Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:55:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708585.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_SRR1708585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708585.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:55:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,283,920
Mapped reads	5,190,226 / 98.23%
Unmapped reads	93,694 / 1.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	140 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	49,742 / 0.94%
Duplication rate	0.96%
Clipped reads	67,183 / 1.27%

2.2. ACGT Content

Number/percentage of A's	80,150,463 / 30.96%
Number/percentage of C's	49,127,959 / 18.98%
Number/percentage of T's	79,817,692 / 30.83%
Number/percentage of G's	49,778,392 / 19.23%
Number/percentage of N's	5,790 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	0.0836

Standard Deviation	0.3016

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

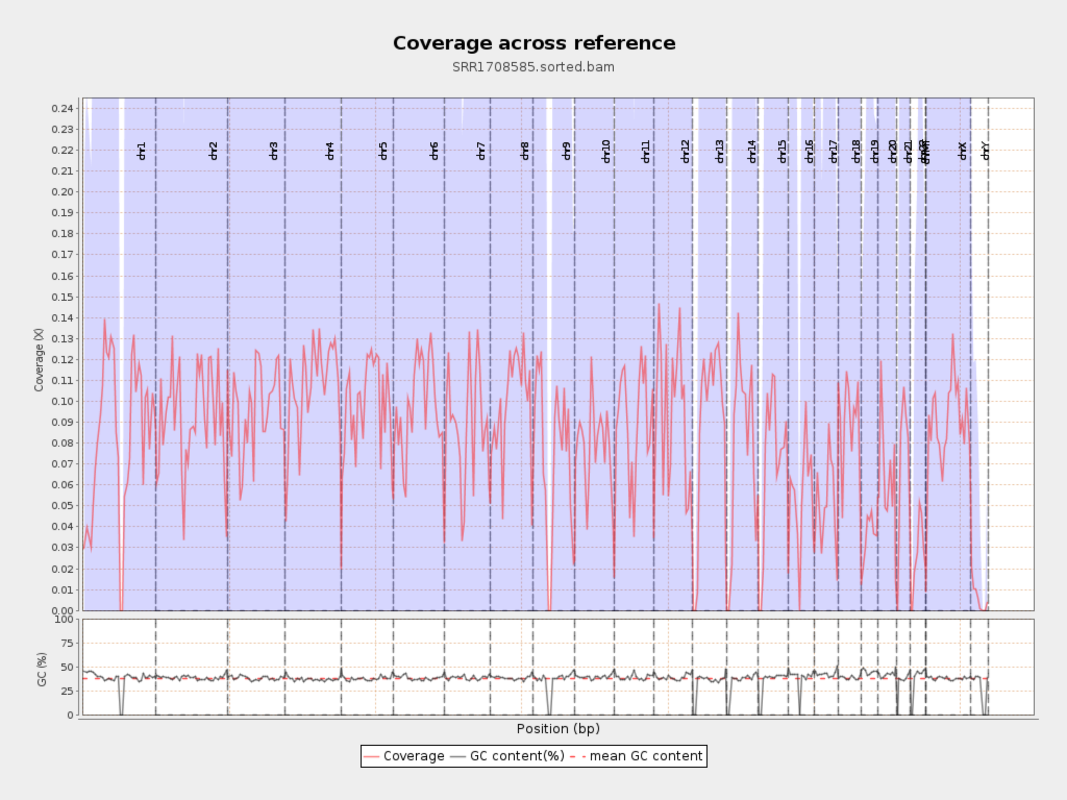
General error rate	0.15%
Mismatches	375,527
Insertions	16,017
Mapped reads with at least one insertion	0.31%
Deletions	13,196
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.32%

2.6. Chromosome stats

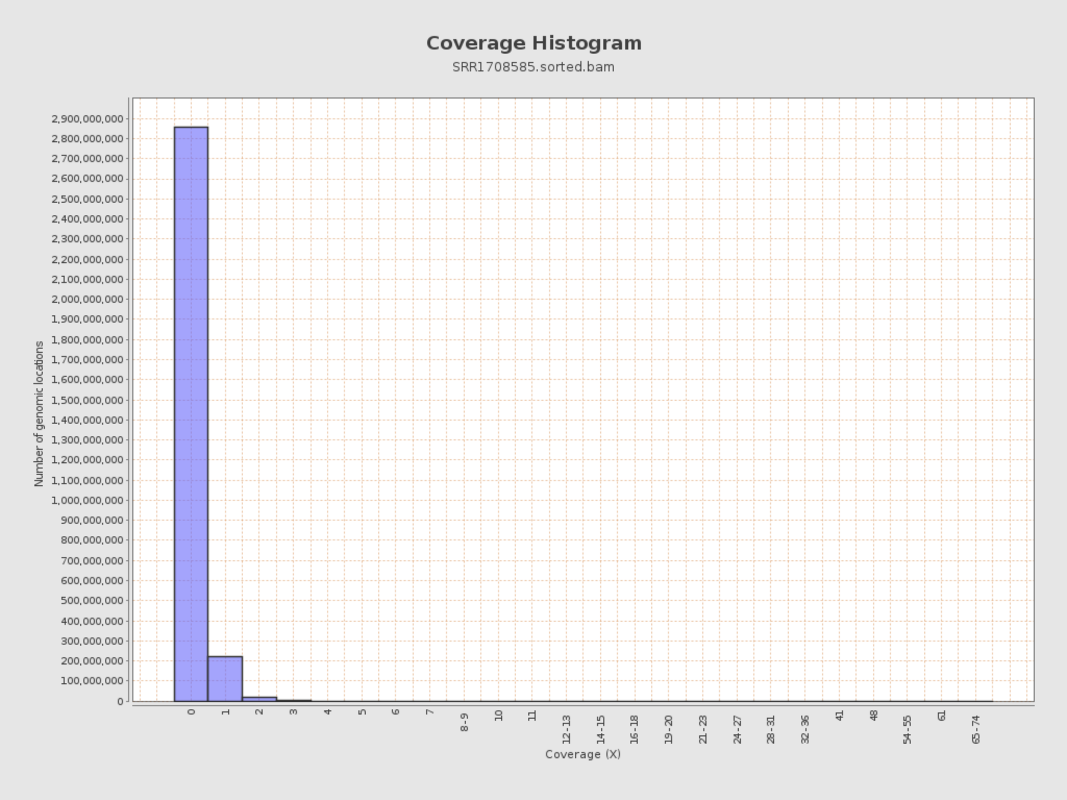
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20692392	0.083	0.3025
chr2	243199373	22411635	0.0922	0.3154
chr3	198022430	18947262	0.0957	0.3207
chr4	191154276	20652218	0.108	0.3406
chr5	180915260	17659723	0.0976	0.3236
chr6	171115067	16802995	0.0982	0.3252
chr7	159138663	13909622	0.0874	0.3074

chr8	146364022	14540378	0.0993	0.3269
chr9	141213431	10509935	0.0744	0.2851
chr10	135534747	10834647	0.0799	0.2932
chr11	135006516	12146988	0.09	0.3133
chr12	133851895	12460281	0.0931	0.3178
chr13	115169878	10279677	0.0893	0.3117
chr14	107349540	8434873	0.0786	0.2942
chr15	102531392	7112496	0.0694	0.2755
chr16	90354753	4867815	0.0539	0.2423
chr17	81195210	4263993	0.0525	0.2387
chr18	78077248	7033309	0.0901	0.3112
chr19	59128983	2155397	0.0365	0.1973
chr20	63025520	4228991	0.0671	0.2703
chr21	48129895	3246216	0.0674	0.2728
chr22	51304566	1382633	0.0269	0.1701
chrMT	16571	150	0.0091	0.0947
chrX	155270560	13978515	0.09	0.3118
chrY	59373566	350581	0.0059	0.0811

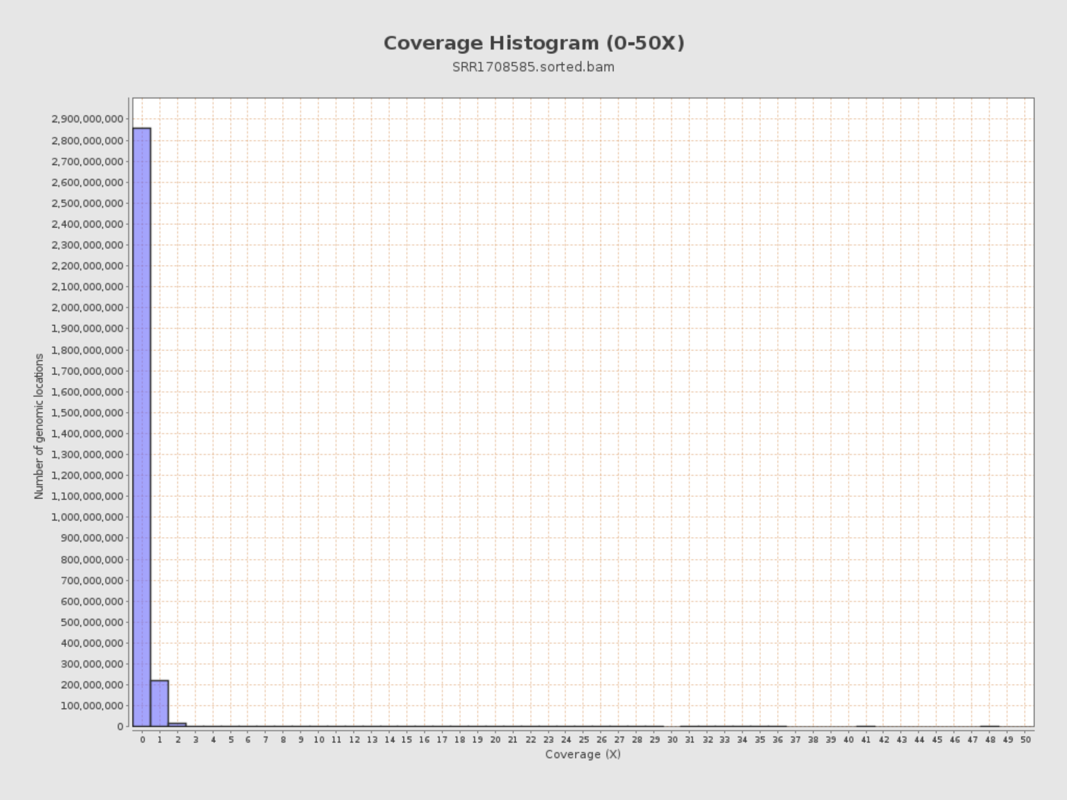
3. Results : Coverage across reference



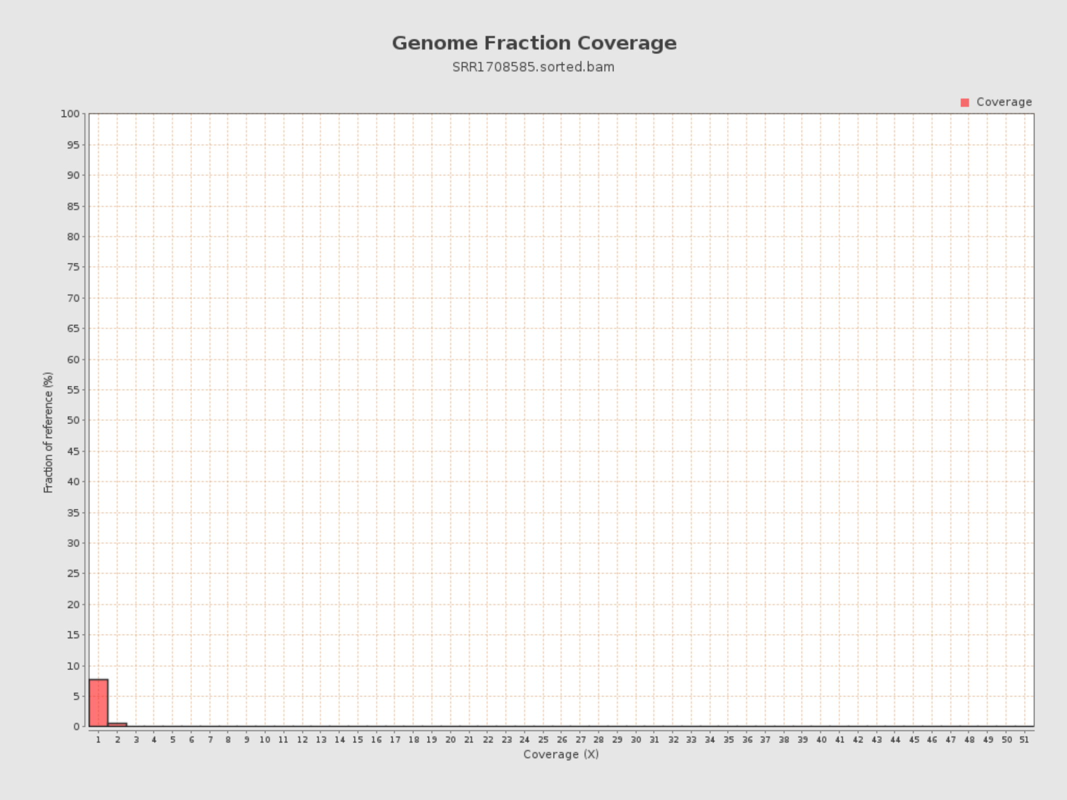
4. Results : Coverage Histogram



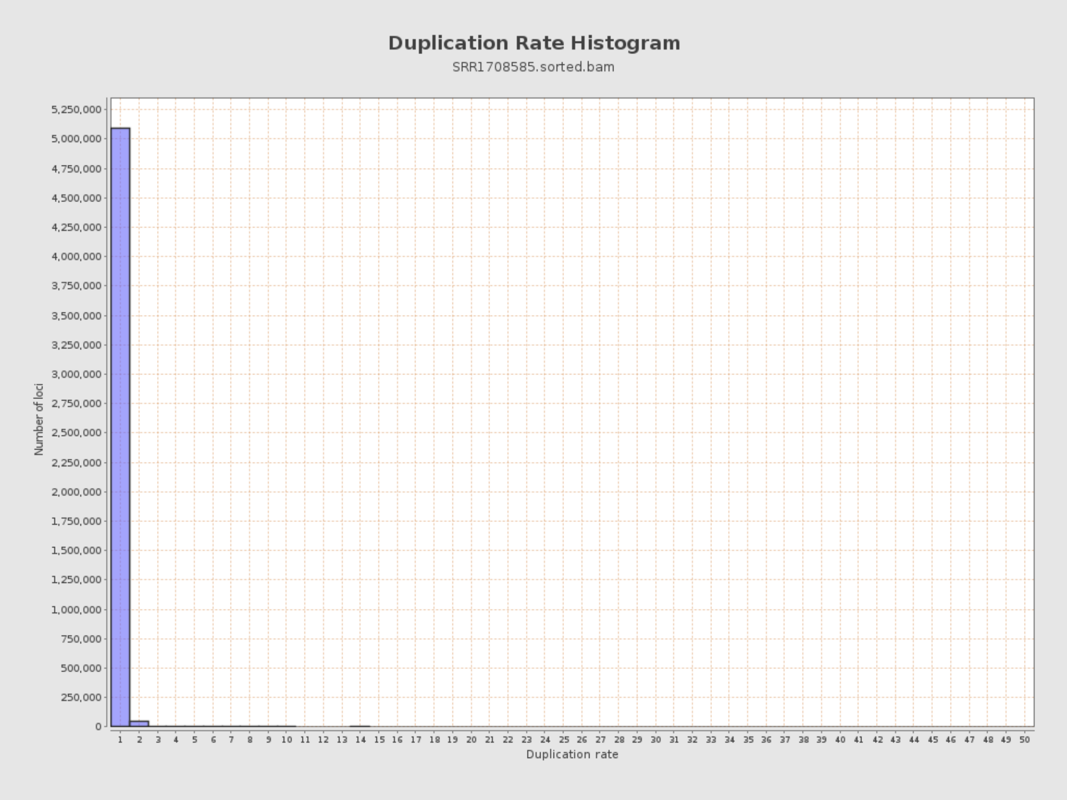
5. Results : Coverage Histogram (0-50X)



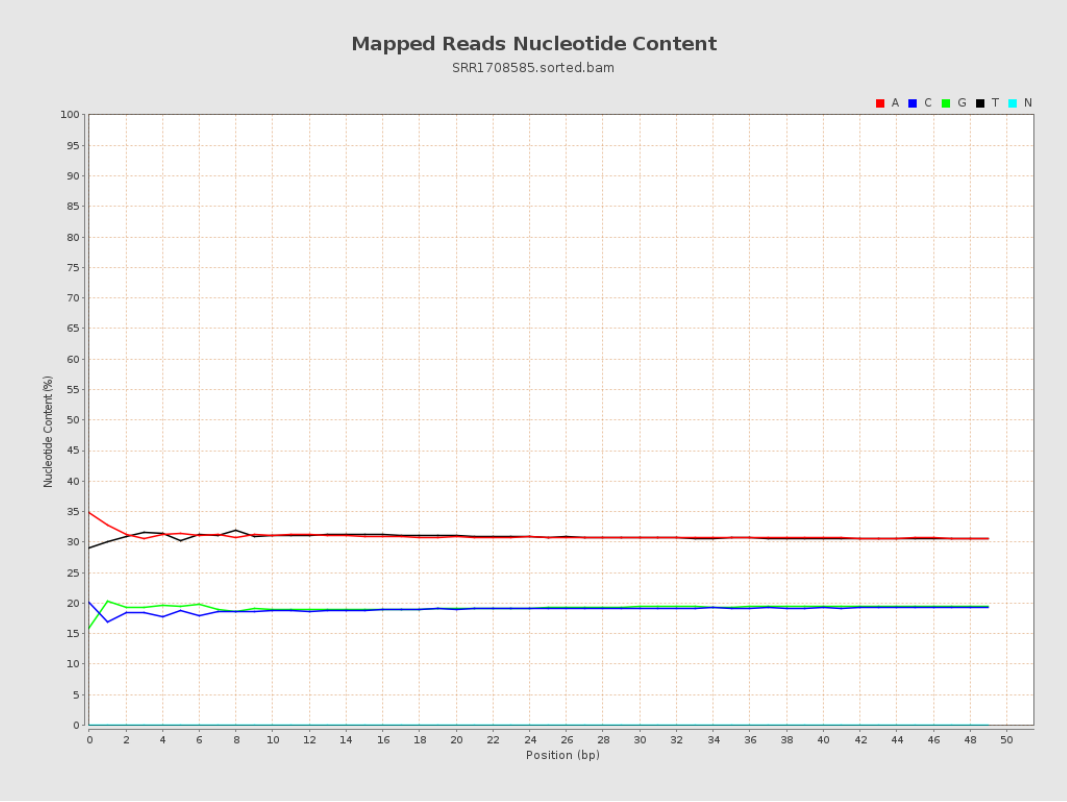
6. Results : Genome Fraction Coverage



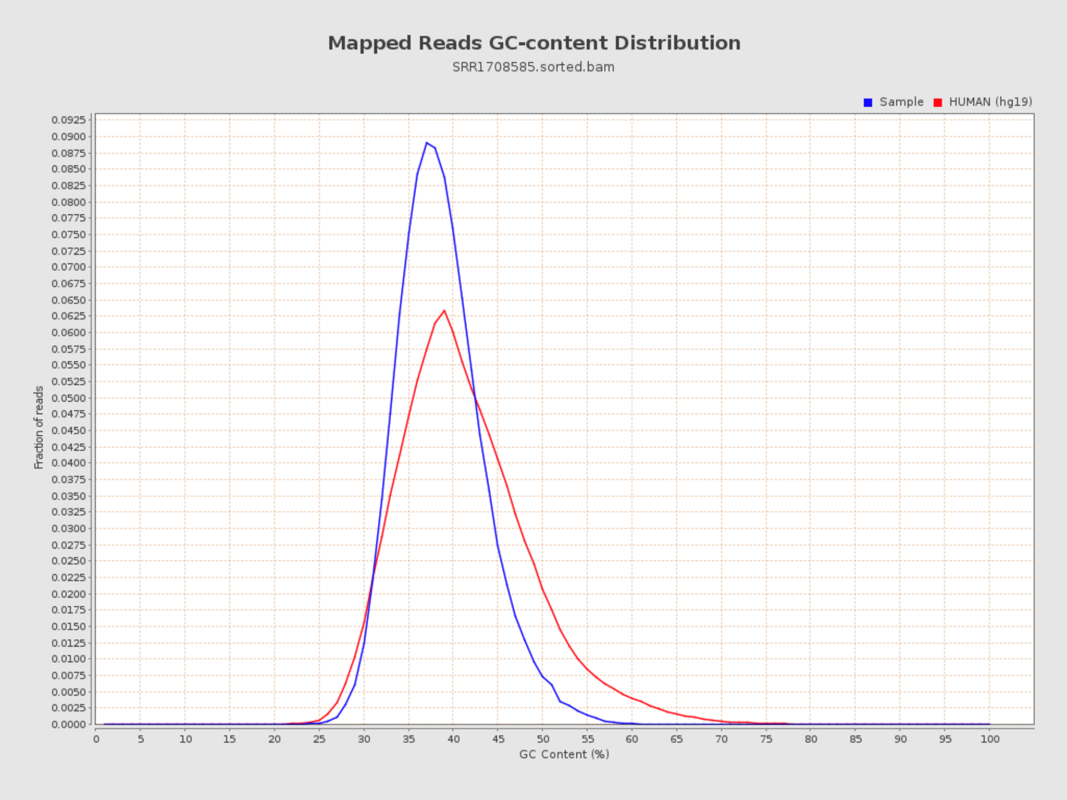
7. Results : Duplication Rate Histogram



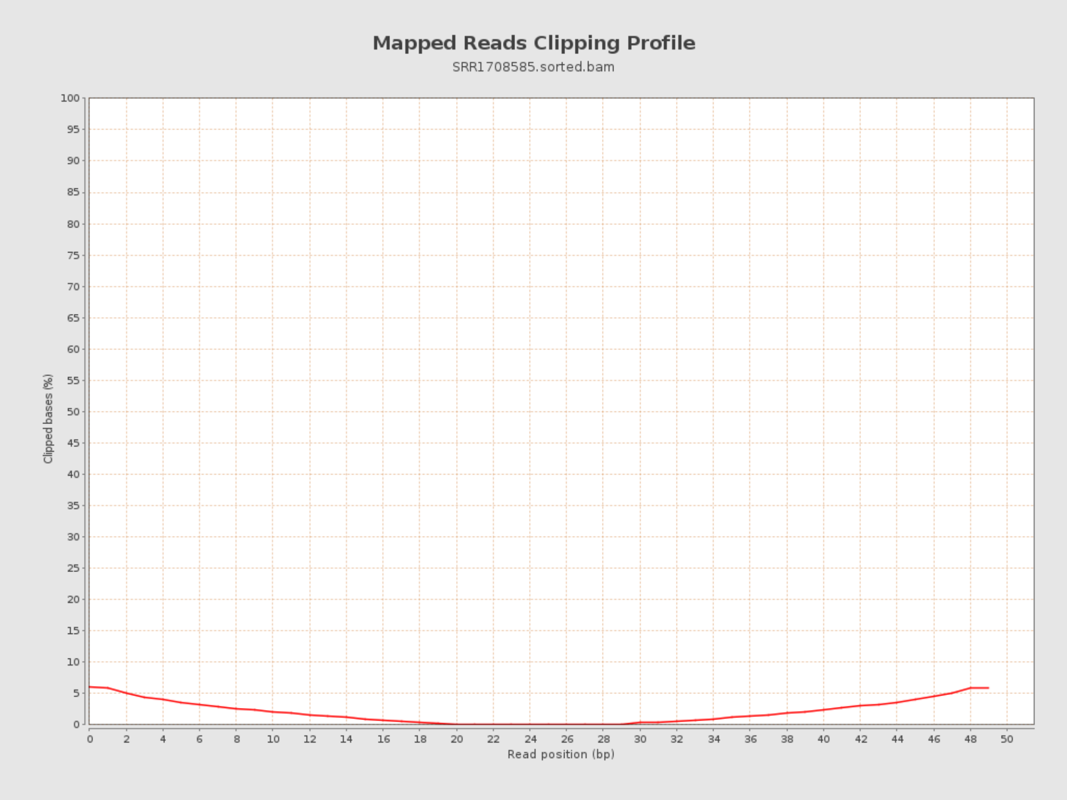
8. Results : Mapped Reads Nucleotide Content



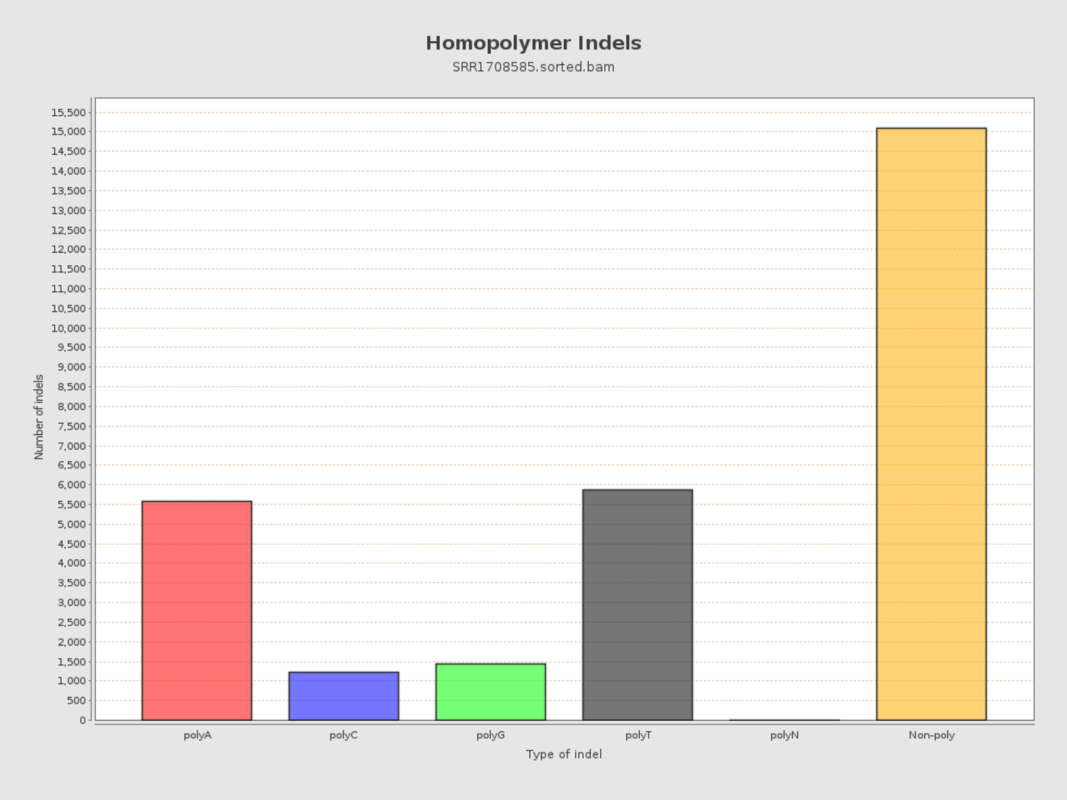
9. Results : Mapped Reads GC-content Distribution



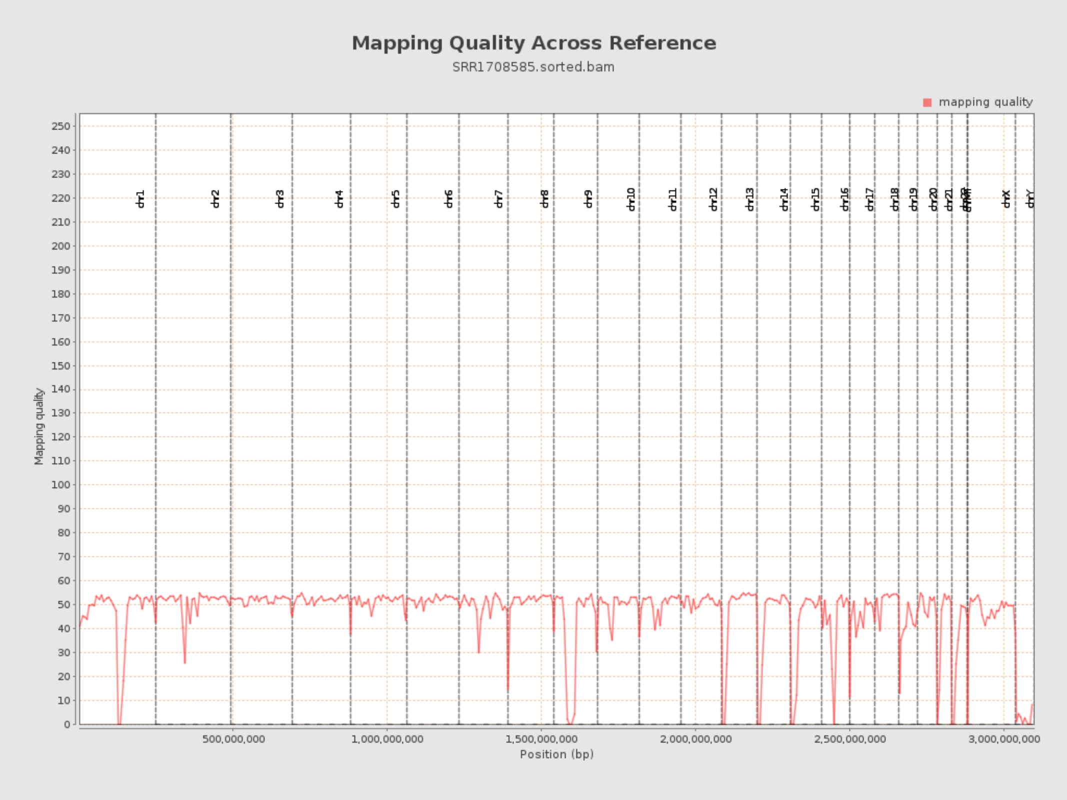
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram