Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:25:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716157.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_SRR9716157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:25:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	695,753
Mapped reads	629,516 / 90.48%
Unmapped reads	66,237 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,606 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,257 / 1.62%
Duplication rate	1.38%
Clipped reads	629,901 / 90.54%

2.2. ACGT Content

Number/percentage of A's	9,020,093 / 24.98%
Number/percentage of C's	6,980,054 / 19.33%
Number/percentage of T's	11,345,128 / 31.41%
Number/percentage of G's	8,770,215 / 24.28%
Number/percentage of N's	674 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.129

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

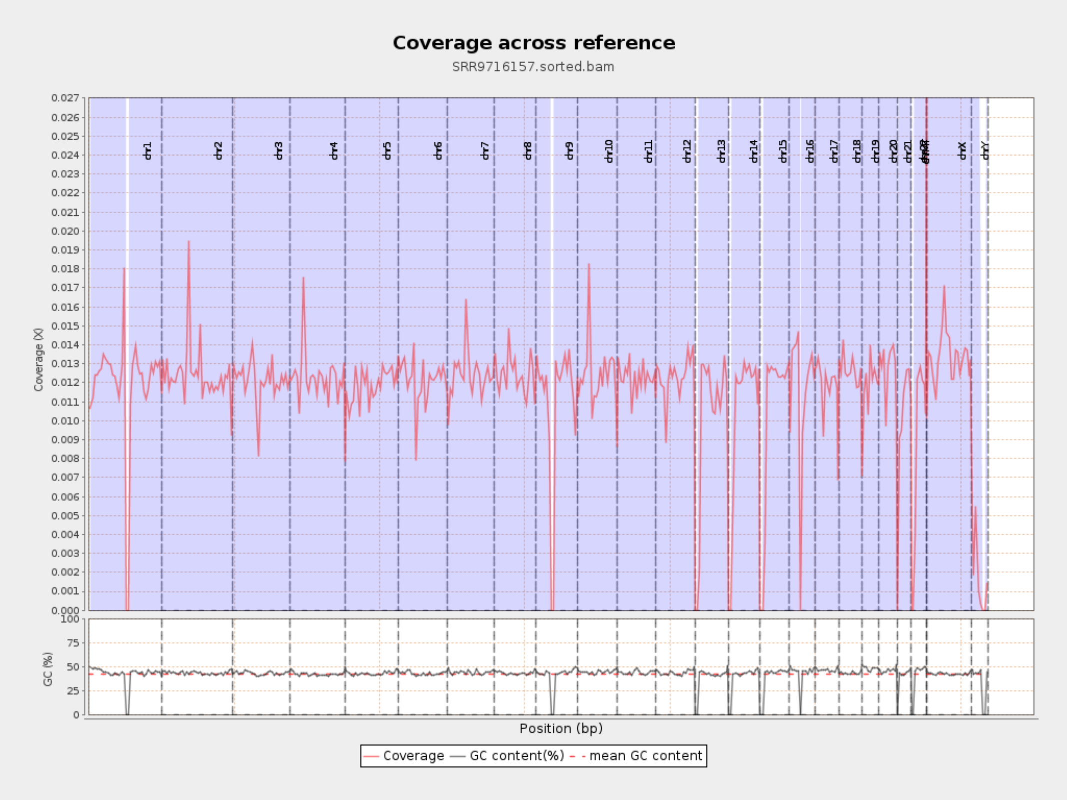
General error rate	0.5%
Mismatches	175,765
Insertions	2,661
Mapped reads with at least one insertion	0.42%
Deletions	5,628
Mapped reads with at least one deletion	0.89%
Homopolymer indels	38.67%

2.6. Chromosome stats

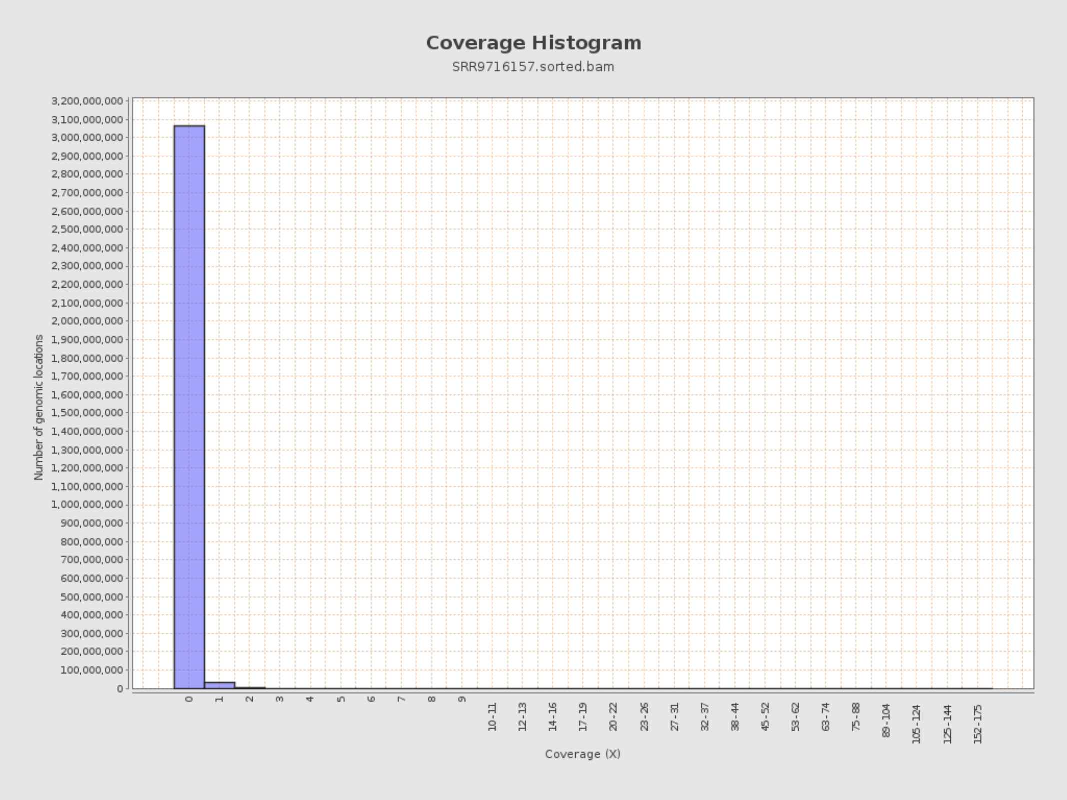
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2943219	0.0118	0.1806
chr2	243199373	3033663	0.0125	0.1367
chr3	198022430	2394408	0.0121	0.1145
chr4	191154276	2352905	0.0123	0.1194
chr5	180915260	2145457	0.0119	0.1136
chr6	171115067	2076972	0.0121	0.1181
chr7	159138663	1984068	0.0125	0.1414

chr8	146364022	1820896	0.0124	0.1279
chr9	141213431	1520282	0.0108	0.1284
chr10	135534747	1694815	0.0125	0.1267
chr11	135006516	1648520	0.0122	0.1309
chr12	133851895	1644946	0.0123	0.1158
chr13	115169878	1142822	0.0099	0.1029
chr14	107349540	1099070	0.0102	0.108
chr15	102531392	1038549	0.0101	0.105
chr16	90354753	1045146	0.0116	0.1149
chr17	81195210	950022	0.0117	0.1148
chr18	78077248	989363	0.0127	0.1907
chr19	59128983	704579	0.0119	0.1456
chr20	63025520	805552	0.0128	0.1186
chr21	48129895	484267	0.0101	0.1099
chr22	51304566	430976	0.0084	0.0948
chrMT	16571	473	0.0285	0.1774
chrX	155270560	2072509	0.0133	0.1279
chrY	59373566	102210	0.0017	0.0506

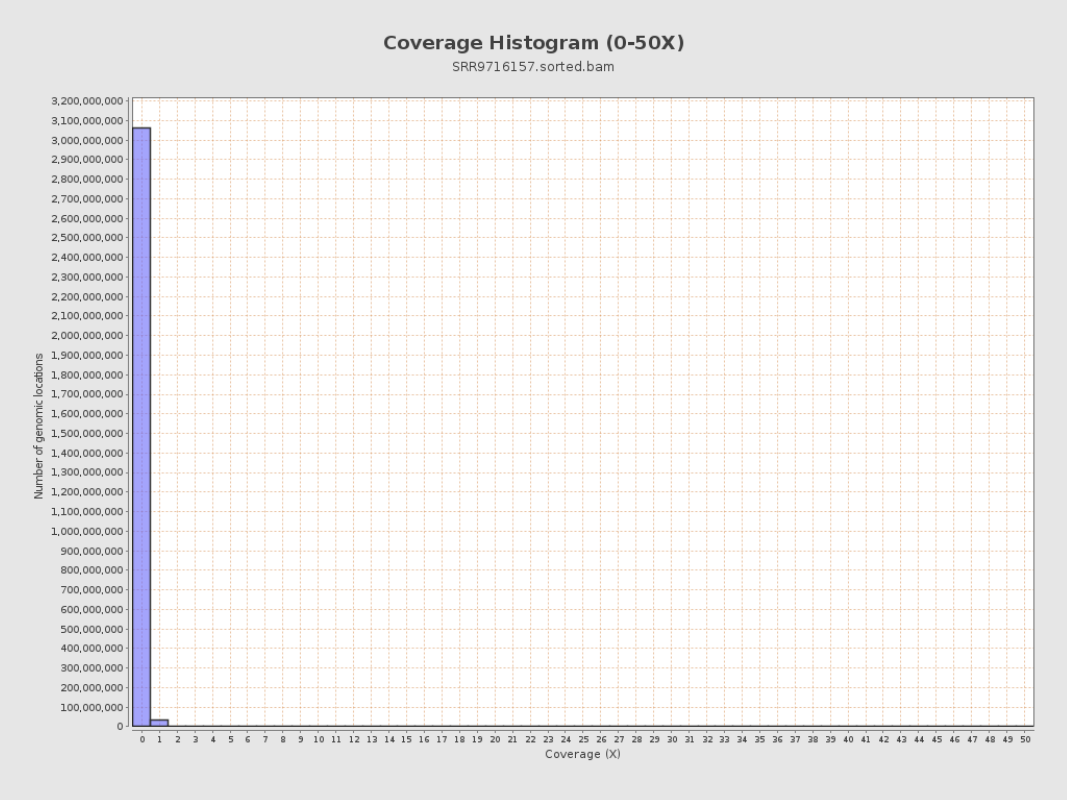
3. Results : Coverage across reference



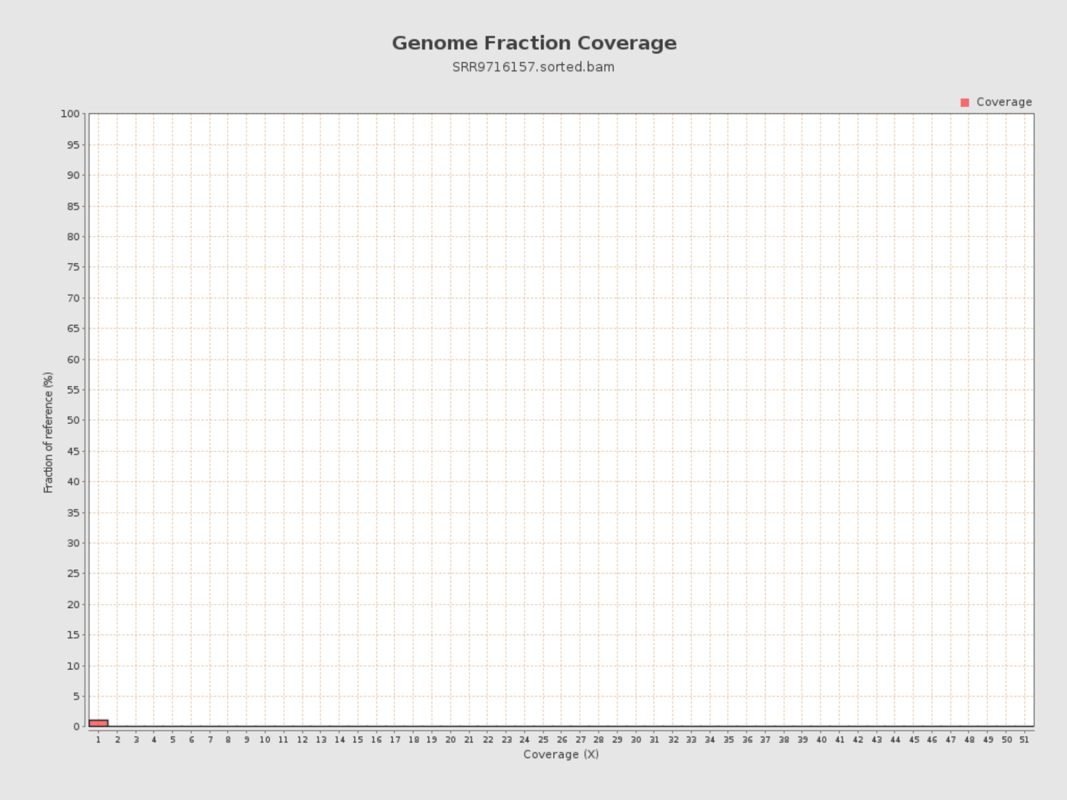
4. Results : Coverage Histogram



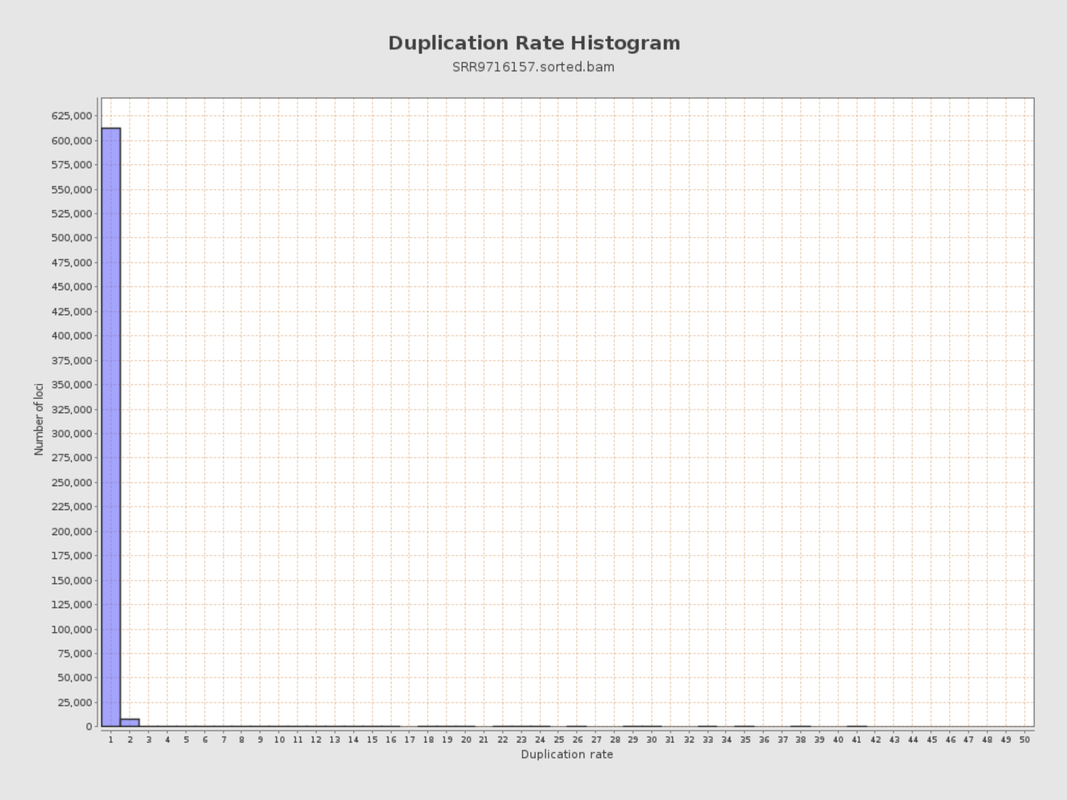
5. Results : Coverage Histogram (0-50X)



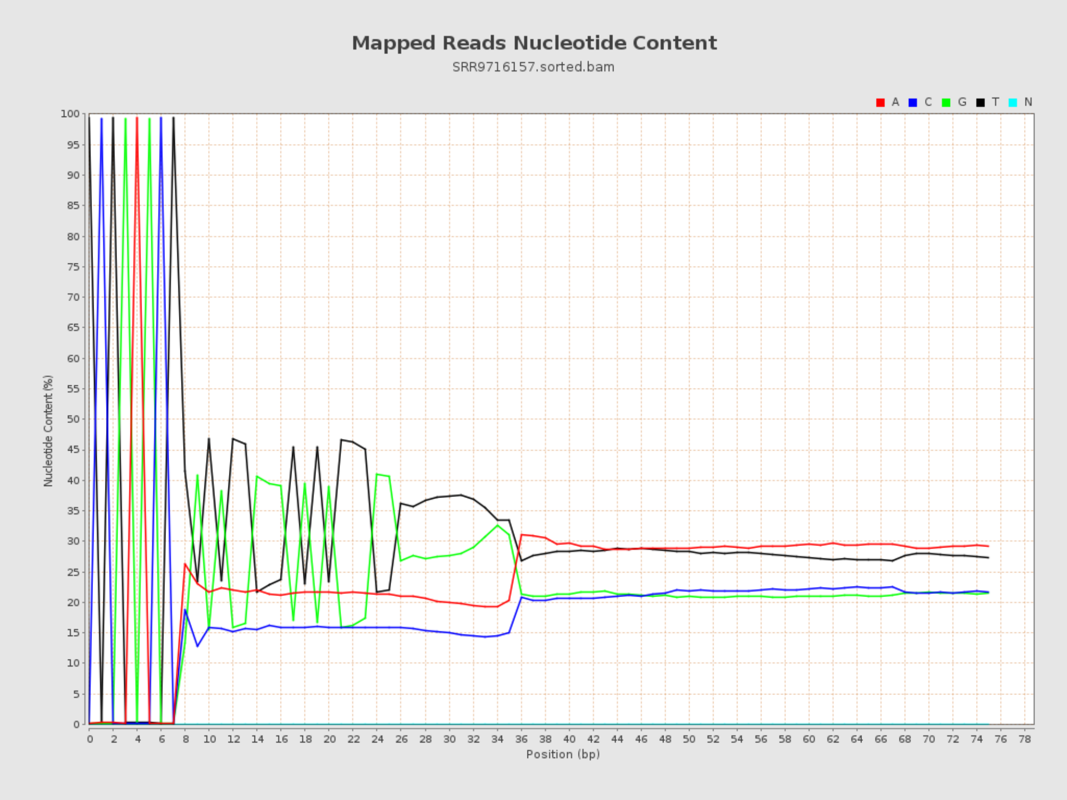
6. Results : Genome Fraction Coverage



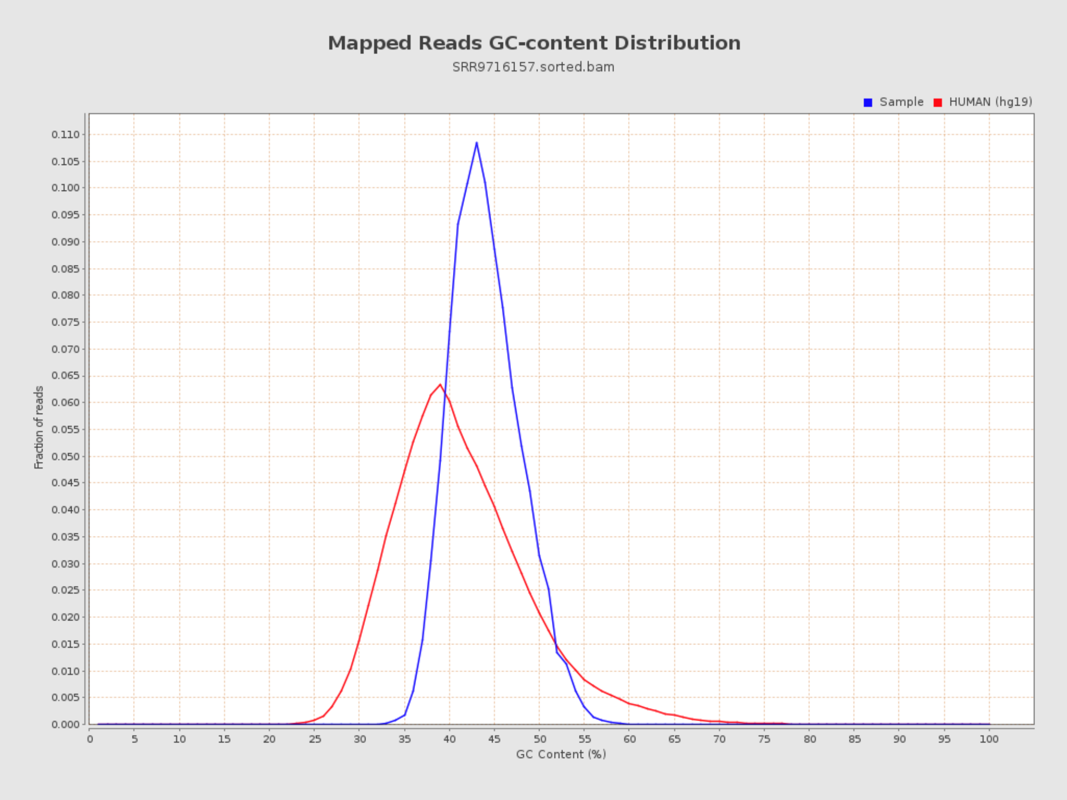
7. Results : Duplication Rate Histogram



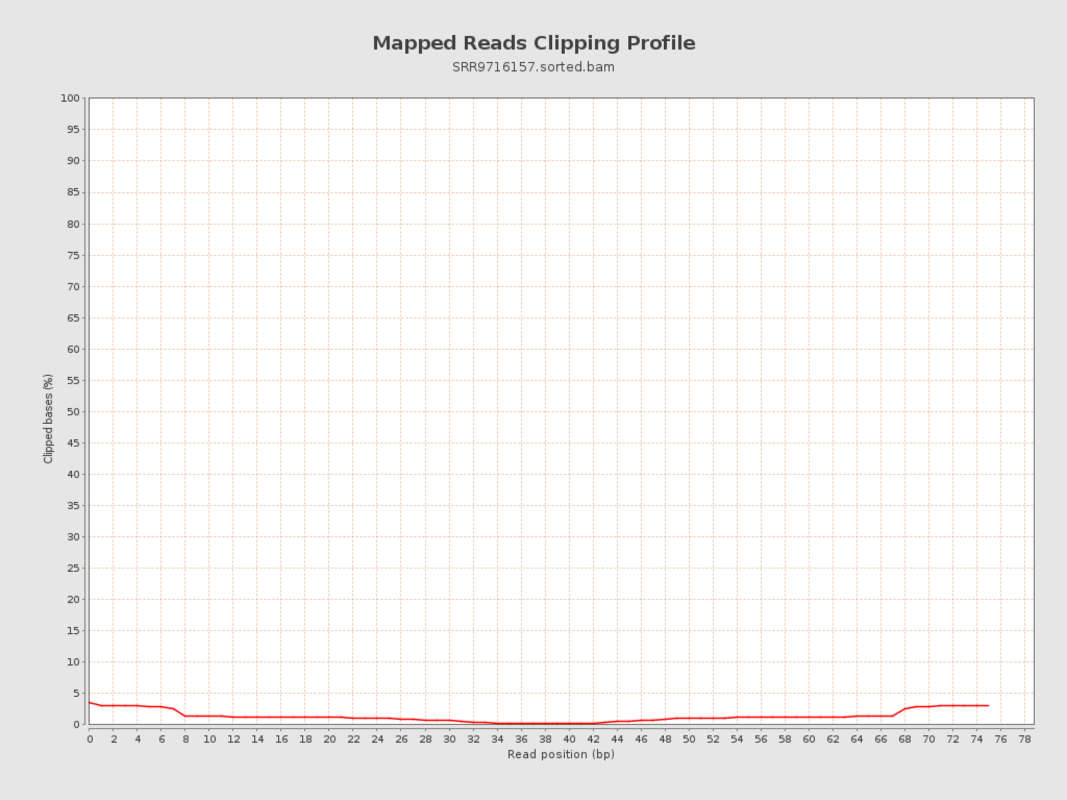
8. Results : Mapped Reads Nucleotide Content



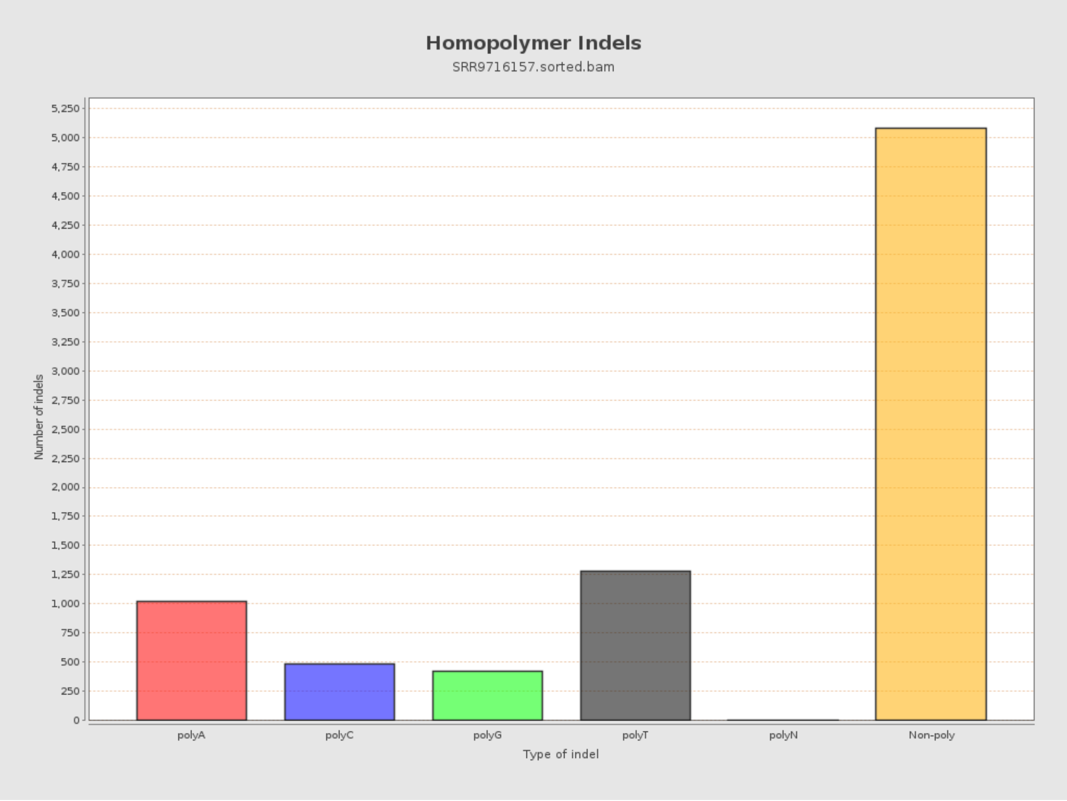
9. Results : Mapped Reads GC-content Distribution



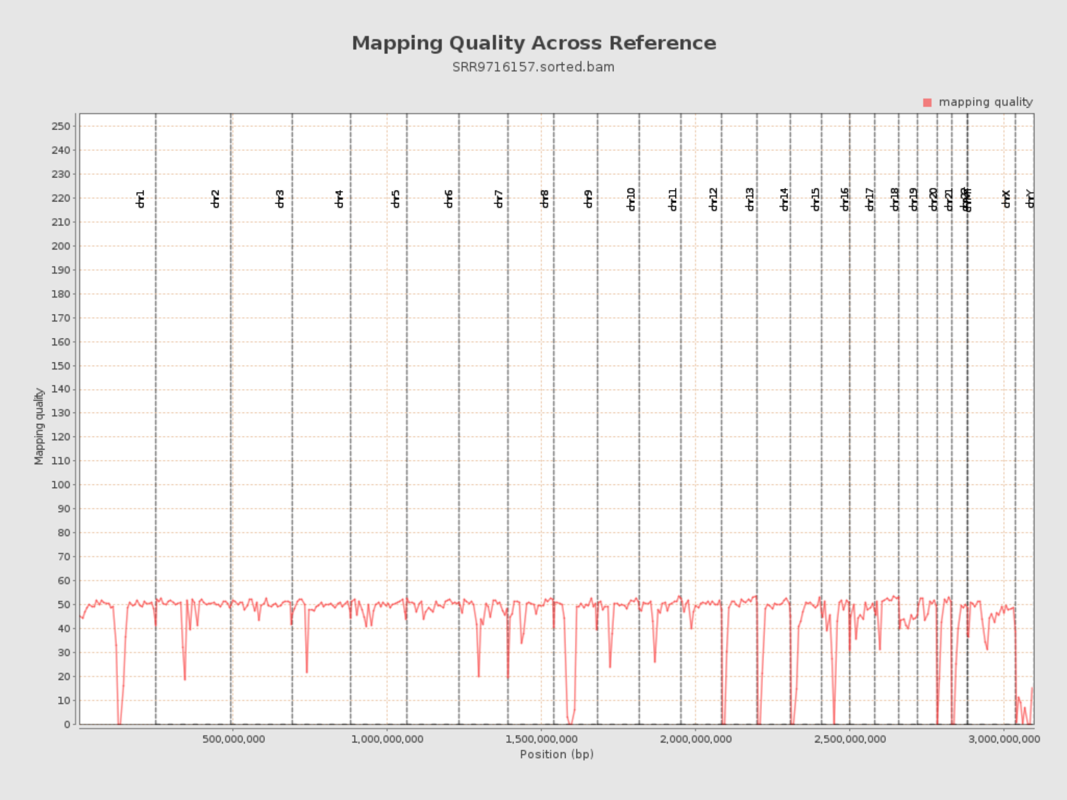
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram