Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:58:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708513.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_SRR1708513 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708513.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:58:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708513.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,984,086
Mapped reads	2,102,438 / 70.46%
Unmapped reads	881,648 / 29.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	469 / 0.02%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	88,812 / 2.98%
Duplication rate	3.33%
Clipped reads	394,405 / 13.22%

2.2. ACGT Content

Number/percentage of A's	29,353,778 / 29.03%
Number/percentage of C's	18,814,066 / 18.61%
Number/percentage of T's	32,317,737 / 31.96%
Number/percentage of G's	20,633,622 / 20.4%
Number/percentage of N's	1,444 / 0%
GC Percentage	39.01%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.3178

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

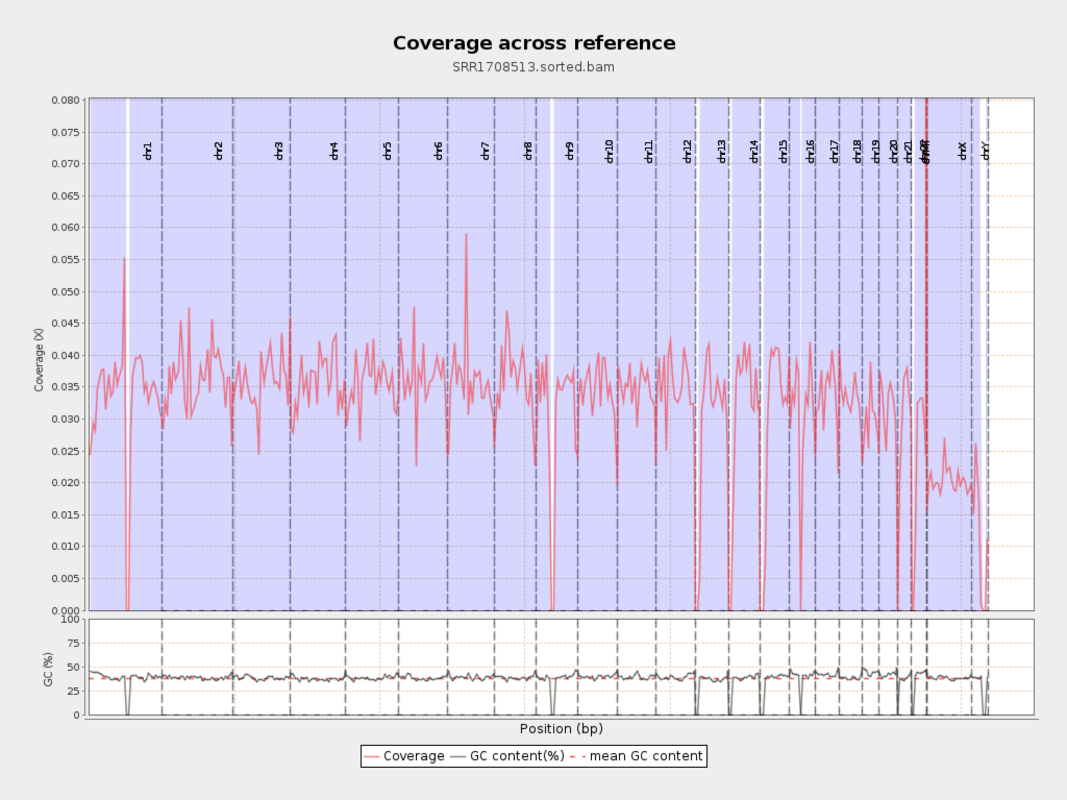
General error rate	0.48%
Mismatches	479,597
Insertions	4,755
Mapped reads with at least one insertion	0.23%
Deletions	11,977
Mapped reads with at least one deletion	0.57%
Homopolymer indels	48.43%

2.6. Chromosome stats

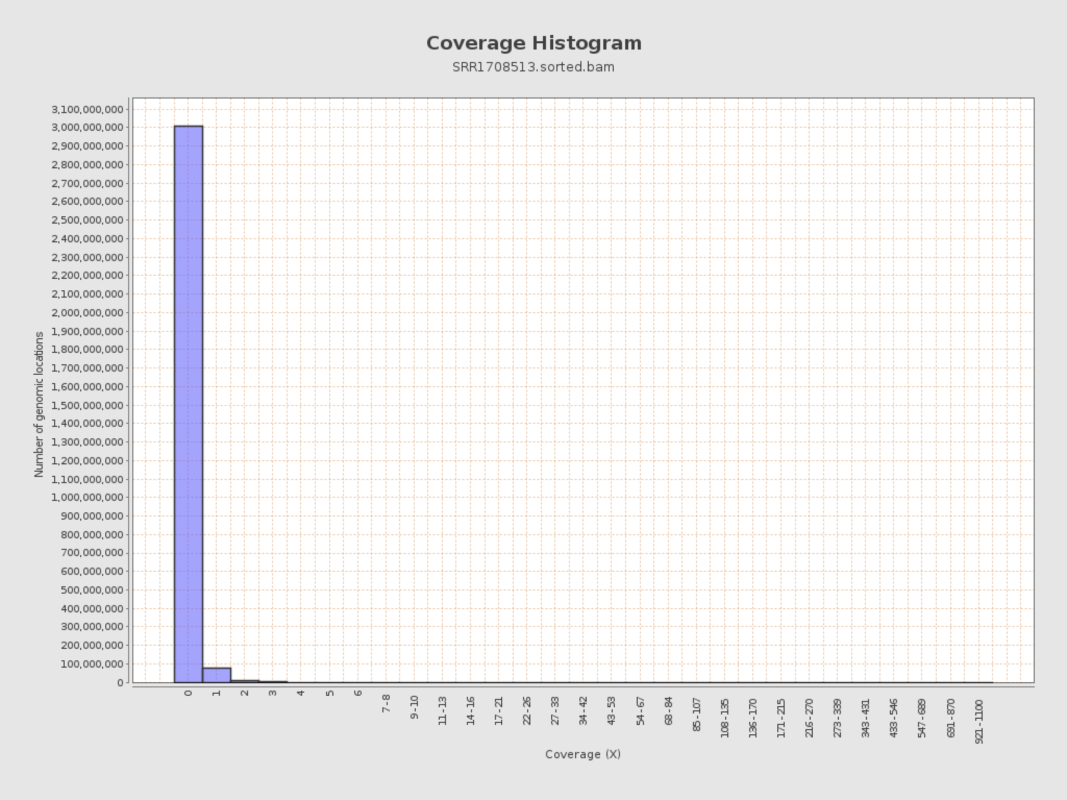
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8297809	0.0333	0.5767
chr2	243199373	8855172	0.0364	0.2736
chr3	198022430	7124004	0.036	0.2137
chr4	191154276	6816427	0.0357	0.2155
chr5	180915260	6436471	0.0356	0.2138
chr6	171115067	6228984	0.0364	0.2543
chr7	159138663	5761346	0.0362	0.4017

chr8	146364022	5261783	0.0359	0.6341
chr9	141213431	4328448	0.0307	0.2383
chr10	135534747	4728442	0.0349	0.2562
chr11	135006516	4681074	0.0347	0.2823
chr12	133851895	4738687	0.0354	0.2147
chr13	115169878	3285493	0.0285	0.1898
chr14	107349540	3288224	0.0306	0.2004
chr15	102531392	2976974	0.029	0.1918
chr16	90354753	2776717	0.0307	0.2024
chr17	81195210	2720022	0.0335	0.2526
chr18	78077248	2629855	0.0337	0.3716
chr19	59128983	1768759	0.0299	0.3927
chr20	63025520	2004103	0.0318	0.2014
chr21	48129895	1365138	0.0284	0.2109
chr22	51304566	1117562	0.0218	0.1802
chrMT	16571	162810	9.825	7.4943
chrX	155270560	3140589	0.0202	0.181
chrY	59373566	644172	0.0108	0.1267

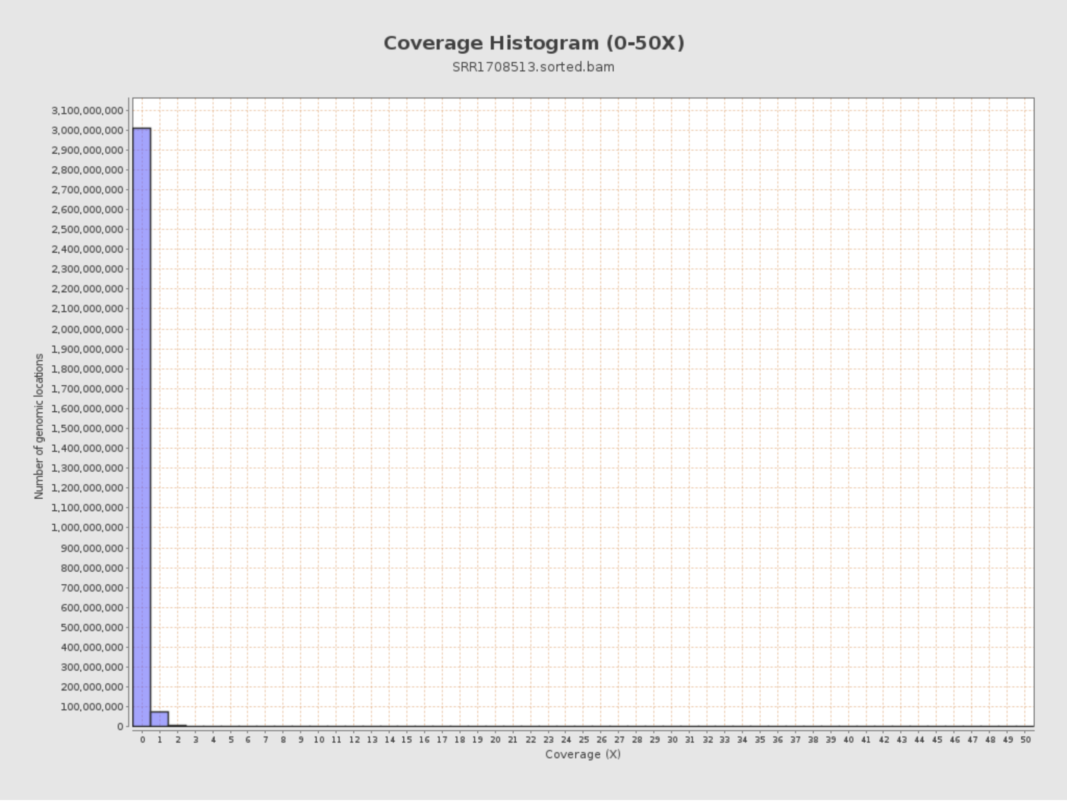
3. Results : Coverage across reference



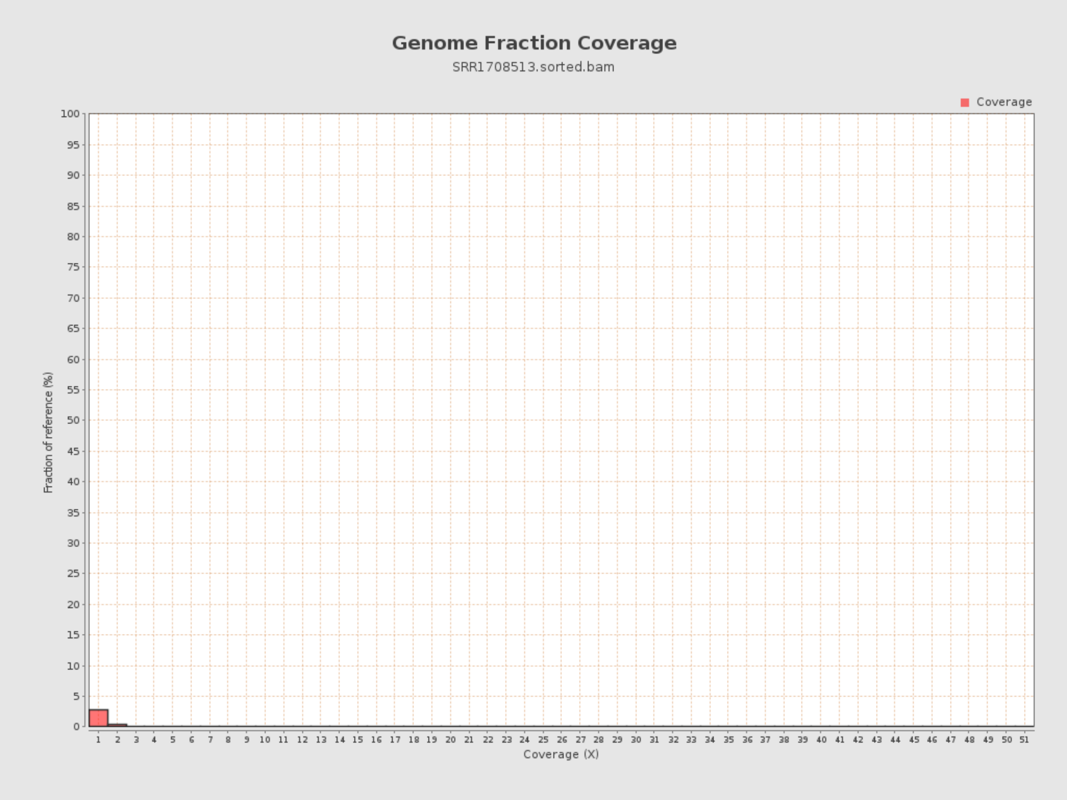
4. Results : Coverage Histogram



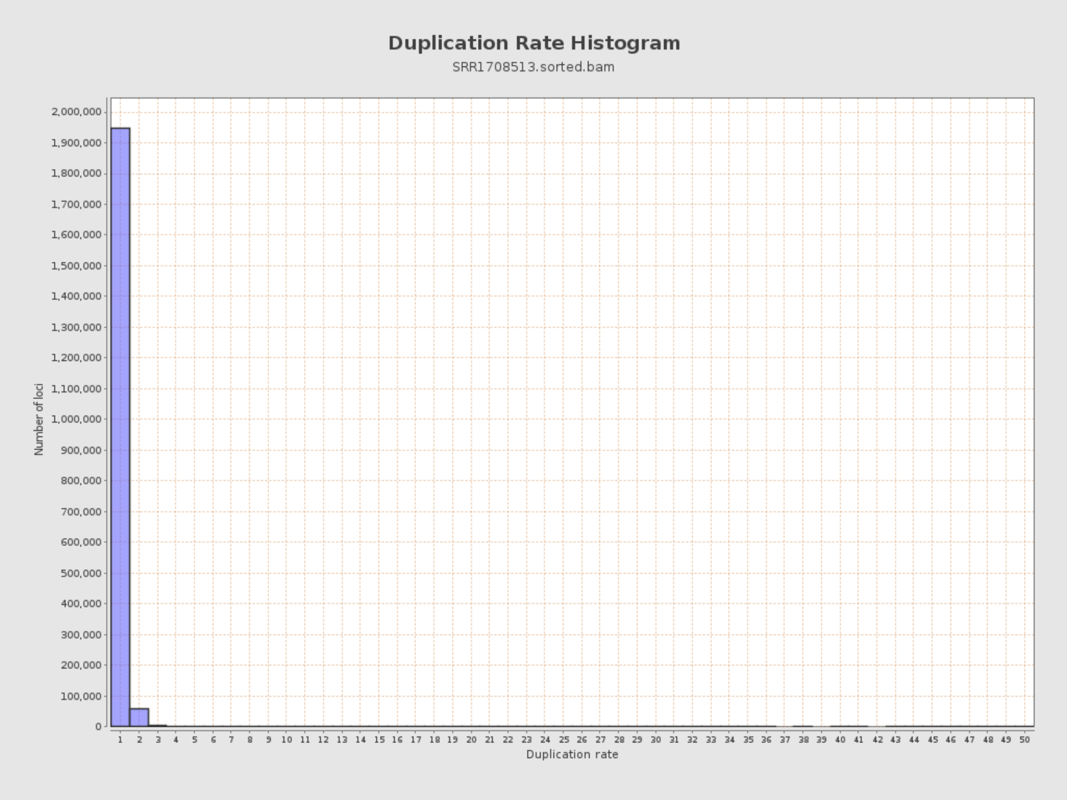
5. Results : Coverage Histogram (0-50X)



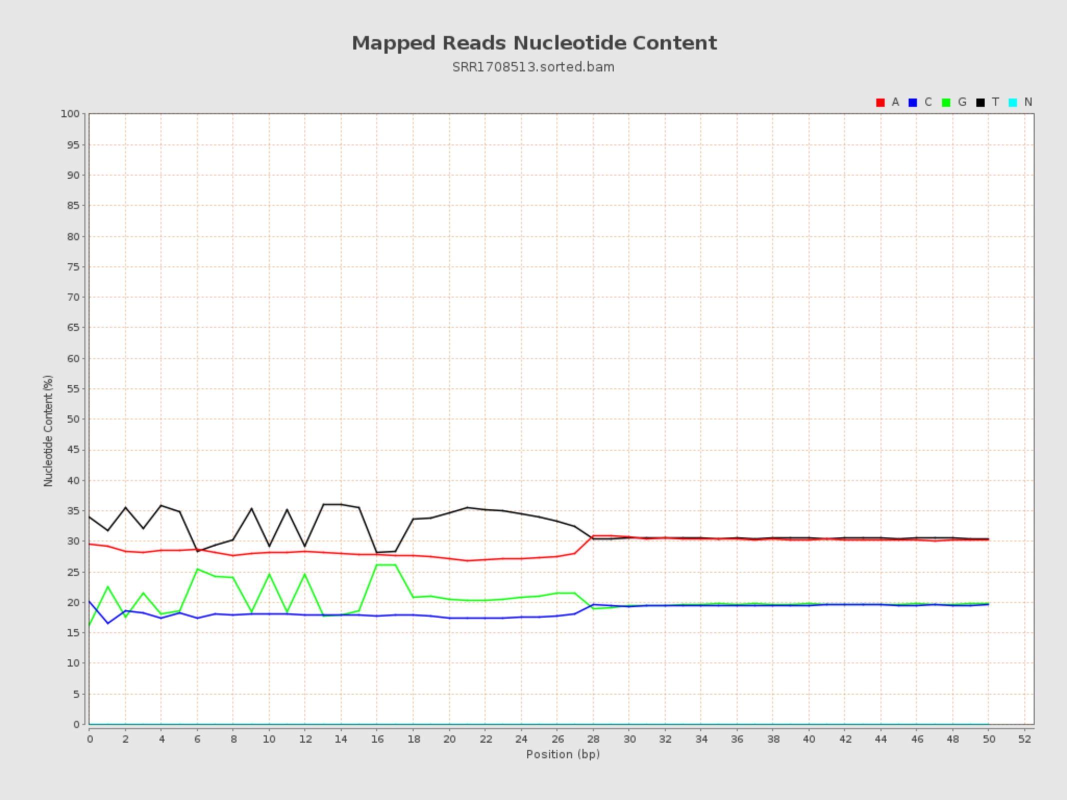
6. Results : Genome Fraction Coverage



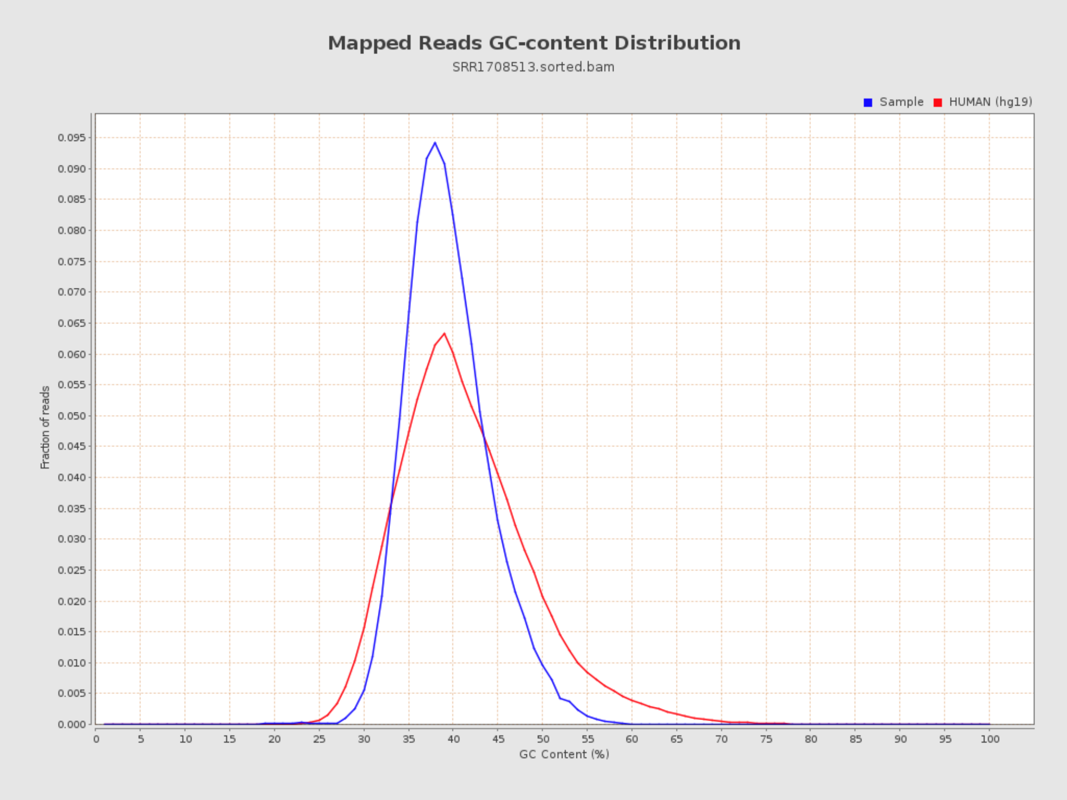
7. Results : Duplication Rate Histogram



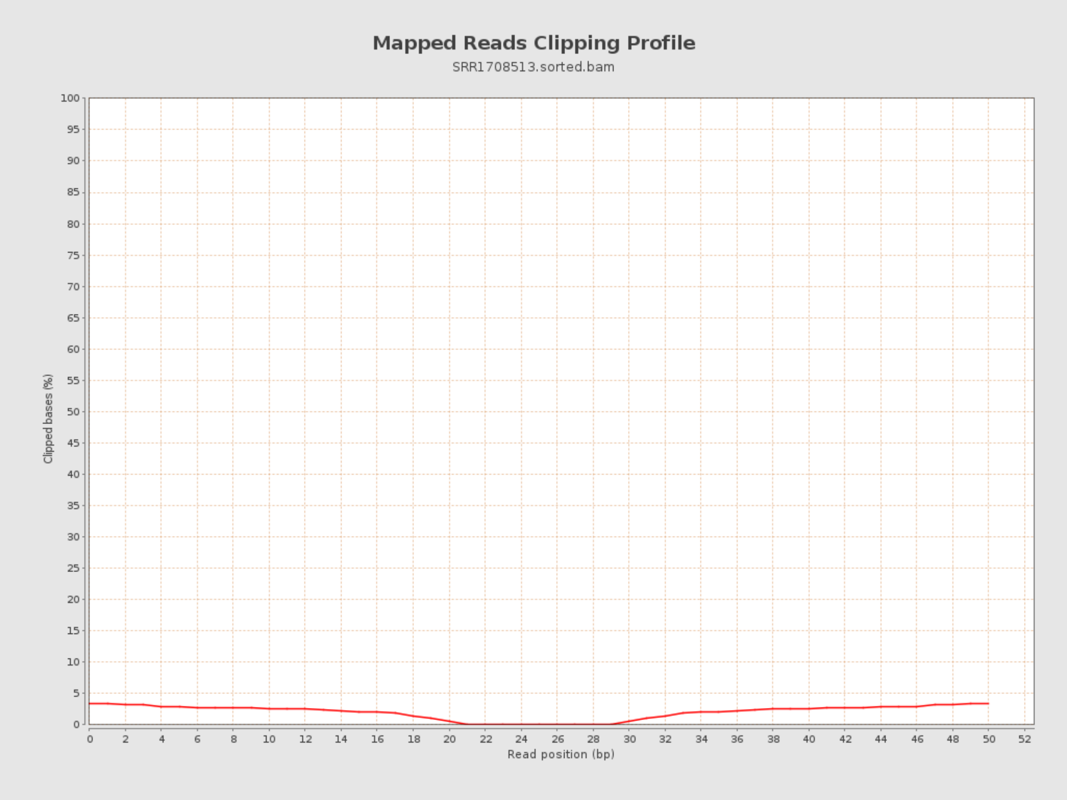
8. Results : Mapped Reads Nucleotide Content



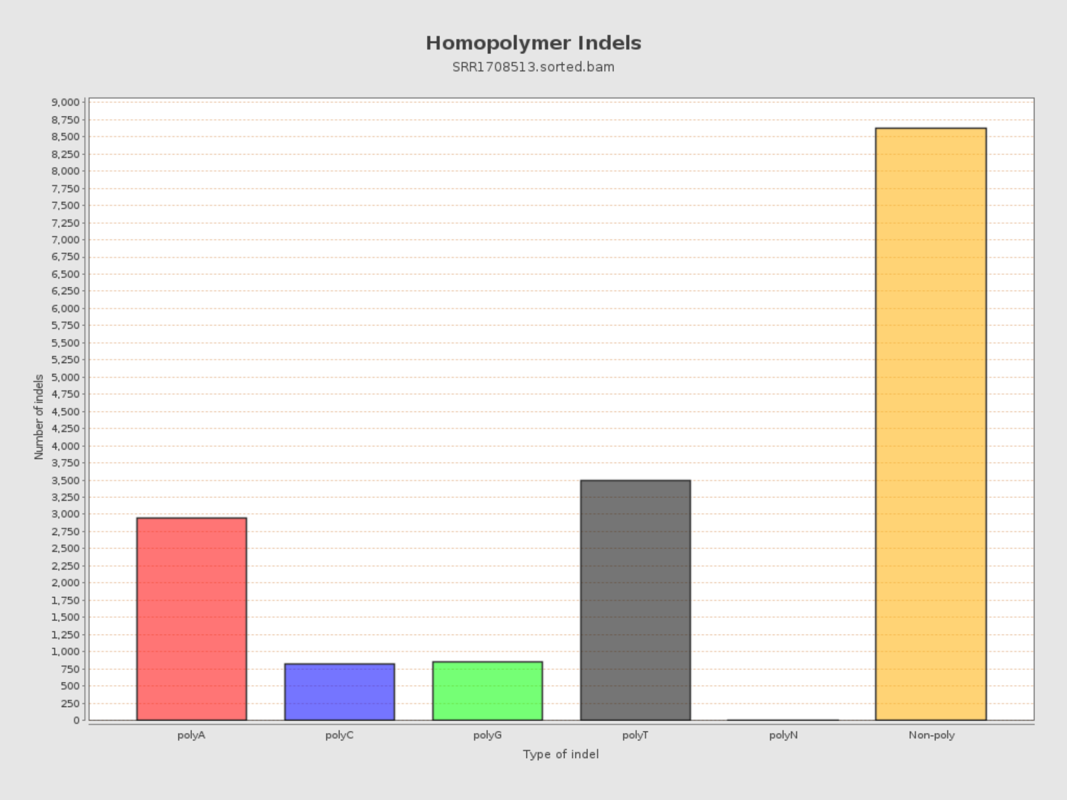
9. Results : Mapped Reads GC-content Distribution



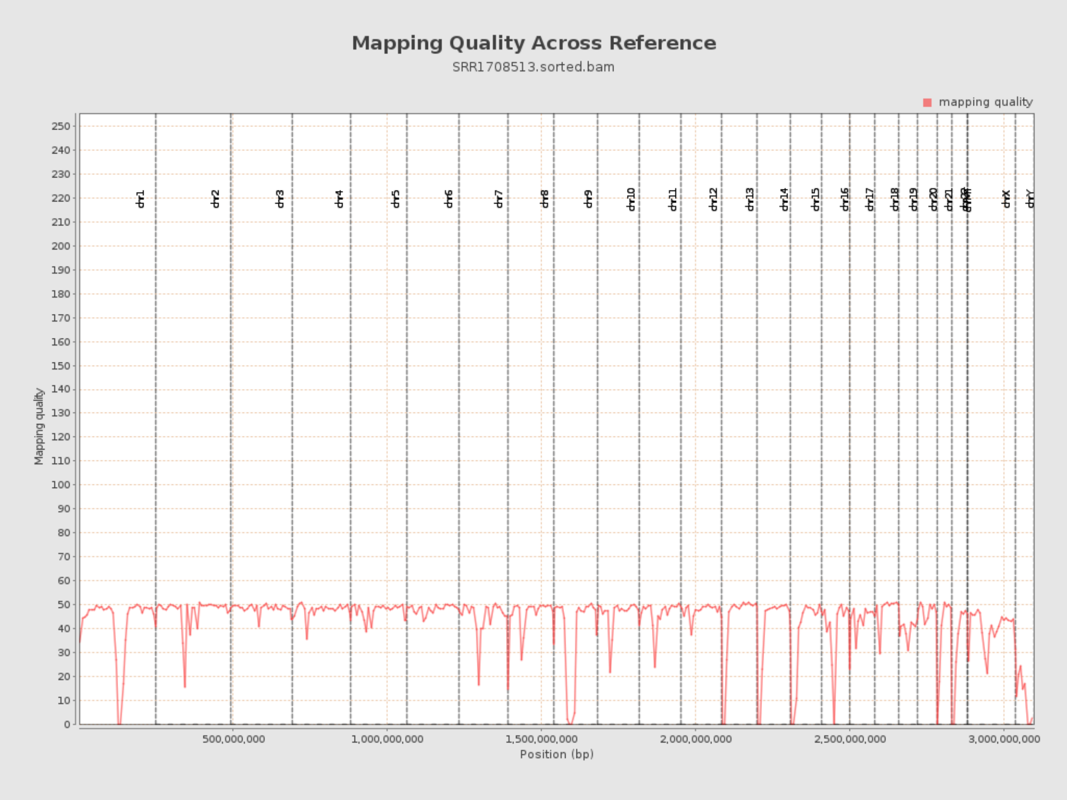
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram