Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:47:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708540.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_SRR1708540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:47:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,013,773
Mapped reads	23,167,785 / 96.48%
Unmapped reads	845,988 / 3.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	523 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	213,431 / 0.89%
Duplication rate	0.91%
Clipped reads	371,745 / 1.55%

2.2. ACGT Content

Number/percentage of A's	361,141,186 / 31.26%
Number/percentage of C's	215,257,403 / 18.63%
Number/percentage of T's	359,309,278 / 31.1%
Number/percentage of G's	219,055,032 / 18.96%
Number/percentage of N's	459,805 / 0.04%
GC Percentage	37.6%

2.3. Coverage

Mean	0.3732

Standard Deviation	0.6829

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

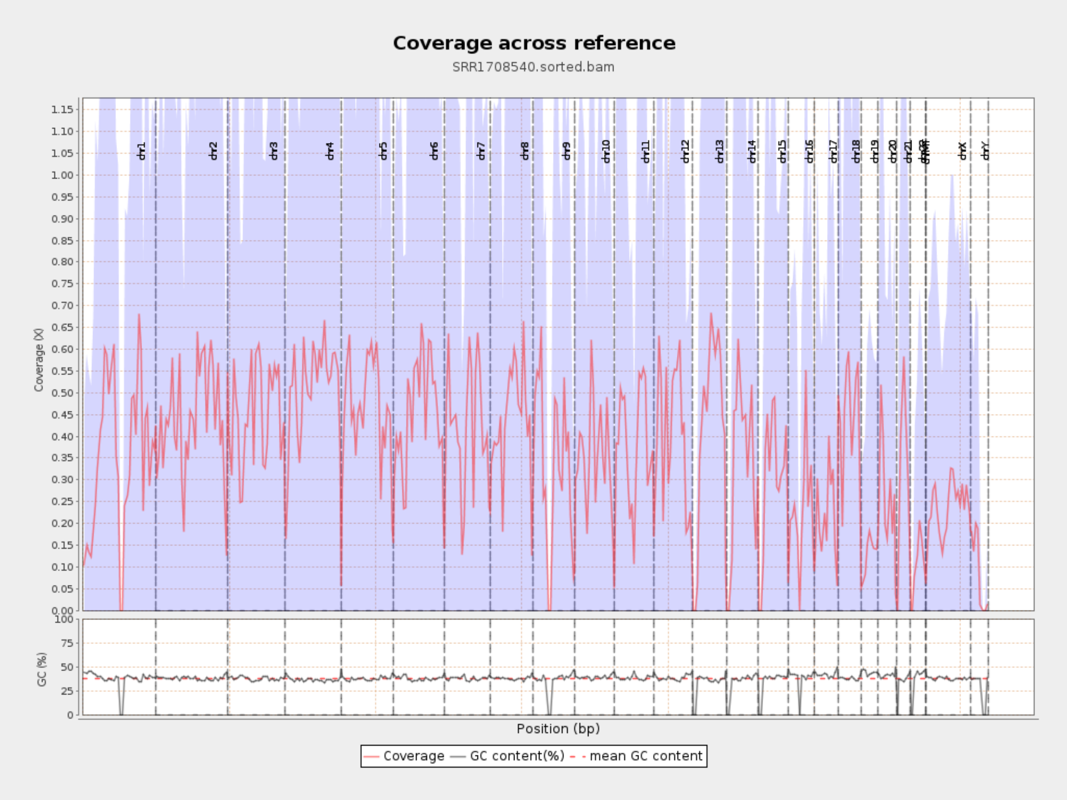
General error rate	0.35%
Mismatches	3,986,038
Insertions	64,178
Mapped reads with at least one insertion	0.28%
Deletions	61,421
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.25%

2.6. Chromosome stats

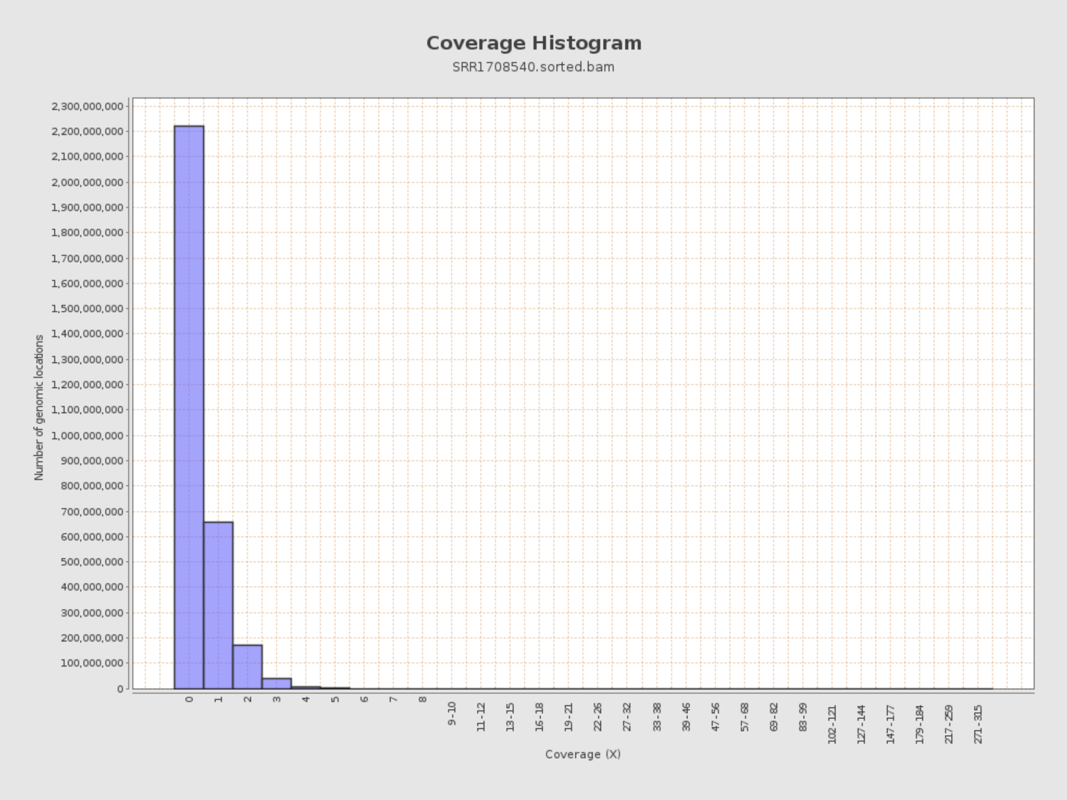
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88100960	0.3535	0.6792
chr2	243199373	107046360	0.4402	0.7259
chr3	198022430	89873988	0.4539	0.732
chr4	191154276	97892967	0.5121	0.7763
chr5	180915260	83315221	0.4605	0.7392
chr6	171115067	78794654	0.4605	0.7427
chr7	159138663	66428800	0.4174	0.7182

chr8	146364022	64609048	0.4414	0.7262
chr9	141213431	47962950	0.3396	0.6588
chr10	135534747	48939331	0.3611	0.6563
chr11	135006516	51300285	0.38	0.6932
chr12	133851895	53427986	0.3992	0.7028
chr13	115169878	49473102	0.4296	0.7346
chr14	107349540	36811246	0.3429	0.6619
chr15	102531392	30631772	0.2988	0.621
chr16	90354753	20273104	0.2244	0.5299
chr17	81195210	17934196	0.2209	0.5336
chr18	78077248	35140024	0.4501	0.734
chr19	59128983	7716973	0.1305	0.3939
chr20	63025520	17147488	0.2721	0.5841
chr21	48129895	15007335	0.3118	0.6545
chr22	51304566	5532741	0.1078	0.3651
chrMT	16571	1027	0.062	0.249
chrX	155270560	36752093	0.2367	0.5128
chrY	59373566	5210930	0.0878	0.3337

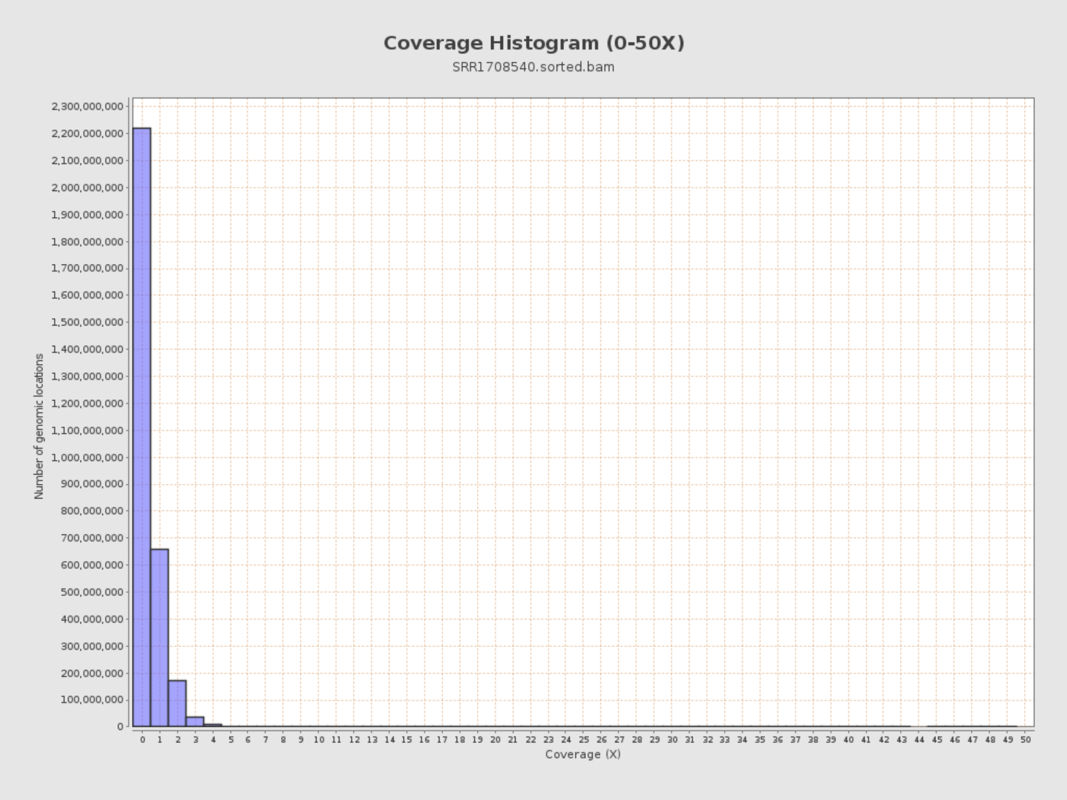
3. Results : Coverage across reference



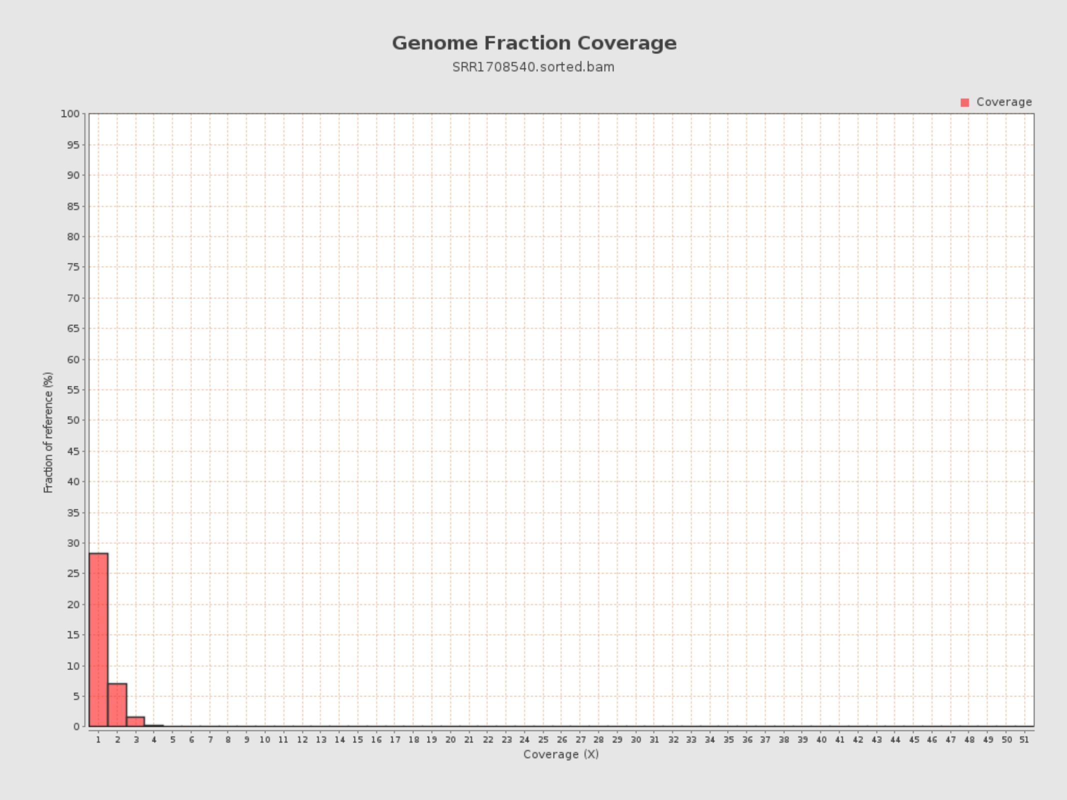
4. Results : Coverage Histogram



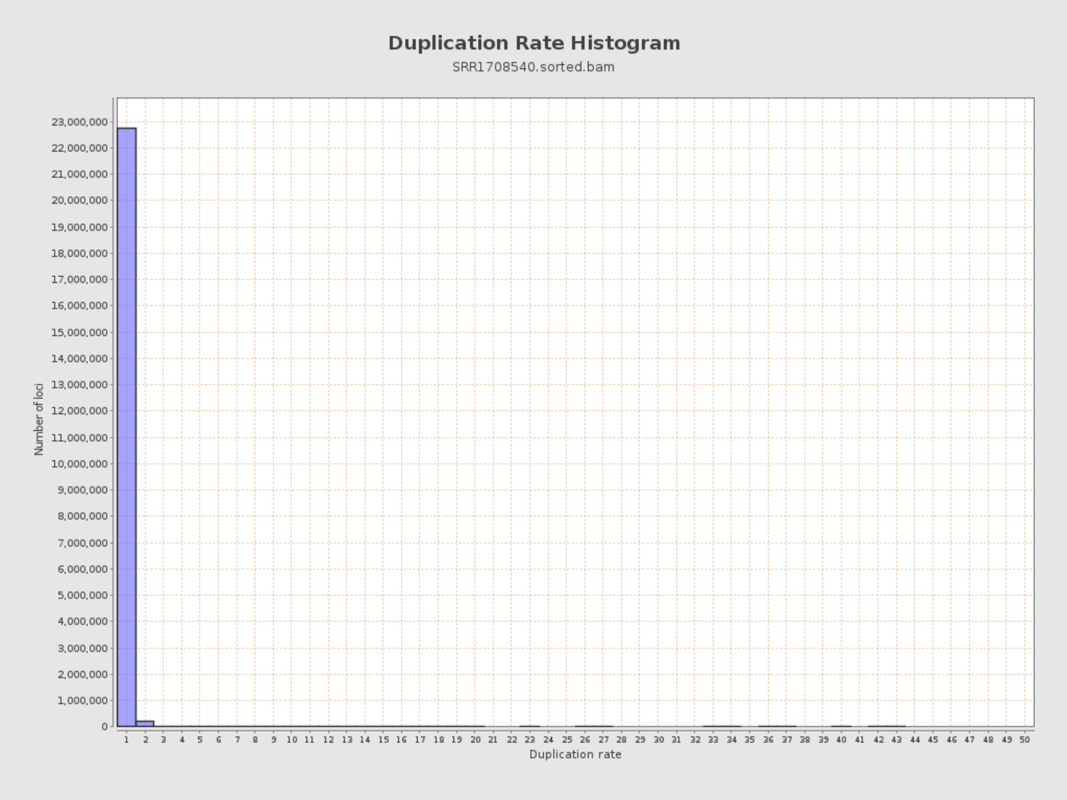
5. Results : Coverage Histogram (0-50X)



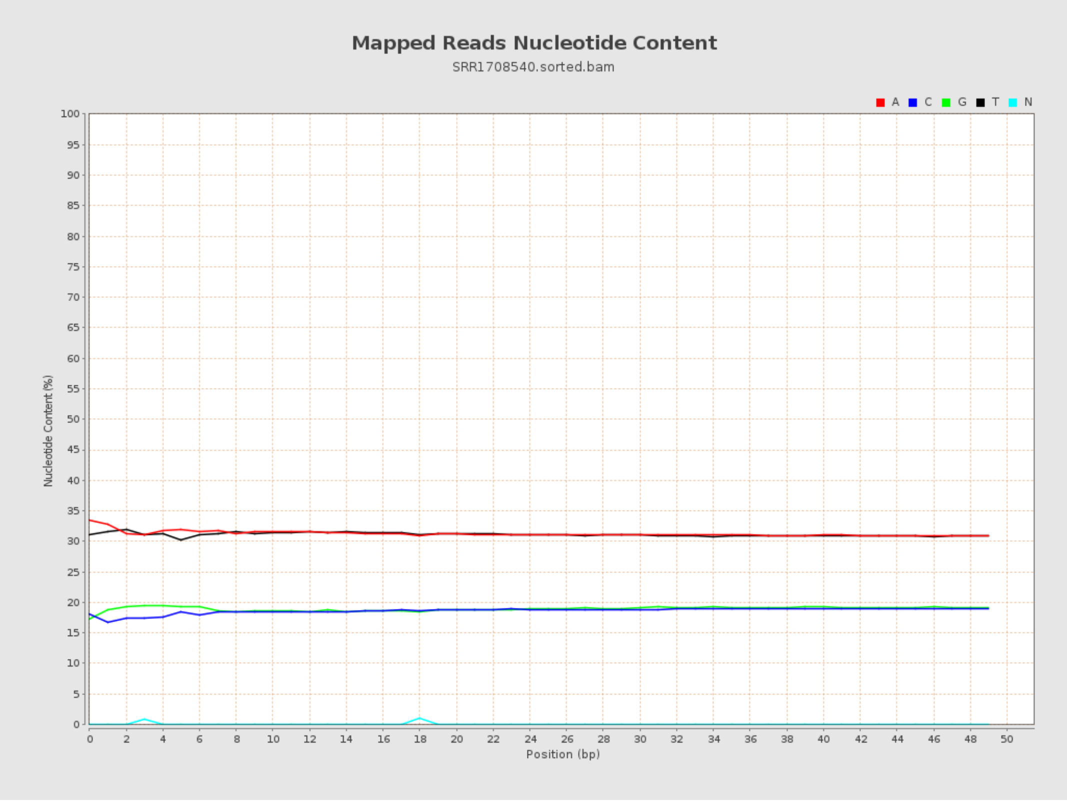
6. Results : Genome Fraction Coverage



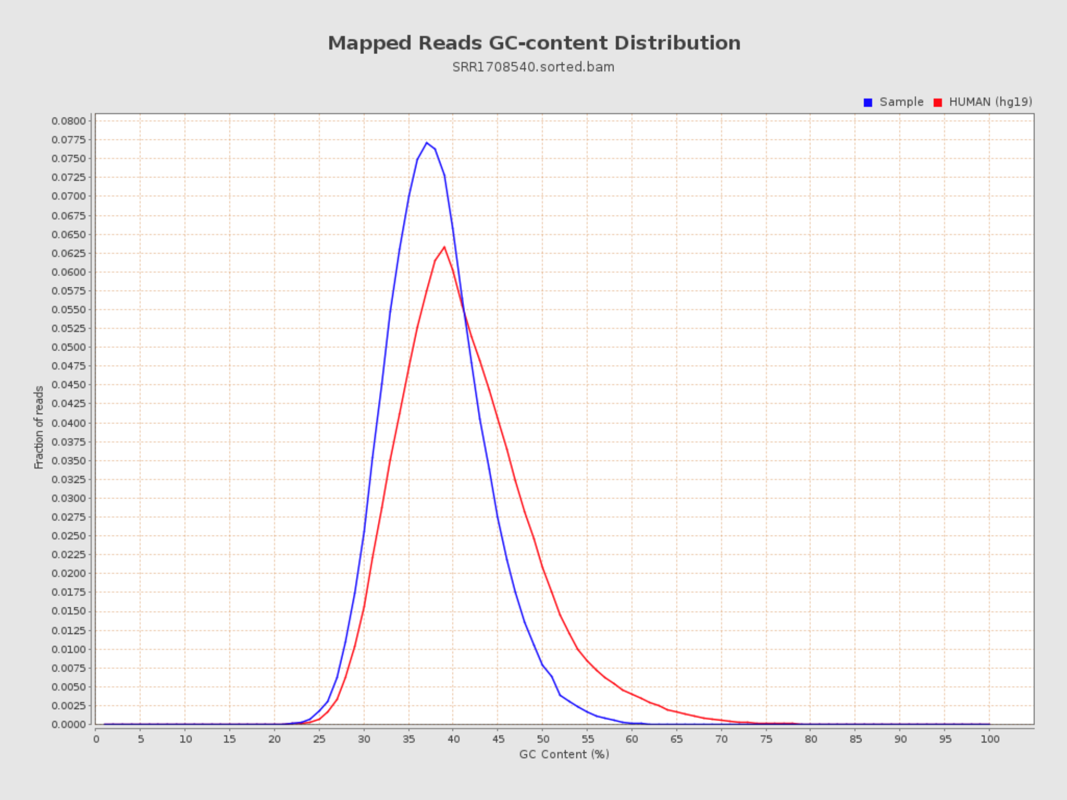
7. Results : Duplication Rate Histogram



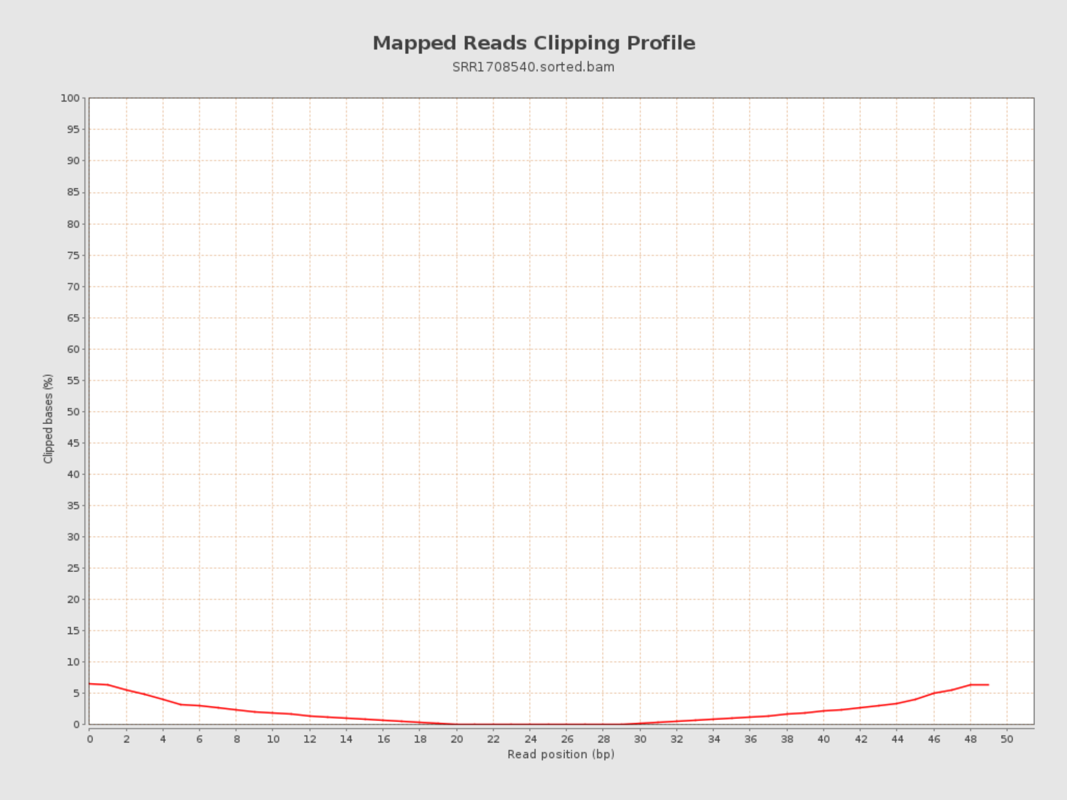
8. Results : Mapped Reads Nucleotide Content



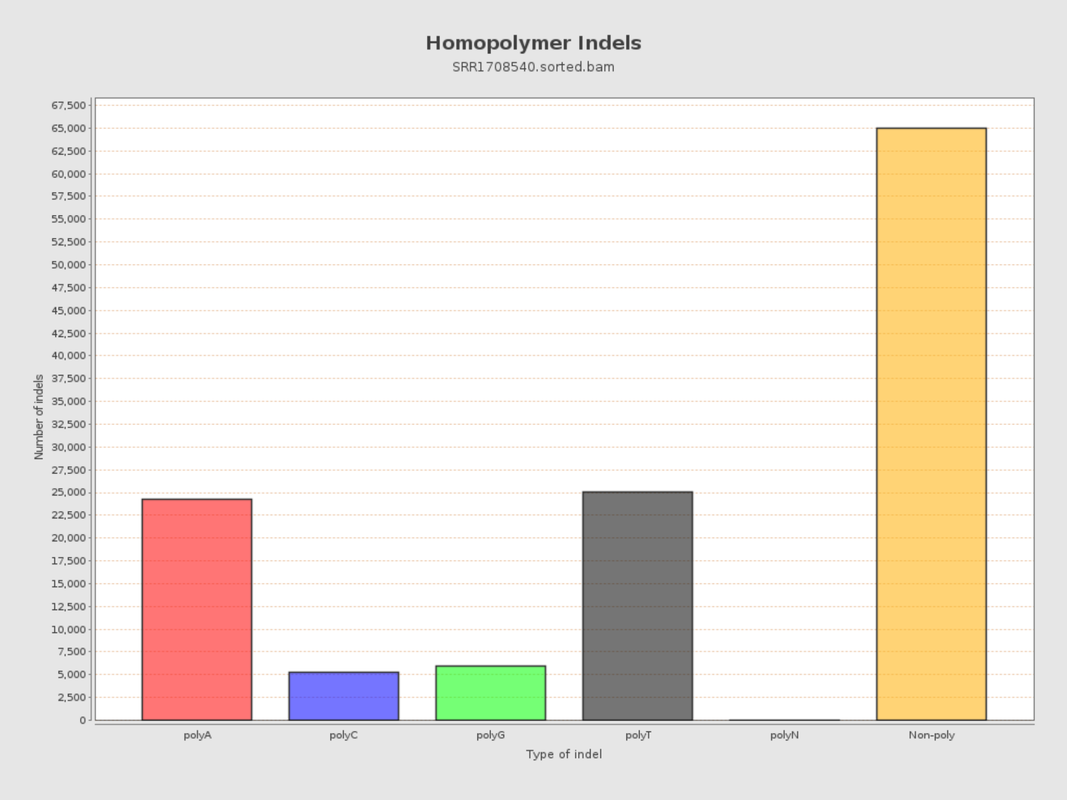
9. Results : Mapped Reads GC-content Distribution



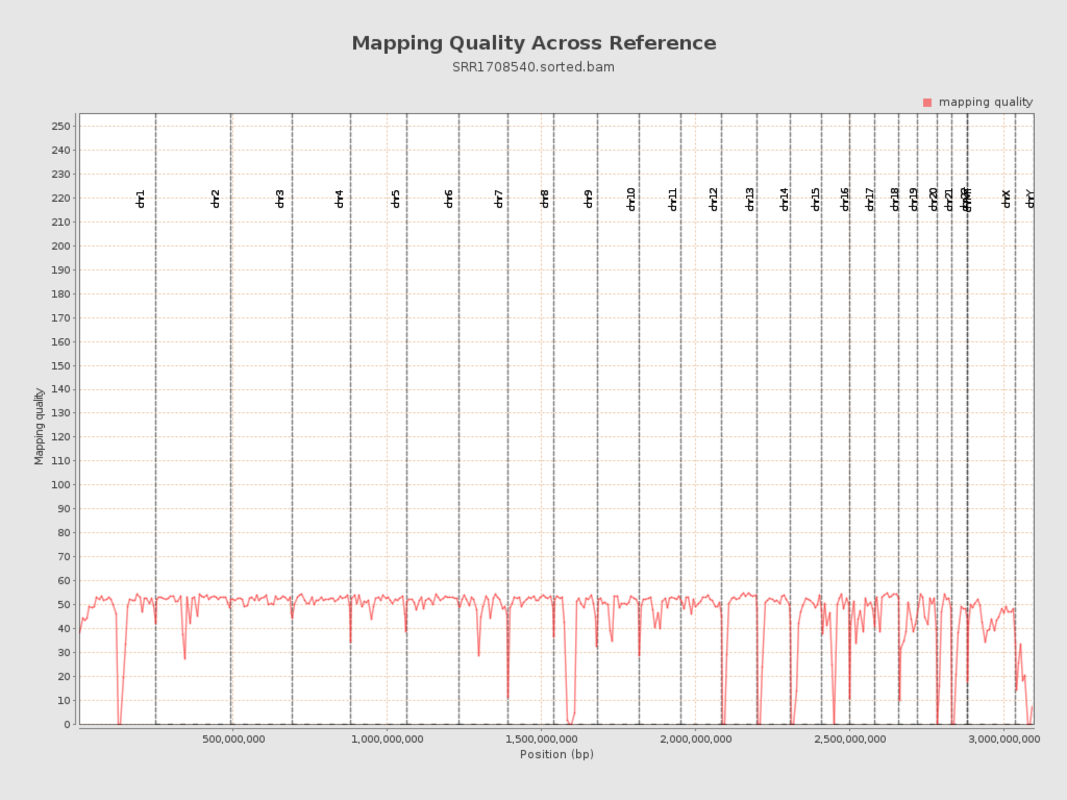
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram