Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:50:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708643.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_SRR1708643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:50:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,646,216
Mapped reads	4,447,875 / 95.73%
Unmapped reads	198,341 / 4.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	114 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	20,613 / 0.44%
Duplication rate	0.46%
Clipped reads	59,792 / 1.29%

2.2. ACGT Content

Number/percentage of A's	68,502,468 / 30.88%
Number/percentage of C's	42,269,042 / 19.06%
Number/percentage of T's	68,423,908 / 30.85%
Number/percentage of G's	42,617,797 / 19.21%
Number/percentage of N's	7,785 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	0.0717

Standard Deviation	0.2791

2.4. Mapping Quality

Mean Mapping Quality	46.53

2.5. Mismatches and indels

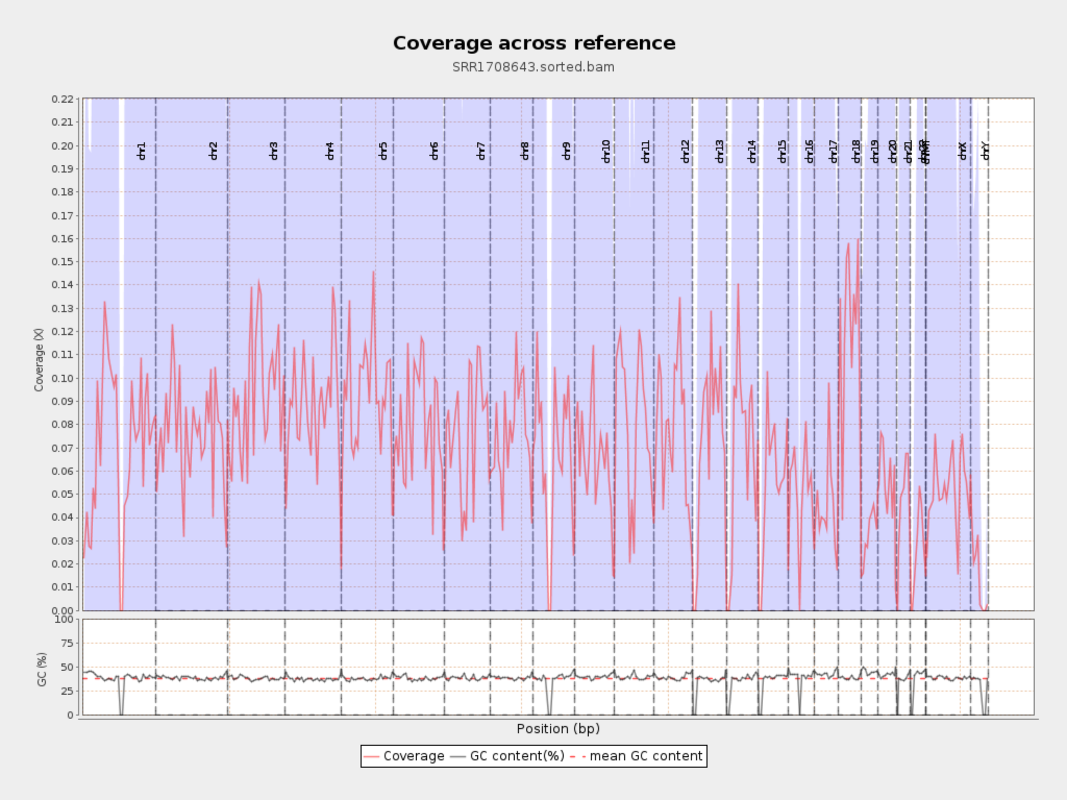
General error rate	0.17%
Mismatches	364,493
Insertions	15,294
Mapped reads with at least one insertion	0.34%
Deletions	13,022
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.67%

2.6. Chromosome stats

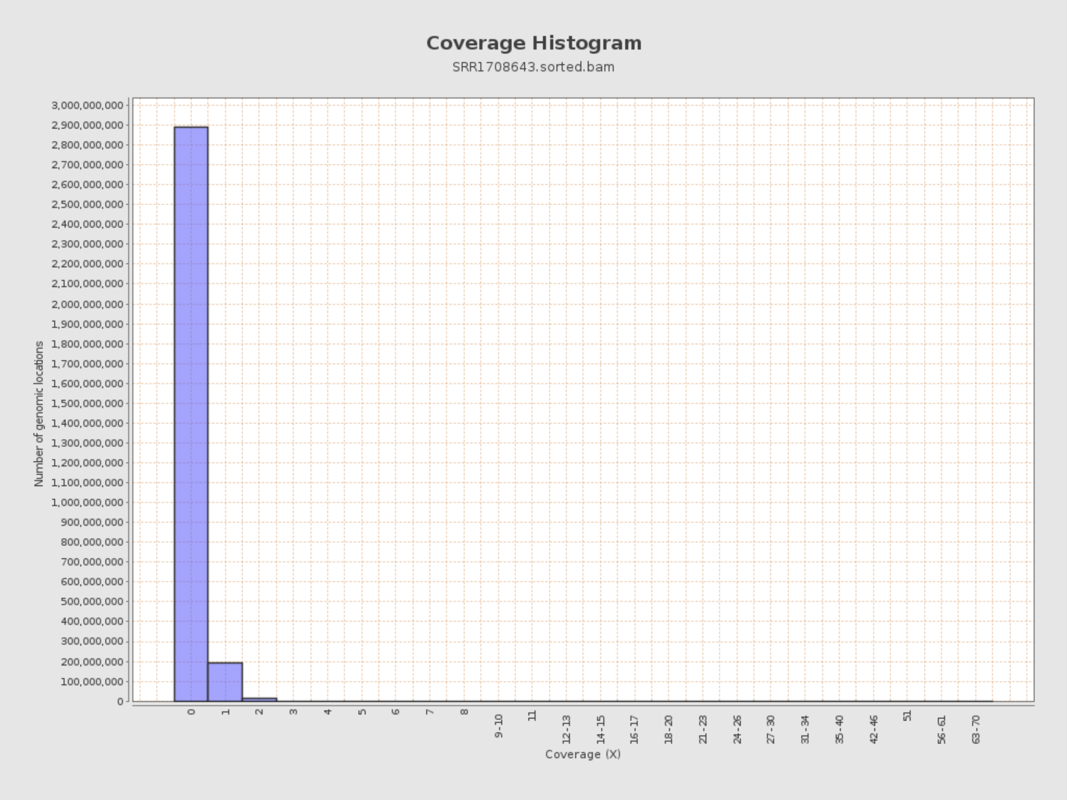
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17748084	0.0712	0.2799
chr2	243199373	18540821	0.0762	0.2869
chr3	198022430	18481687	0.0933	0.3171
chr4	191154276	16912847	0.0885	0.3083
chr5	180915260	16584050	0.0917	0.3138
chr6	171115067	13775449	0.0805	0.2944
chr7	159138663	12033127	0.0756	0.2866

chr8	146364022	11050347	0.0755	0.2849
chr9	141213431	9415764	0.0667	0.2694
chr10	135534747	9223048	0.068	0.27
chr11	135006516	10904605	0.0808	0.2977
chr12	133851895	10337453	0.0772	0.2895
chr13	115169878	8304245	0.0721	0.2802
chr14	107349540	7426327	0.0692	0.2749
chr15	102531392	5566679	0.0543	0.2432
chr16	90354753	4490131	0.0497	0.2311
chr17	81195210	3705804	0.0456	0.2231
chr18	78077248	9324068	0.1194	0.3606
chr19	59128983	1960071	0.0331	0.1877
chr20	63025520	3526493	0.056	0.2446
chr21	48129895	2180519	0.0453	0.2227
chr22	51304566	1367411	0.0267	0.1695
chrMT	16571	500	0.0302	0.1711
chrX	155270560	8128499	0.0524	0.2366
chrY	59373566	855406	0.0144	0.1246

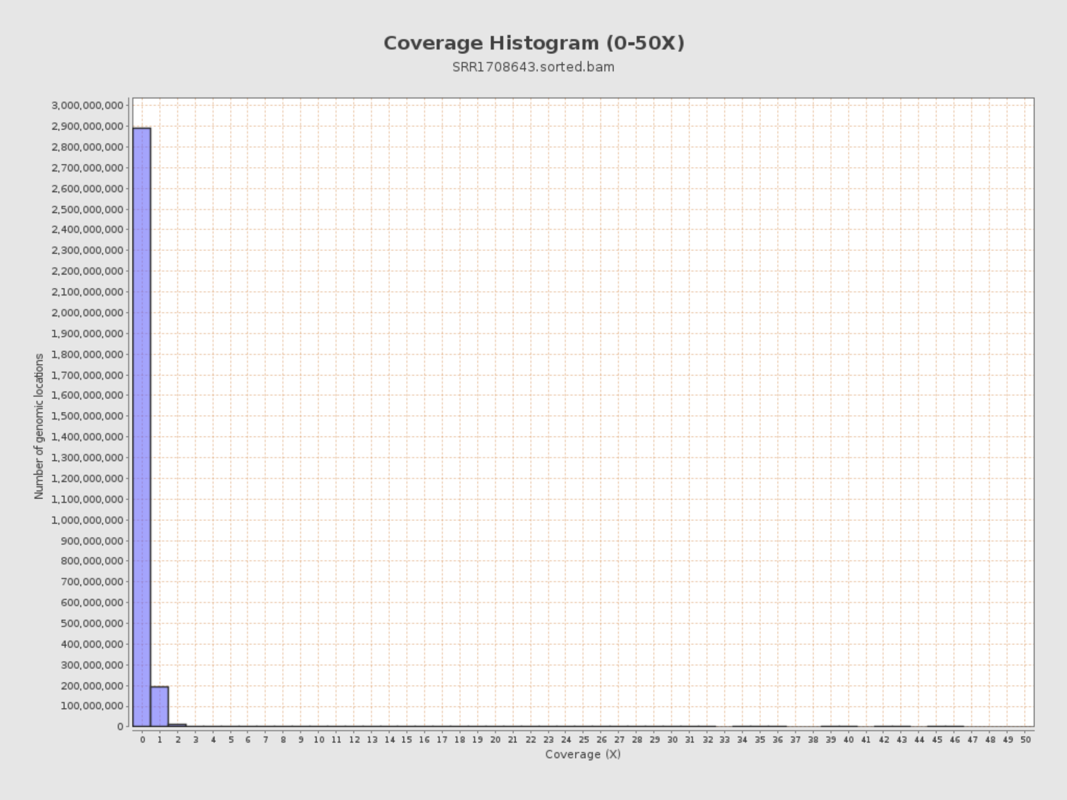
3. Results : Coverage across reference



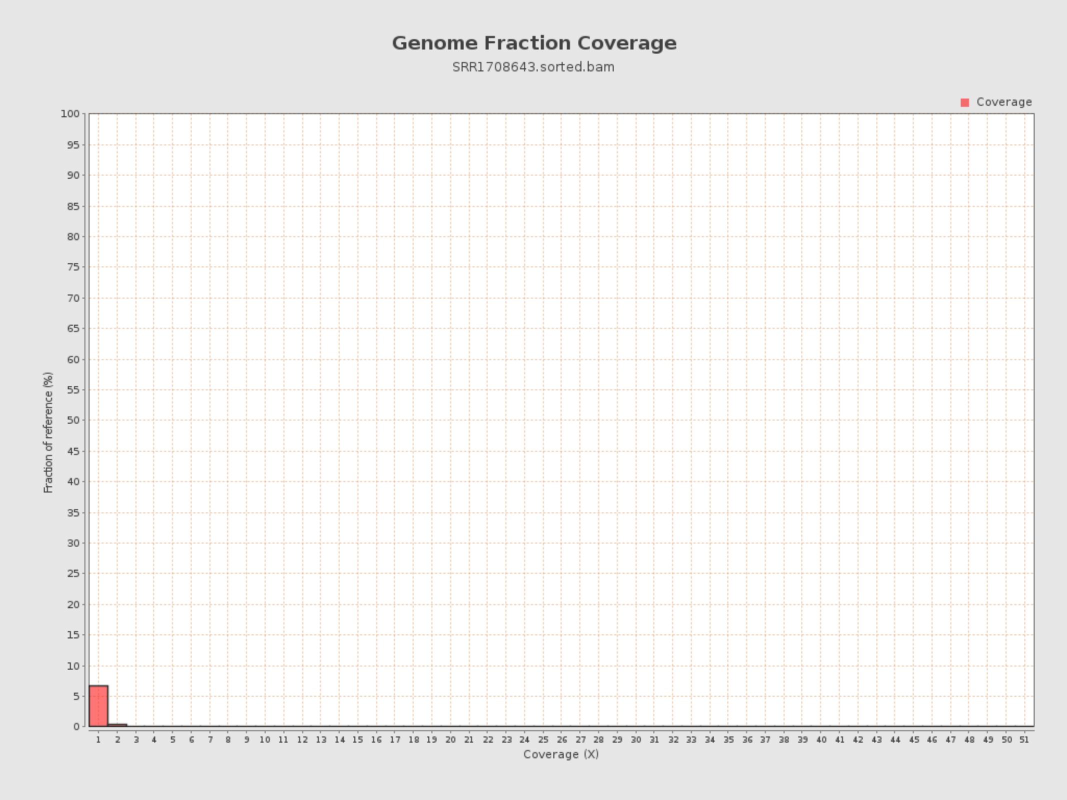
4. Results : Coverage Histogram



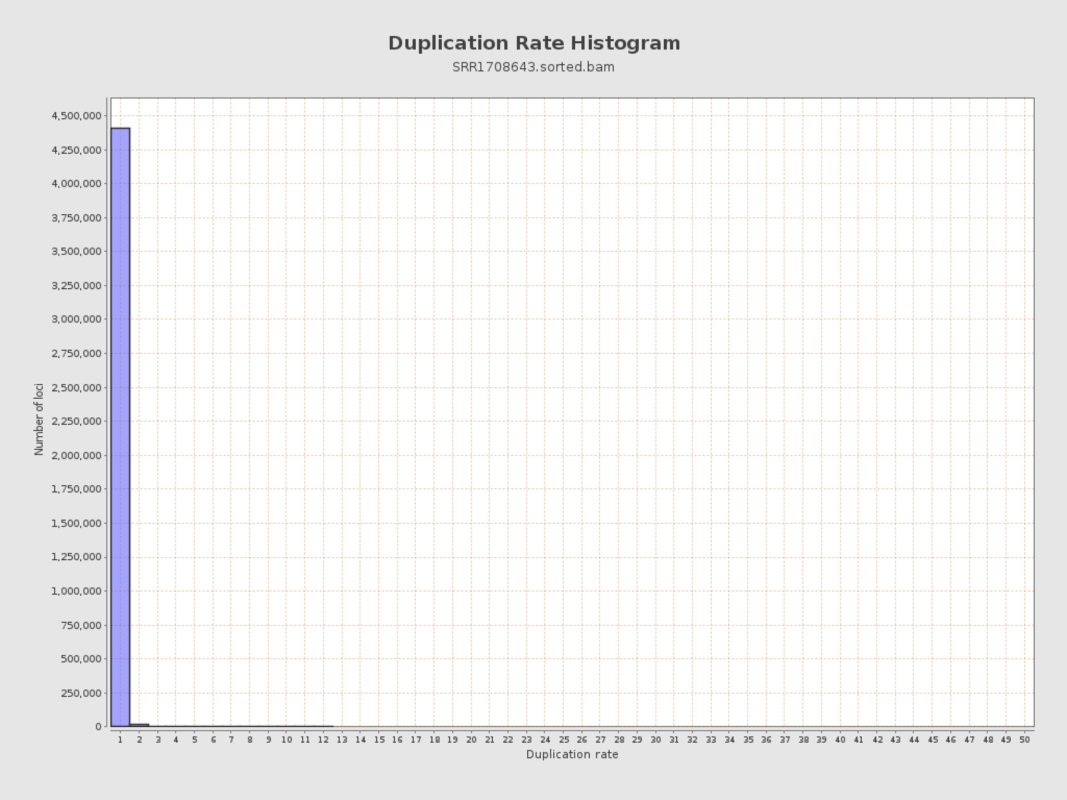
5. Results : Coverage Histogram (0-50X)



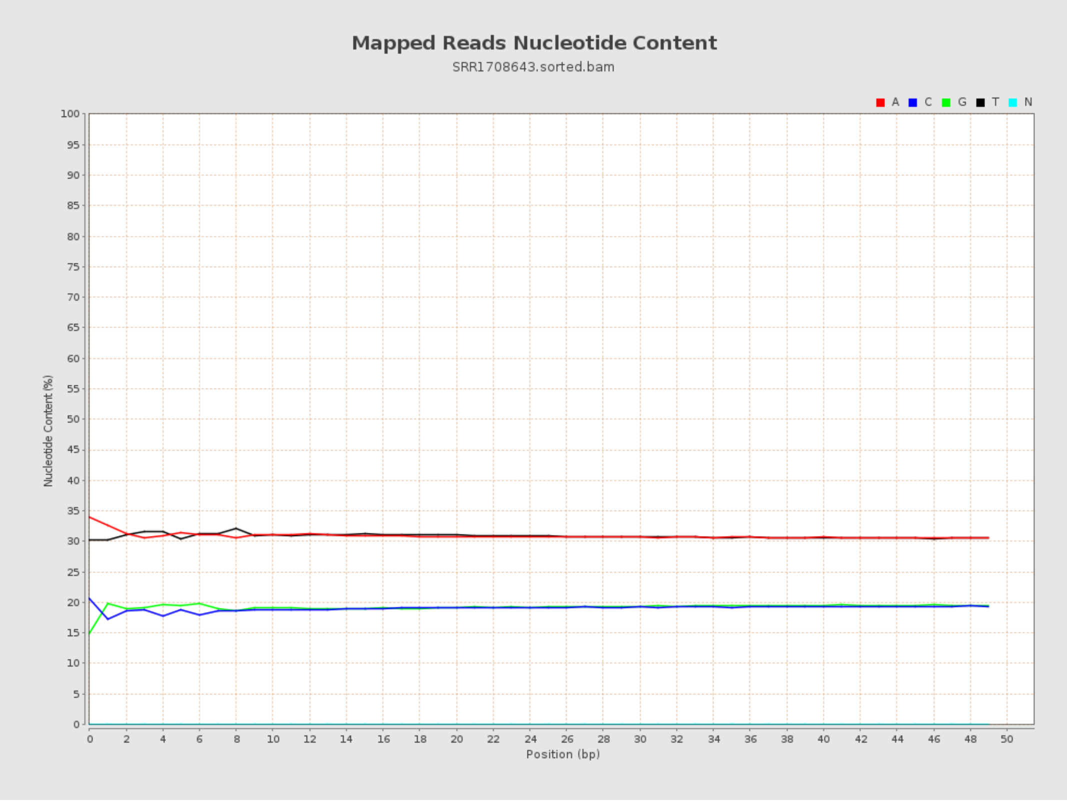
6. Results : Genome Fraction Coverage



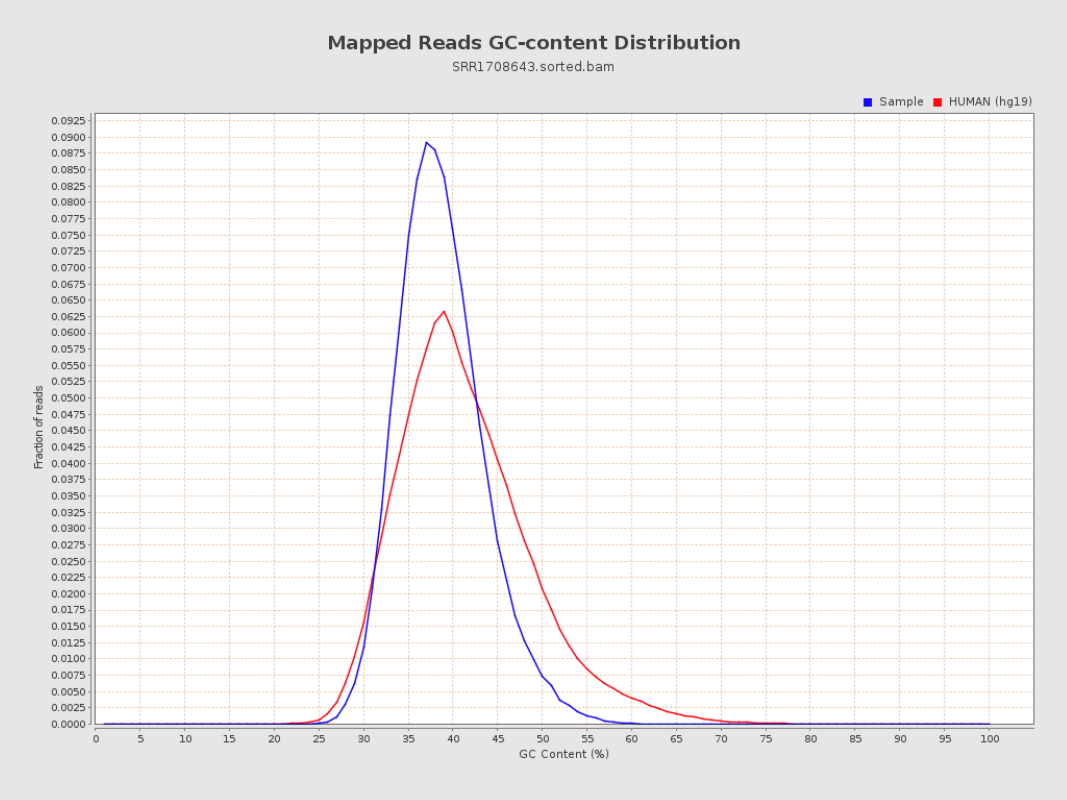
7. Results : Duplication Rate Histogram



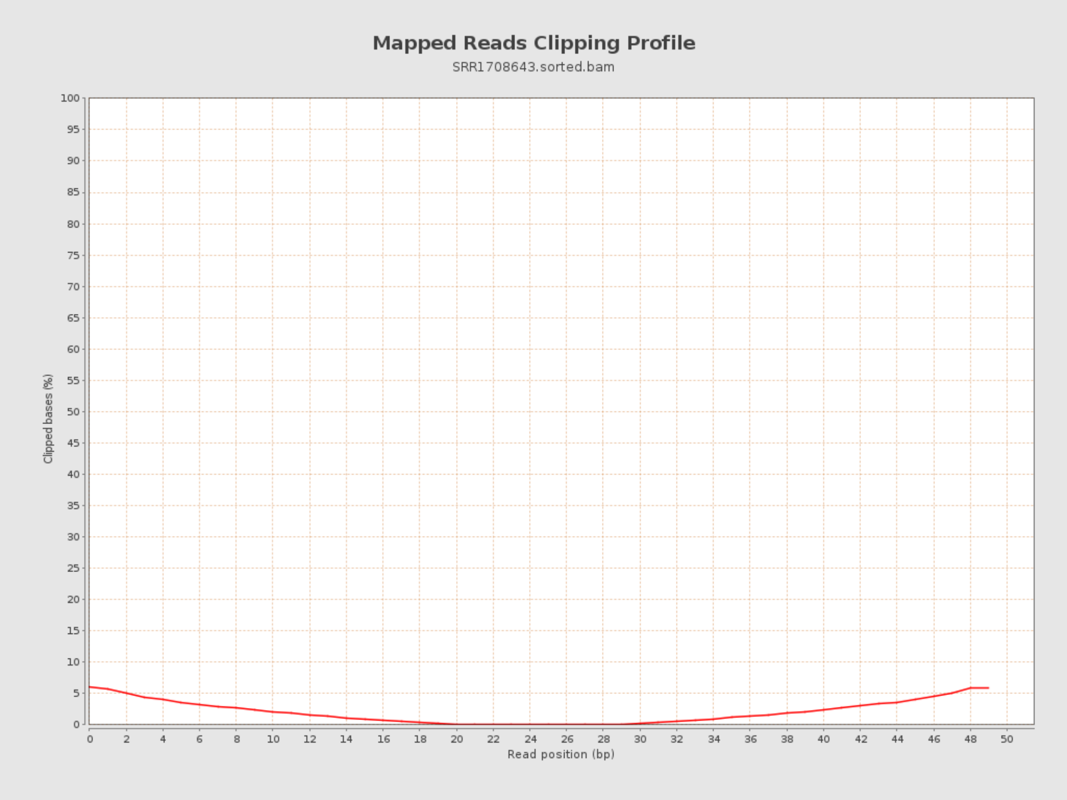
8. Results : Mapped Reads Nucleotide Content



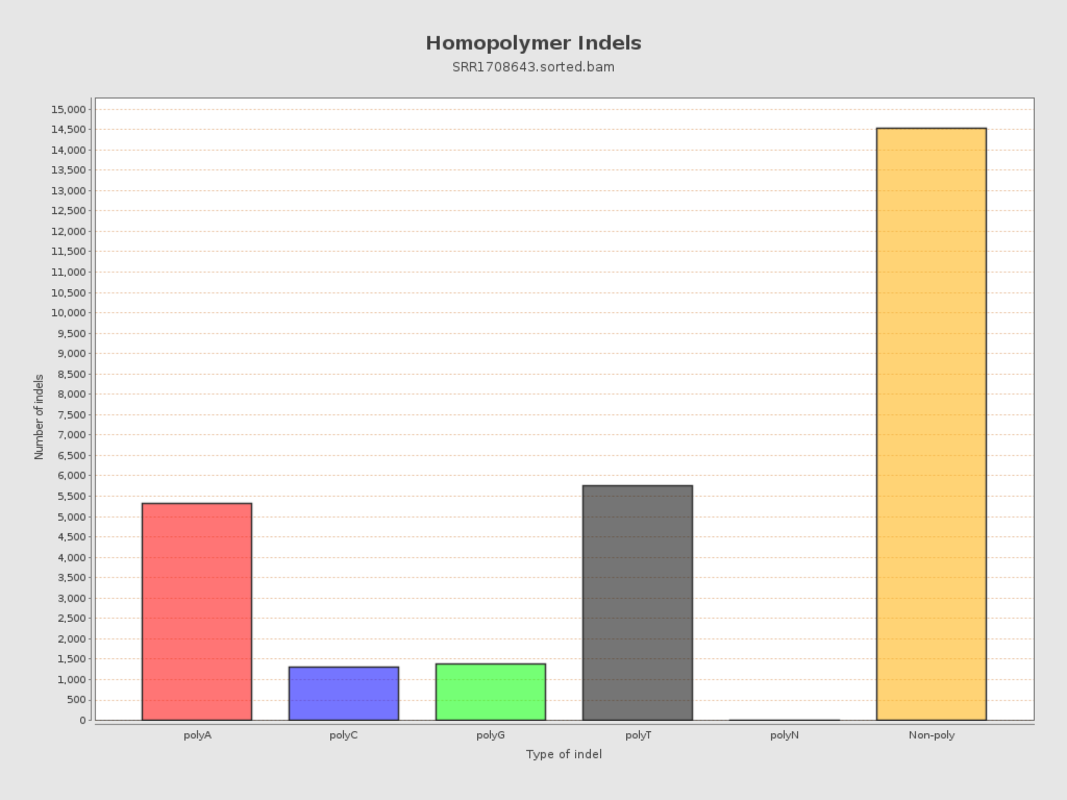
9. Results : Mapped Reads GC-content Distribution



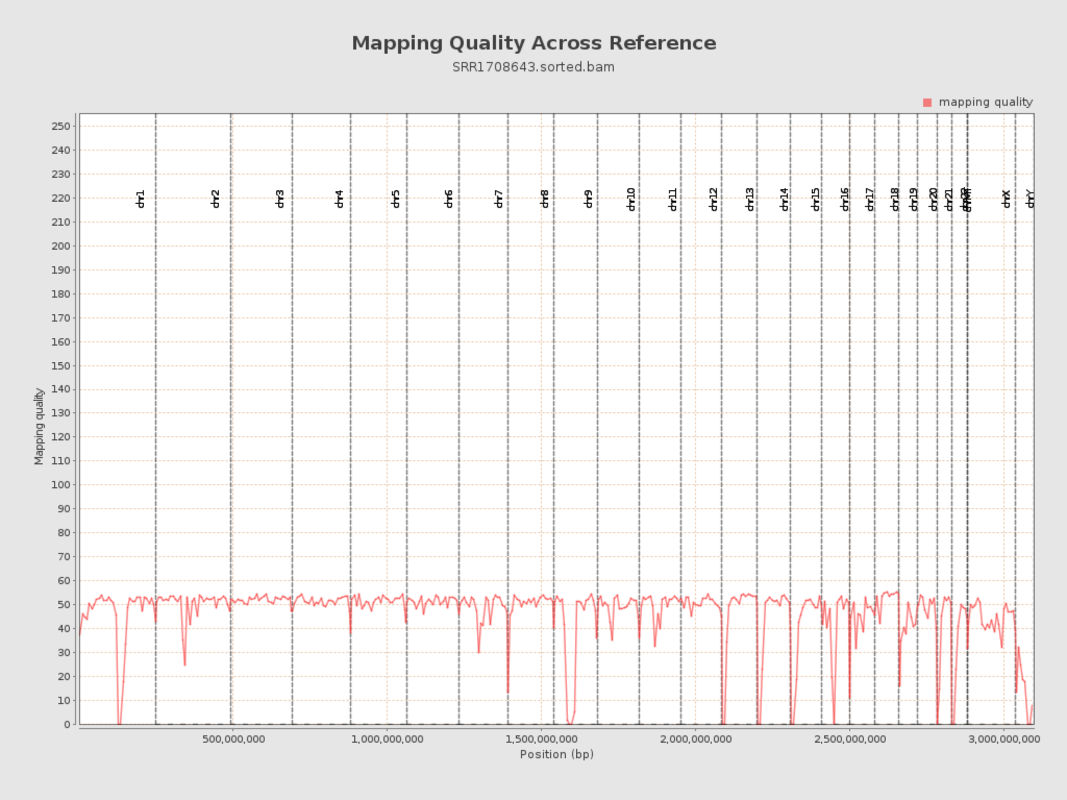
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram