Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716737.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_SRR9716737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:33:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	407,316
Mapped reads	374,292 / 91.89%
Unmapped reads	33,024 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,310 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	5,589 / 1.37%
Duplication rate	1.1%
Clipped reads	375,517 / 92.19%

2.2. ACGT Content

Number/percentage of A's	5,909,842 / 26.36%
Number/percentage of C's	4,643,252 / 20.71%
Number/percentage of T's	6,732,051 / 30.03%
Number/percentage of G's	5,131,603 / 22.89%
Number/percentage of N's	358 / 0%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0072

Standard Deviation	0.1026

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

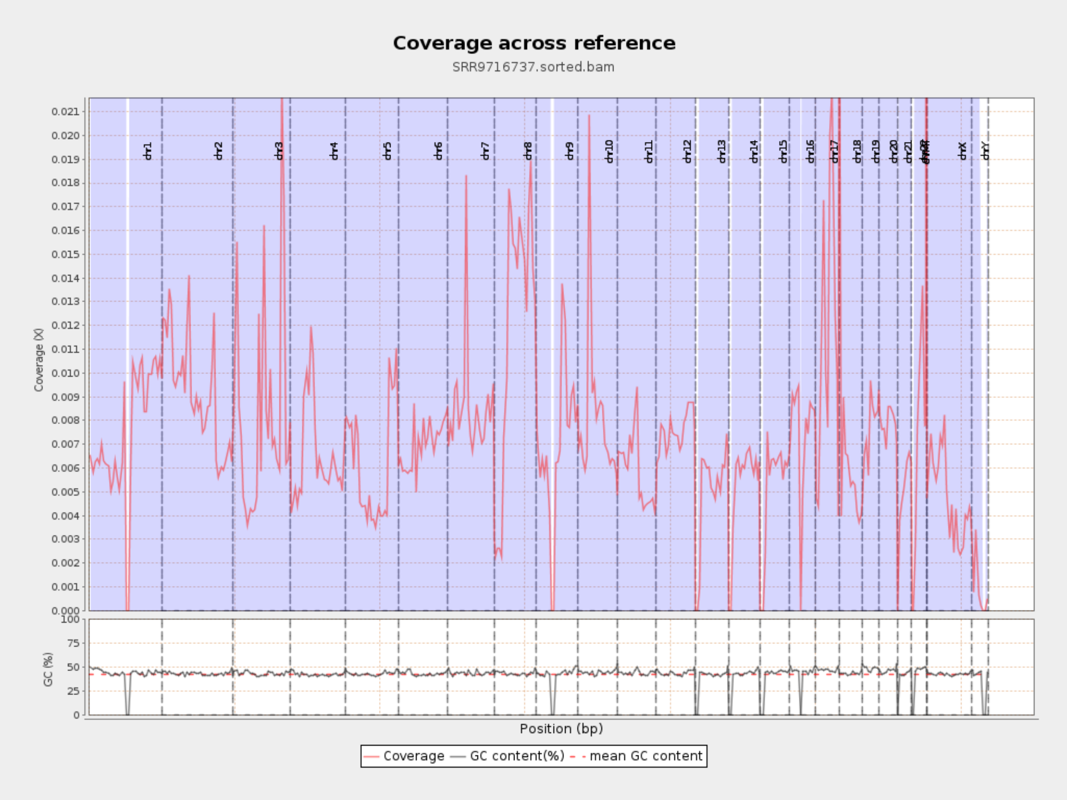
General error rate	0.49%
Mismatches	106,912
Insertions	1,753
Mapped reads with at least one insertion	0.47%
Deletions	4,176
Mapped reads with at least one deletion	1.11%
Homopolymer indels	39.59%

2.6. Chromosome stats

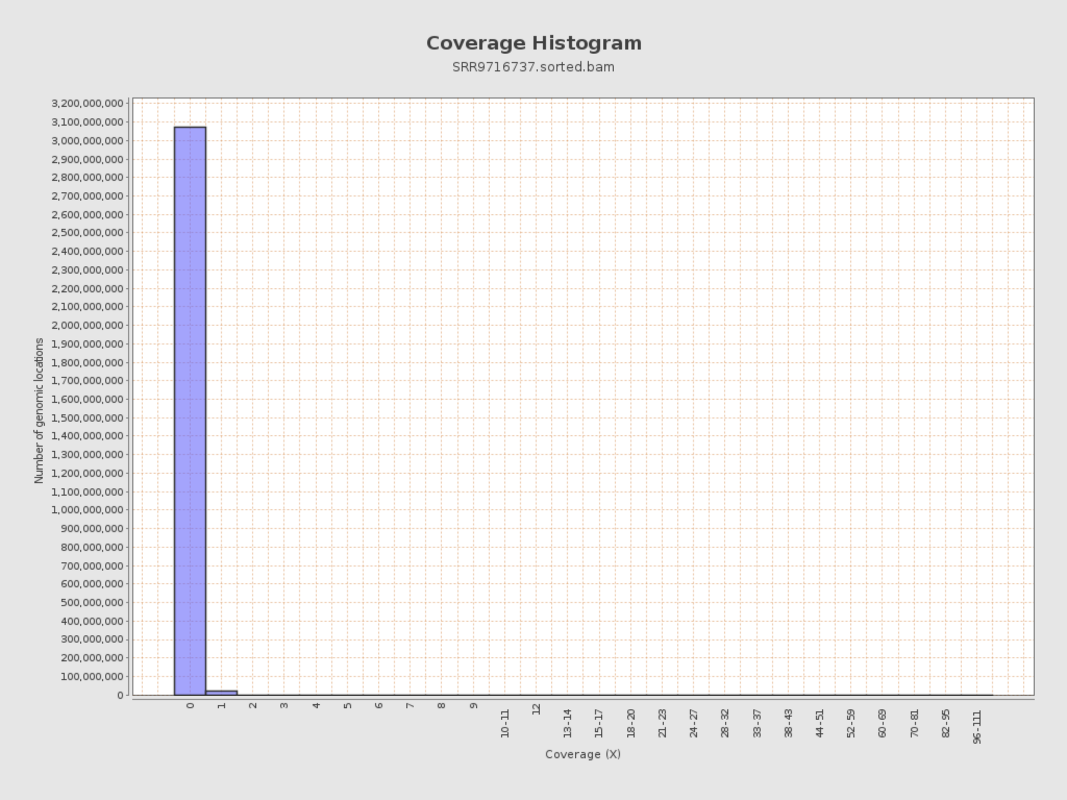
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1835312	0.0074	0.1231
chr2	243199373	2252882	0.0093	0.1167
chr3	198022430	1653270	0.0083	0.0949
chr4	191154276	1247348	0.0065	0.0867
chr5	180915260	1106113	0.0061	0.0804
chr6	171115067	1194021	0.007	0.0872
chr7	159138663	1366324	0.0086	0.1716

chr8	146364022	1763447	0.012	0.1267
chr9	141213431	961758	0.0068	0.0888
chr10	135534747	1099596	0.0081	0.1304
chr11	135006516	792882	0.0059	0.0825
chr12	133851895	1009742	0.0075	0.0925
chr13	115169878	562223	0.0049	0.0718
chr14	107349540	557765	0.0052	0.0736
chr15	102531392	525473	0.0051	0.0732
chr16	90354753	679399	0.0075	0.0912
chr17	81195210	942711	0.0116	0.1115
chr18	78077248	510378	0.0065	0.1076
chr19	59128983	452680	0.0077	0.1104
chr20	63025520	497193	0.0079	0.0927
chr21	48129895	235806	0.0049	0.0764
chr22	51304566	350730	0.0068	0.0844
chrMT	16571	13975	0.8433	1.0352
chrX	155270560	757692	0.0049	0.0743
chrY	59373566	55124	0.0009	0.0404

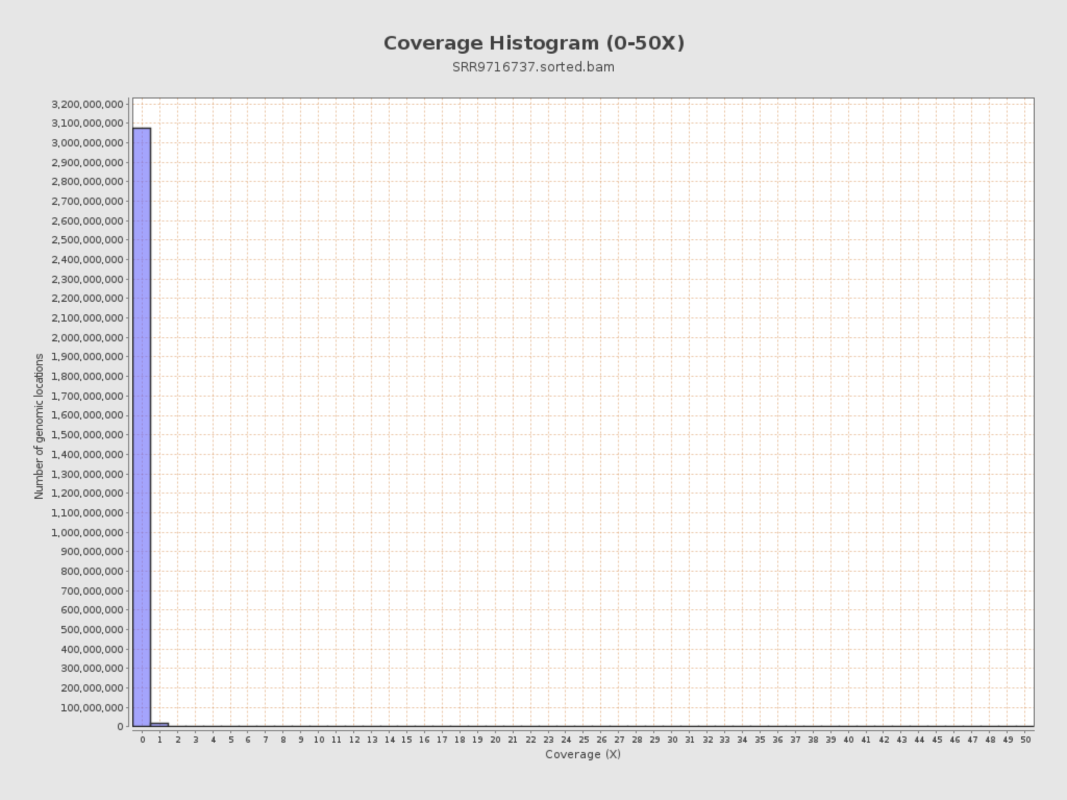
3. Results : Coverage across reference



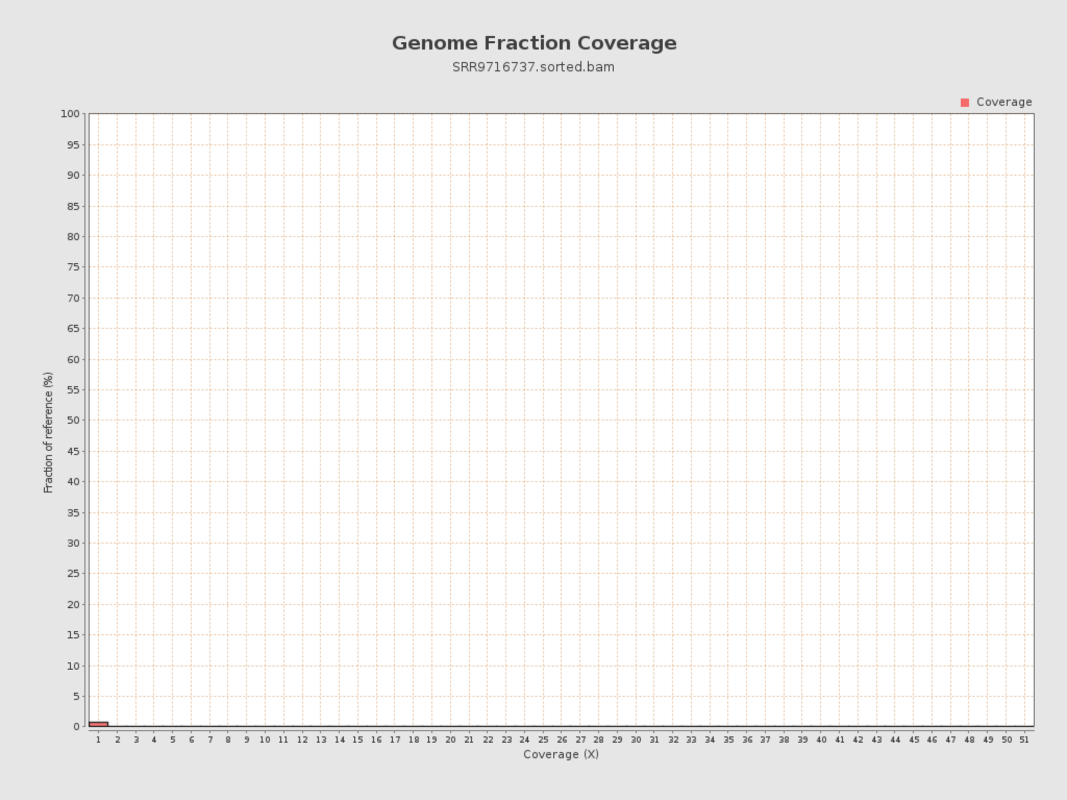
4. Results : Coverage Histogram



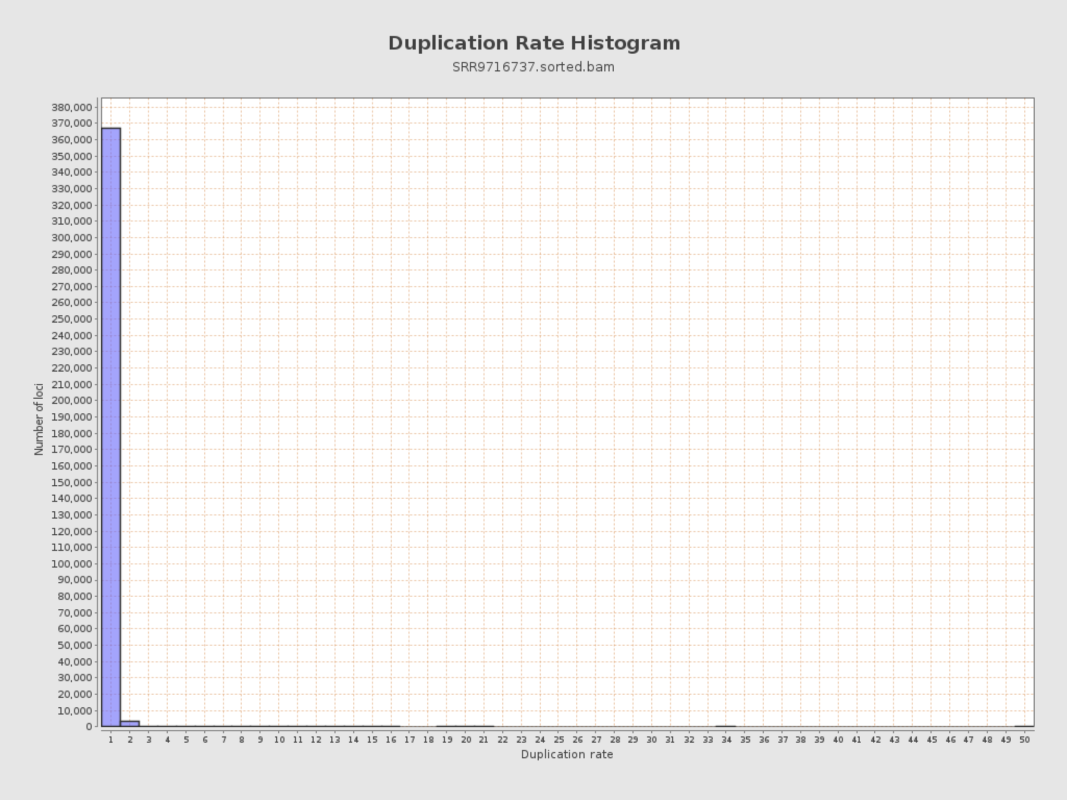
5. Results : Coverage Histogram (0-50X)



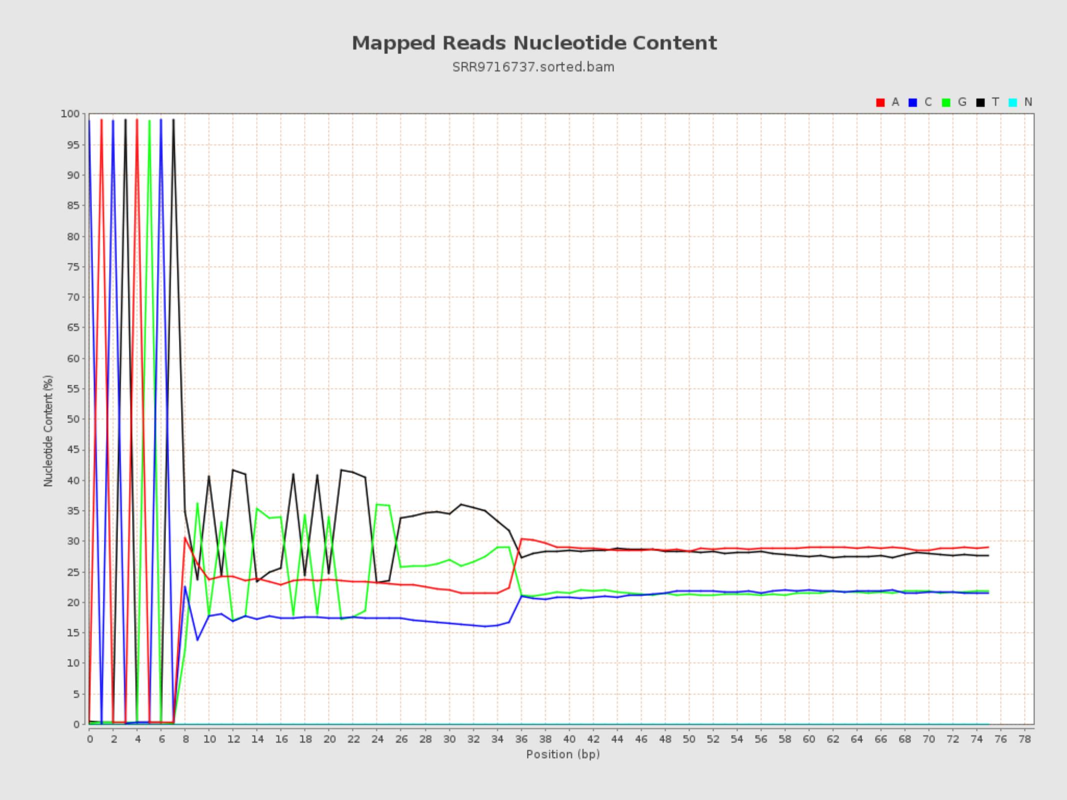
6. Results : Genome Fraction Coverage



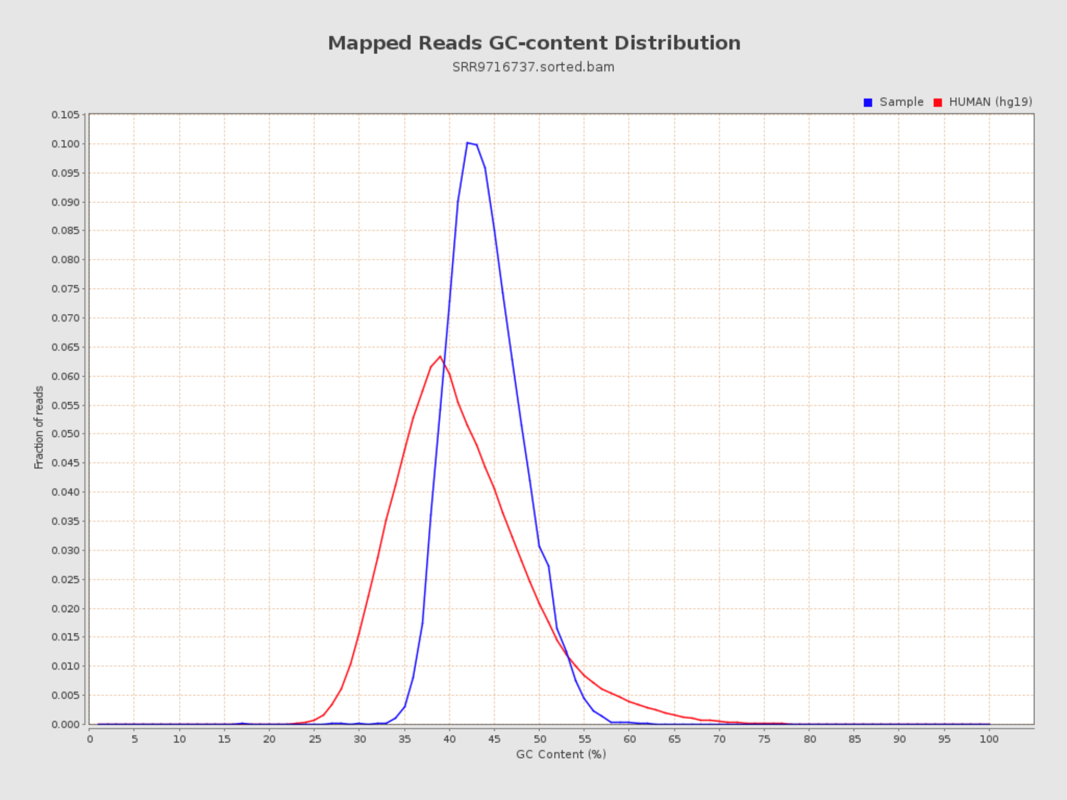
7. Results : Duplication Rate Histogram



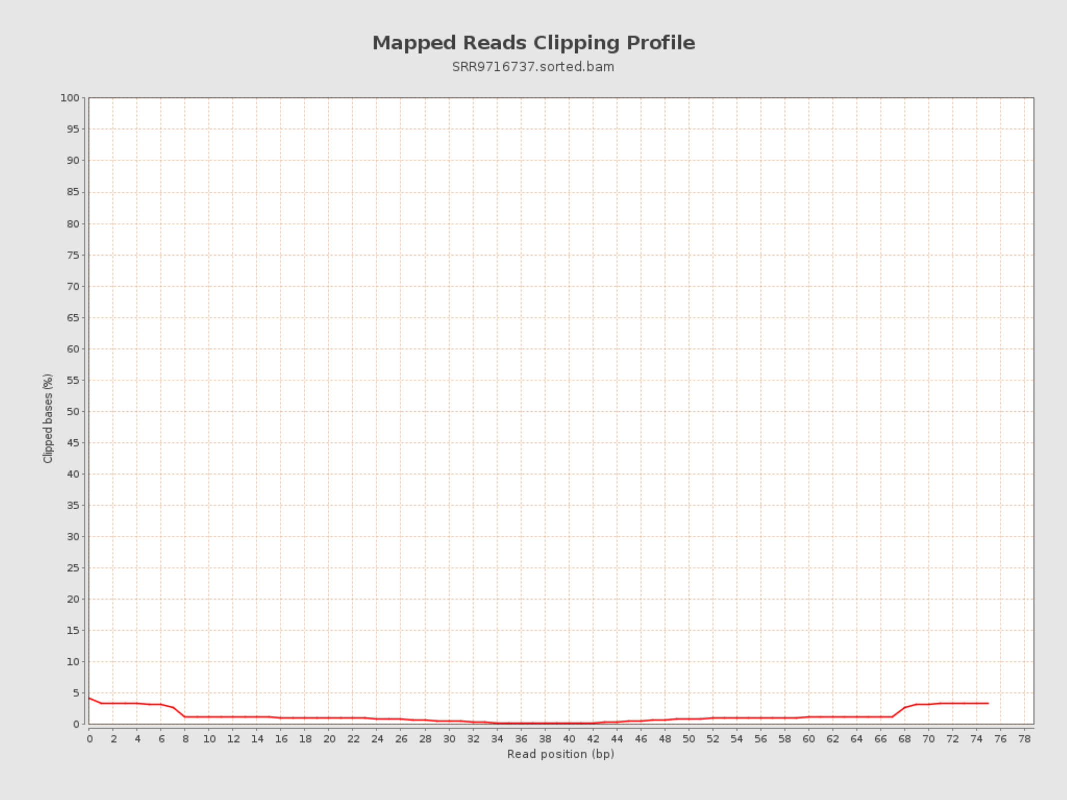
8. Results : Mapped Reads Nucleotide Content



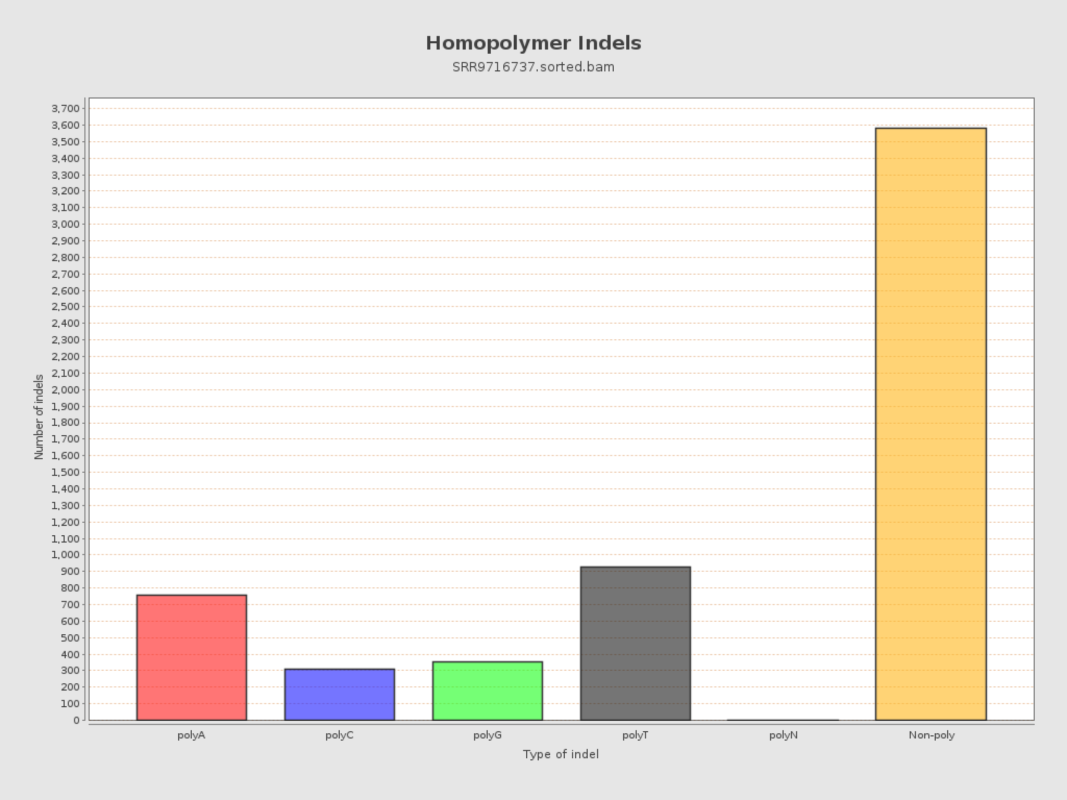
9. Results : Mapped Reads GC-content Distribution



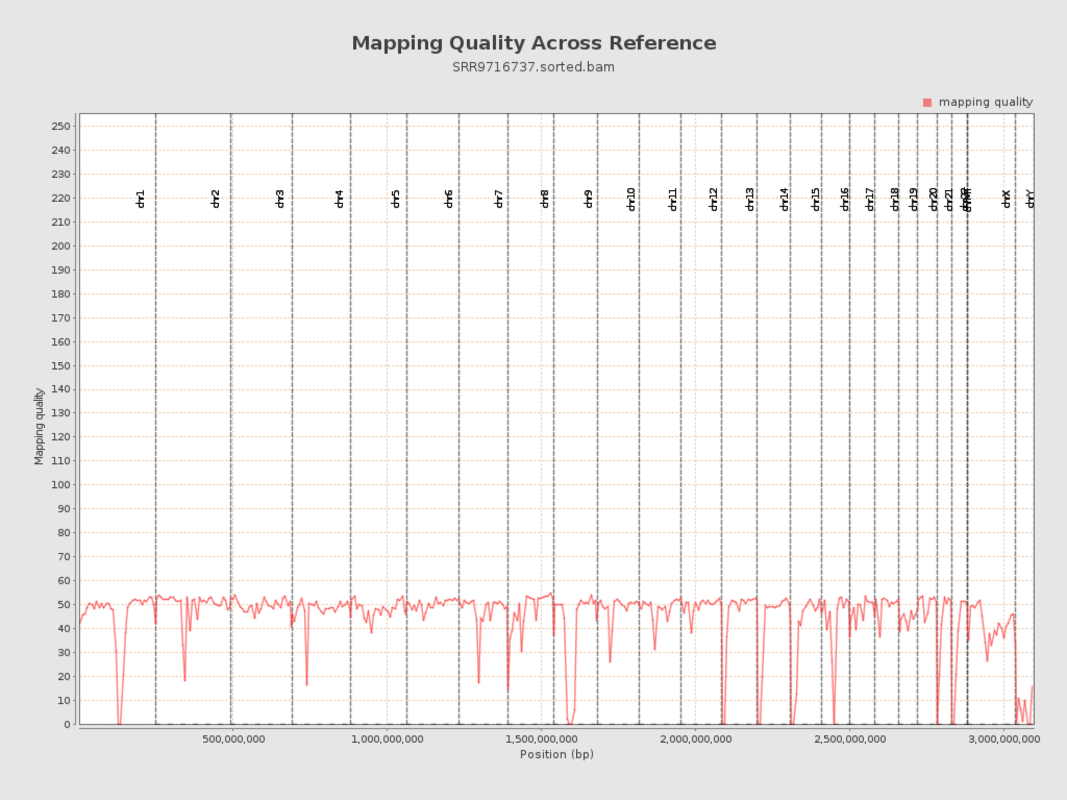
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram