Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:35:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716369.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_SRR9716369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716369.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:35:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,009,460
Mapped reads	6,334,171 / 90.37%
Unmapped reads	675,289 / 9.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	143,649 / 2.05%
Read min/max/mean length	30 / 101 / 101.73
Duplicated reads (estimated)	567,260 / 8.09%
Duplication rate	6.54%
Clipped reads	6,467,032 / 92.26%

2.2. ACGT Content

Number/percentage of A's	128,578,654 / 26.3%
Number/percentage of C's	94,004,021 / 19.23%
Number/percentage of T's	151,753,808 / 31.04%
Number/percentage of G's	114,473,587 / 23.42%
Number/percentage of N's	33,898 / 0.01%
GC Percentage	42.65%

2.3. Coverage

Mean	0.158

Standard Deviation	1.2994

2.4. Mapping Quality

Mean Mapping Quality	46.79

2.5. Mismatches and indels

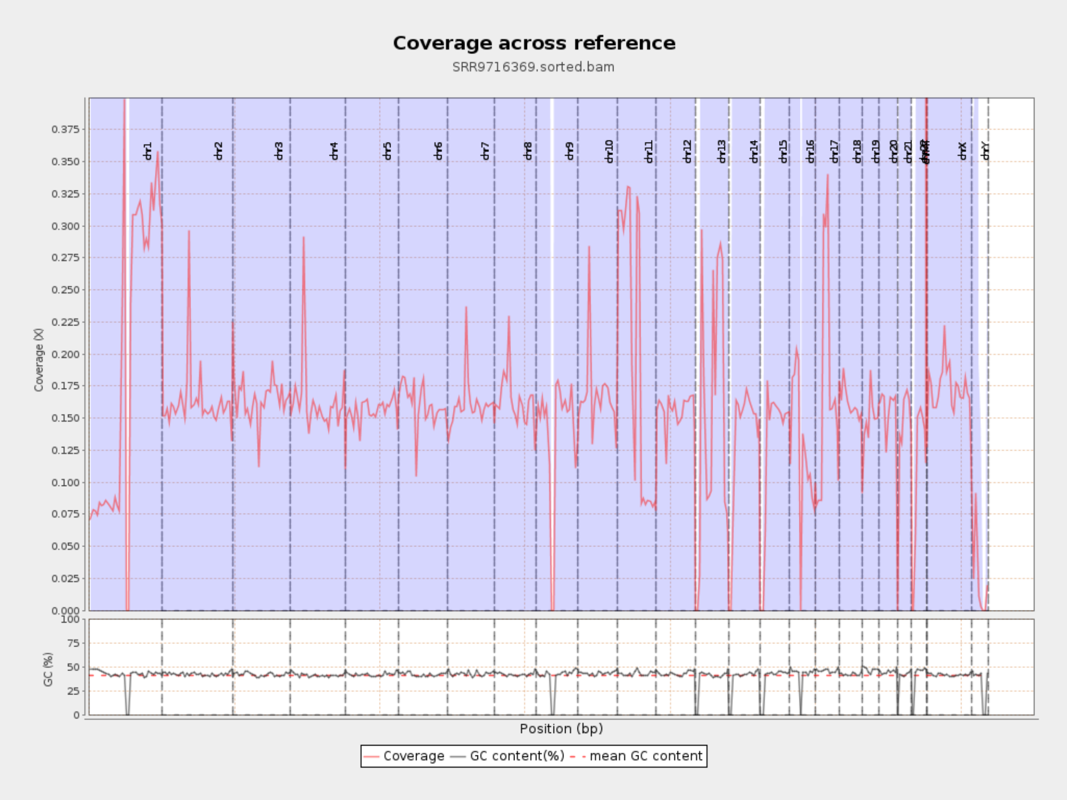
General error rate	0.71%
Mismatches	3,369,343
Insertions	42,458
Mapped reads with at least one insertion	0.66%
Deletions	109,444
Mapped reads with at least one deletion	1.7%
Homopolymer indels	42.47%

2.6. Chromosome stats

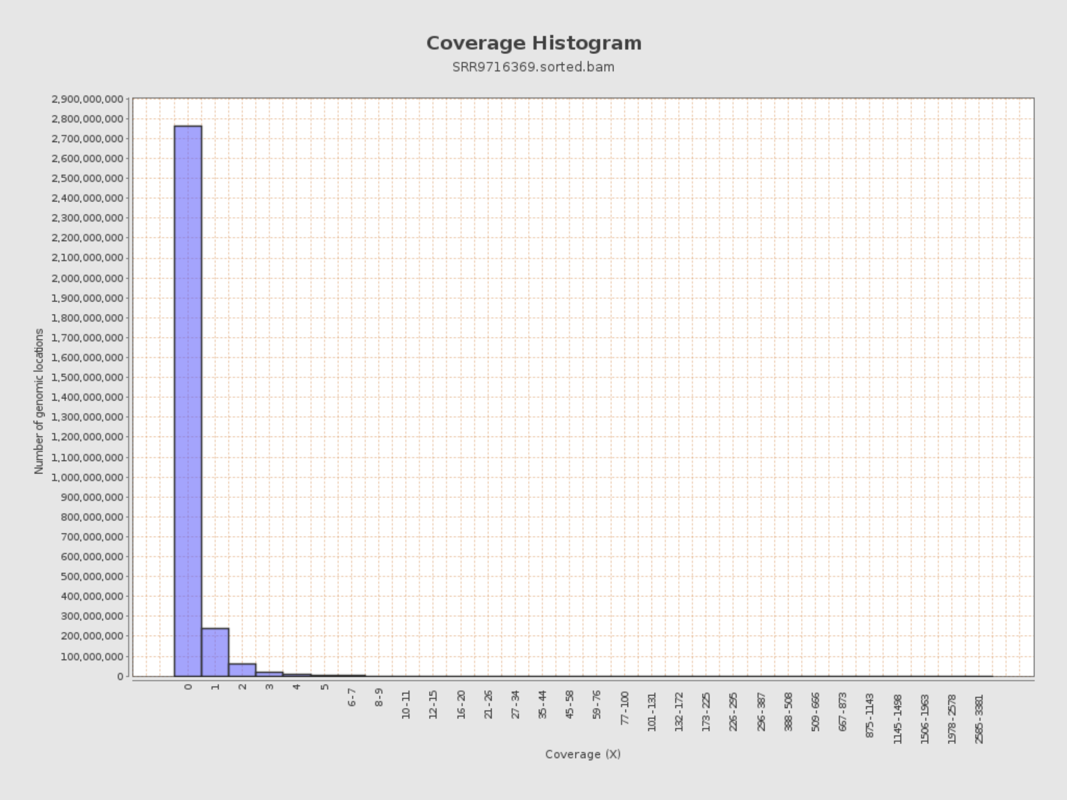
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47543348	0.1907	2.914
chr2	243199373	39678002	0.1632	1.4178
chr3	198022430	32878453	0.166	0.5545
chr4	191154276	31154879	0.163	0.8266
chr5	180915260	28259727	0.1562	0.5485
chr6	171115067	27484440	0.1606	0.6575
chr7	159138663	25671895	0.1613	1.6123

chr8	146364022	24019268	0.1641	1.5126
chr9	141213431	19557905	0.1385	1.0234
chr10	135534747	22792021	0.1682	1.2756
chr11	135006516	26990362	0.1999	1.3783
chr12	133851895	20933103	0.1564	0.5465
chr13	115169878	17185908	0.1492	0.5381
chr14	107349540	14064762	0.131	0.5867
chr15	102531392	13119113	0.128	0.4942
chr16	90354753	11410491	0.1263	0.6041
chr17	81195210	14503347	0.1786	0.826
chr18	78077248	12703019	0.1627	1.8436
chr19	59128983	8836360	0.1494	2.0688
chr20	63025520	9810290	0.1557	0.6212
chr21	48129895	6629619	0.1377	0.6796
chr22	51304566	5314304	0.1036	0.4431
chrMT	16571	171826	10.3691	7.3096
chrX	155270560	26867147	0.173	0.7747
chrY	59373566	1473958	0.0248	0.727

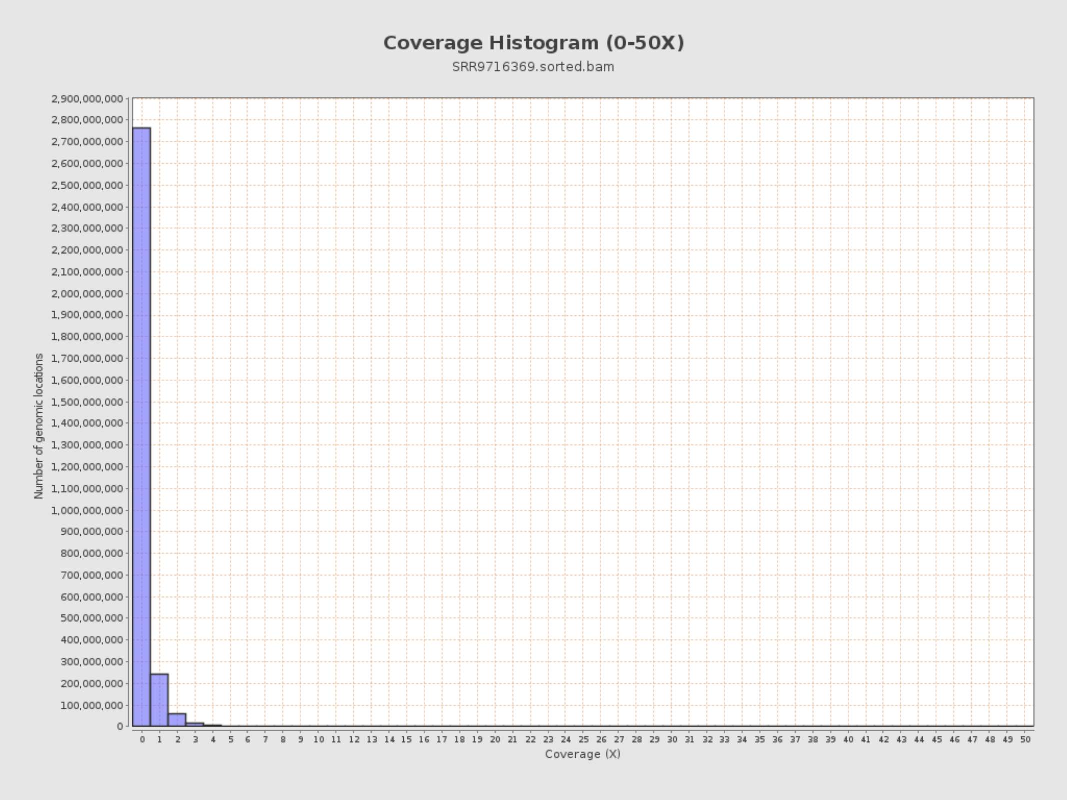
3. Results : Coverage across reference



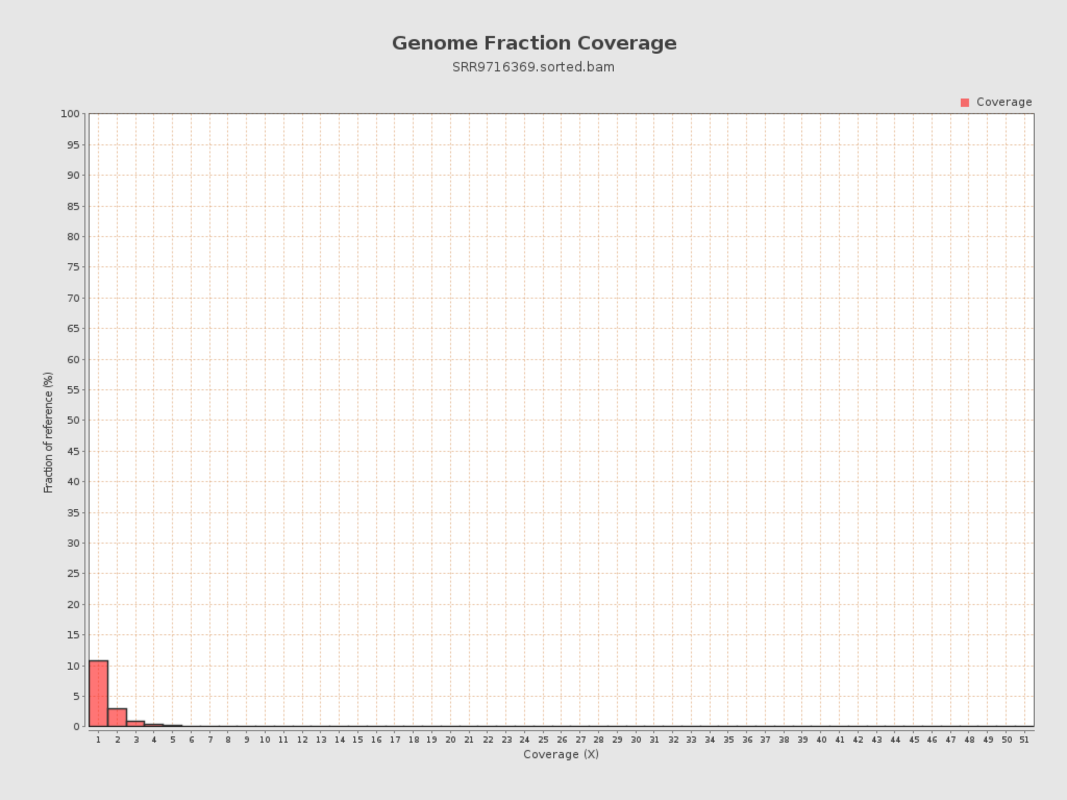
4. Results : Coverage Histogram



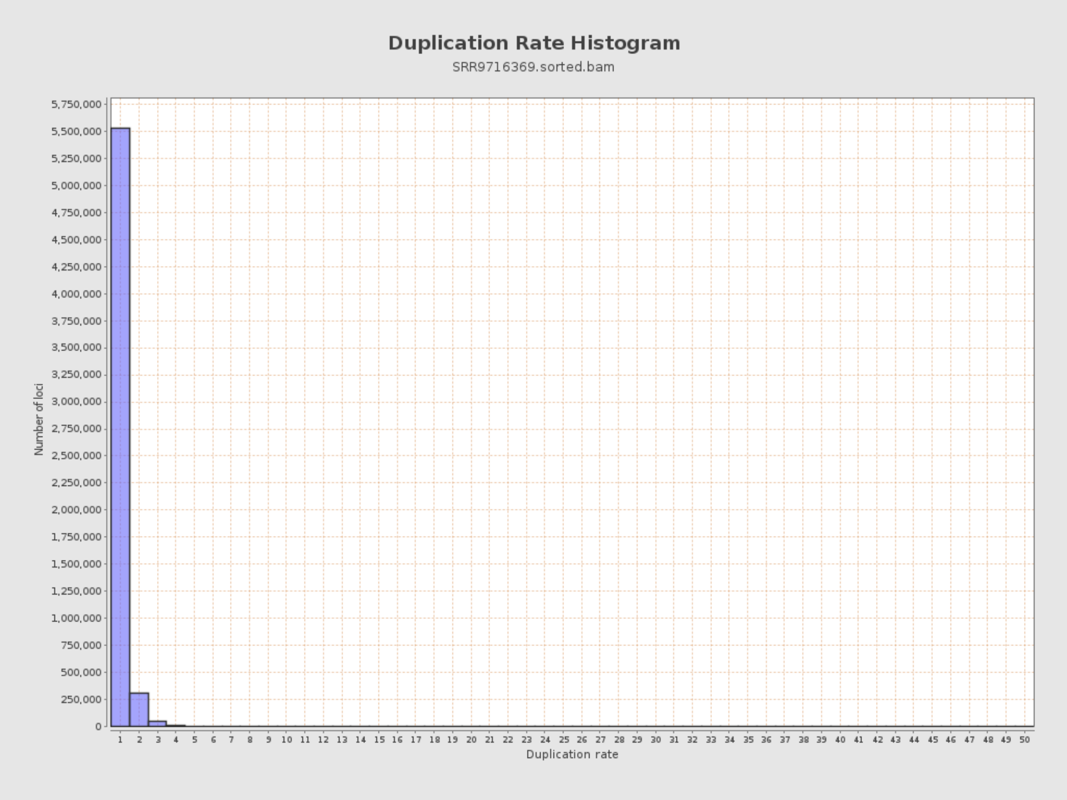
5. Results : Coverage Histogram (0-50X)



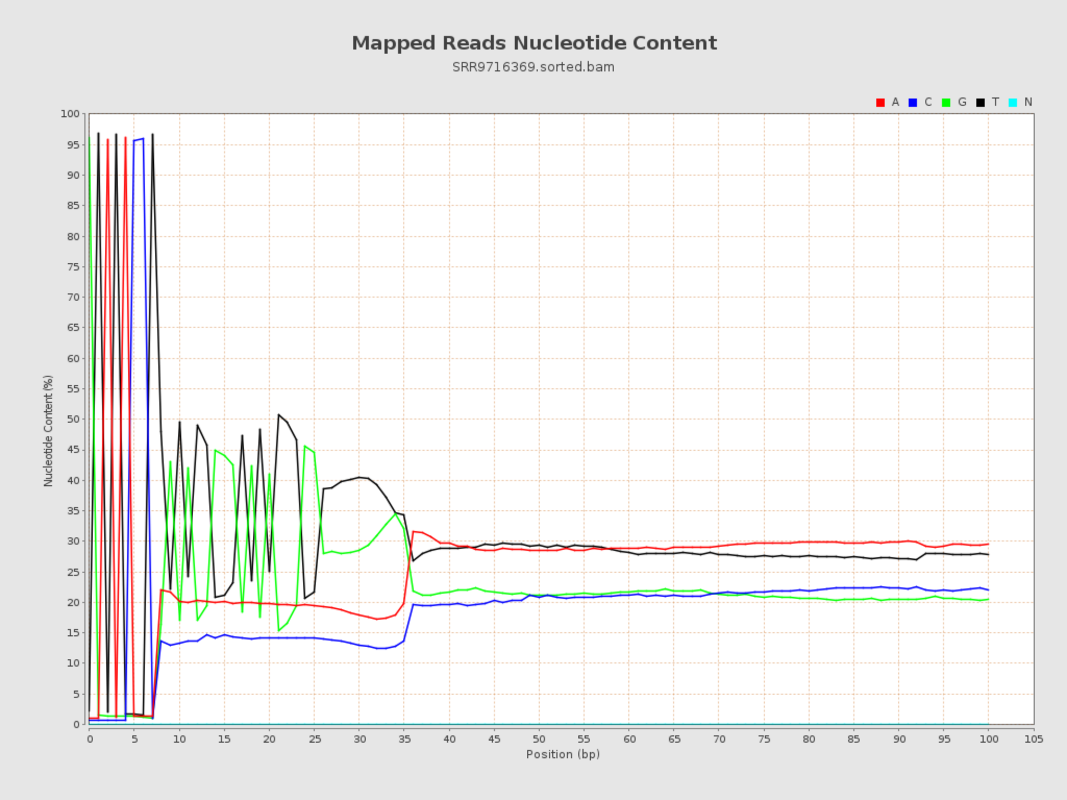
6. Results : Genome Fraction Coverage



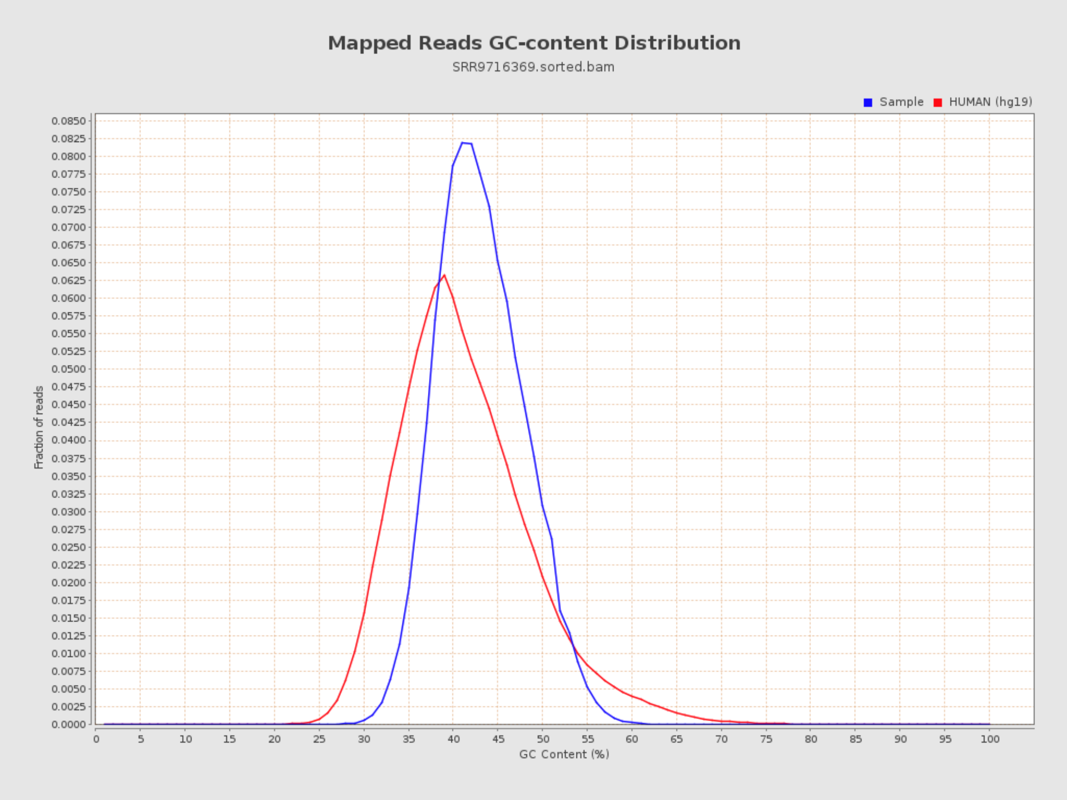
7. Results : Duplication Rate Histogram



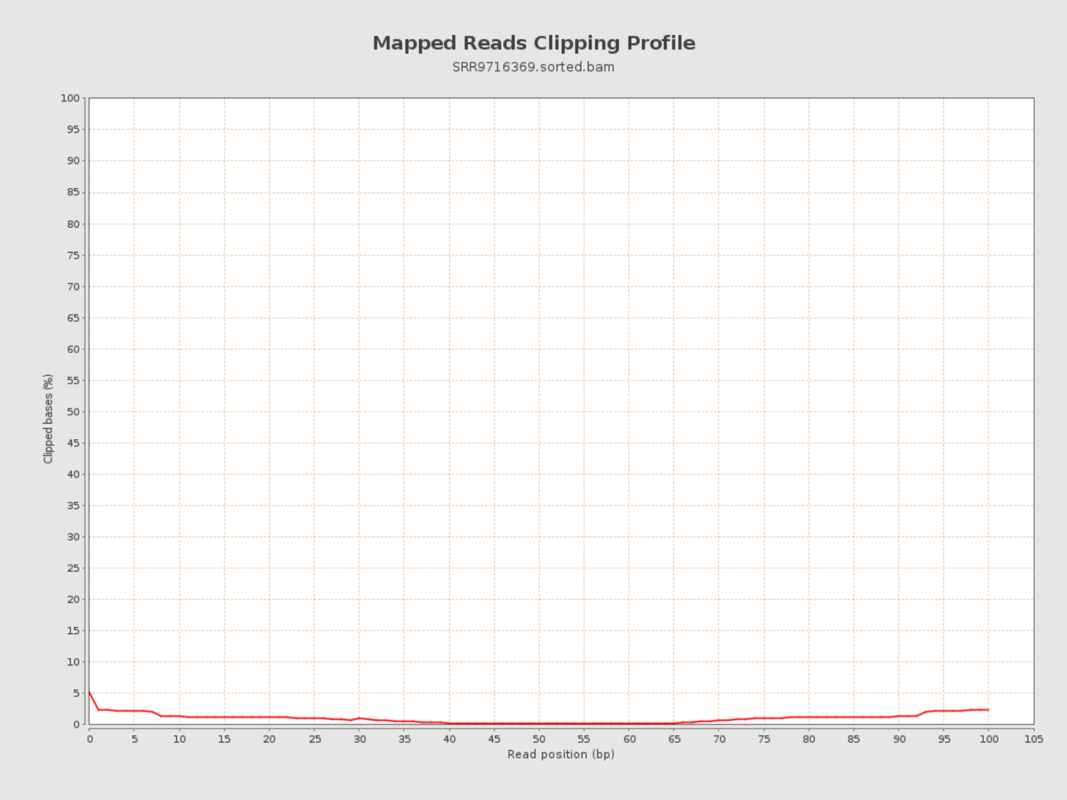
8. Results : Mapped Reads Nucleotide Content



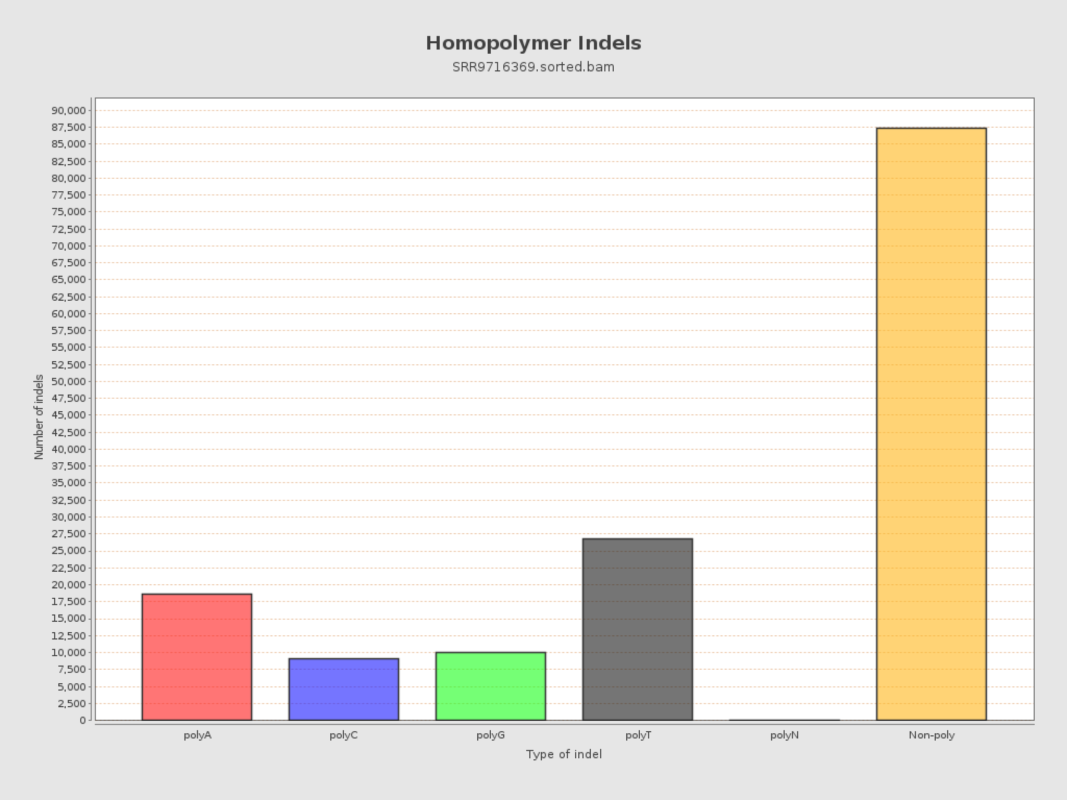
9. Results : Mapped Reads GC-content Distribution



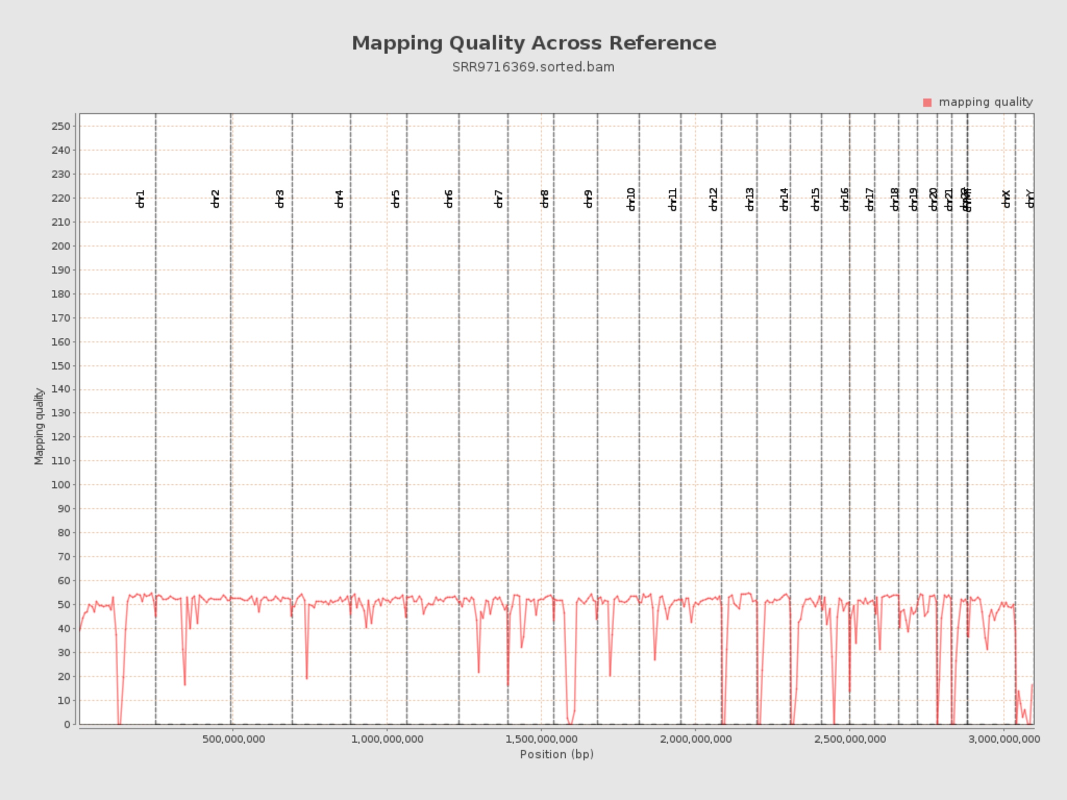
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram