Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:29:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716487.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_SRR9716487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716487.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:29:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,483,987
Mapped reads	607,915 / 40.96%
Unmapped reads	876,072 / 59.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,847 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	13,866 / 0.93%
Duplication rate	1.78%
Clipped reads	608,700 / 41.02%

2.2. ACGT Content

Number/percentage of A's	8,604,249 / 24.65%
Number/percentage of C's	7,171,707 / 20.54%
Number/percentage of T's	11,122,346 / 31.86%
Number/percentage of G's	8,010,162 / 22.95%
Number/percentage of N's	415 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1331

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

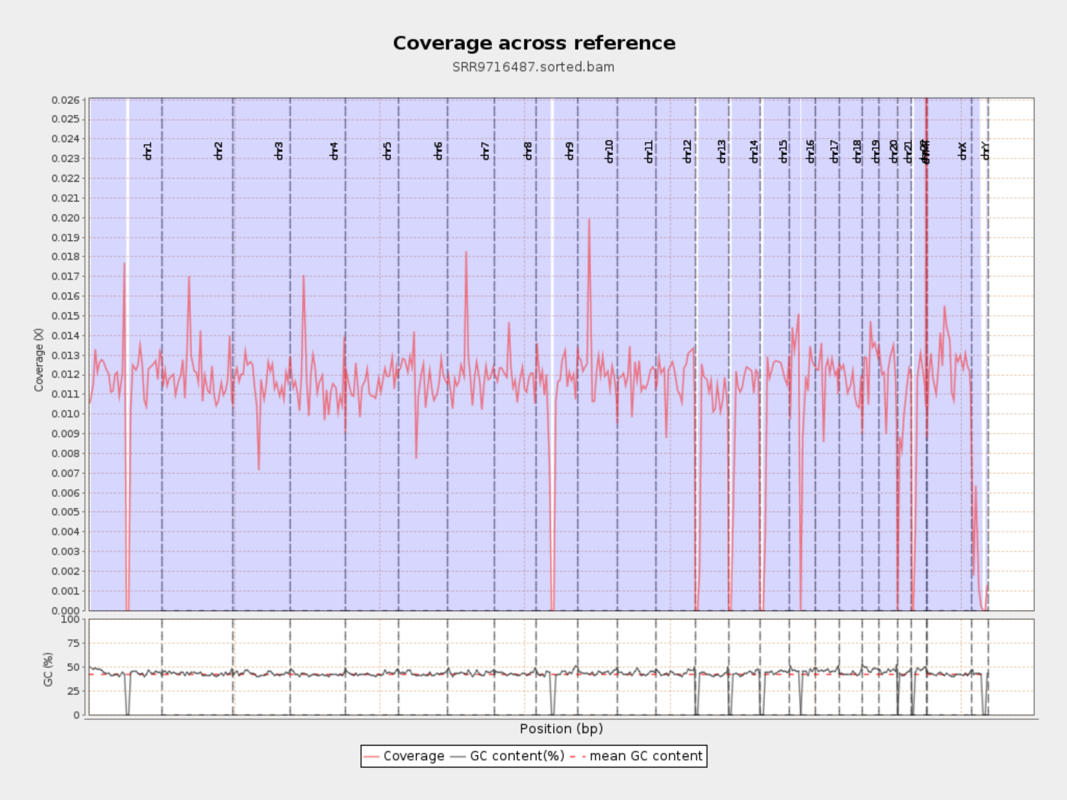
General error rate	0.52%
Mismatches	175,934
Insertions	2,902
Mapped reads with at least one insertion	0.47%
Deletions	6,625
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.98%

2.6. Chromosome stats

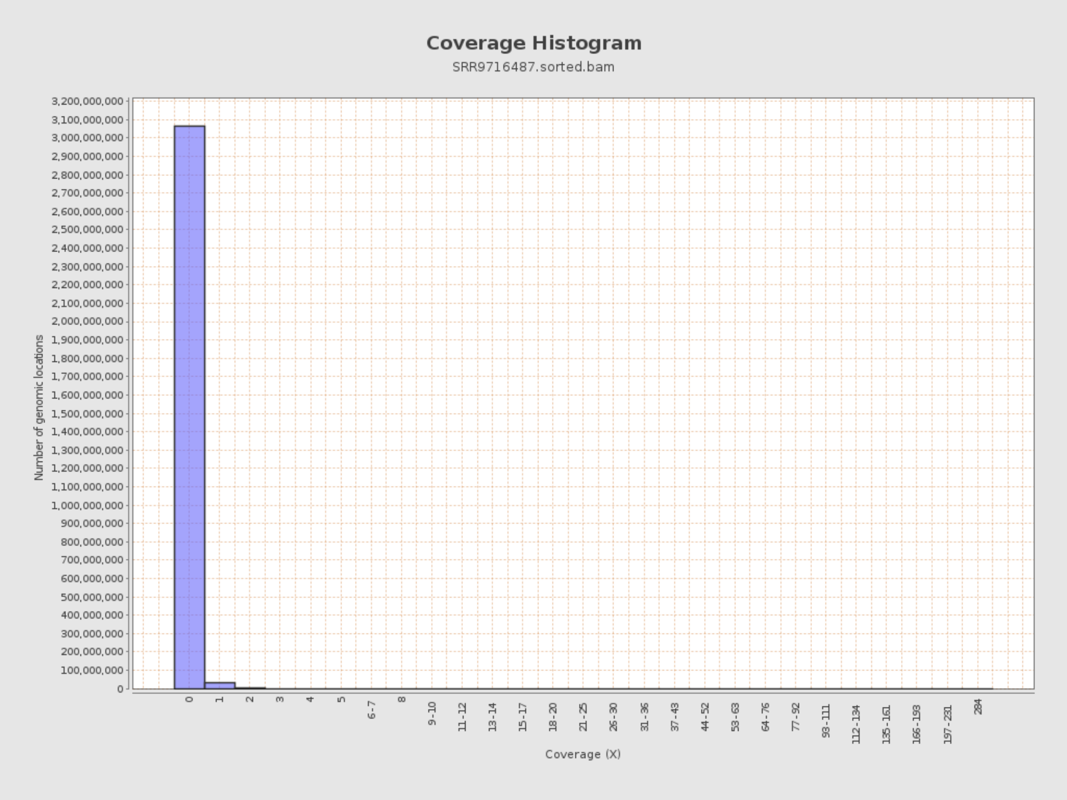
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2858918	0.0115	0.2061
chr2	243199373	2909519	0.012	0.165
chr3	198022430	2301867	0.0116	0.1128
chr4	191154276	2212253	0.0116	0.1162
chr5	180915260	2091051	0.0116	0.1125
chr6	171115067	2020897	0.0118	0.1215
chr7	159138663	1913841	0.012	0.1503

chr8	146364022	1742358	0.0119	0.1244
chr9	141213431	1456824	0.0103	0.1187
chr10	135534747	1696972	0.0125	0.1361
chr11	135006516	1596607	0.0118	0.1258
chr12	133851895	1607099	0.012	0.1151
chr13	115169878	1076353	0.0093	0.1007
chr14	107349540	1054035	0.0098	0.1052
chr15	102531392	1019129	0.0099	0.1048
chr16	90354753	1038468	0.0115	0.1155
chr17	81195210	977946	0.012	0.1178
chr18	78077248	900670	0.0115	0.1556
chr19	59128983	757644	0.0128	0.1553
chr20	63025520	751743	0.0119	0.1148
chr21	48129895	450595	0.0094	0.104
chr22	51304566	428406	0.0084	0.0966
chrMT	16571	3561	0.2149	0.4937
chrX	155270560	1944106	0.0125	0.1214
chrY	59373566	108323	0.0018	0.0611

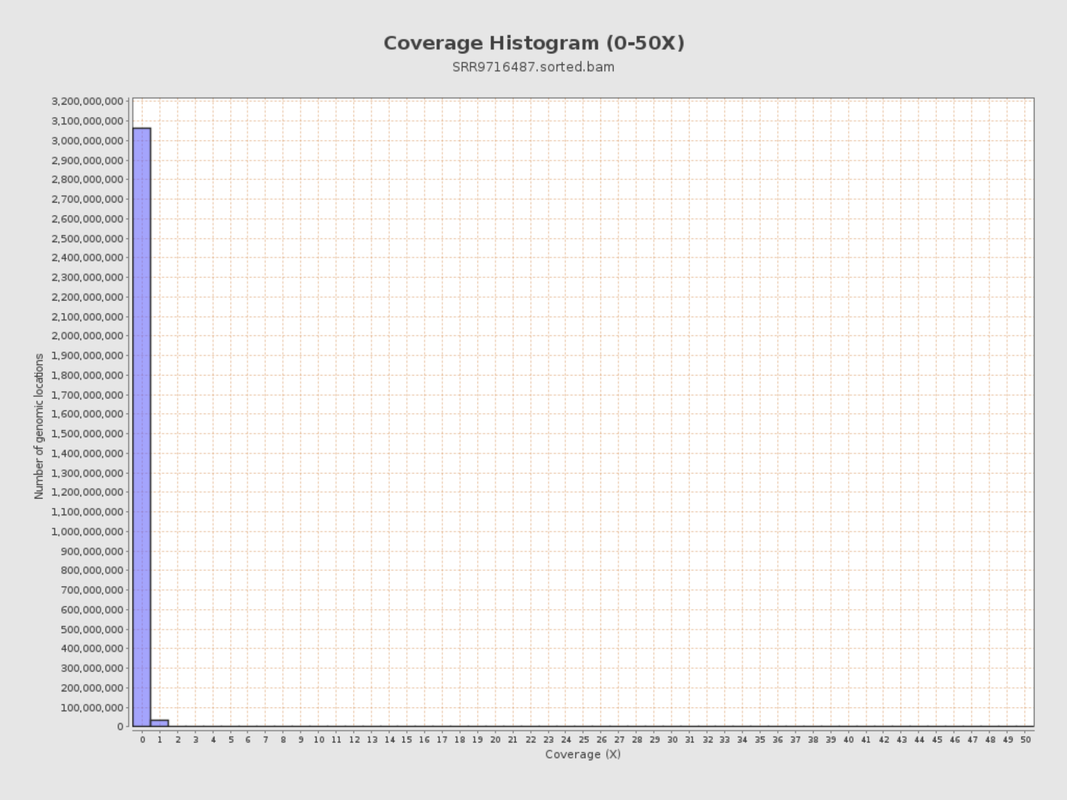
3. Results : Coverage across reference



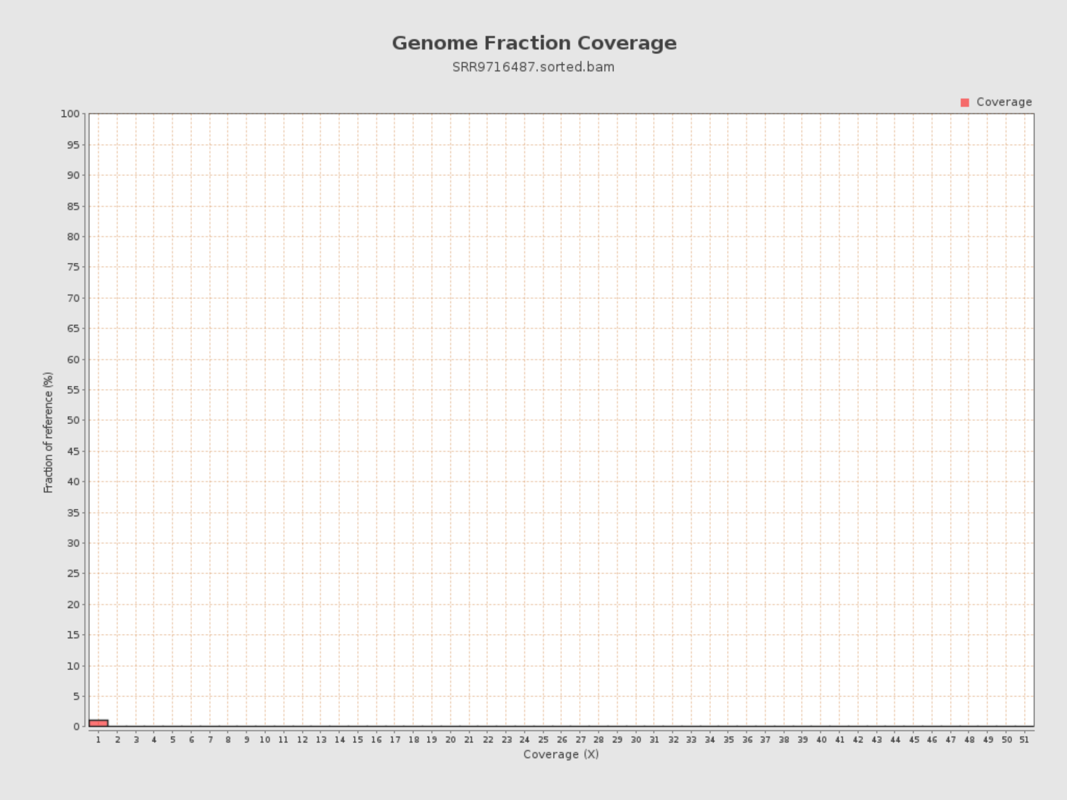
4. Results : Coverage Histogram



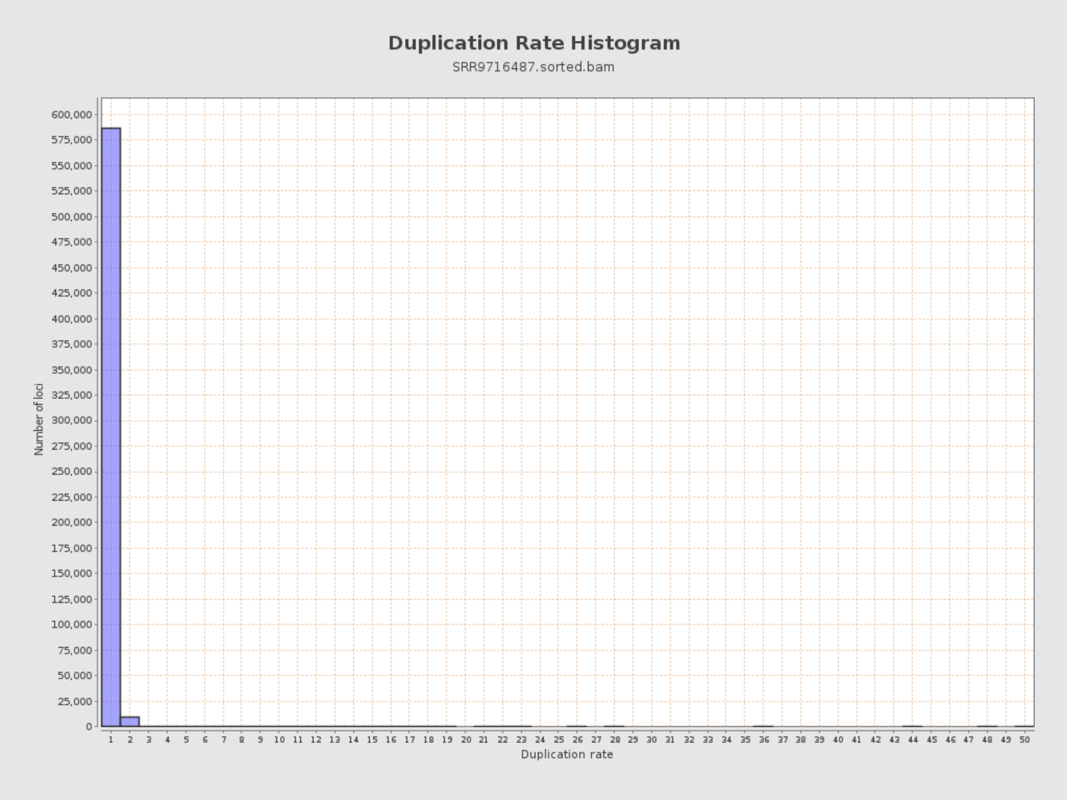
5. Results : Coverage Histogram (0-50X)



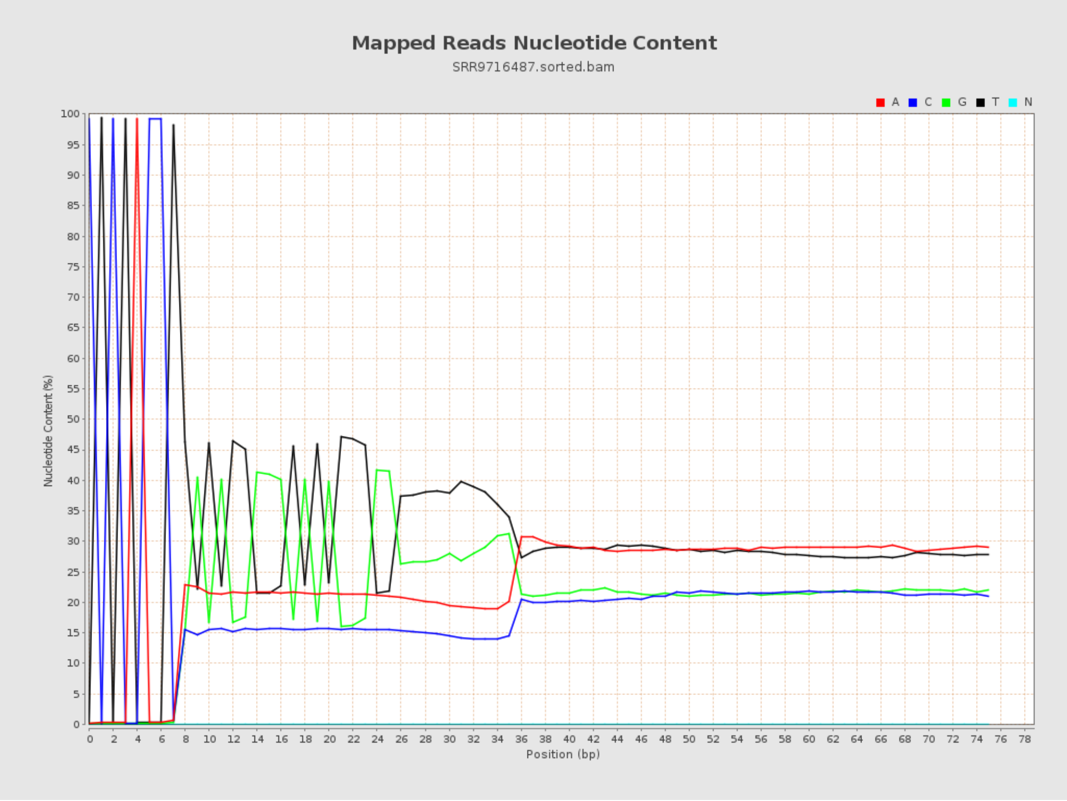
6. Results : Genome Fraction Coverage



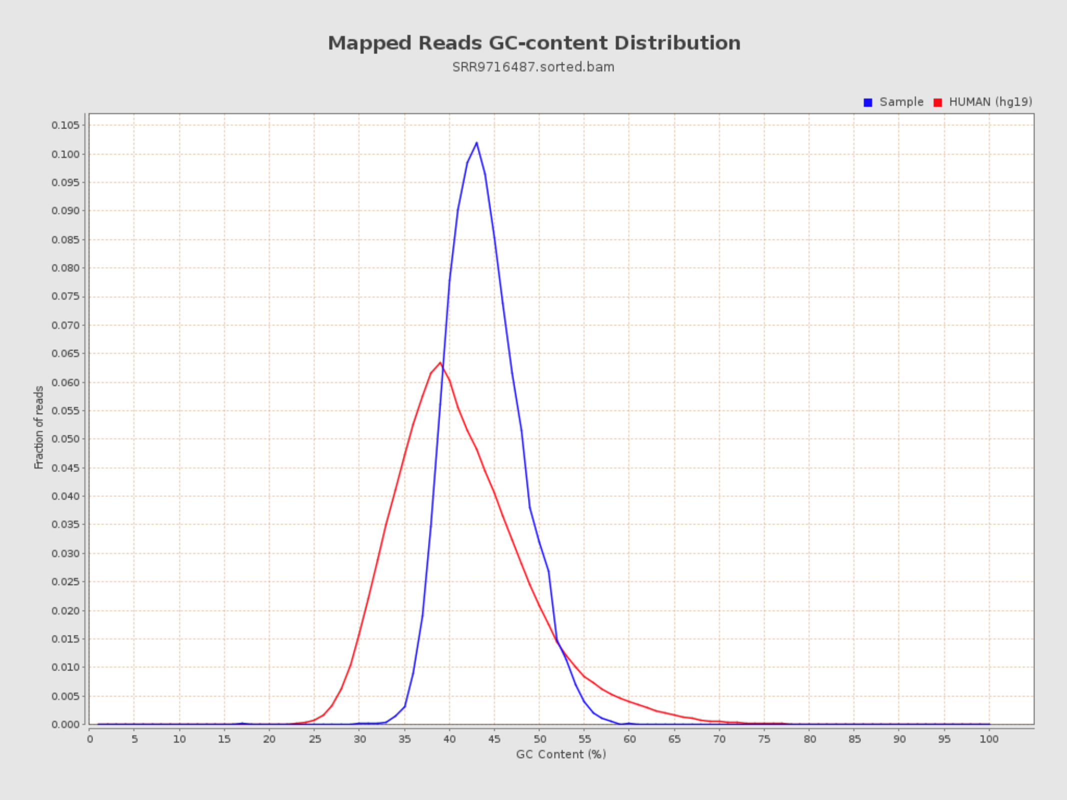
7. Results : Duplication Rate Histogram



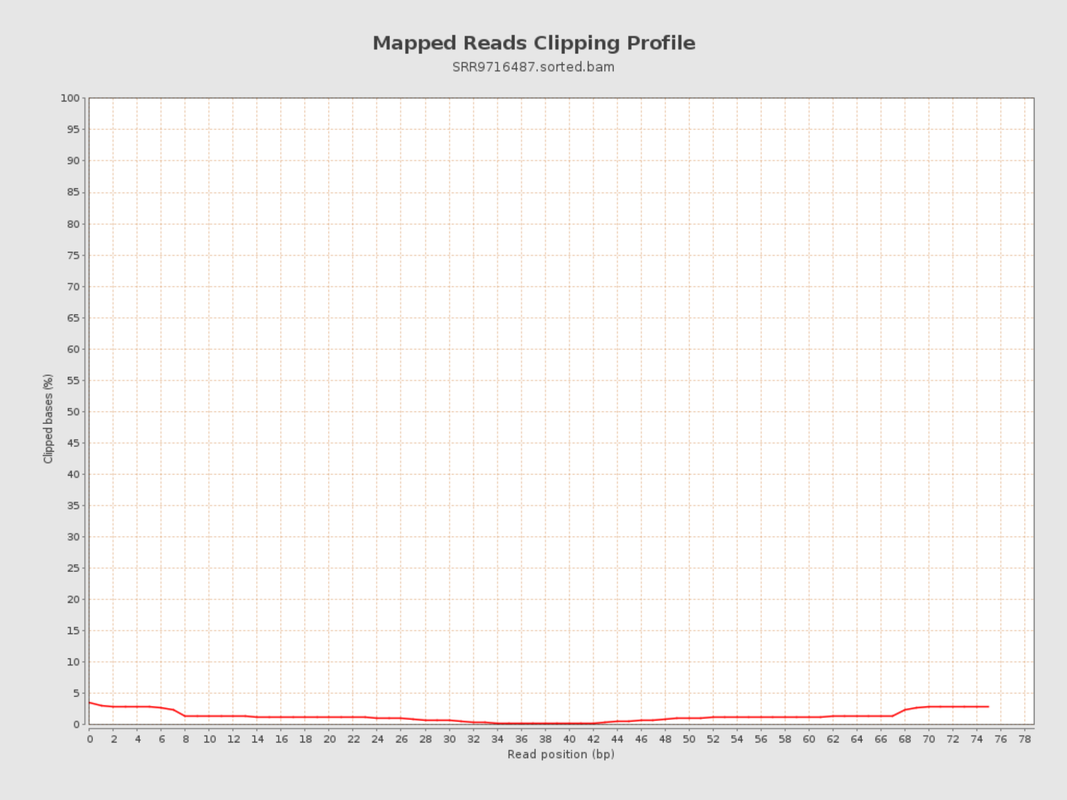
8. Results : Mapped Reads Nucleotide Content



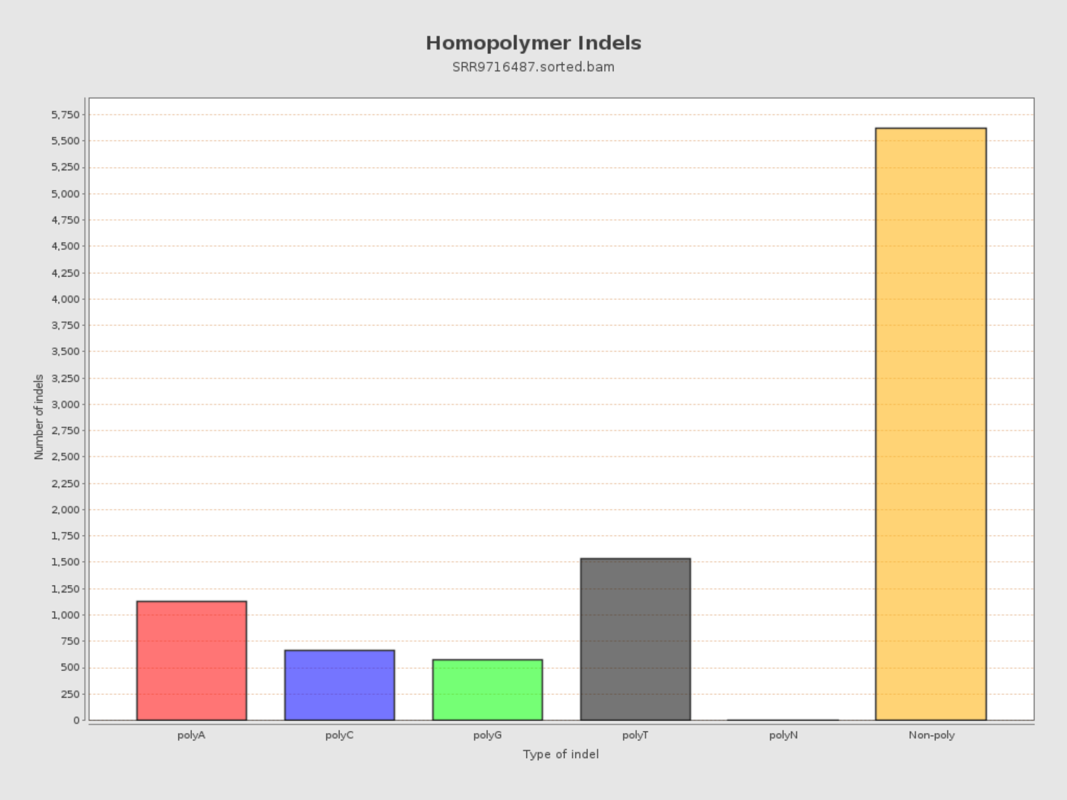
9. Results : Mapped Reads GC-content Distribution



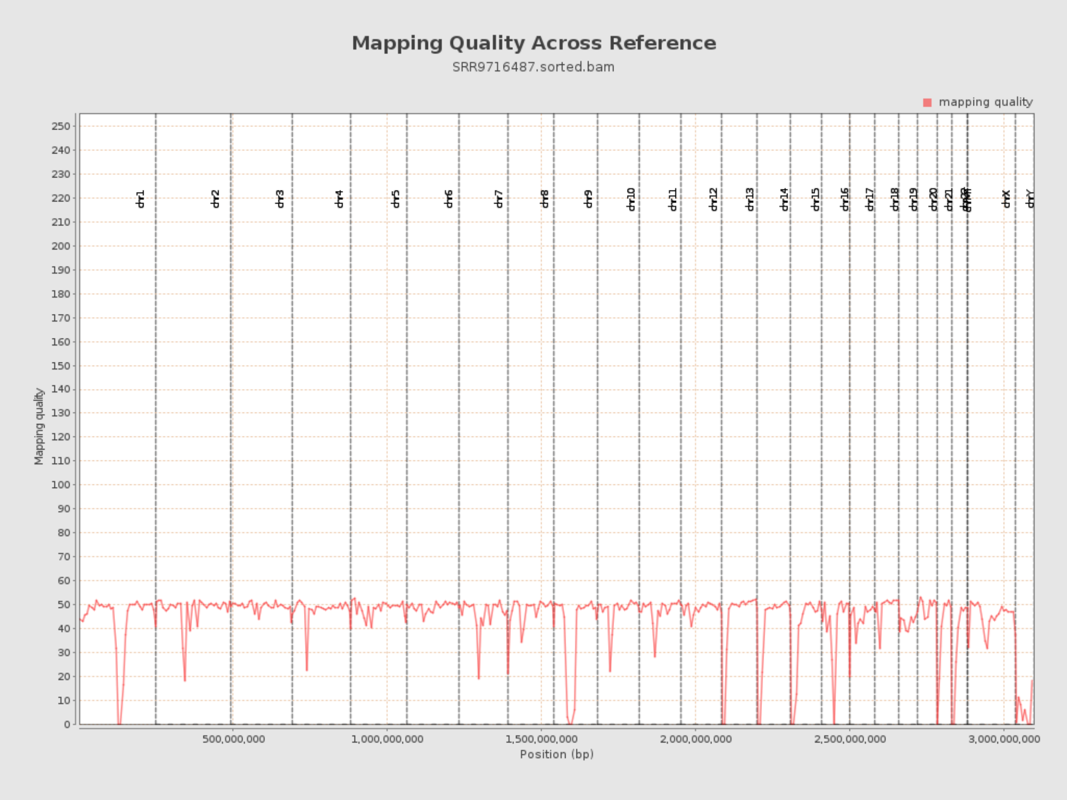
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram