Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:30:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708573.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_SRR1708573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:30:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,373,513
Mapped reads	3,591,375 / 82.12%
Unmapped reads	782,138 / 17.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	94 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	20,018 / 0.46%
Duplication rate	0.55%
Clipped reads	50,207 / 1.15%

2.2. ACGT Content

Number/percentage of A's	55,387,019 / 30.93%
Number/percentage of C's	34,136,674 / 19.06%
Number/percentage of T's	55,053,523 / 30.74%
Number/percentage of G's	34,483,602 / 19.26%
Number/percentage of N's	6,533 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.2565

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

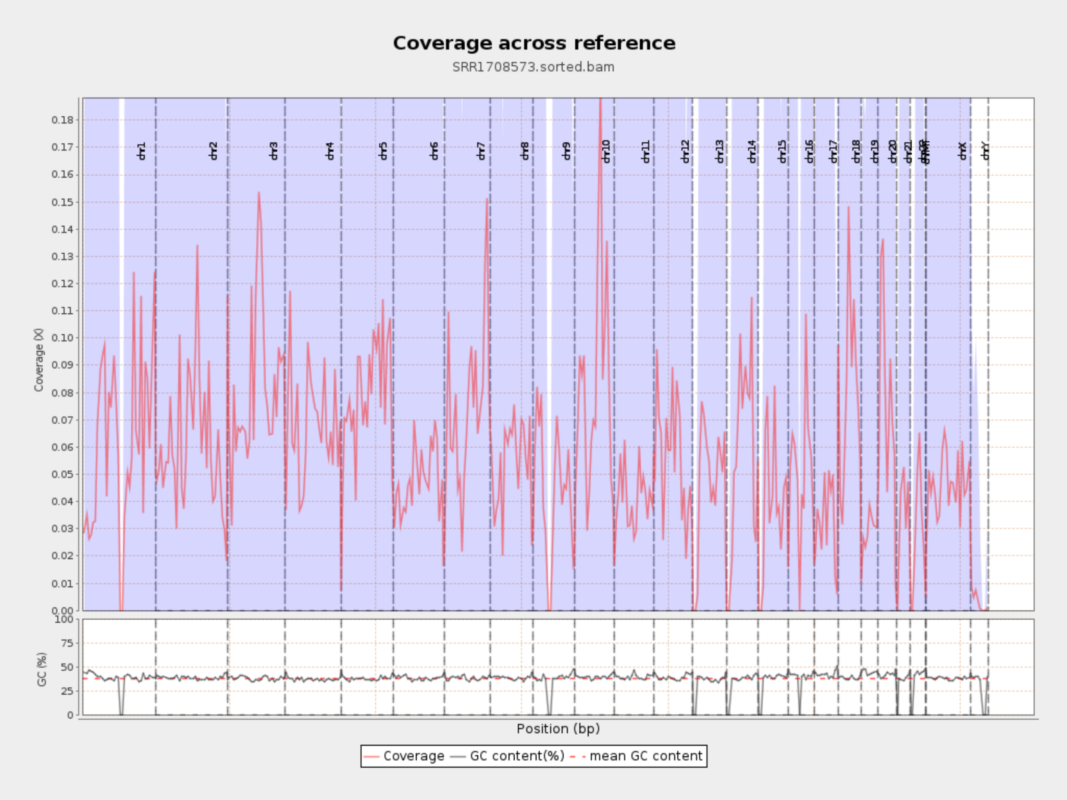
General error rate	0.17%
Mismatches	283,332
Insertions	12,281
Mapped reads with at least one insertion	0.34%
Deletions	9,594
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48%

2.6. Chromosome stats

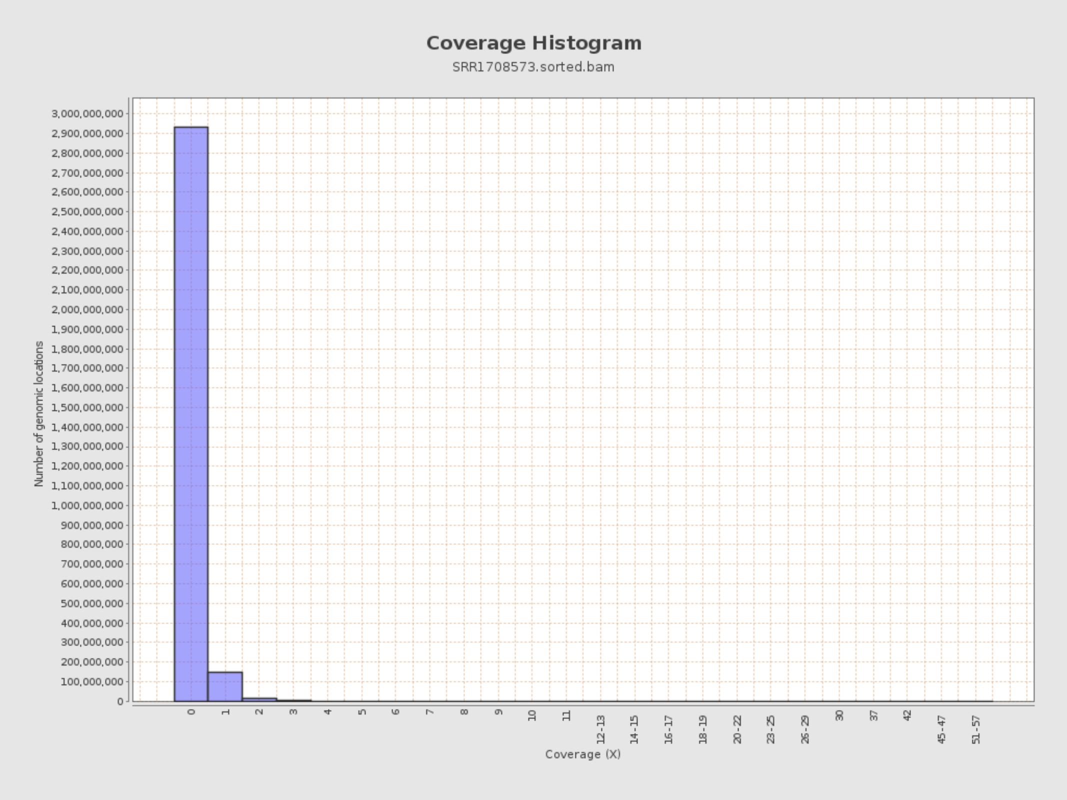
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15552989	0.0624	0.2689
chr2	243199373	14938863	0.0614	0.2633
chr3	198022430	16380816	0.0827	0.3071
chr4	191154276	12986879	0.0679	0.2763
chr5	180915260	14181633	0.0784	0.299
chr6	171115067	8214360	0.048	0.2305
chr7	159138663	11856671	0.0745	0.2921

chr8	146364022	7909650	0.054	0.244
chr9	141213431	6339216	0.0449	0.2237
chr10	135534747	11307151	0.0834	0.3098
chr11	135006516	5531948	0.041	0.2132
chr12	133851895	7556842	0.0565	0.2526
chr13	115169878	5345821	0.0464	0.2282
chr14	107349540	6158226	0.0574	0.2545
chr15	102531392	3991015	0.0389	0.2101
chr16	90354753	4539504	0.0502	0.2362
chr17	81195210	2693252	0.0332	0.1933
chr18	78077248	6283559	0.0805	0.3032
chr19	59128983	1758210	0.0297	0.179
chr20	63025520	5075982	0.0805	0.3038
chr21	48129895	1555390	0.0323	0.1909
chr22	51304566	1511901	0.0295	0.182
chrMT	16571	300	0.0181	0.1333
chrX	155270560	7227838	0.0465	0.2281
chrY	59373566	185637	0.0031	0.0588

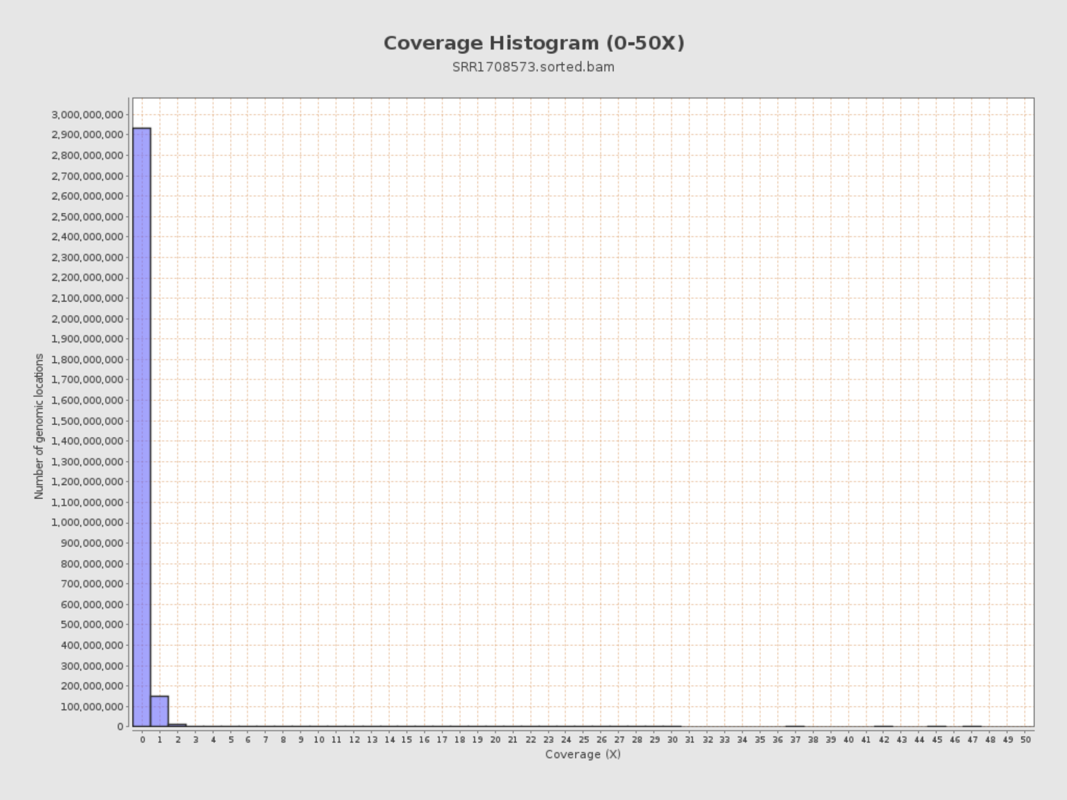
3. Results : Coverage across reference



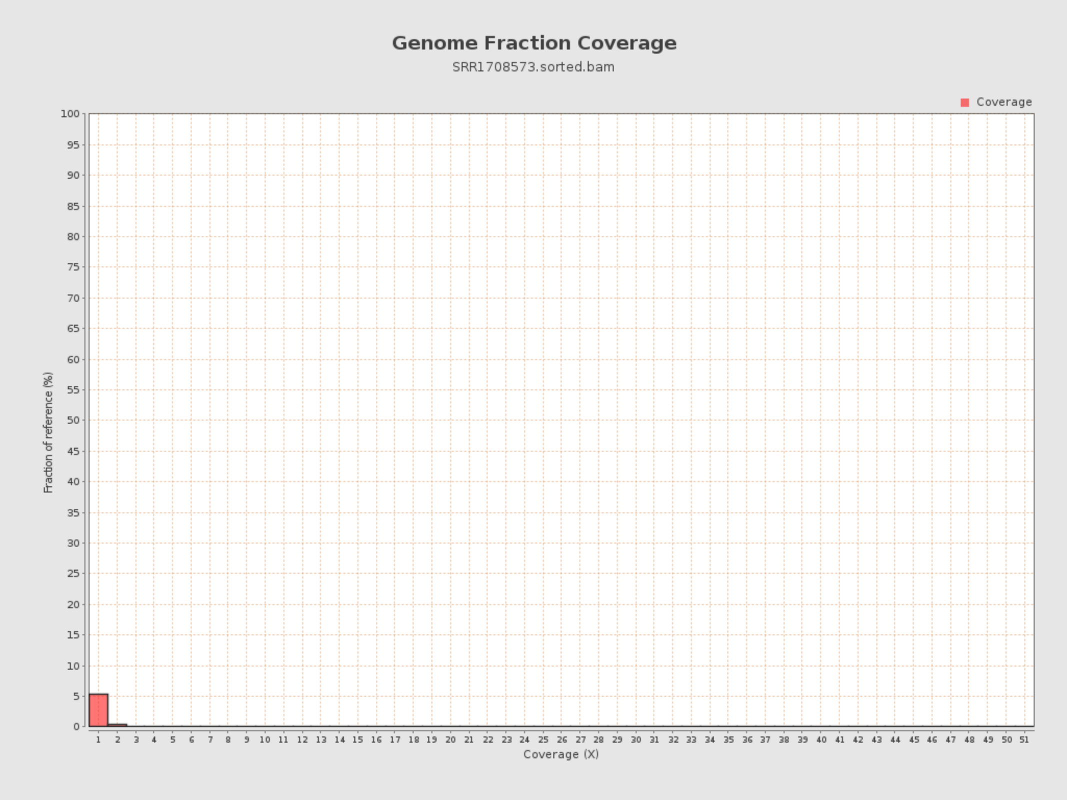
4. Results : Coverage Histogram



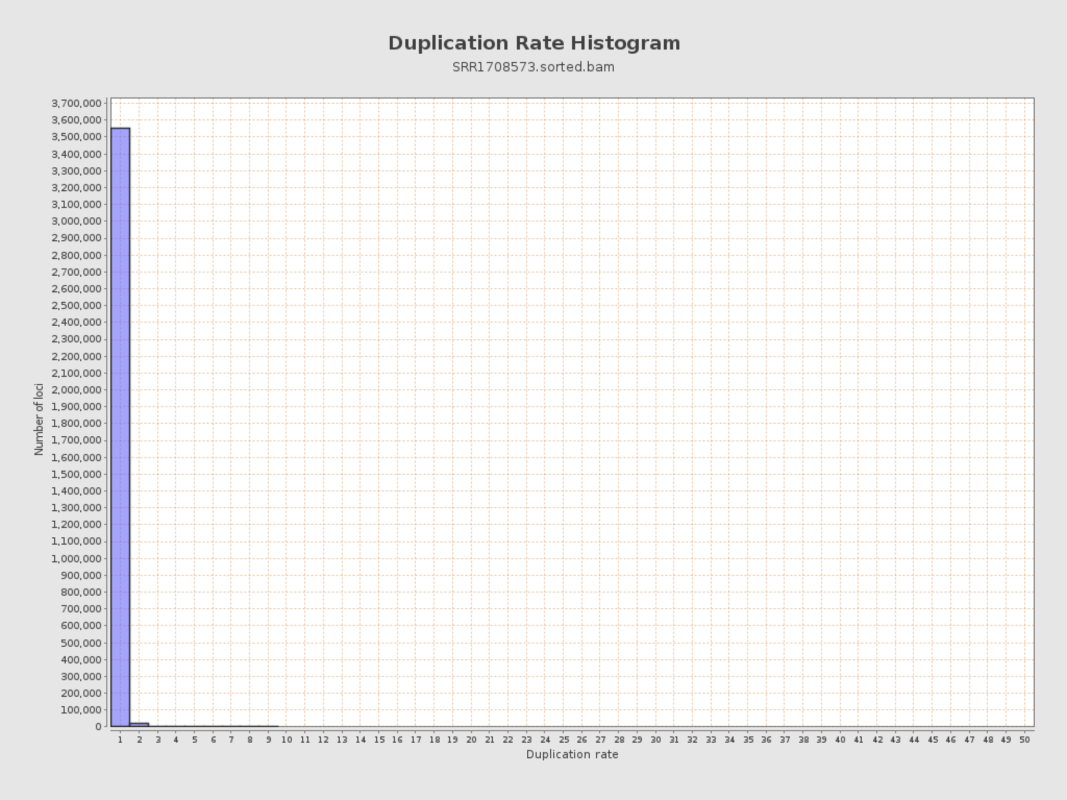
5. Results : Coverage Histogram (0-50X)



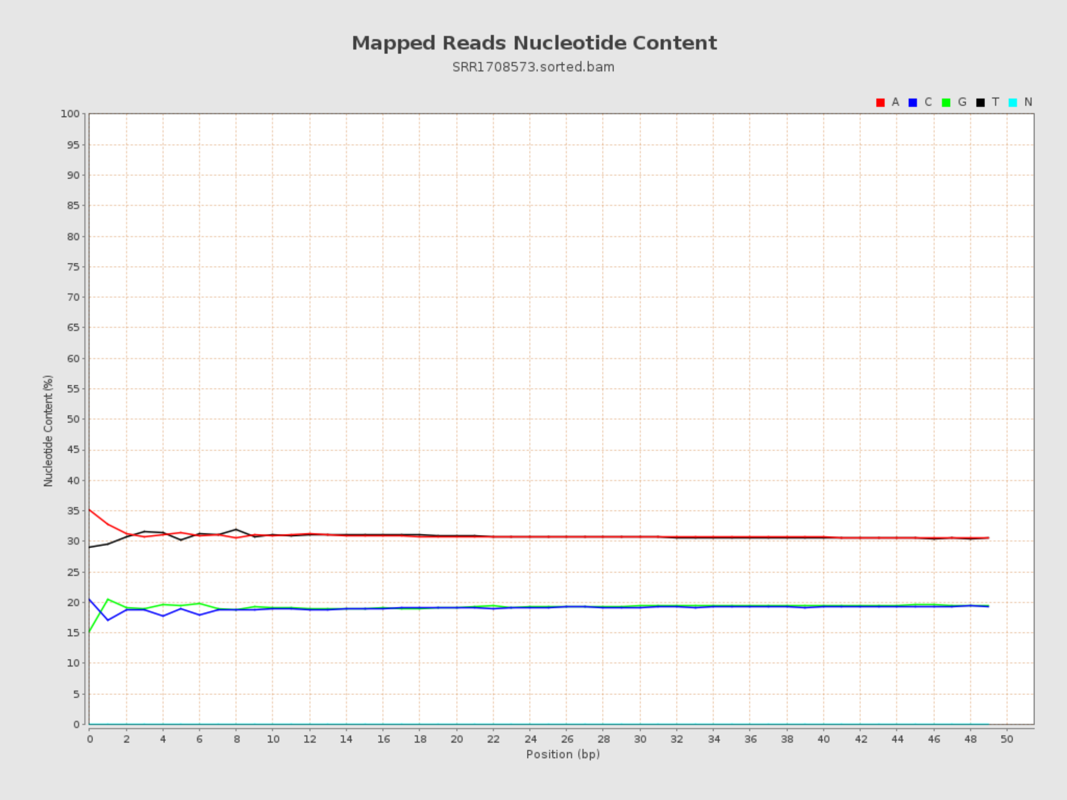
6. Results : Genome Fraction Coverage



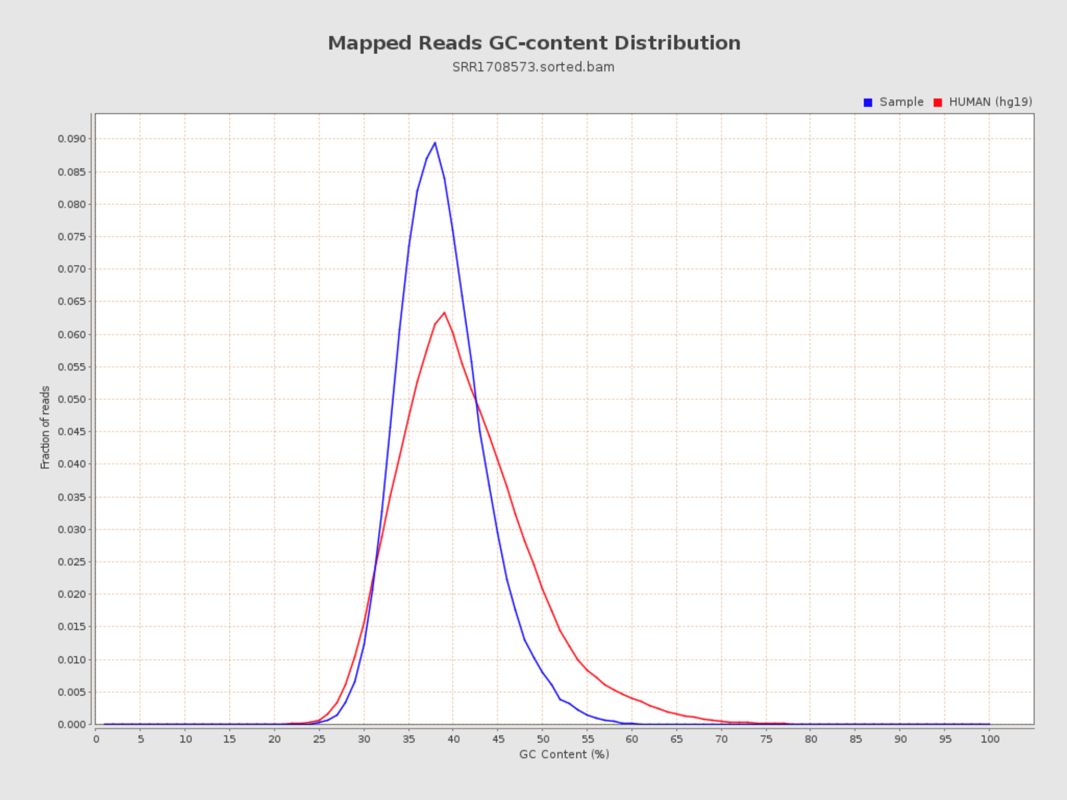
7. Results : Duplication Rate Histogram



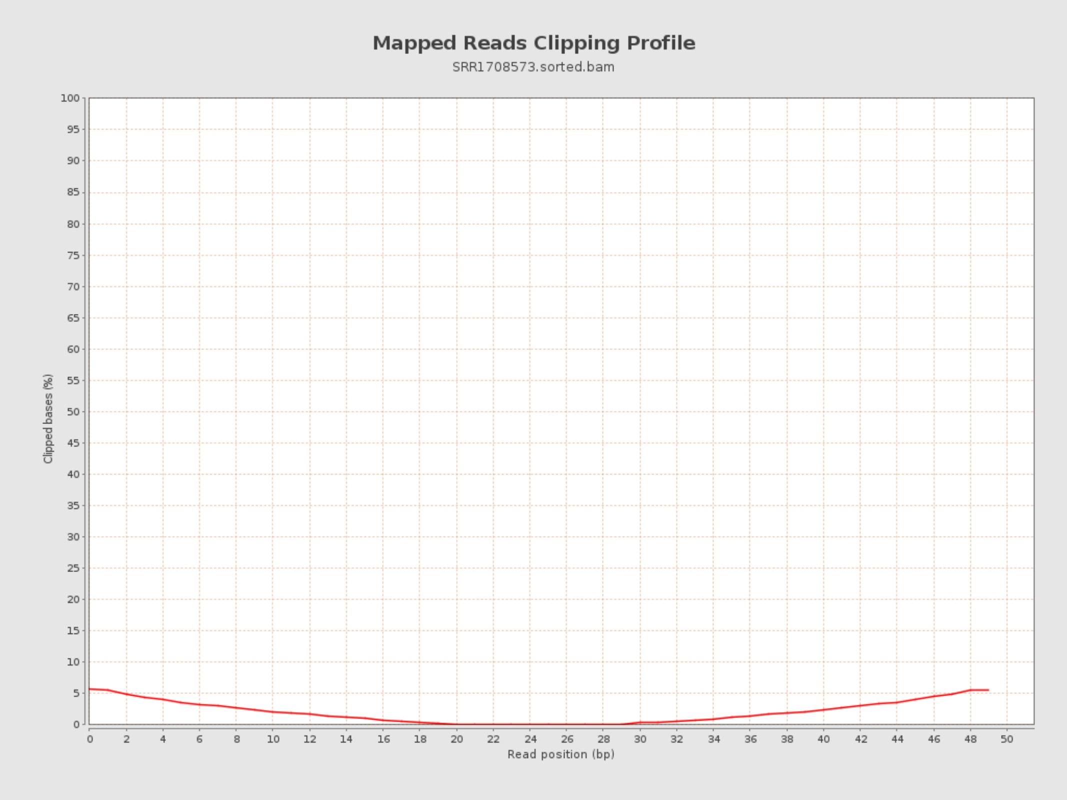
8. Results : Mapped Reads Nucleotide Content



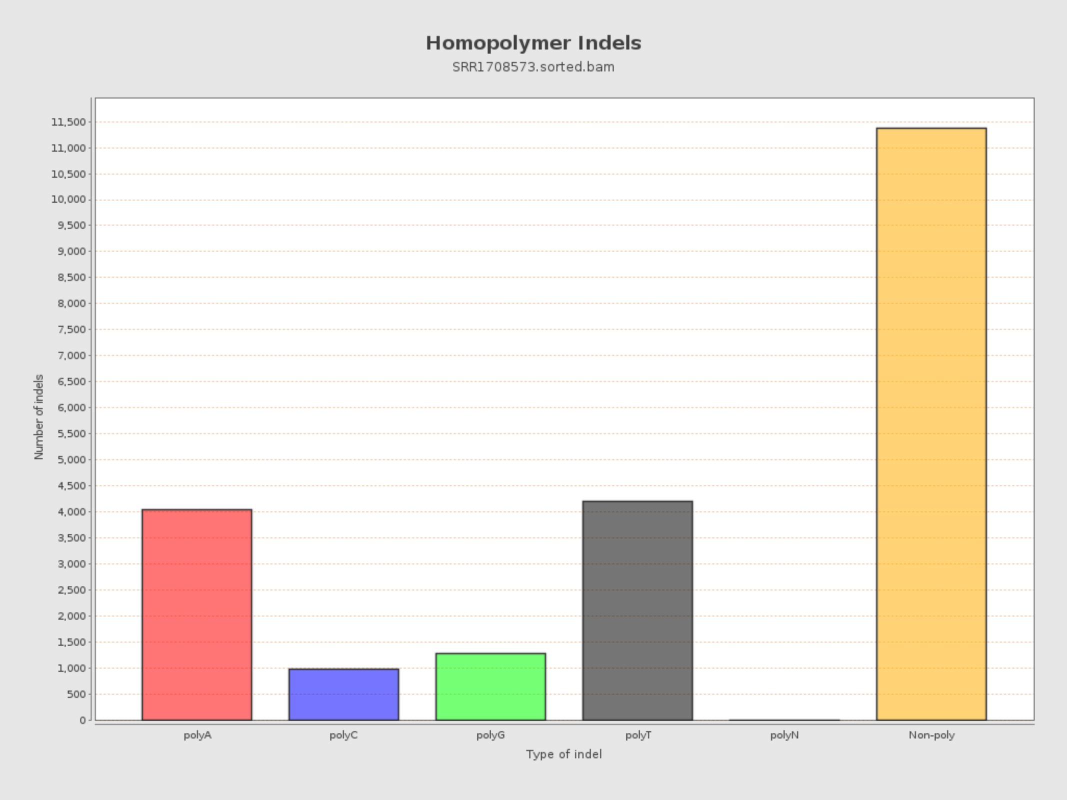
9. Results : Mapped Reads GC-content Distribution



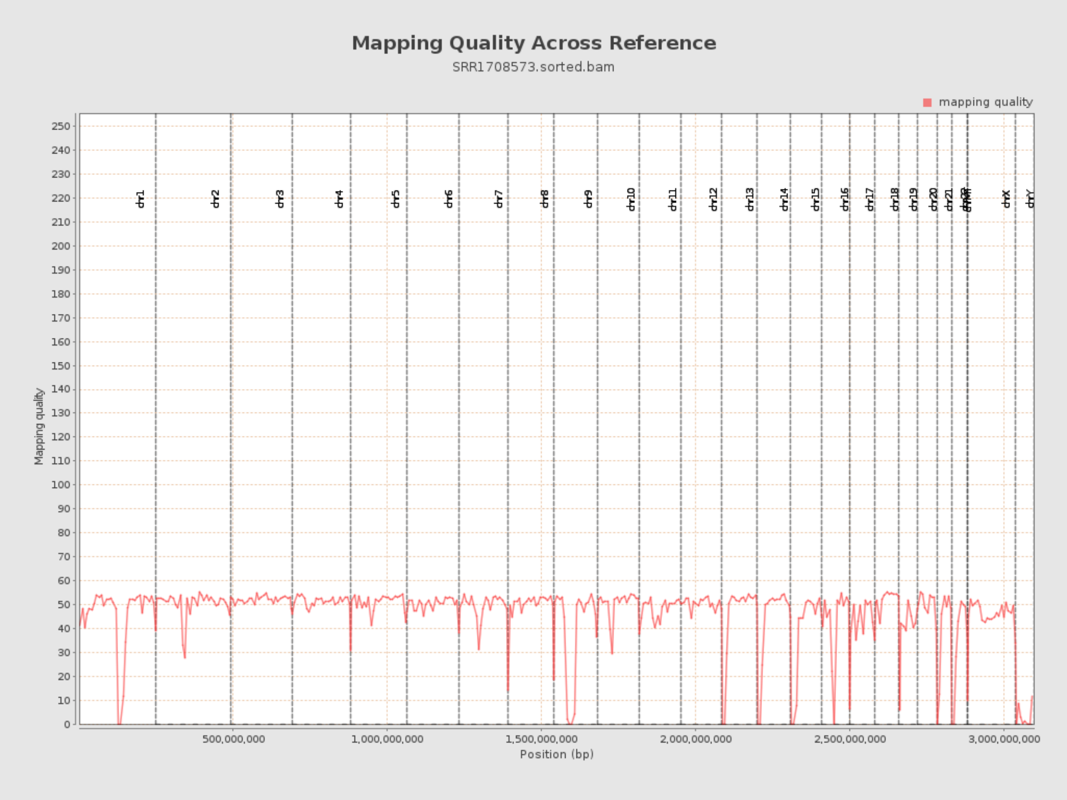
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram