Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:08:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708622.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_SRR1708622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708622.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:08:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,311,902
Mapped reads	2,401,878 / 72.52%
Unmapped reads	910,024 / 27.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	786 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	88,889 / 2.68%
Duplication rate	2.57%
Clipped reads	374,062 / 11.29%

2.2. ACGT Content

Number/percentage of A's	34,529,947 / 29.53%
Number/percentage of C's	21,962,607 / 18.79%
Number/percentage of T's	36,913,698 / 31.57%
Number/percentage of G's	23,497,428 / 20.1%
Number/percentage of N's	10,155 / 0.01%
GC Percentage	38.88%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3988

2.4. Mapping Quality

Mean Mapping Quality	43.13

2.5. Mismatches and indels

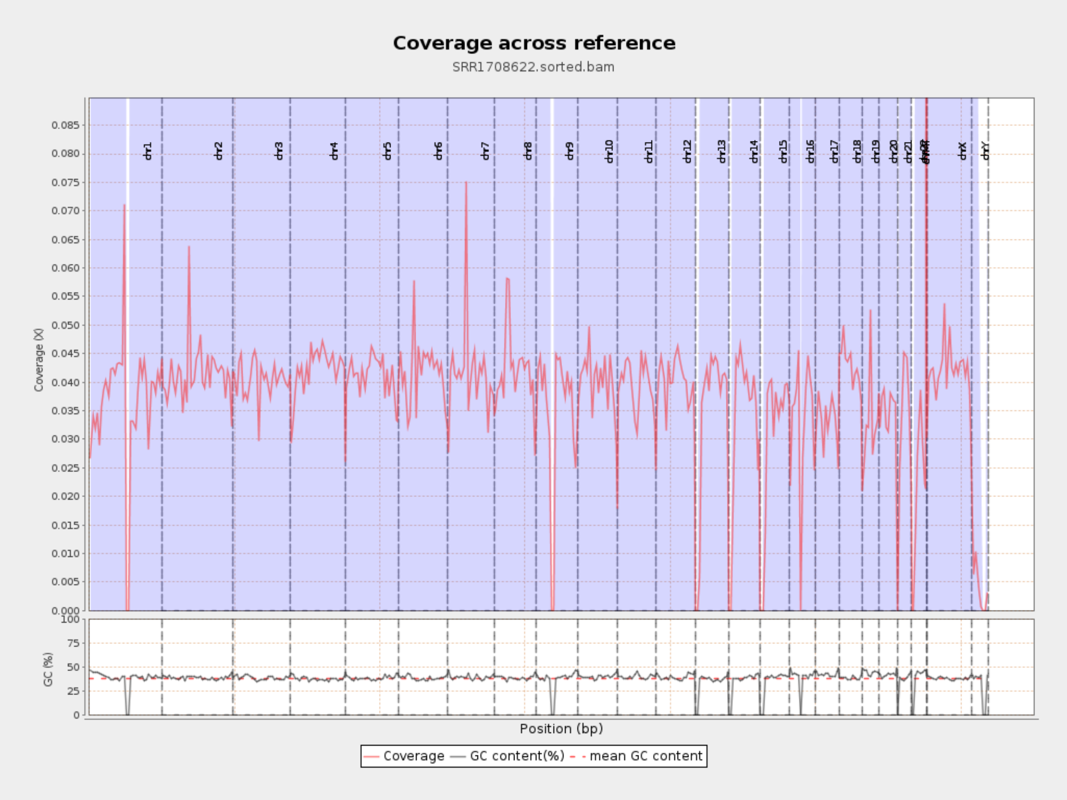
General error rate	0.65%
Mismatches	746,339
Insertions	5,497
Mapped reads with at least one insertion	0.23%
Deletions	14,649
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.33%

2.6. Chromosome stats

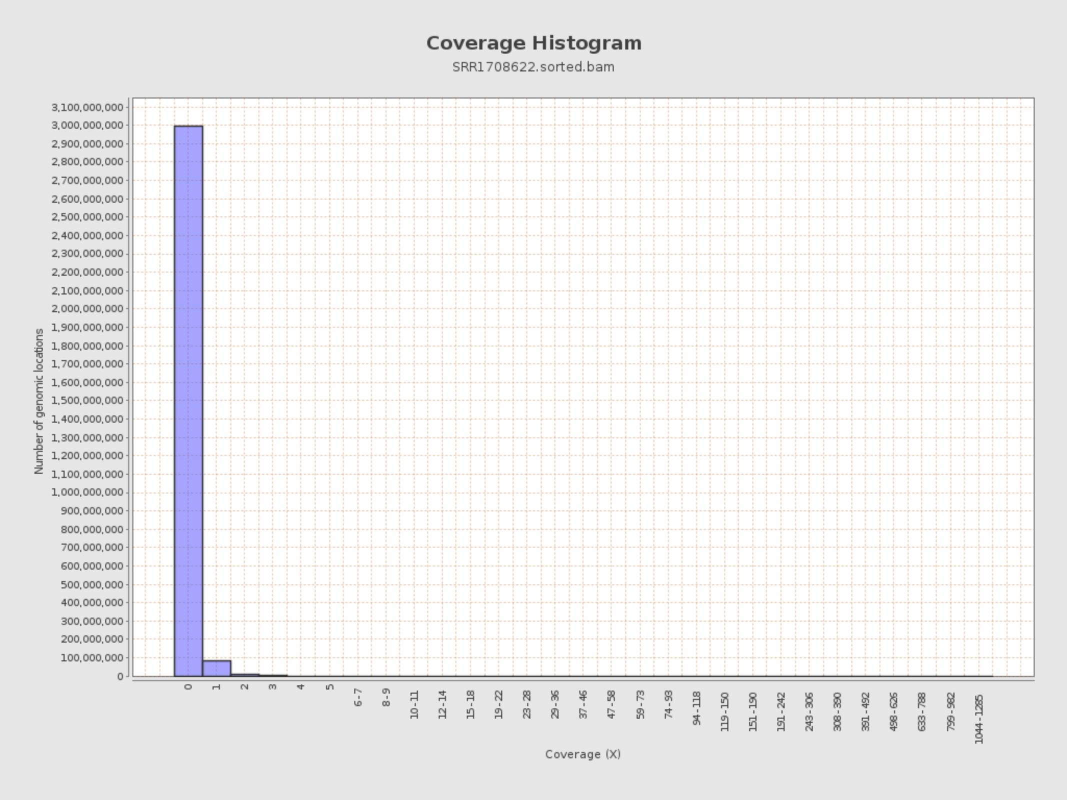
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9123848	0.0366	0.7464
chr2	243199373	10108596	0.0416	0.4096
chr3	198022430	8022940	0.0405	0.2319
chr4	191154276	8098530	0.0424	0.2405
chr5	180915260	7464911	0.0413	0.2357
chr6	171115067	7162850	0.0419	0.3176
chr7	159138663	6686745	0.042	0.5524

chr8	146364022	6145116	0.042	0.7453
chr9	141213431	4885912	0.0346	0.3023
chr10	135534747	5485925	0.0405	0.3111
chr11	135006516	5280952	0.0391	0.3028
chr12	133851895	5376111	0.0402	0.2389
chr13	115169878	3918851	0.034	0.2142
chr14	107349540	3542922	0.033	0.2283
chr15	102531392	3095358	0.0302	0.1993
chr16	90354753	2985235	0.033	0.221
chr17	81195210	2674476	0.0329	0.2407
chr18	78077248	3358963	0.043	0.6055
chr19	59128983	1957058	0.0331	0.5413
chr20	63025520	2178665	0.0346	0.2202
chr21	48129895	1536914	0.0319	0.2159
chr22	51304566	1049692	0.0205	0.1619
chrMT	16571	8420	0.5081	0.9118
chrX	155270560	6524044	0.042	0.2606
chrY	59373566	263340	0.0044	0.0834

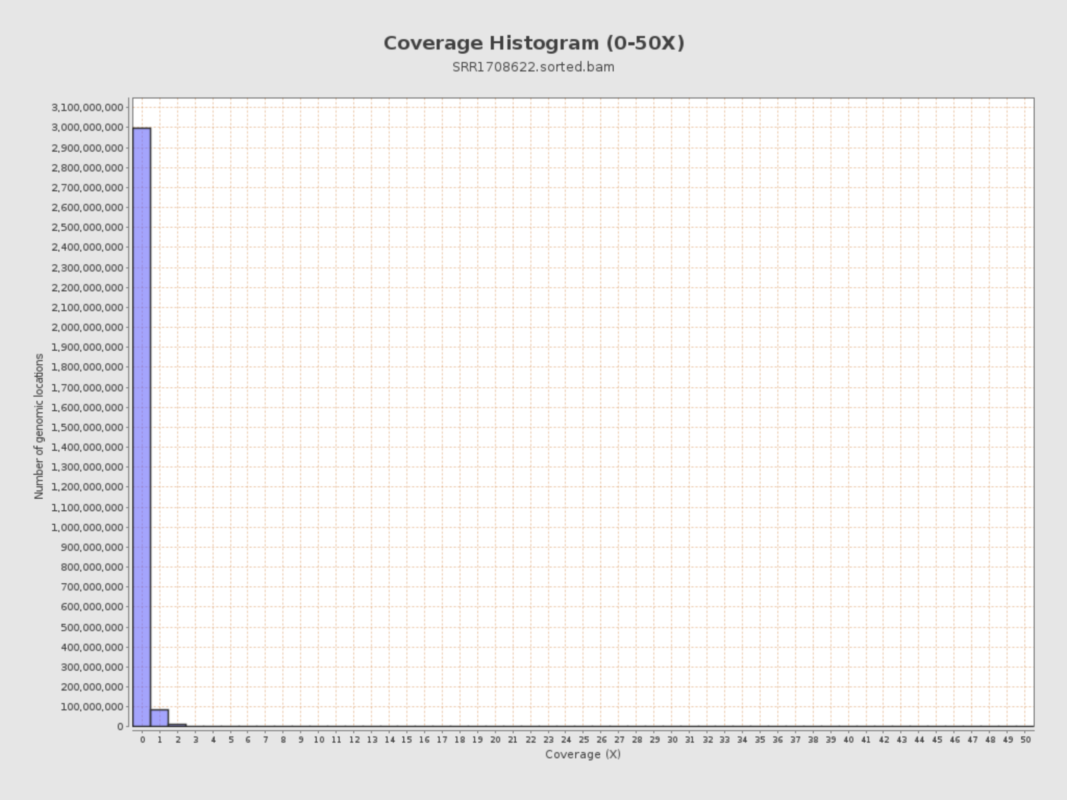
3. Results : Coverage across reference



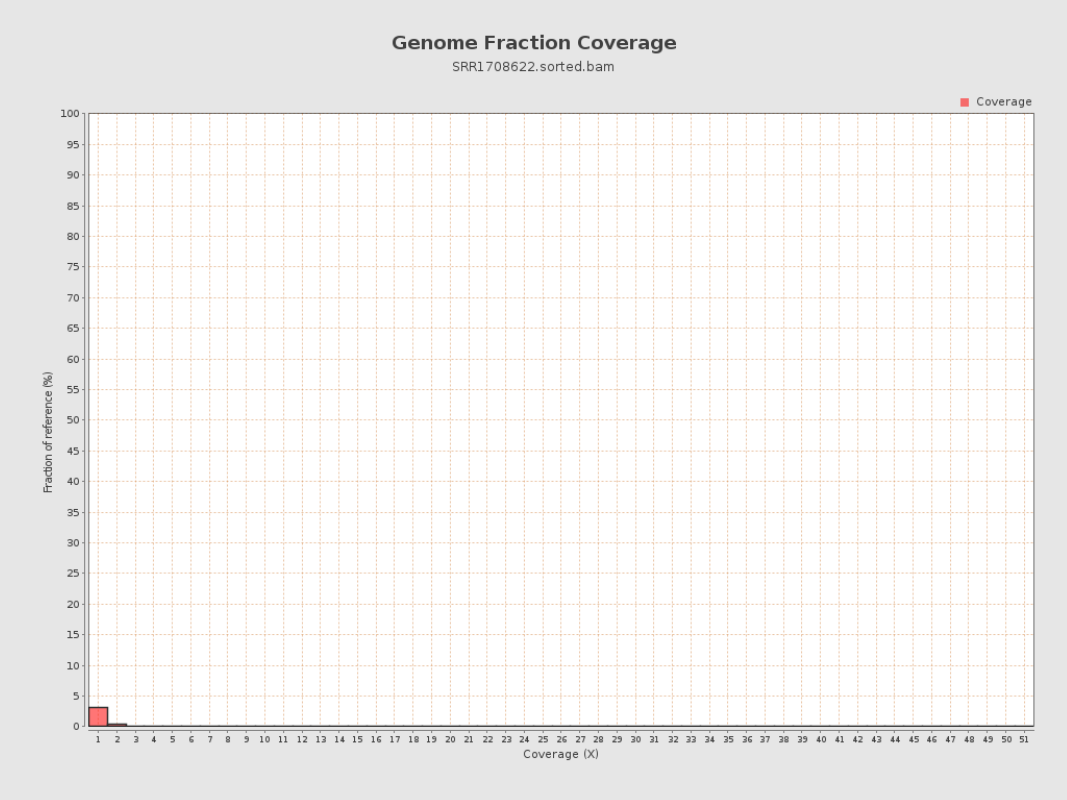
4. Results : Coverage Histogram



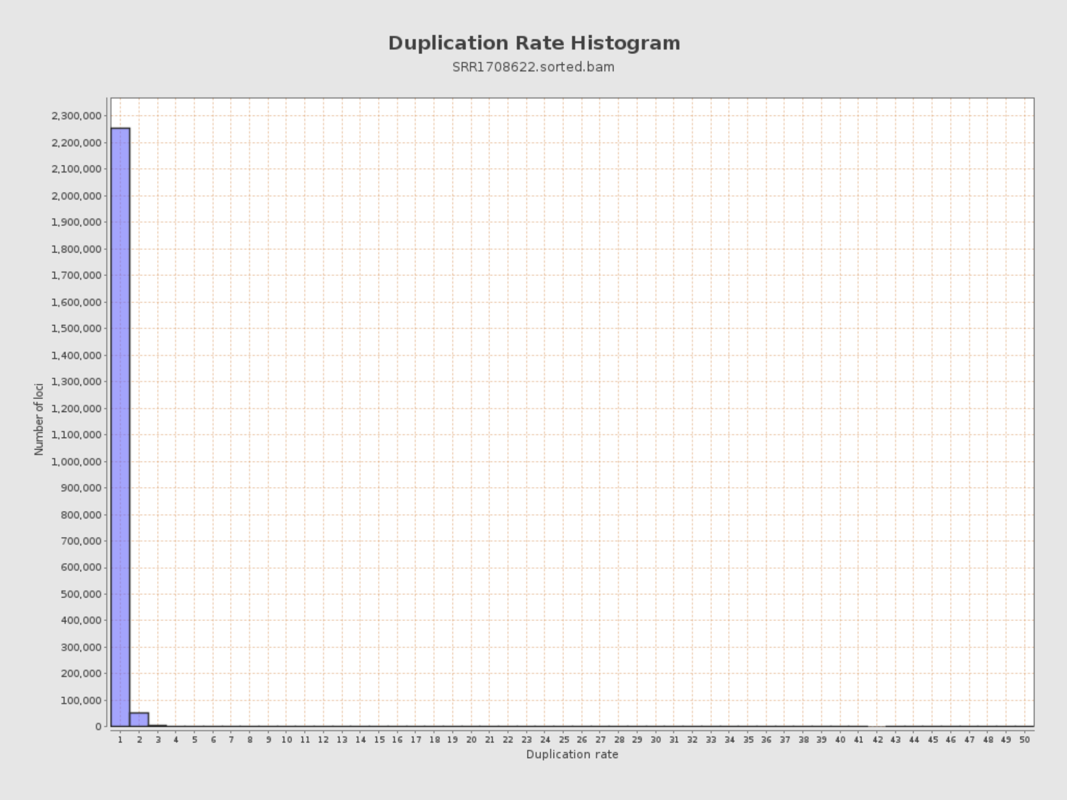
5. Results : Coverage Histogram (0-50X)



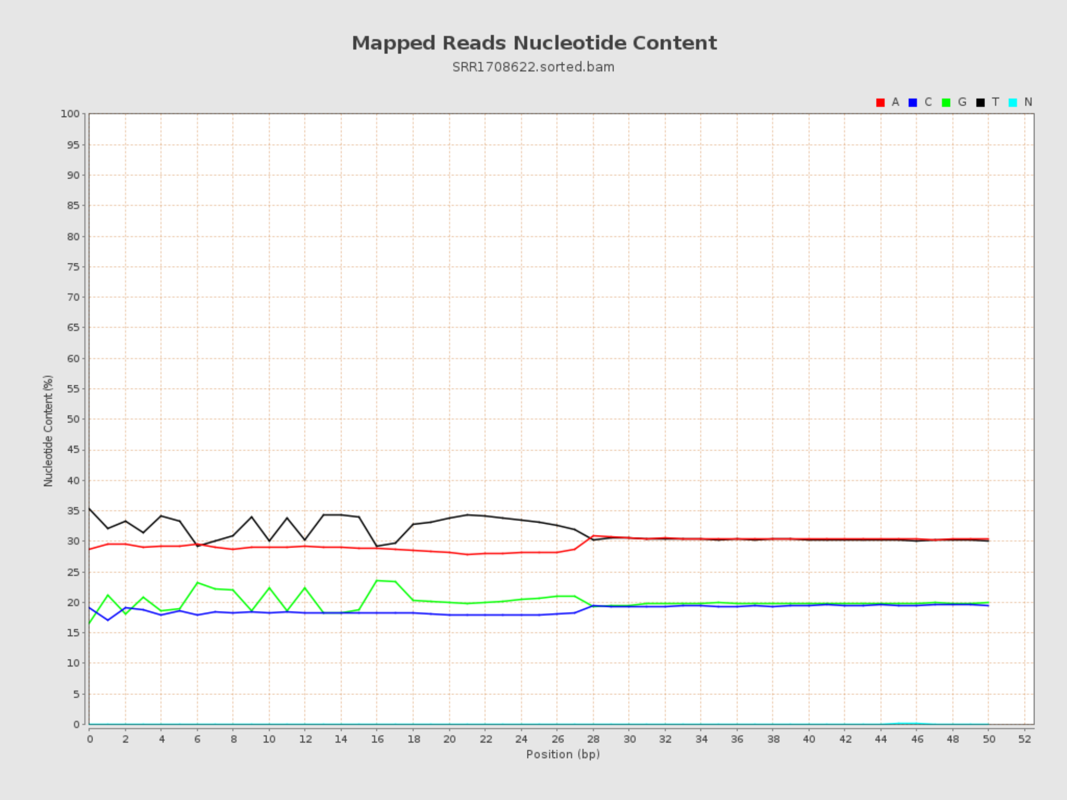
6. Results : Genome Fraction Coverage



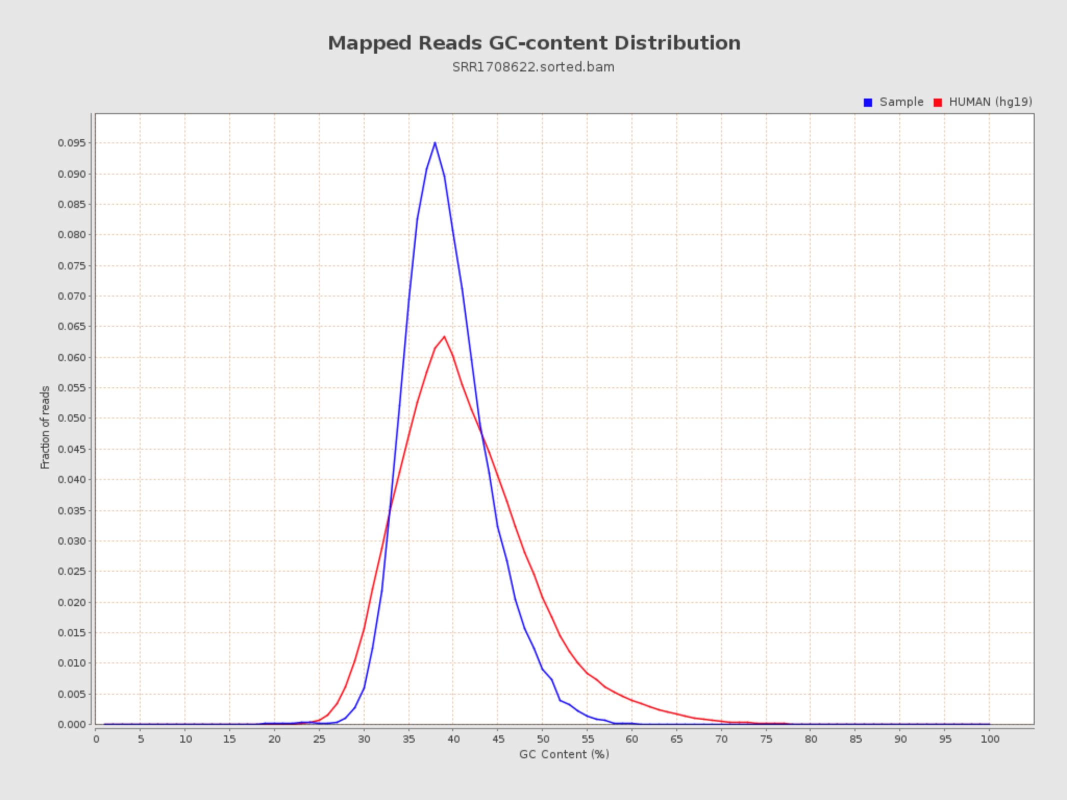
7. Results : Duplication Rate Histogram



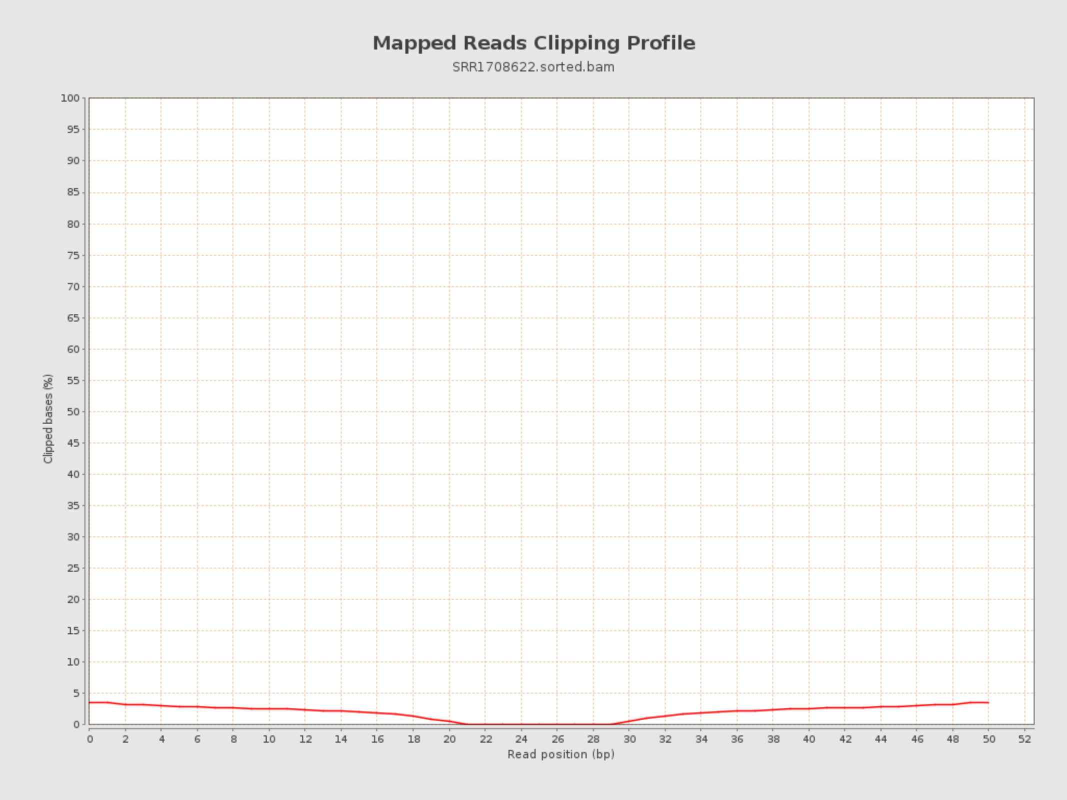
8. Results : Mapped Reads Nucleotide Content



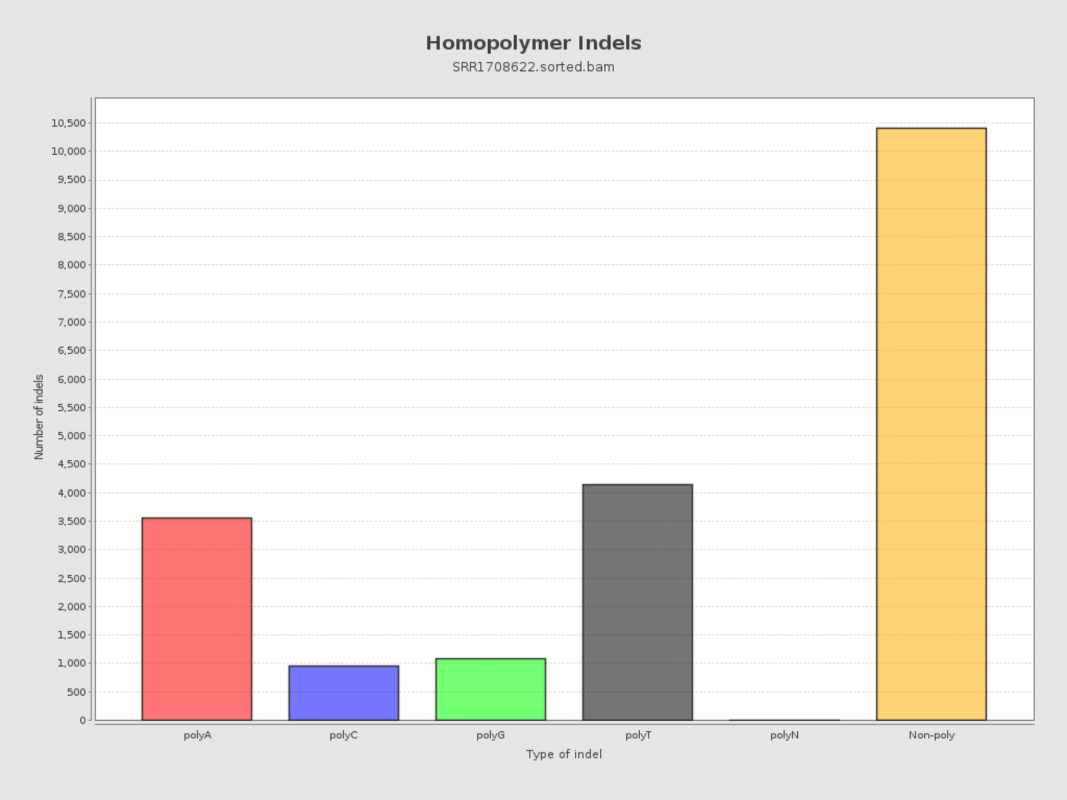
9. Results : Mapped Reads GC-content Distribution



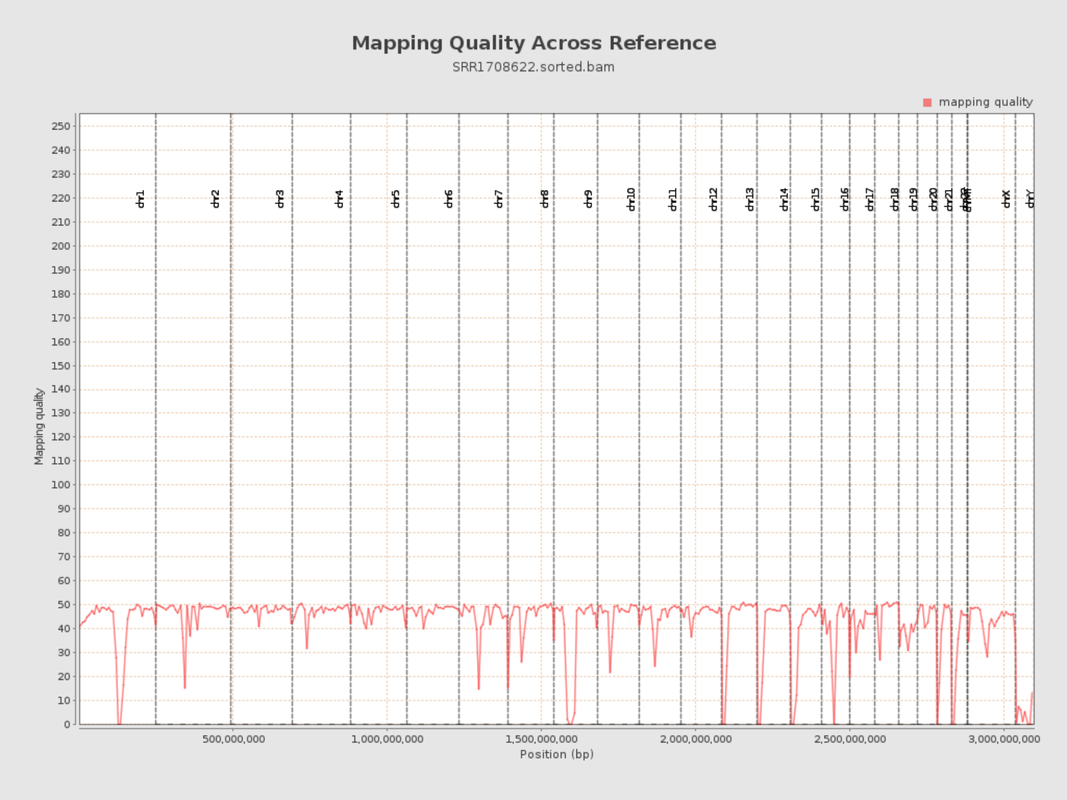
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram