Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716728.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_SRR9716728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716728.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:09:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,412,845
Mapped reads	1,304,696 / 92.35%
Unmapped reads	108,149 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,409 / 2.29%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	33,132 / 2.35%
Duplication rate	1.66%
Clipped reads	1,335,364 / 94.52%

2.2. ACGT Content

Number/percentage of A's	25,966,818 / 25.89%
Number/percentage of C's	19,704,962 / 19.65%
Number/percentage of T's	30,141,329 / 30.05%
Number/percentage of G's	24,476,062 / 24.4%
Number/percentage of N's	12,258 / 0.01%
GC Percentage	44.05%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.2927

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

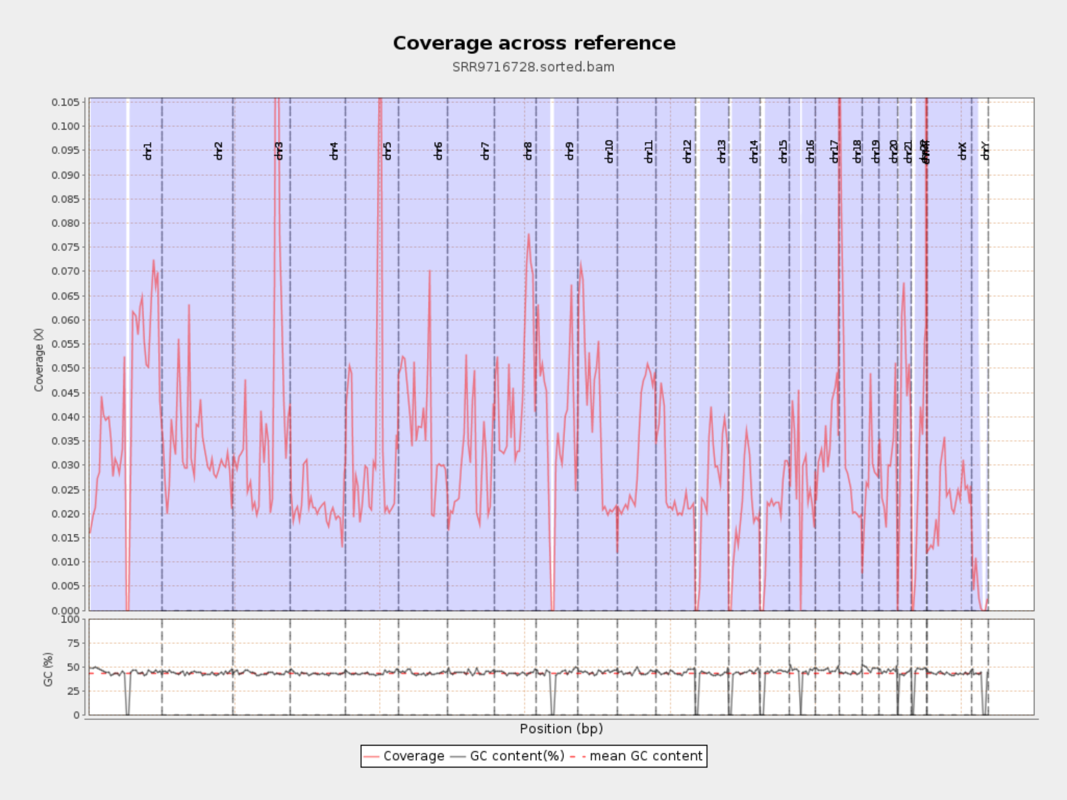
General error rate	0.75%
Mismatches	734,639
Insertions	8,017
Mapped reads with at least one insertion	0.61%
Deletions	21,415
Mapped reads with at least one deletion	1.62%
Homopolymer indels	39.79%

2.6. Chromosome stats

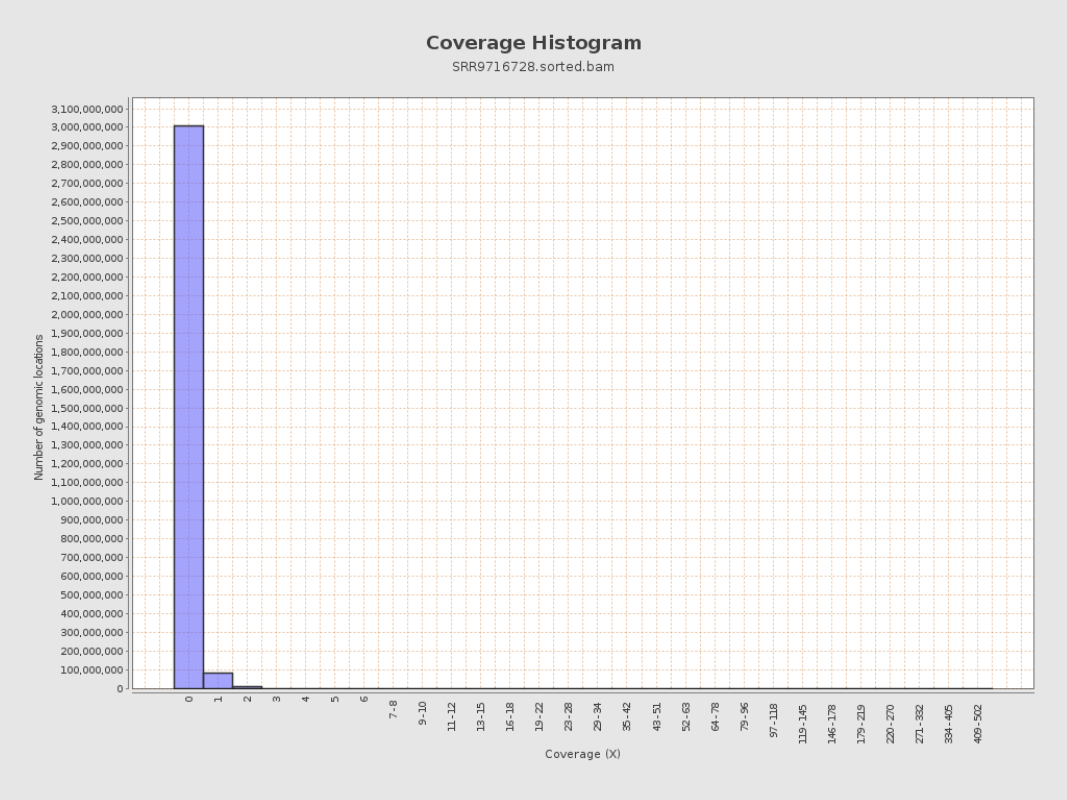
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10326902	0.0414	0.4553
chr2	243199373	8097513	0.0333	0.4156
chr3	198022430	8154209	0.0412	0.2258
chr4	191154276	4077518	0.0213	0.1671
chr5	180915260	6434135	0.0356	0.2078
chr6	171115067	6699180	0.0392	0.2495
chr7	159138663	4774711	0.03	0.4125

chr8	146364022	6898848	0.0471	0.3665
chr9	141213431	5281328	0.0374	0.2711
chr10	135534747	5507914	0.0406	0.2871
chr11	135006516	4503800	0.0334	0.245
chr12	133851895	3446214	0.0257	0.1754
chr13	115169878	3013321	0.0262	0.1746
chr14	107349540	2034936	0.019	0.1694
chr15	102531392	2010549	0.0196	0.1503
chr16	90354753	2439119	0.027	0.1931
chr17	81195210	2893361	0.0356	0.2284
chr18	78077248	2915519	0.0373	0.4844
chr19	59128983	1681430	0.0284	0.3537
chr20	63025520	1897020	0.0301	0.2087
chr21	48129895	2082337	0.0433	0.2355
chr22	51304566	1371201	0.0267	0.1794
chrMT	16571	98178	5.9247	4.4552
chrX	155270560	3492453	0.0225	0.1965
chrY	59373566	206184	0.0035	0.1086

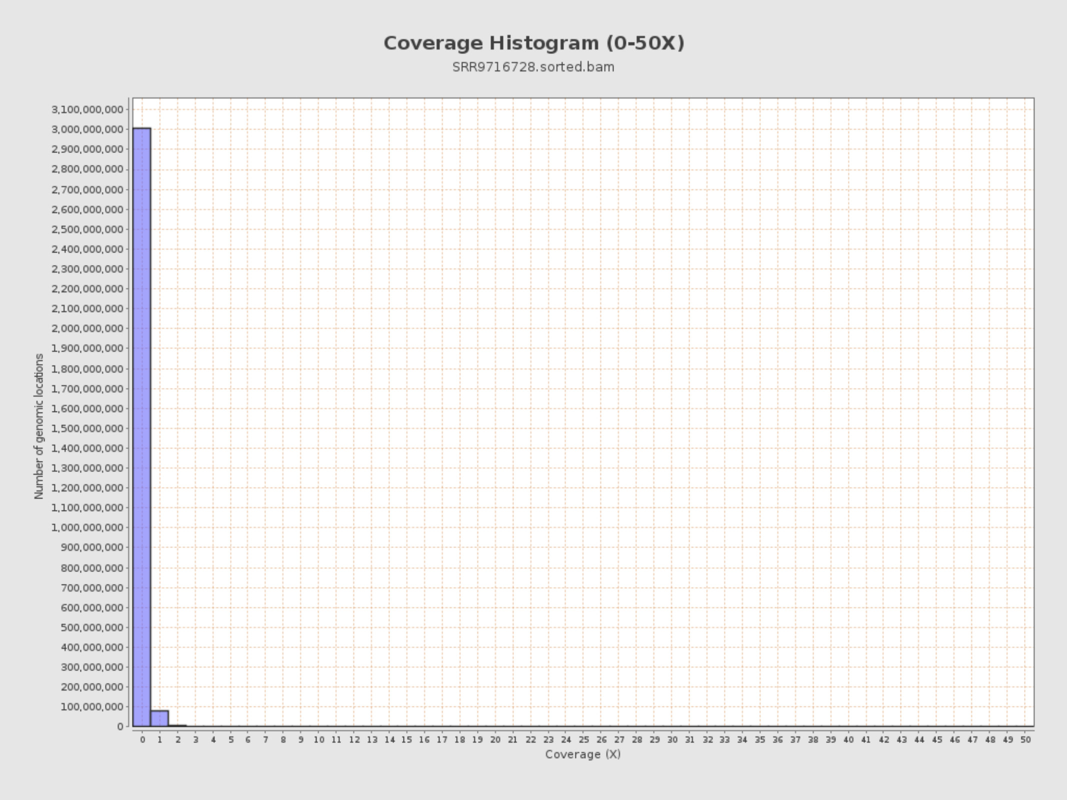
3. Results : Coverage across reference



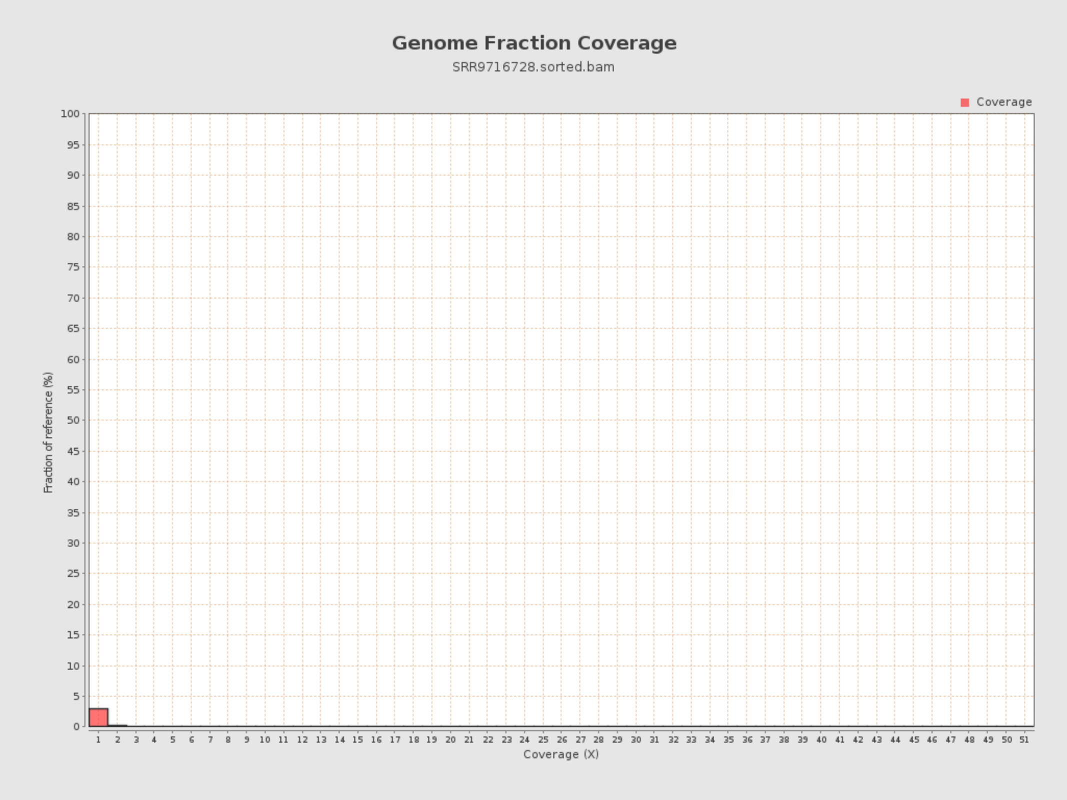
4. Results : Coverage Histogram



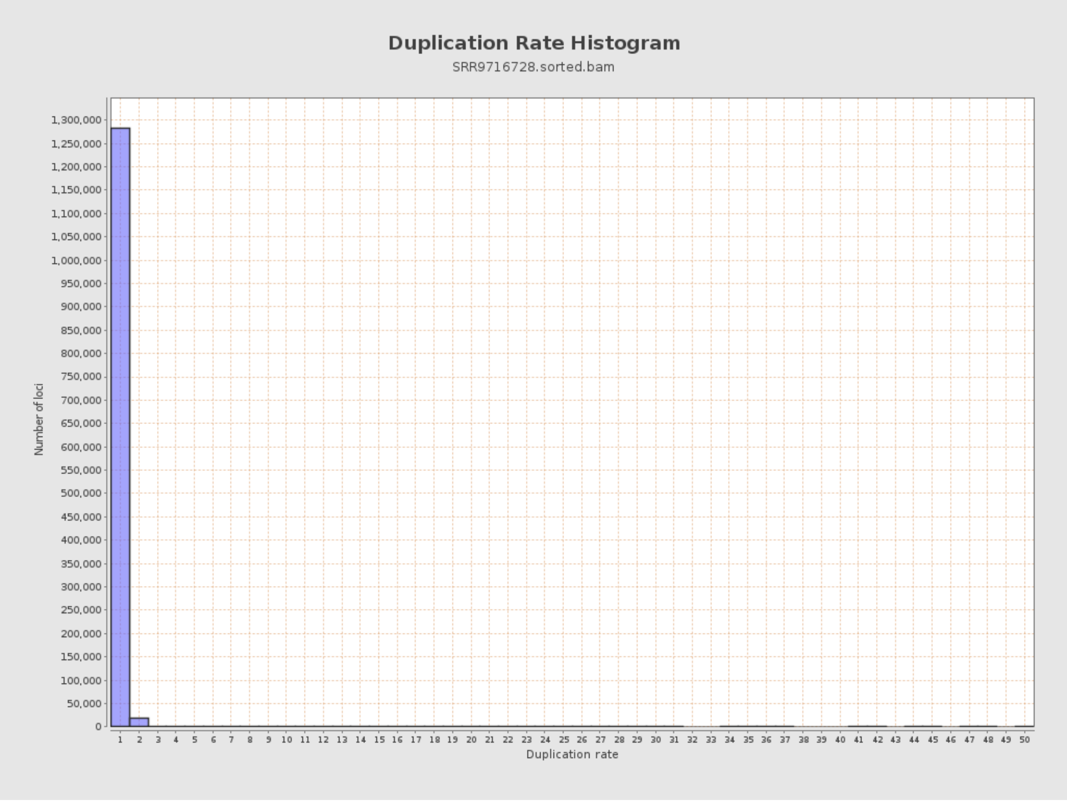
5. Results : Coverage Histogram (0-50X)



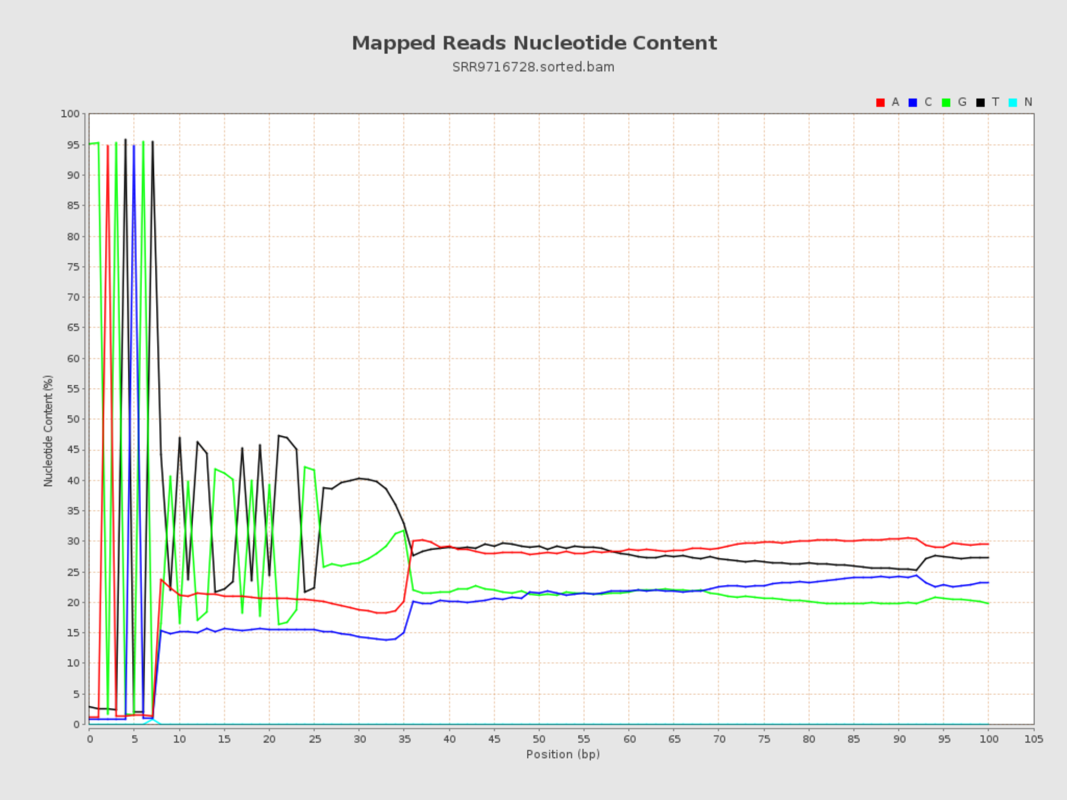
6. Results : Genome Fraction Coverage



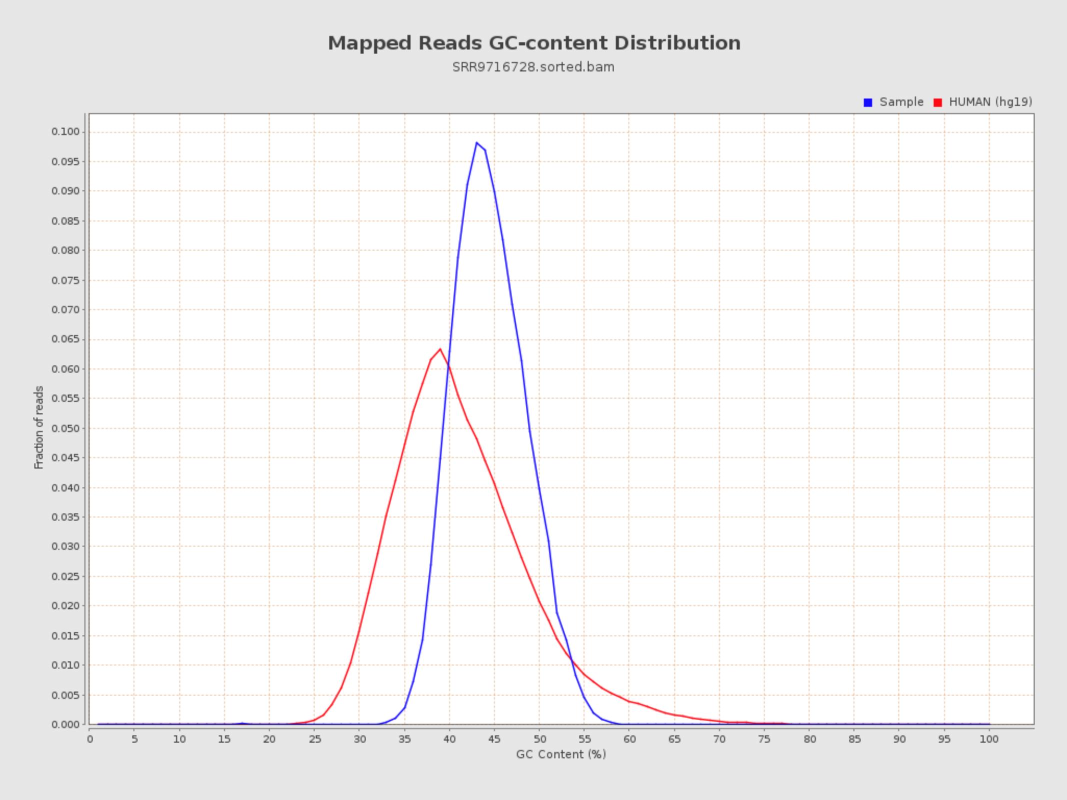
7. Results : Duplication Rate Histogram



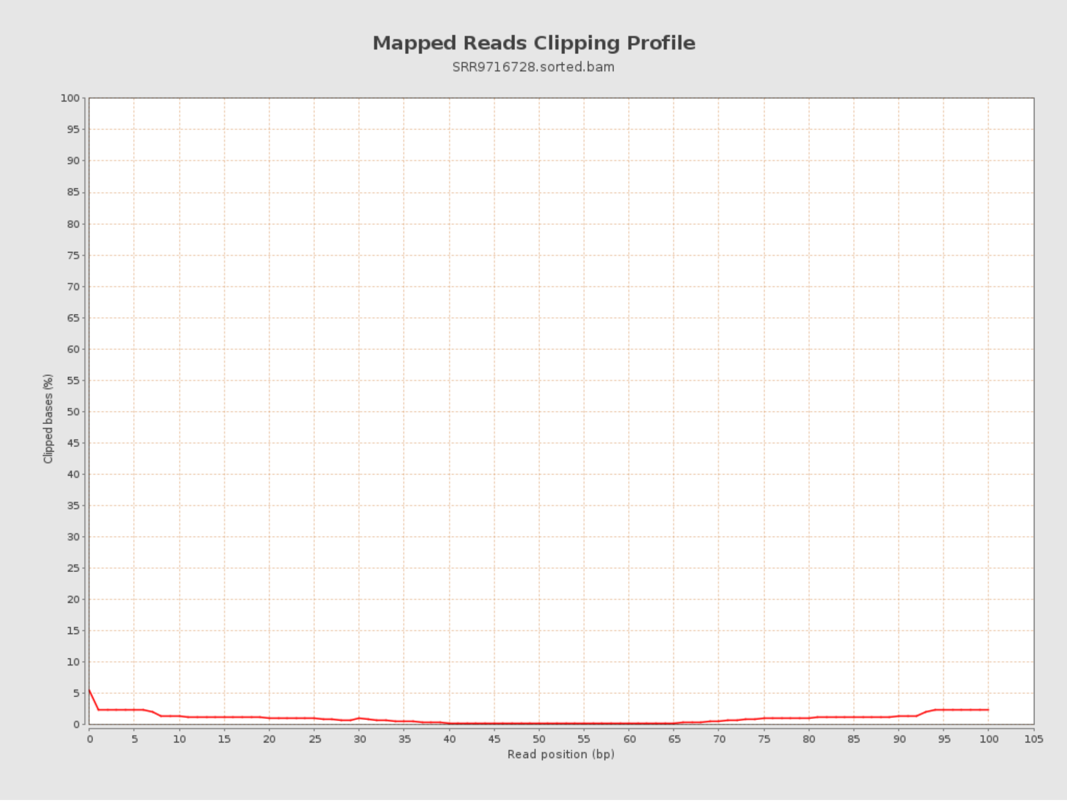
8. Results : Mapped Reads Nucleotide Content



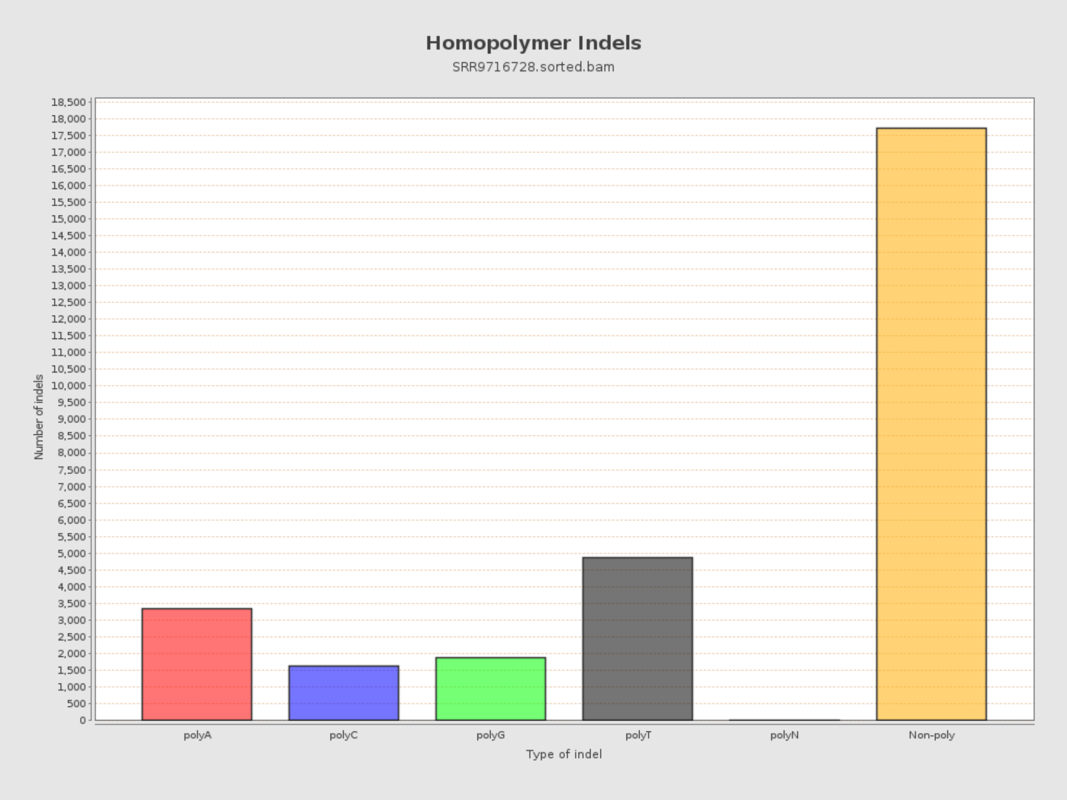
9. Results : Mapped Reads GC-content Distribution



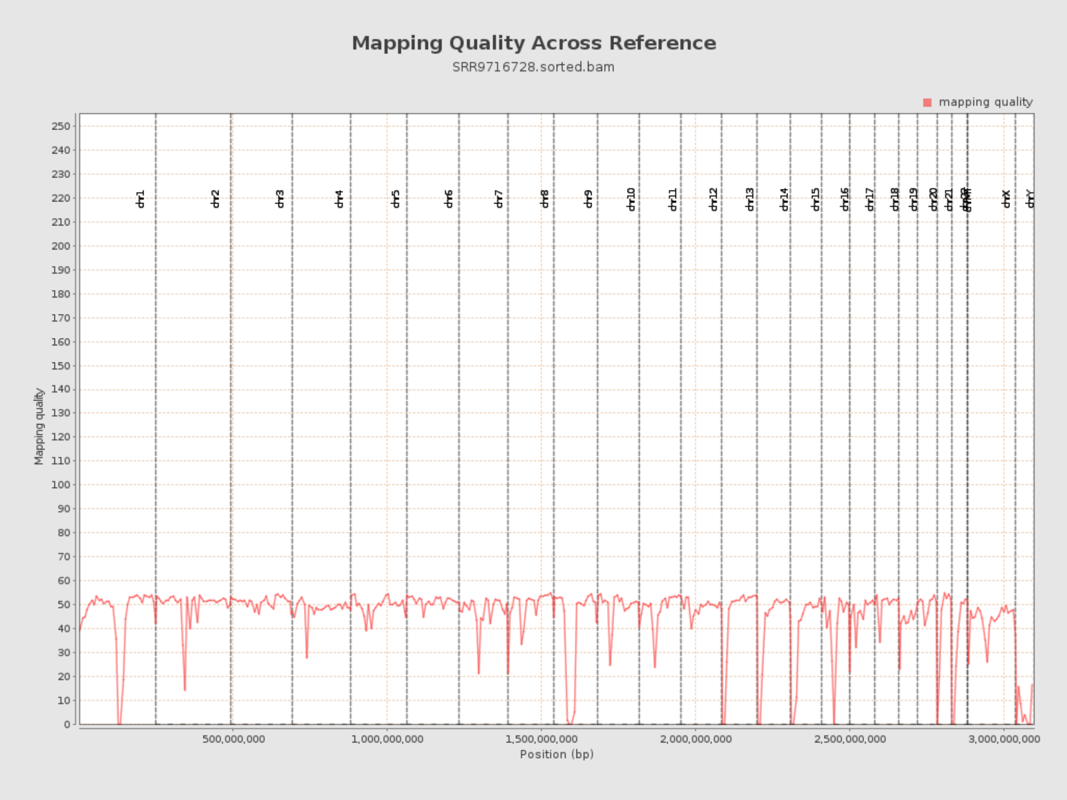
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram