Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:40:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708589.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_SRR1708589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708589.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:40:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,752,197
Mapped reads	4,646,477 / 97.78%
Unmapped reads	105,720 / 2.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	109 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	46,723 / 0.98%
Duplication rate	1.01%
Clipped reads	61,912 / 1.3%

2.2. ACGT Content

Number/percentage of A's	71,872,881 / 31.01%
Number/percentage of C's	43,862,770 / 18.93%
Number/percentage of T's	71,519,039 / 30.86%
Number/percentage of G's	44,477,375 / 19.19%
Number/percentage of N's	8,226 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0749

Standard Deviation	0.2892

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

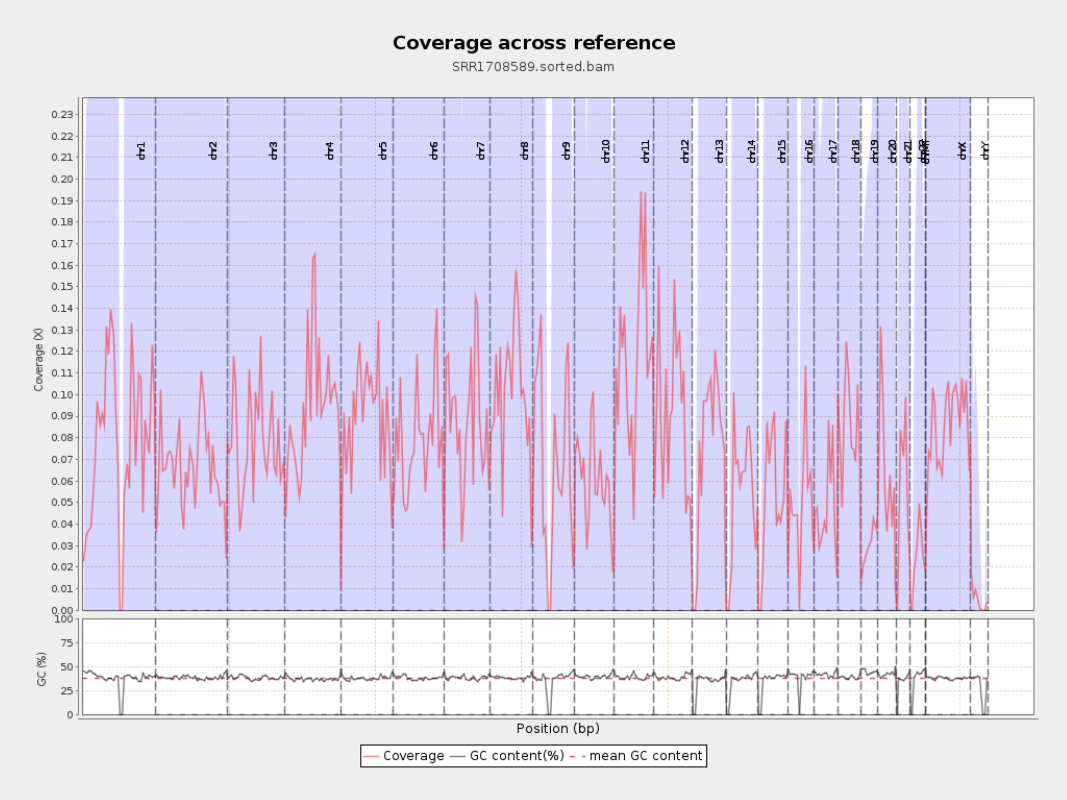
General error rate	0.16%
Mismatches	341,970
Insertions	14,529
Mapped reads with at least one insertion	0.31%
Deletions	11,753
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.86%

2.6. Chromosome stats

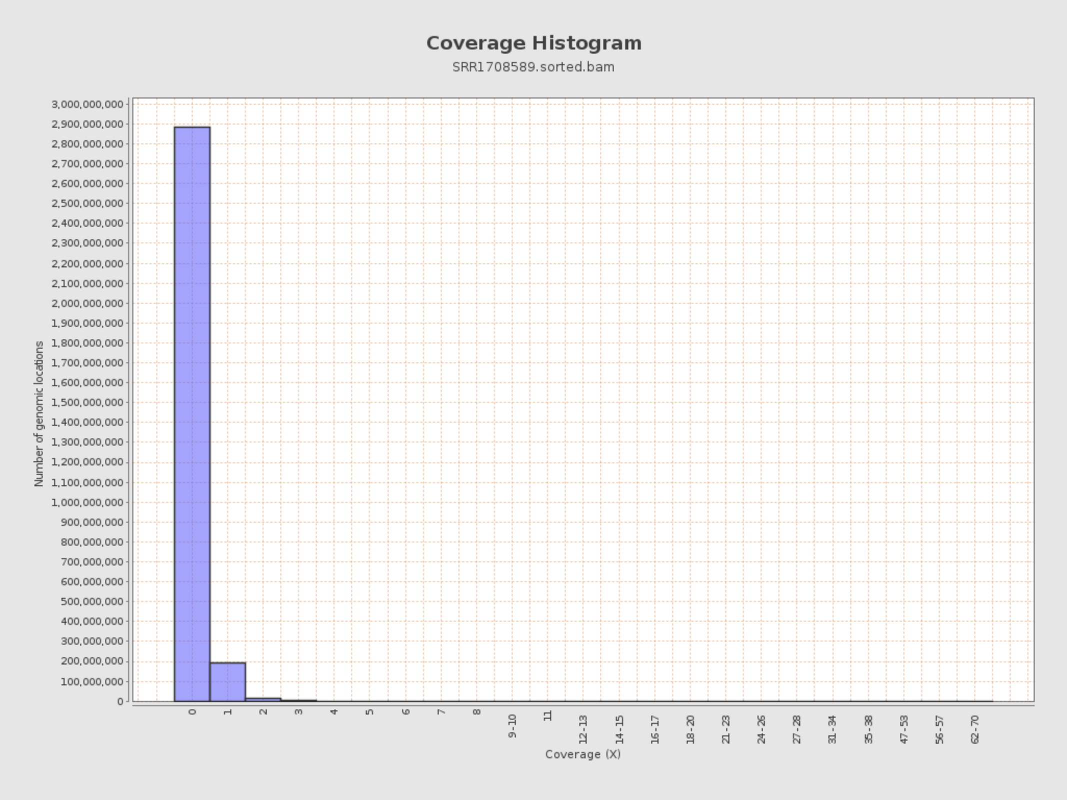
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19452755	0.078	0.2962
chr2	243199373	16160457	0.0664	0.2693
chr3	198022430	15534739	0.0784	0.2937
chr4	191154276	18056765	0.0945	0.3239
chr5	180915260	16043921	0.0887	0.3123
chr6	171115067	13614224	0.0796	0.2973
chr7	159138663	13826236	0.0869	0.3114

chr8	146364022	14822887	0.1013	0.3363
chr9	141213431	9710635	0.0688	0.278
chr10	135534747	8267178	0.061	0.2578
chr11	135006516	15787663	0.1169	0.3644
chr12	133851895	12030673	0.0899	0.3173
chr13	115169878	8554117	0.0743	0.2885
chr14	107349540	5901048	0.055	0.2471
chr15	102531392	5460641	0.0533	0.244
chr16	90354753	4521732	0.05	0.2347
chr17	81195210	3927650	0.0484	0.2321
chr18	78077248	6699834	0.0858	0.3076
chr19	59128983	1788664	0.0303	0.1802
chr20	63025520	4128520	0.0655	0.2699
chr21	48129895	2578009	0.0536	0.2461
chr22	51304566	1252038	0.0244	0.1637
chrMT	16571	295	0.0178	0.1322
chrX	155270560	13343548	0.0859	0.3076
chrY	59373566	296221	0.005	0.0745

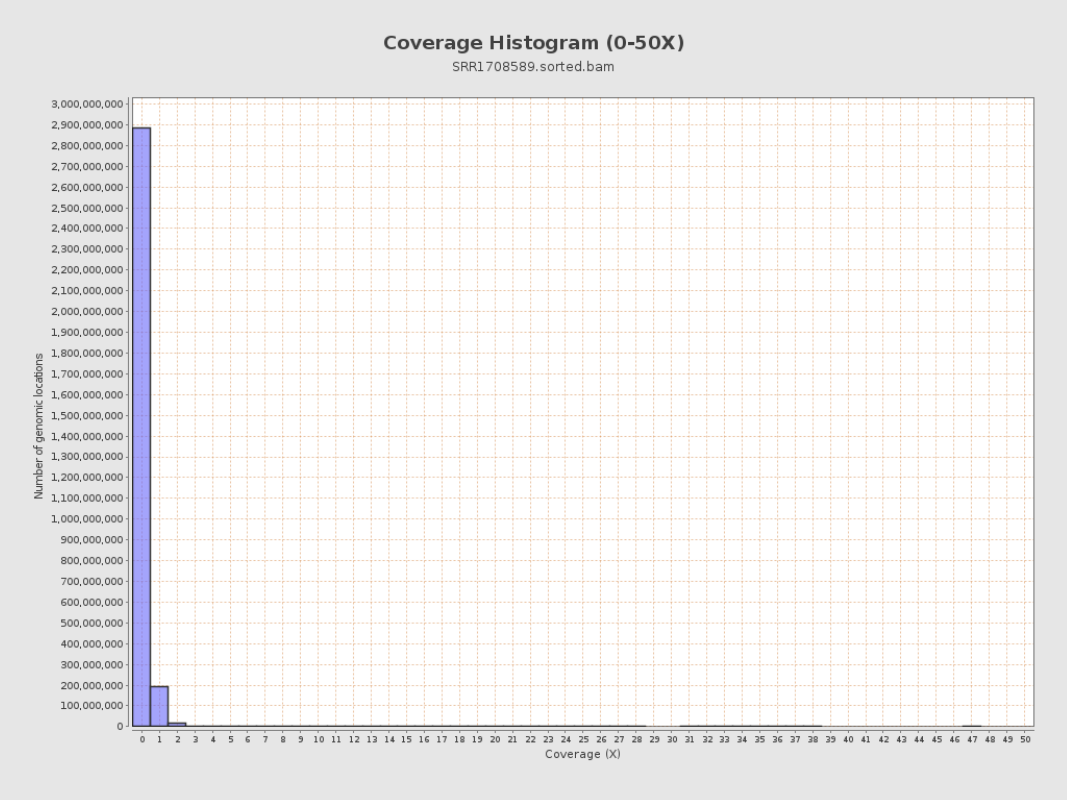
3. Results : Coverage across reference



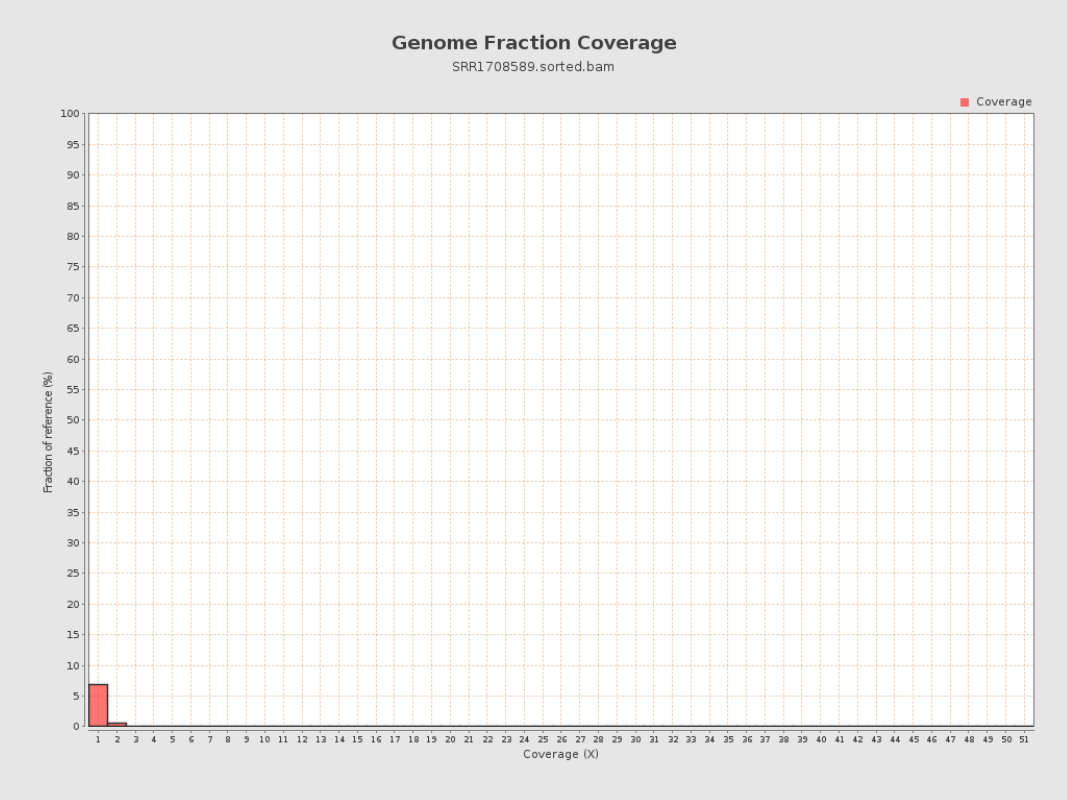
4. Results : Coverage Histogram



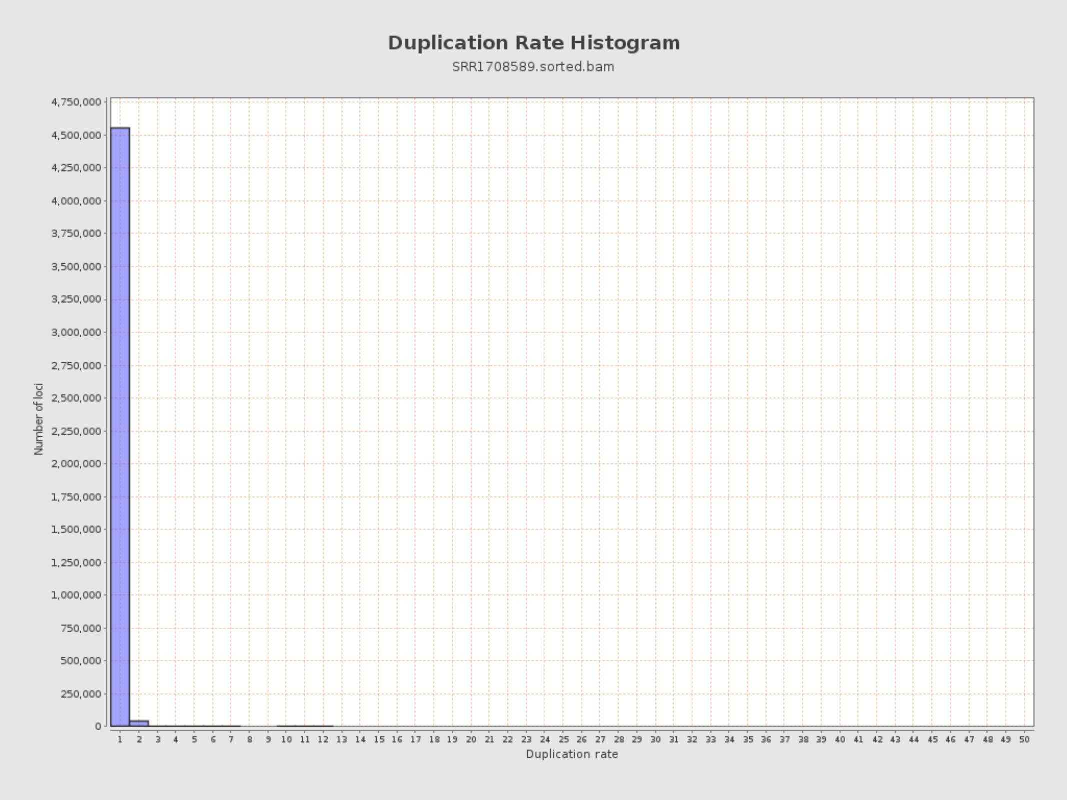
5. Results : Coverage Histogram (0-50X)



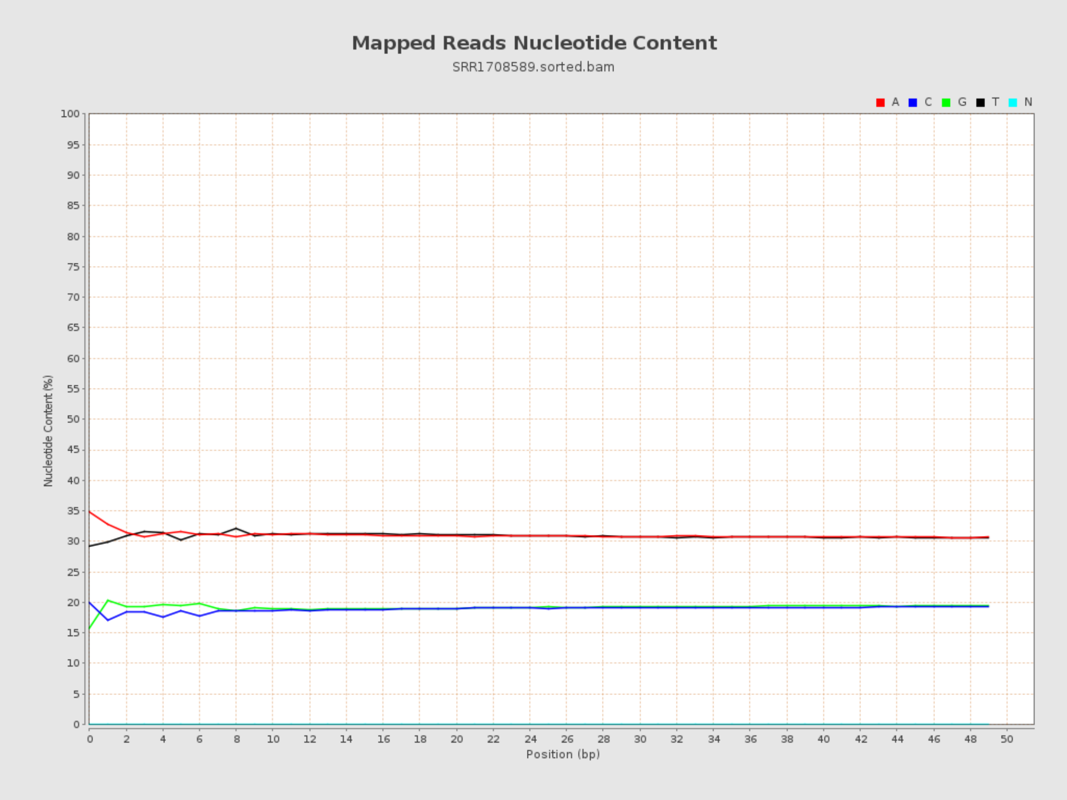
6. Results : Genome Fraction Coverage



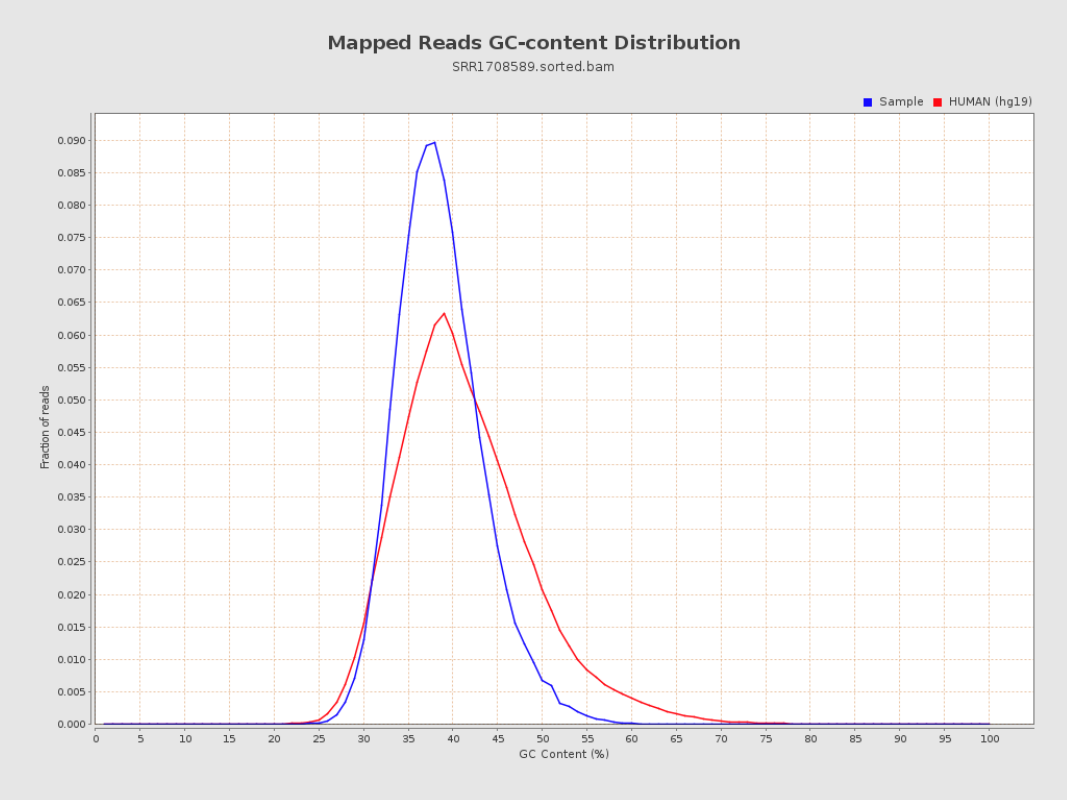
7. Results : Duplication Rate Histogram



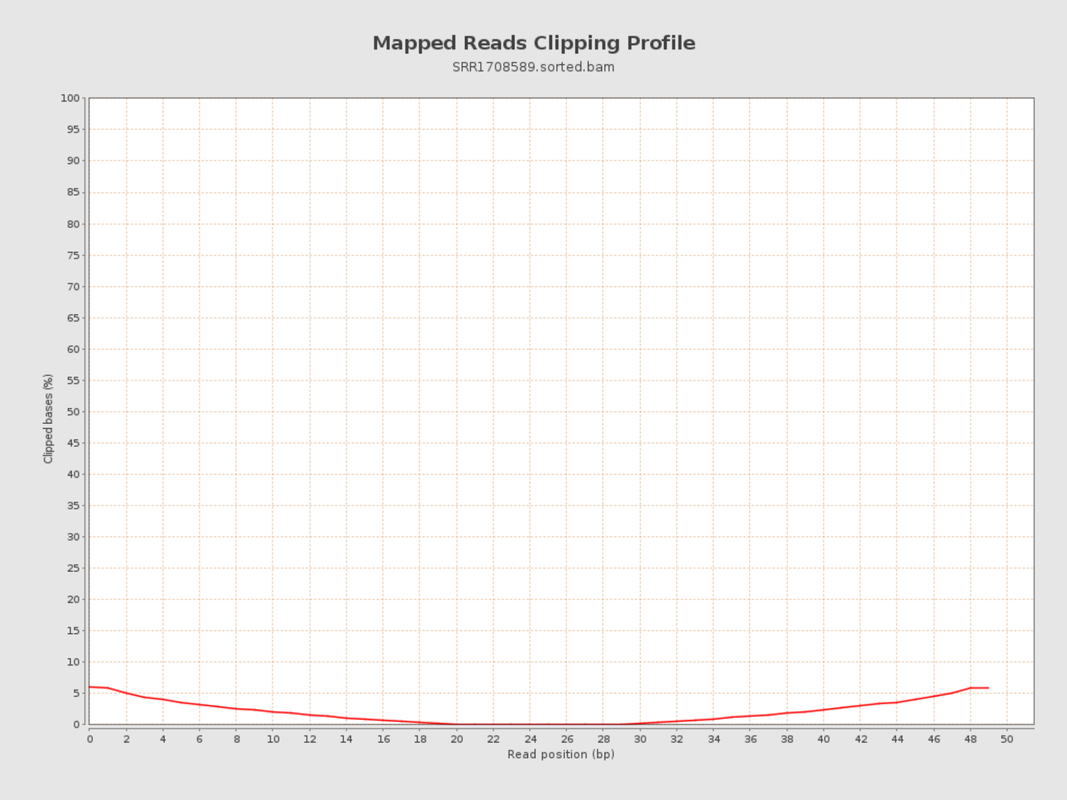
8. Results : Mapped Reads Nucleotide Content



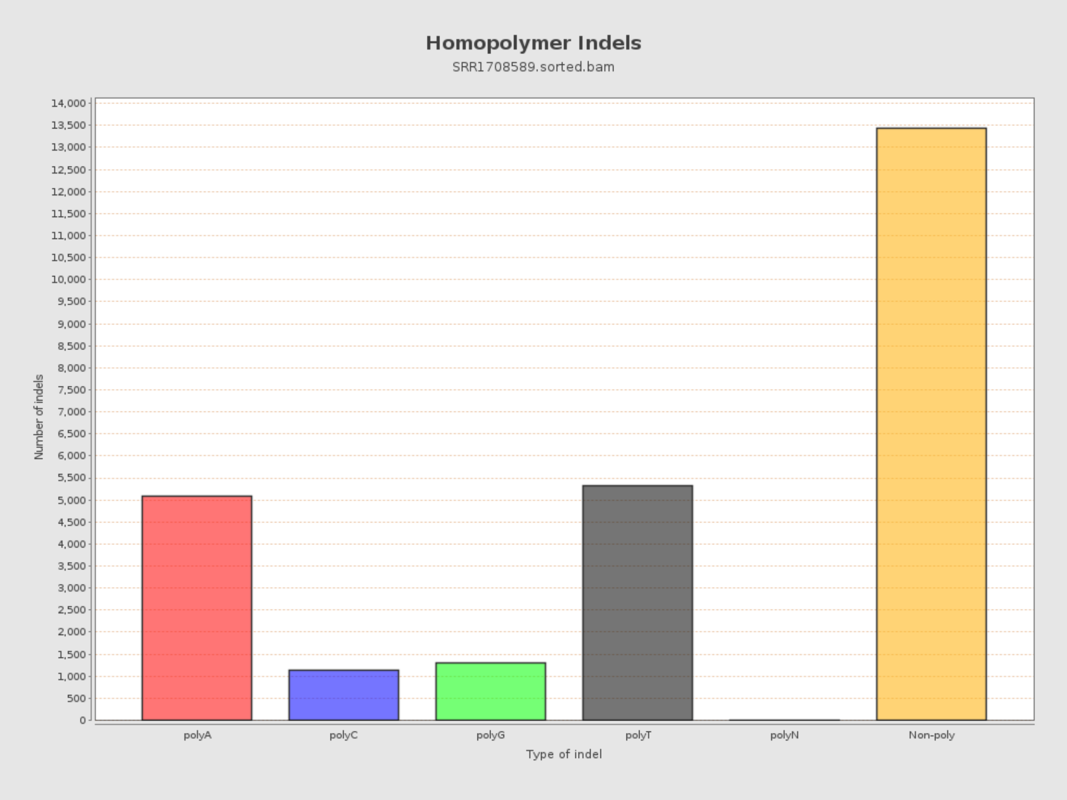
9. Results : Mapped Reads GC-content Distribution



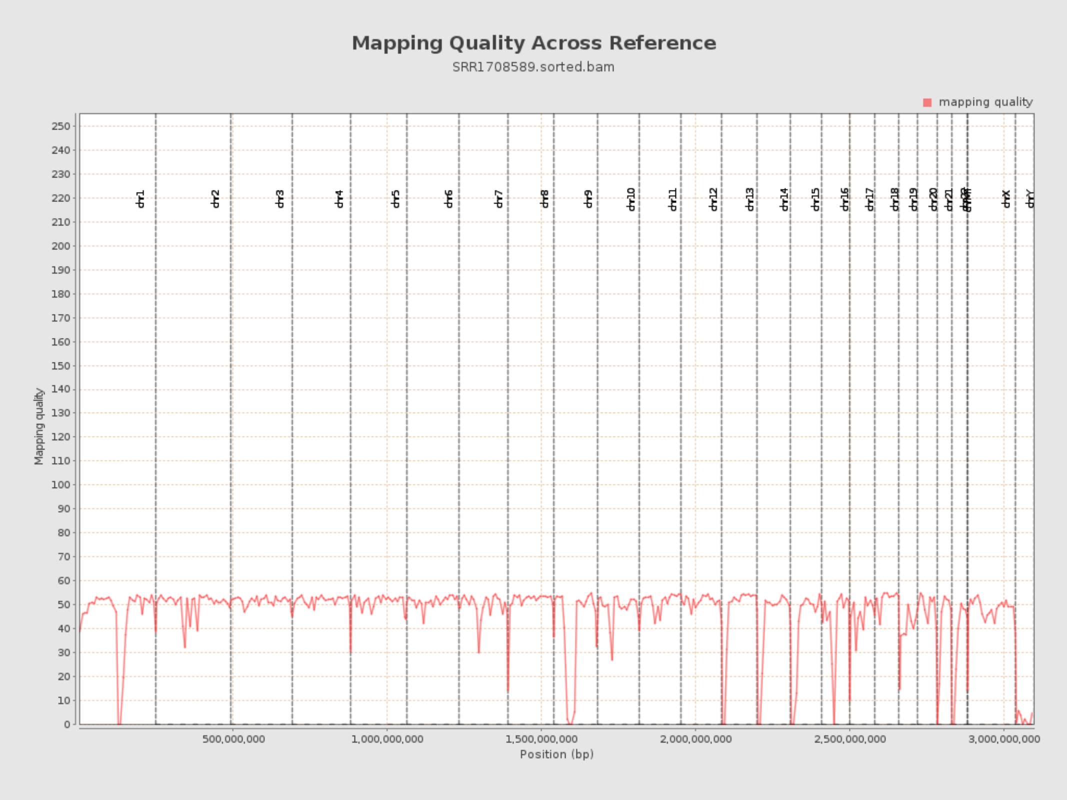
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram