Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:49:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008706.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_SRR6008706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008706.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:49:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,937,900
Mapped reads	502,573 / 17.11%
Unmapped reads	2,435,327 / 82.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,253 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	37,596 / 1.28%
Duplication rate	4.04%
Clipped reads	389,488 / 13.26%

2.2. ACGT Content

Number/percentage of A's	7,745,180 / 27.15%
Number/percentage of C's	4,279,709 / 15%
Number/percentage of T's	9,594,243 / 33.64%
Number/percentage of G's	6,899,085 / 24.19%
Number/percentage of N's	5,679 / 0.02%
GC Percentage	39.19%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.286

2.4. Mapping Quality

Mean Mapping Quality	40.77

2.5. Mismatches and indels

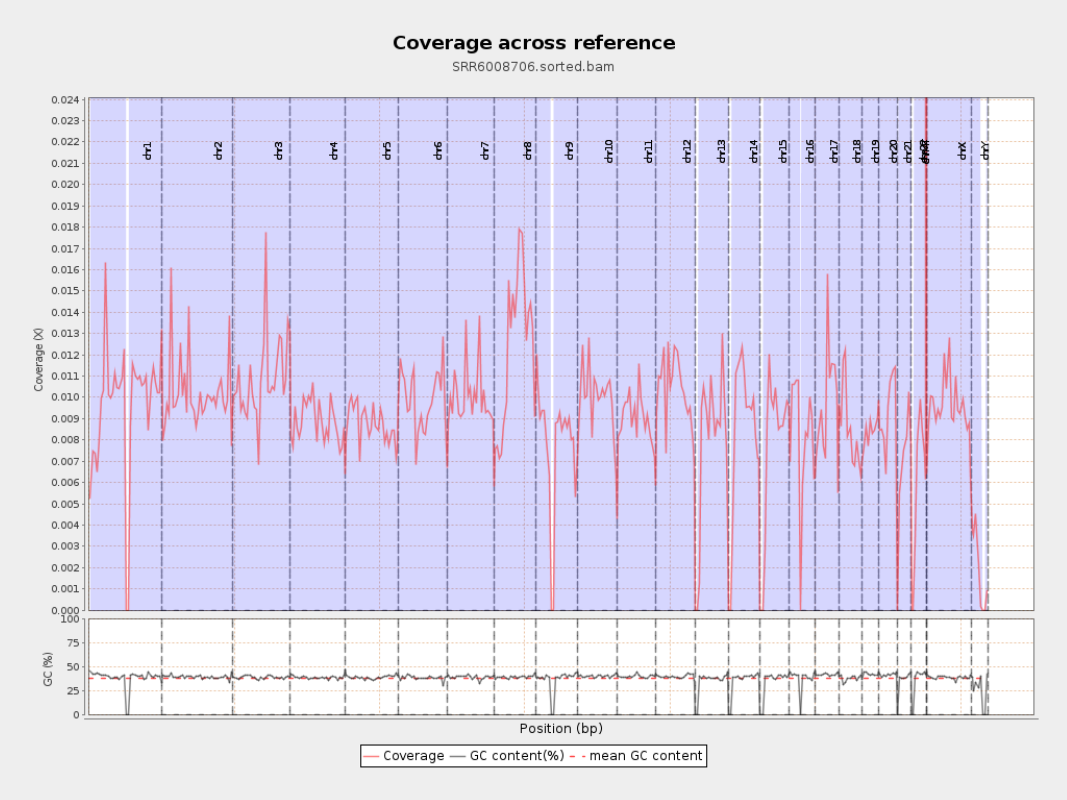
General error rate	1.1%
Mismatches	310,105
Insertions	2,846
Mapped reads with at least one insertion	0.56%
Deletions	10,851
Mapped reads with at least one deletion	2.14%
Homopolymer indels	46.1%

2.6. Chromosome stats

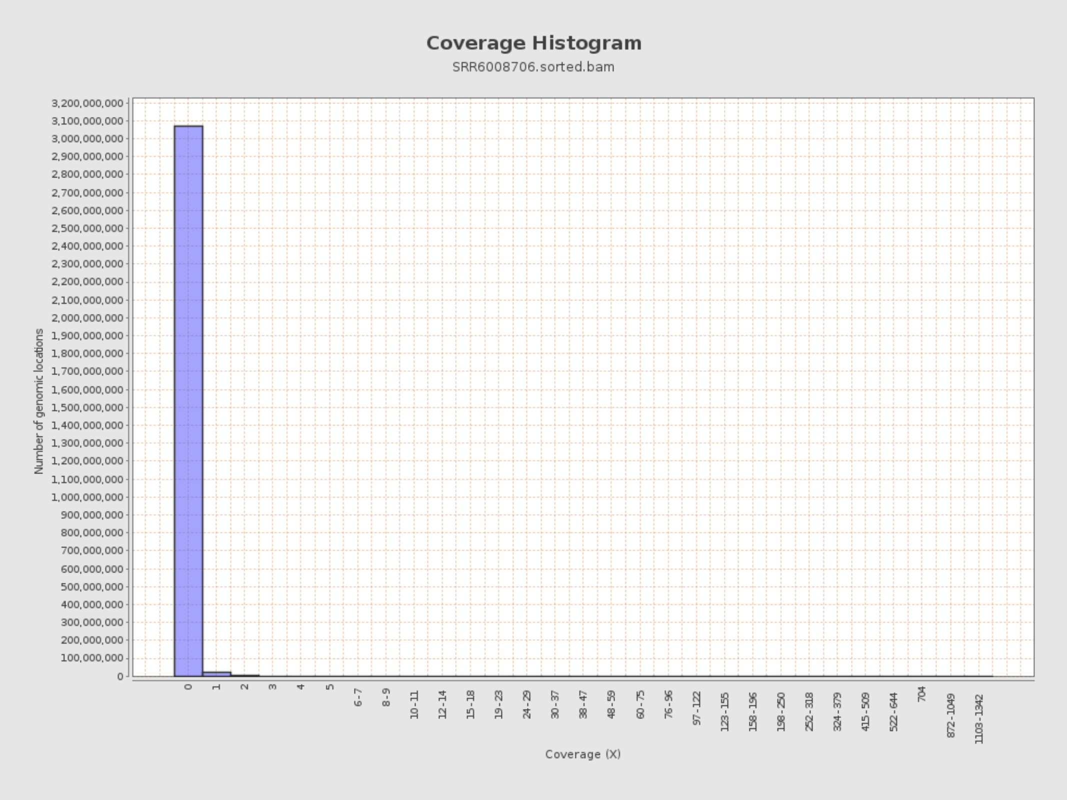
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2373459	0.0095	0.1513
chr2	243199373	2484125	0.0102	0.4466
chr3	198022430	2145006	0.0108	0.1595
chr4	191154276	1693909	0.0089	0.1473
chr5	180915260	1583832	0.0088	0.1301
chr6	171115067	1692308	0.0099	0.3723
chr7	159138663	1605851	0.0101	0.2884

chr8	146364022	1815111	0.0124	0.187
chr9	141213431	1074127	0.0076	0.1281
chr10	135534747	1365248	0.0101	0.2123
chr11	135006516	1208841	0.009	0.129
chr12	133851895	1390853	0.0104	0.1554
chr13	115169878	904660	0.0079	0.1992
chr14	107349540	904809	0.0084	0.1221
chr15	102531392	791096	0.0077	0.1724
chr16	90354753	737370	0.0082	0.1933
chr17	81195210	792872	0.0098	1.0194
chr18	78077248	670579	0.0086	0.4682
chr19	59128983	495633	0.0084	0.1778
chr20	63025520	579131	0.0092	0.121
chr21	48129895	332791	0.0069	0.1084
chr22	51304566	296309	0.0058	0.0978
chrMT	16571	11573	0.6984	1.1053
chrX	155270560	1483862	0.0096	0.2528
chrY	59373566	107037	0.0018	0.2225

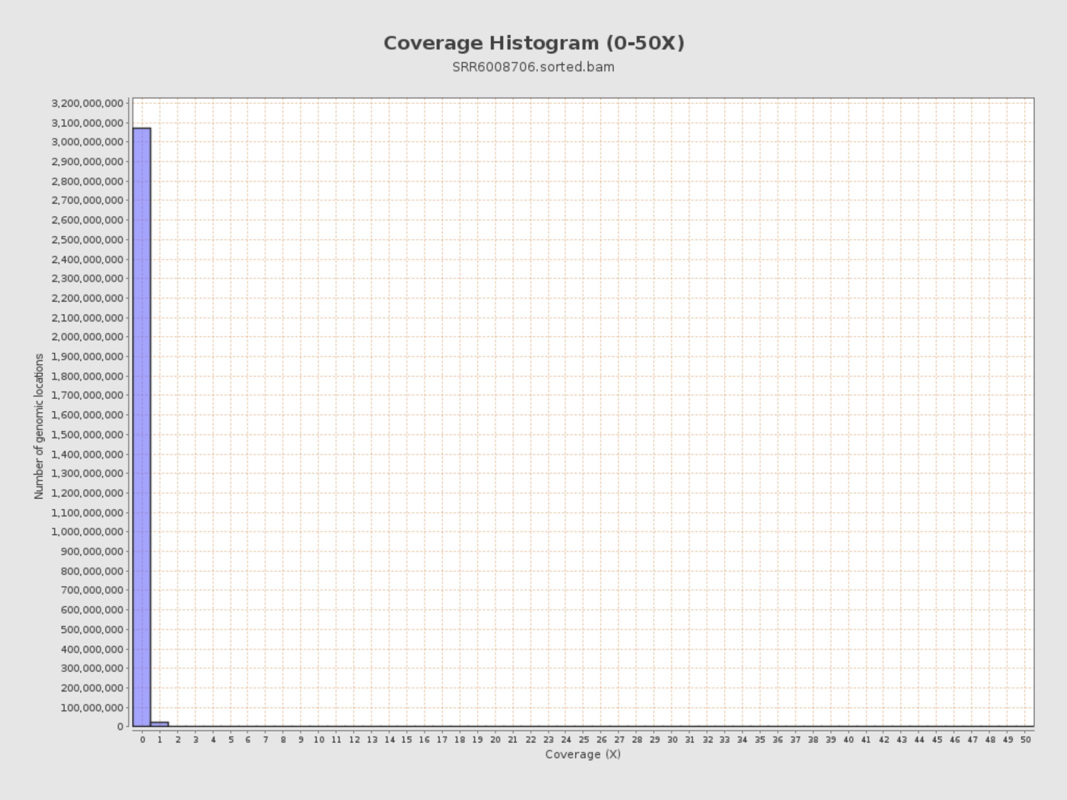
3. Results : Coverage across reference



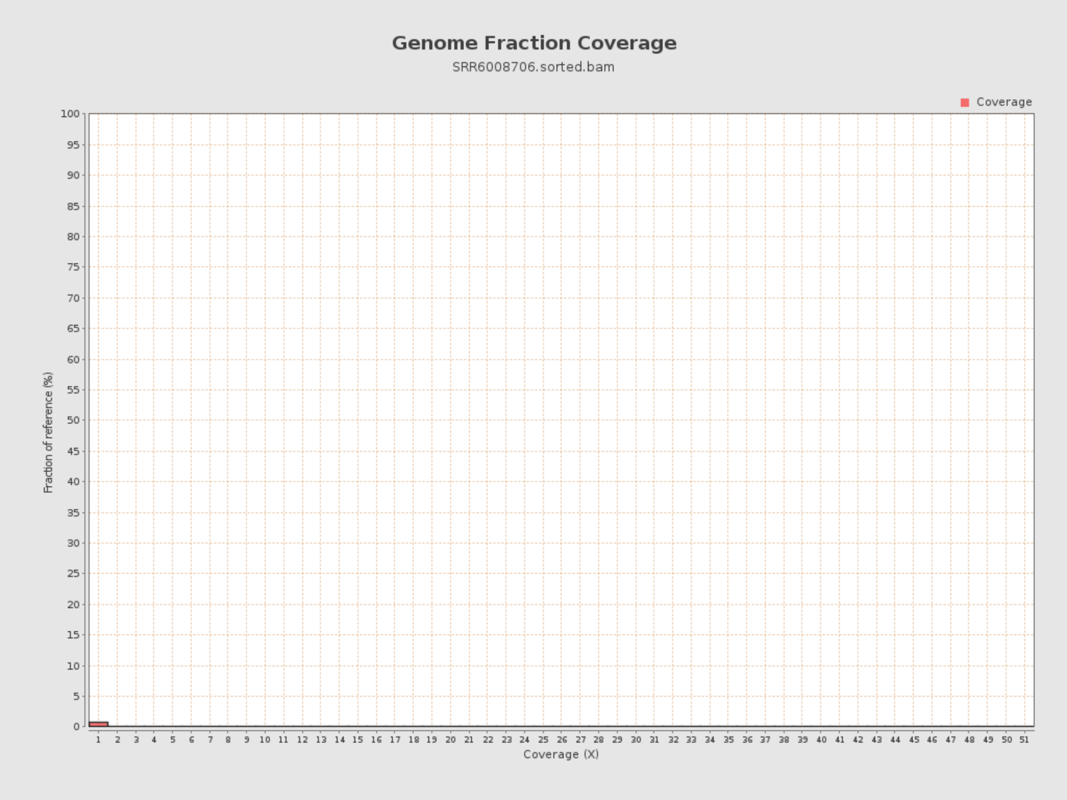
4. Results : Coverage Histogram



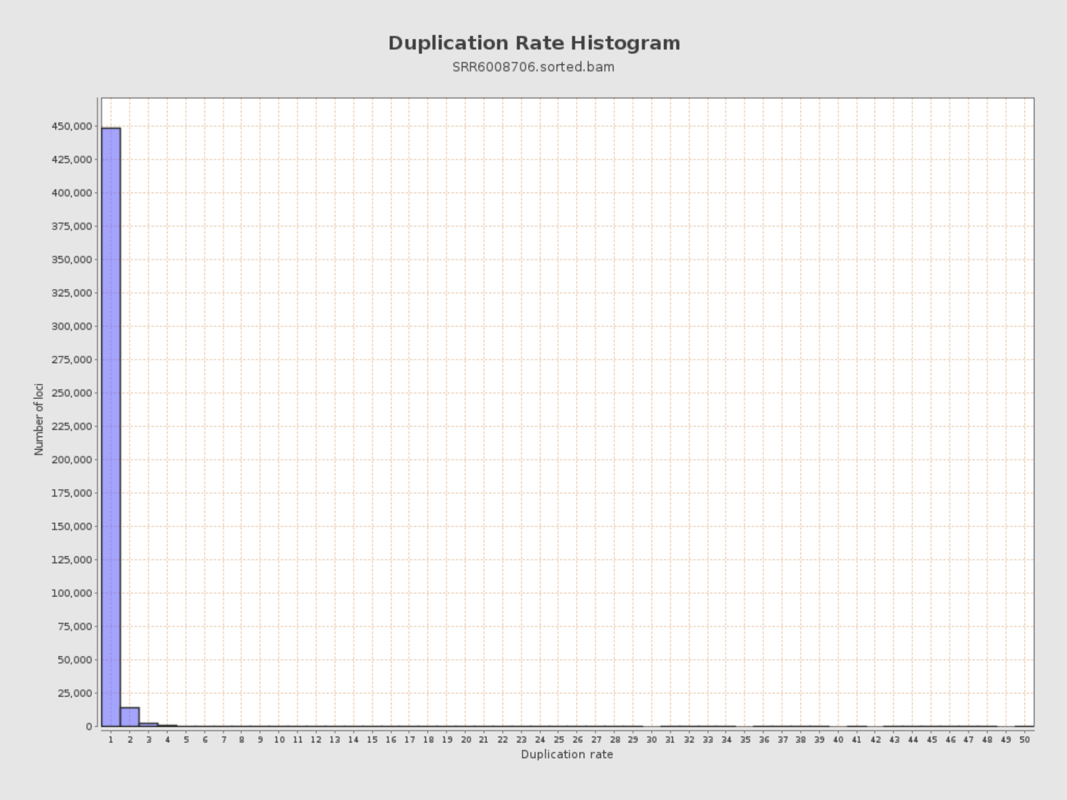
5. Results : Coverage Histogram (0-50X)



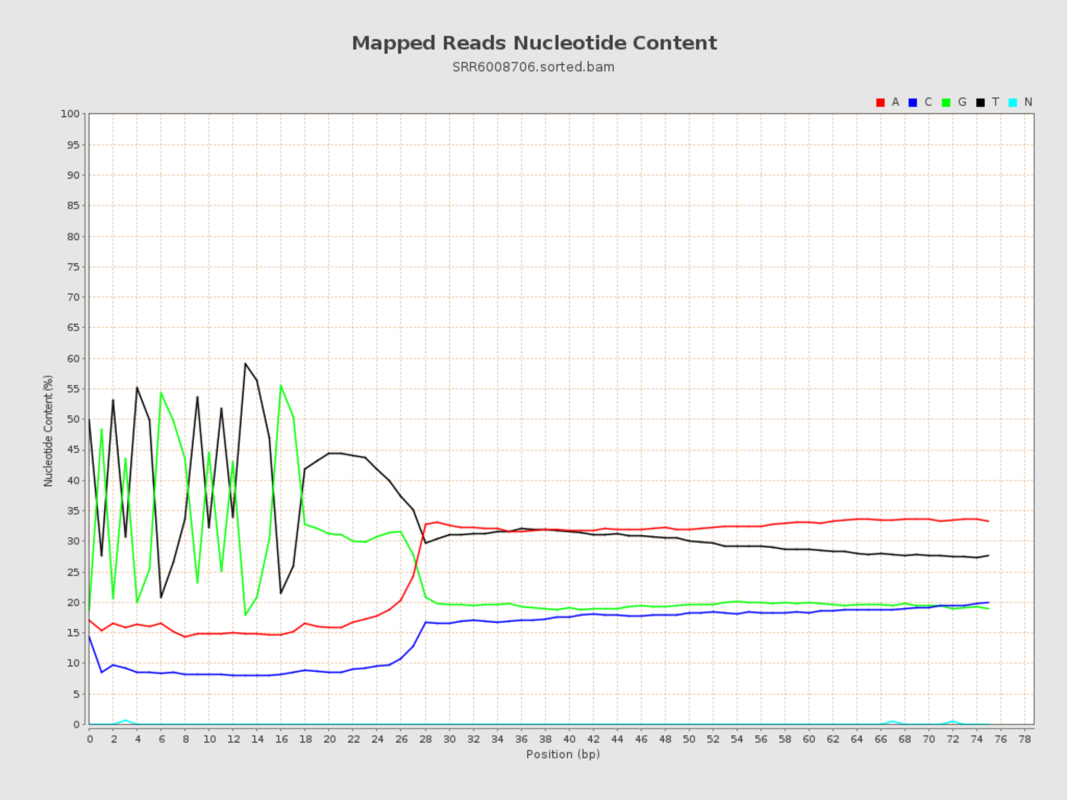
6. Results : Genome Fraction Coverage



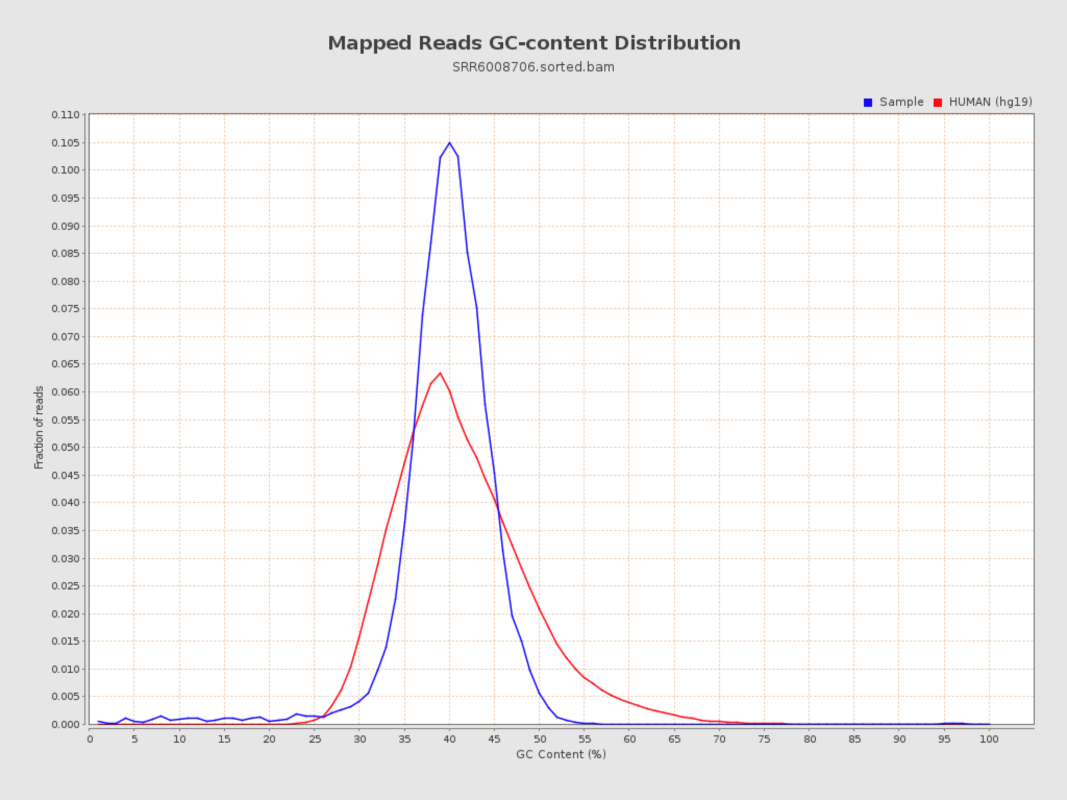
7. Results : Duplication Rate Histogram



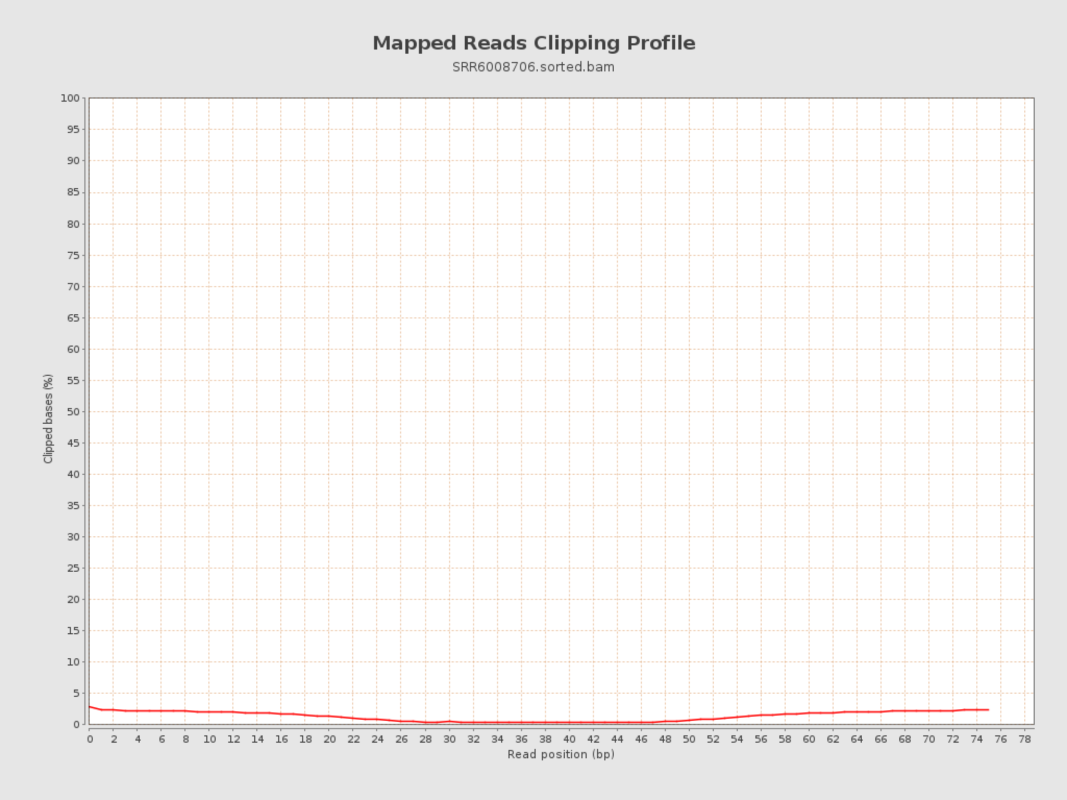
8. Results : Mapped Reads Nucleotide Content



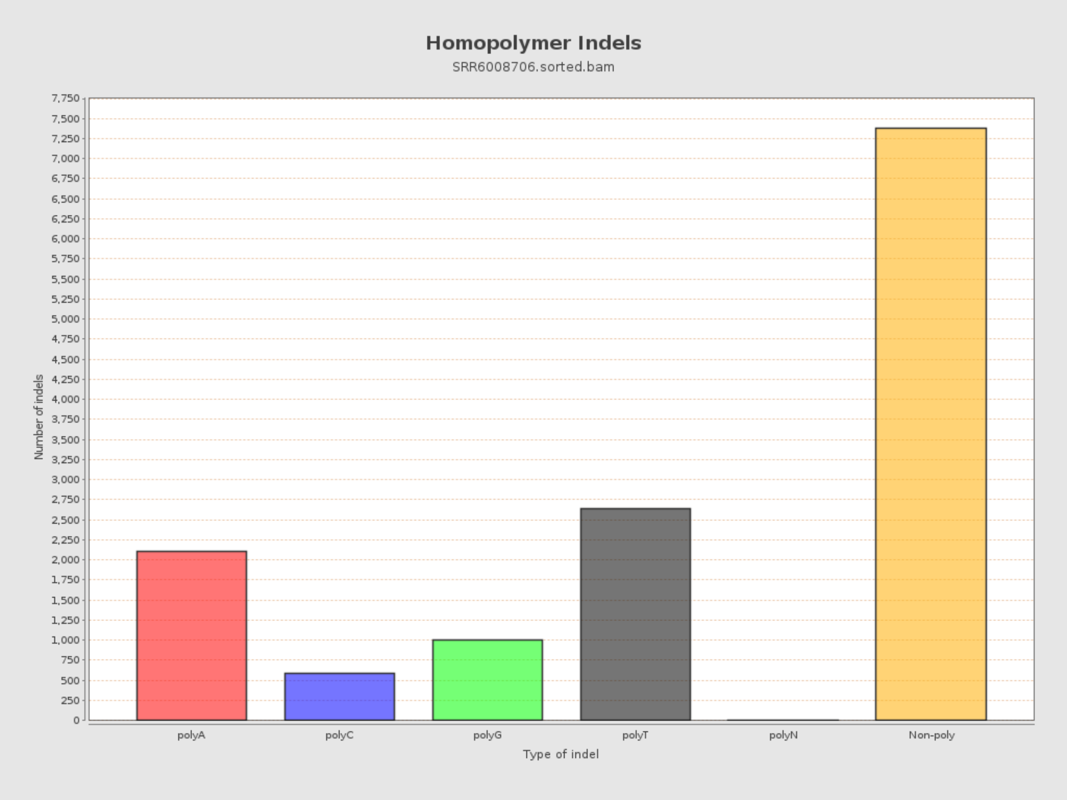
9. Results : Mapped Reads GC-content Distribution



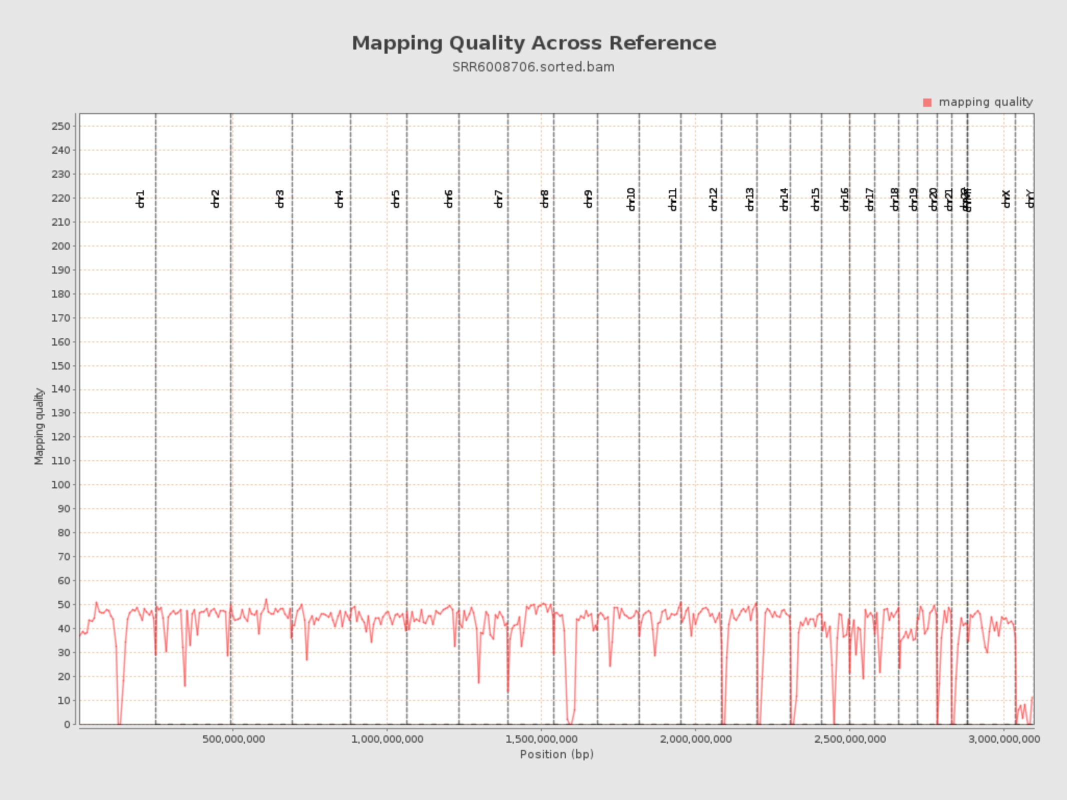
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram