Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:06:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708607.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_SRR1708607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:06:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,104,164
Mapped reads	5,968,203 / 97.77%
Unmapped reads	135,961 / 2.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	186 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	61,808 / 1.01%
Duplication rate	1.03%
Clipped reads	77,175 / 1.26%

2.2. ACGT Content

Number/percentage of A's	92,163,117 / 30.96%
Number/percentage of C's	56,560,981 / 19%
Number/percentage of T's	91,619,761 / 30.78%
Number/percentage of G's	57,325,069 / 19.26%
Number/percentage of N's	10,241 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	0.0962

Standard Deviation	0.3268

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

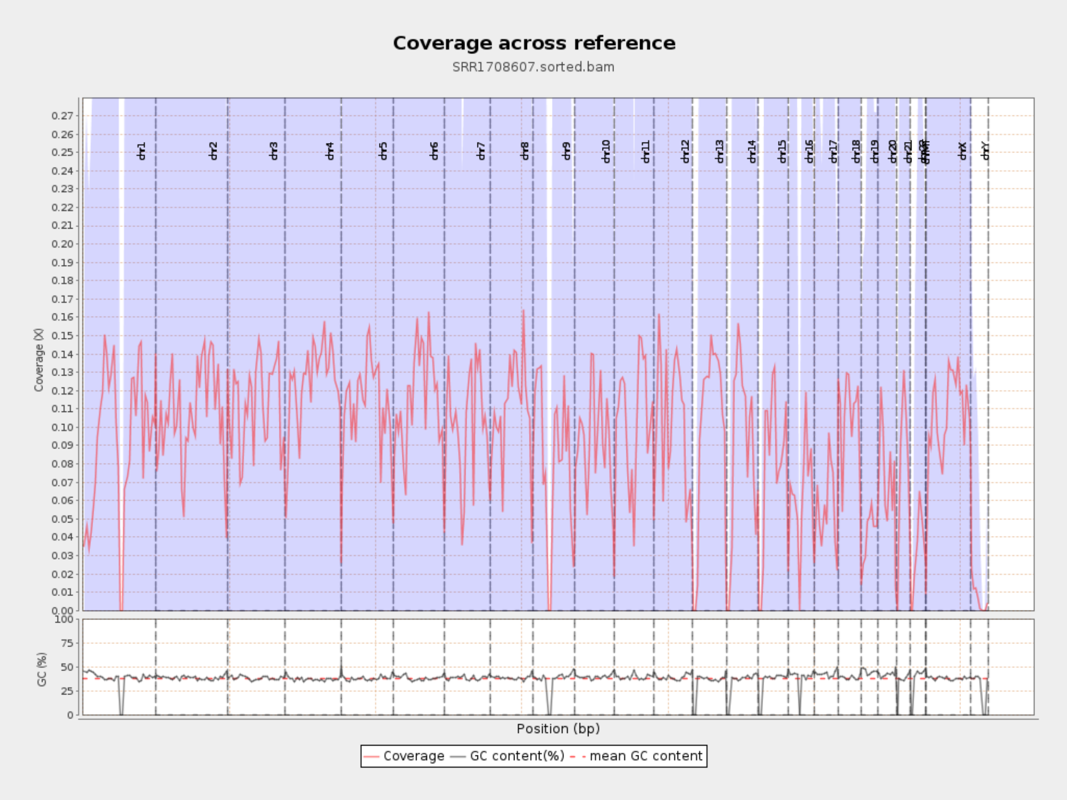
General error rate	0.15%
Mismatches	425,827
Insertions	18,860
Mapped reads with at least one insertion	0.32%
Deletions	14,893
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.26%

2.6. Chromosome stats

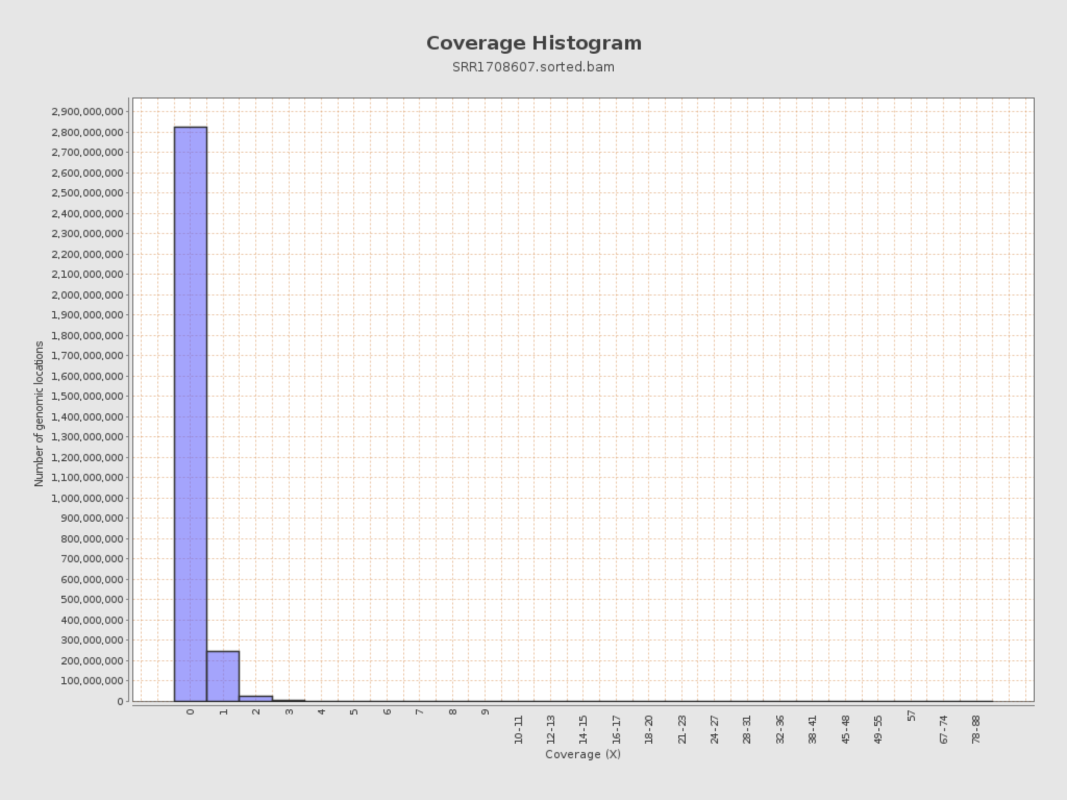
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23002699	0.0923	0.3221
chr2	243199373	26173229	0.1076	0.3438
chr3	198022430	22365113	0.1129	0.3518
chr4	191154276	23877478	0.1249	0.3698
chr5	180915260	20205367	0.1117	0.3496
chr6	171115067	19998774	0.1169	0.359
chr7	159138663	16057722	0.1009	0.3345

chr8	146364022	16171266	0.1105	0.3485
chr9	141213431	11783099	0.0834	0.3042
chr10	135534747	12790800	0.0944	0.3214
chr11	135006516	13967863	0.1035	0.3407
chr12	133851895	13735495	0.1026	0.3374
chr13	115169878	11666956	0.1013	0.3356
chr14	107349540	9638910	0.0898	0.3179
chr15	102531392	8062756	0.0786	0.2969
chr16	90354753	5517002	0.0611	0.2591
chr17	81195210	4648961	0.0573	0.2516
chr18	78077248	8329996	0.1067	0.3418
chr19	59128983	2507142	0.0424	0.2146
chr20	63025520	4722561	0.0749	0.288
chr21	48129895	3661556	0.0761	0.2927
chr22	51304566	1708500	0.0333	0.1913
chrMT	16571	150	0.0091	0.0947
chrX	155270560	16718707	0.1077	0.3447
chrY	59373566	392293	0.0066	0.0864

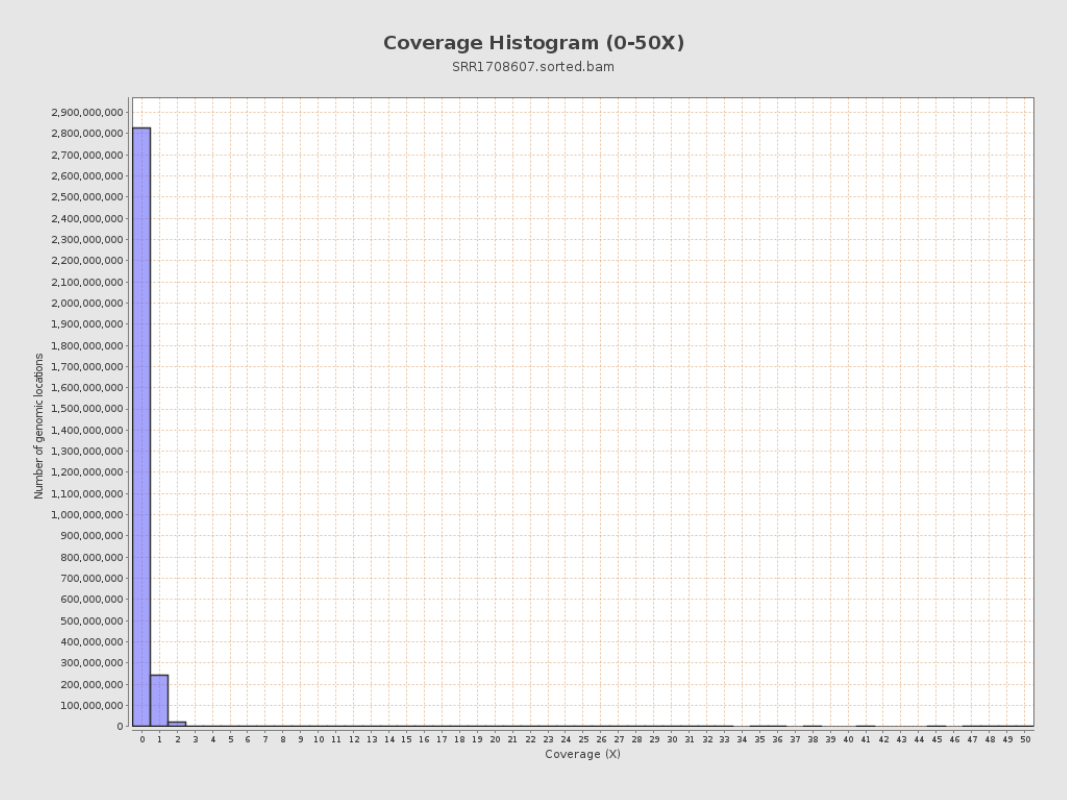
3. Results : Coverage across reference



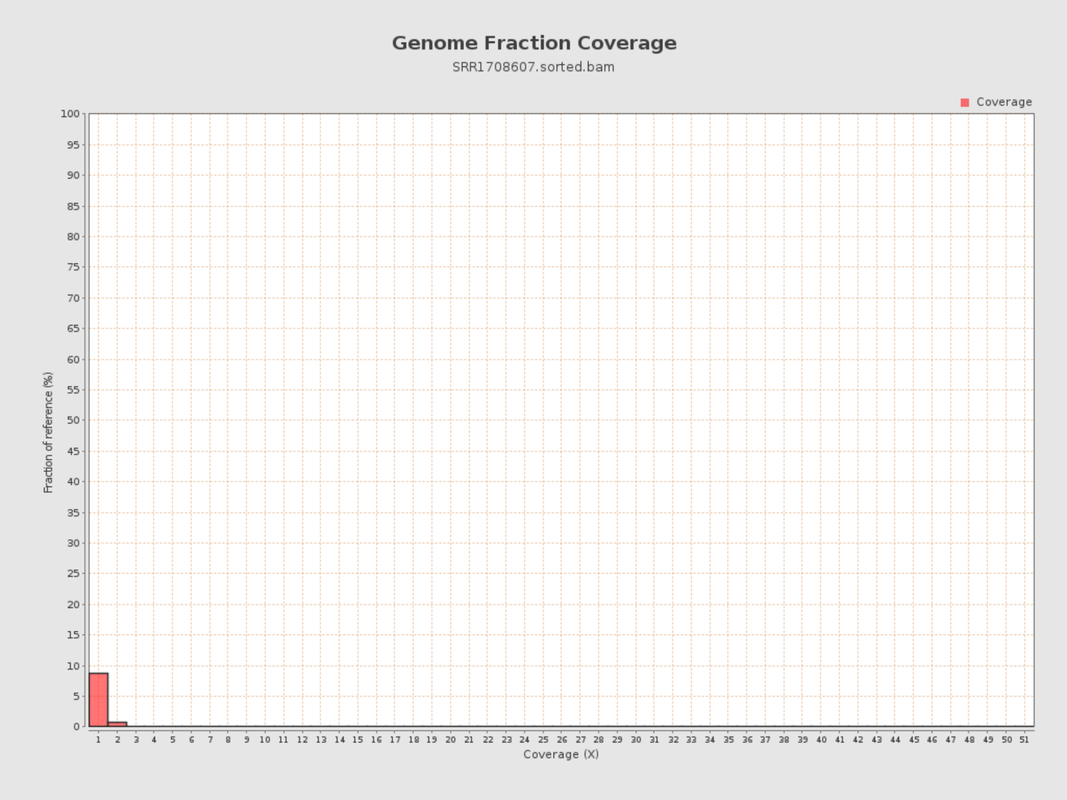
4. Results : Coverage Histogram



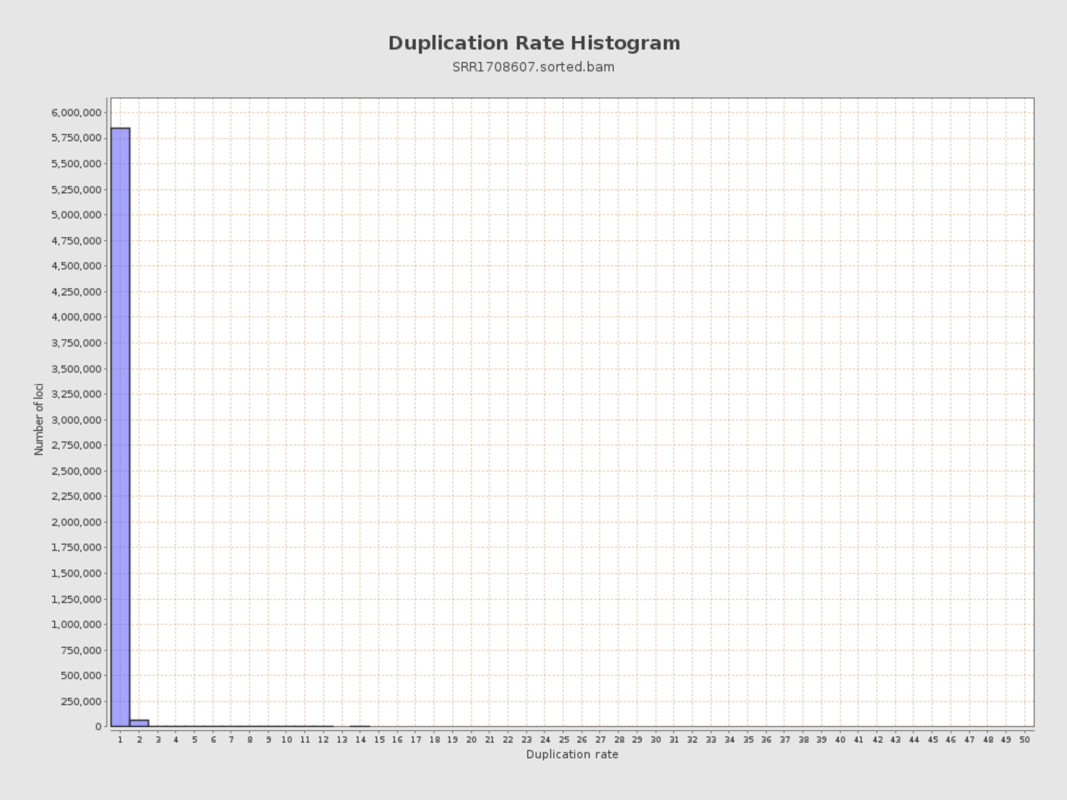
5. Results : Coverage Histogram (0-50X)



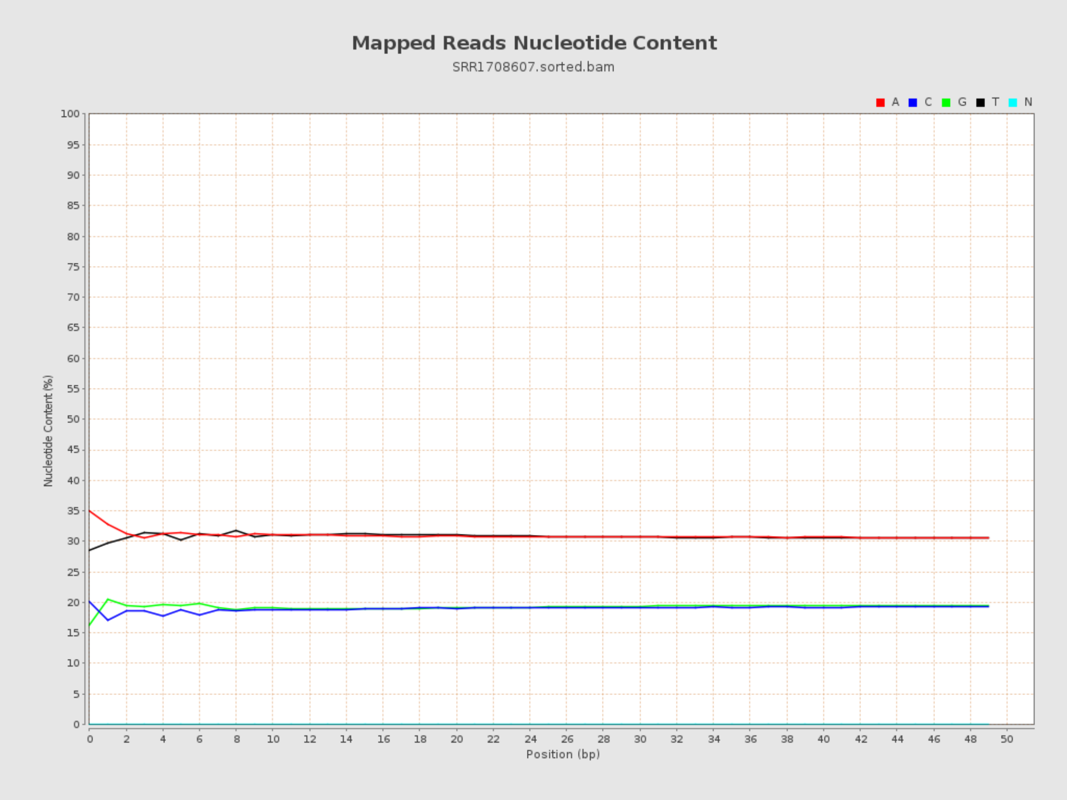
6. Results : Genome Fraction Coverage



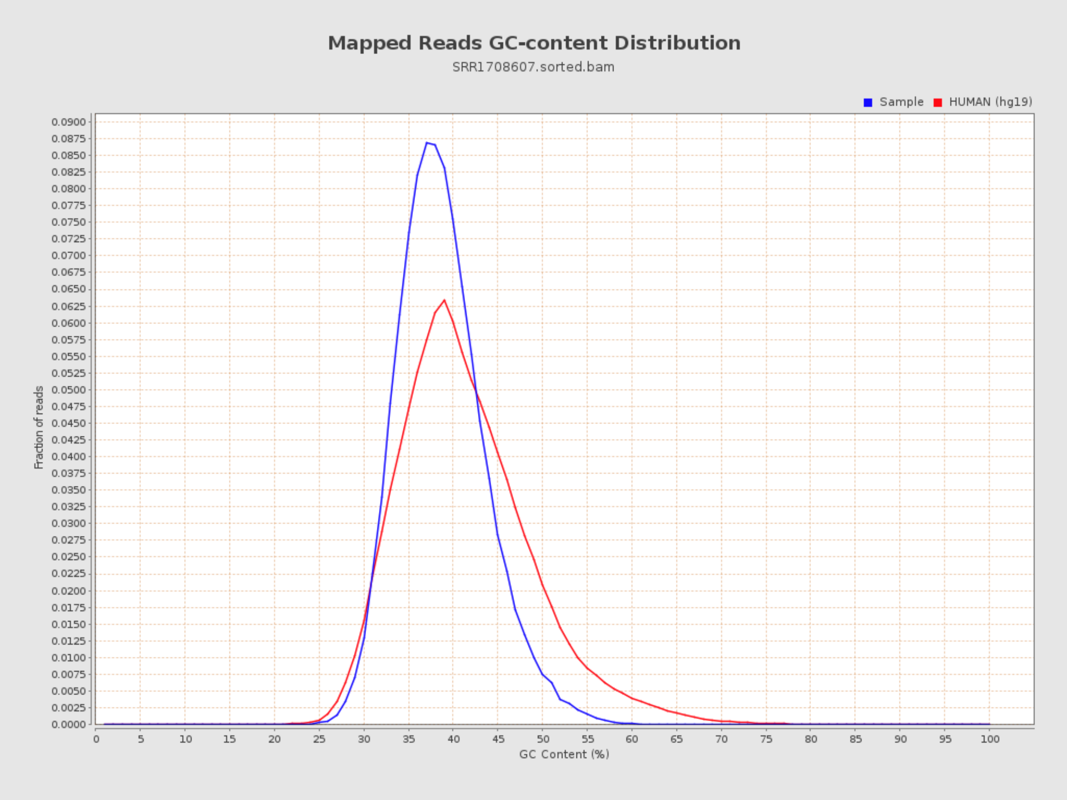
7. Results : Duplication Rate Histogram



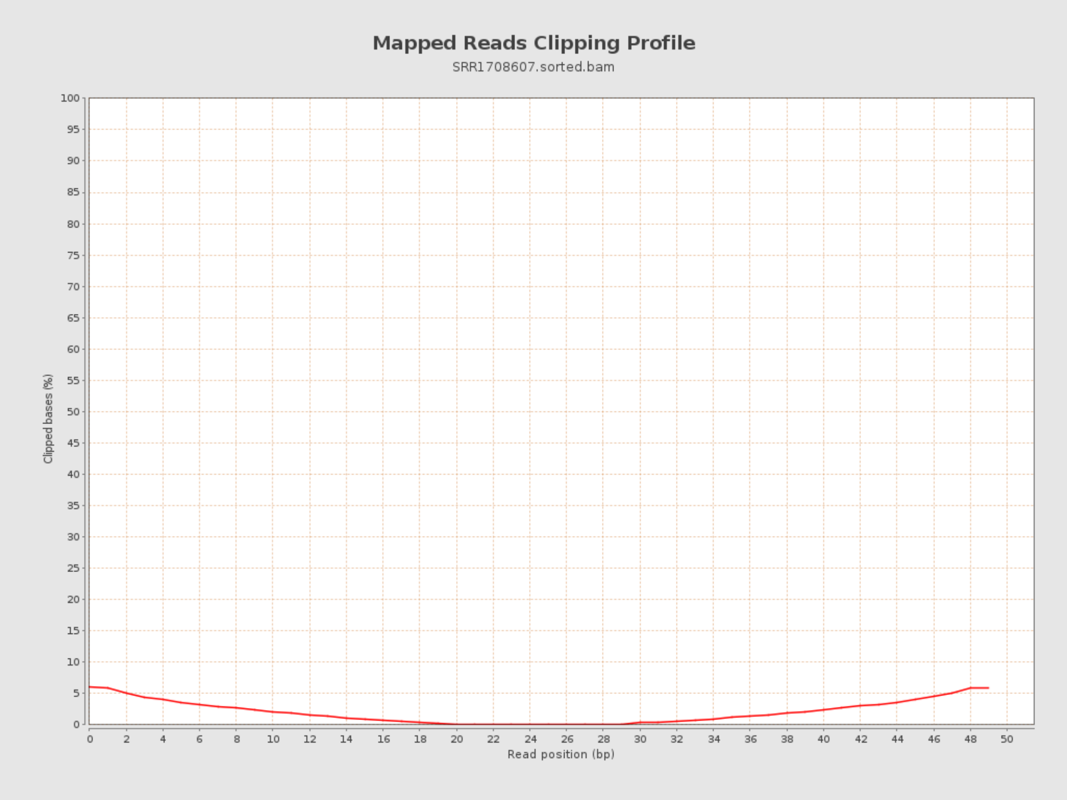
8. Results : Mapped Reads Nucleotide Content



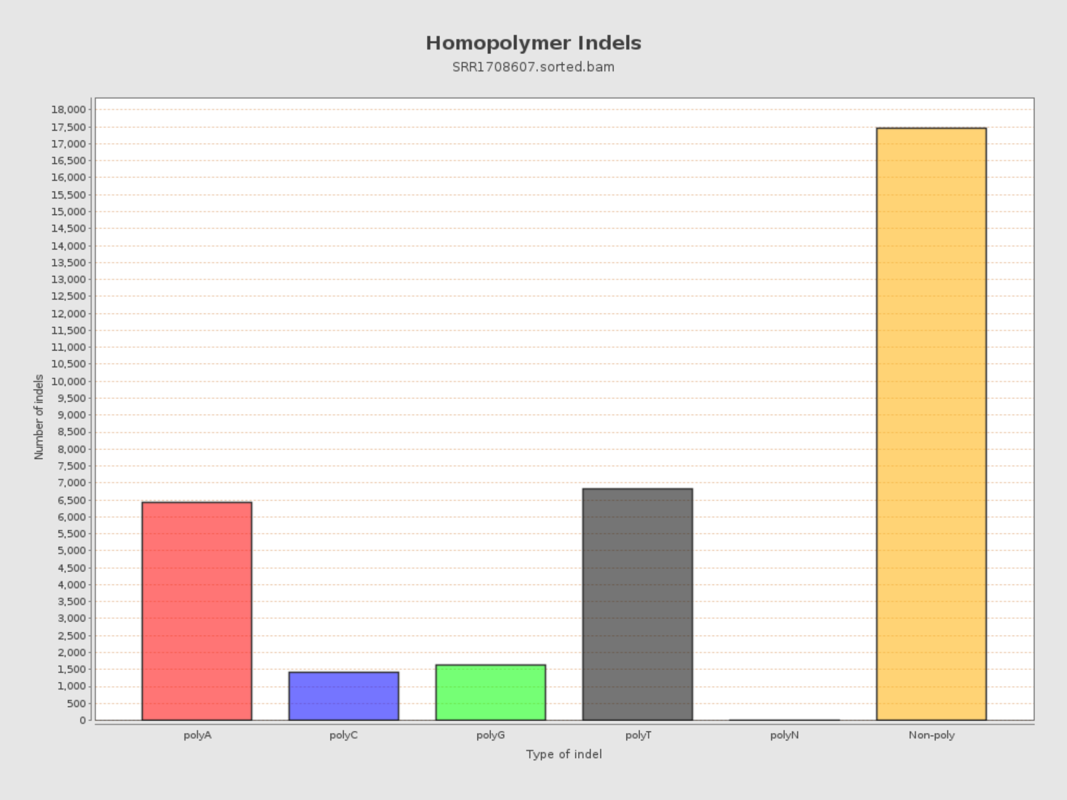
9. Results : Mapped Reads GC-content Distribution



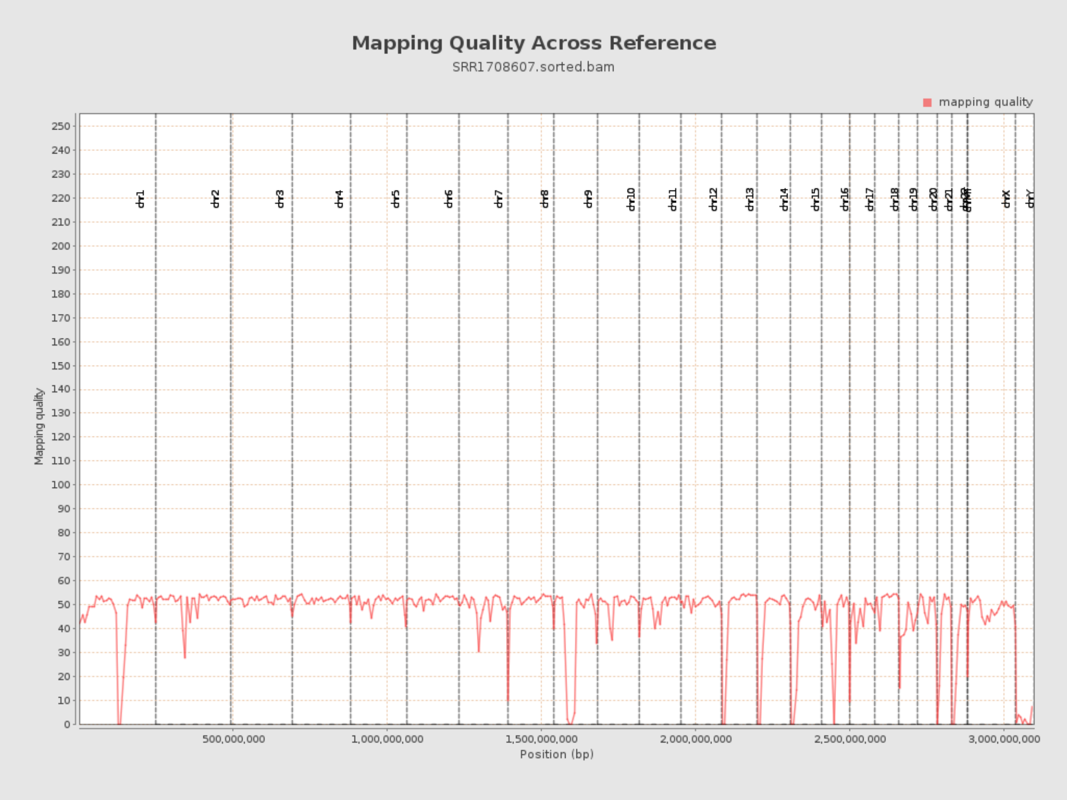
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram