Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:12:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716667.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_SRR9716667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:12:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,611,774
Mapped reads	2,427,422 / 92.94%
Unmapped reads	184,352 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,048 / 1.69%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	125,735 / 4.81%
Duplication rate	3.77%
Clipped reads	2,466,783 / 94.45%

2.2. ACGT Content

Number/percentage of A's	50,293,574 / 26.1%
Number/percentage of C's	38,525,704 / 19.99%
Number/percentage of T's	58,347,297 / 30.27%
Number/percentage of G's	45,544,833 / 23.63%
Number/percentage of N's	13,534 / 0.01%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0623

Standard Deviation	0.5452

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

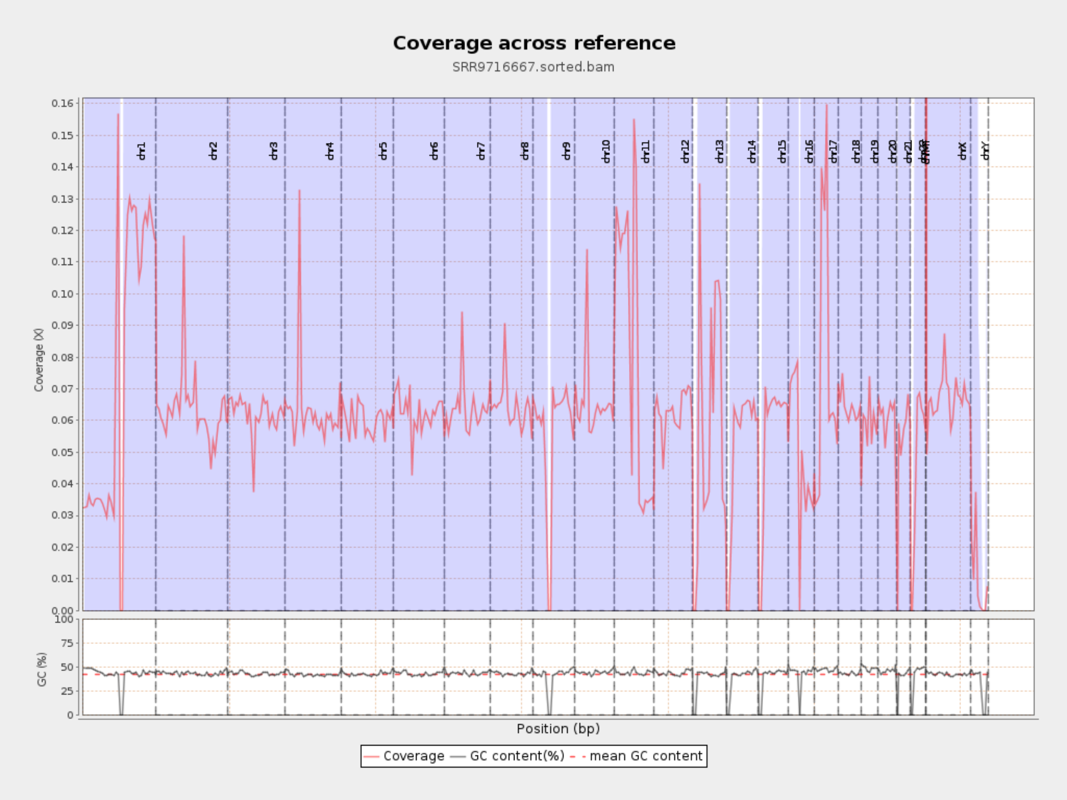
General error rate	0.69%
Mismatches	1,285,334
Insertions	15,841
Mapped reads with at least one insertion	0.64%
Deletions	46,743
Mapped reads with at least one deletion	1.9%
Homopolymer indels	44.01%

2.6. Chromosome stats

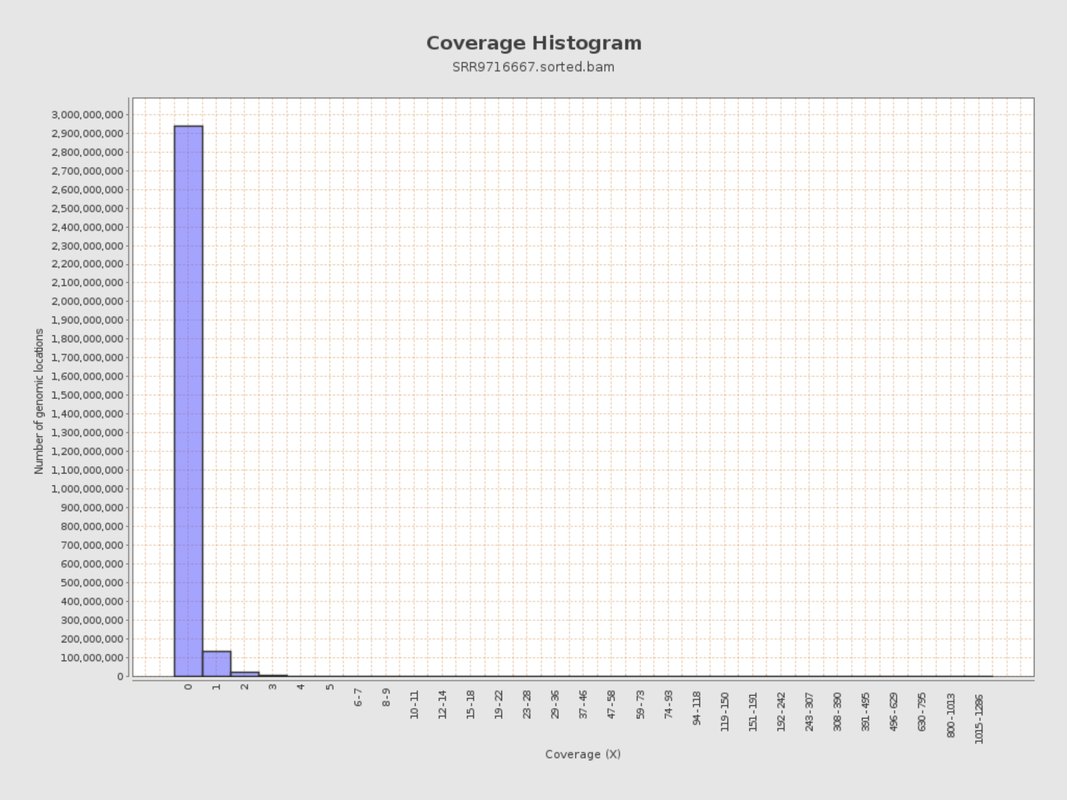
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18782994	0.0754	1.1075
chr2	243199373	15494834	0.0637	0.6085
chr3	198022430	12263398	0.0619	0.2885
chr4	191154276	12184088	0.0637	0.4066
chr5	180915260	10915777	0.0603	0.2894
chr6	171115067	10721867	0.0627	0.3252
chr7	159138663	10144660	0.0637	0.6724

chr8	146364022	9406814	0.0643	0.633
chr9	141213431	7892983	0.0559	0.4528
chr10	135534747	8891314	0.0656	0.5275
chr11	135006516	10979800	0.0813	0.6364
chr12	133851895	8456649	0.0632	0.2968
chr13	115169878	6717721	0.0583	0.2839
chr14	107349540	5644223	0.0526	0.2993
chr15	102531392	5475154	0.0534	0.2696
chr16	90354753	4367519	0.0483	0.299
chr17	81195210	6203171	0.0764	0.4164
chr18	78077248	5024204	0.0643	0.7868
chr19	59128983	3476912	0.0588	0.8187
chr20	63025520	3859187	0.0612	0.3124
chr21	48129895	2567339	0.0533	0.3294
chr22	51304566	2298346	0.0448	0.2503
chrMT	16571	79378	4.7902	3.3398
chrX	155270560	10383460	0.0669	0.3743
chrY	59373566	583672	0.0098	0.3109

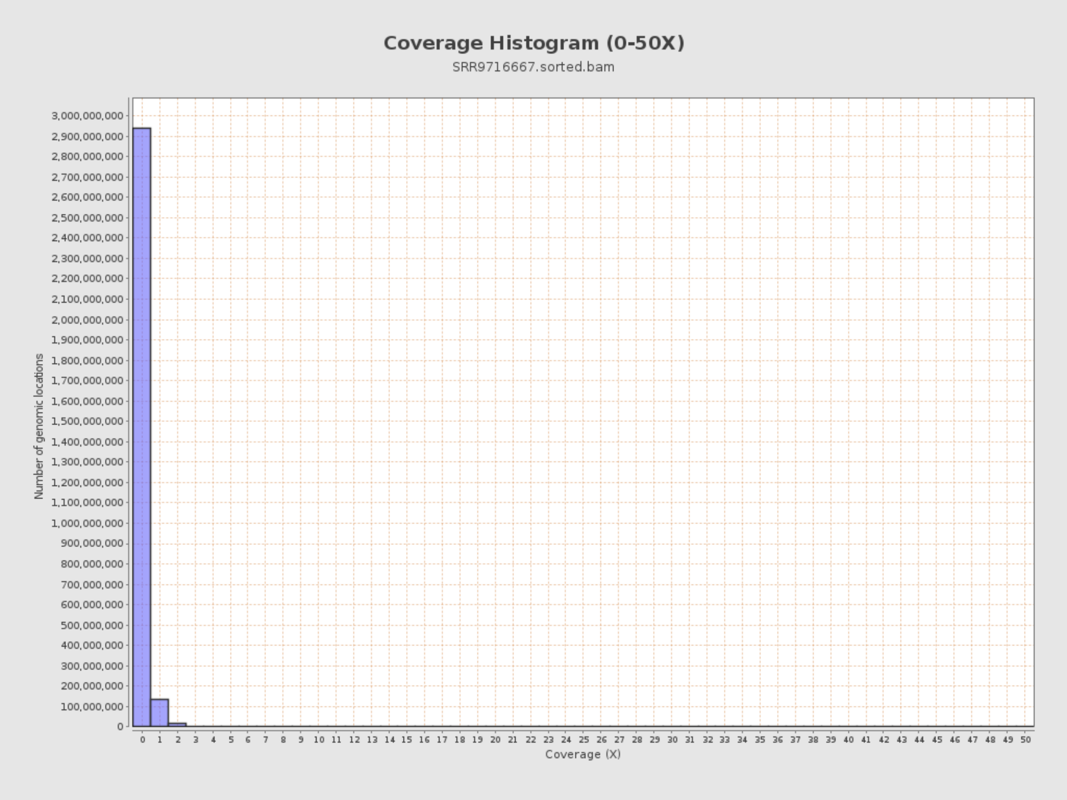
3. Results : Coverage across reference



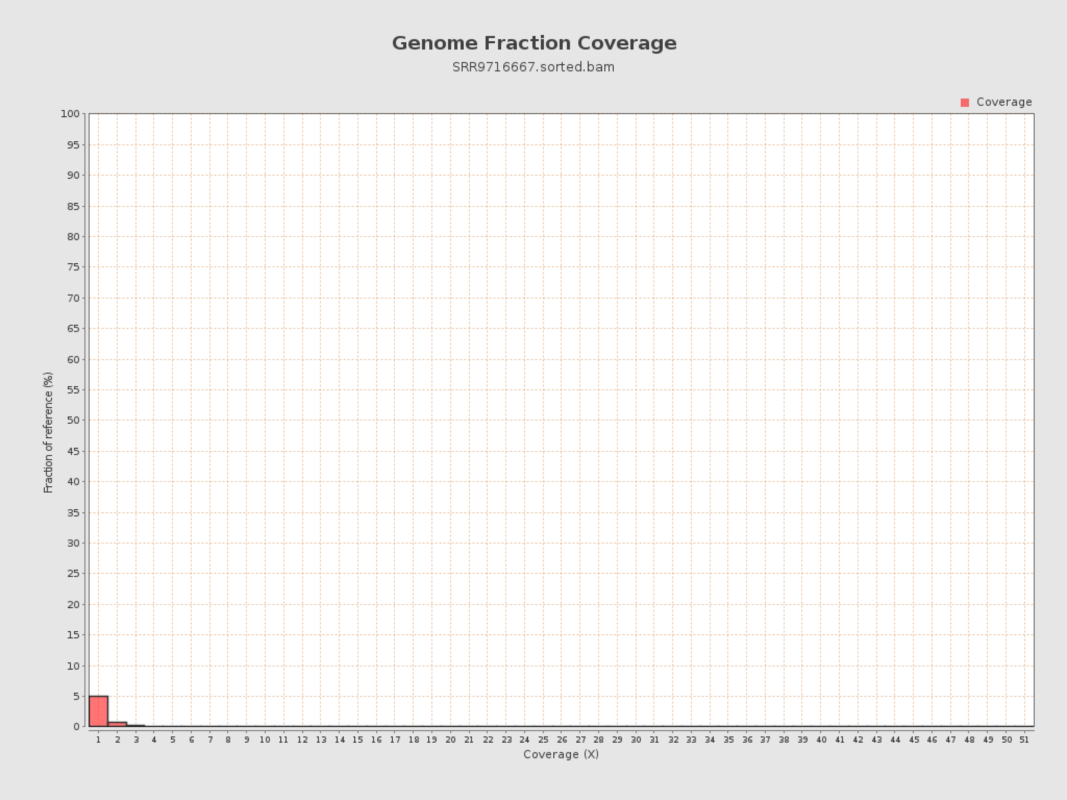
4. Results : Coverage Histogram



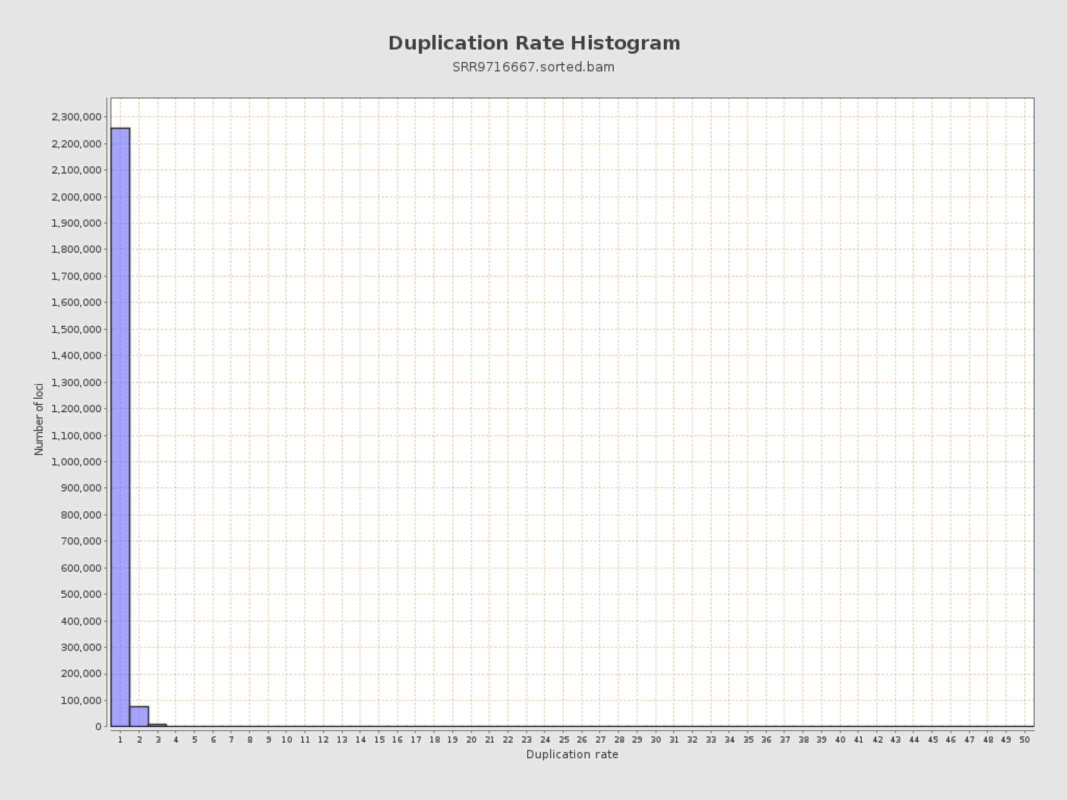
5. Results : Coverage Histogram (0-50X)



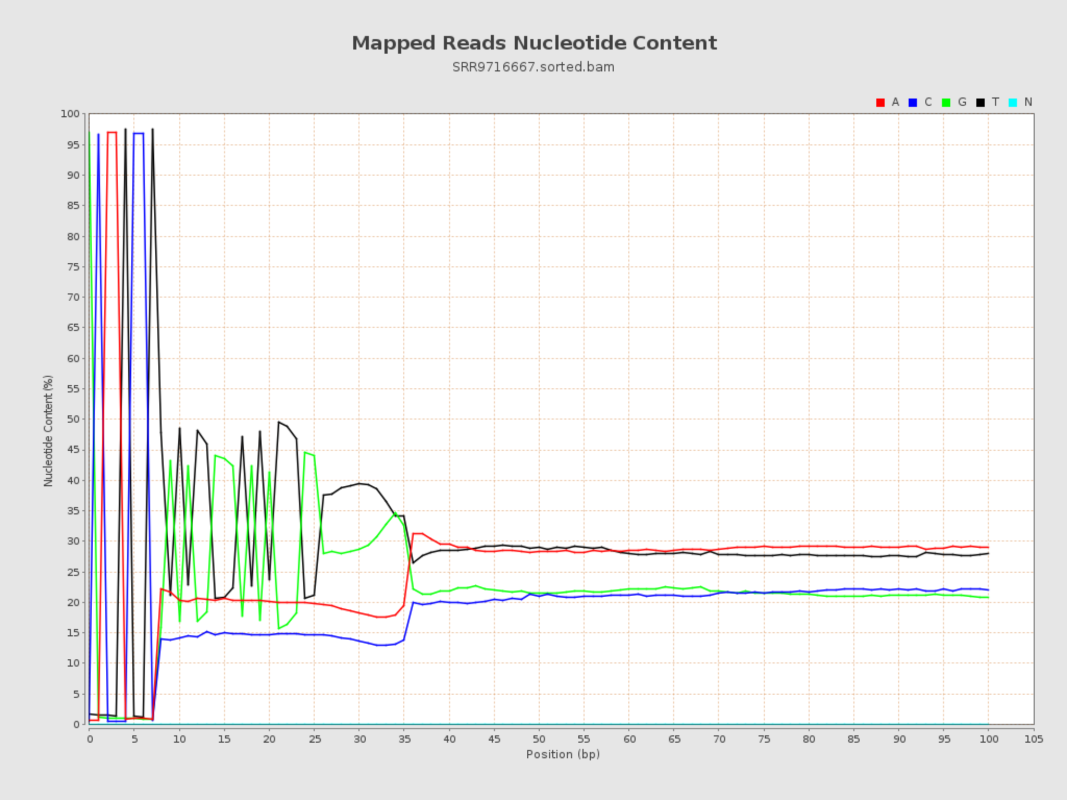
6. Results : Genome Fraction Coverage



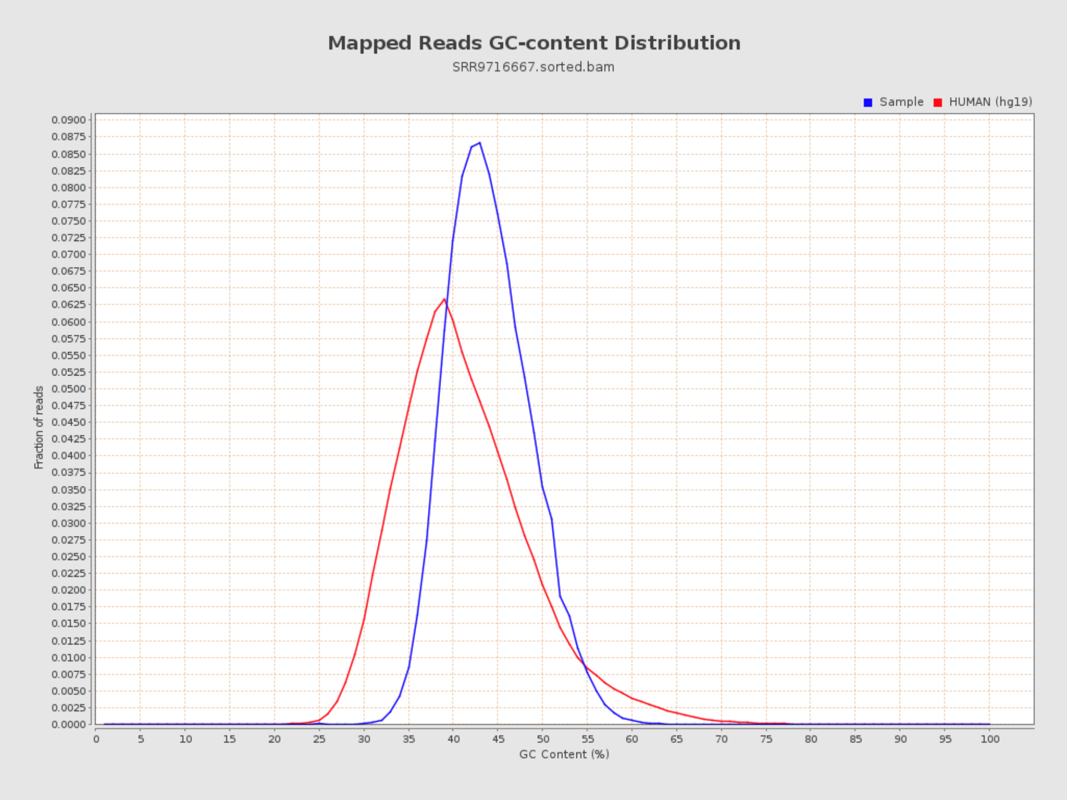
7. Results : Duplication Rate Histogram



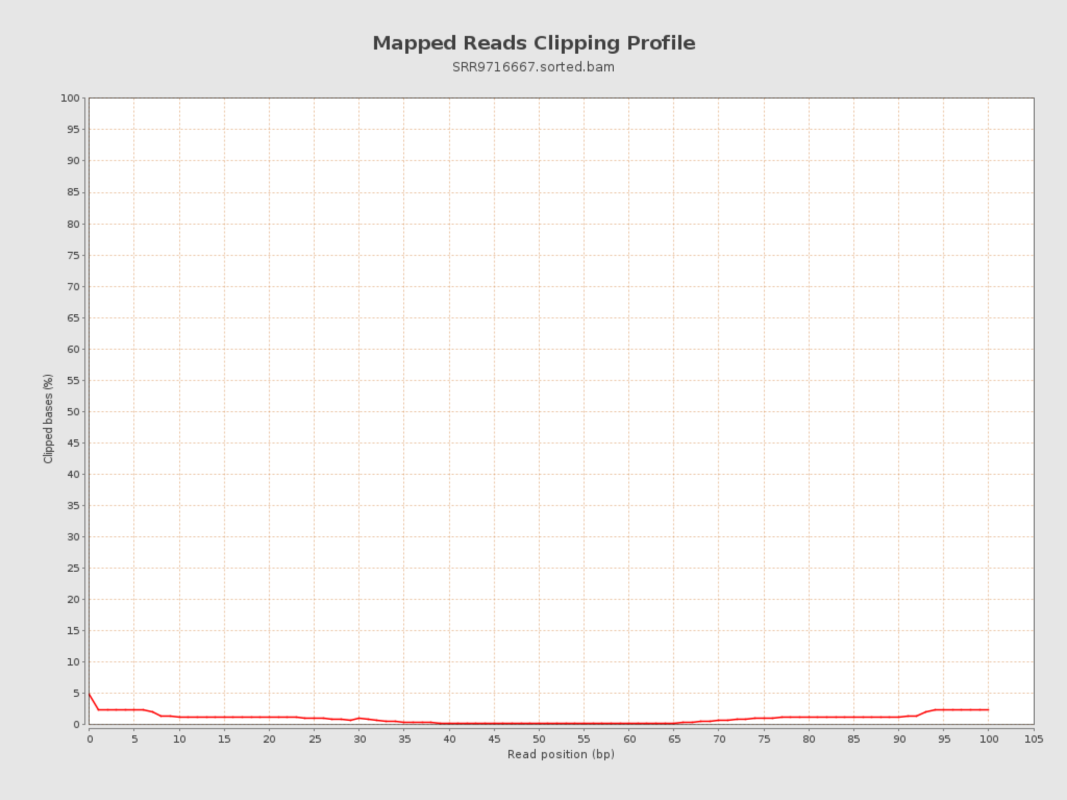
8. Results : Mapped Reads Nucleotide Content



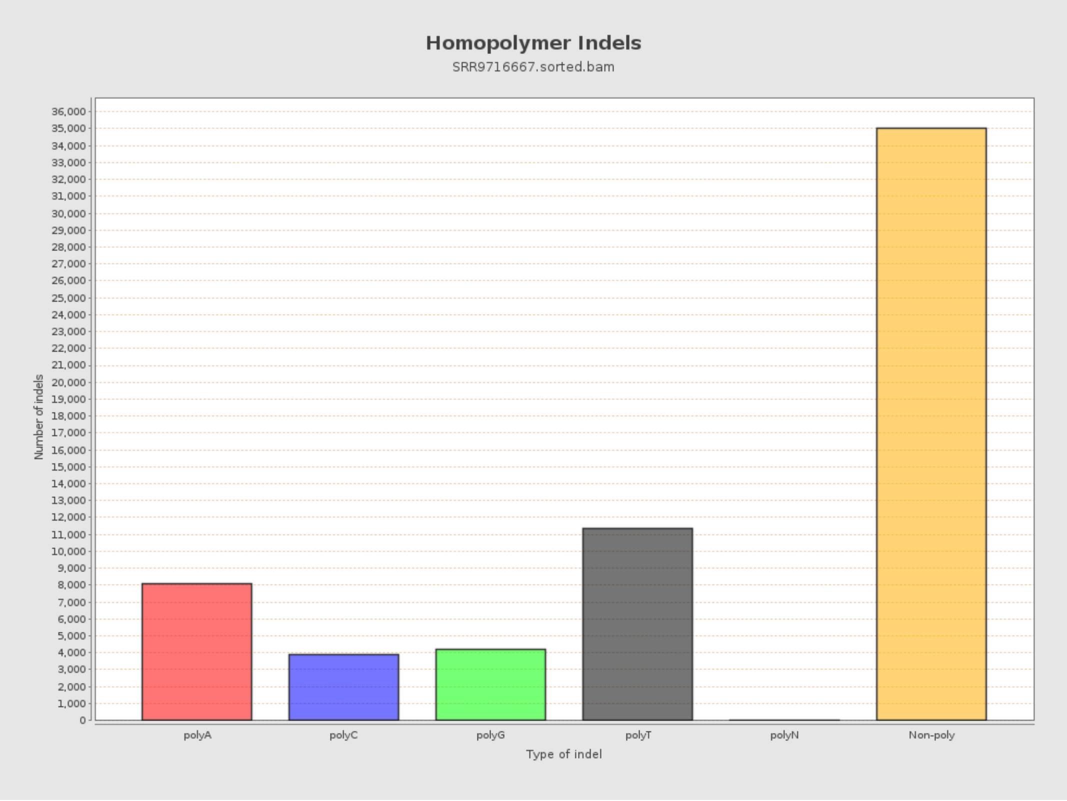
9. Results : Mapped Reads GC-content Distribution



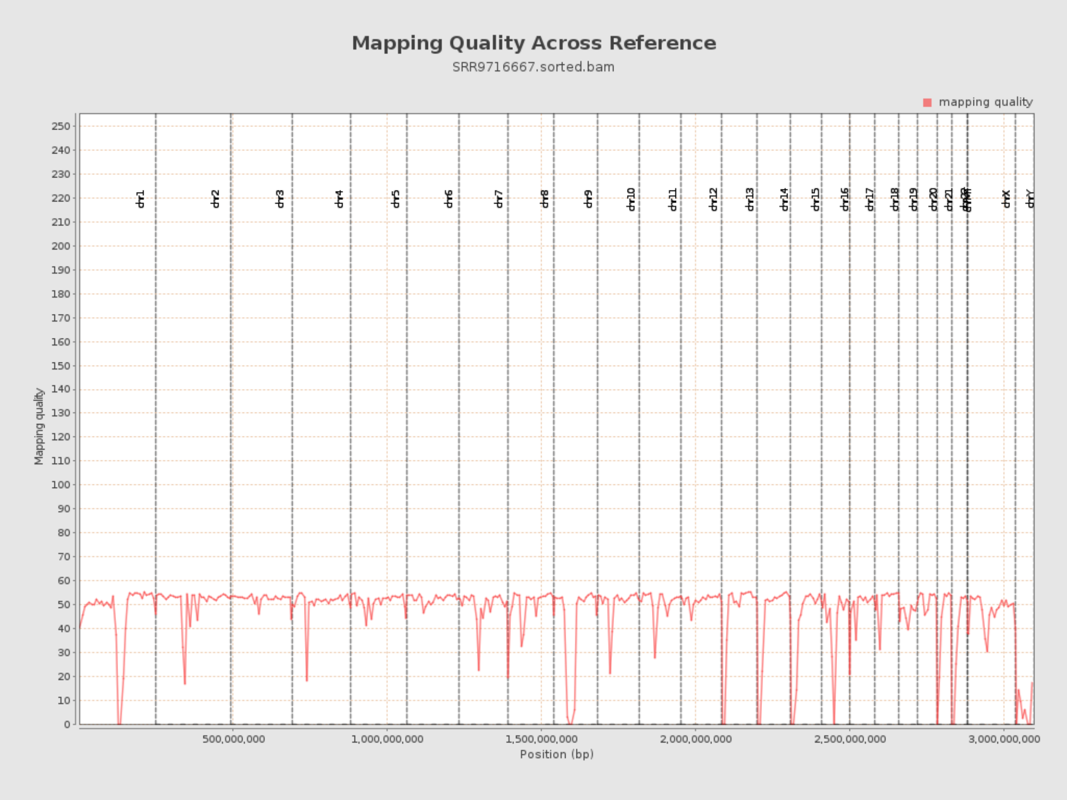
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram