Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:43:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708568.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_SRR1708568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:43:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,131,111
Mapped reads	3,411,722 / 82.59%
Unmapped reads	719,389 / 17.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	90 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,680 / 0.43%
Duplication rate	0.52%
Clipped reads	46,623 / 1.13%

2.2. ACGT Content

Number/percentage of A's	52,766,264 / 31.02%
Number/percentage of C's	32,239,683 / 18.95%
Number/percentage of T's	52,480,202 / 30.85%
Number/percentage of G's	32,628,422 / 19.18%
Number/percentage of N's	7,461 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	0.055

Standard Deviation	0.2469

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

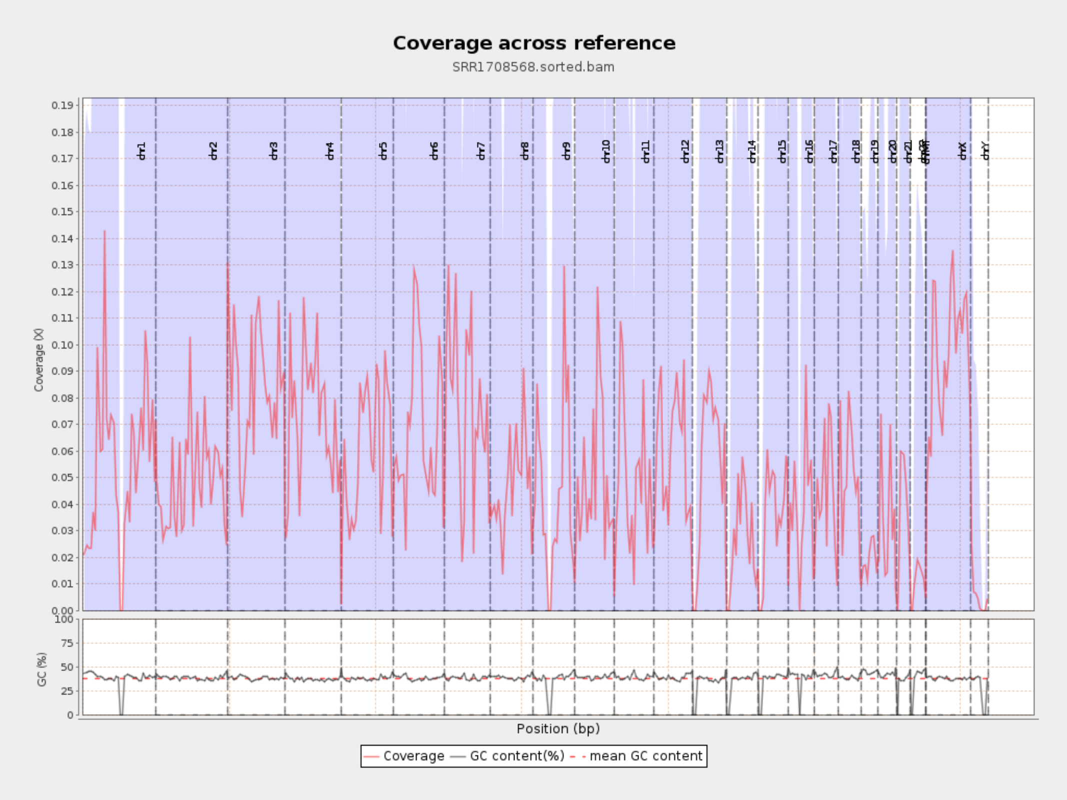
General error rate	0.16%
Mismatches	265,263
Insertions	11,520
Mapped reads with at least one insertion	0.34%
Deletions	8,817
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.66%

2.6. Chromosome stats

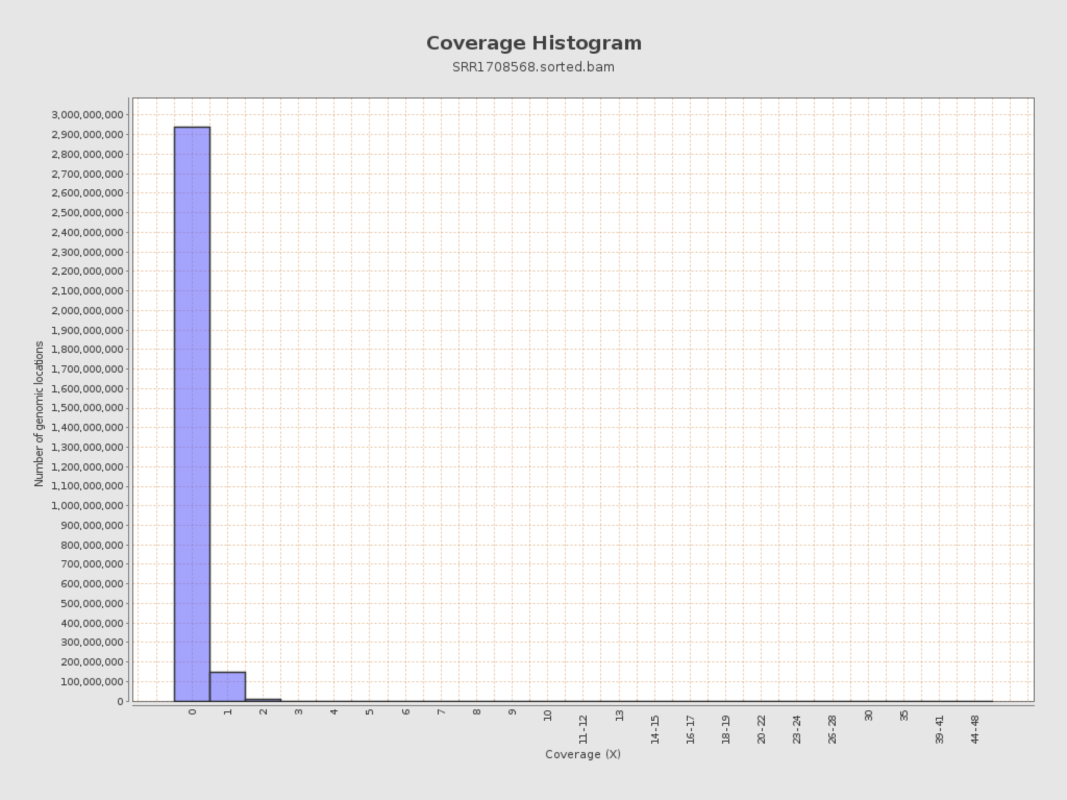
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13745207	0.0551	0.2474
chr2	243199373	11785550	0.0485	0.2299
chr3	198022430	16774335	0.0847	0.305
chr4	191154276	13981504	0.0731	0.2831
chr5	180915260	10711456	0.0592	0.2546
chr6	171115067	11792745	0.0689	0.276
chr7	159138663	11889942	0.0747	0.2885

chr8	146364022	6979399	0.0477	0.2278
chr9	141213431	6384276	0.0452	0.2239
chr10	135534747	6654124	0.0491	0.2327
chr11	135006516	6572865	0.0487	0.2324
chr12	133851895	8037292	0.06	0.2568
chr13	115169878	6385066	0.0554	0.2473
chr14	107349540	2860996	0.0267	0.1716
chr15	102531392	3616623	0.0353	0.197
chr16	90354753	3350636	0.0371	0.202
chr17	81195210	3645146	0.0449	0.2221
chr18	78077248	3993364	0.0511	0.2373
chr19	59128983	1135235	0.0192	0.1426
chr20	63025520	2222189	0.0353	0.1963
chr21	48129895	1705796	0.0354	0.1985
chr22	51304566	571843	0.0111	0.1085
chrMT	16571	200	0.0121	0.1092
chrX	155270560	15035756	0.0968	0.3282
chrY	59373566	305544	0.0051	0.0751

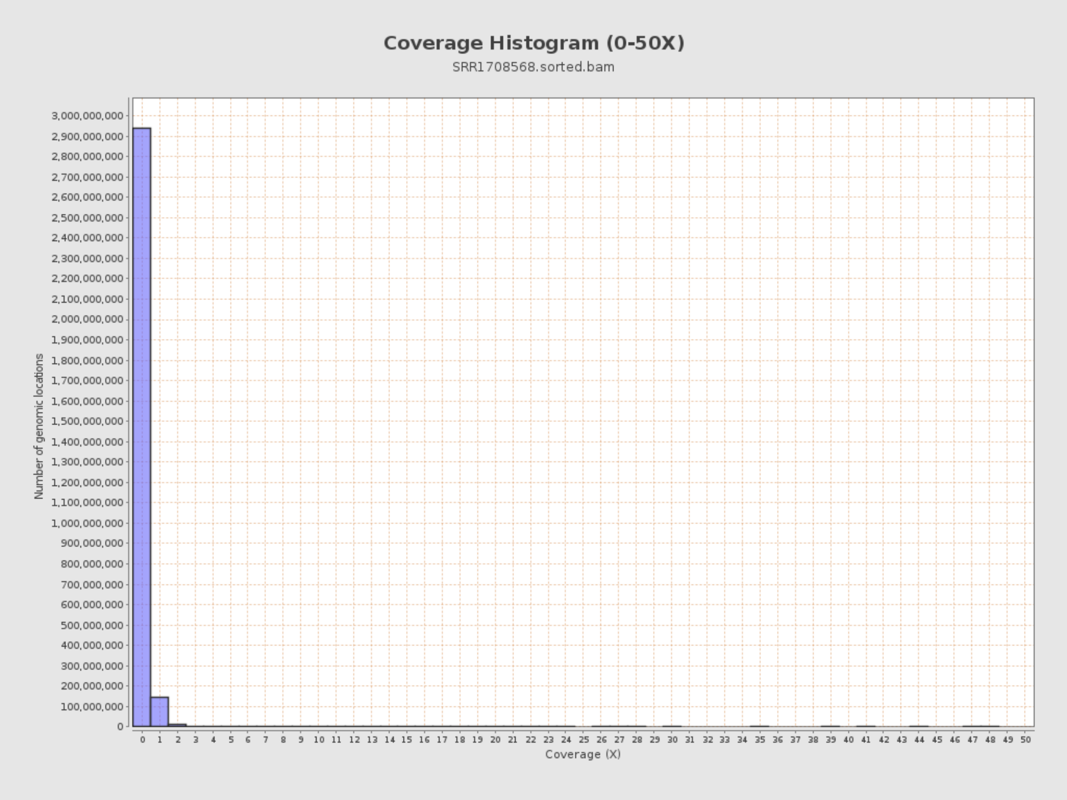
3. Results : Coverage across reference



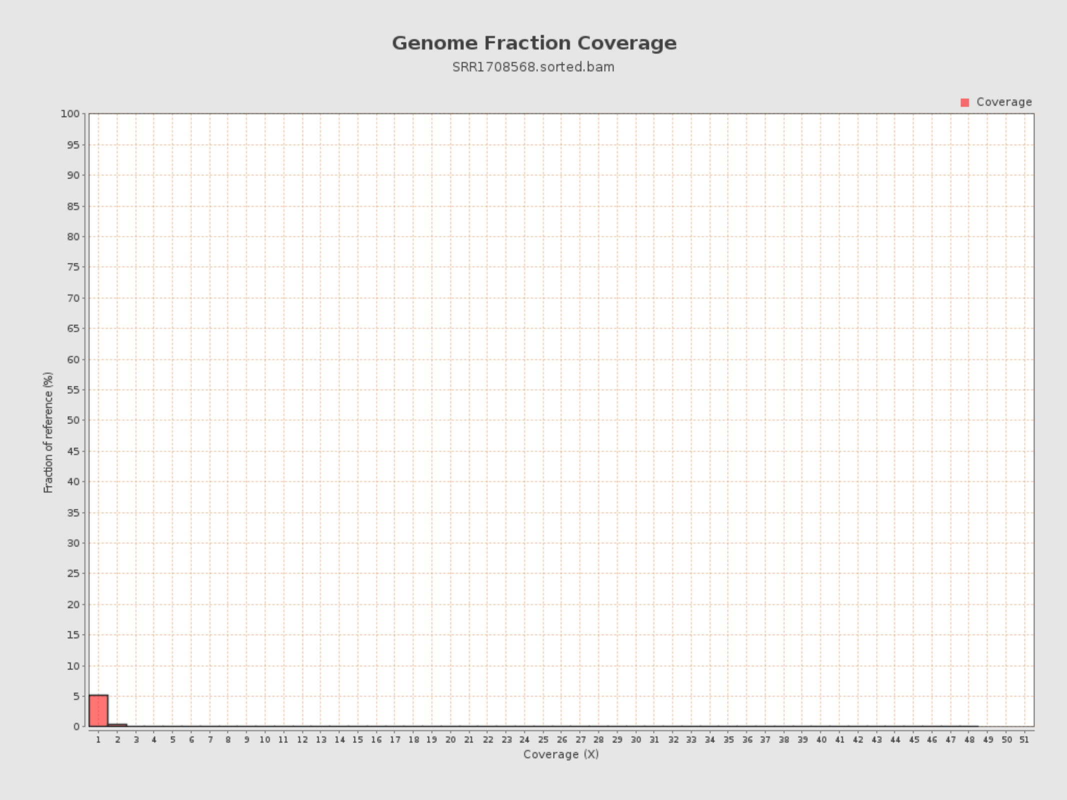
4. Results : Coverage Histogram



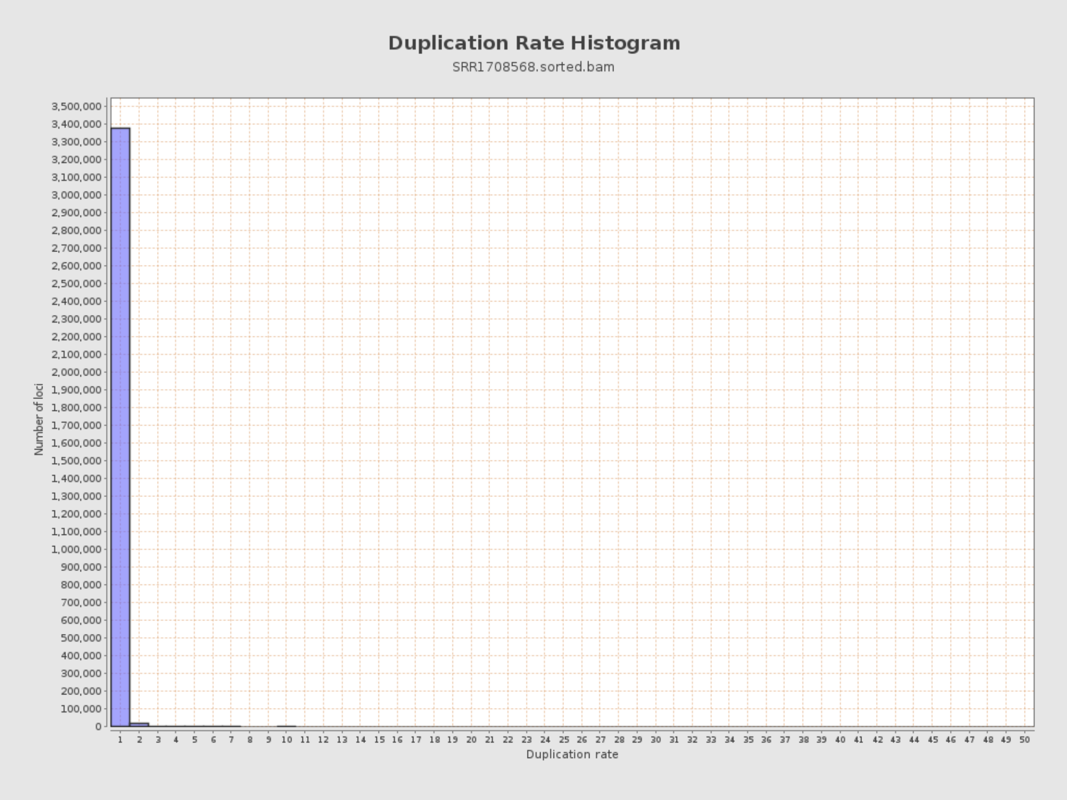
5. Results : Coverage Histogram (0-50X)



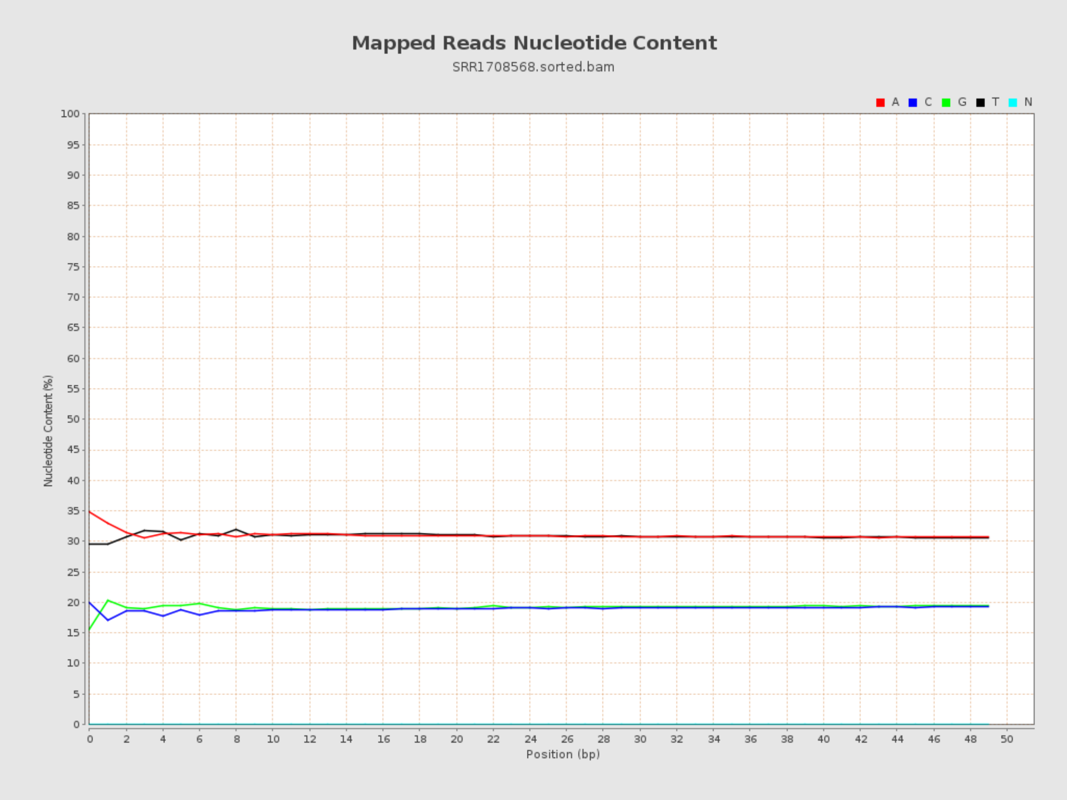
6. Results : Genome Fraction Coverage



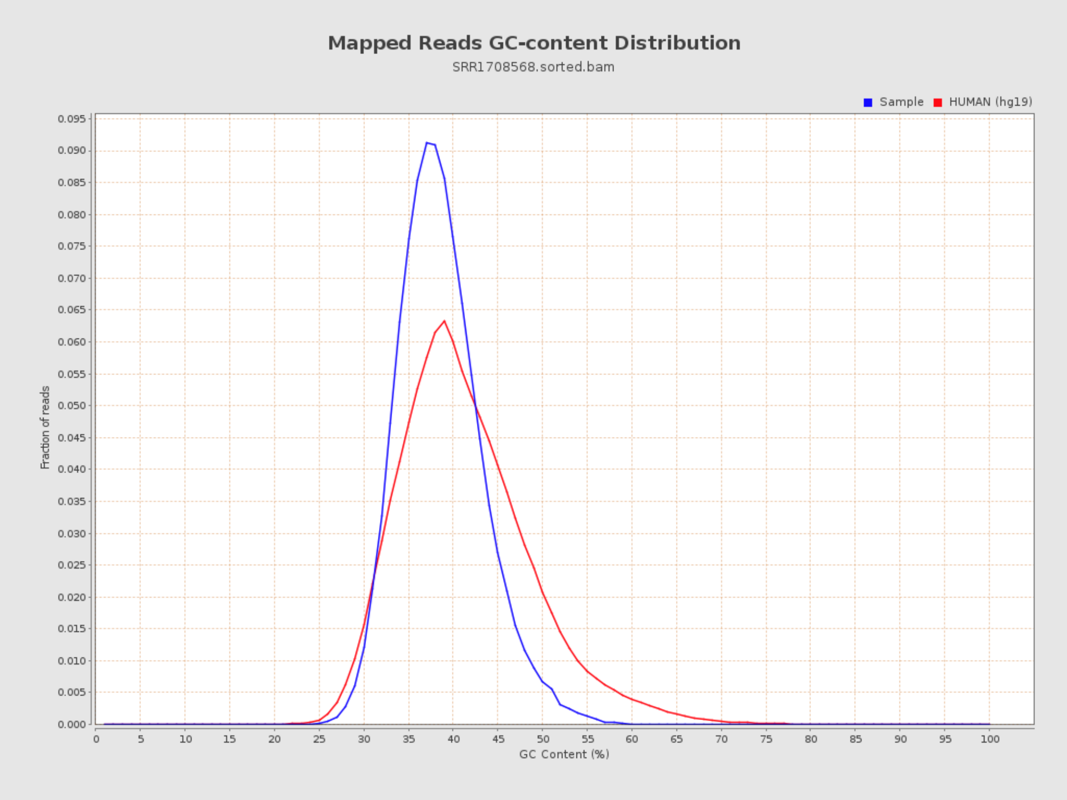
7. Results : Duplication Rate Histogram



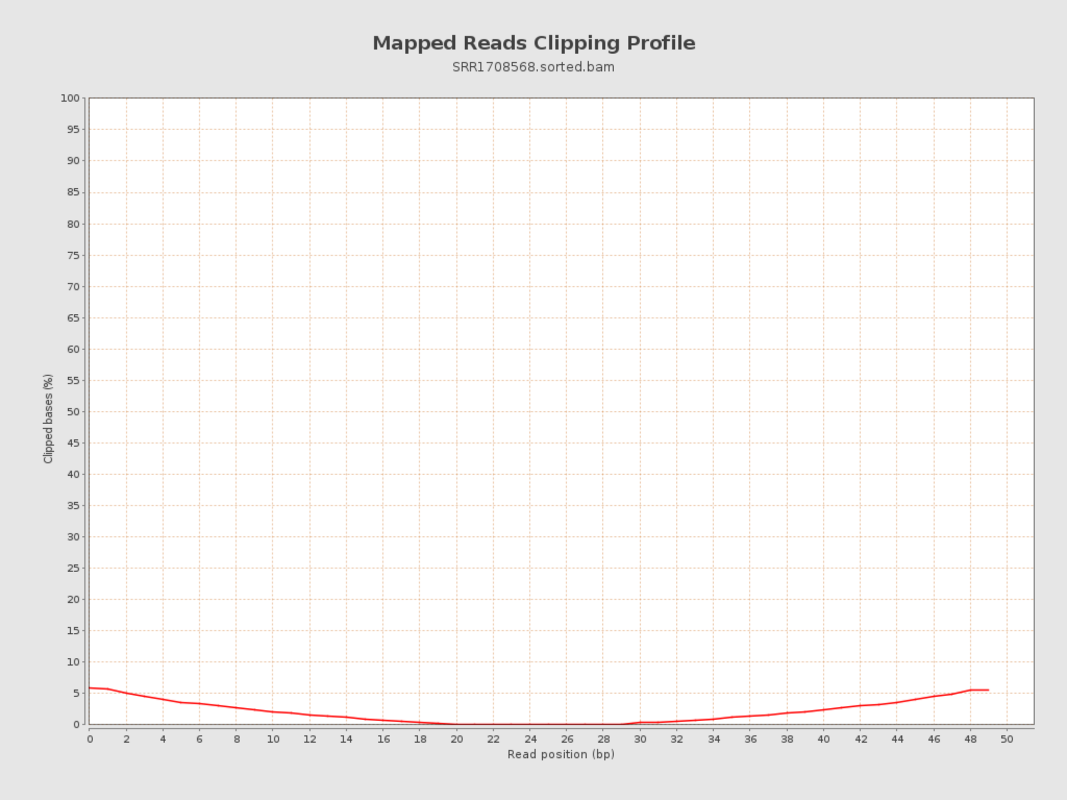
8. Results : Mapped Reads Nucleotide Content



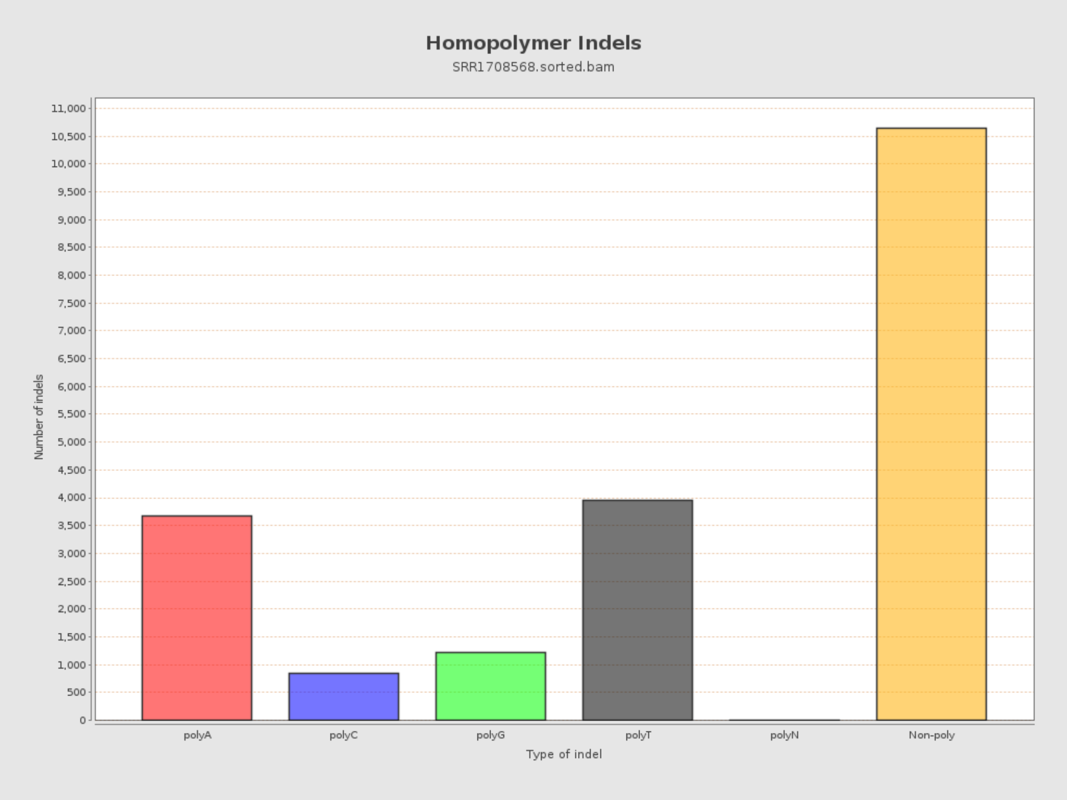
9. Results : Mapped Reads GC-content Distribution



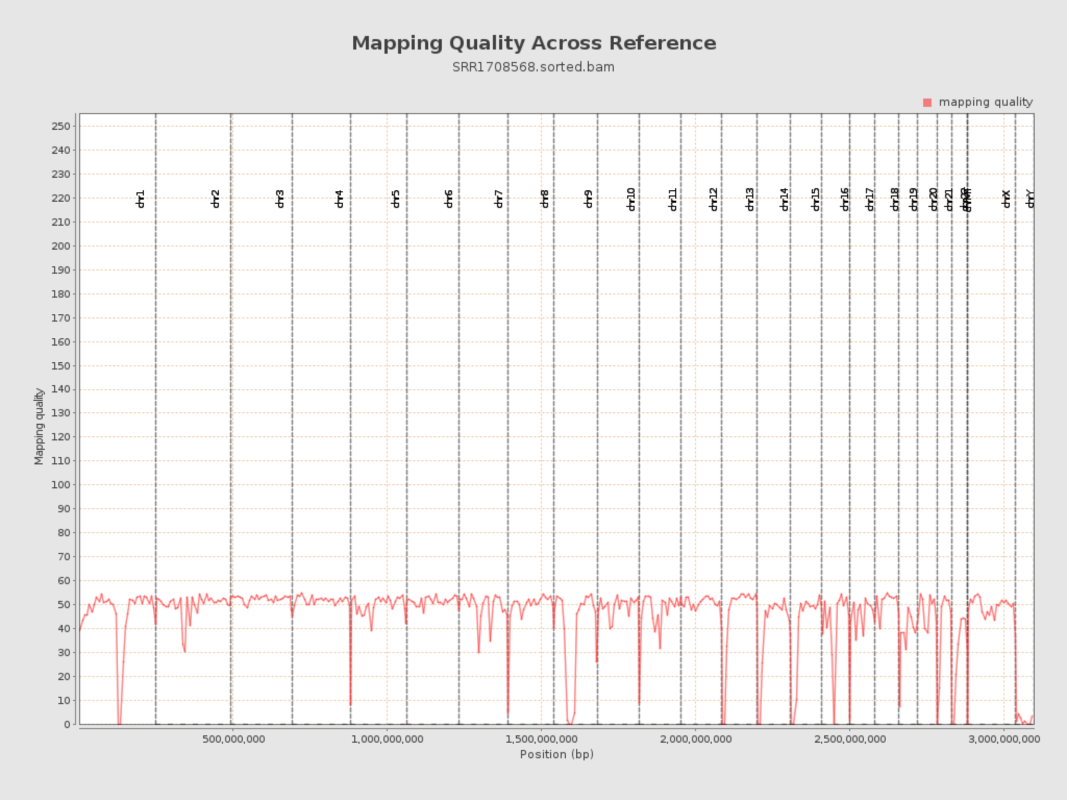
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram