Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:27:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708650.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_SRR1708650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:27:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,654,662
Mapped reads	4,423,168 / 95.03%
Unmapped reads	231,494 / 4.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	116 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	21,644 / 0.46%
Duplication rate	0.48%
Clipped reads	58,156 / 1.25%

2.2. ACGT Content

Number/percentage of A's	68,052,256 / 30.85%
Number/percentage of C's	42,034,518 / 19.05%
Number/percentage of T's	68,050,389 / 30.85%
Number/percentage of G's	42,455,237 / 19.25%
Number/percentage of N's	7,241 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	0.0713

Standard Deviation	0.2787

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

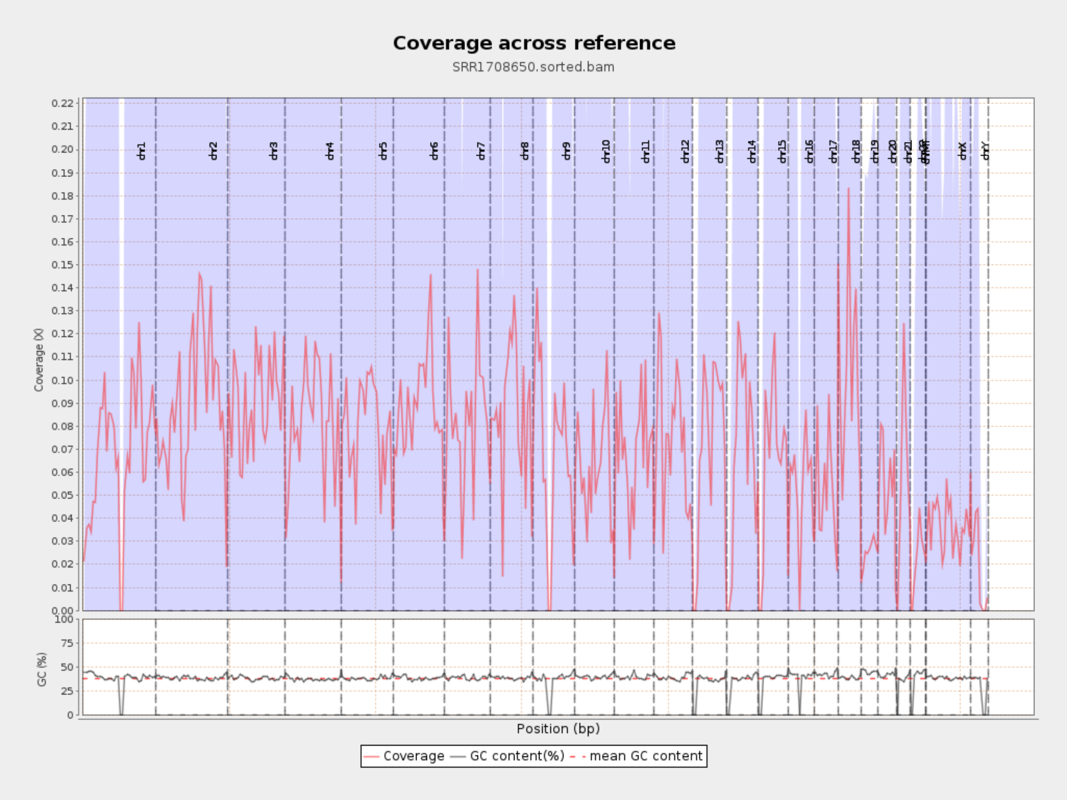
General error rate	0.17%
Mismatches	358,722
Insertions	14,634
Mapped reads with at least one insertion	0.33%
Deletions	12,617
Mapped reads with at least one deletion	0.28%
Homopolymer indels	49.11%

2.6. Chromosome stats

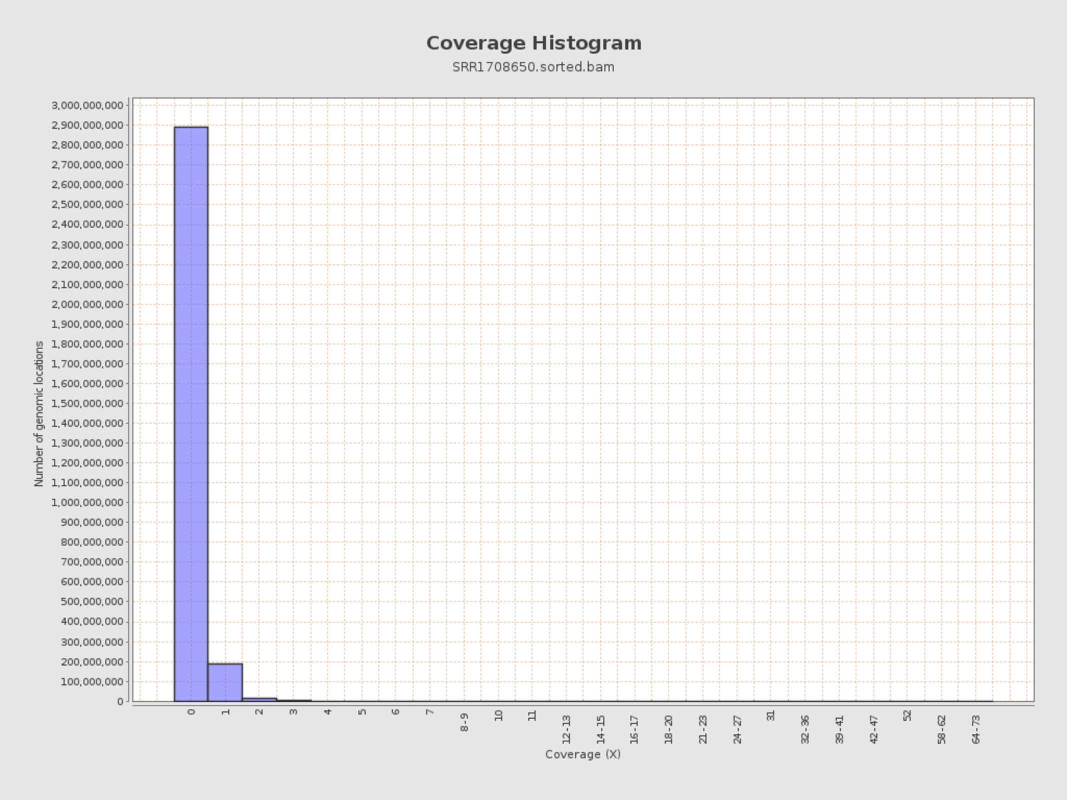
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16883421	0.0677	0.2724
chr2	243199373	21751448	0.0894	0.3123
chr3	198022430	18003242	0.0909	0.3133
chr4	191154276	15751496	0.0824	0.2976
chr5	180915260	14138752	0.0782	0.2898
chr6	171115067	15426285	0.0902	0.3123
chr7	159138663	12949991	0.0814	0.2971

chr8	146364022	12635712	0.0863	0.3059
chr9	141213431	9971935	0.0706	0.2779
chr10	135534747	8740758	0.0645	0.2636
chr11	135006516	9346592	0.0692	0.2751
chr12	133851895	9850529	0.0736	0.2829
chr13	115169878	8156245	0.0708	0.2774
chr14	107349540	7376291	0.0687	0.275
chr15	102531392	6688835	0.0652	0.2674
chr16	90354753	4678609	0.0518	0.2365
chr17	81195210	4323200	0.0532	0.2414
chr18	78077248	8095263	0.1037	0.3363
chr19	59128983	1508178	0.0255	0.1637
chr20	63025520	3565852	0.0566	0.2466
chr21	48129895	2745288	0.057	0.2505
chr22	51304566	1149057	0.0224	0.1543
chrMT	16571	340	0.0205	0.1418
chrX	155270560	5788527	0.0373	0.1995
chrY	59373566	1095679	0.0185	0.141

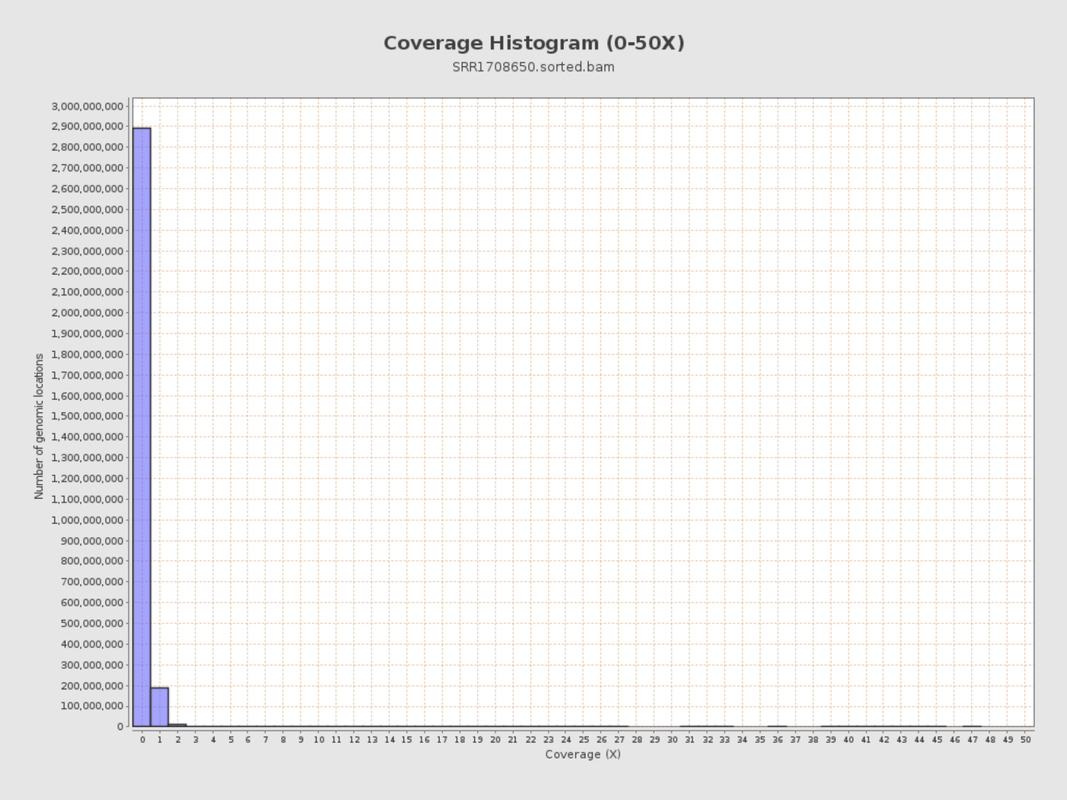
3. Results : Coverage across reference



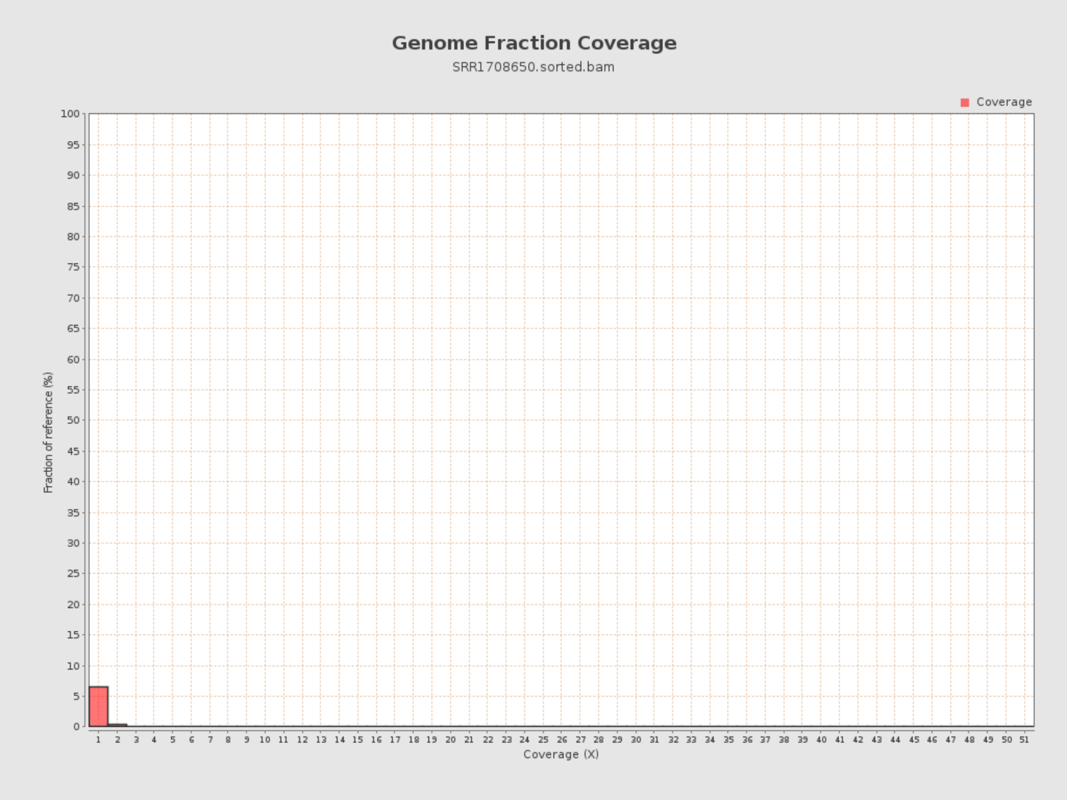
4. Results : Coverage Histogram



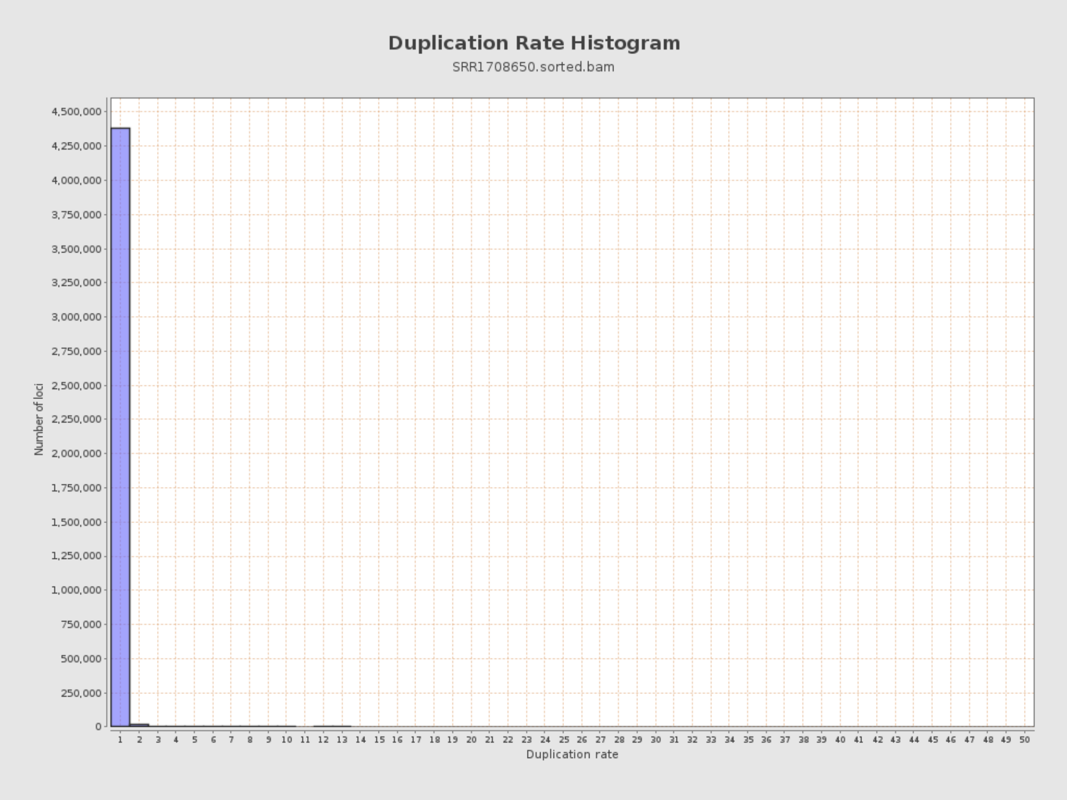
5. Results : Coverage Histogram (0-50X)



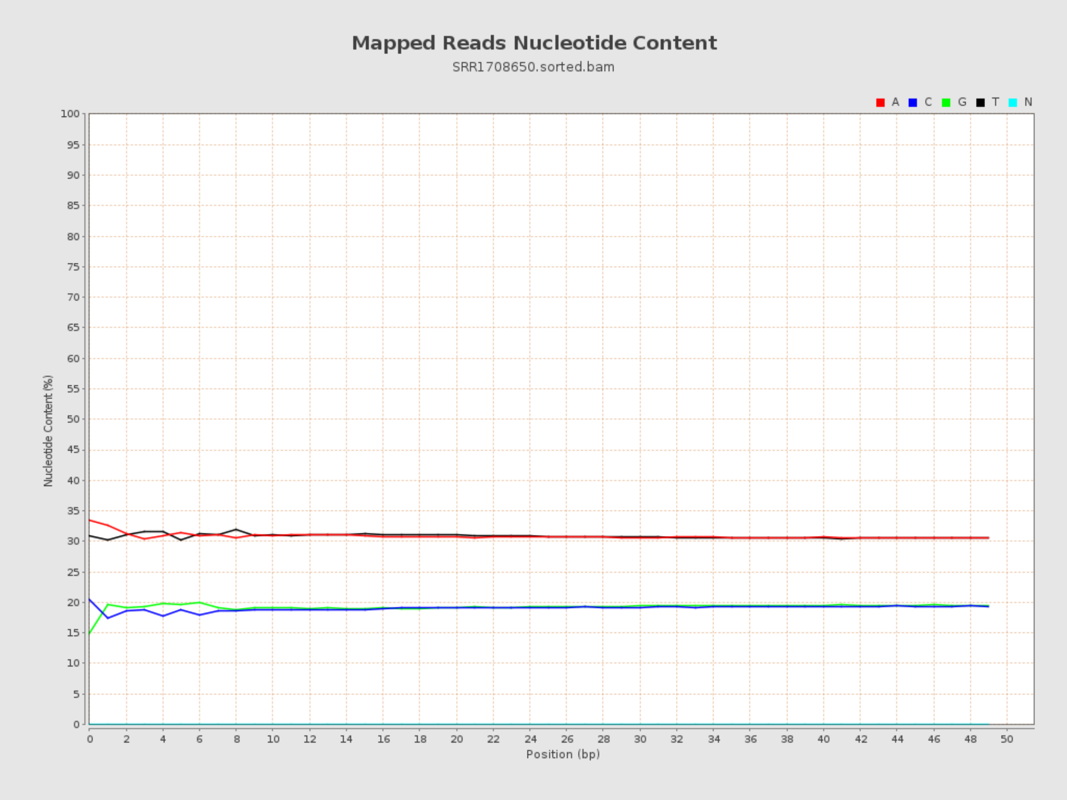
6. Results : Genome Fraction Coverage



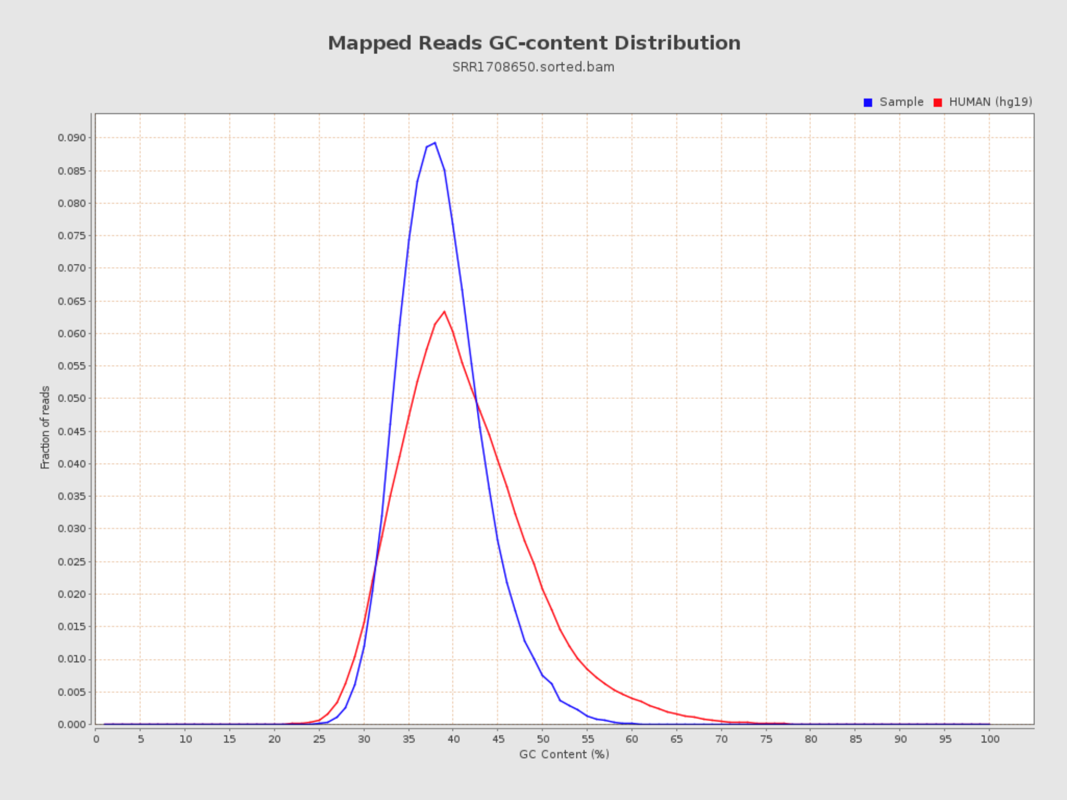
7. Results : Duplication Rate Histogram



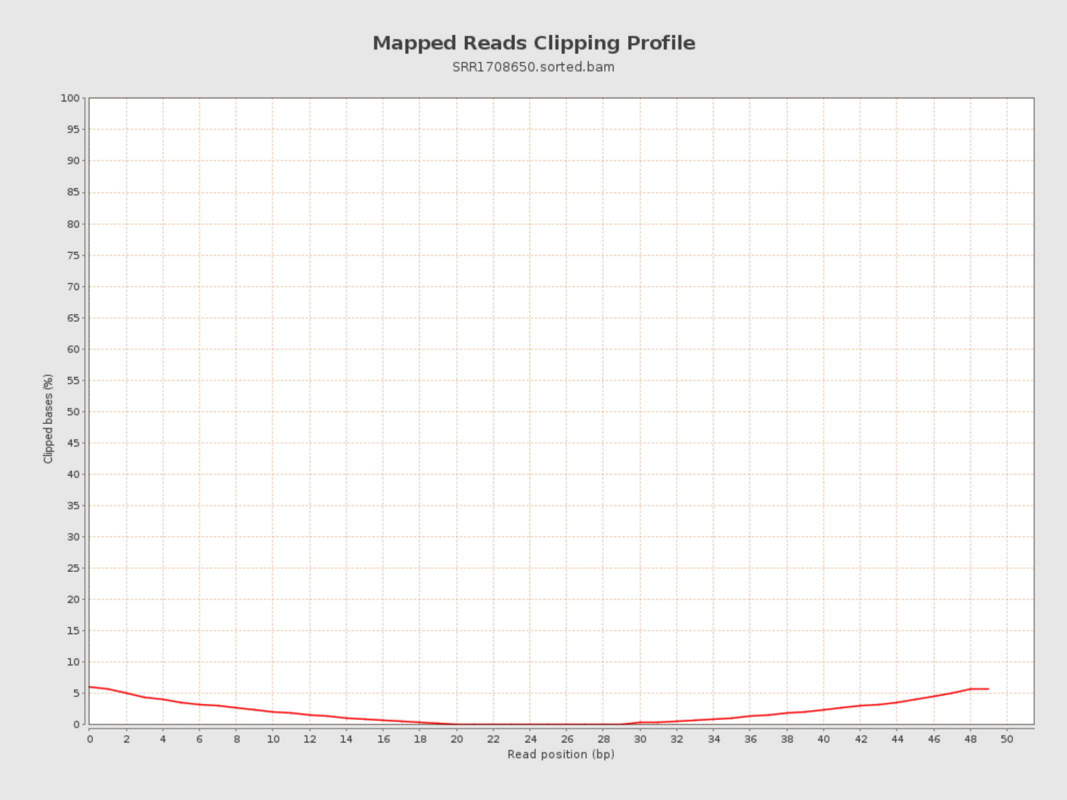
8. Results : Mapped Reads Nucleotide Content



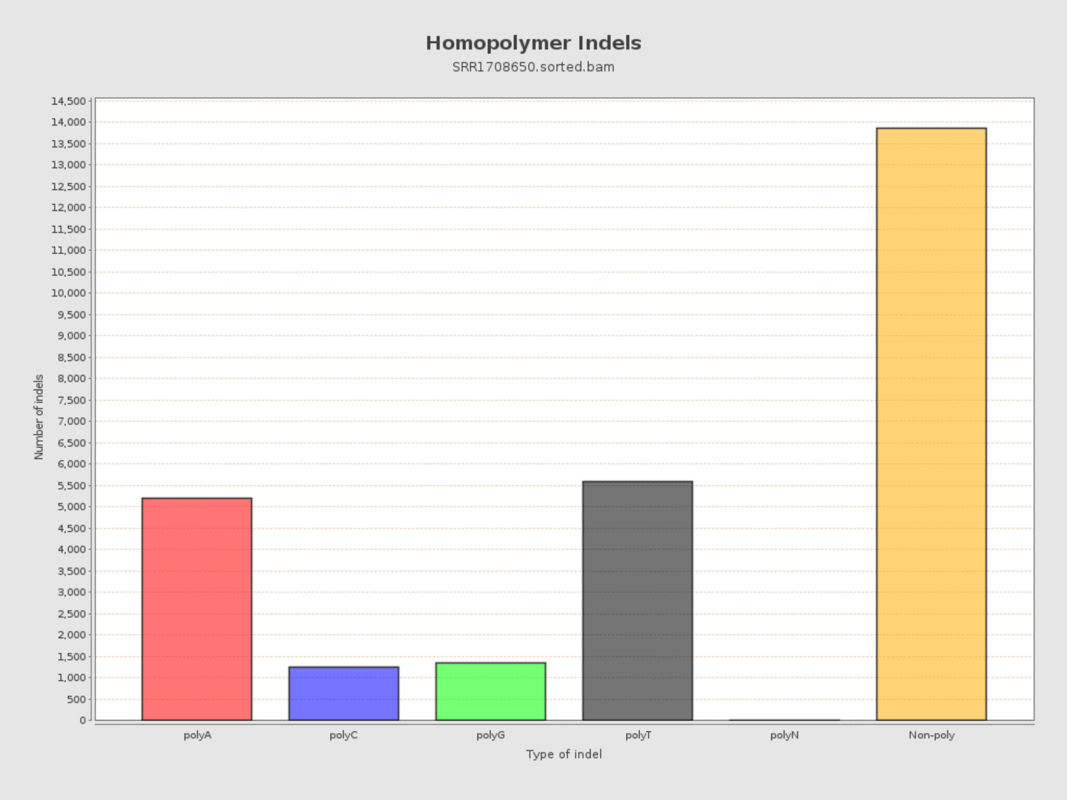
9. Results : Mapped Reads GC-content Distribution



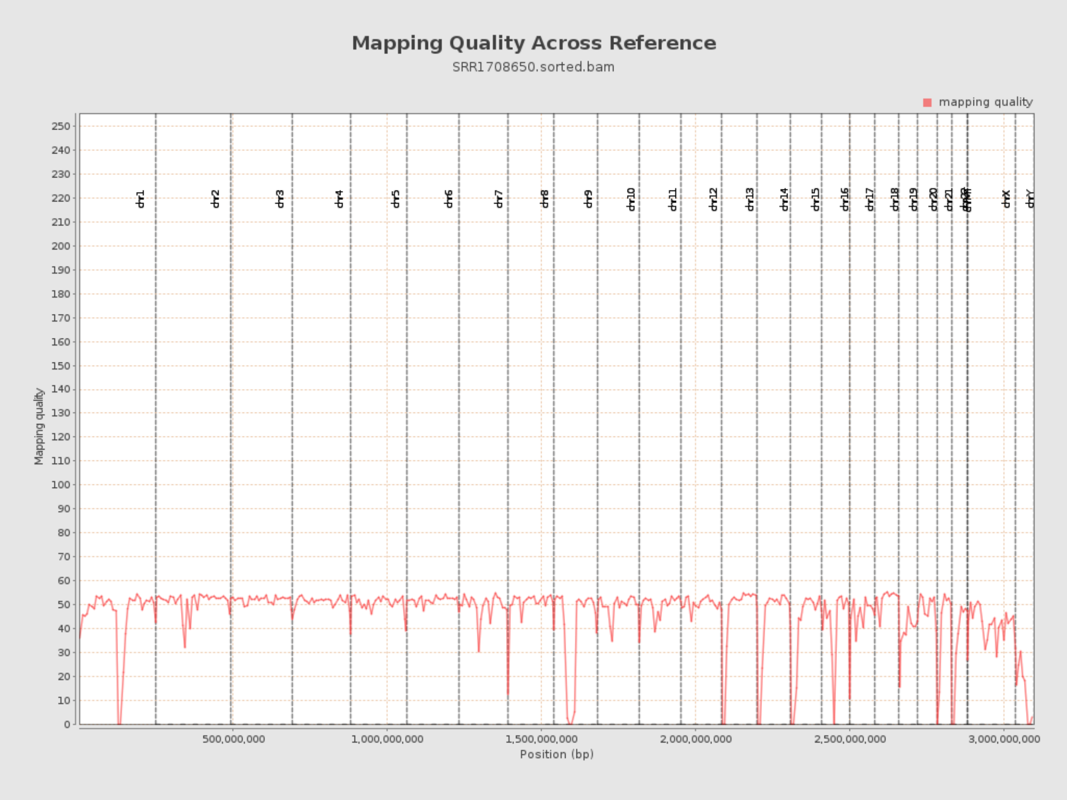
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram