Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:40:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708603.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_SRR1708603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:40:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,013,205
Mapped reads	4,917,678 / 98.09%
Unmapped reads	95,527 / 1.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	170 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	49,394 / 0.99%
Duplication rate	1.01%
Clipped reads	65,423 / 1.31%

2.2. ACGT Content

Number/percentage of A's	76,018,429 / 30.99%
Number/percentage of C's	46,427,945 / 18.93%
Number/percentage of T's	75,673,127 / 30.85%
Number/percentage of G's	47,138,908 / 19.22%
Number/percentage of N's	9,190 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0792

Standard Deviation	0.2943

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

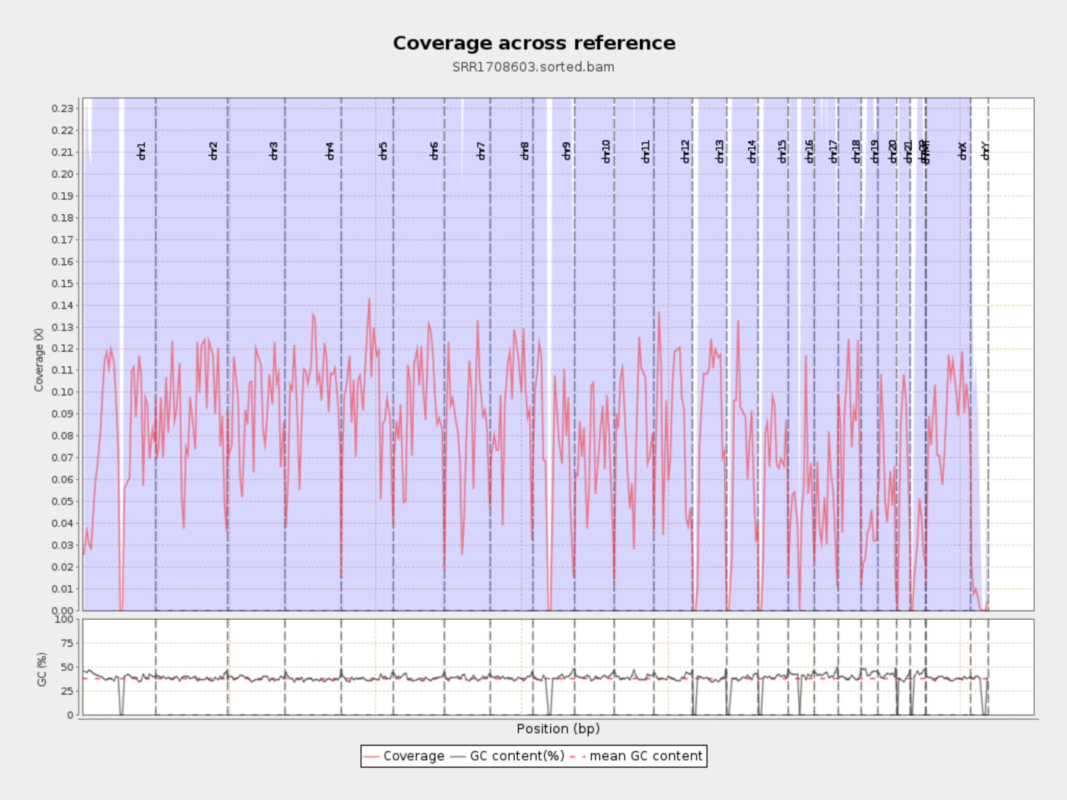
General error rate	0.15%
Mismatches	354,748
Insertions	15,714
Mapped reads with at least one insertion	0.32%
Deletions	12,085
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.31%

2.6. Chromosome stats

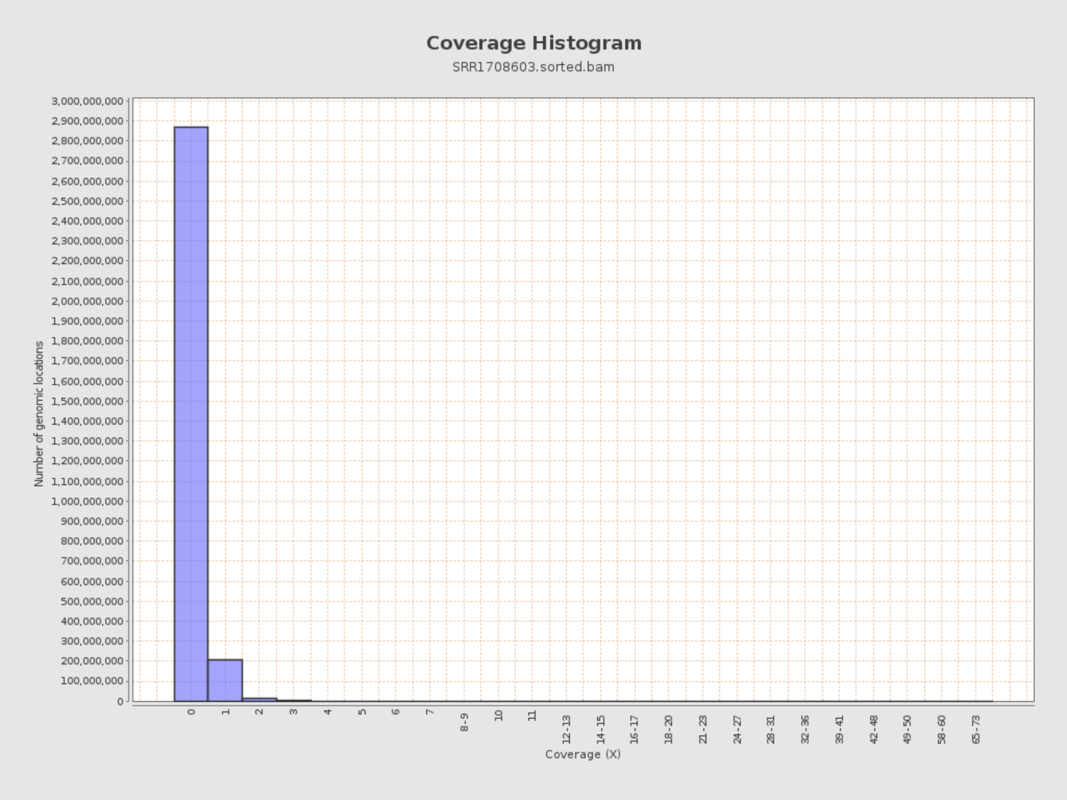
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18807715	0.0755	0.2889
chr2	243199373	22150630	0.0911	0.314
chr3	198022430	18313511	0.0925	0.3161
chr4	191154276	19195792	0.1004	0.3291
chr5	180915260	17653983	0.0976	0.3248
chr6	171115067	16226355	0.0948	0.3203
chr7	159138663	13295803	0.0835	0.302

chr8	146364022	13686848	0.0935	0.3184
chr9	141213431	10395018	0.0736	0.2841
chr10	135534747	9919639	0.0732	0.2811
chr11	135006516	11084513	0.0821	0.3011
chr12	133851895	11233007	0.0839	0.3026
chr13	115169878	9661859	0.0839	0.3032
chr14	107349540	7320245	0.0682	0.2737
chr15	102531392	6416797	0.0626	0.2623
chr16	90354753	4432081	0.0491	0.2308
chr17	81195210	3831268	0.0472	0.2263
chr18	78077248	7000766	0.0897	0.3107
chr19	59128983	1927096	0.0326	0.1867
chr20	63025520	3945630	0.0626	0.2612
chr21	48129895	3118176	0.0648	0.2686
chr22	51304566	1329004	0.0259	0.1677
chrMT	16571	200	0.0121	0.1092
chrX	155270560	14022568	0.0903	0.313
chrY	59373566	319748	0.0054	0.0774

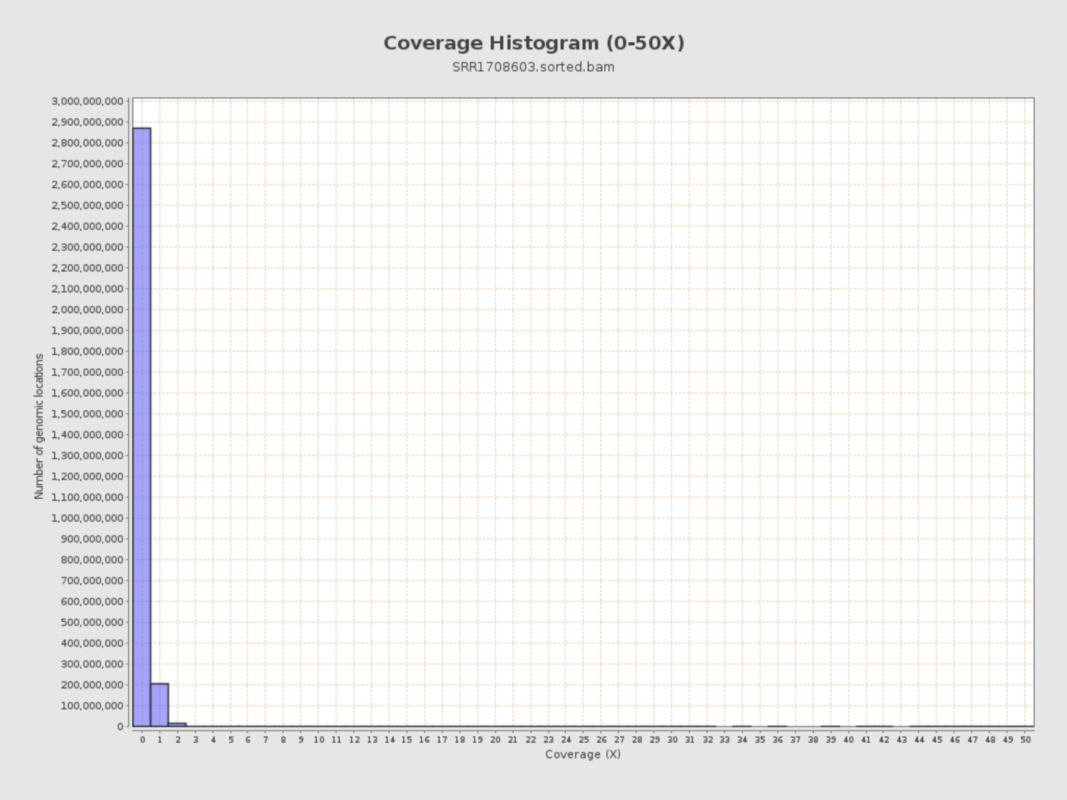
3. Results : Coverage across reference



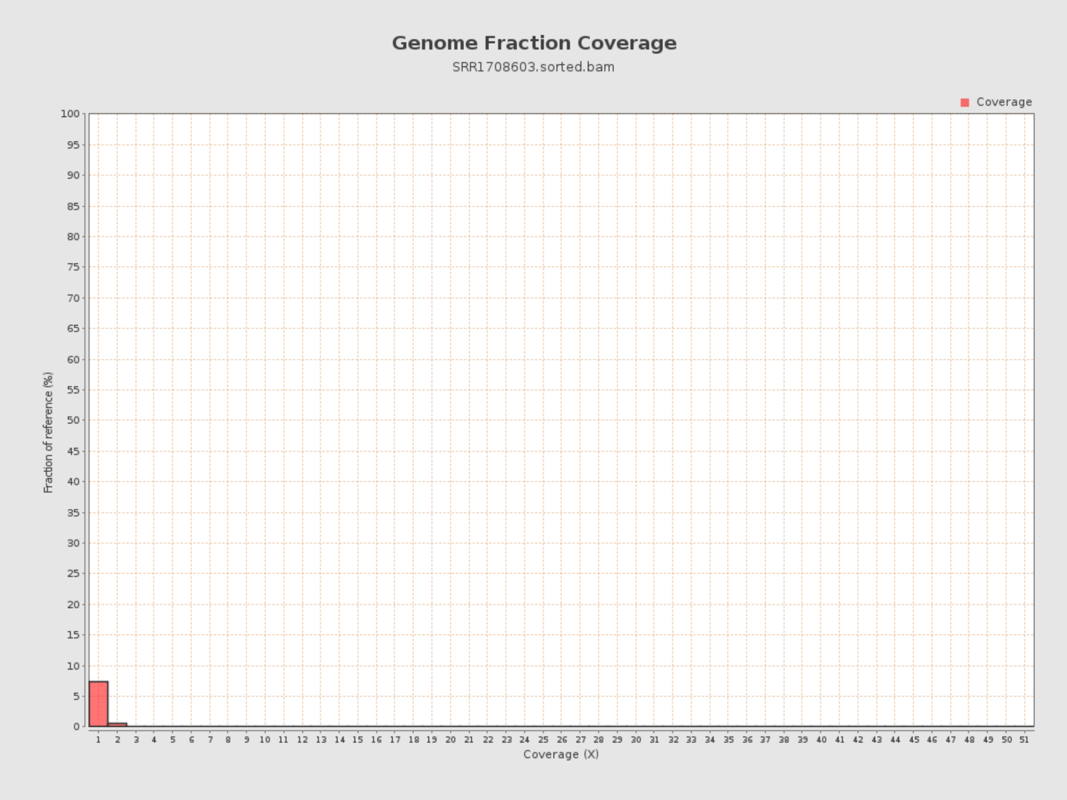
4. Results : Coverage Histogram



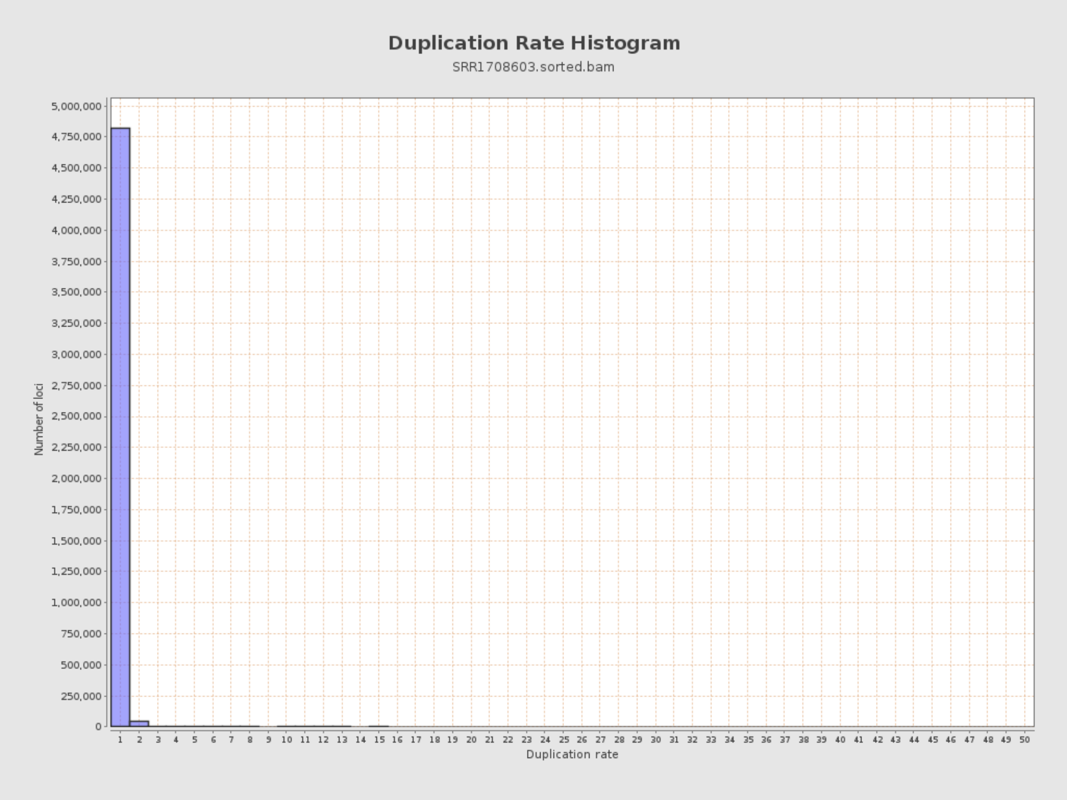
5. Results : Coverage Histogram (0-50X)



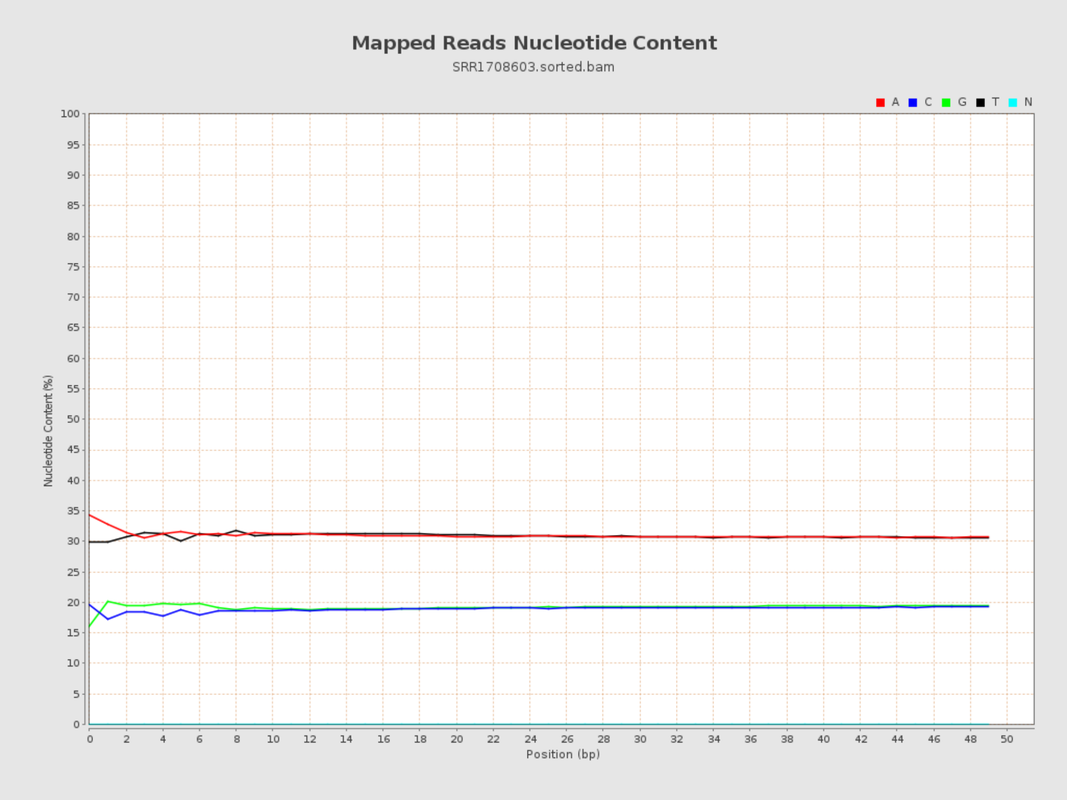
6. Results : Genome Fraction Coverage



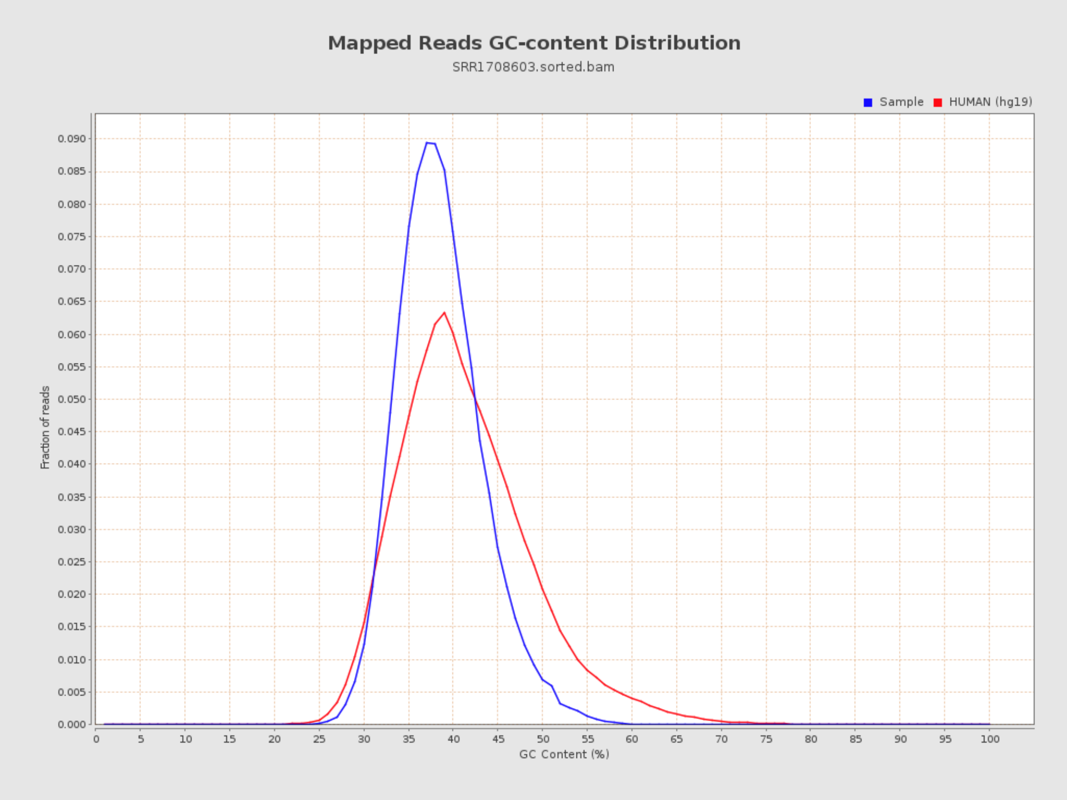
7. Results : Duplication Rate Histogram



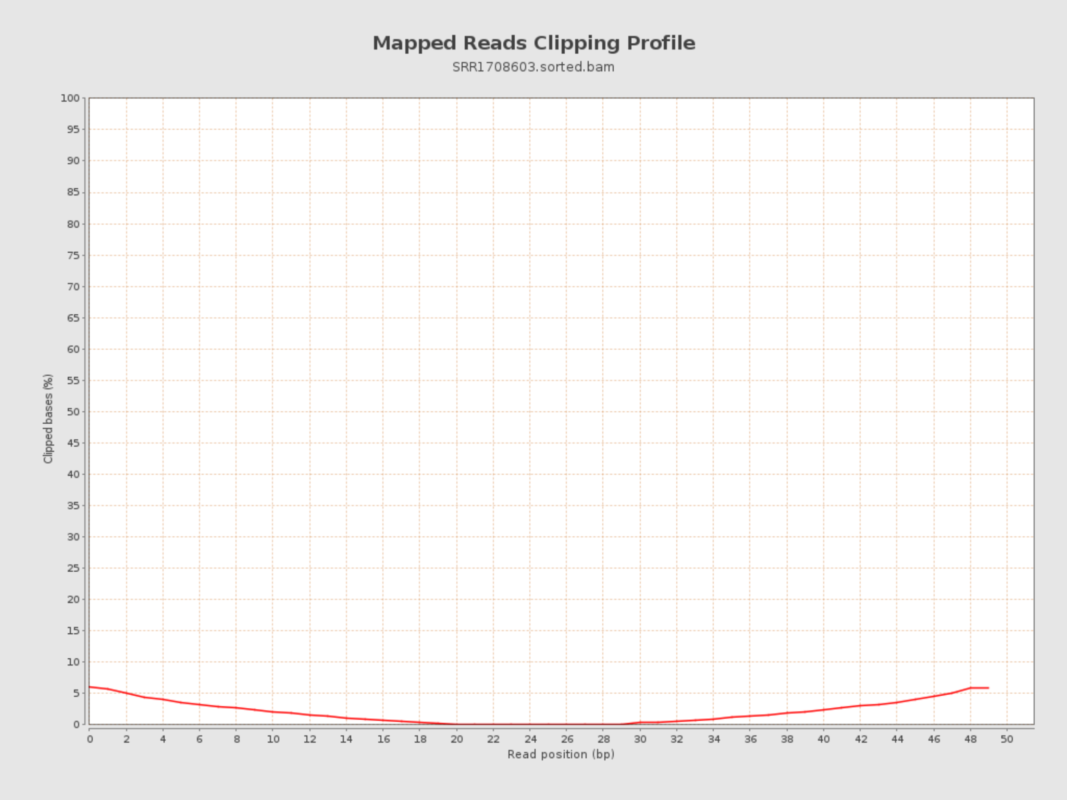
8. Results : Mapped Reads Nucleotide Content



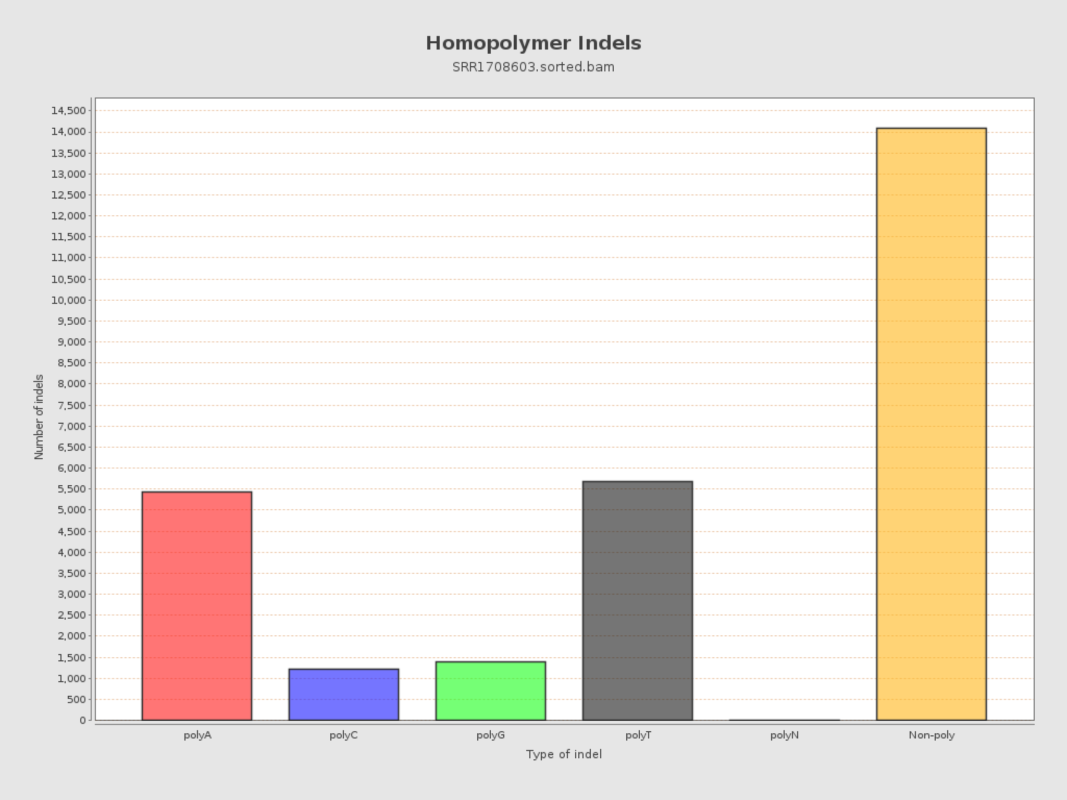
9. Results : Mapped Reads GC-content Distribution



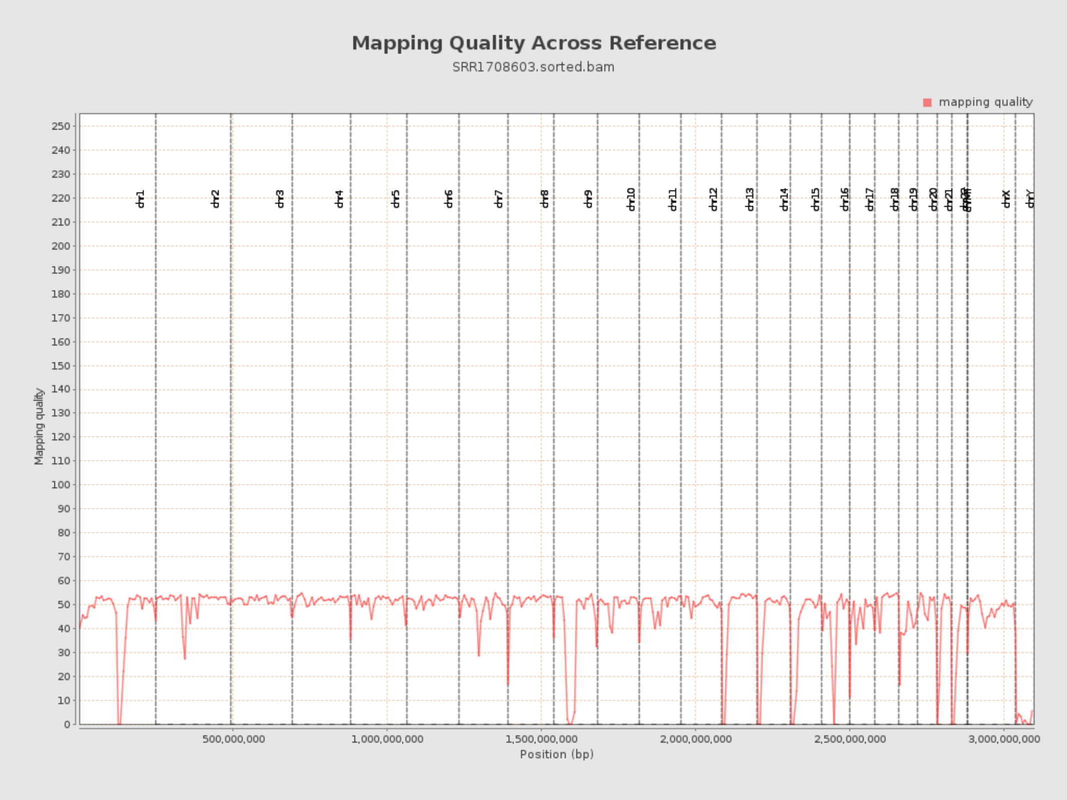
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram