Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:24:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716556.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_SRR9716556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716556.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	645,740
Mapped reads	574,833 / 89.02%
Unmapped reads	70,907 / 10.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,320 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,427 / 1.46%
Duplication rate	1.32%
Clipped reads	576,284 / 89.24%

2.2. ACGT Content

Number/percentage of A's	7,942,227 / 24.33%
Number/percentage of C's	6,218,180 / 19.05%
Number/percentage of T's	10,347,116 / 31.7%
Number/percentage of G's	8,133,042 / 24.92%
Number/percentage of N's	691 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1173

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

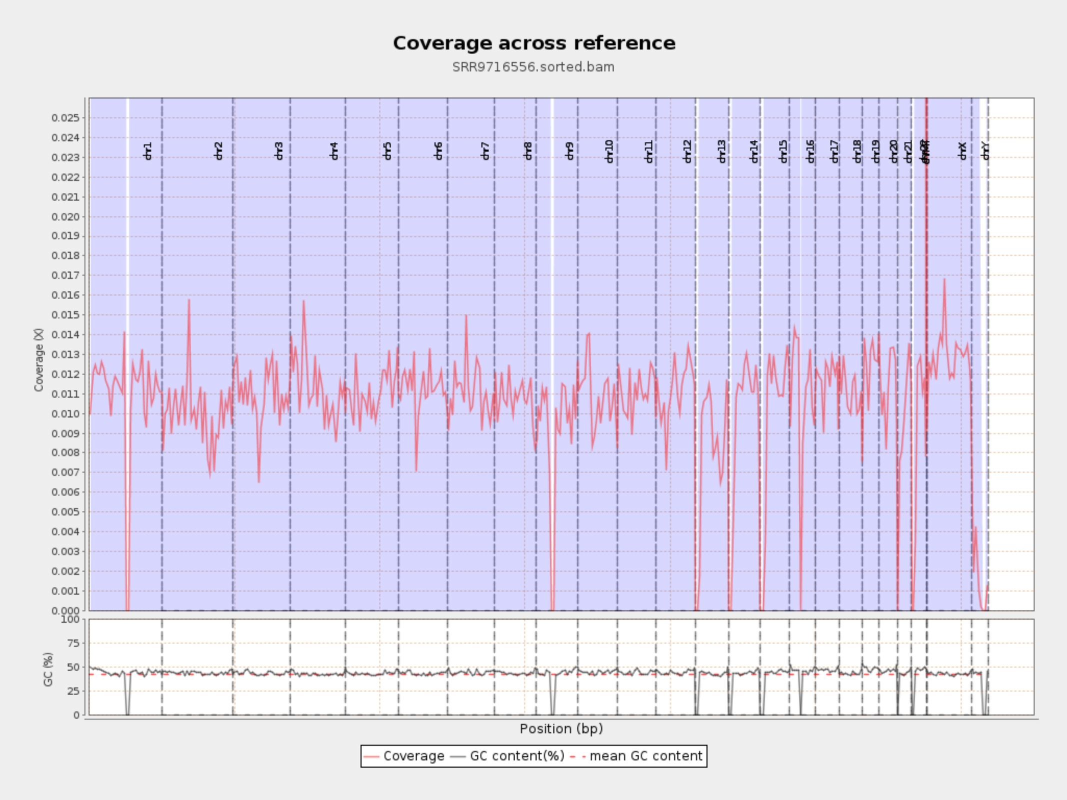
General error rate	0.48%
Mismatches	154,273
Insertions	1,777
Mapped reads with at least one insertion	0.31%
Deletions	4,931
Mapped reads with at least one deletion	0.85%
Homopolymer indels	41.46%

2.6. Chromosome stats

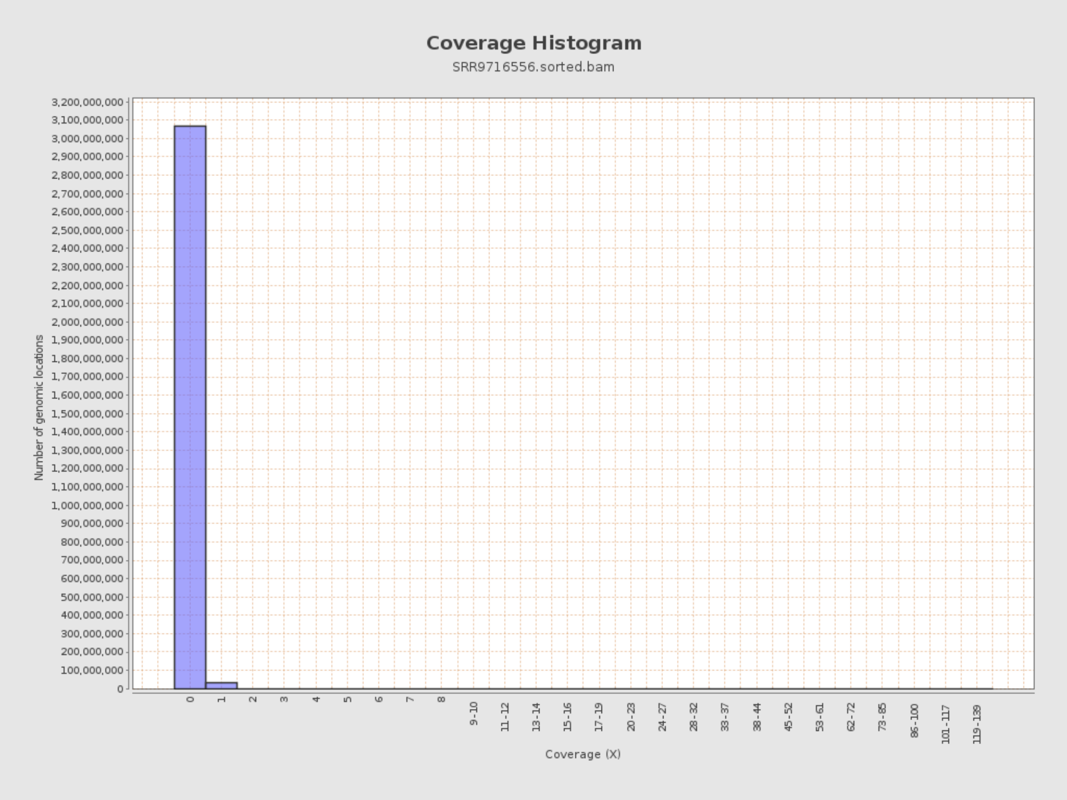
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2703937	0.0108	0.1521
chr2	243199373	2437799	0.01	0.1202
chr3	198022430	2173774	0.011	0.1091
chr4	191154276	2163561	0.0113	0.1123
chr5	180915260	2001453	0.0111	0.1093
chr6	171115067	1929139	0.0113	0.1121
chr7	159138663	1768859	0.0111	0.1236

chr8	146364022	1581741	0.0108	0.1149
chr9	141213431	1266980	0.009	0.1107
chr10	135534747	1480529	0.0109	0.1163
chr11	135006516	1496788	0.0111	0.1187
chr12	133851895	1496170	0.0112	0.11
chr13	115169878	905979	0.0079	0.0916
chr14	107349540	1030456	0.0096	0.1023
chr15	102531392	989833	0.0097	0.1018
chr16	90354753	973659	0.0108	0.1101
chr17	81195210	952488	0.0117	0.1148
chr18	78077248	872125	0.0112	0.164
chr19	59128983	738954	0.0125	0.1367
chr20	63025520	718374	0.0114	0.1109
chr21	48129895	449955	0.0093	0.1032
chr22	51304566	415486	0.0081	0.0935
chrMT	16571	6539	0.3946	0.6511
chrX	155270560	2002778	0.0129	0.1229
chrY	59373566	92205	0.0016	0.0472

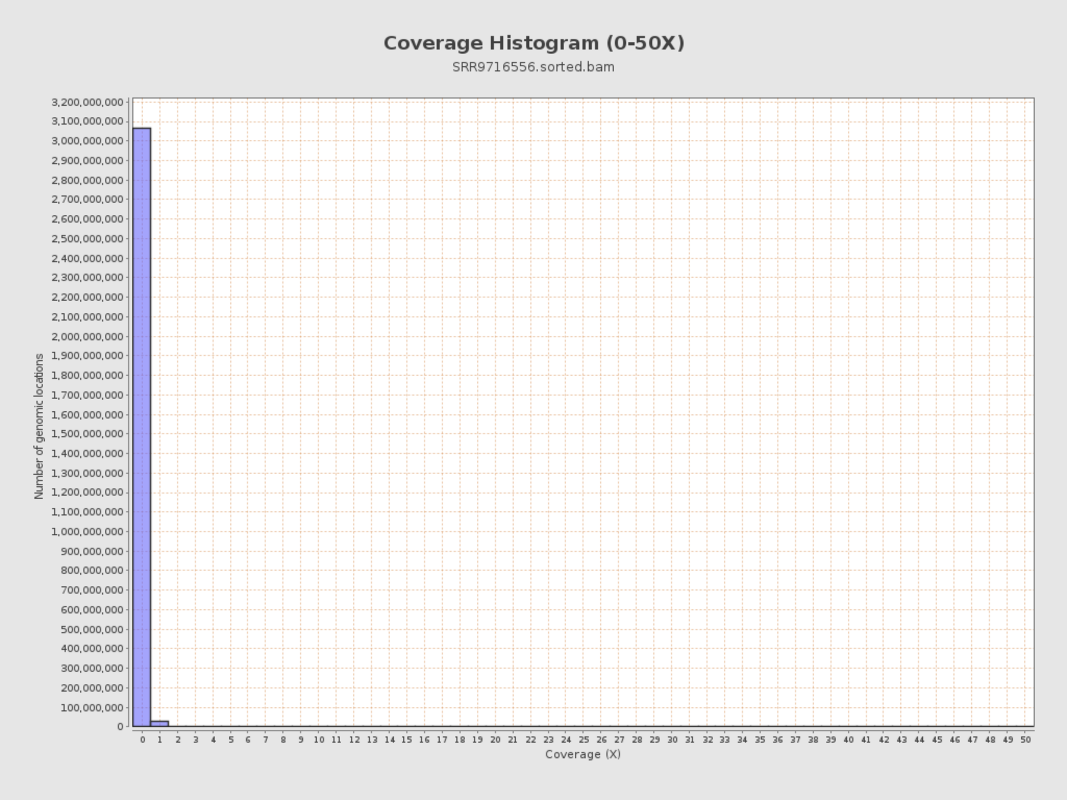
3. Results : Coverage across reference



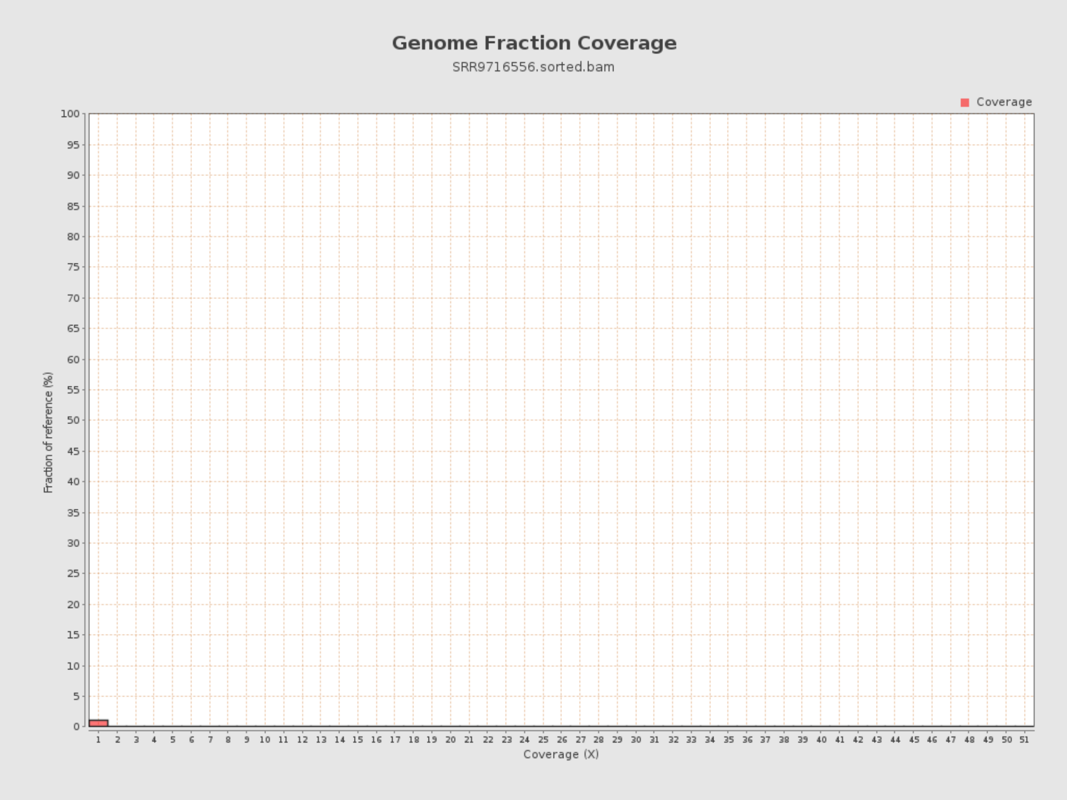
4. Results : Coverage Histogram



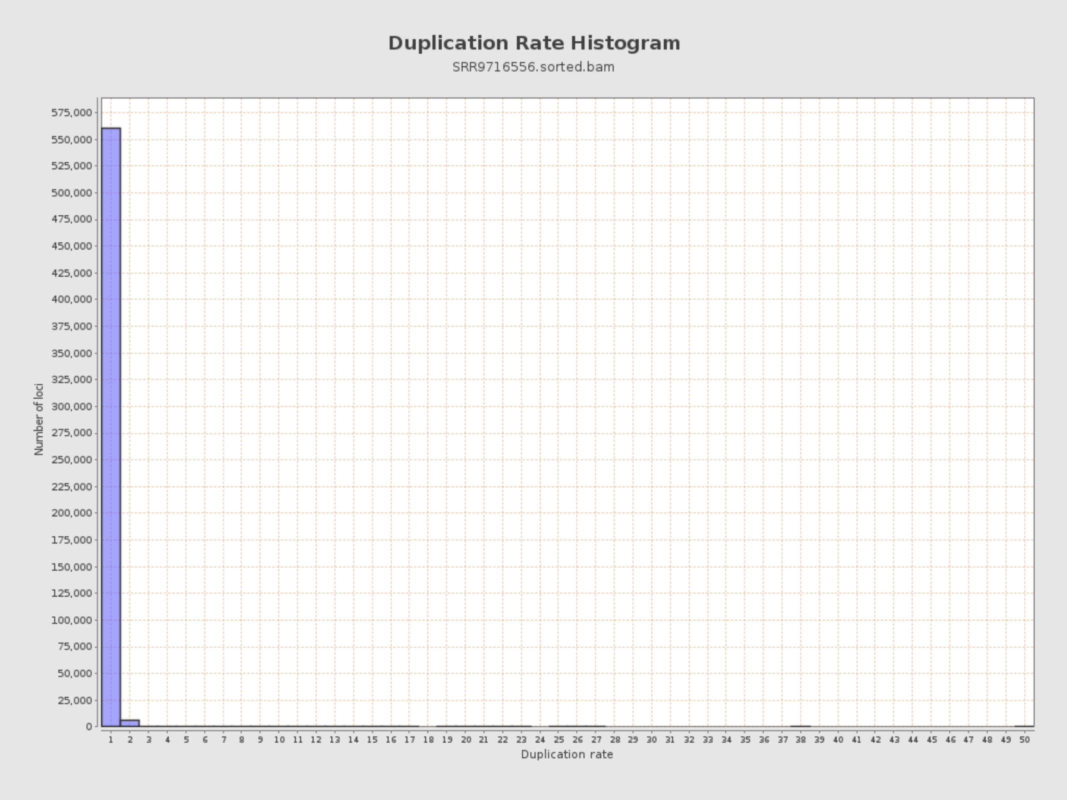
5. Results : Coverage Histogram (0-50X)



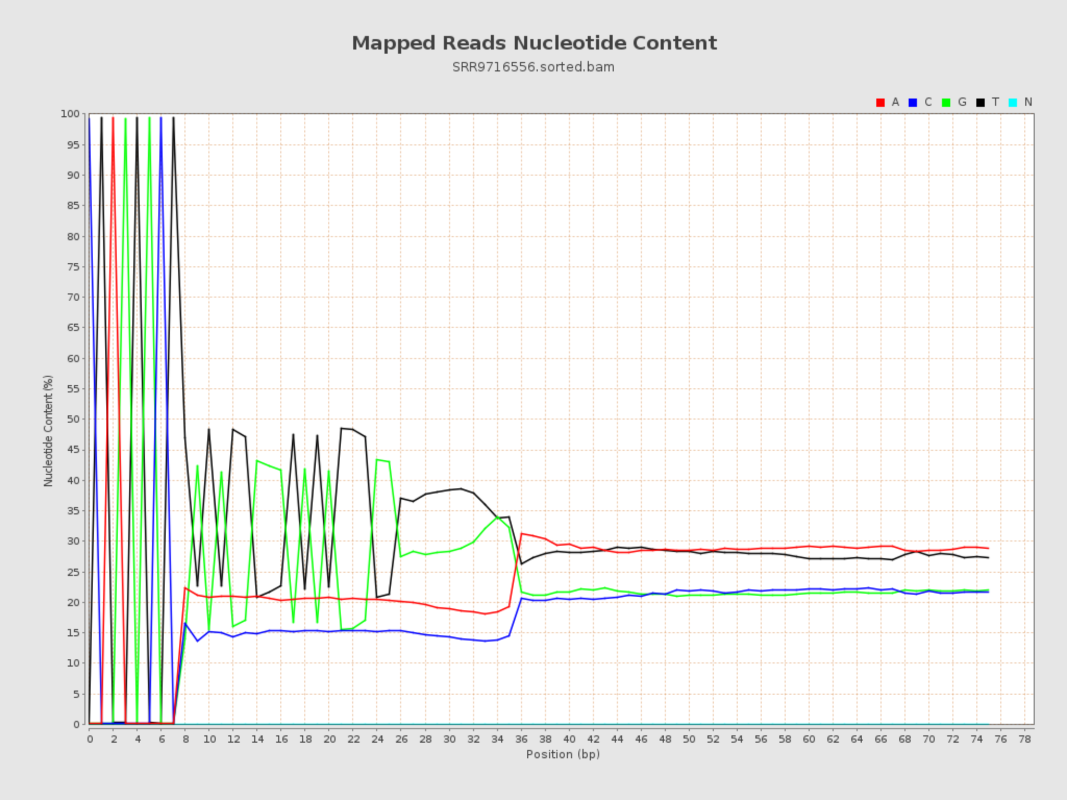
6. Results : Genome Fraction Coverage



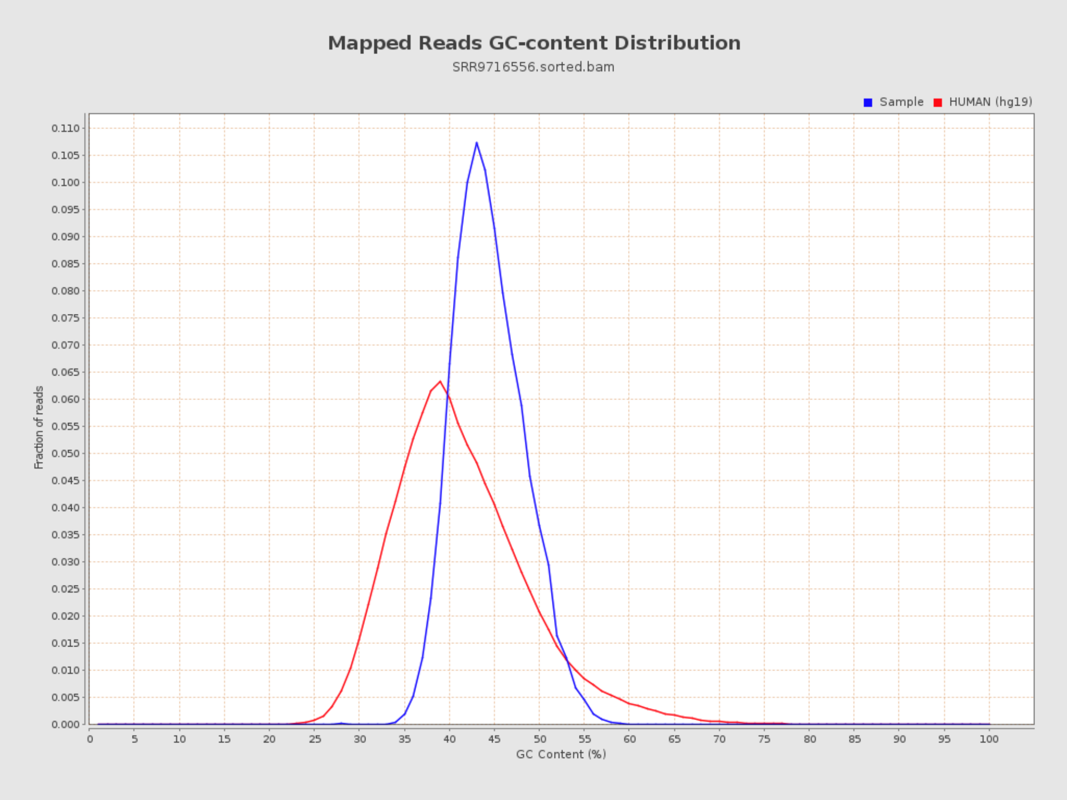
7. Results : Duplication Rate Histogram



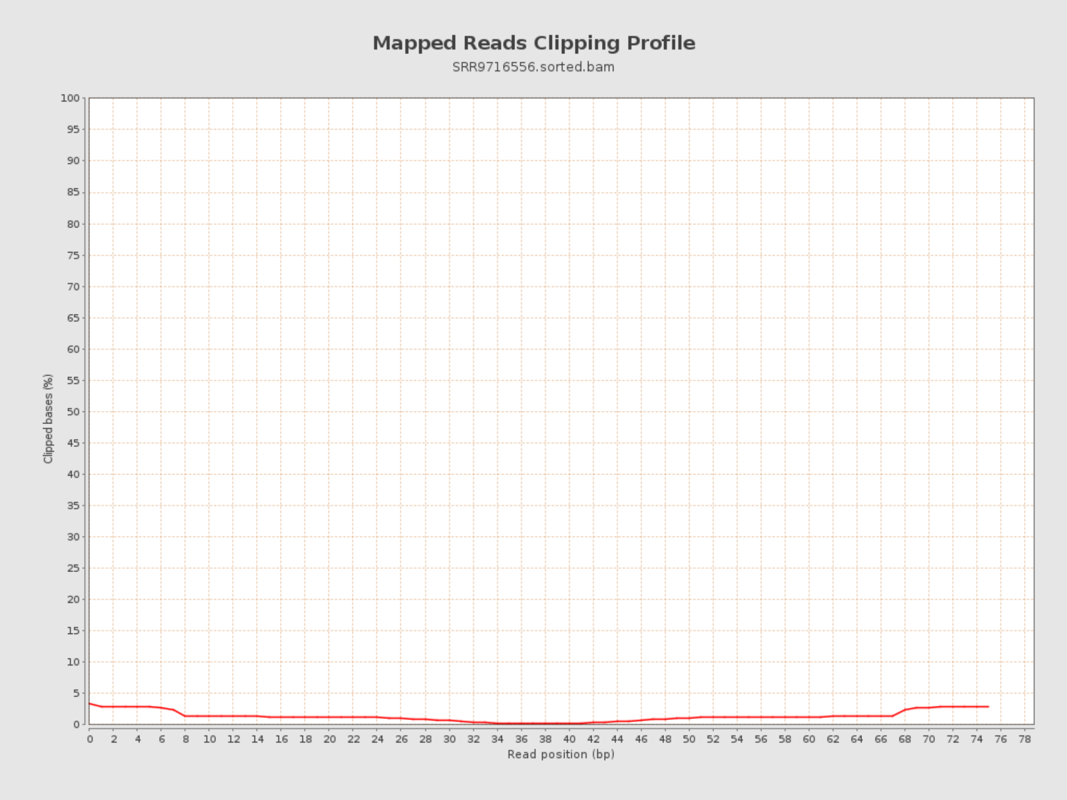
8. Results : Mapped Reads Nucleotide Content



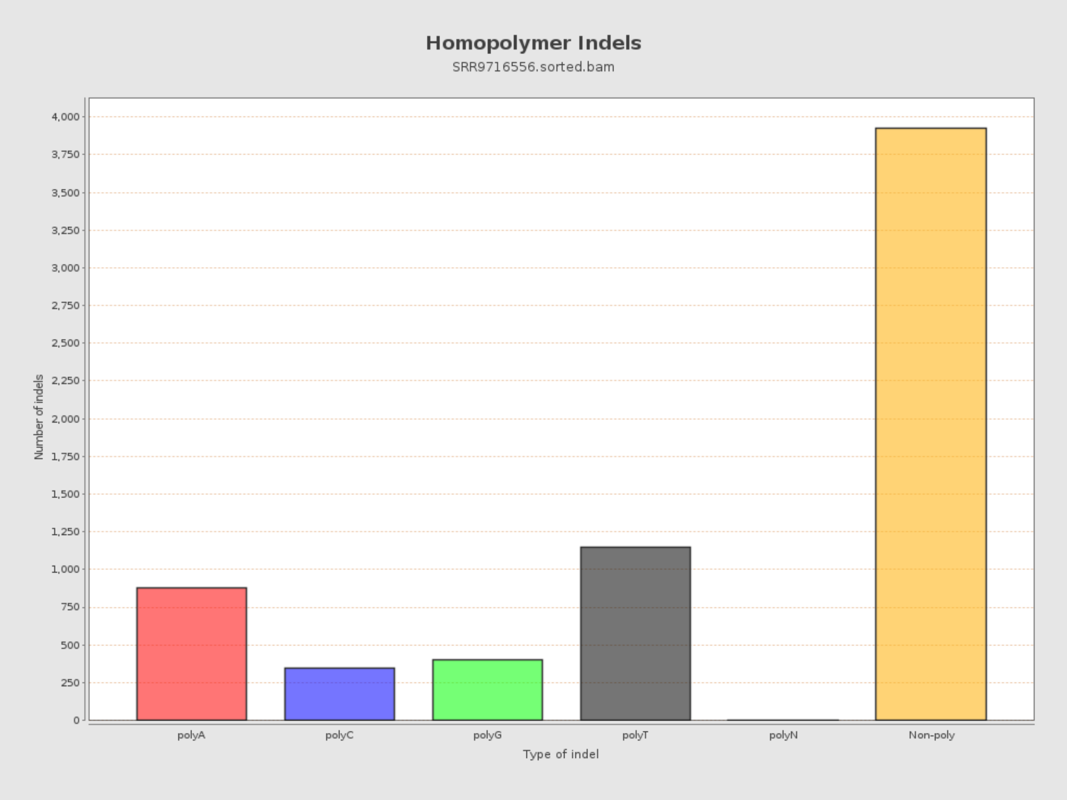
9. Results : Mapped Reads GC-content Distribution



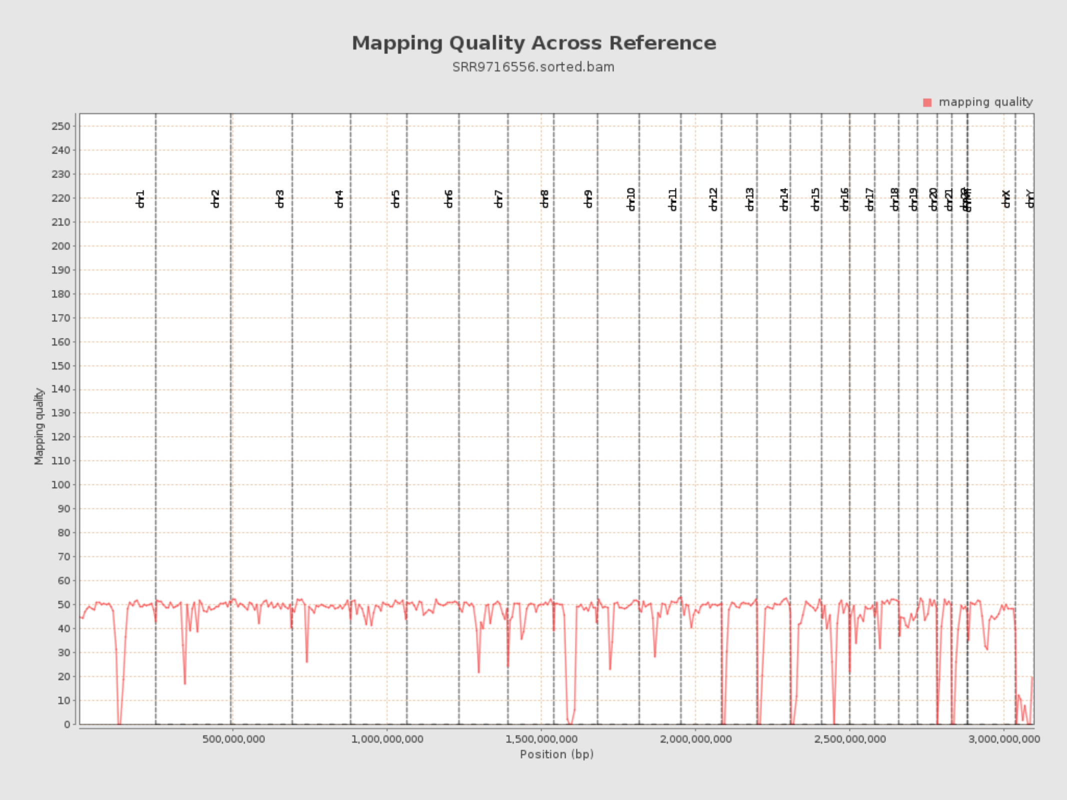
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram