Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:53:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708597.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_SRR1708597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:53:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,790,891
Mapped reads	4,668,683 / 97.45%
Unmapped reads	122,208 / 2.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	138 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	45,456 / 0.95%
Duplication rate	0.94%
Clipped reads	63,579 / 1.33%

2.2. ACGT Content

Number/percentage of A's	72,024,983 / 30.94%
Number/percentage of C's	44,244,794 / 19%
Number/percentage of T's	71,753,403 / 30.82%
Number/percentage of G's	44,786,999 / 19.24%
Number/percentage of N's	8,260 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	0.0752

Standard Deviation	0.3014

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

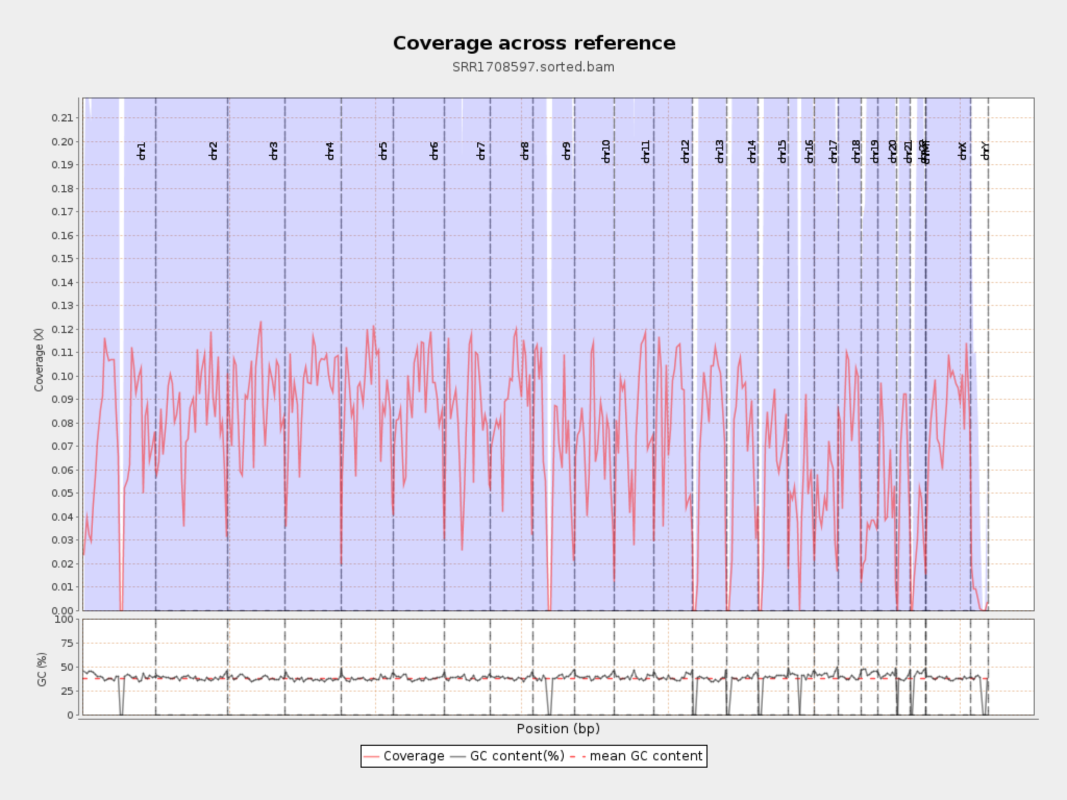
General error rate	0.15%
Mismatches	334,857
Insertions	14,459
Mapped reads with at least one insertion	0.31%
Deletions	11,671
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.54%

2.6. Chromosome stats

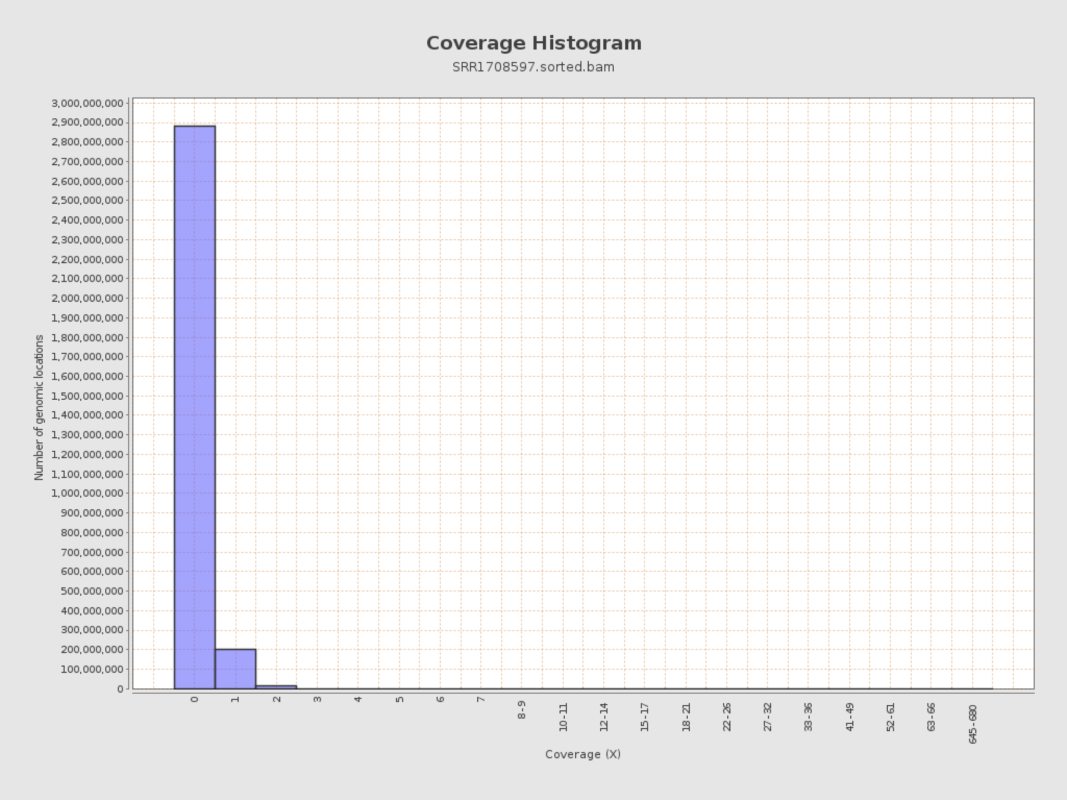
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17803191	0.0714	0.2793
chr2	243199373	20172042	0.0829	0.2979
chr3	198022430	17962526	0.0907	0.3114
chr4	191154276	18058068	0.0945	0.3172
chr5	180915260	16261594	0.0899	0.3098
chr6	171115067	15514859	0.0907	0.3113
chr7	159138663	12985174	0.0816	0.2965

chr8	146364022	12986510	0.0887	0.3081
chr9	141213431	9670824	0.0685	0.2723
chr10	135534747	9936507	0.0733	0.2798
chr11	135006516	10691429	0.0792	0.555
chr12	133851895	10897000	0.0814	0.2958
chr13	115169878	8718417	0.0757	0.2855
chr14	107349540	7164777	0.0667	0.2689
chr15	102531392	6103978	0.0595	0.2537
chr16	90354753	4164143	0.0461	0.2223
chr17	81195210	3807193	0.0469	0.2249
chr18	78077248	6633085	0.085	0.301
chr19	59128983	1868883	0.0316	0.1832
chr20	63025520	3593621	0.057	0.2477
chr21	48129895	2810775	0.0584	0.253
chr22	51304566	1375725	0.0268	0.1696
chrMT	16571	450	0.0272	0.1716
chrX	155270560	13347712	0.086	0.3034
chrY	59373566	309838	0.0052	0.0757

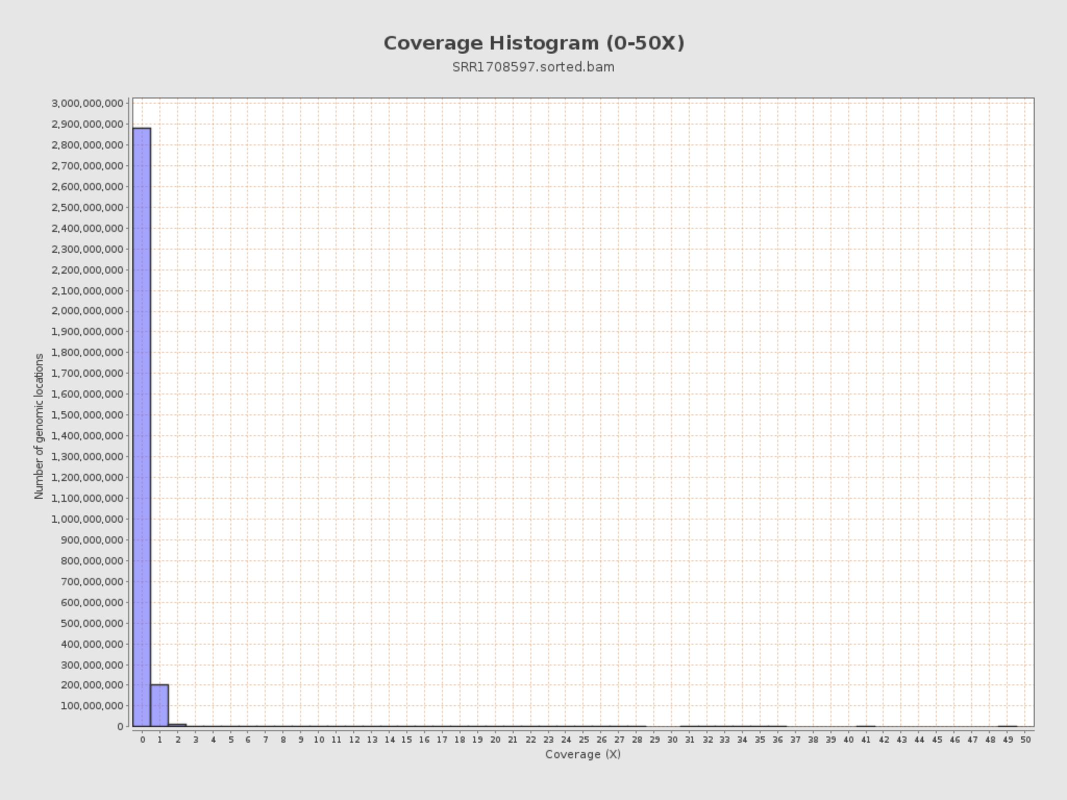
3. Results : Coverage across reference



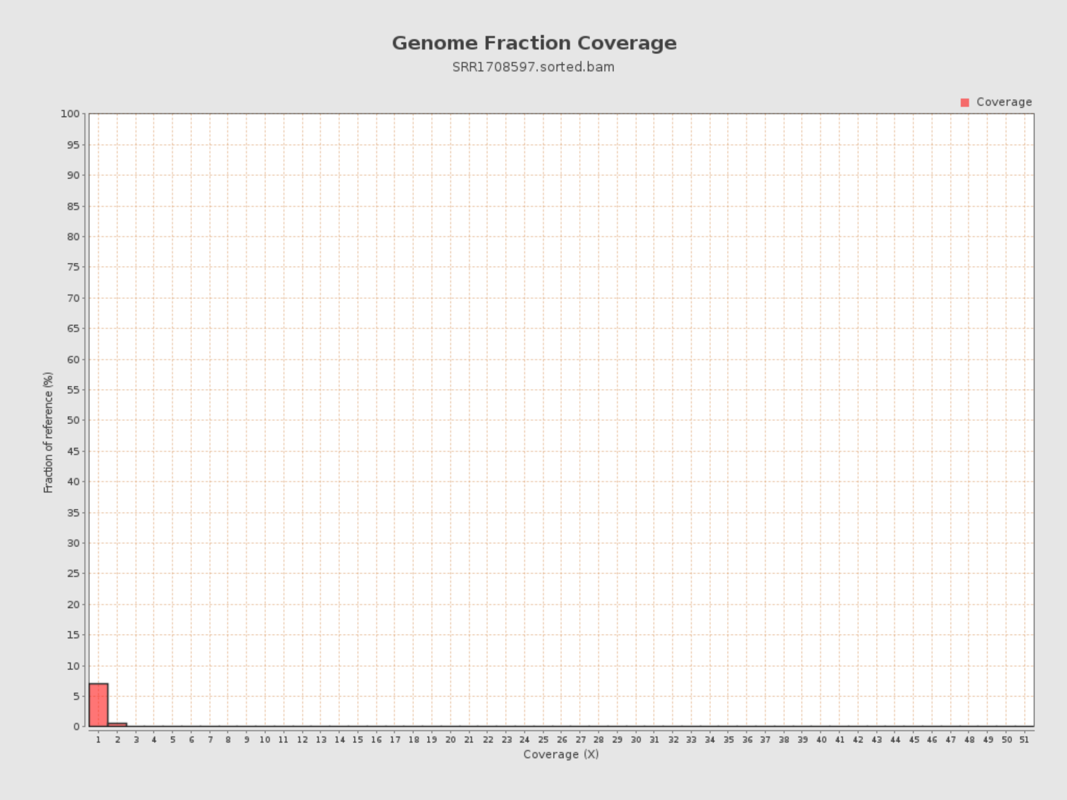
4. Results : Coverage Histogram



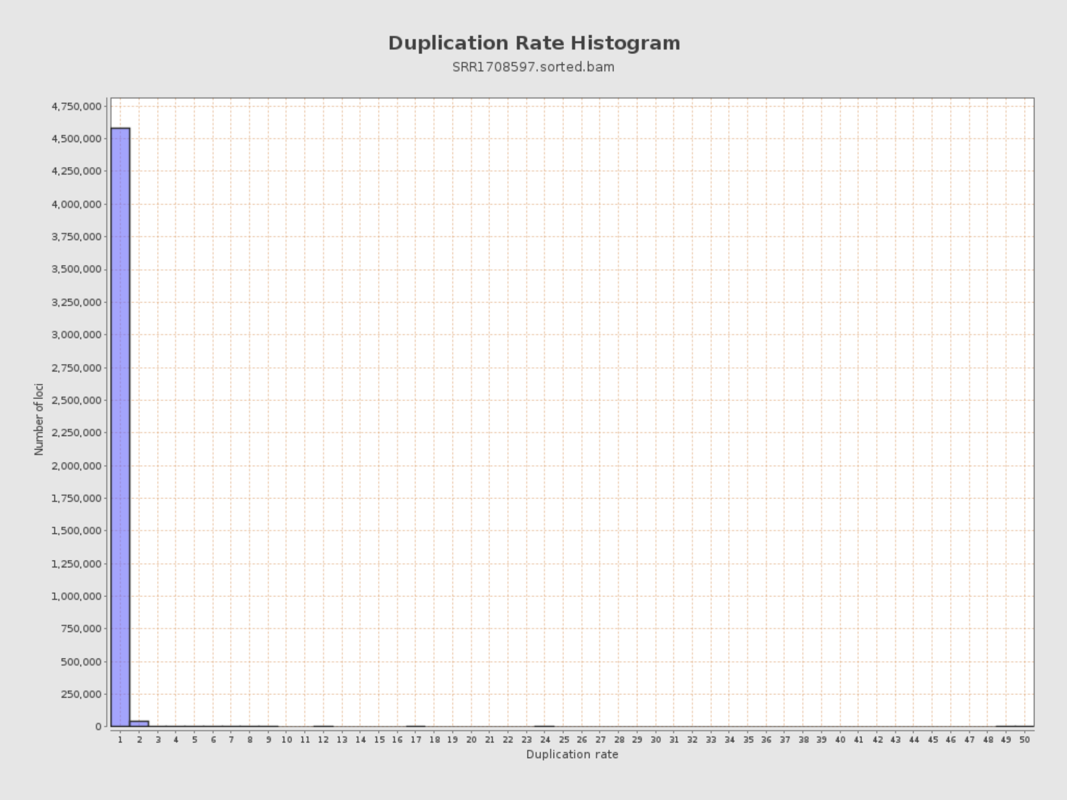
5. Results : Coverage Histogram (0-50X)



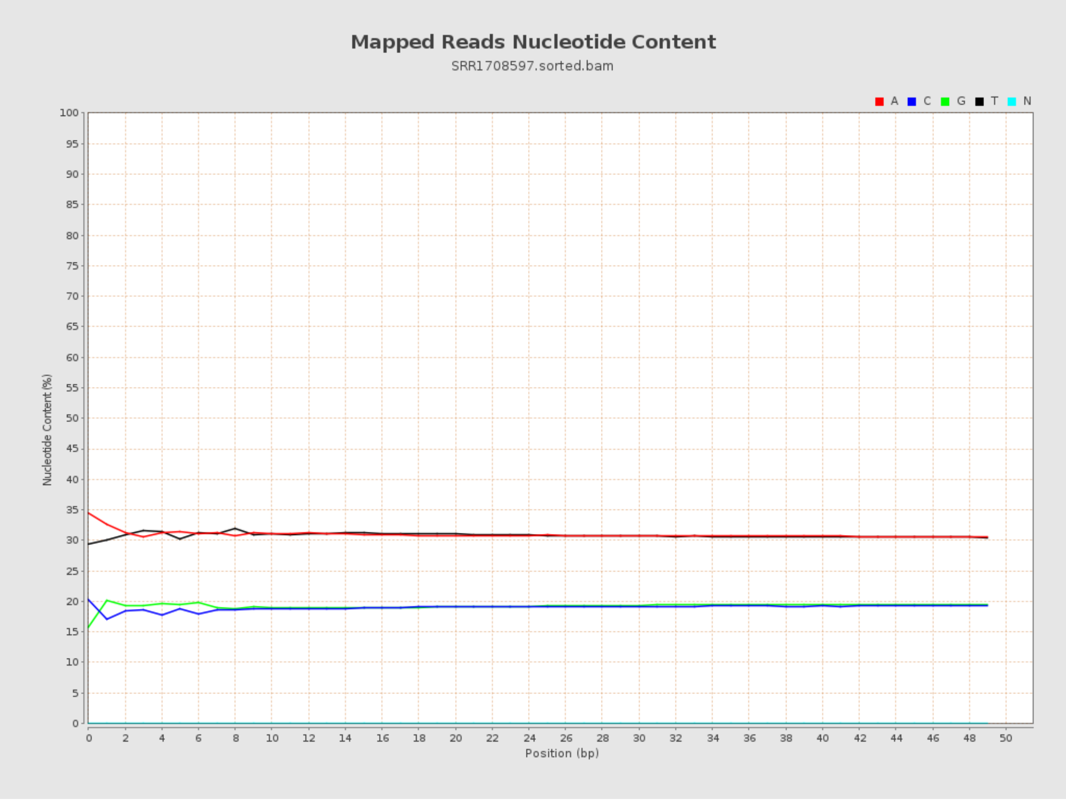
6. Results : Genome Fraction Coverage



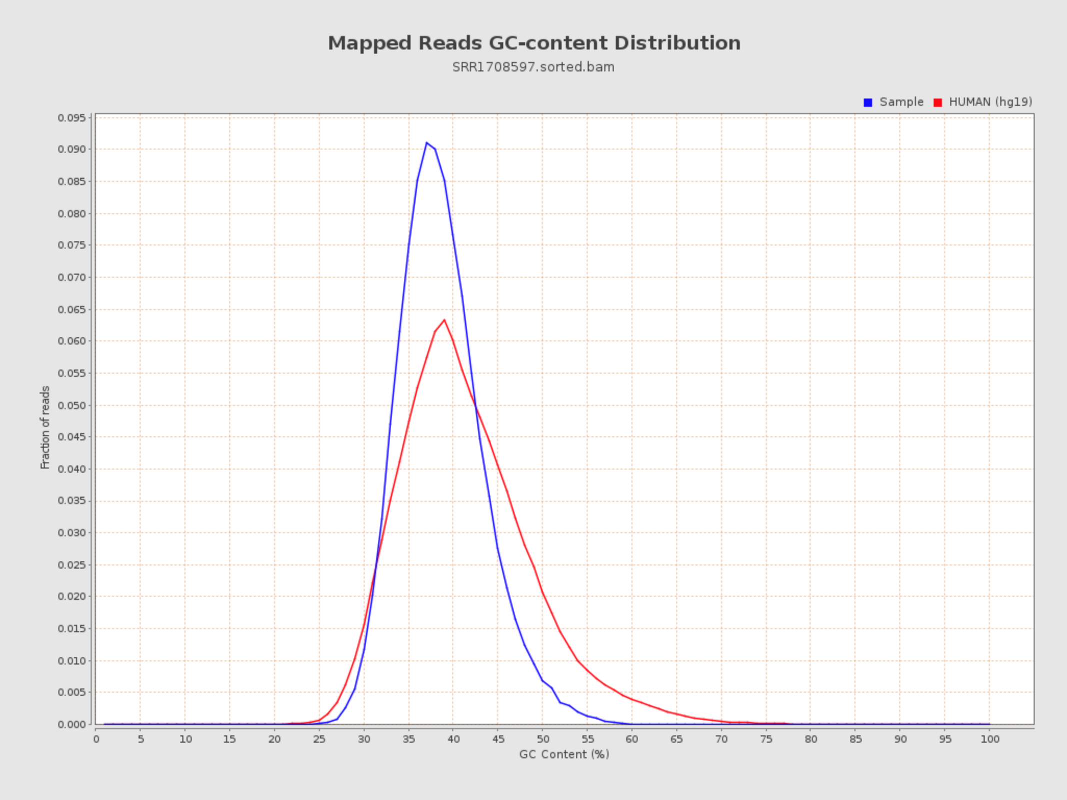
7. Results : Duplication Rate Histogram



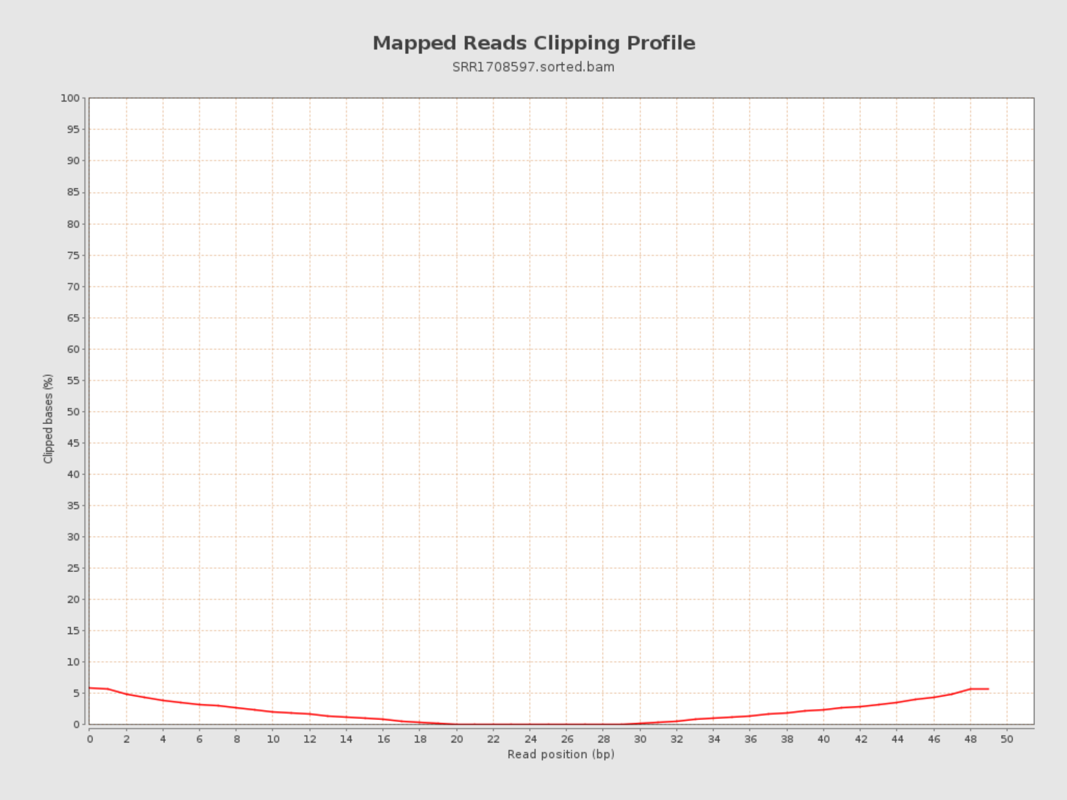
8. Results : Mapped Reads Nucleotide Content



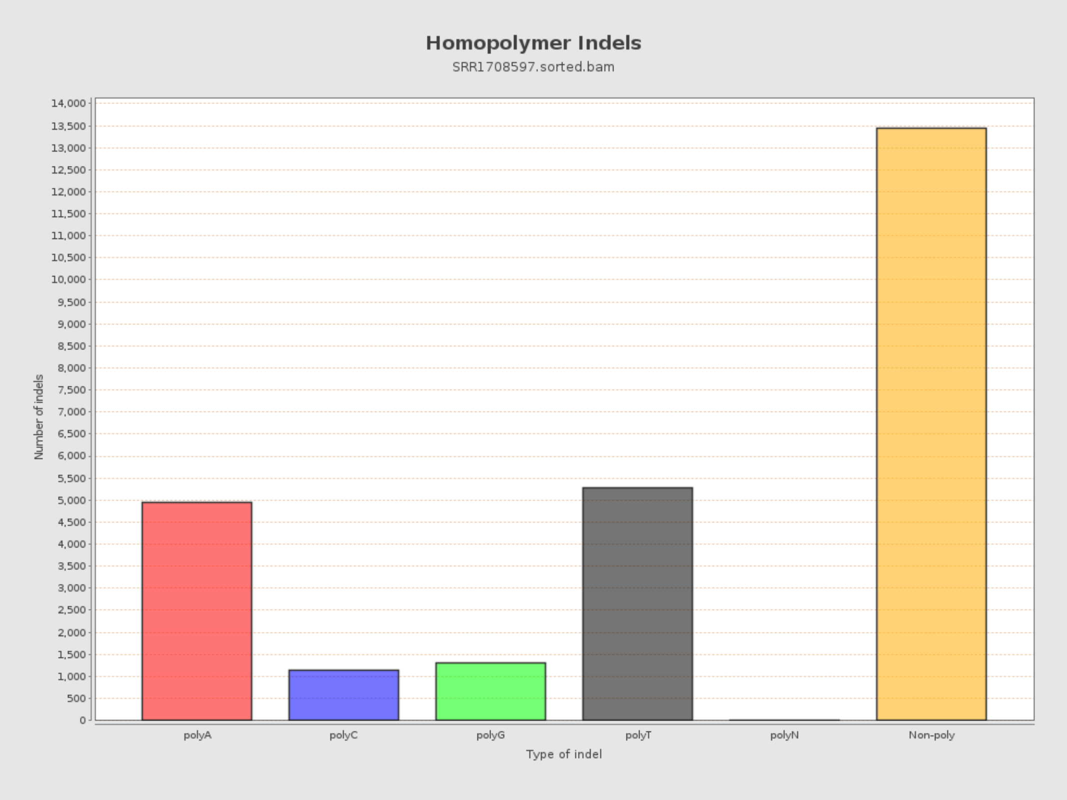
9. Results : Mapped Reads GC-content Distribution



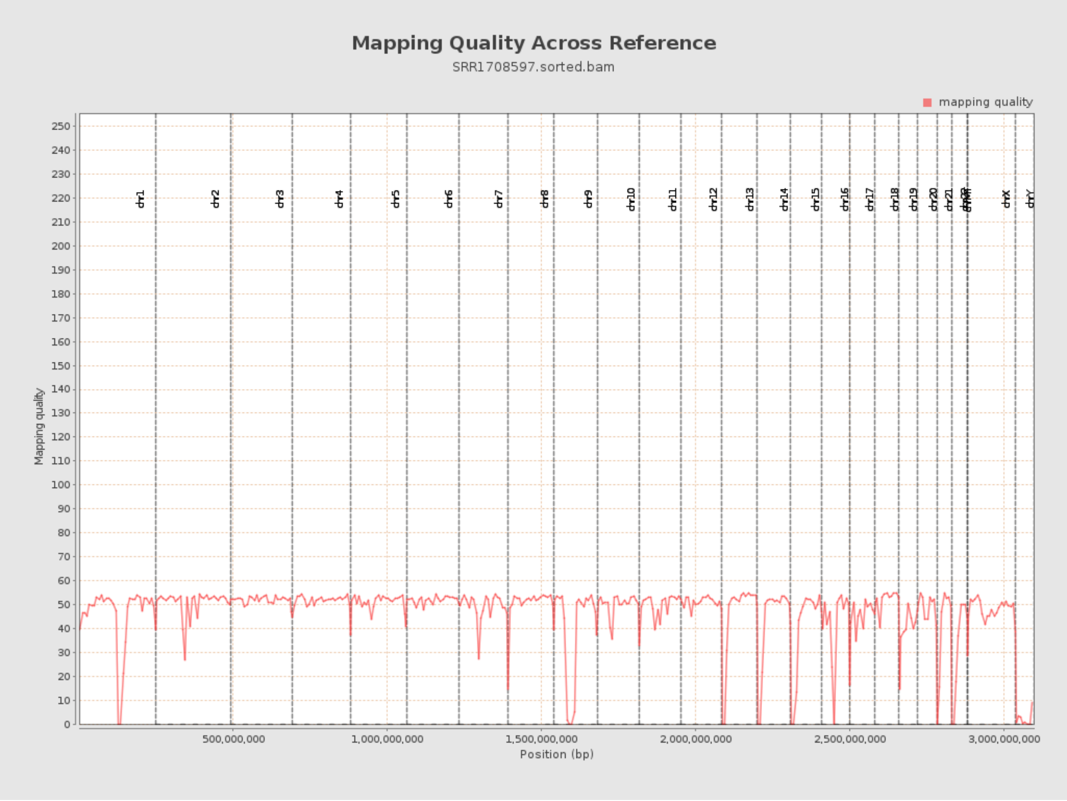
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram