Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:26:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716668.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_SRR9716668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:26:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,442,257
Mapped reads	1,325,135 / 91.88%
Unmapped reads	117,122 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,450 / 1.9%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	41,057 / 2.85%
Duplication rate	2.14%
Clipped reads	1,349,454 / 93.57%

2.2. ACGT Content

Number/percentage of A's	27,374,057 / 26.25%
Number/percentage of C's	20,147,982 / 19.32%
Number/percentage of T's	32,359,738 / 31.03%
Number/percentage of G's	24,397,204 / 23.39%
Number/percentage of N's	7,257 / 0.01%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.3311

2.4. Mapping Quality

Mean Mapping Quality	47.23

2.5. Mismatches and indels

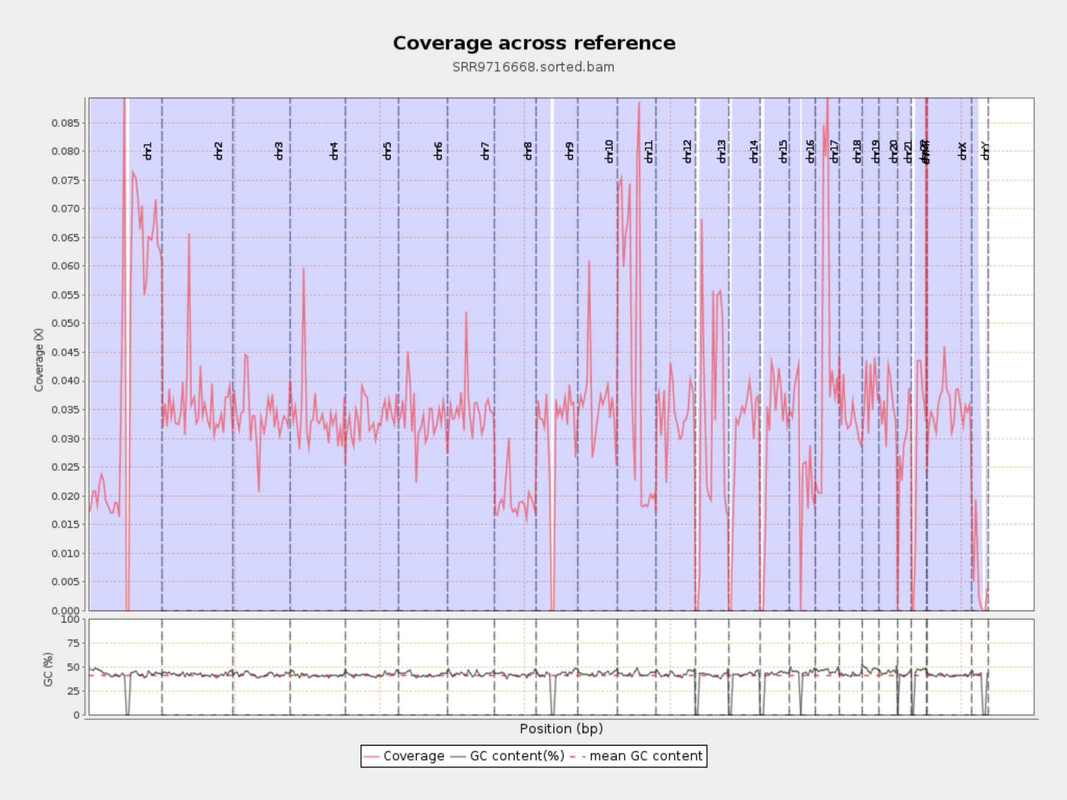
General error rate	0.69%
Mismatches	699,146
Insertions	9,242
Mapped reads with at least one insertion	0.69%
Deletions	25,785
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.49%

2.6. Chromosome stats

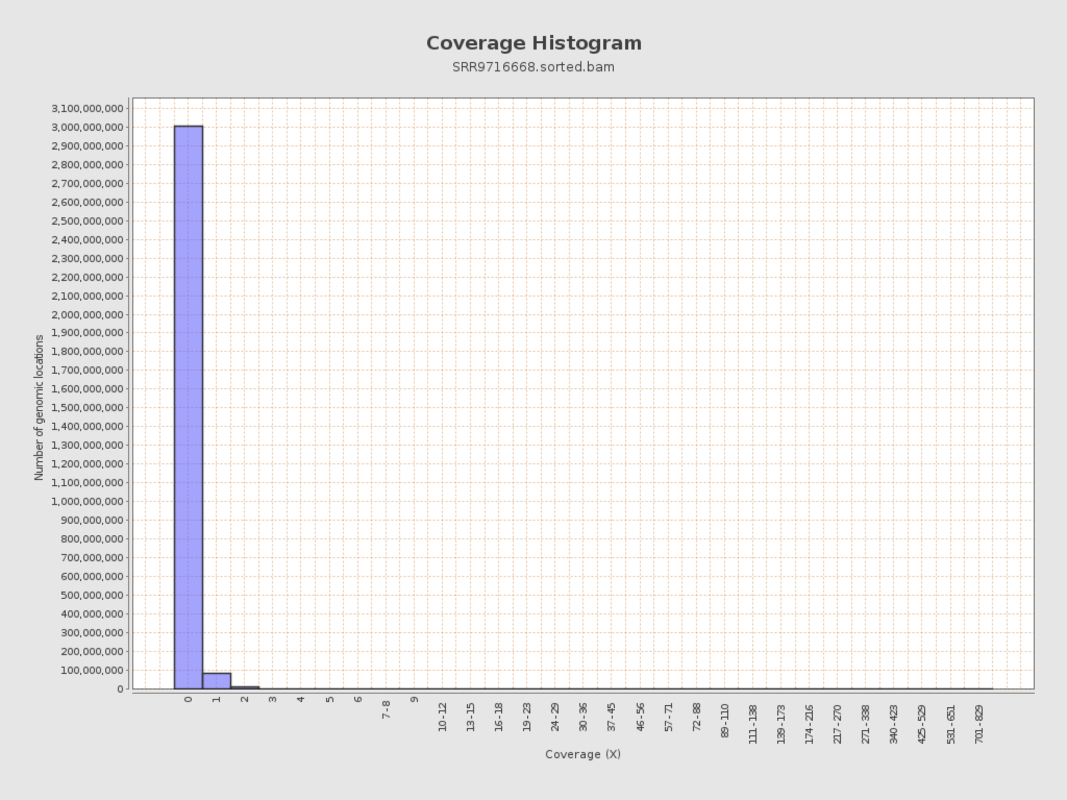
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10479132	0.042	0.7152
chr2	243199373	8750295	0.036	0.3323
chr3	198022430	6699104	0.0338	0.2005
chr4	191154276	6457751	0.0338	0.2377
chr5	180915260	6060979	0.0335	0.1989
chr6	171115067	5733685	0.0335	0.2126
chr7	159138663	5593640	0.0351	0.3755

chr8	146364022	2805658	0.0192	0.3268
chr9	141213431	4280880	0.0303	0.2747
chr10	135534747	4913201	0.0363	0.3102
chr11	135006516	6152080	0.0456	0.347
chr12	133851895	4623629	0.0345	0.2024
chr13	115169878	3635649	0.0316	0.1937
chr14	107349540	3141252	0.0293	0.1985
chr15	102531392	3070902	0.03	0.1874
chr16	90354753	2449064	0.0271	0.1911
chr17	81195210	3815577	0.047	0.282
chr18	78077248	2641898	0.0338	0.4251
chr19	59128983	2241562	0.0379	0.502
chr20	63025520	2229226	0.0354	0.2115
chr21	48129895	1321994	0.0275	0.2005
chr22	51304566	1392061	0.0271	0.1784
chrMT	16571	64704	3.9047	2.8319
chrX	155270560	5484211	0.0353	0.2327
chrY	59373566	297628	0.005	0.1683

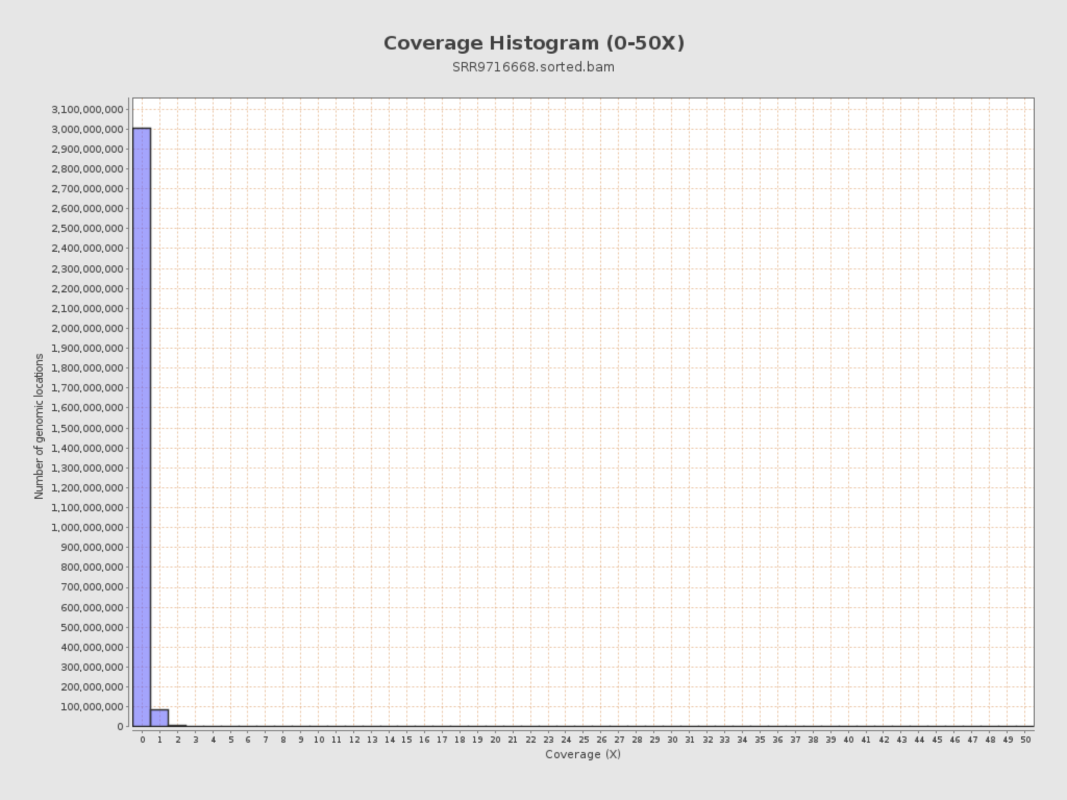
3. Results : Coverage across reference



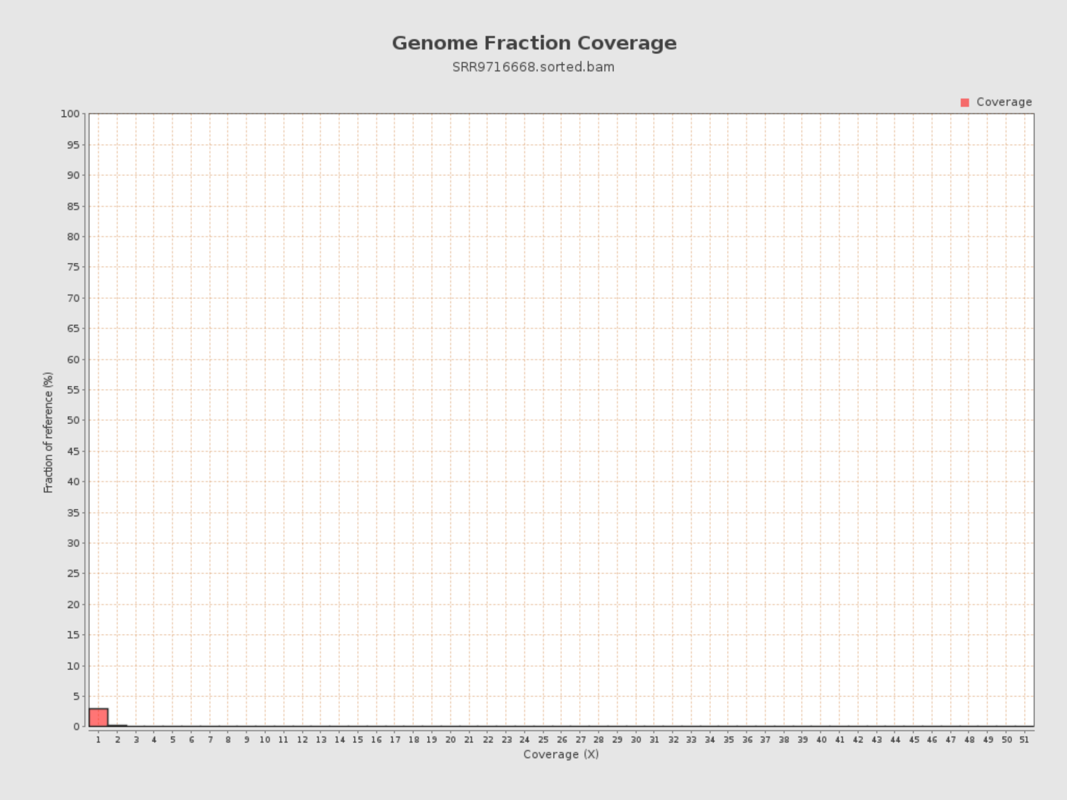
4. Results : Coverage Histogram



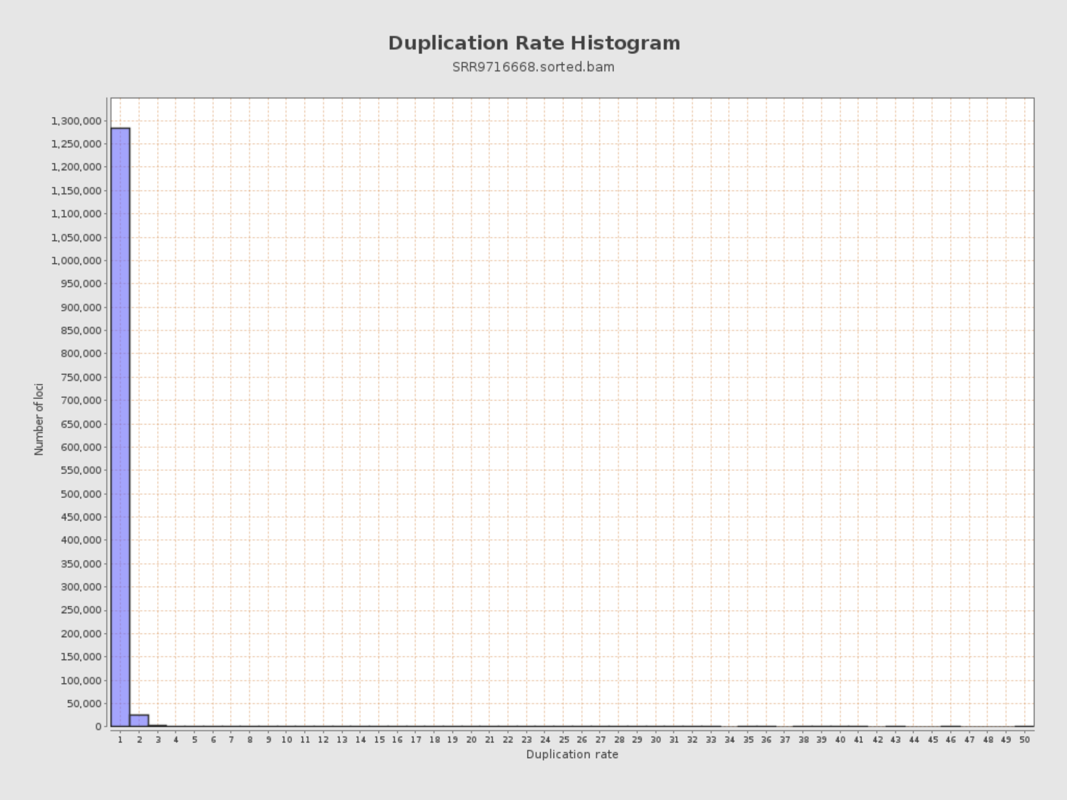
5. Results : Coverage Histogram (0-50X)



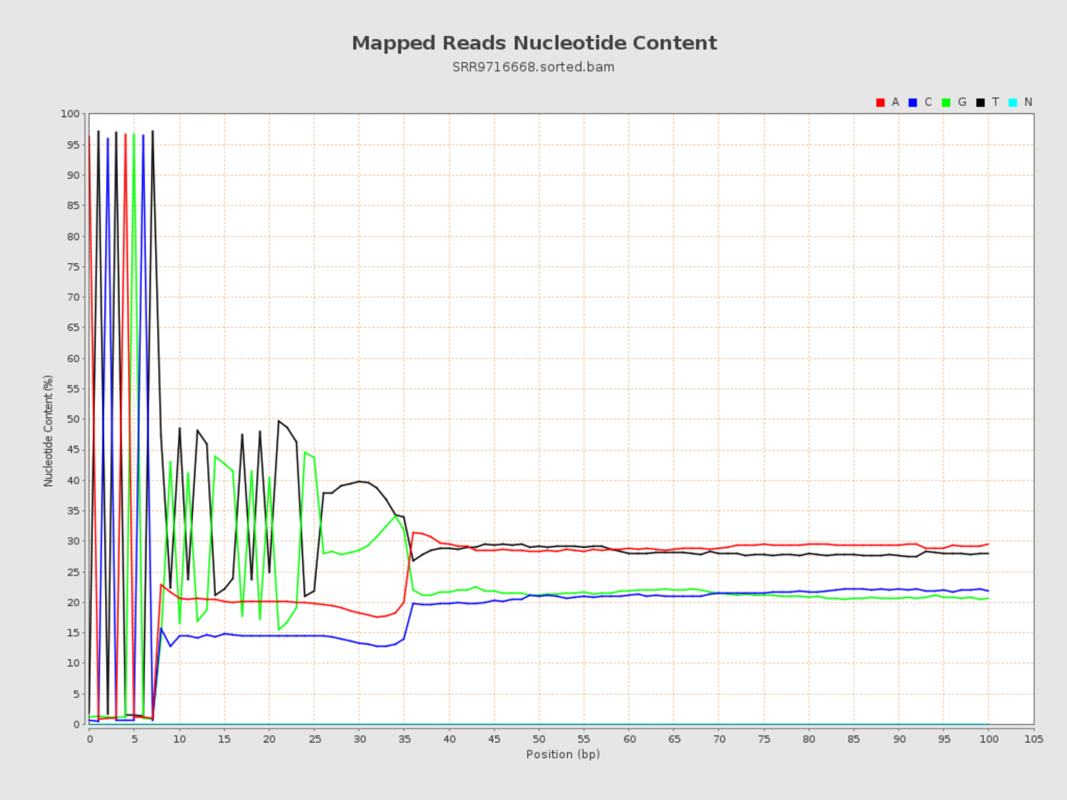
6. Results : Genome Fraction Coverage



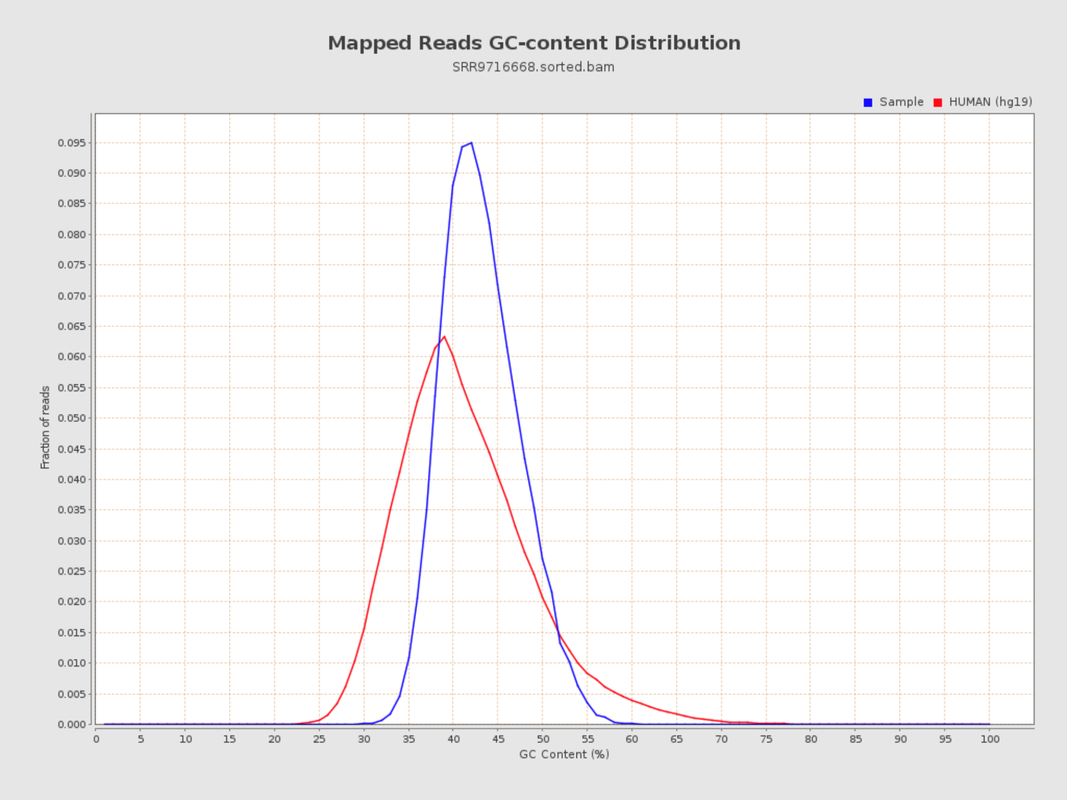
7. Results : Duplication Rate Histogram



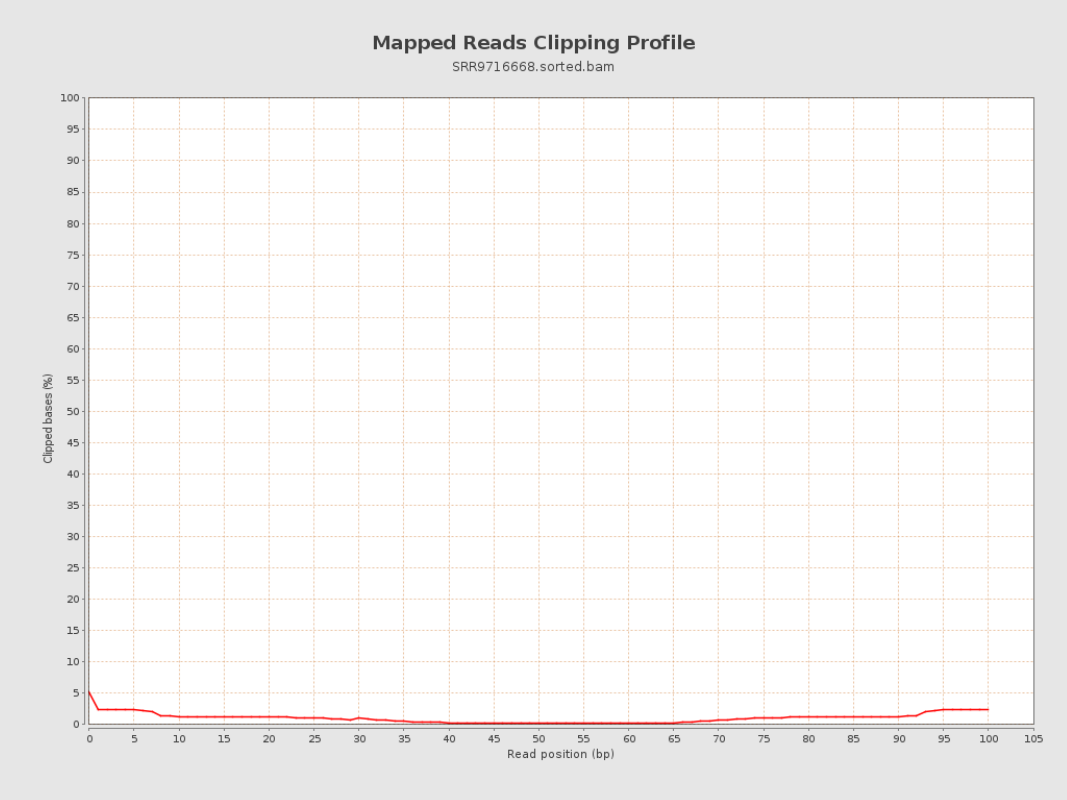
8. Results : Mapped Reads Nucleotide Content



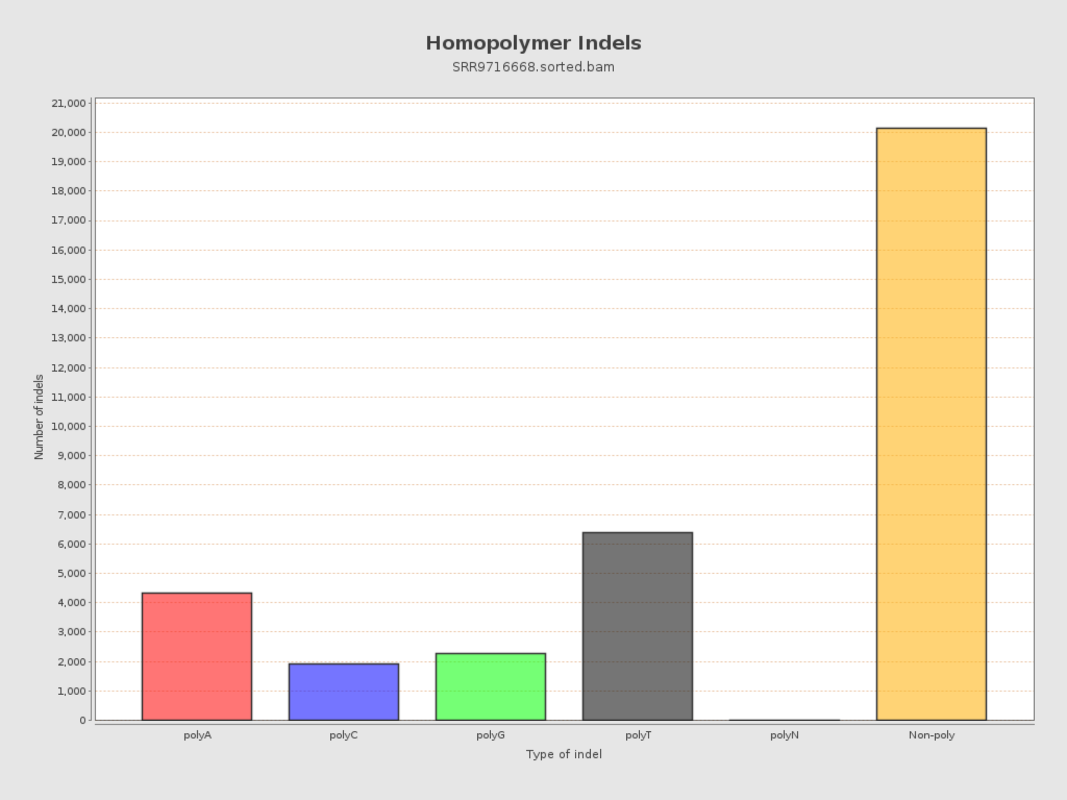
9. Results : Mapped Reads GC-content Distribution



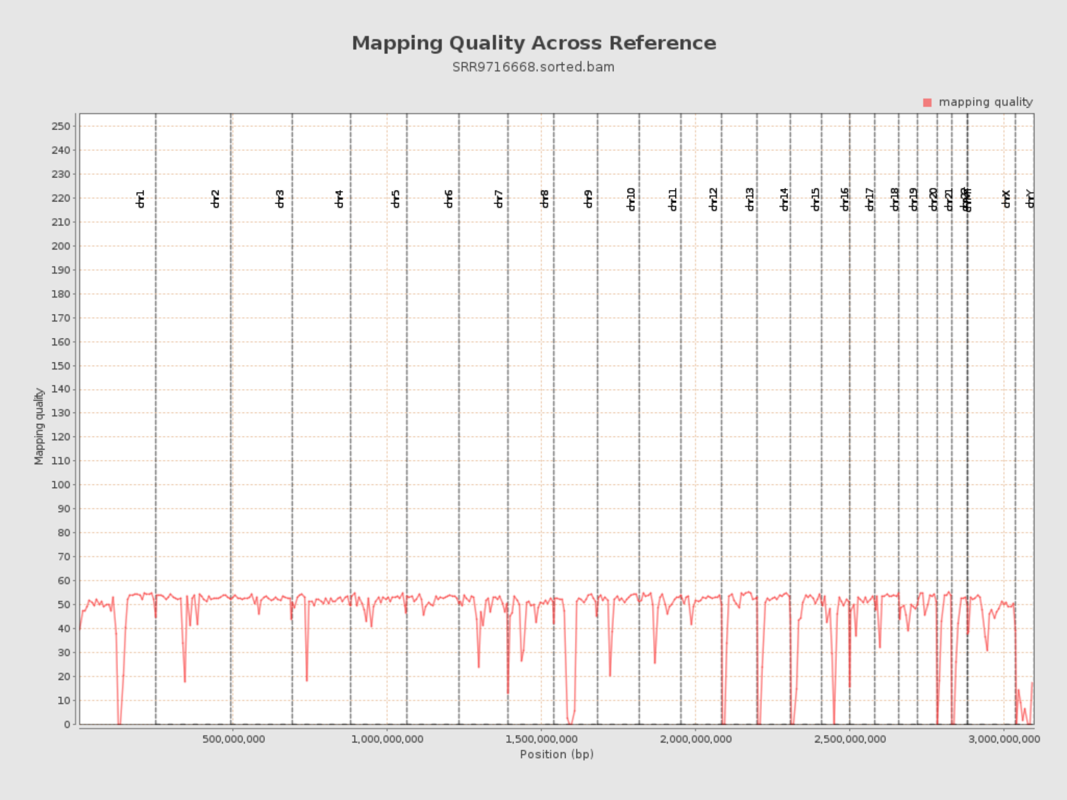
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram