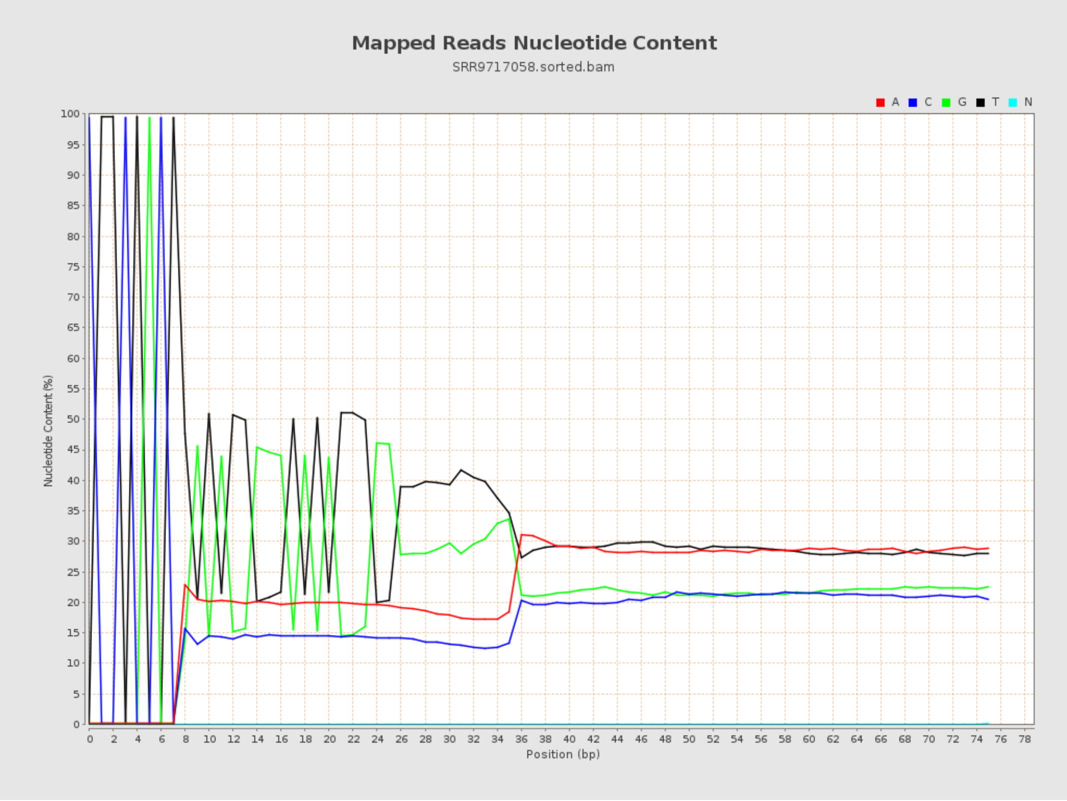
6. Results : Genome Fraction Coverage



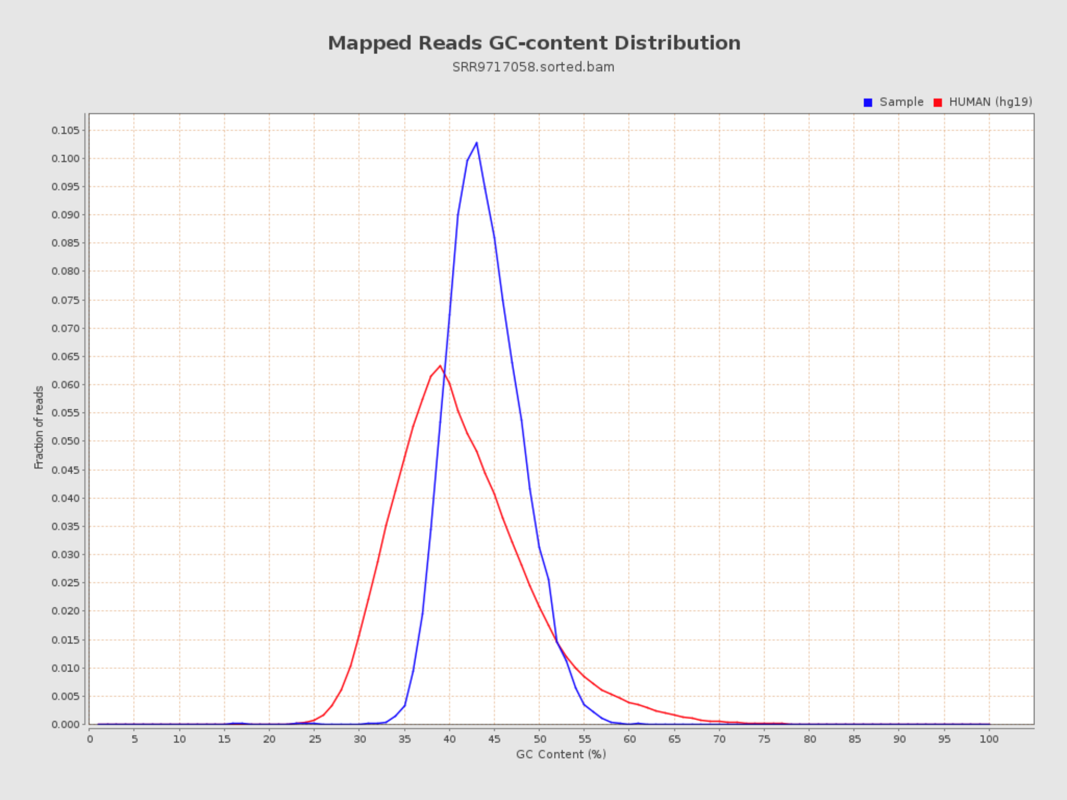
7. Results : Duplication Rate Histogram



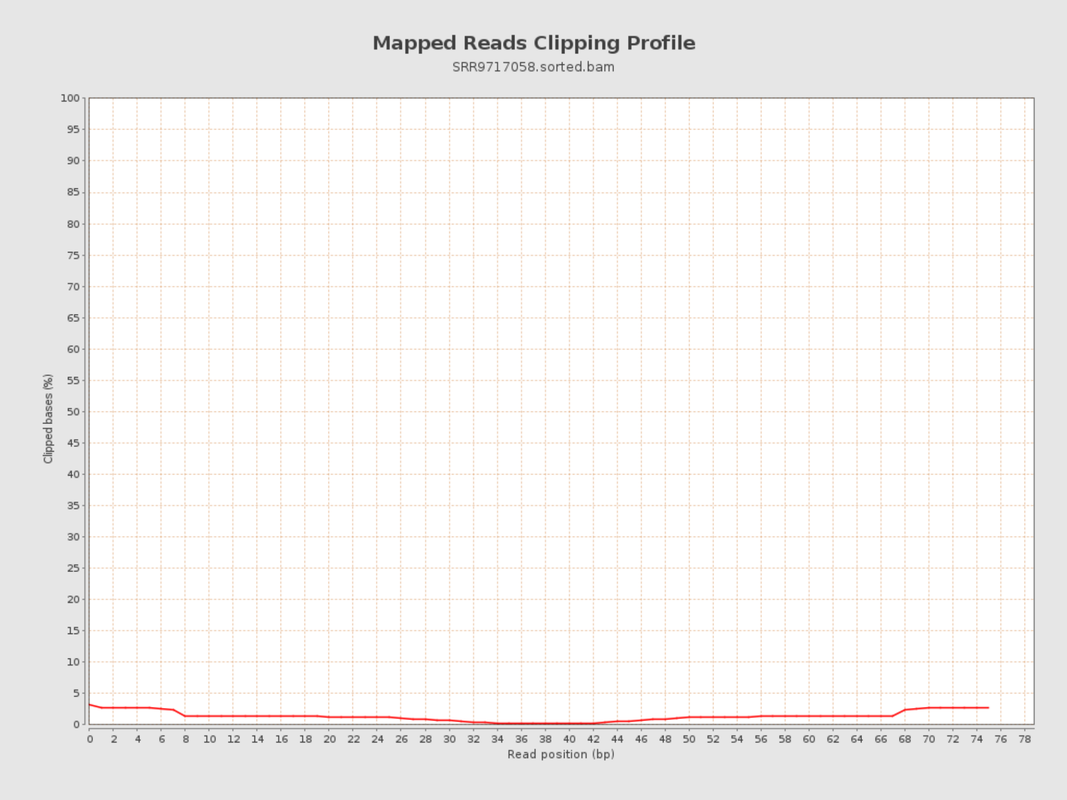
8. Results : Mapped Reads Nucleotide Content



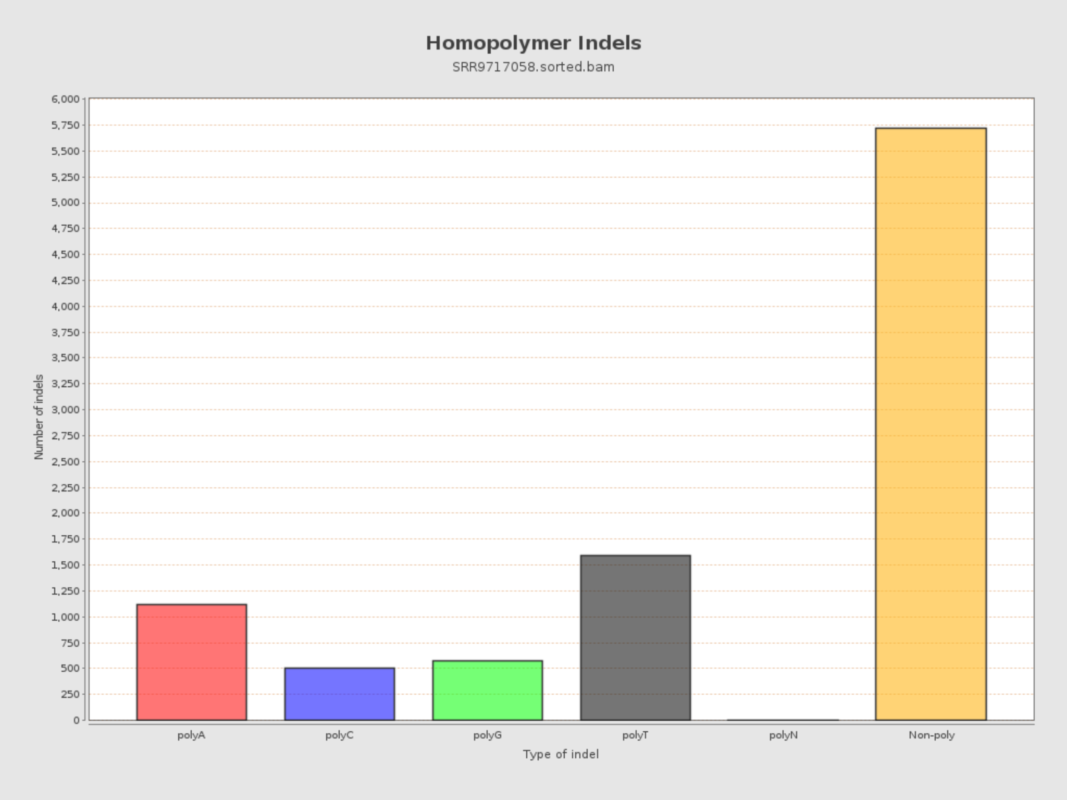
9. Results : Mapped Reads GC-content Distribution



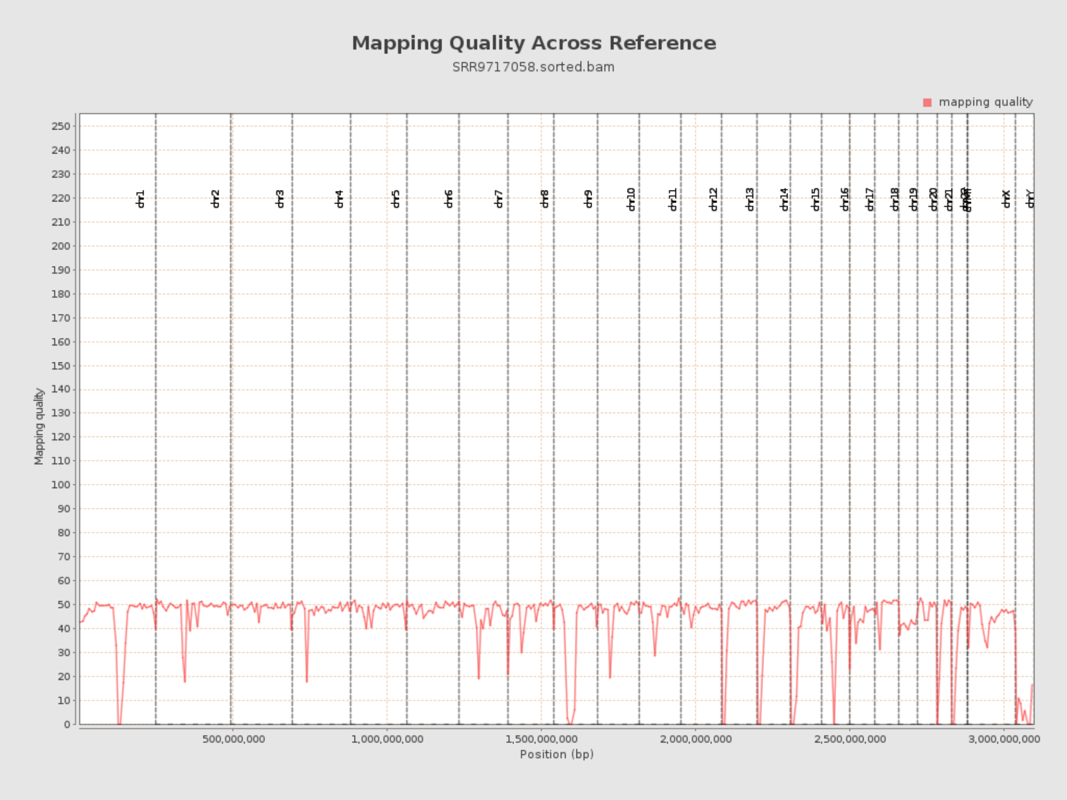
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram