Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:37:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708561.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_SRR1708561 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708561.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:37:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708561.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,177,035
Mapped reads	3,421,638 / 81.92%
Unmapped reads	755,397 / 18.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	101 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,753 / 0.43%
Duplication rate	0.52%
Clipped reads	46,669 / 1.12%

2.2. ACGT Content

Number/percentage of A's	52,980,707 / 31.05%
Number/percentage of C's	32,284,805 / 18.92%
Number/percentage of T's	52,813,847 / 30.96%
Number/percentage of G's	32,529,496 / 19.07%
Number/percentage of N's	5,895 / 0%
GC Percentage	37.99%

2.3. Coverage

Mean	0.0551

Standard Deviation	0.2475

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

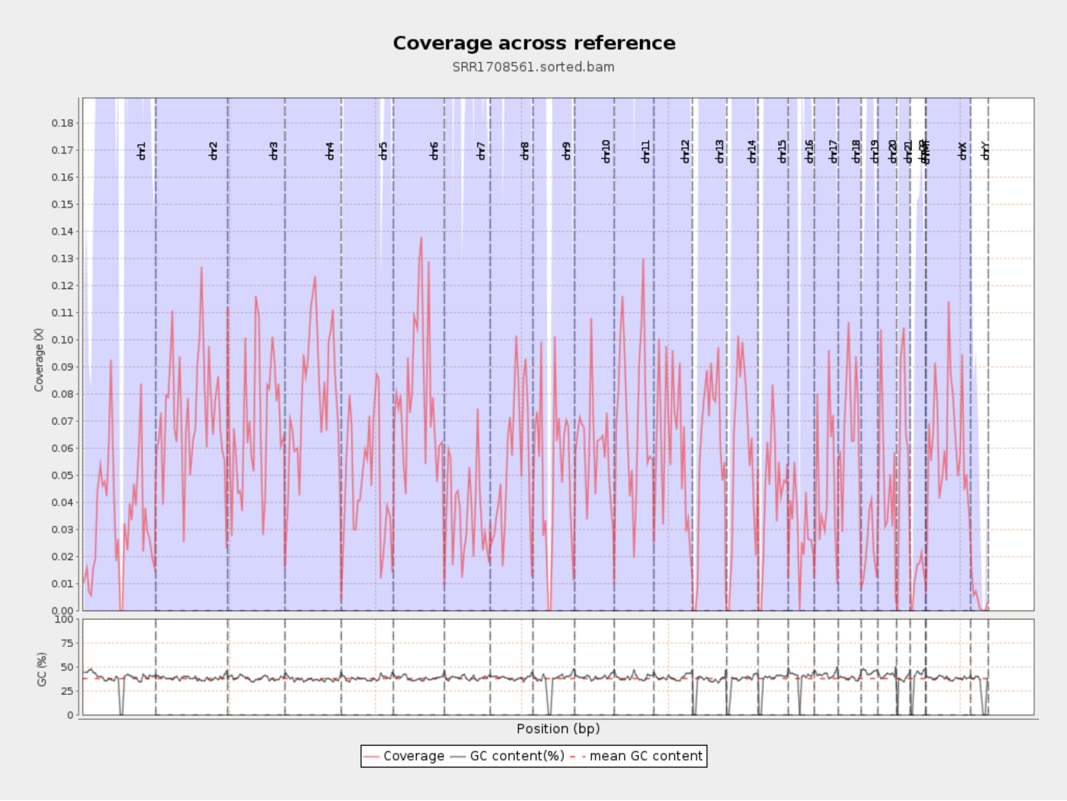
General error rate	0.17%
Mismatches	267,813
Insertions	11,590
Mapped reads with at least one insertion	0.34%
Deletions	9,060
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.82%

2.6. Chromosome stats

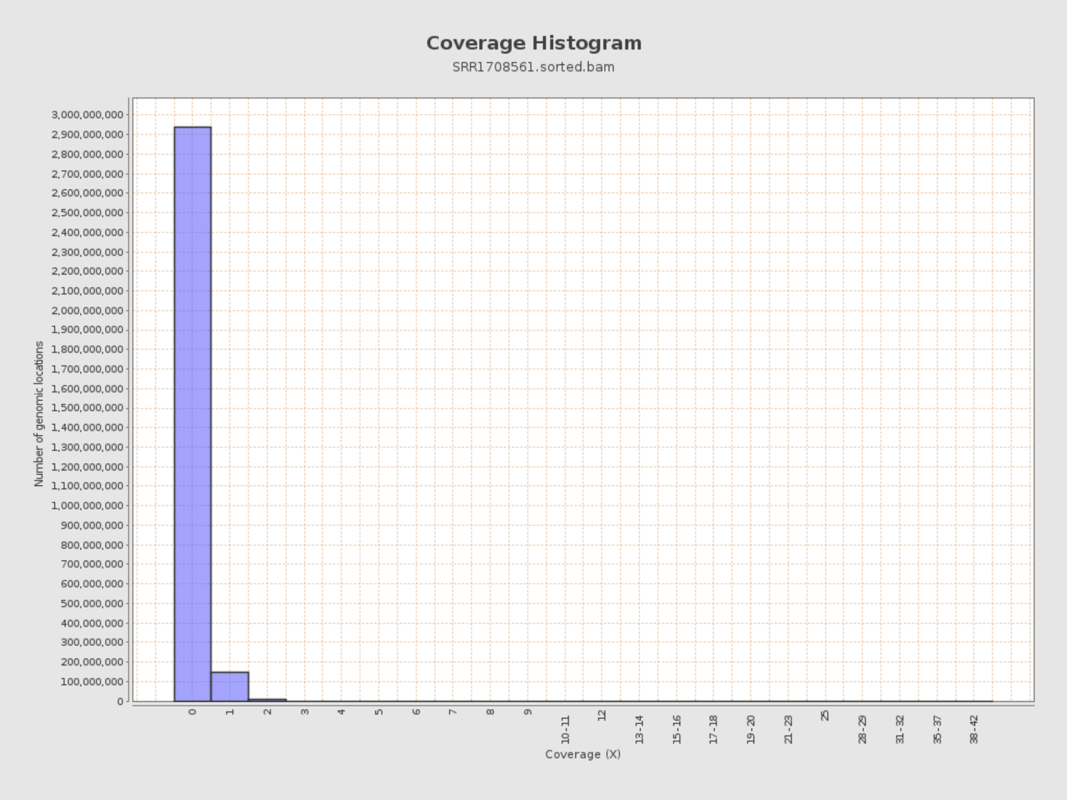
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8269250	0.0332	0.1919
chr2	243199373	17679411	0.0727	0.2829
chr3	198022430	13445364	0.0679	0.2736
chr4	191154276	15265536	0.0799	0.2972
chr5	180915260	8332598	0.0461	0.2255
chr6	171115067	13752546	0.0804	0.2984
chr7	159138663	5611565	0.0353	0.1966

chr8	146364022	7998974	0.0547	0.2453
chr9	141213431	7213177	0.0511	0.2377
chr10	135534747	8233907	0.0608	0.2584
chr11	135006516	9732187	0.0721	0.284
chr12	133851895	8110577	0.0606	0.2587
chr13	115169878	6792152	0.059	0.2549
chr14	107349540	6124596	0.0571	0.2524
chr15	102531392	4387144	0.0428	0.2176
chr16	90354753	2582963	0.0286	0.1767
chr17	81195210	3872963	0.0477	0.2298
chr18	78077248	5334560	0.0683	0.274
chr19	59128983	1385243	0.0234	0.1588
chr20	63025520	3187007	0.0506	0.2361
chr21	48129895	2786428	0.0579	0.258
chr22	51304566	642080	0.0125	0.115
chrMT	16571	100	0.006	0.0774
chrX	155270560	9659141	0.0622	0.2628
chrY	59373566	230466	0.0039	0.0647

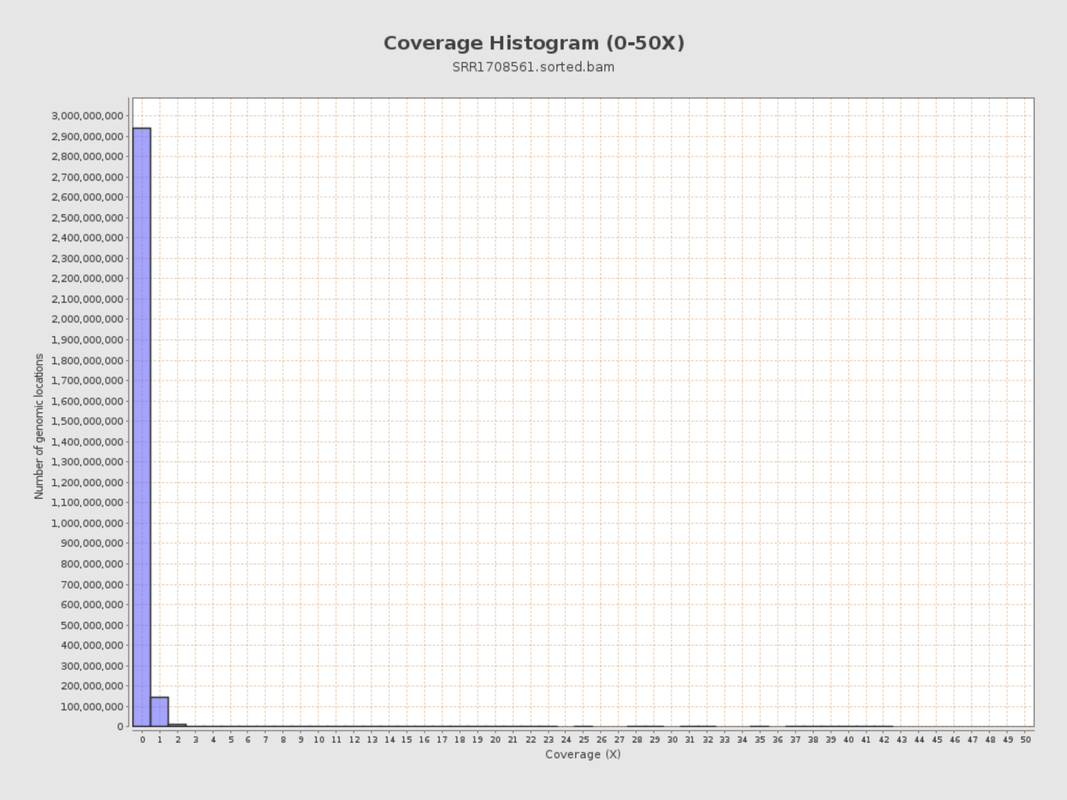
3. Results : Coverage across reference



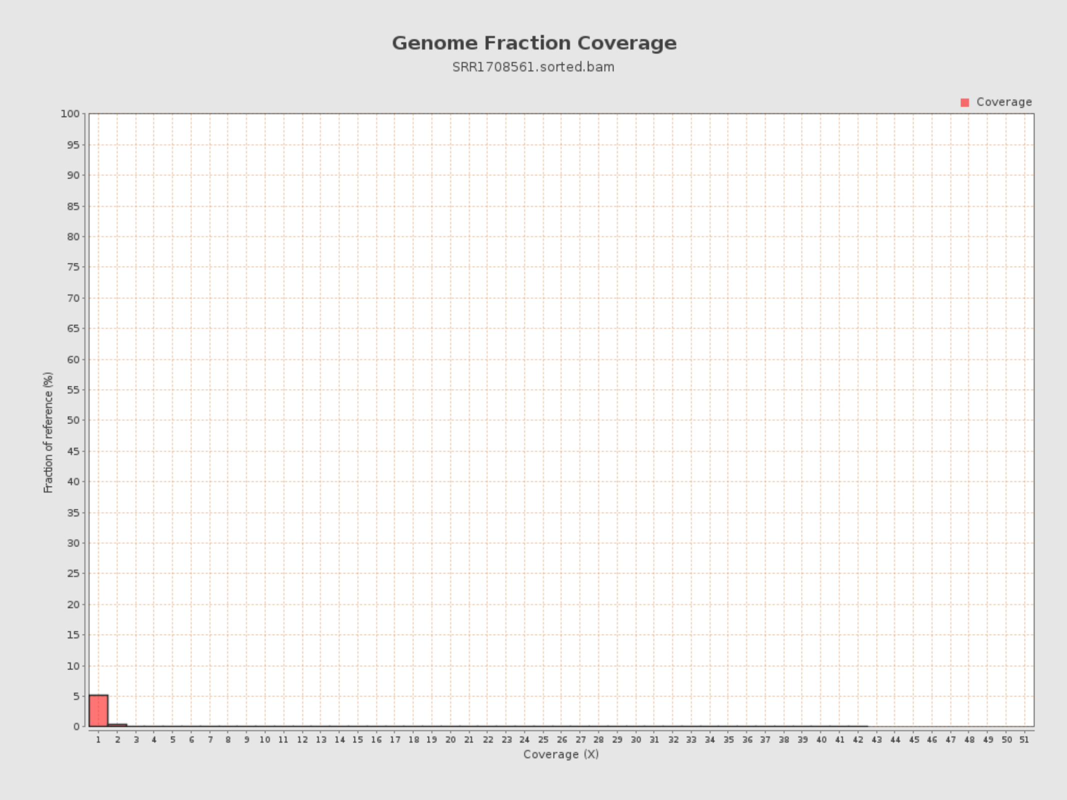
4. Results : Coverage Histogram



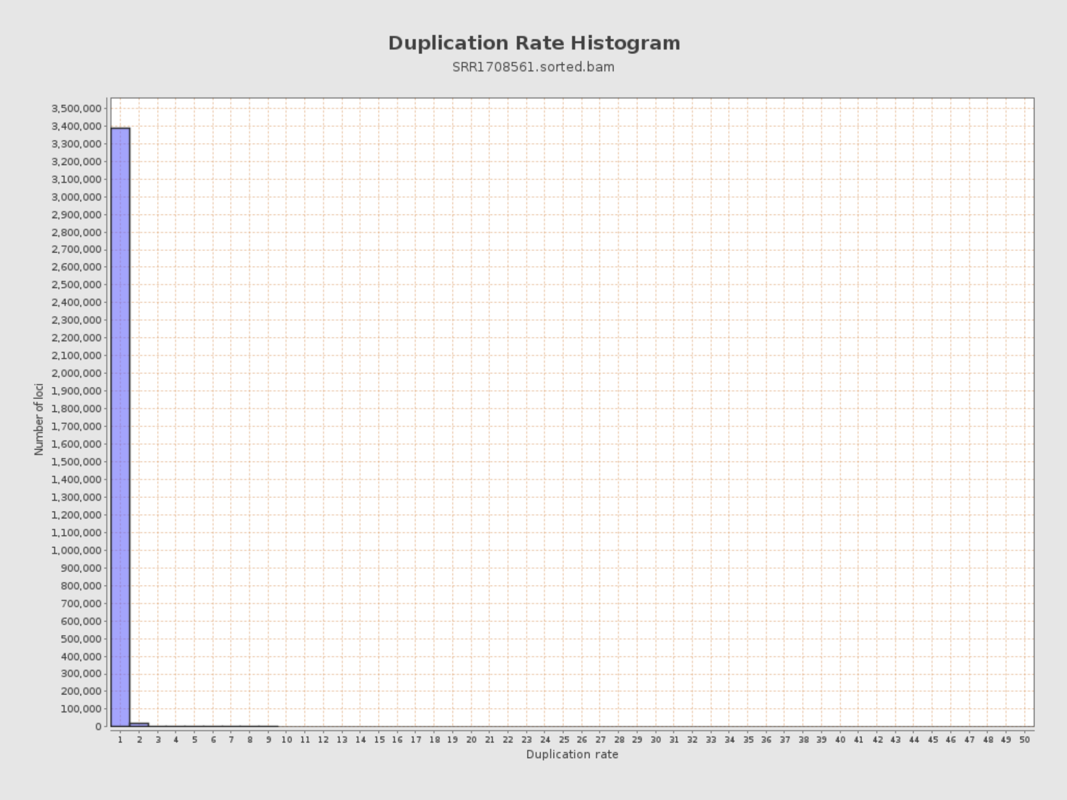
5. Results : Coverage Histogram (0-50X)



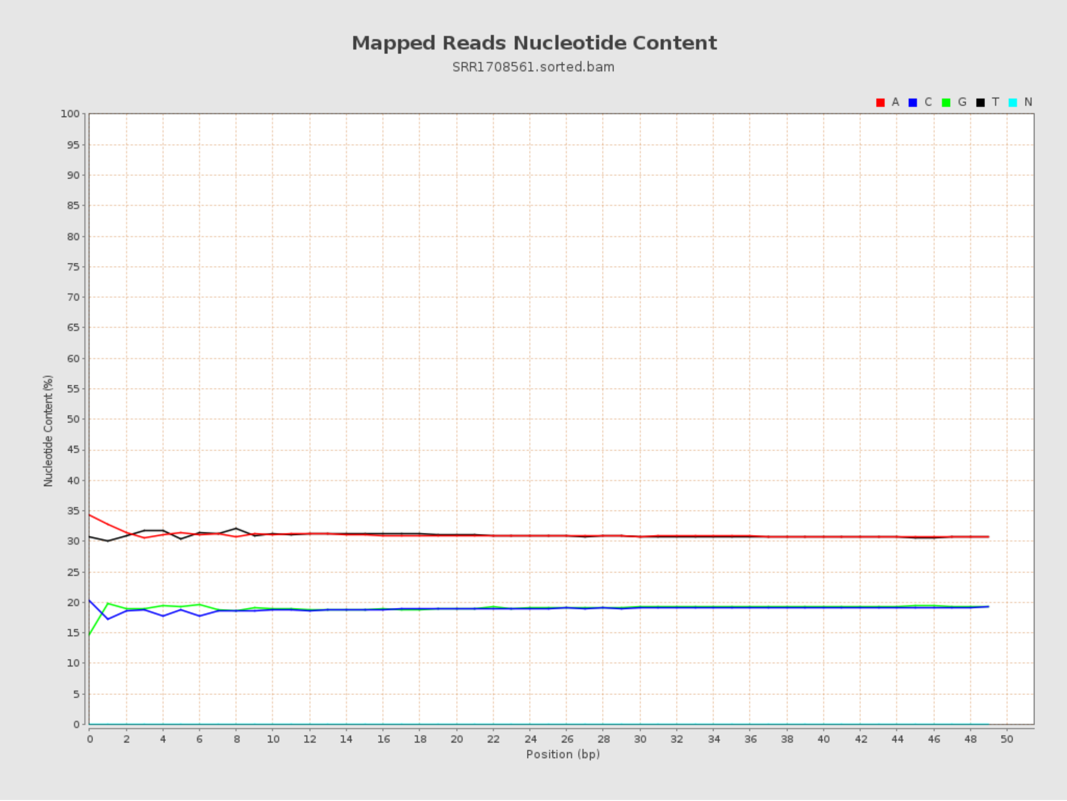
6. Results : Genome Fraction Coverage



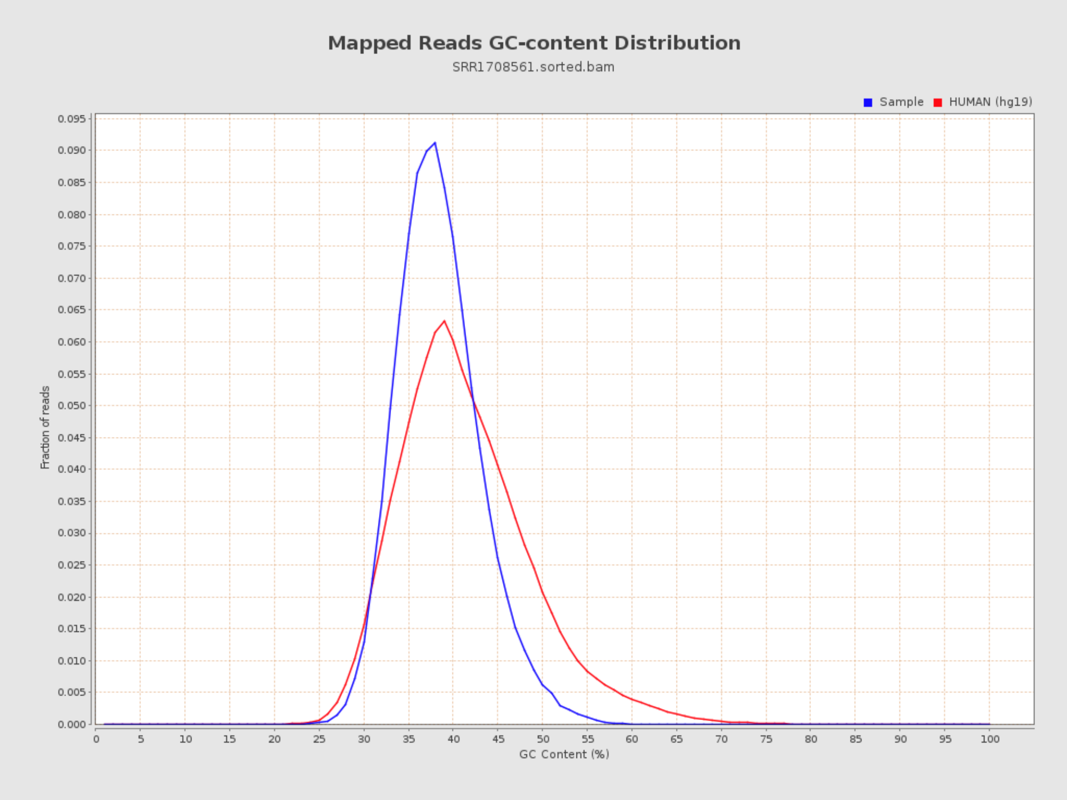
7. Results : Duplication Rate Histogram



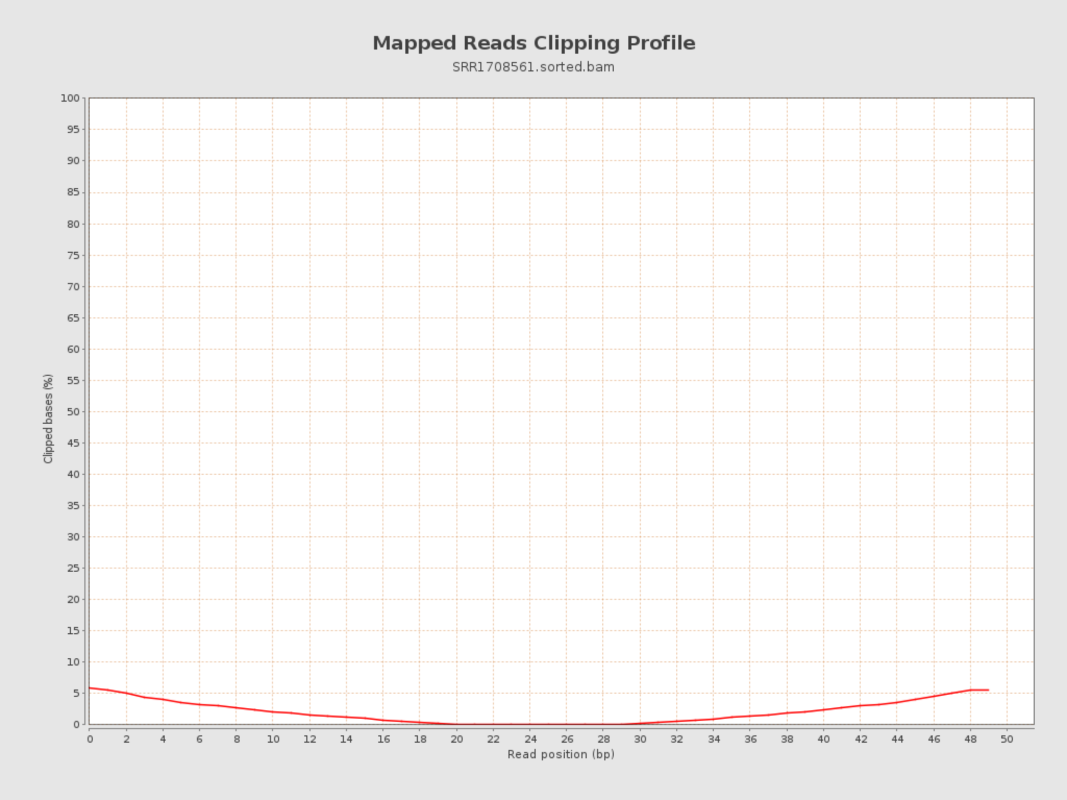
8. Results : Mapped Reads Nucleotide Content



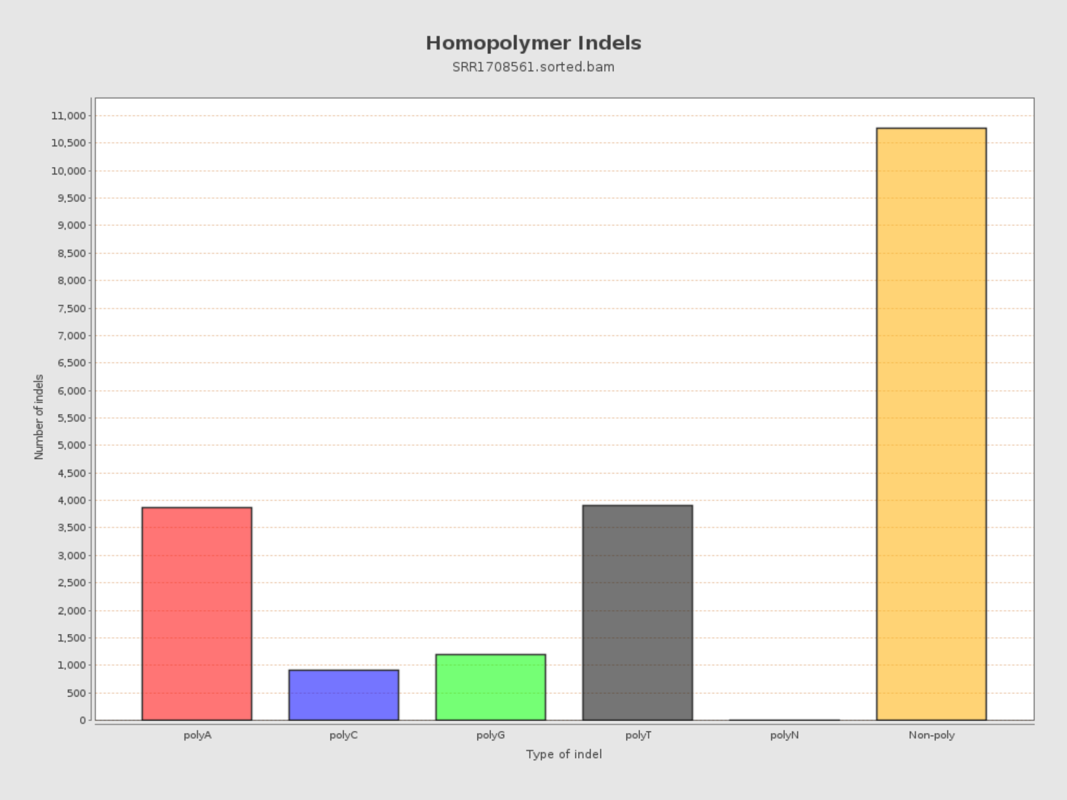
9. Results : Mapped Reads GC-content Distribution



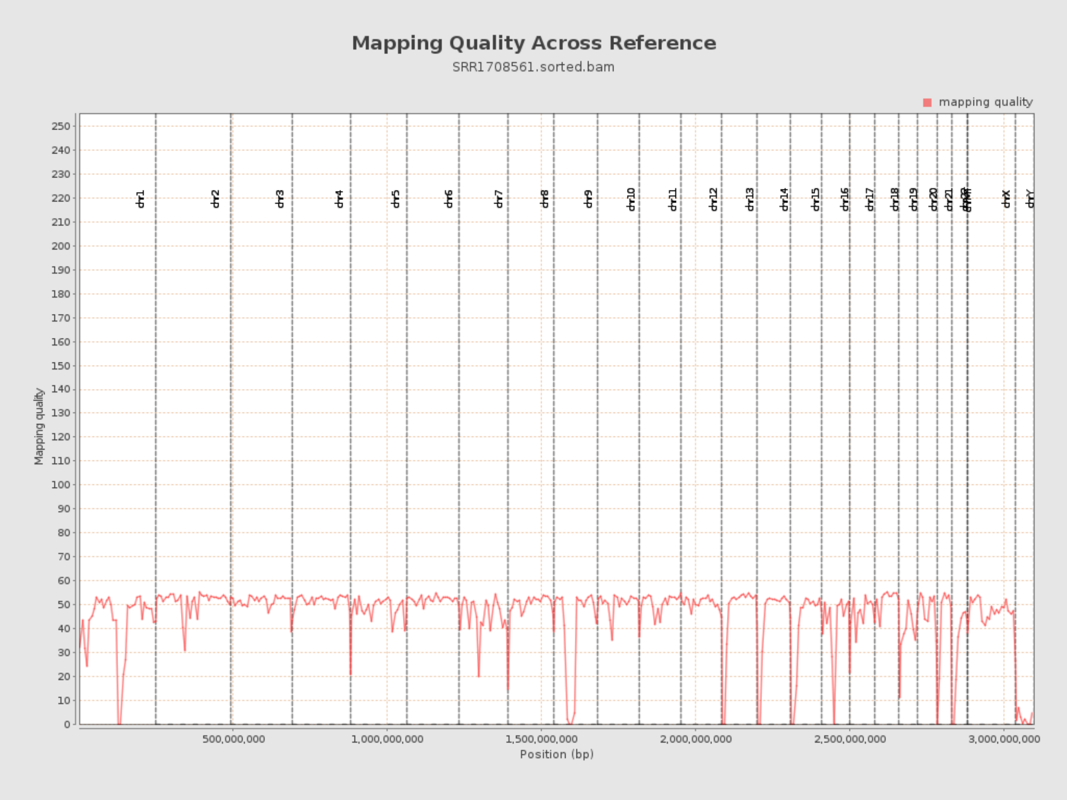
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram