Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:25:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716137.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_SRR9716137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:25:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	545,596
Mapped reads	479,405 / 87.87%
Unmapped reads	66,191 / 12.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,459 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	8,627 / 1.58%
Duplication rate	1.39%
Clipped reads	479,818 / 87.94%

2.2. ACGT Content

Number/percentage of A's	6,773,887 / 24.78%
Number/percentage of C's	5,245,995 / 19.19%
Number/percentage of T's	8,698,342 / 31.81%
Number/percentage of G's	6,622,725 / 24.22%
Number/percentage of N's	232 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1112

2.4. Mapping Quality

Mean Mapping Quality	43.65

2.5. Mismatches and indels

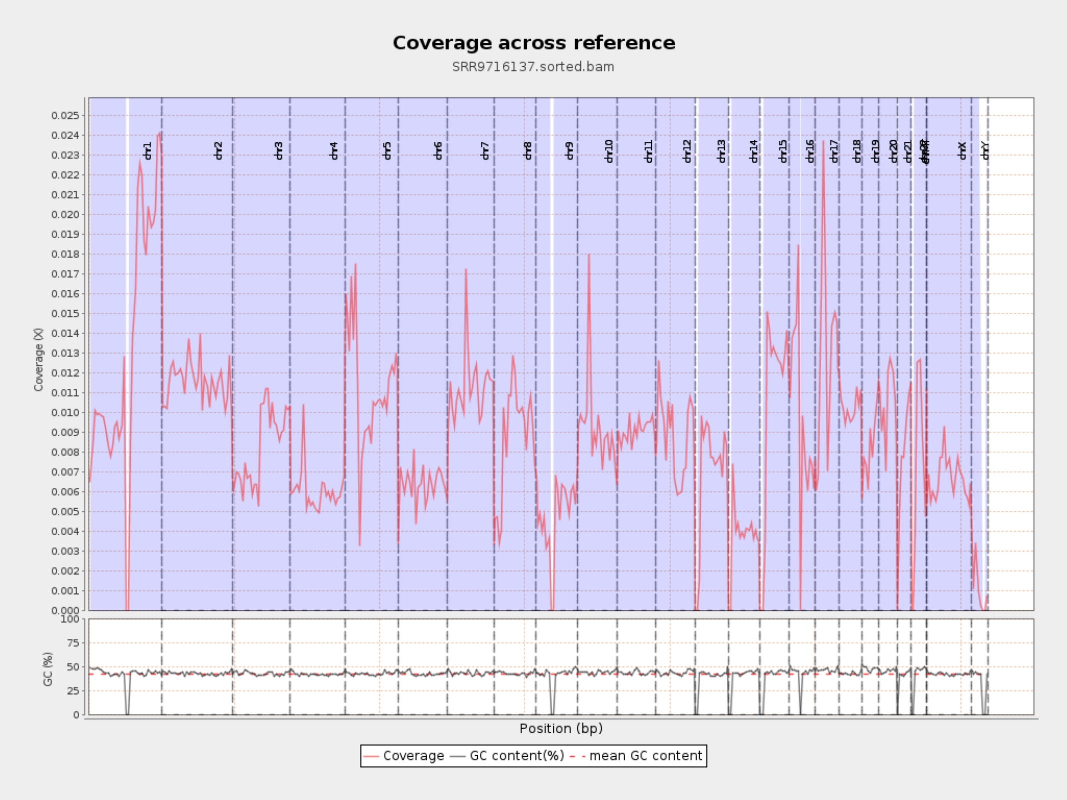
General error rate	0.51%
Mismatches	136,350
Insertions	1,764
Mapped reads with at least one insertion	0.37%
Deletions	5,147
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.39%

2.6. Chromosome stats

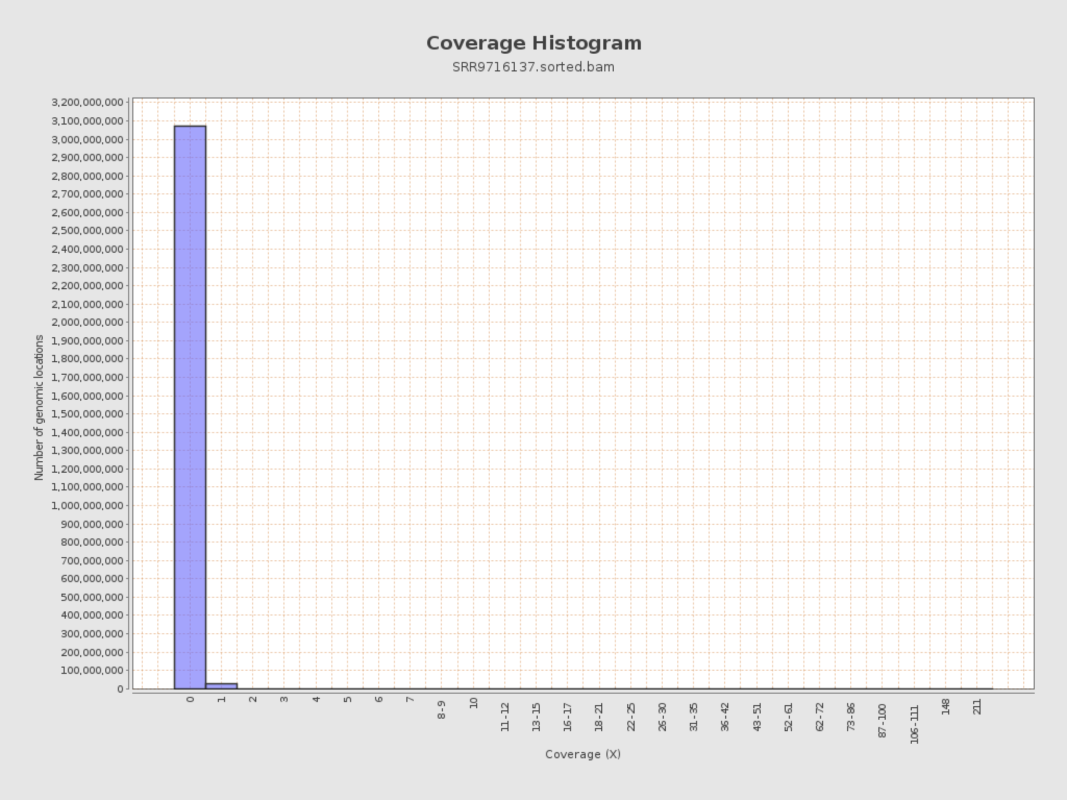
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3260083	0.0131	0.1503
chr2	243199373	2808890	0.0115	0.1429
chr3	198022430	1628344	0.0082	0.0944
chr4	191154276	1152135	0.006	0.0817
chr5	180915260	2033155	0.0112	0.1094
chr6	171115067	1081561	0.0063	0.0865
chr7	159138663	1805247	0.0113	0.1477

chr8	146364022	1289574	0.0088	0.102
chr9	141213431	654367	0.0046	0.0822
chr10	135534747	1257754	0.0093	0.1288
chr11	135006516	1221195	0.009	0.1098
chr12	133851895	1168802	0.0087	0.0964
chr13	115169878	793966	0.0069	0.0854
chr14	107349540	397717	0.0037	0.0643
chr15	102531392	1087287	0.0106	0.1077
chr16	90354753	867596	0.0096	0.1065
chr17	81195210	1063386	0.0131	0.1213
chr18	78077248	802556	0.0103	0.1471
chr19	59128983	491367	0.0083	0.1274
chr20	63025520	660947	0.0105	0.1063
chr21	48129895	375223	0.0078	0.0917
chr22	51304566	351653	0.0069	0.0853
chrMT	16571	186	0.0112	0.1053
chrX	155270560	1031213	0.0066	0.0879
chrY	59373566	65060	0.0011	0.0372

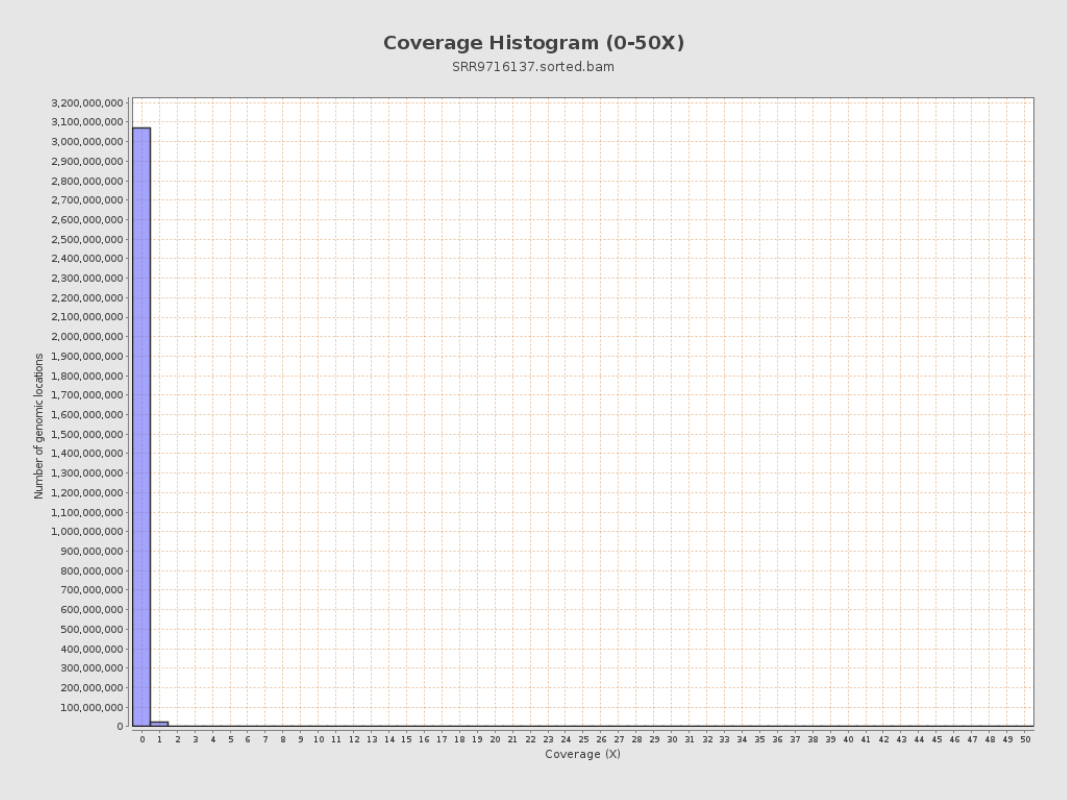
3. Results : Coverage across reference



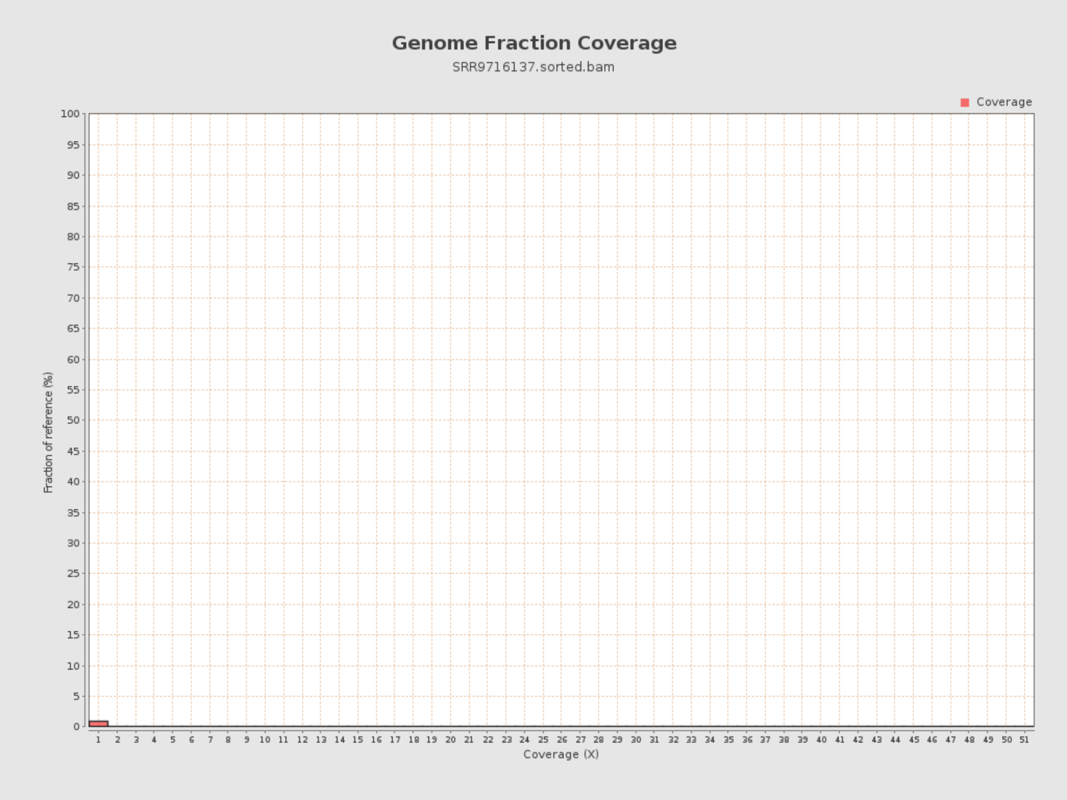
4. Results : Coverage Histogram



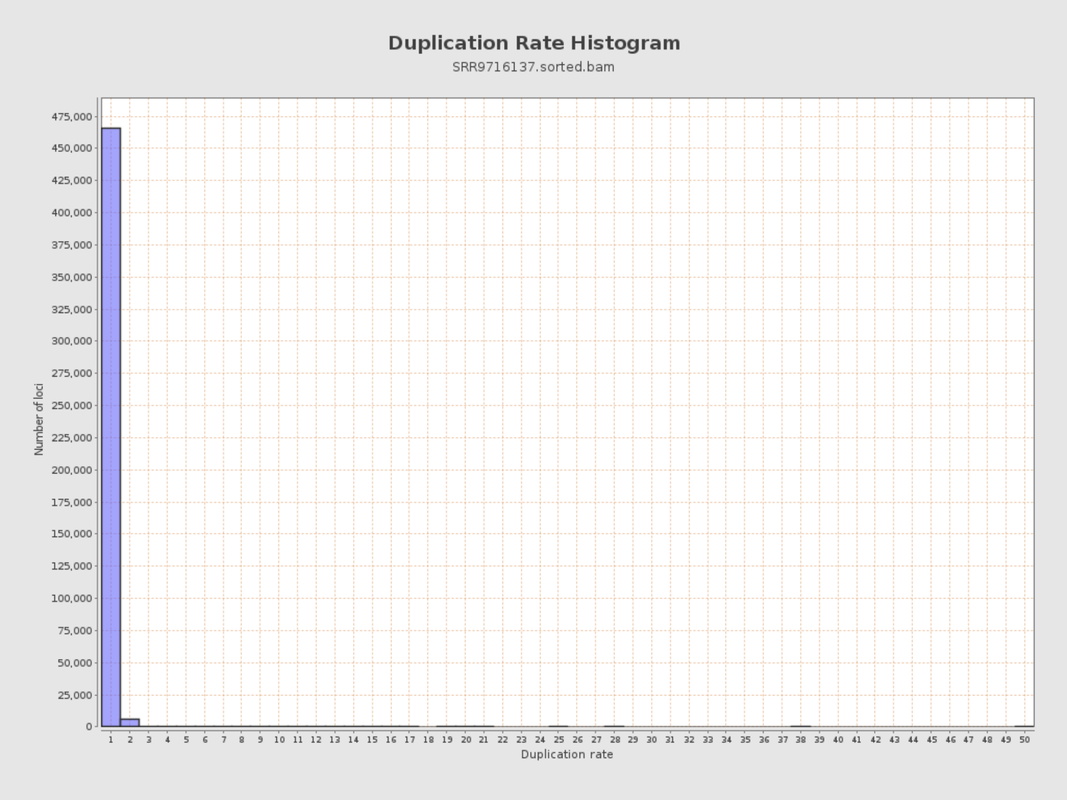
5. Results : Coverage Histogram (0-50X)



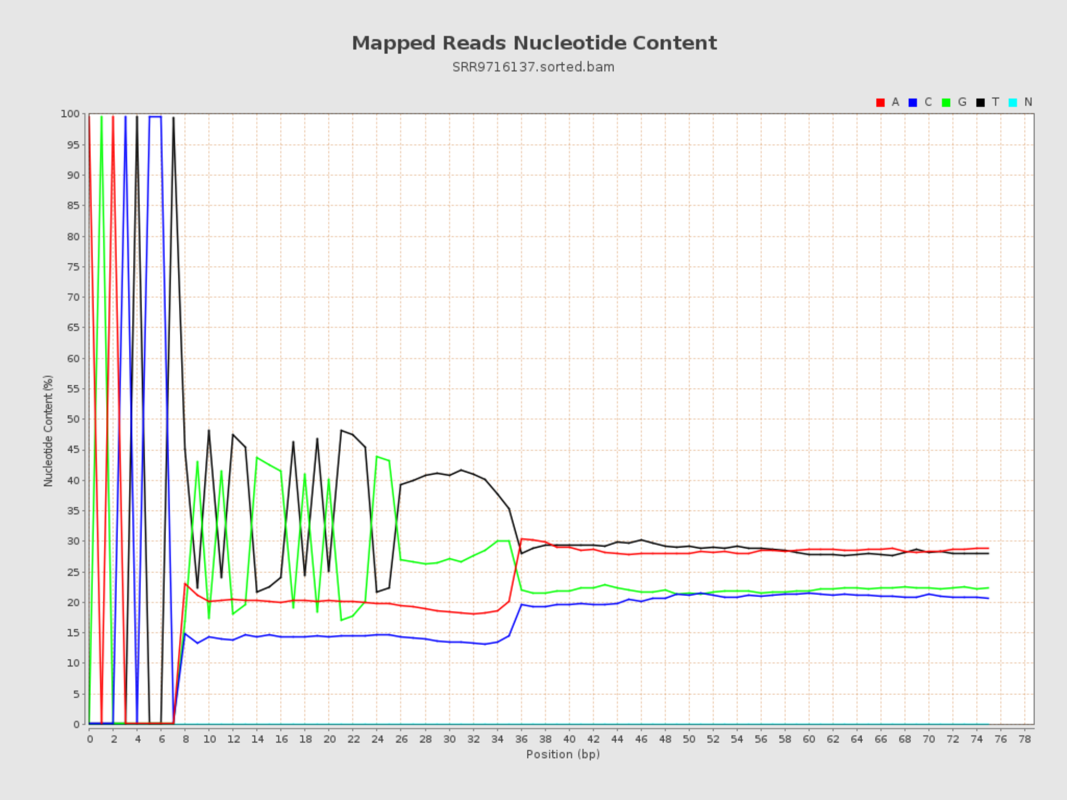
6. Results : Genome Fraction Coverage



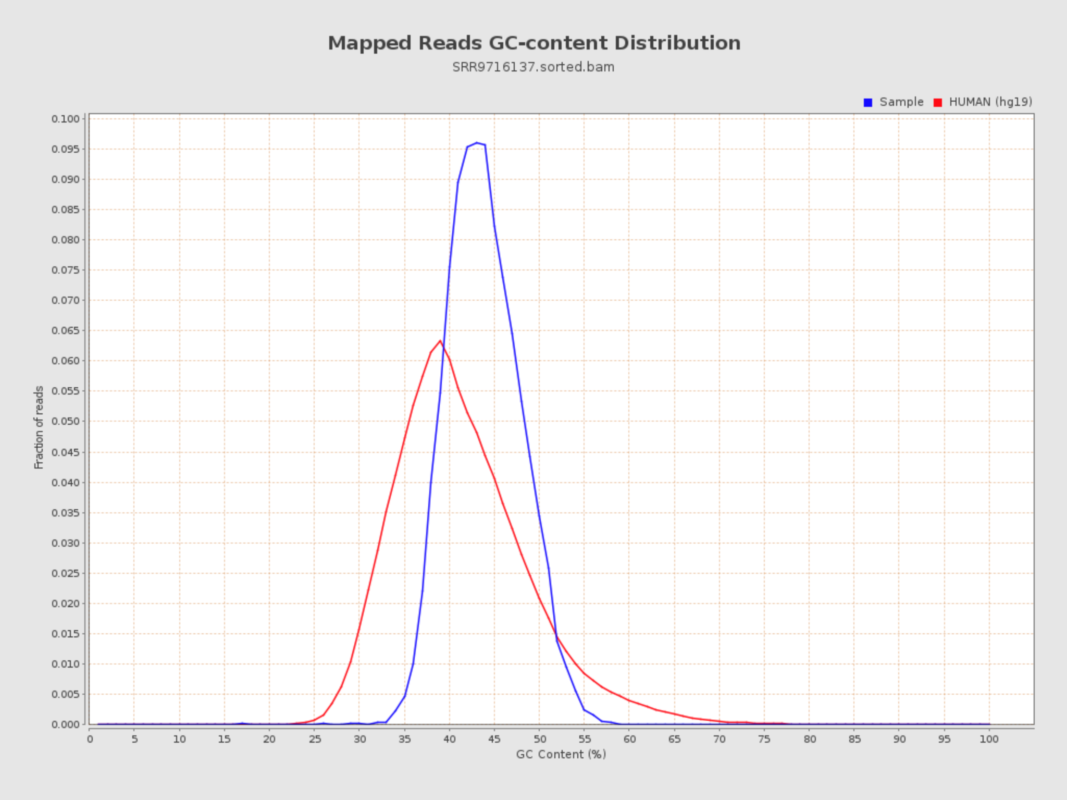
7. Results : Duplication Rate Histogram



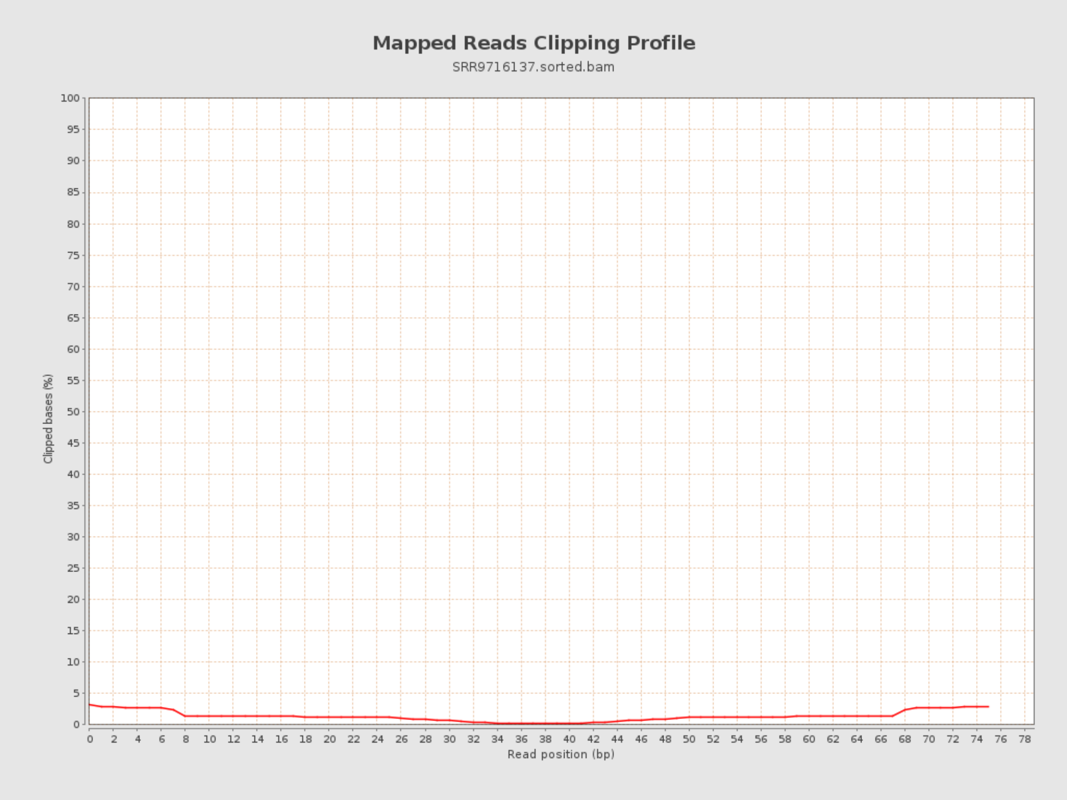
8. Results : Mapped Reads Nucleotide Content



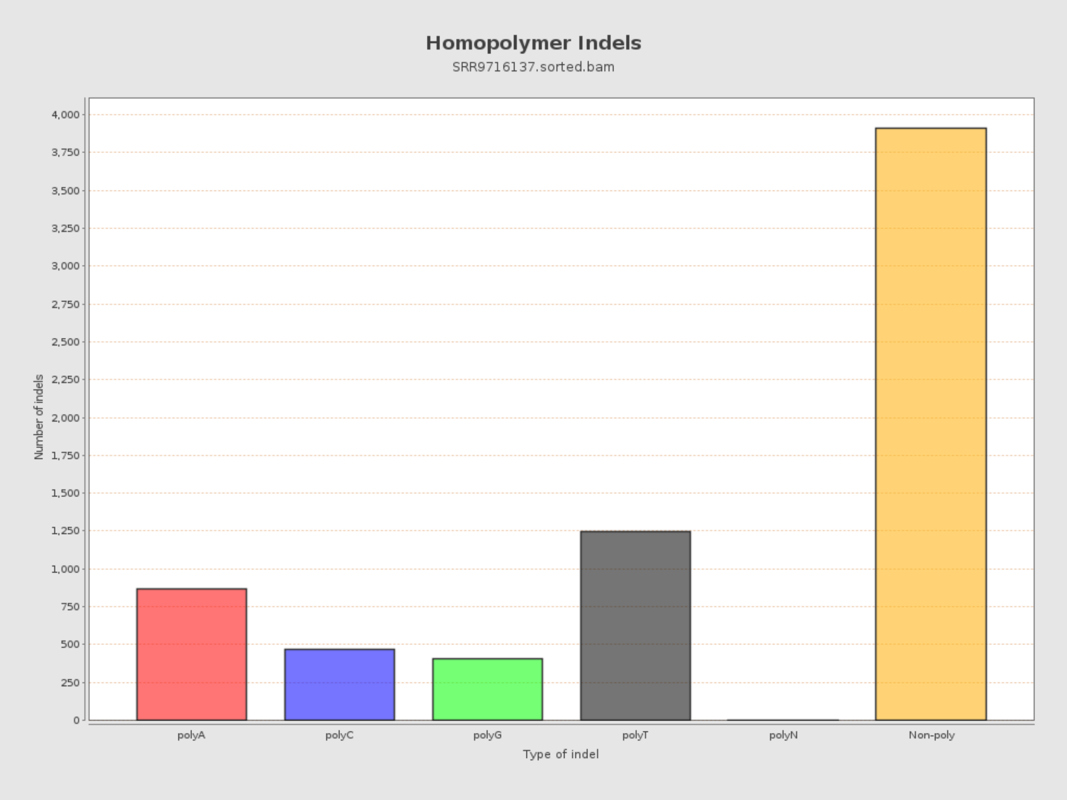
9. Results : Mapped Reads GC-content Distribution



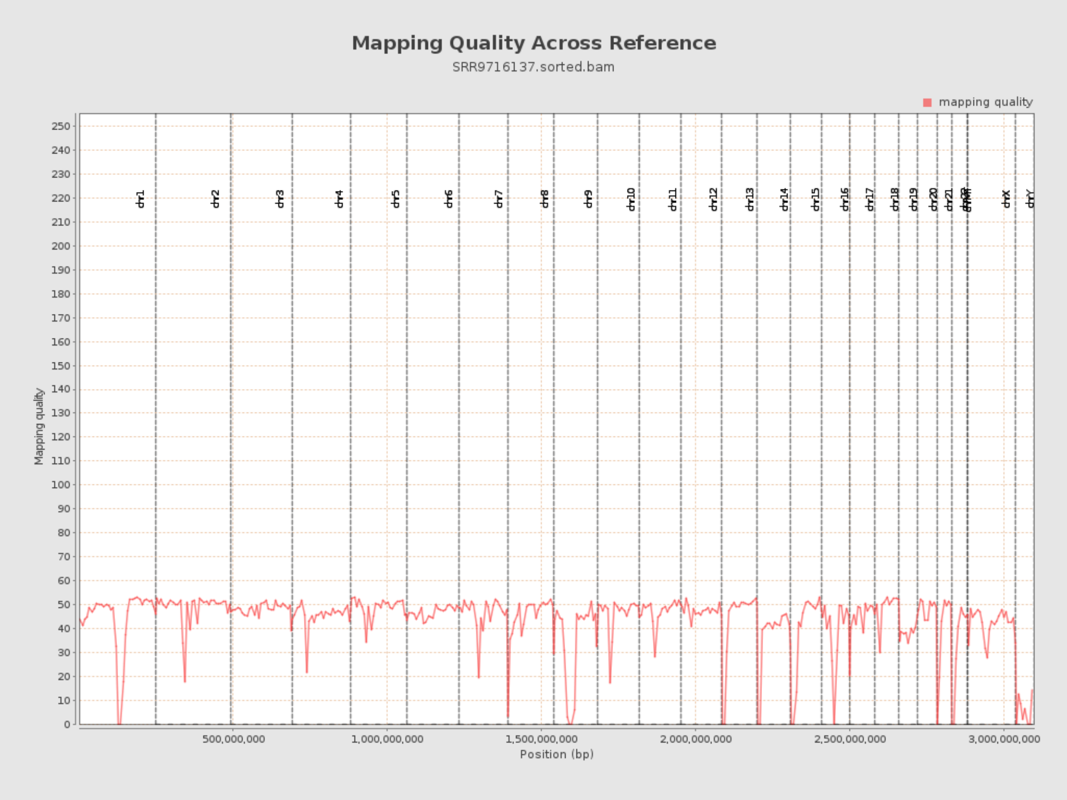
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram