Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708507.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_SRR1708507 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708507.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:25:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708507.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,995,372
Mapped reads	2,014,644 / 67.26%
Unmapped reads	980,728 / 32.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	489 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	90,524 / 3.02%
Duplication rate	3.43%
Clipped reads	447,921 / 14.95%

2.2. ACGT Content

Number/percentage of A's	27,109,572 / 28.34%
Number/percentage of C's	17,698,860 / 18.5%
Number/percentage of T's	30,673,161 / 32.07%
Number/percentage of G's	20,161,781 / 21.08%
Number/percentage of N's	1,353 / 0%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2922

2.4. Mapping Quality

Mean Mapping Quality	40.23

2.5. Mismatches and indels

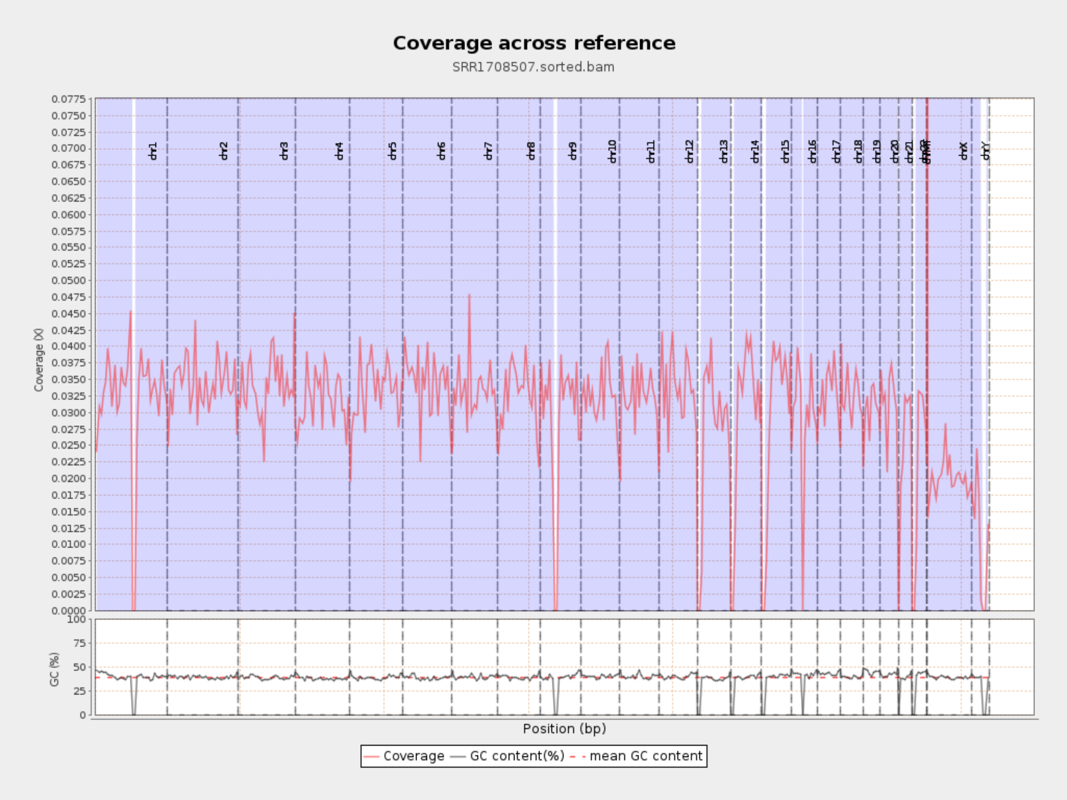
General error rate	0.51%
Mismatches	482,792
Insertions	5,172
Mapped reads with at least one insertion	0.26%
Deletions	14,876
Mapped reads with at least one deletion	0.74%
Homopolymer indels	48.29%

2.6. Chromosome stats

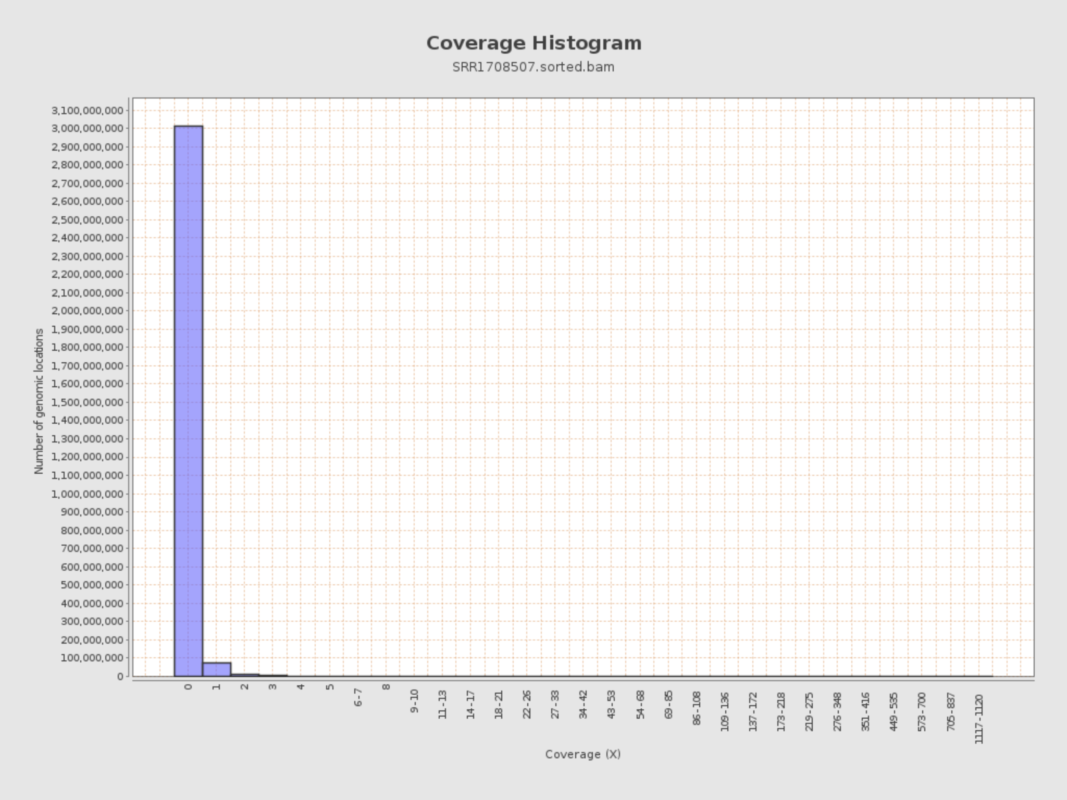
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7977333	0.032	0.3807
chr2	243199373	8380940	0.0345	0.5079
chr3	198022430	6707887	0.0339	0.2184
chr4	191154276	6120929	0.032	0.218
chr5	180915260	6085572	0.0336	0.2141
chr6	171115067	5912191	0.0346	0.2896
chr7	159138663	5312901	0.0334	0.3271

chr8	146364022	4782358	0.0327	0.4363
chr9	141213431	4090072	0.029	0.2309
chr10	135534747	4411960	0.0326	0.2278
chr11	135006516	4456943	0.033	0.2583
chr12	133851895	4545771	0.034	0.2187
chr13	115169878	3059235	0.0266	0.2346
chr14	107349540	3146958	0.0293	0.2031
chr15	102531392	2933218	0.0286	0.2015
chr16	90354753	2599189	0.0288	0.2017
chr17	81195210	2676911	0.033	0.2294
chr18	78077248	2554363	0.0327	0.3137
chr19	59128983	1808962	0.0306	0.3029
chr20	63025520	1969653	0.0313	0.2087
chr21	48129895	1201091	0.025	0.1932
chr22	51304566	1096105	0.0214	0.1755
chrMT	16571	97184	5.8647	4.0981
chrX	155270560	3104293	0.02	0.1872
chrY	59373566	634963	0.0107	0.1319

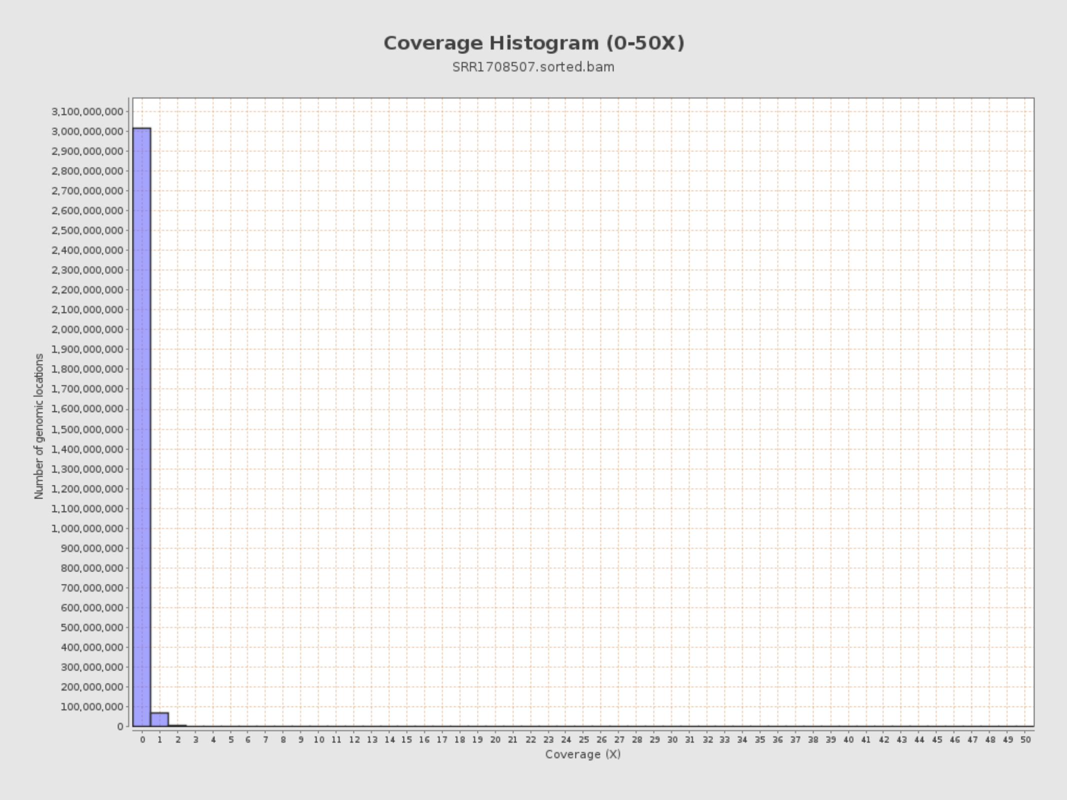
3. Results : Coverage across reference



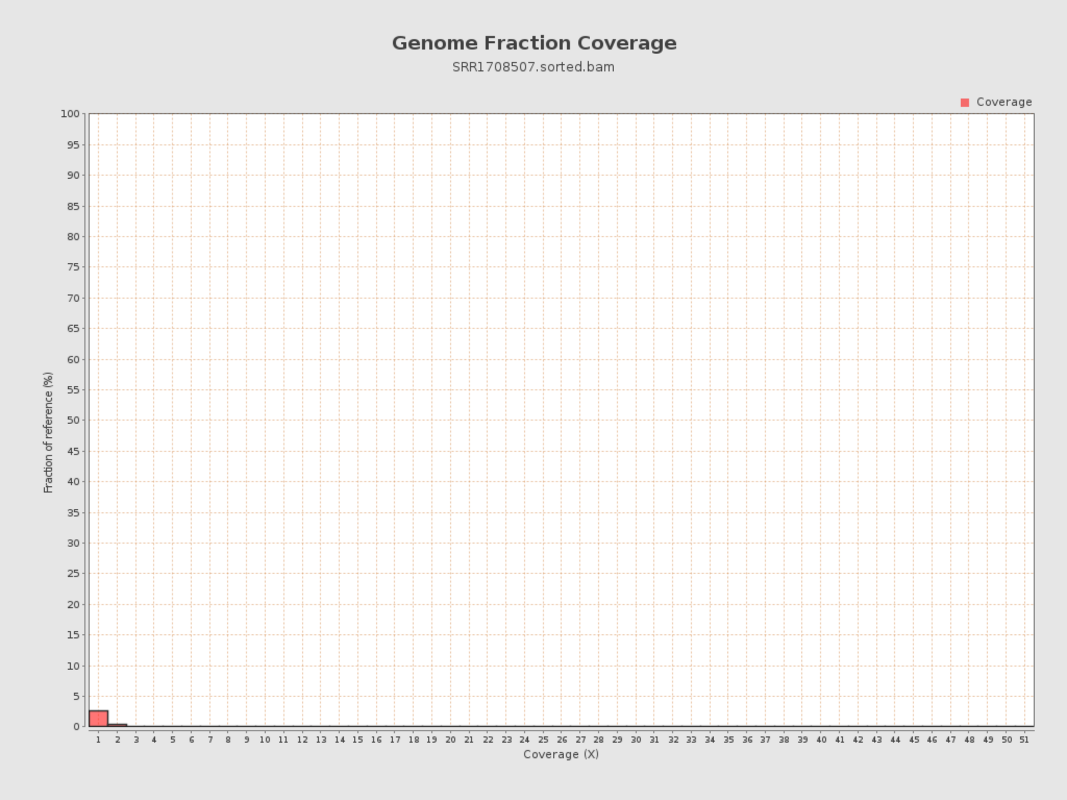
4. Results : Coverage Histogram



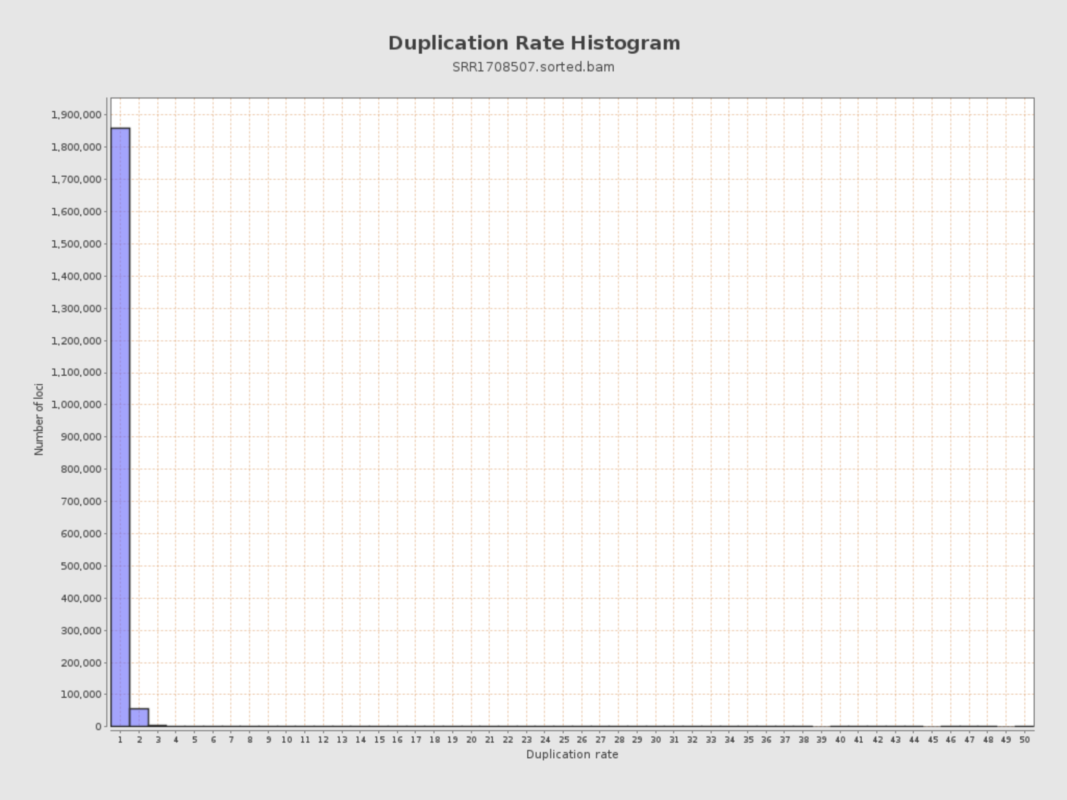
5. Results : Coverage Histogram (0-50X)



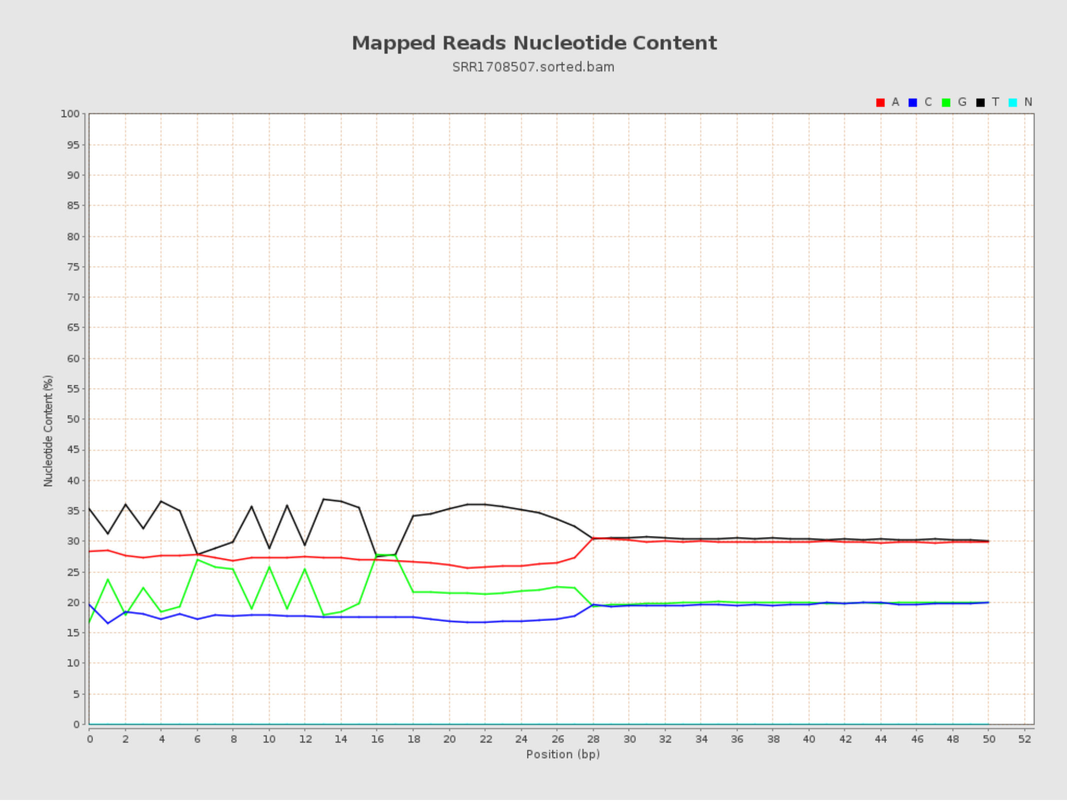
6. Results : Genome Fraction Coverage



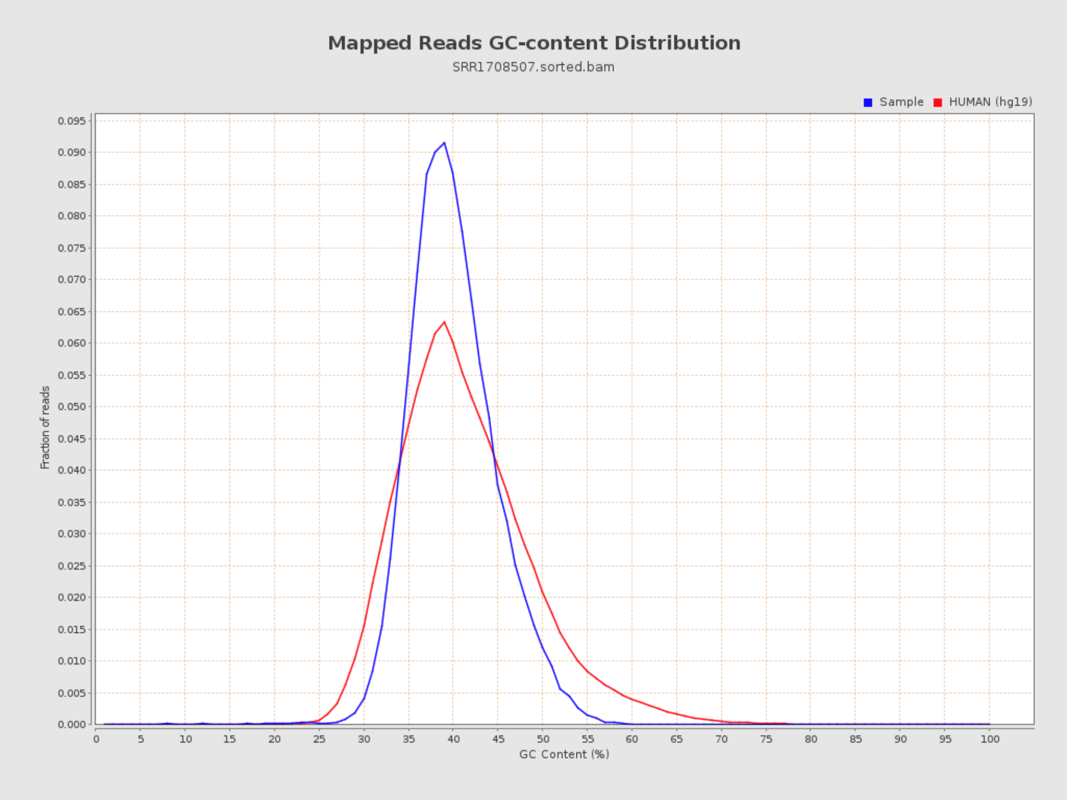
7. Results : Duplication Rate Histogram



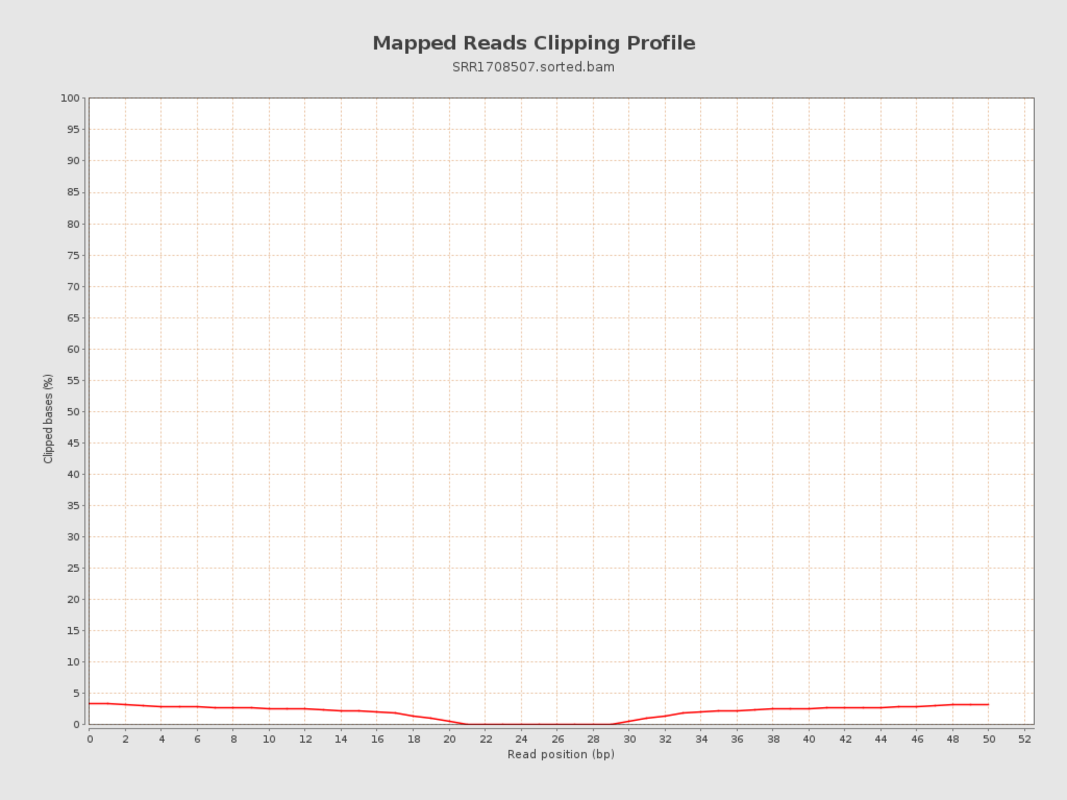
8. Results : Mapped Reads Nucleotide Content



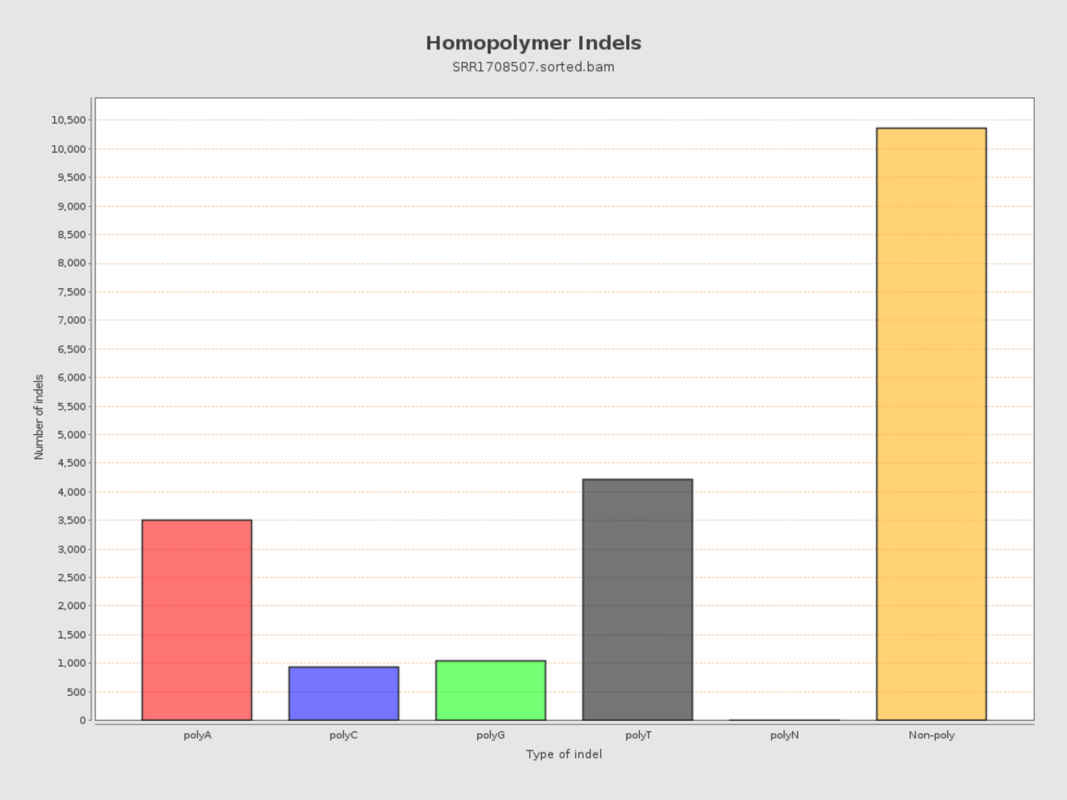
9. Results : Mapped Reads GC-content Distribution



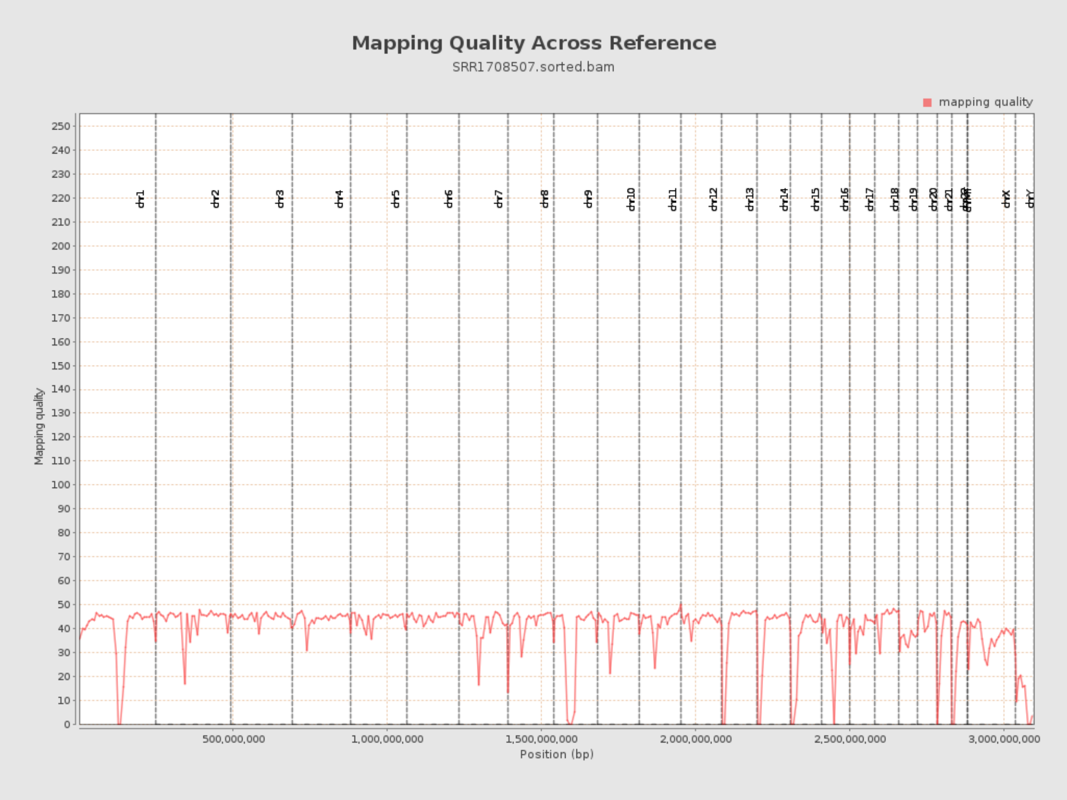
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram