Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:48:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716272.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_SRR9716272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:48:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	605,213
Mapped reads	554,023 / 91.54%
Unmapped reads	51,190 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,150 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,804 / 1.95%
Duplication rate	1.66%
Clipped reads	555,571 / 91.8%

2.2. ACGT Content

Number/percentage of A's	7,907,850 / 24.44%
Number/percentage of C's	5,799,183 / 17.92%
Number/percentage of T's	10,624,883 / 32.83%
Number/percentage of G's	8,025,925 / 24.8%
Number/percentage of N's	863 / 0%
GC Percentage	42.72%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1277

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

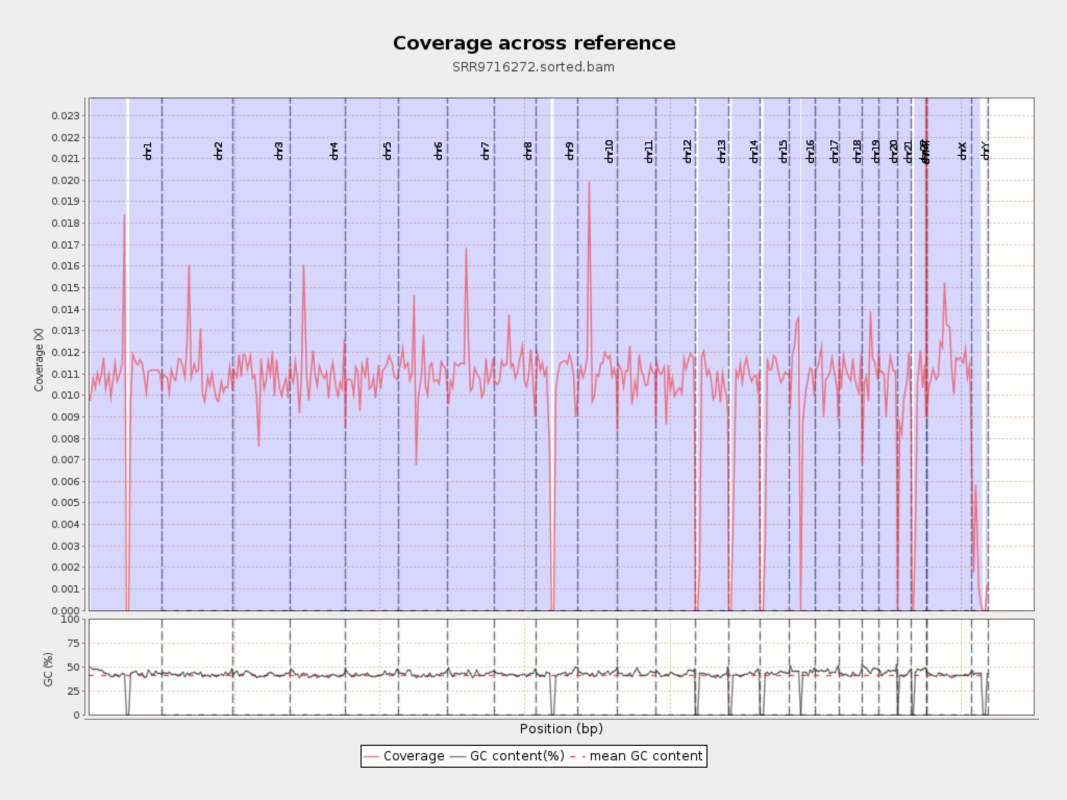
General error rate	0.51%
Mismatches	162,715
Insertions	1,843
Mapped reads with at least one insertion	0.33%
Deletions	6,296
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.17%

2.6. Chromosome stats

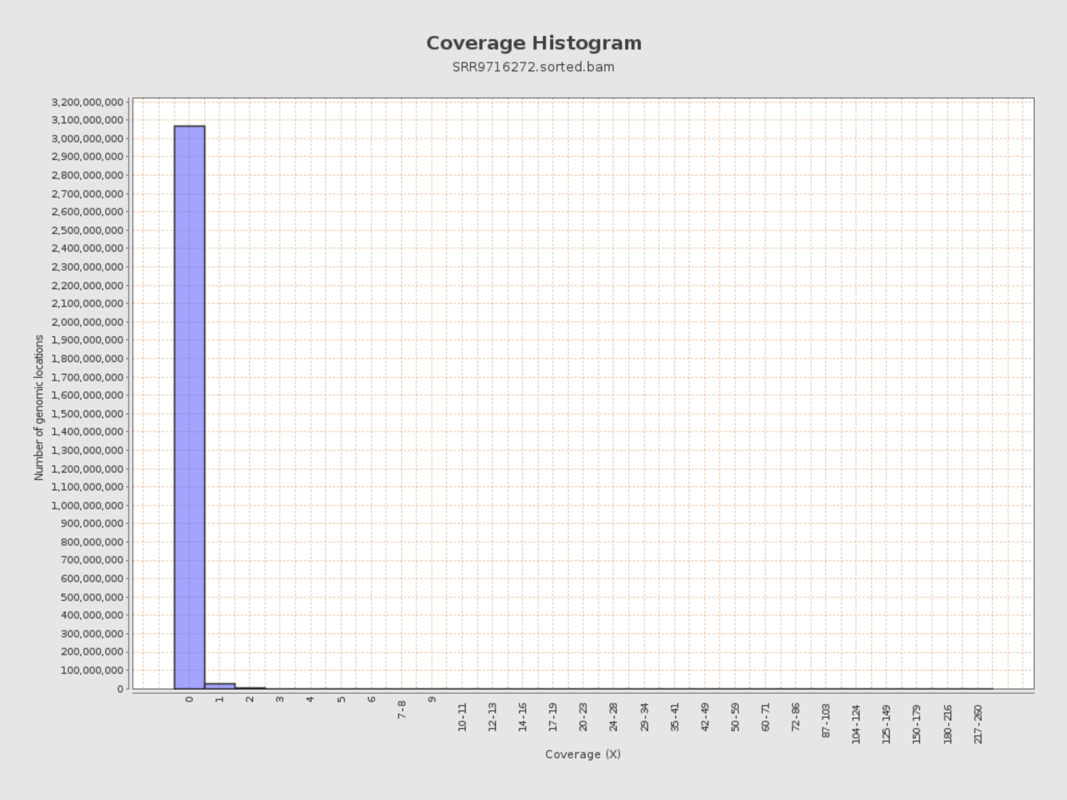
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2616106	0.0105	0.205
chr2	243199373	2682309	0.011	0.1428
chr3	198022430	2147486	0.0108	0.1079
chr4	191154276	2107297	0.011	0.1126
chr5	180915260	1964738	0.0109	0.1087
chr6	171115067	1893245	0.0111	0.1175
chr7	159138663	1794216	0.0113	0.144

chr8	146364022	1638773	0.0112	0.1221
chr9	141213431	1373877	0.0097	0.1152
chr10	135534747	1574311	0.0116	0.1308
chr11	135006516	1471500	0.0109	0.1206
chr12	133851895	1451599	0.0108	0.1094
chr13	115169878	1028531	0.0089	0.099
chr14	107349540	974535	0.0091	0.0999
chr15	102531392	926200	0.009	0.0989
chr16	90354753	927071	0.0103	0.1088
chr17	81195210	879628	0.0108	0.1099
chr18	78077248	859585	0.011	0.1584
chr19	59128983	656394	0.0111	0.1529
chr20	63025520	678874	0.0108	0.1086
chr21	48129895	428059	0.0089	0.1024
chr22	51304566	387308	0.0075	0.0902
chrMT	16571	5660	0.3416	0.6096
chrX	155270560	1800462	0.0116	0.1166
chrY	59373566	101215	0.0017	0.0587

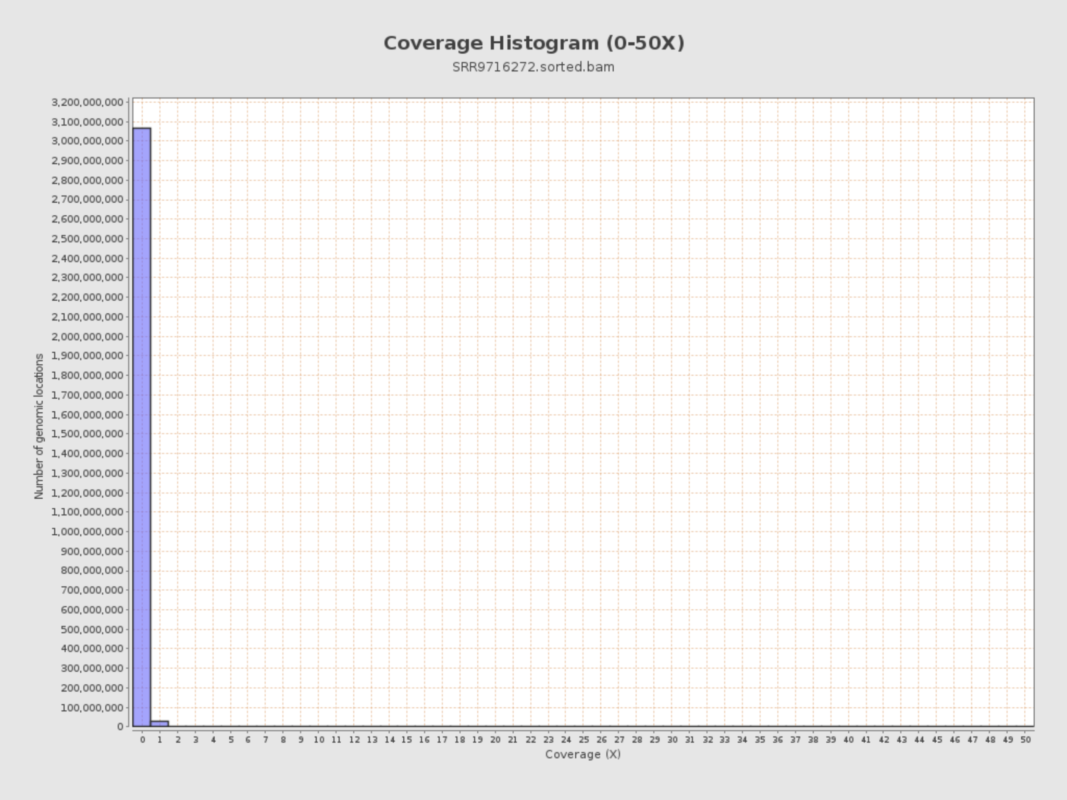
3. Results : Coverage across reference



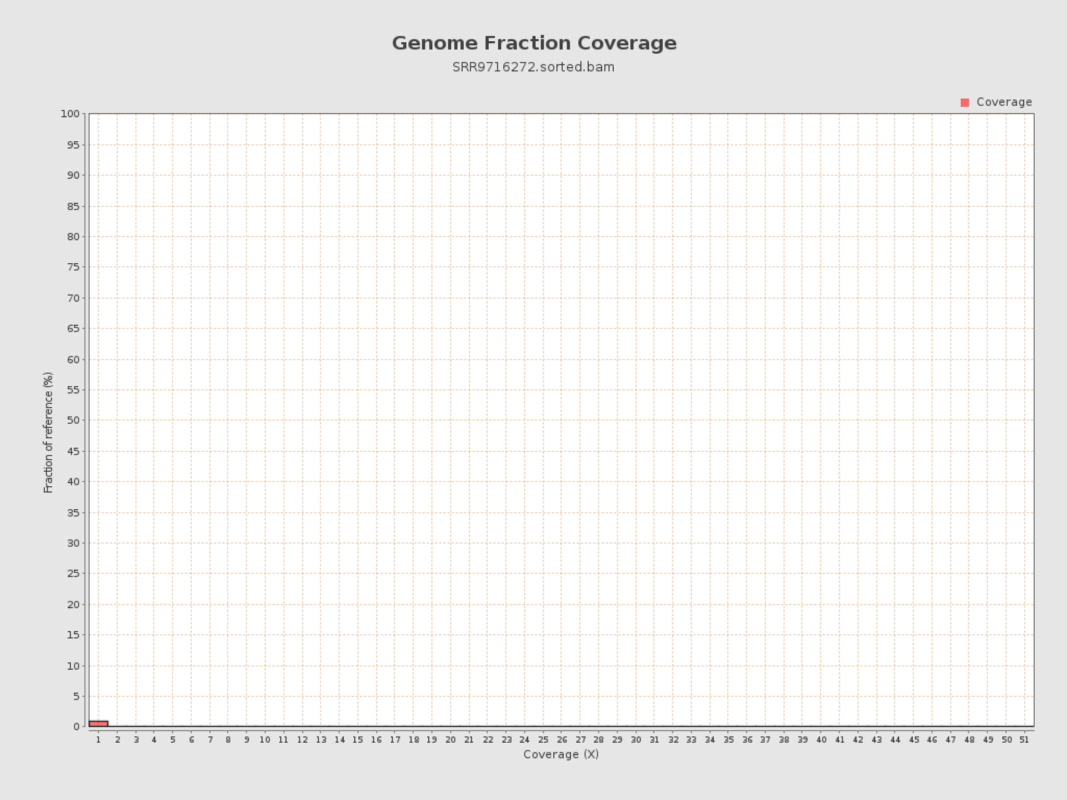
4. Results : Coverage Histogram



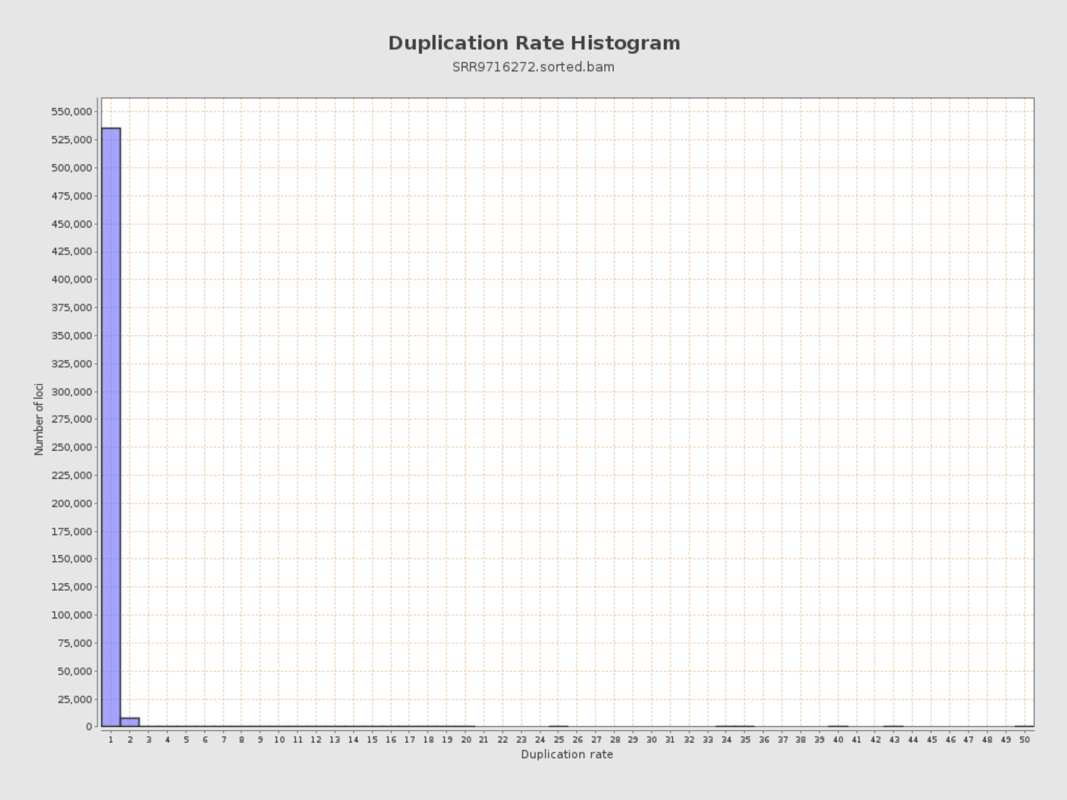
5. Results : Coverage Histogram (0-50X)



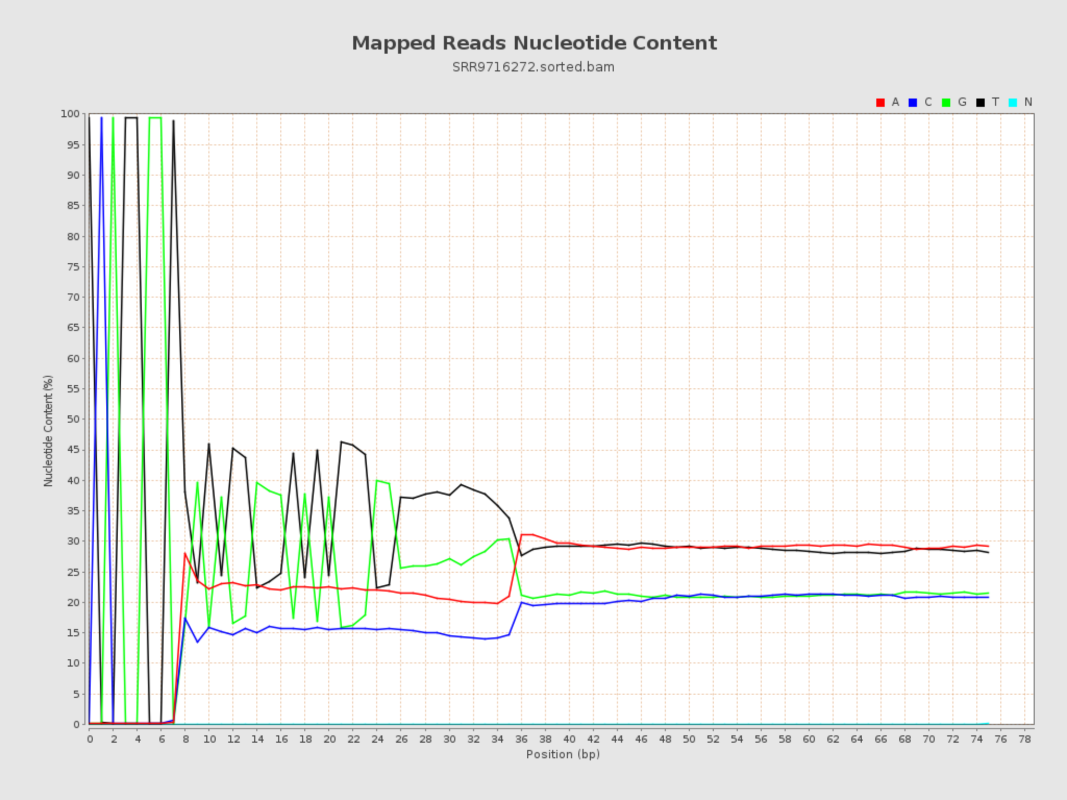
6. Results : Genome Fraction Coverage



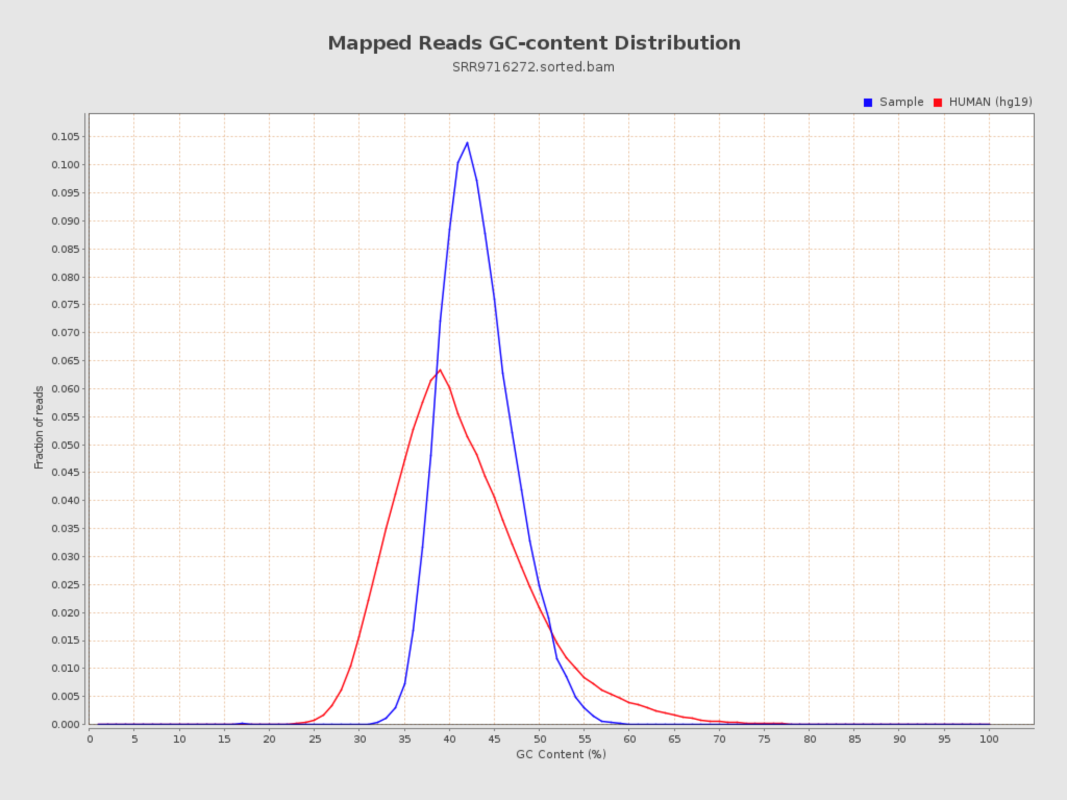
7. Results : Duplication Rate Histogram



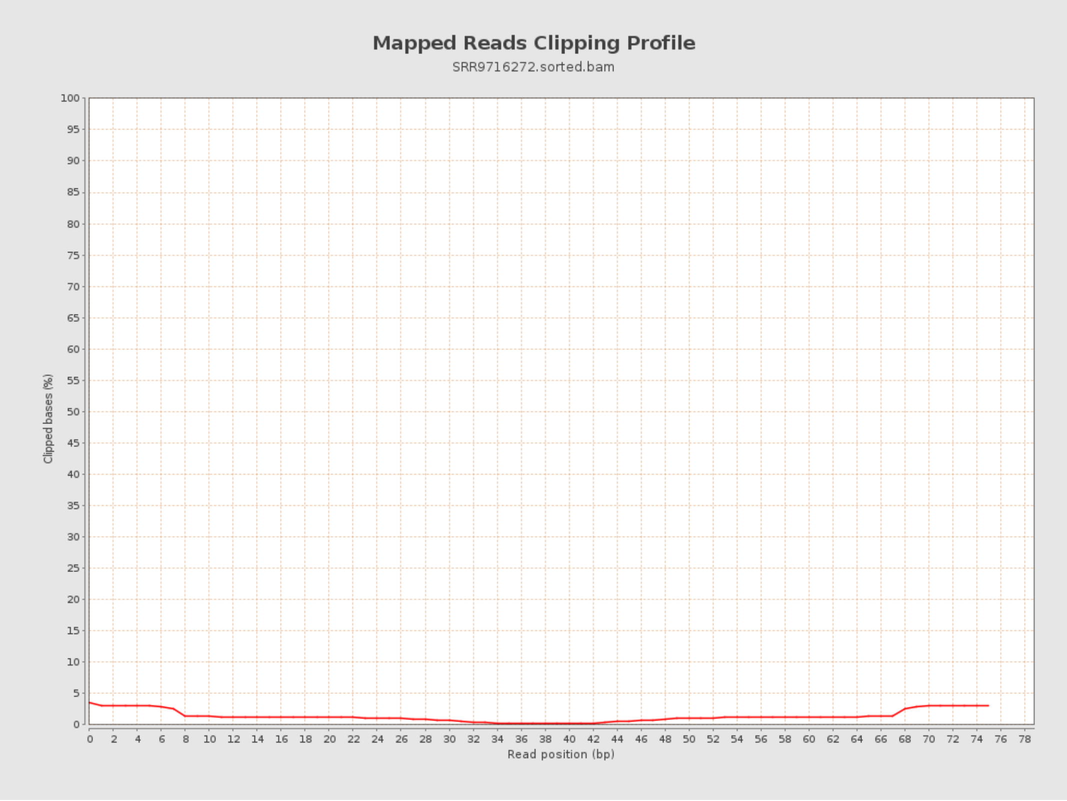
8. Results : Mapped Reads Nucleotide Content



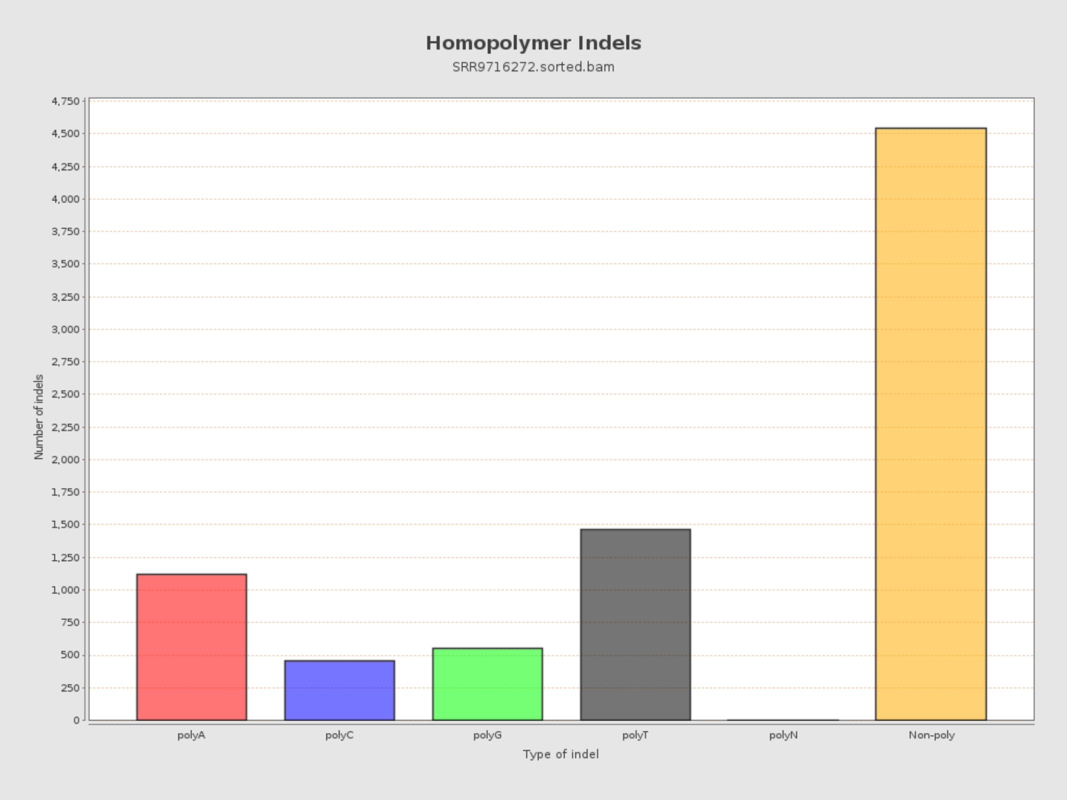
9. Results : Mapped Reads GC-content Distribution



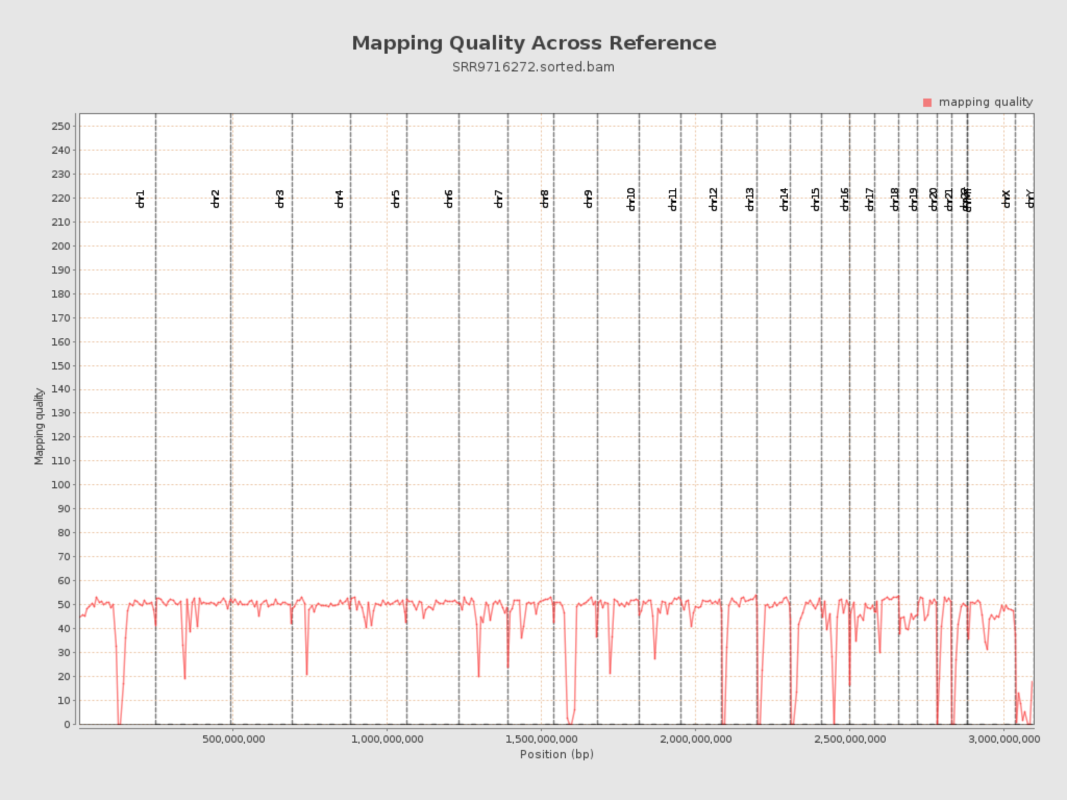
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram