Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:10:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708555.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_SRR1708555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708555.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:10:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708555.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,377,755
Mapped reads	3,612,636 / 82.52%
Unmapped reads	765,119 / 17.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	110 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,160 / 0.37%
Duplication rate	0.44%
Clipped reads	49,941 / 1.14%

2.2. ACGT Content

Number/percentage of A's	55,645,631 / 30.89%
Number/percentage of C's	34,328,405 / 19.06%
Number/percentage of T's	55,460,081 / 30.79%
Number/percentage of G's	34,698,559 / 19.26%
Number/percentage of N's	5,065 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.2485

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Mismatches and indels

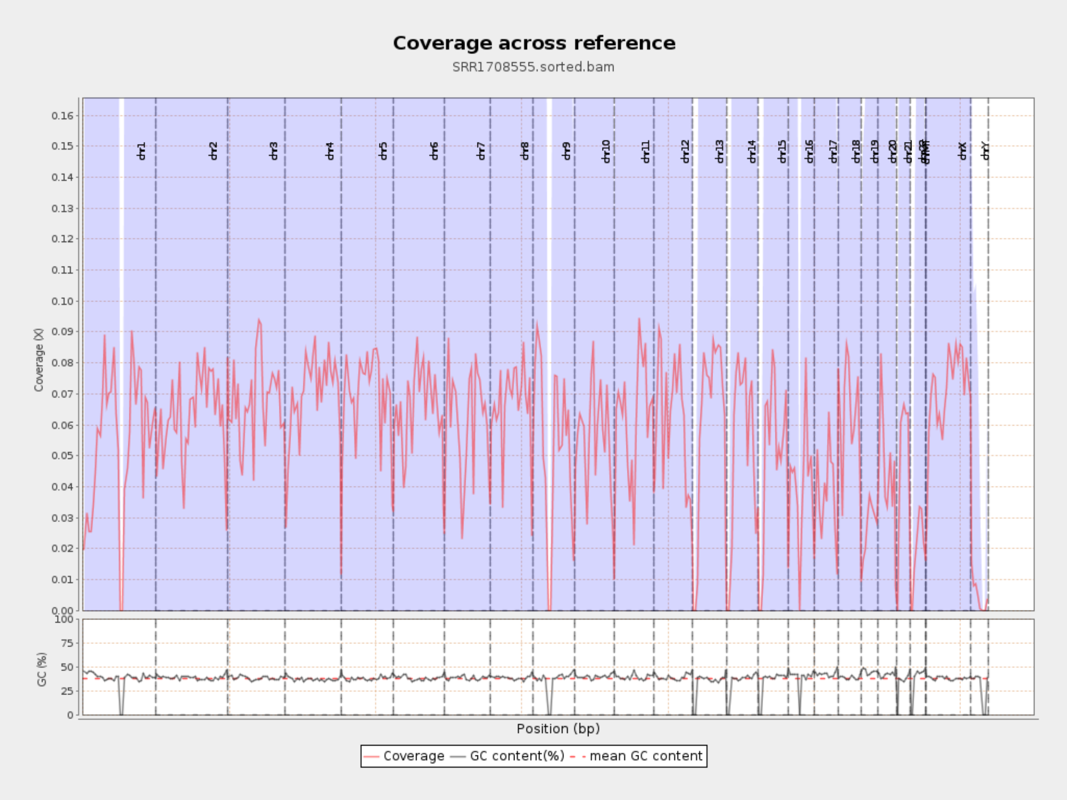
General error rate	0.17%
Mismatches	285,427
Insertions	11,922
Mapped reads with at least one insertion	0.33%
Deletions	9,718
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.47%

2.6. Chromosome stats

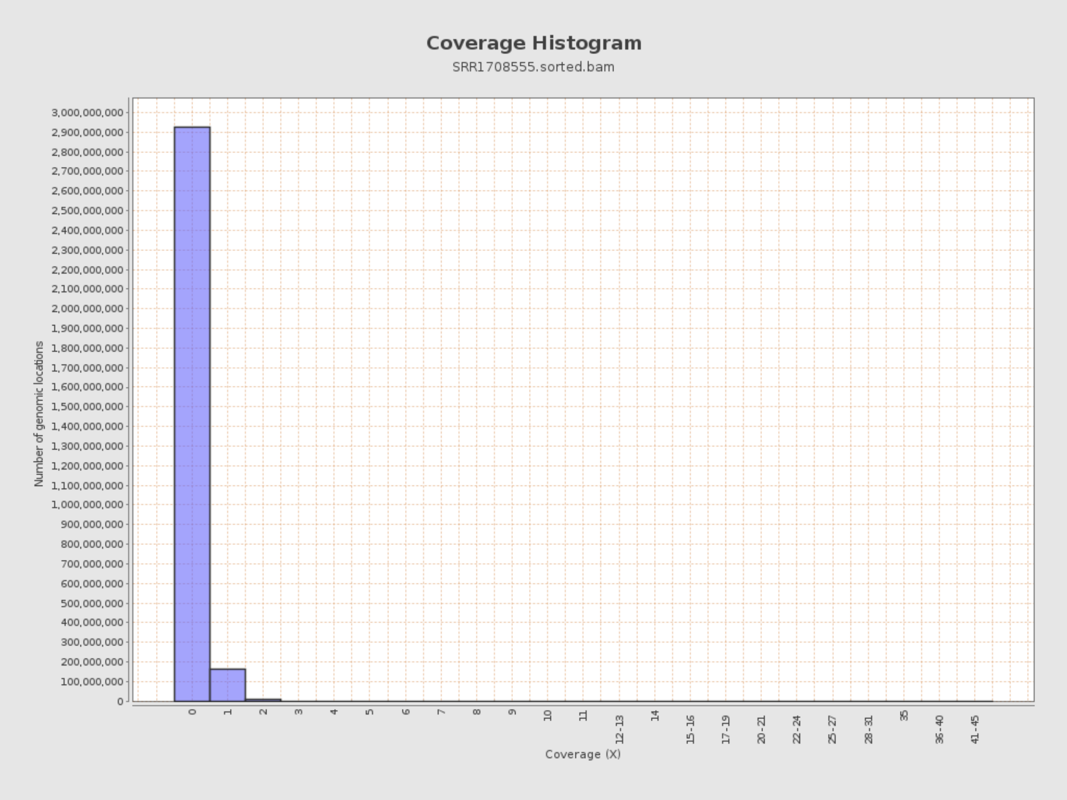
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13656623	0.0548	0.242
chr2	243199373	15362746	0.0632	0.2579
chr3	198022430	13438875	0.0679	0.2672
chr4	191154276	13430507	0.0703	0.2721
chr5	180915260	12494051	0.0691	0.2695
chr6	171115067	11319400	0.0662	0.2637
chr7	159138663	9649061	0.0606	0.2534

chr8	146364022	9747346	0.0666	0.2649
chr9	141213431	7641877	0.0541	0.2404
chr10	135534747	7740782	0.0571	0.2453
chr11	135006516	8465605	0.0627	0.2589
chr12	133851895	8286795	0.0619	0.2561
chr13	115169878	7096048	0.0616	0.2558
chr14	107349540	5716831	0.0533	0.2383
chr15	102531392	5075096	0.0495	0.2305
chr16	90354753	3571003	0.0395	0.2047
chr17	81195210	3141655	0.0387	0.2027
chr18	78077248	5019381	0.0643	0.2602
chr19	59128983	1628025	0.0275	0.1698
chr20	63025520	2980876	0.0473	0.2239
chr21	48129895	2245765	0.0467	0.2241
chr22	51304566	1014629	0.0198	0.1437
chrMT	16571	350	0.0211	0.1707
chrX	155270560	11151764	0.0718	0.276
chrY	59373566	279011	0.0047	0.0714

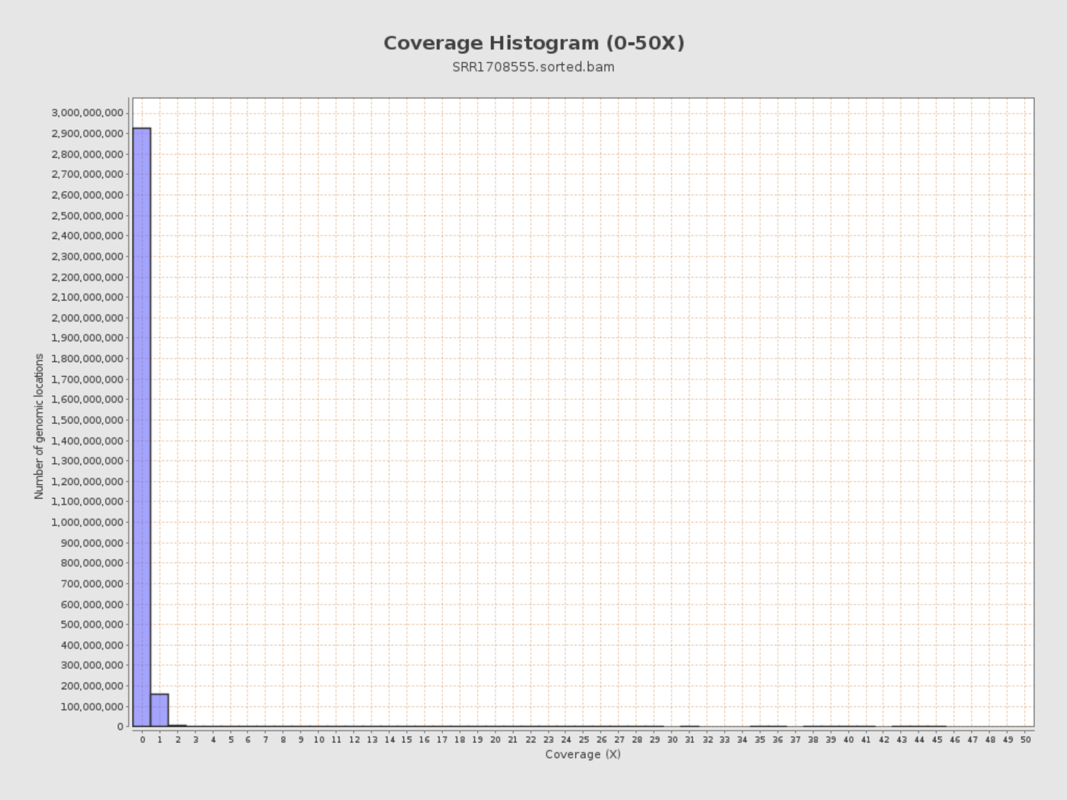
3. Results : Coverage across reference



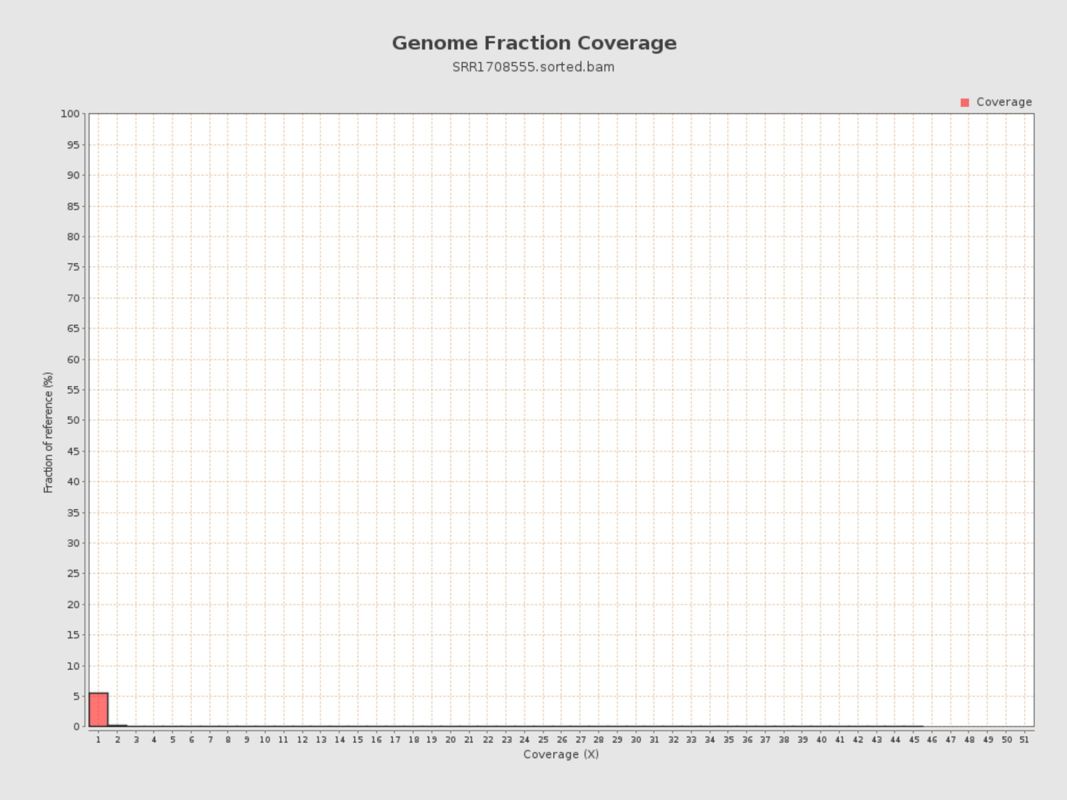
4. Results : Coverage Histogram



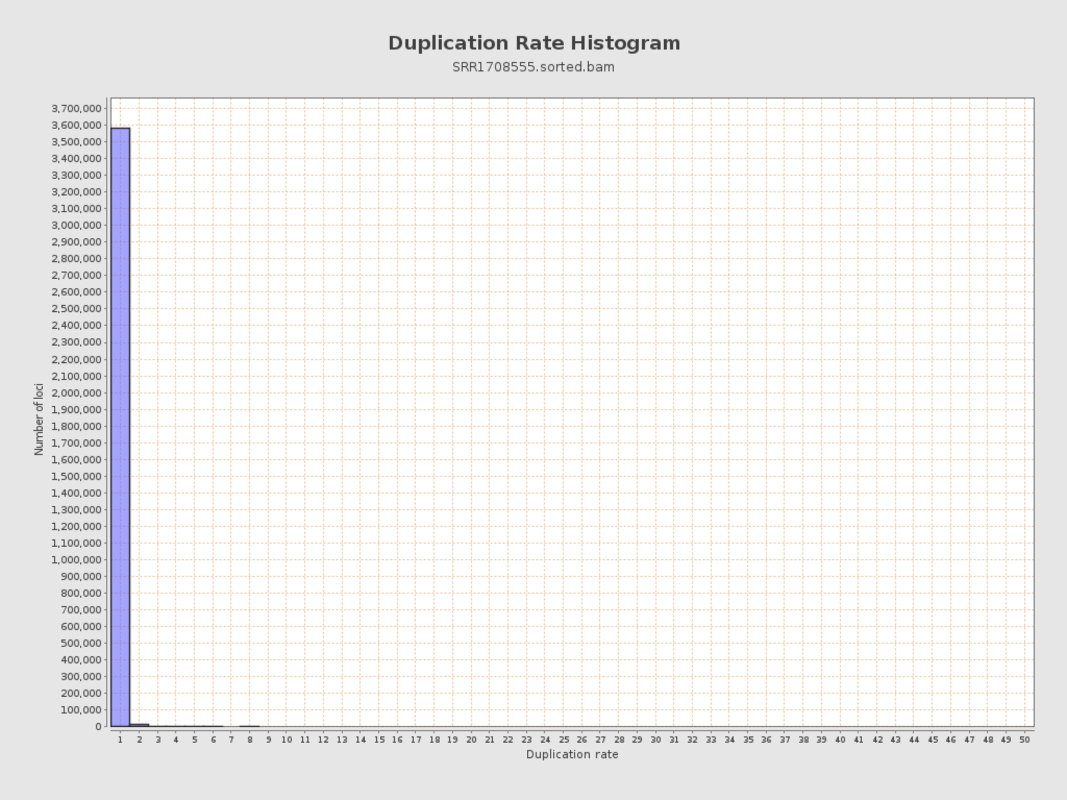
5. Results : Coverage Histogram (0-50X)



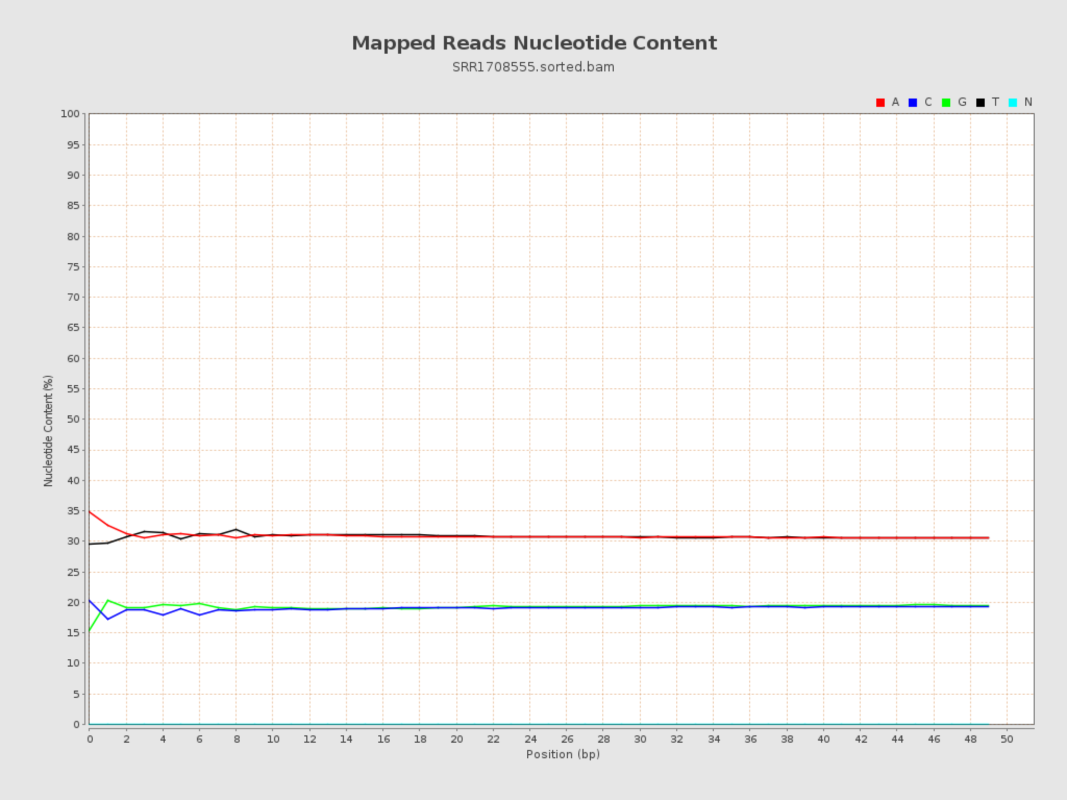
6. Results : Genome Fraction Coverage



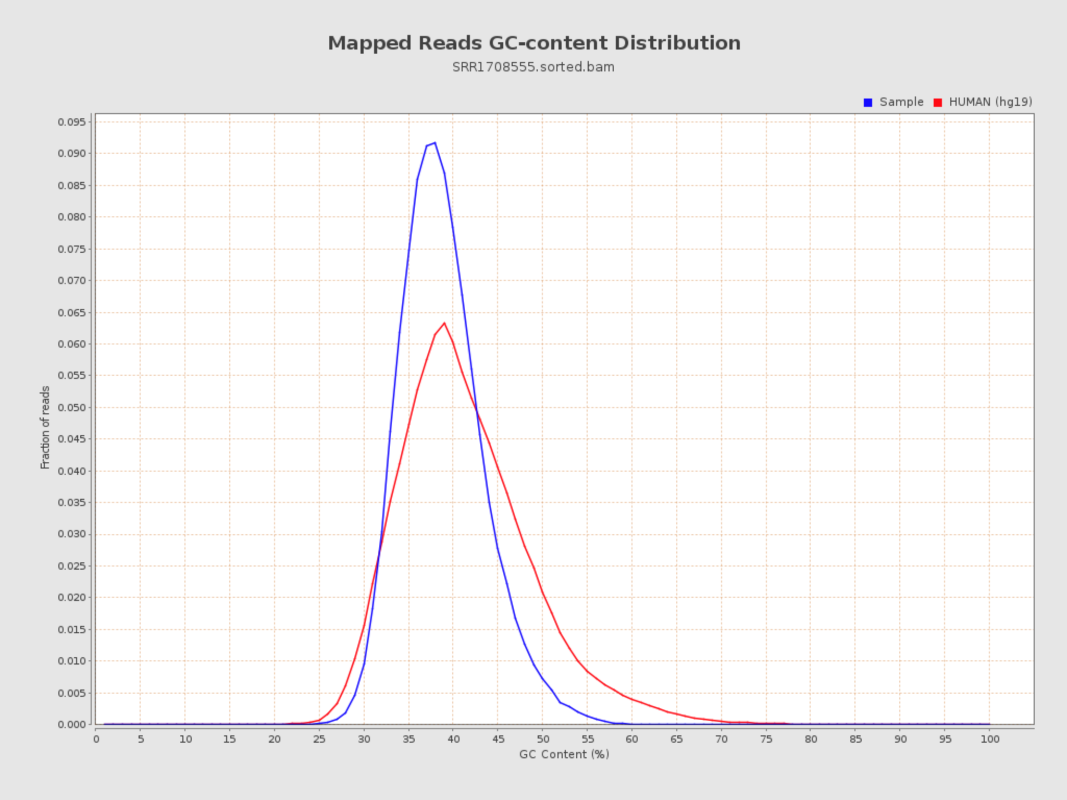
7. Results : Duplication Rate Histogram



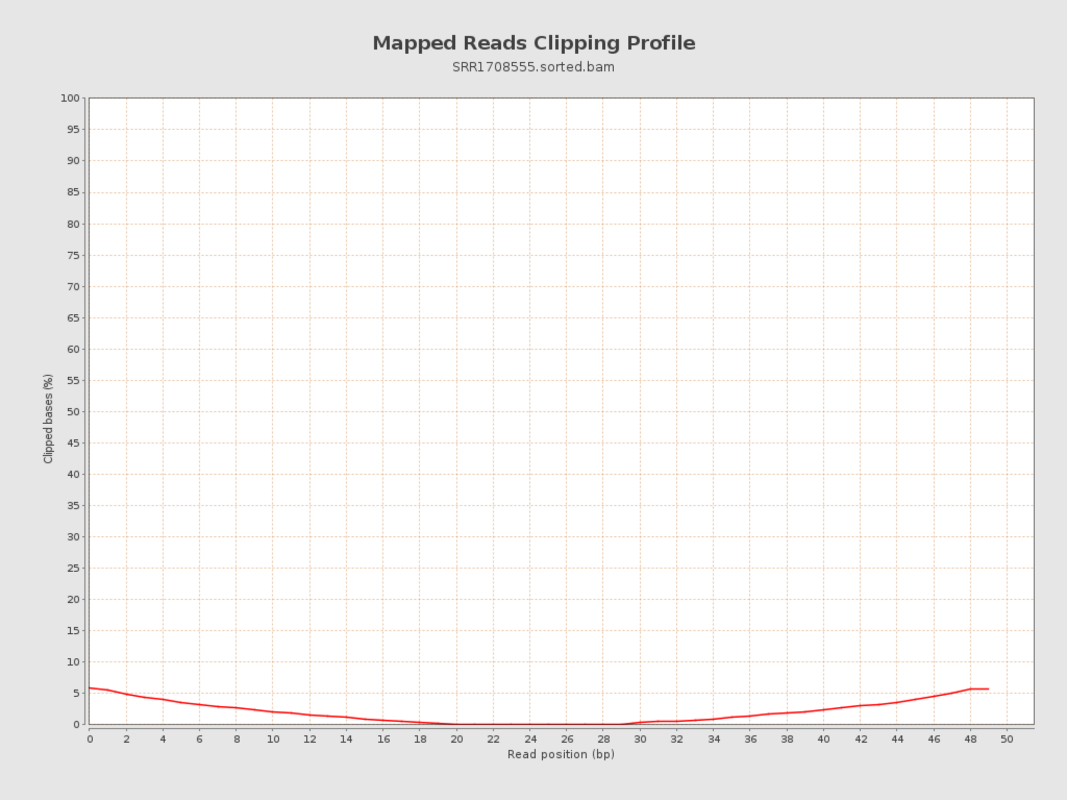
8. Results : Mapped Reads Nucleotide Content



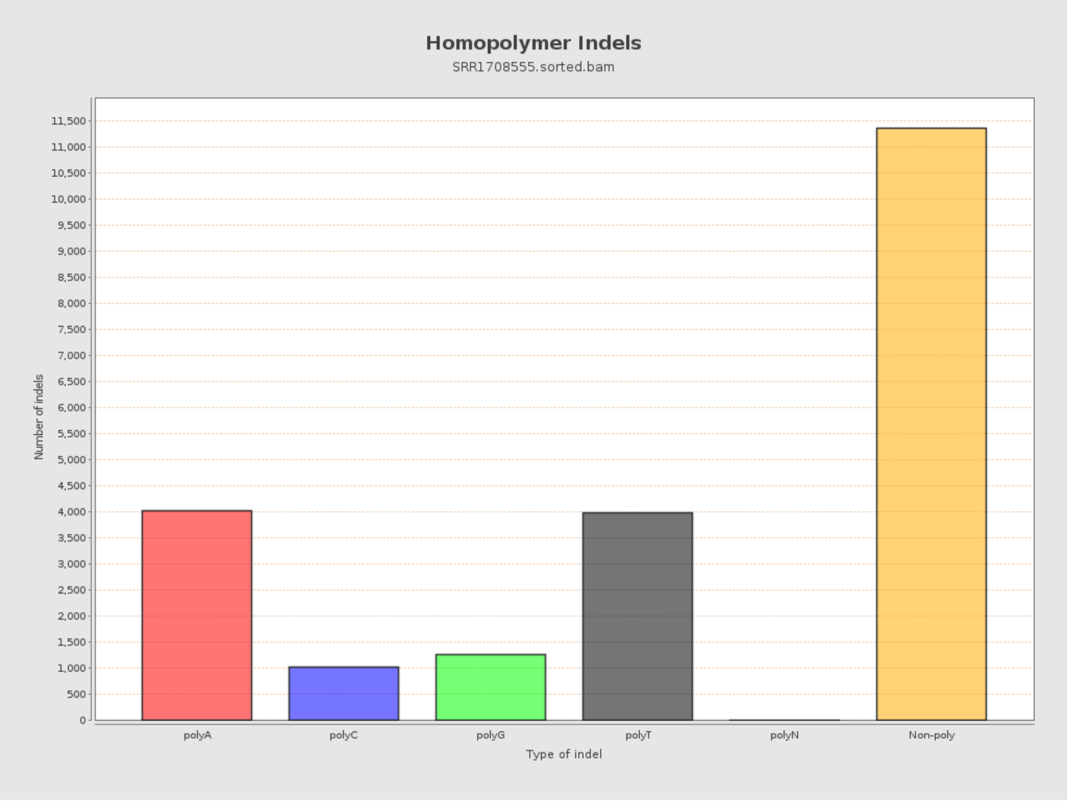
9. Results : Mapped Reads GC-content Distribution



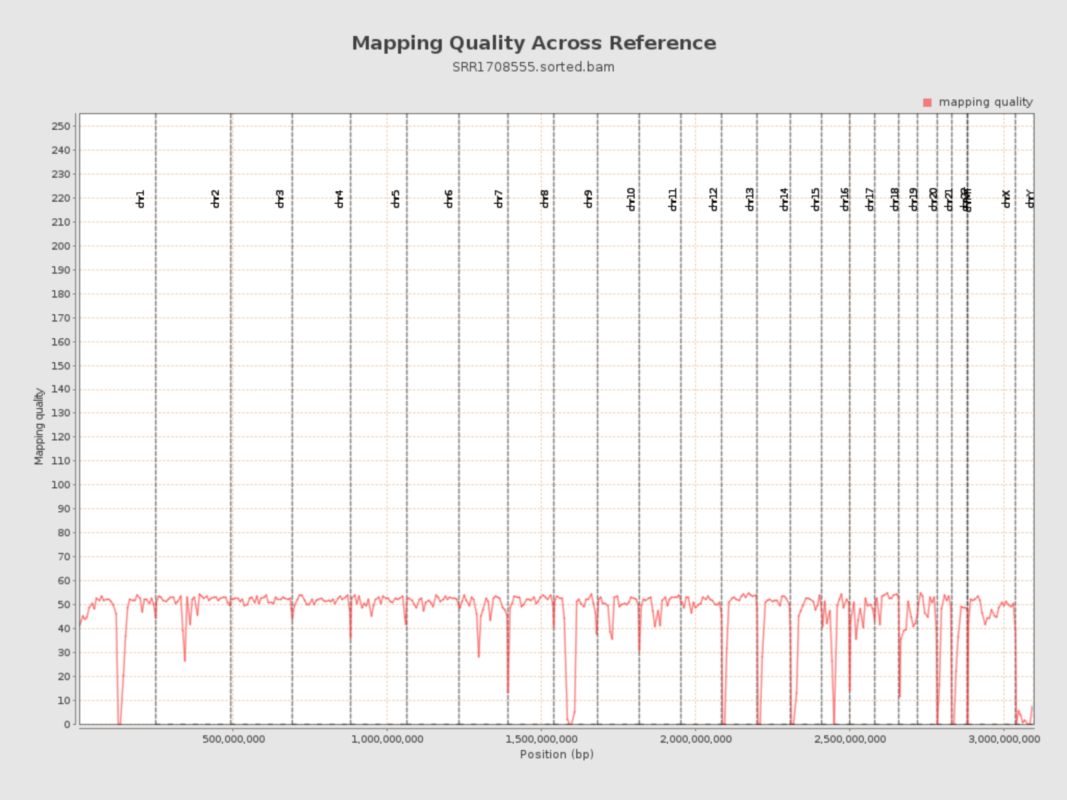
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram