Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:10:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708647.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_SRR1708647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708647.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:10:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,530,321
Mapped reads	4,395,064 / 97.01%
Unmapped reads	135,257 / 2.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	118 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	22,555 / 0.5%
Duplication rate	0.51%
Clipped reads	58,155 / 1.28%

2.2. ACGT Content

Number/percentage of A's	67,795,941 / 30.93%
Number/percentage of C's	41,646,625 / 19%
Number/percentage of T's	67,713,489 / 30.89%
Number/percentage of G's	42,035,234 / 19.18%
Number/percentage of N's	7,361 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	0.0708

Standard Deviation	0.2815

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

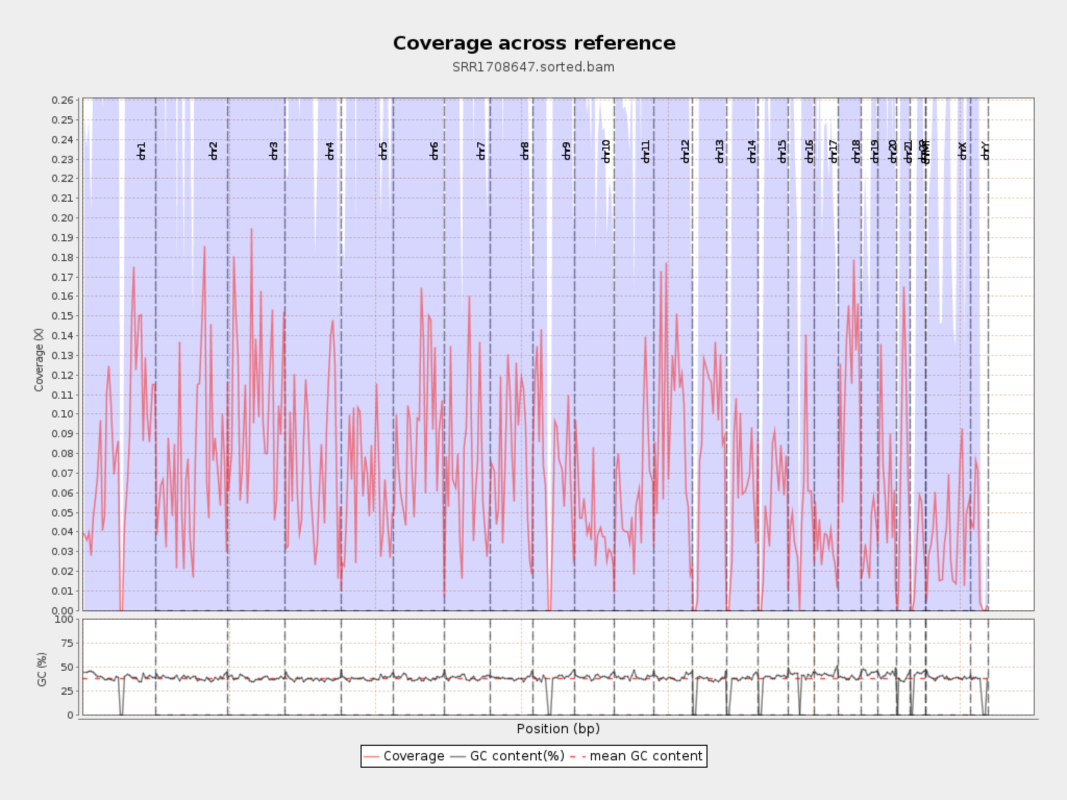
General error rate	0.17%
Mismatches	353,276
Insertions	14,915
Mapped reads with at least one insertion	0.34%
Deletions	12,380
Mapped reads with at least one deletion	0.28%
Homopolymer indels	49.16%

2.6. Chromosome stats

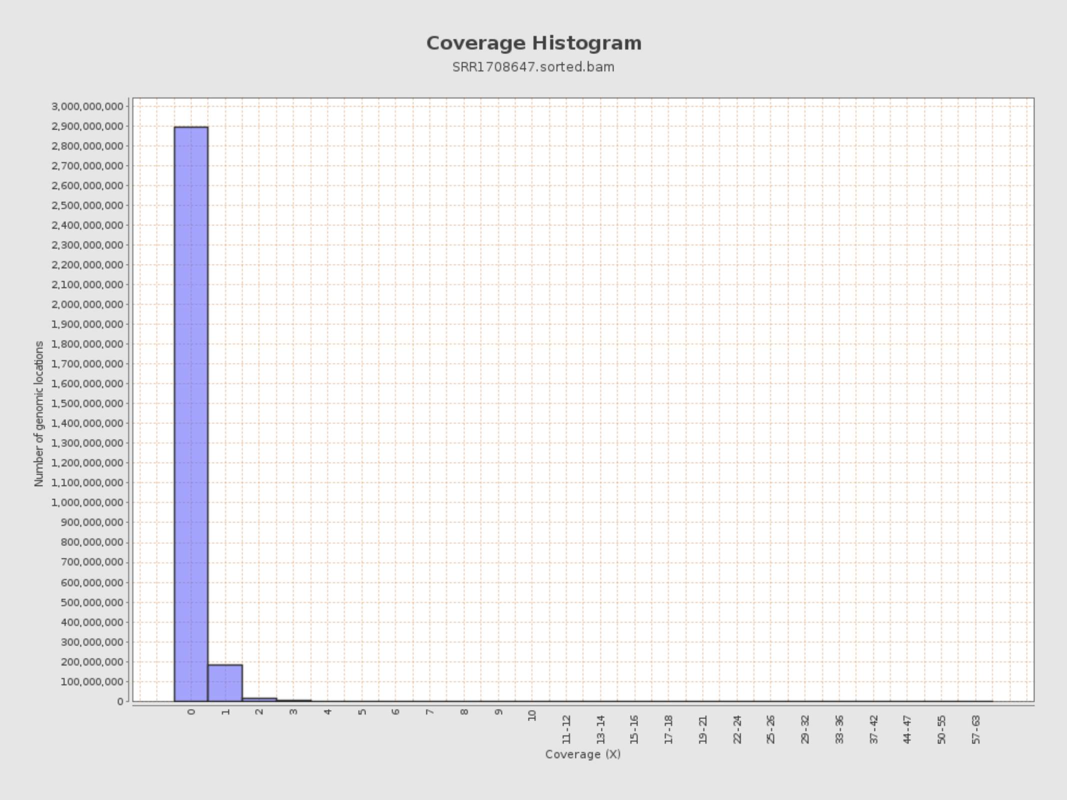
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20672497	0.0829	0.3063
chr2	243199373	18090149	0.0744	0.2869
chr3	198022430	21008418	0.1061	0.3448
chr4	191154276	14094248	0.0737	0.2861
chr5	180915260	11224222	0.062	0.2607
chr6	171115067	15814323	0.0924	0.3202
chr7	159138663	11130166	0.0699	0.2785

chr8	146364022	11431493	0.0781	0.2945
chr9	141213431	10456682	0.074	0.2868
chr10	135534747	6138602	0.0453	0.2222
chr11	135006516	8291275	0.0614	0.2635
chr12	133851895	12998406	0.0971	0.3306
chr13	115169878	10025231	0.087	0.3115
chr14	107349540	6433194	0.0599	0.2568
chr15	102531392	5451344	0.0532	0.2439
chr16	90354753	4442375	0.0492	0.2323
chr17	81195210	2814539	0.0347	0.1939
chr18	78077248	9601343	0.123	0.3699
chr19	59128983	2011026	0.034	0.1913
chr20	63025520	4222679	0.067	0.2717
chr21	48129895	3529245	0.0733	0.2881
chr22	51304566	1515012	0.0295	0.1798
chrMT	16571	150	0.0091	0.1225
chrX	155270560	6066460	0.0391	0.2072
chrY	59373566	1756842	0.0296	0.1805

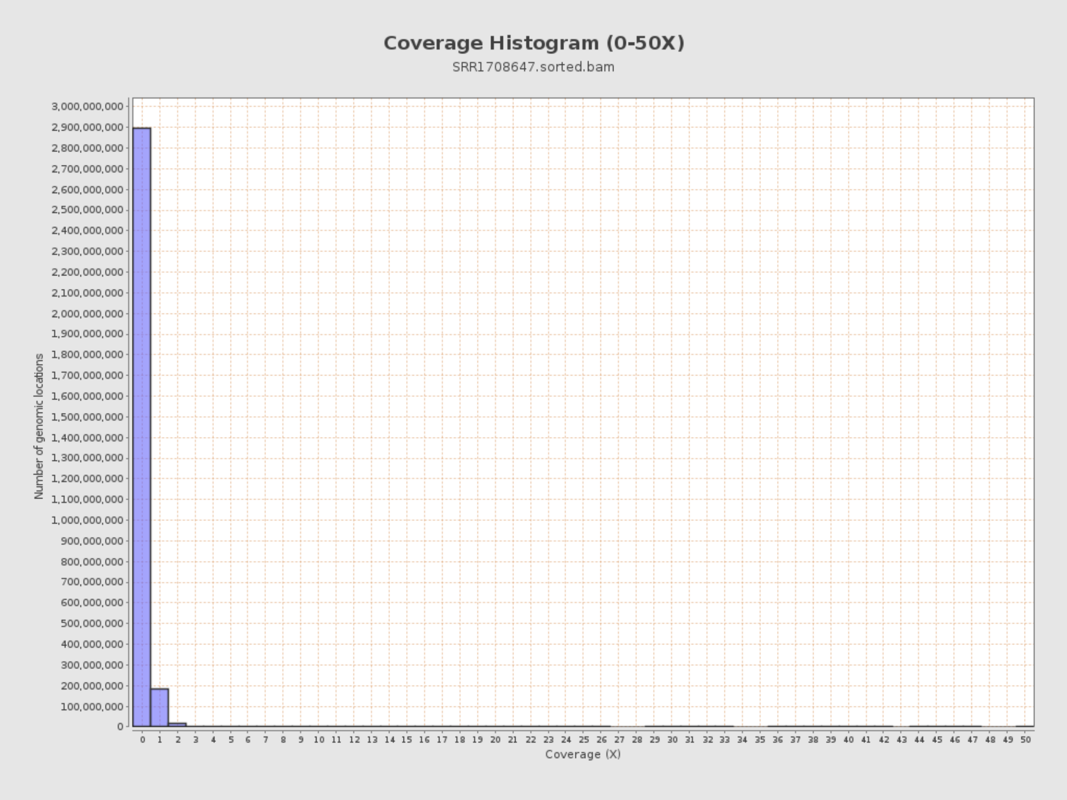
3. Results : Coverage across reference



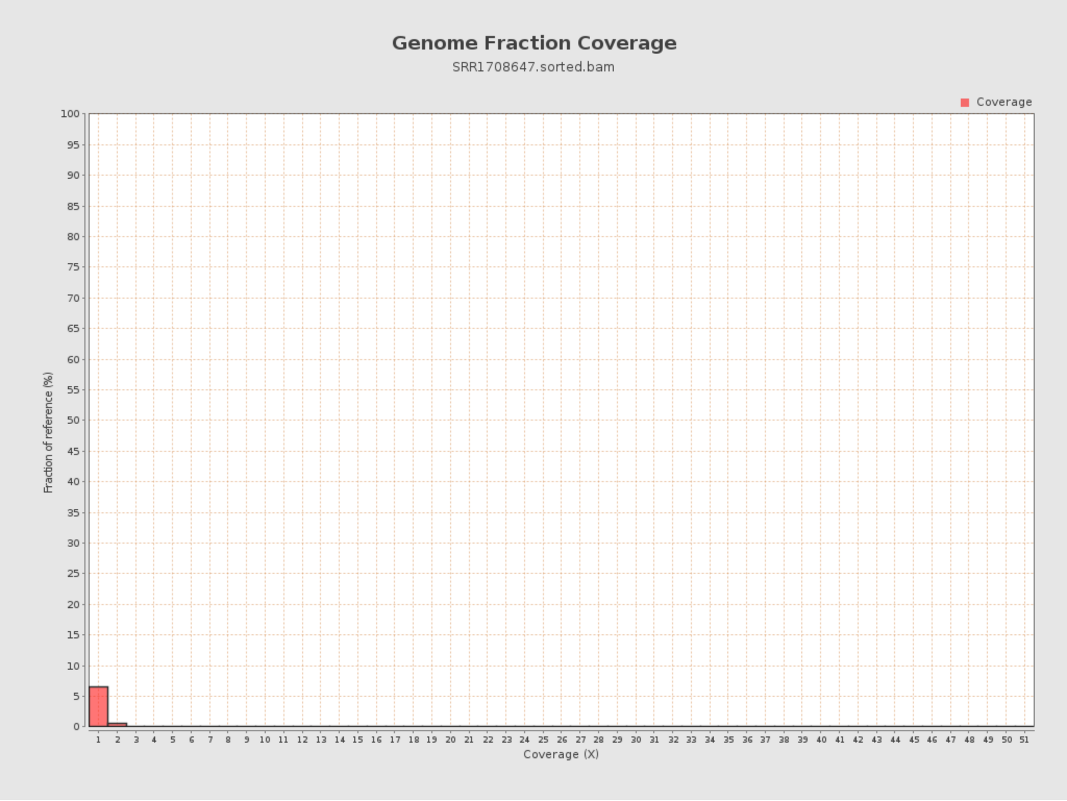
4. Results : Coverage Histogram



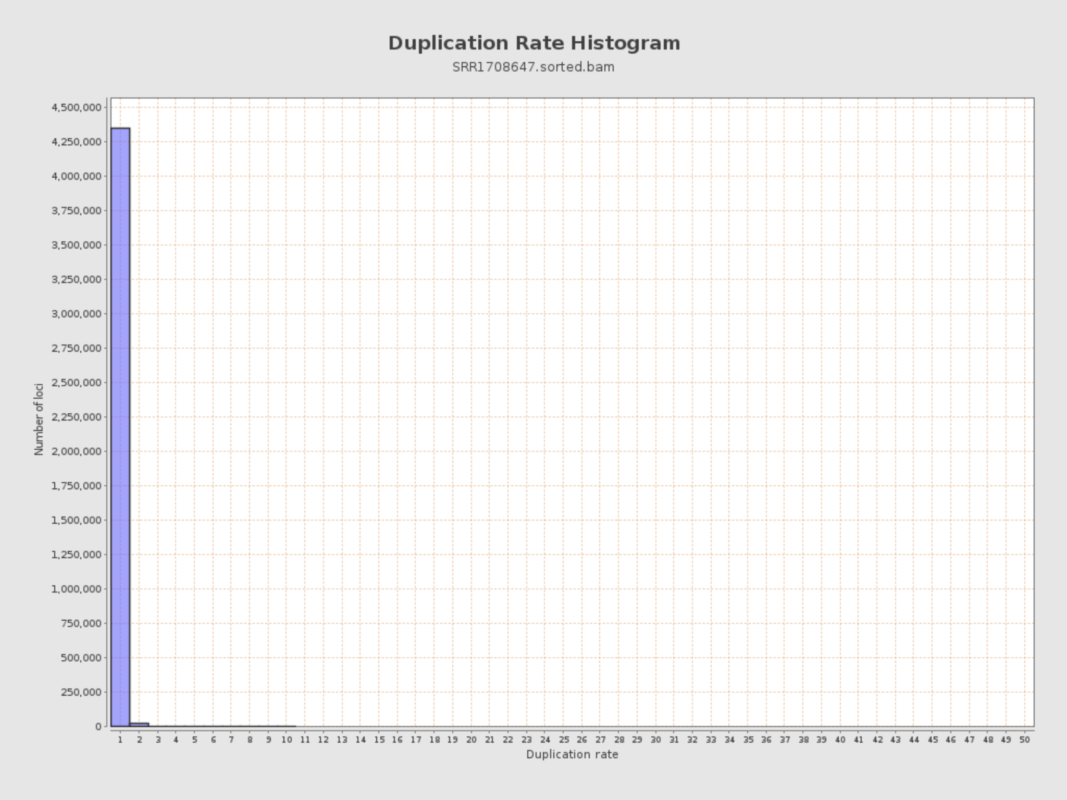
5. Results : Coverage Histogram (0-50X)



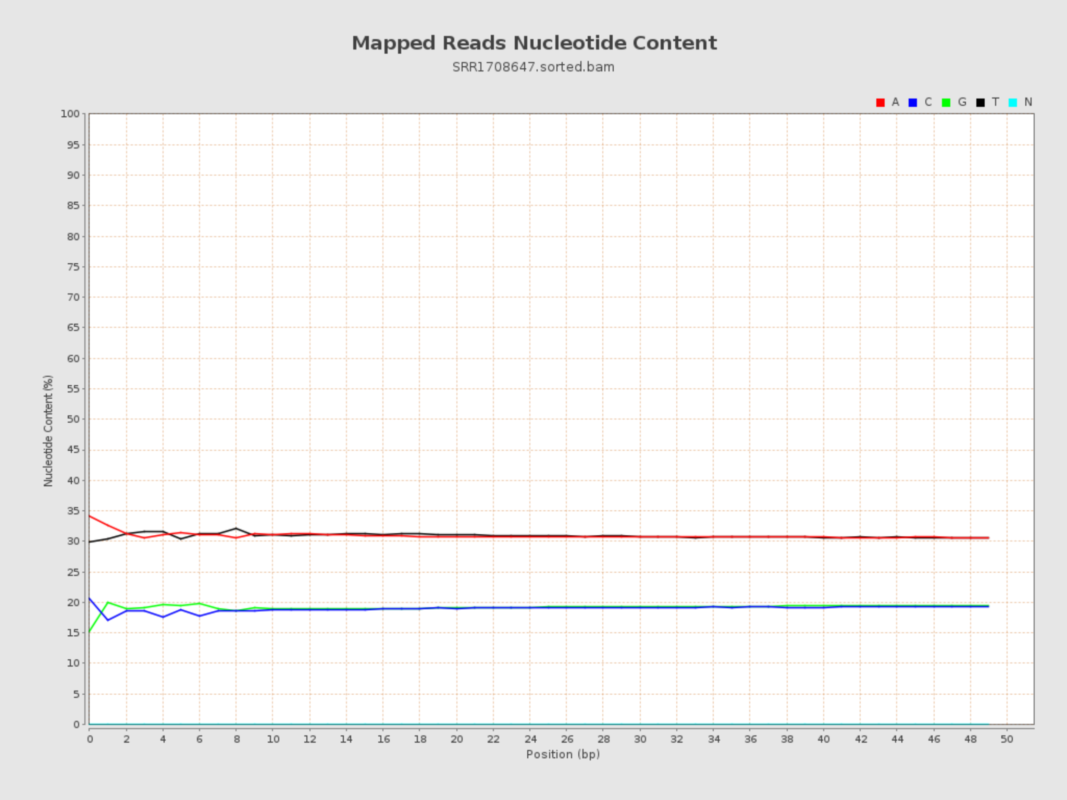
6. Results : Genome Fraction Coverage



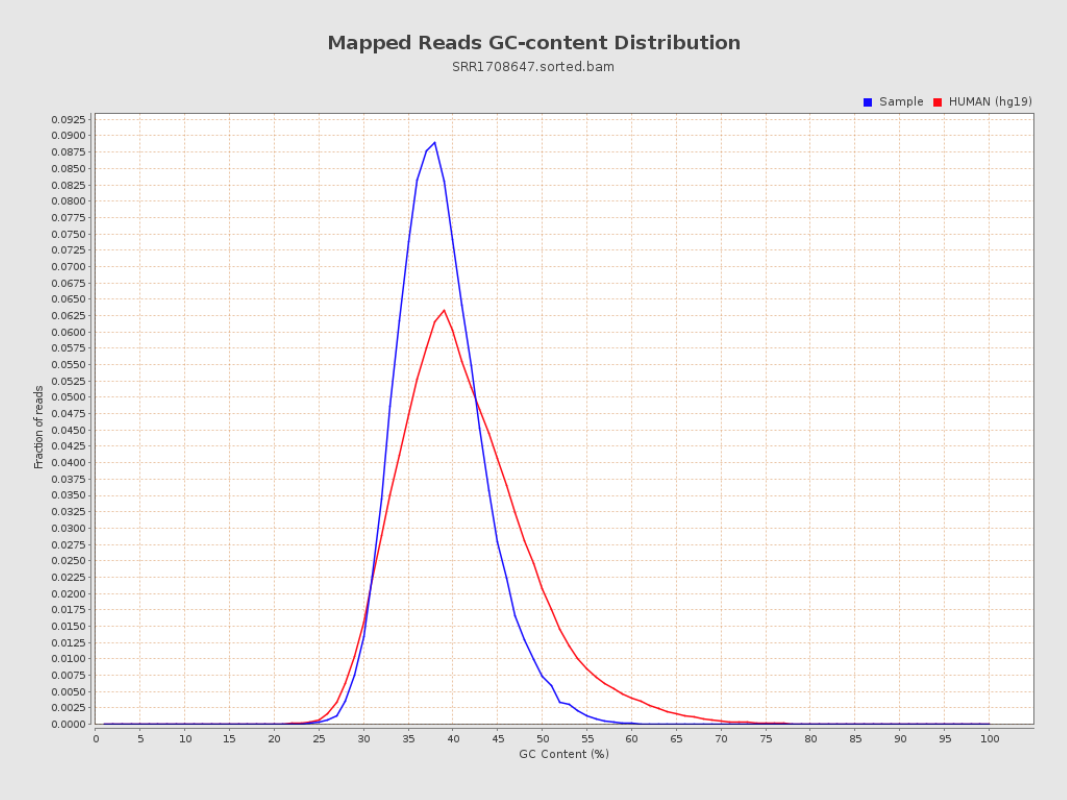
7. Results : Duplication Rate Histogram



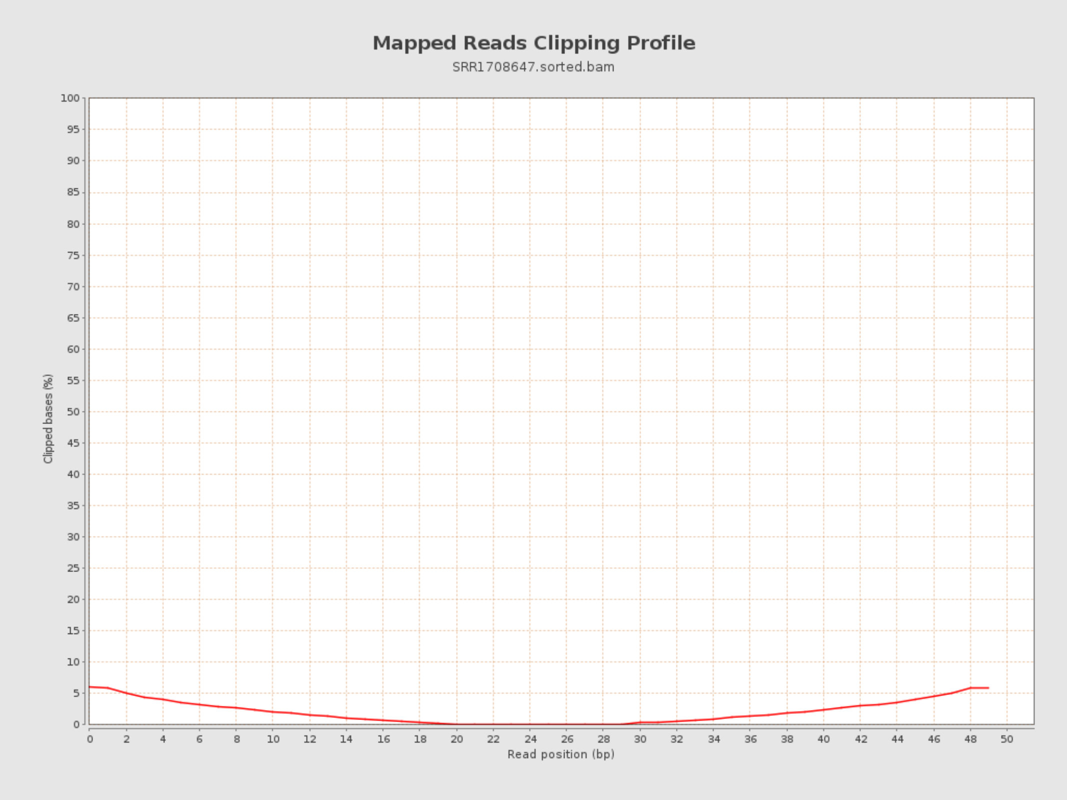
8. Results : Mapped Reads Nucleotide Content



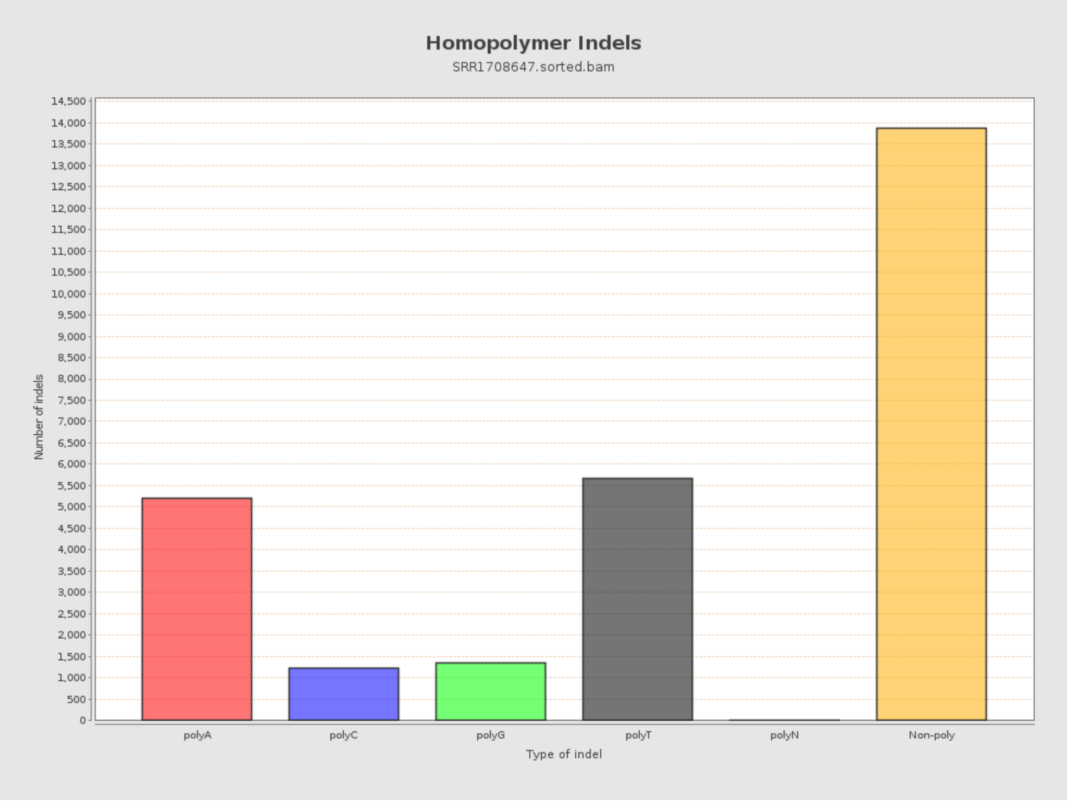
9. Results : Mapped Reads GC-content Distribution



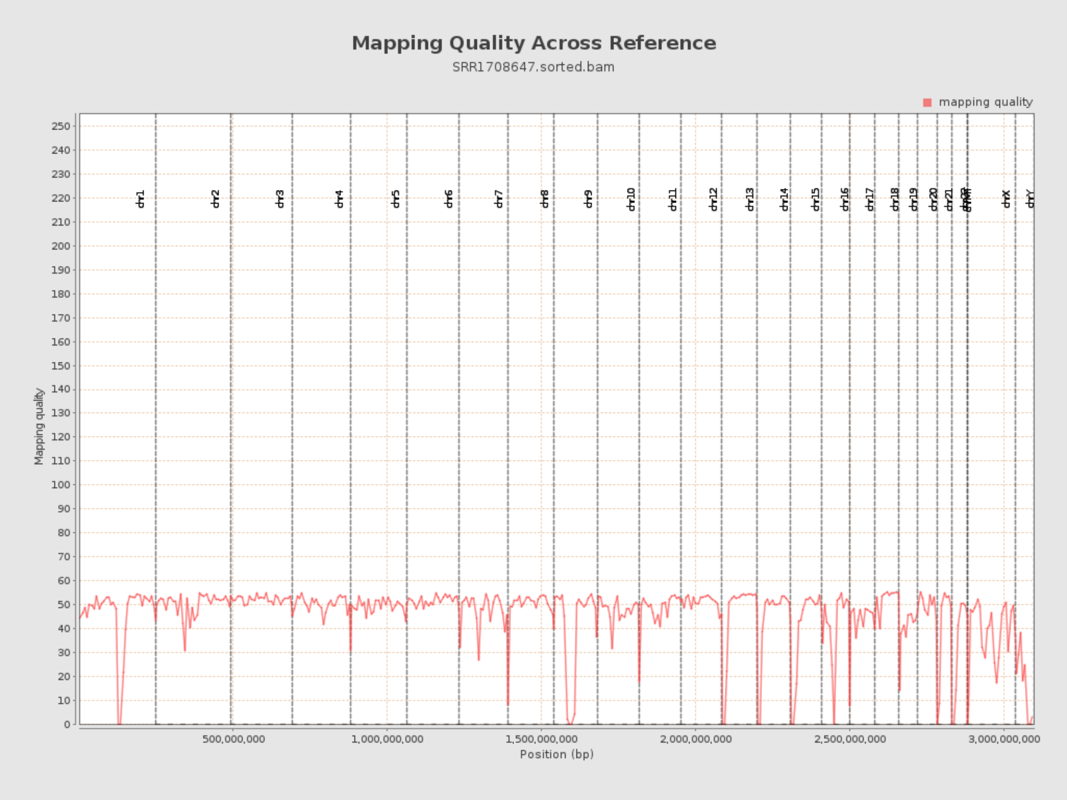
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram