Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:04:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708592.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_SRR1708592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:04:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,759,503
Mapped reads	5,641,022 / 97.94%
Unmapped reads	118,481 / 2.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	155 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	55,763 / 0.97%
Duplication rate	0.99%
Clipped reads	77,312 / 1.34%

2.2. ACGT Content

Number/percentage of A's	87,204,222 / 31%
Number/percentage of C's	53,294,003 / 18.94%
Number/percentage of T's	86,785,929 / 30.85%
Number/percentage of G's	54,028,840 / 19.21%
Number/percentage of N's	9,269 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0909

Standard Deviation	0.3155

2.4. Mapping Quality

Mean Mapping Quality	46.81

2.5. Mismatches and indels

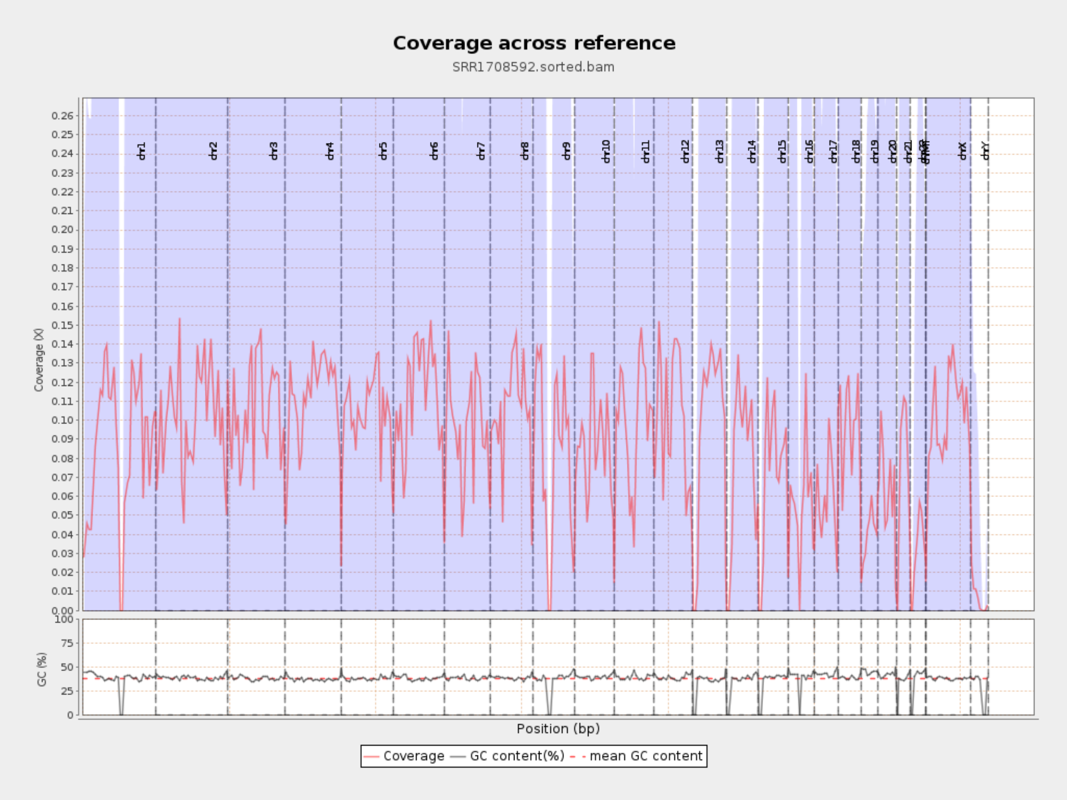
General error rate	0.16%
Mismatches	413,937
Insertions	18,036
Mapped reads with at least one insertion	0.32%
Deletions	14,061
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.23%

2.6. Chromosome stats

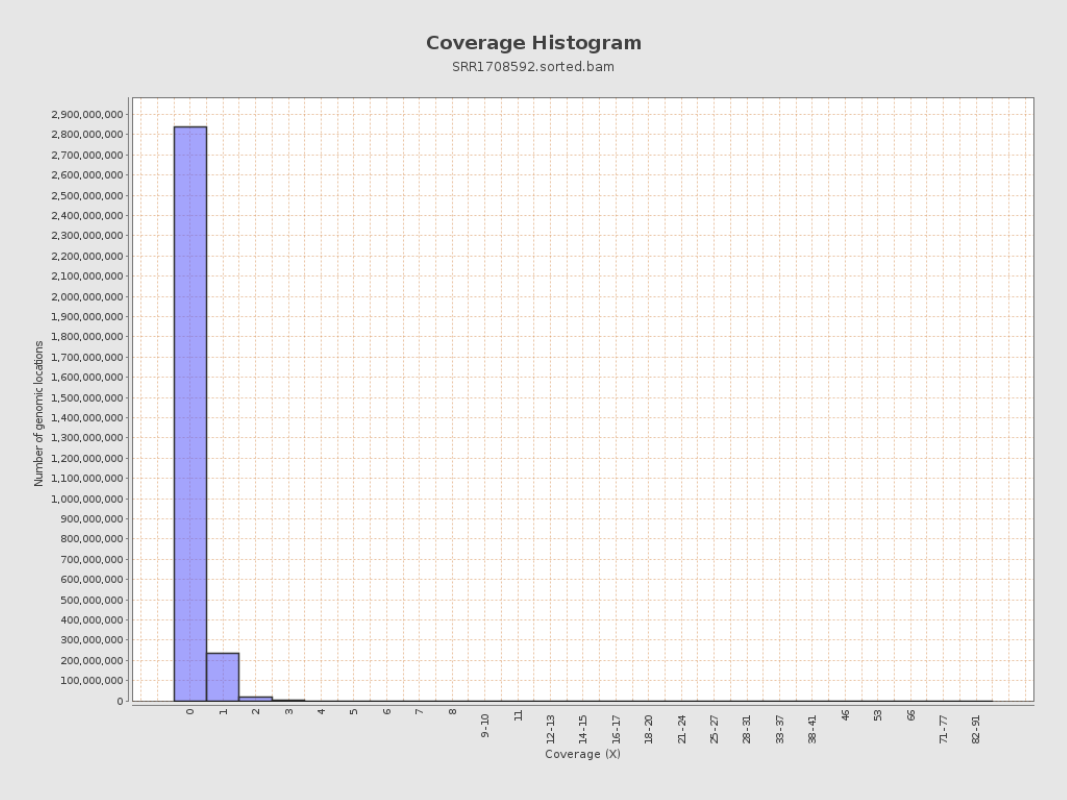
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21704592	0.0871	0.3111
chr2	243199373	24794617	0.102	0.3325
chr3	198022430	20901062	0.1055	0.338
chr4	191154276	21491504	0.1124	0.3484
chr5	180915260	18651261	0.1031	0.3335
chr6	171115067	19488614	0.1139	0.3519
chr7	159138663	15146345	0.0952	0.3225

chr8	146364022	15520306	0.106	0.3389
chr9	141213431	11874230	0.0841	0.3045
chr10	135534747	11897783	0.0878	0.3078
chr11	135006516	13371064	0.099	0.3302
chr12	133851895	13585532	0.1015	0.3327
chr13	115169878	11393679	0.0989	0.3298
chr14	107349540	8567027	0.0798	0.2967
chr15	102531392	7404887	0.0722	0.2824
chr16	90354753	4984171	0.0552	0.2456
chr17	81195210	4888354	0.0602	0.2565
chr18	78077248	7672743	0.0983	0.3257
chr19	59128983	2429410	0.0411	0.2093
chr20	63025520	4185380	0.0664	0.2684
chr21	48129895	3459921	0.0719	0.2838
chr22	51304566	1654333	0.0322	0.1873
chrMT	16571	250	0.0151	0.1219
chrX	155270560	15898167	0.1024	0.3331
chrY	59373566	380798	0.0064	0.0846

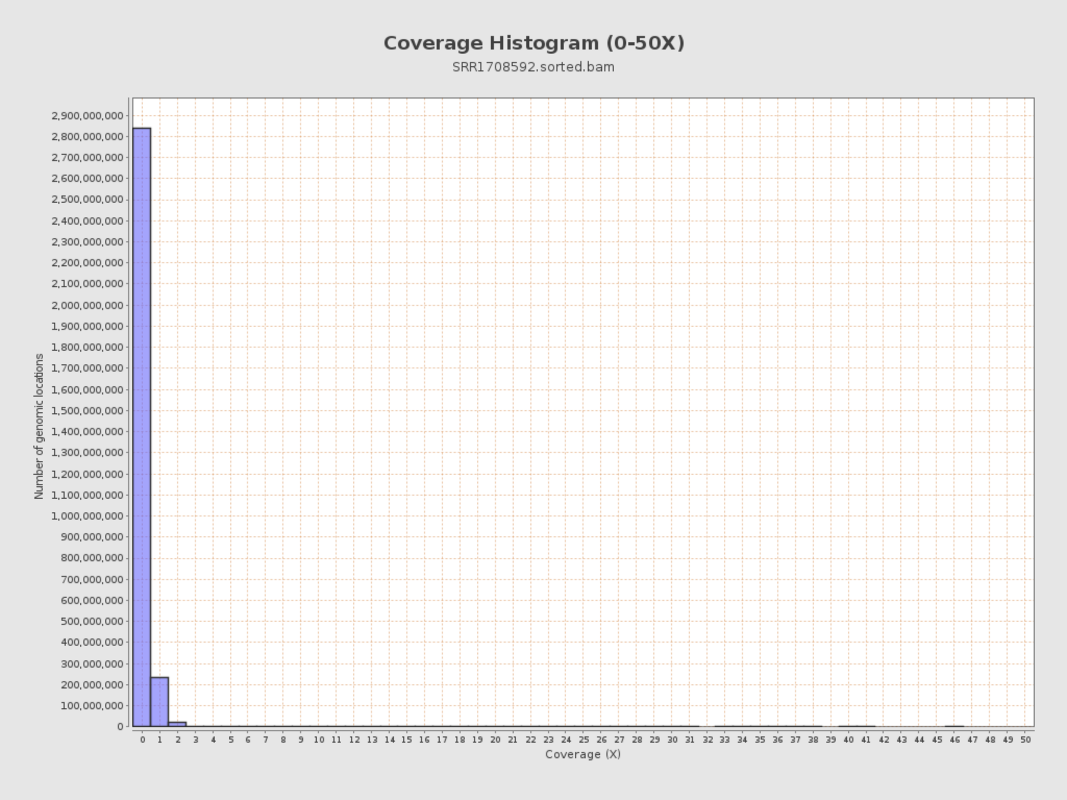
3. Results : Coverage across reference



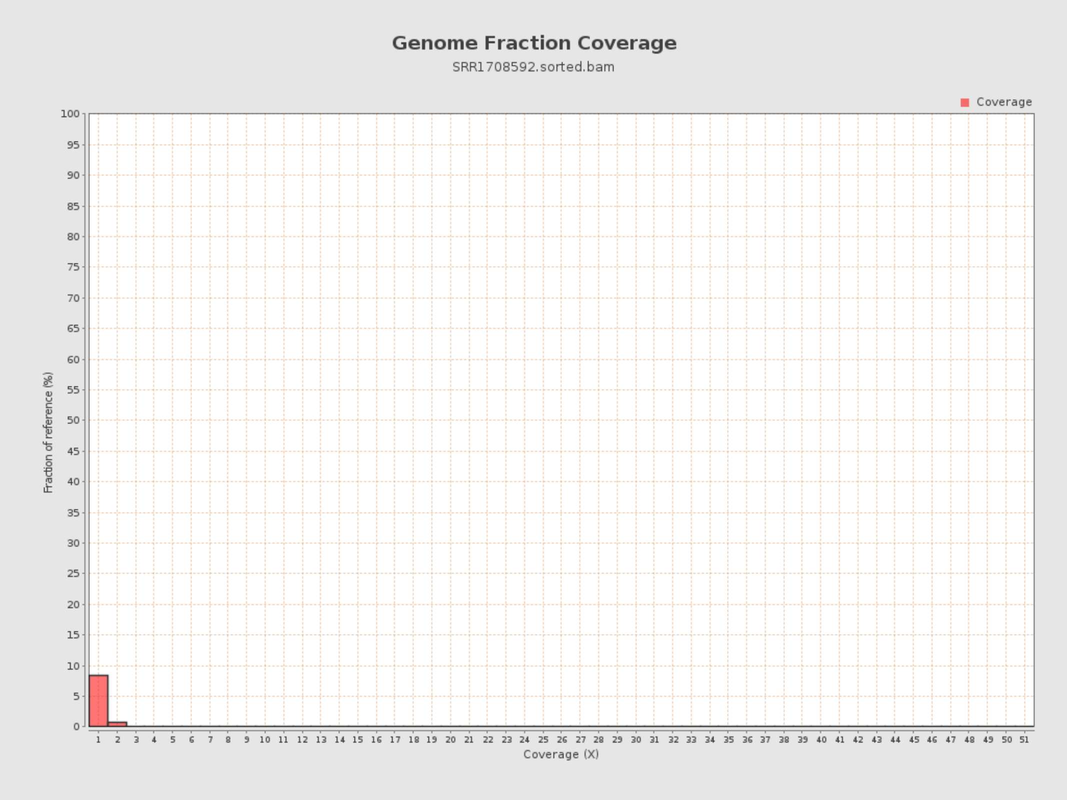
4. Results : Coverage Histogram



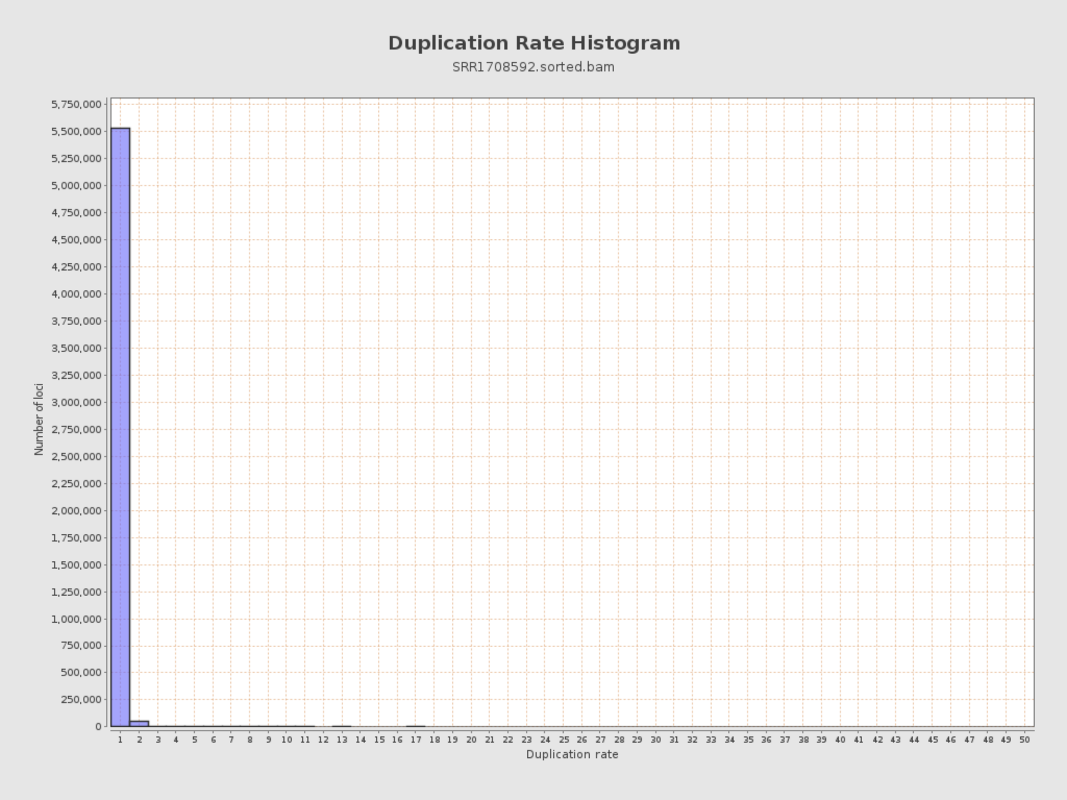
5. Results : Coverage Histogram (0-50X)



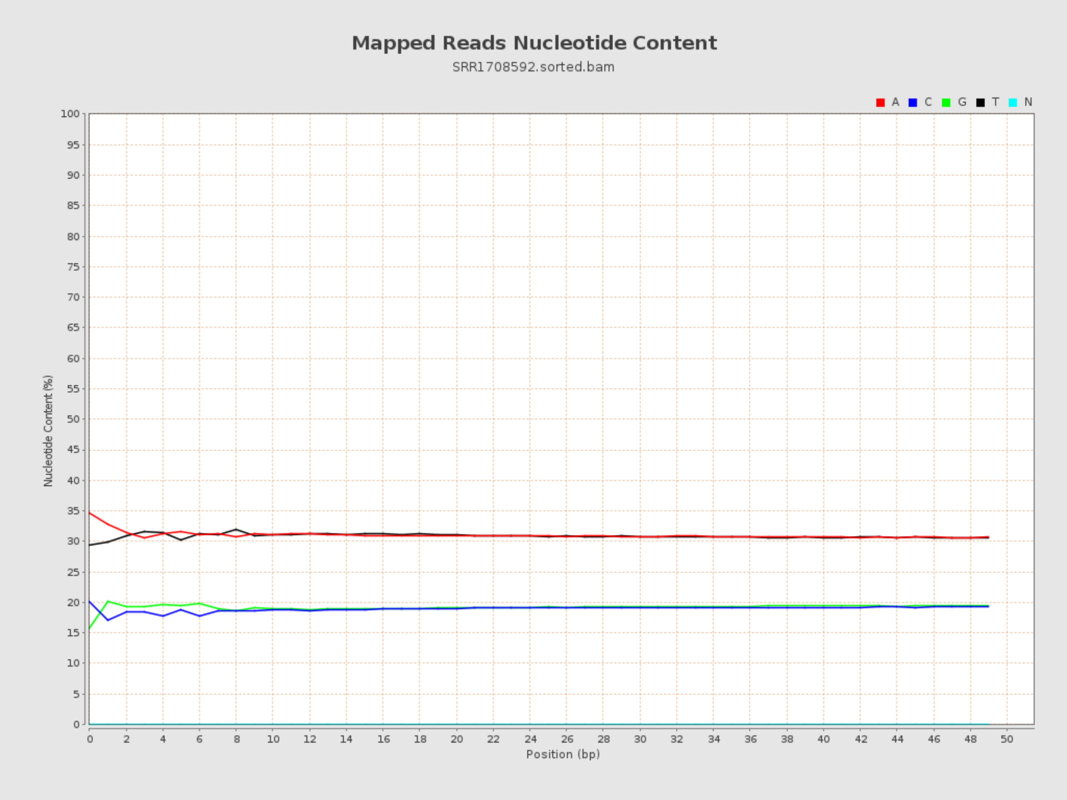
6. Results : Genome Fraction Coverage



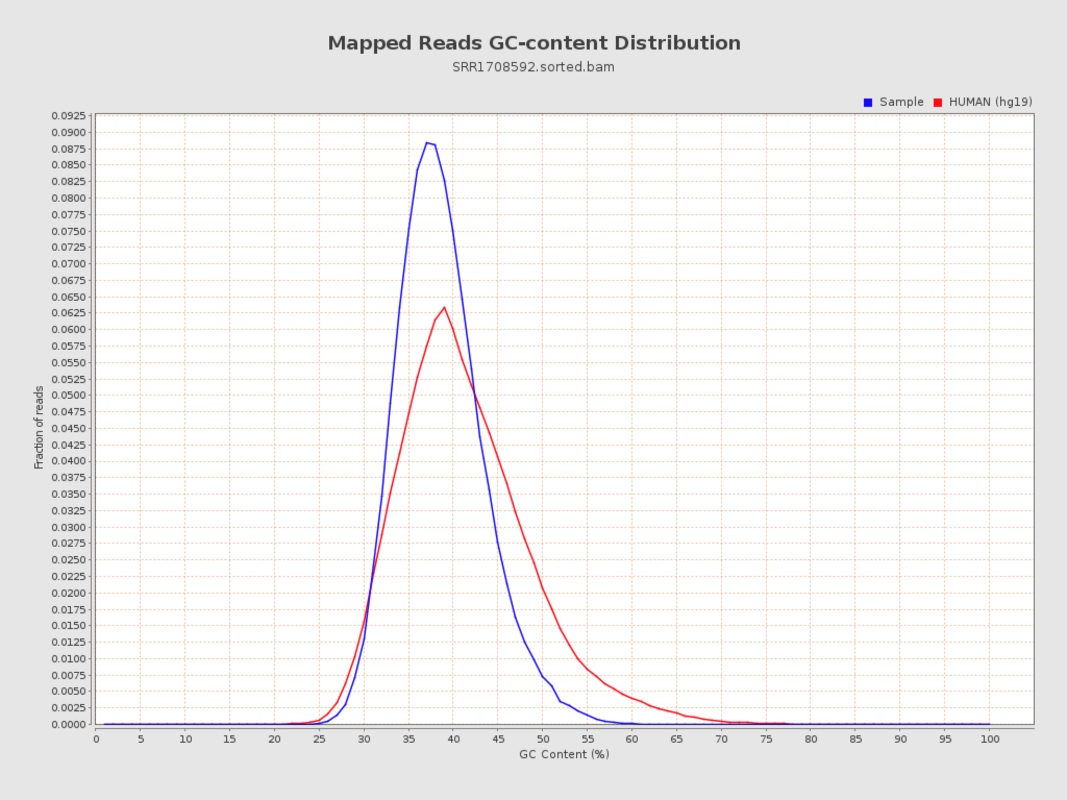
7. Results : Duplication Rate Histogram



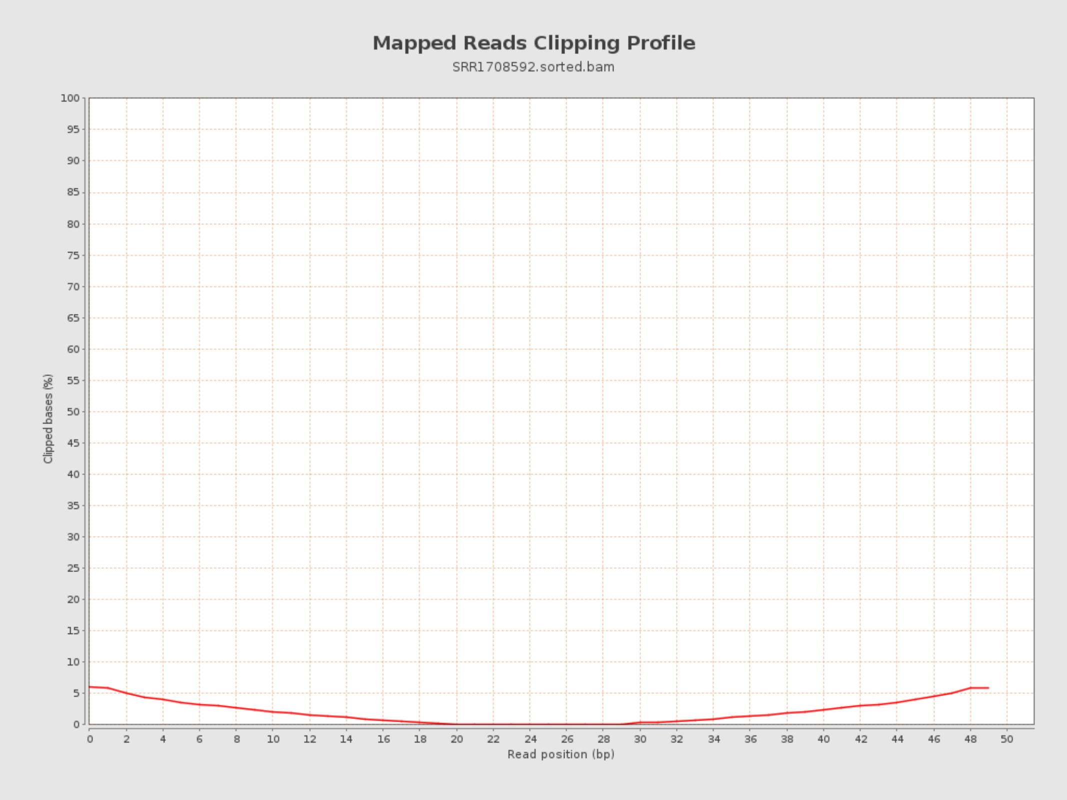
8. Results : Mapped Reads Nucleotide Content



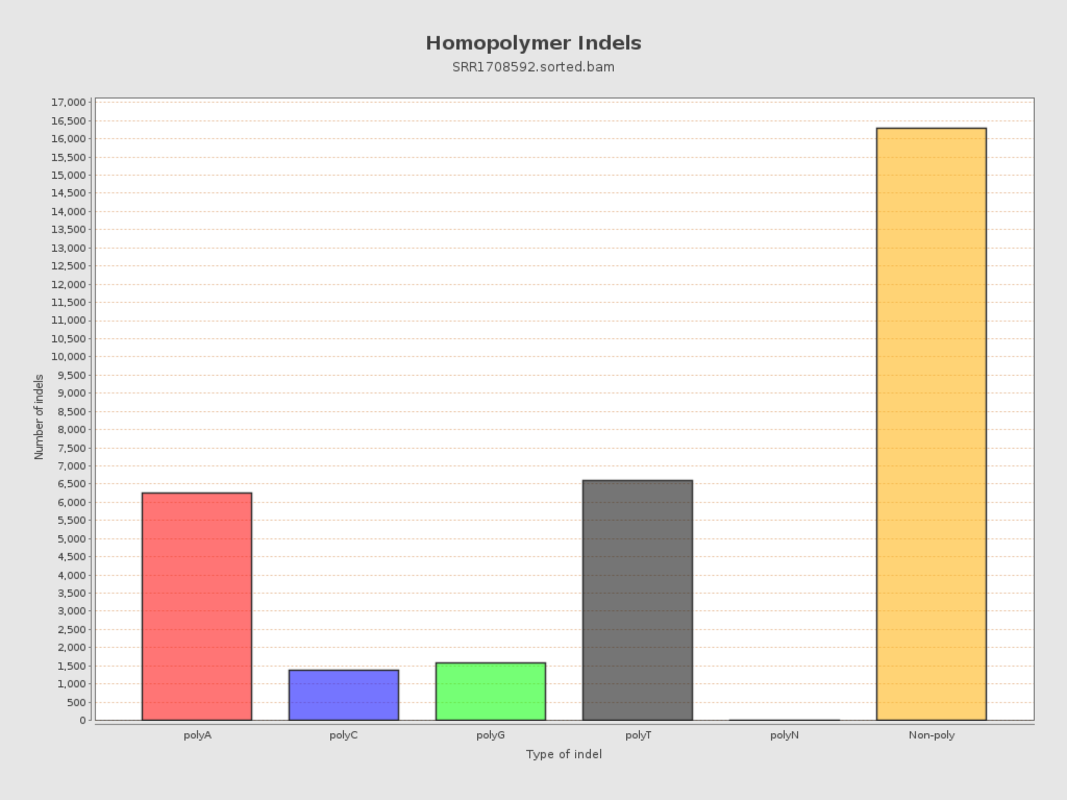
9. Results : Mapped Reads GC-content Distribution



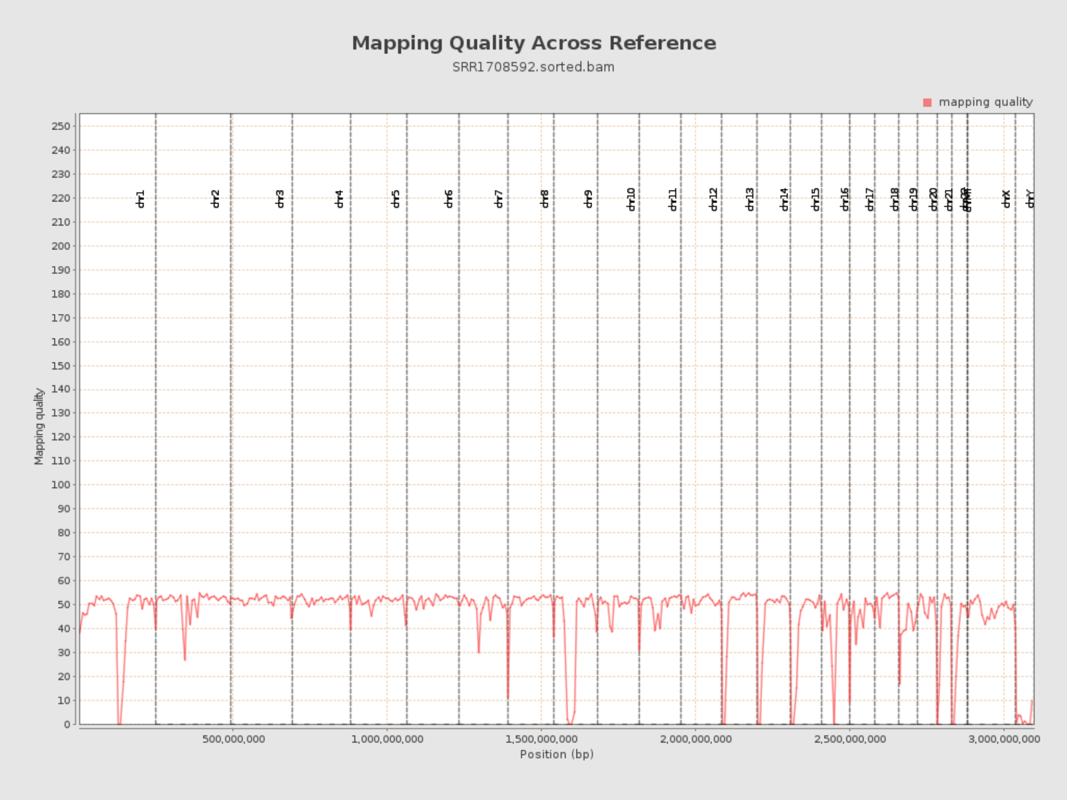
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram