Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:00:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708620.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_SRR1708620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:00:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,575,942
Mapped reads	2,584,359 / 72.27%
Unmapped reads	991,583 / 27.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	836 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	96,675 / 2.7%
Duplication rate	2.57%
Clipped reads	390,645 / 10.92%

2.2. ACGT Content

Number/percentage of A's	37,077,714 / 29.43%
Number/percentage of C's	23,902,397 / 18.97%
Number/percentage of T's	39,594,734 / 31.42%
Number/percentage of G's	25,418,035 / 20.17%
Number/percentage of N's	11,046 / 0.01%
GC Percentage	39.14%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.4083

2.4. Mapping Quality

Mean Mapping Quality	42.55

2.5. Mismatches and indels

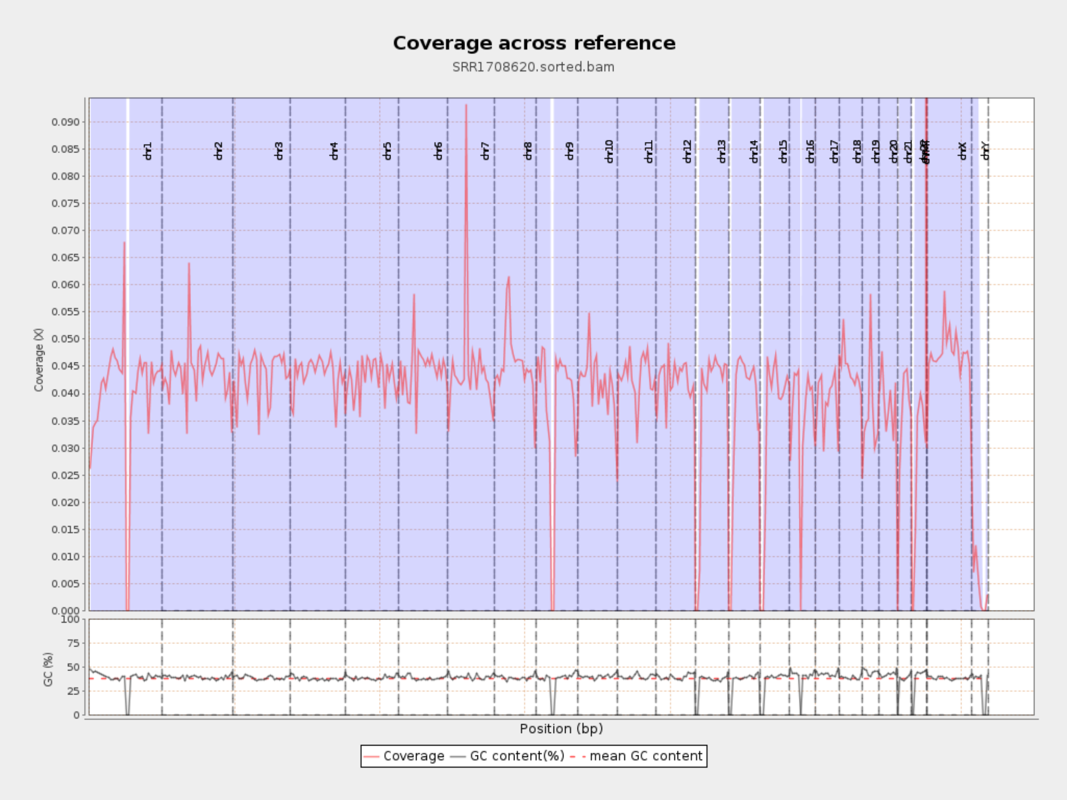
General error rate	0.64%
Mismatches	802,667
Insertions	6,014
Mapped reads with at least one insertion	0.23%
Deletions	16,465
Mapped reads with at least one deletion	0.64%
Homopolymer indels	48.08%

2.6. Chromosome stats

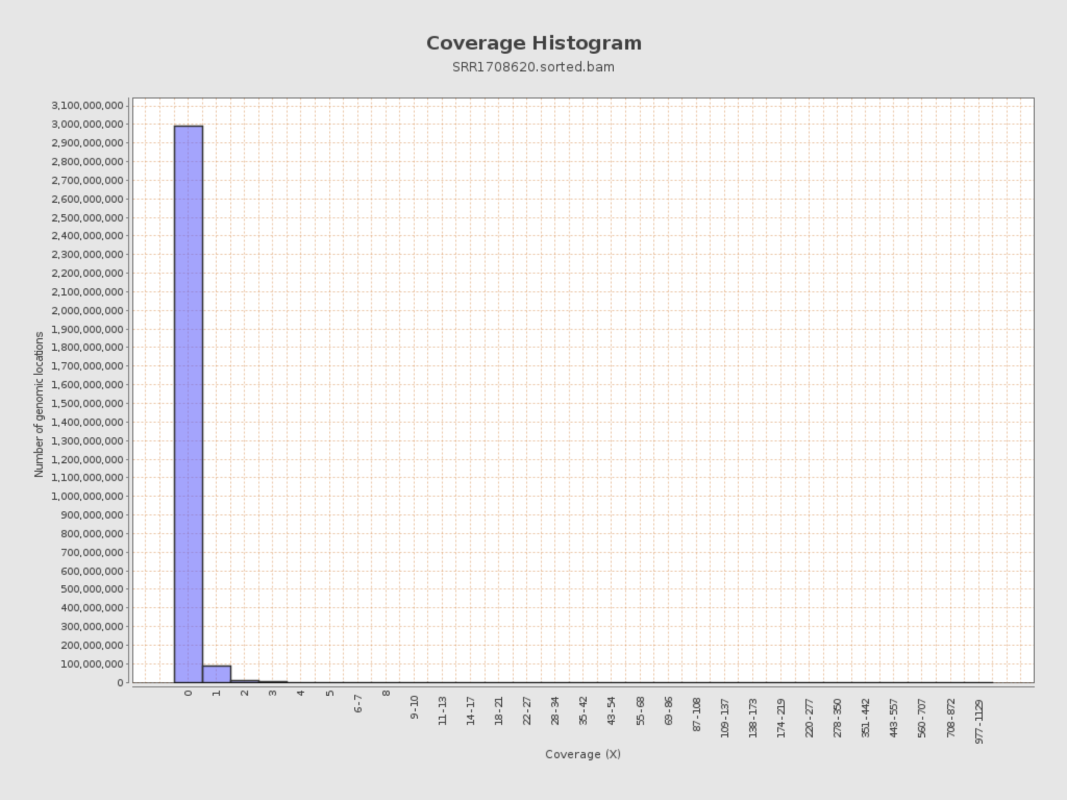
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9952859	0.0399	0.6887
chr2	243199373	10733095	0.0441	0.4354
chr3	198022430	8630269	0.0436	0.245
chr4	191154276	8369365	0.0438	0.2485
chr5	180915260	7766836	0.0429	0.2454
chr6	171115067	7605151	0.0444	0.3422
chr7	159138663	7164364	0.045	0.6981

chr8	146364022	6679217	0.0456	0.6773
chr9	141213431	5313152	0.0376	0.3231
chr10	135534747	5724563	0.0422	0.3286
chr11	135006516	5769113	0.0427	0.3301
chr12	133851895	5675954	0.0424	0.2495
chr13	115169878	4242193	0.0368	0.2305
chr14	107349540	3896070	0.0363	0.2467
chr15	102531392	3552817	0.0347	0.2175
chr16	90354753	3208198	0.0355	0.234
chr17	81195210	3098589	0.0382	0.2623
chr18	78077248	3480667	0.0446	0.6747
chr19	59128983	2178471	0.0368	0.5157
chr20	63025520	2402935	0.0381	0.2379
chr21	48129895	1638100	0.034	0.234
chr22	51304566	1304810	0.0254	0.1843
chrMT	16571	18370	1.1086	1.2304
chrX	155270560	7325920	0.0472	0.2803
chrY	59373566	297782	0.005	0.0894

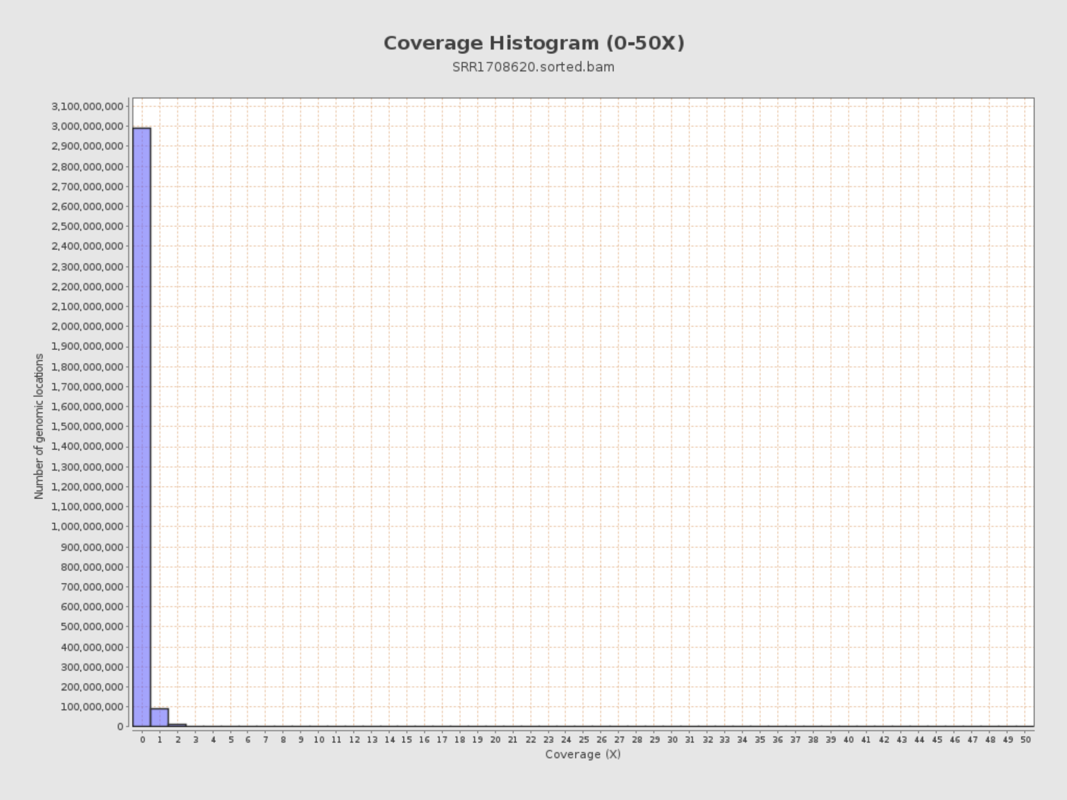
3. Results : Coverage across reference



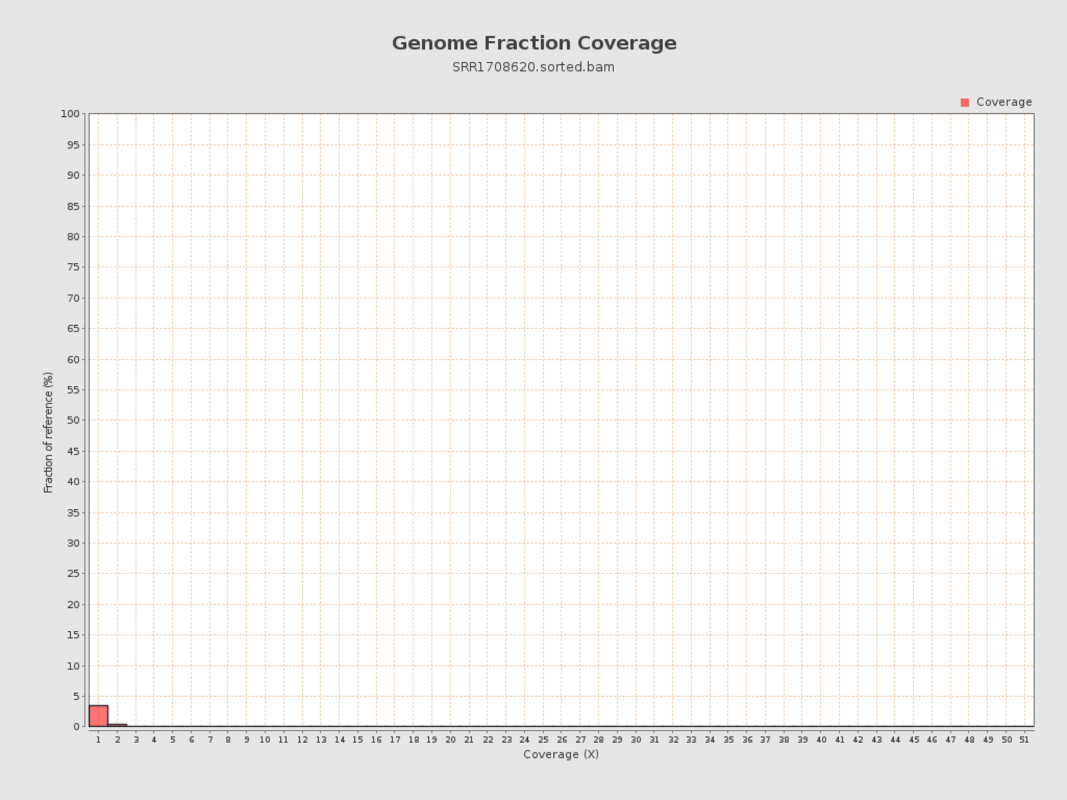
4. Results : Coverage Histogram



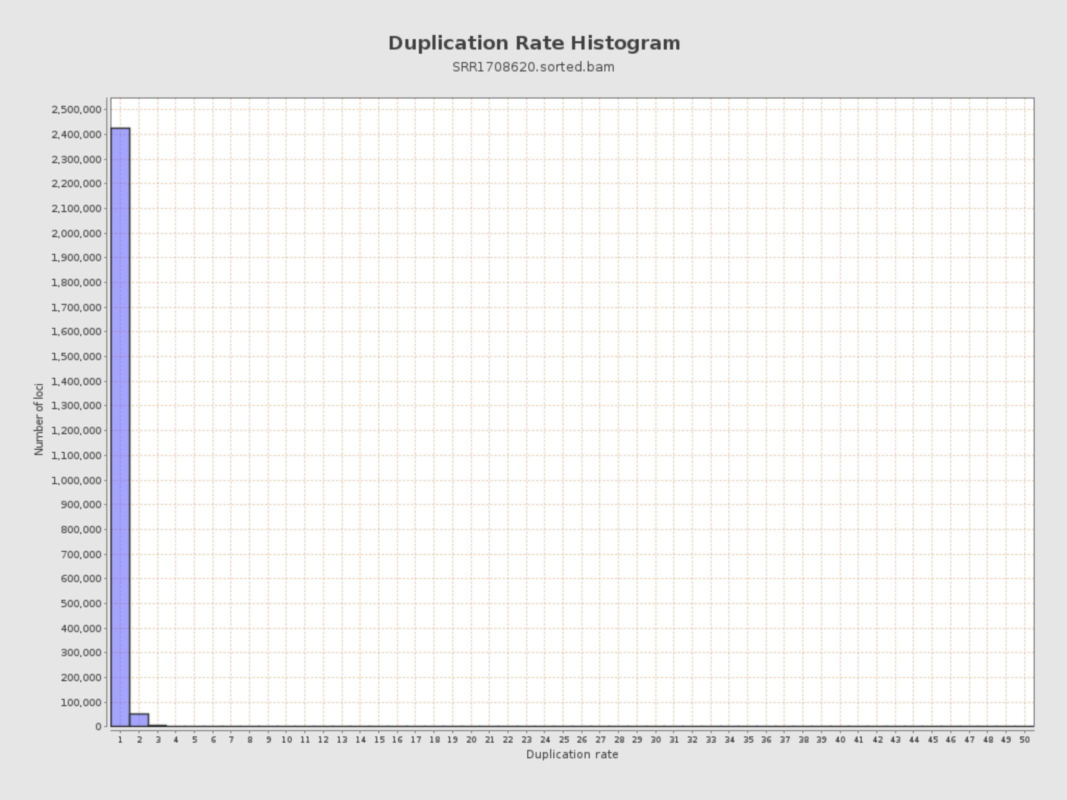
5. Results : Coverage Histogram (0-50X)



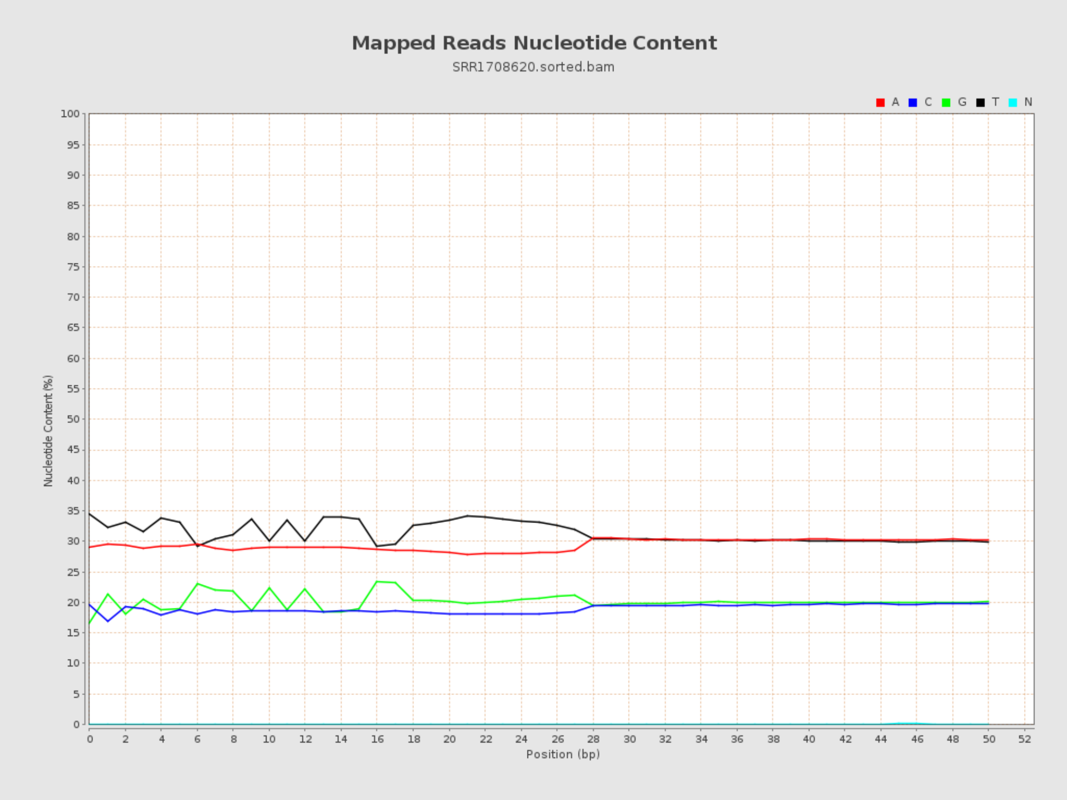
6. Results : Genome Fraction Coverage



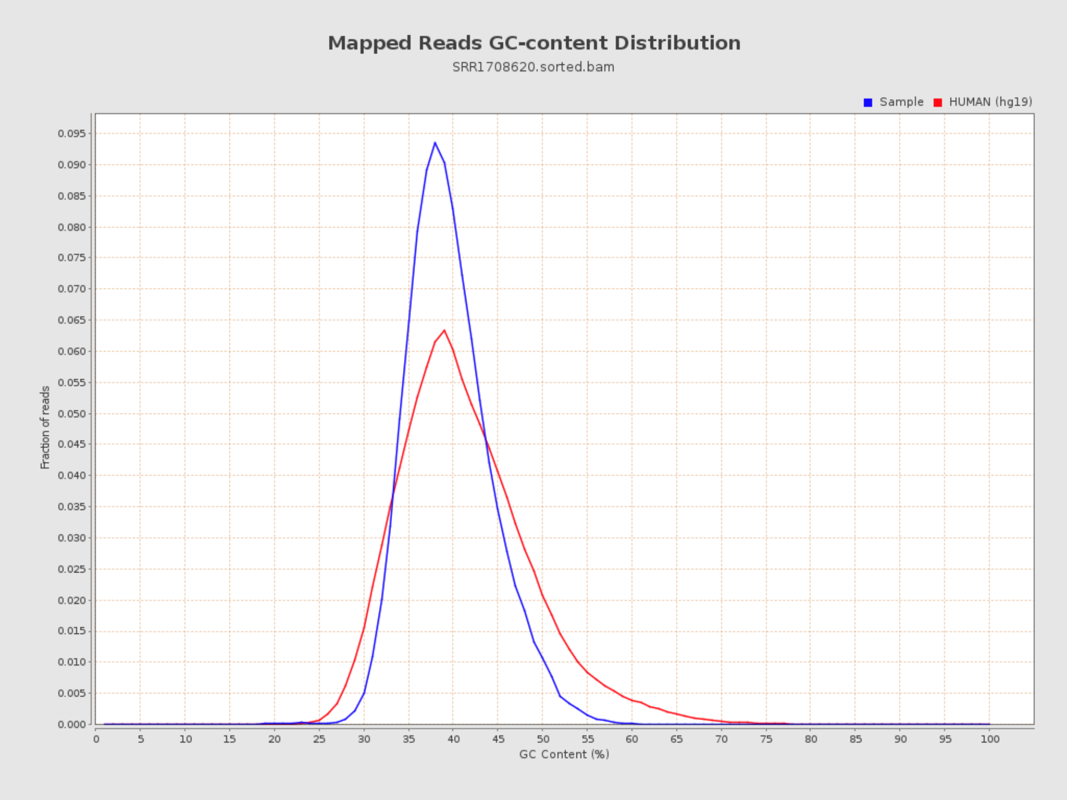
7. Results : Duplication Rate Histogram



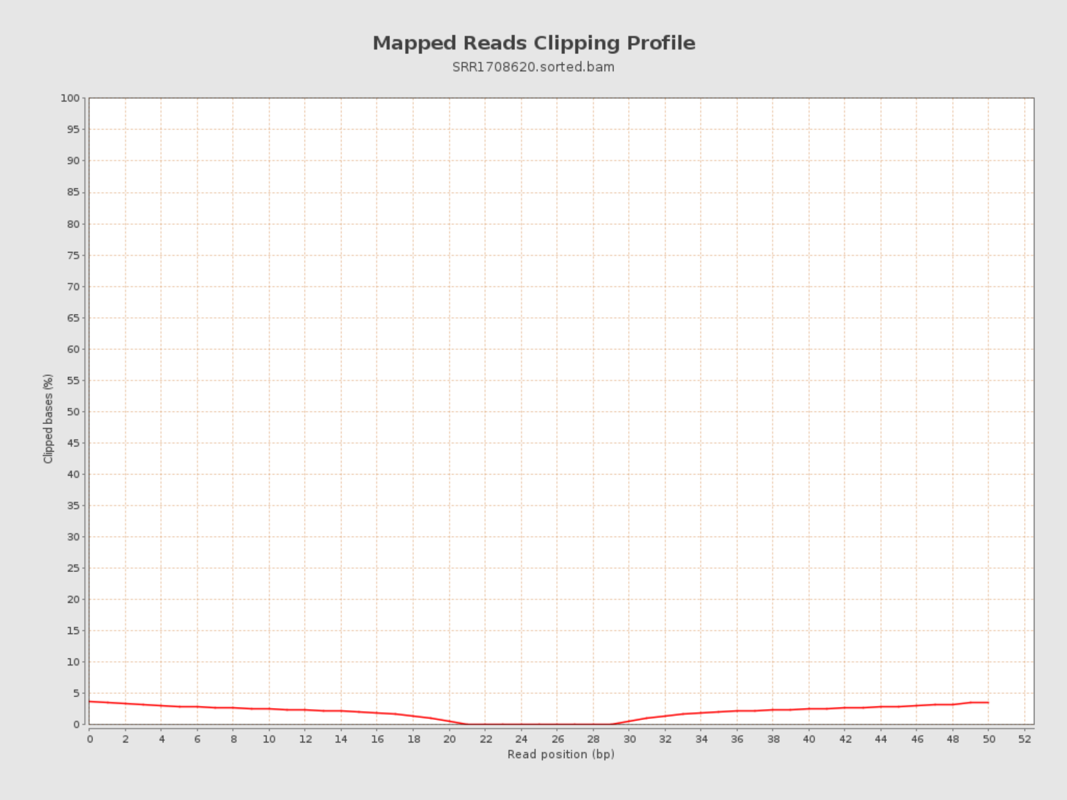
8. Results : Mapped Reads Nucleotide Content



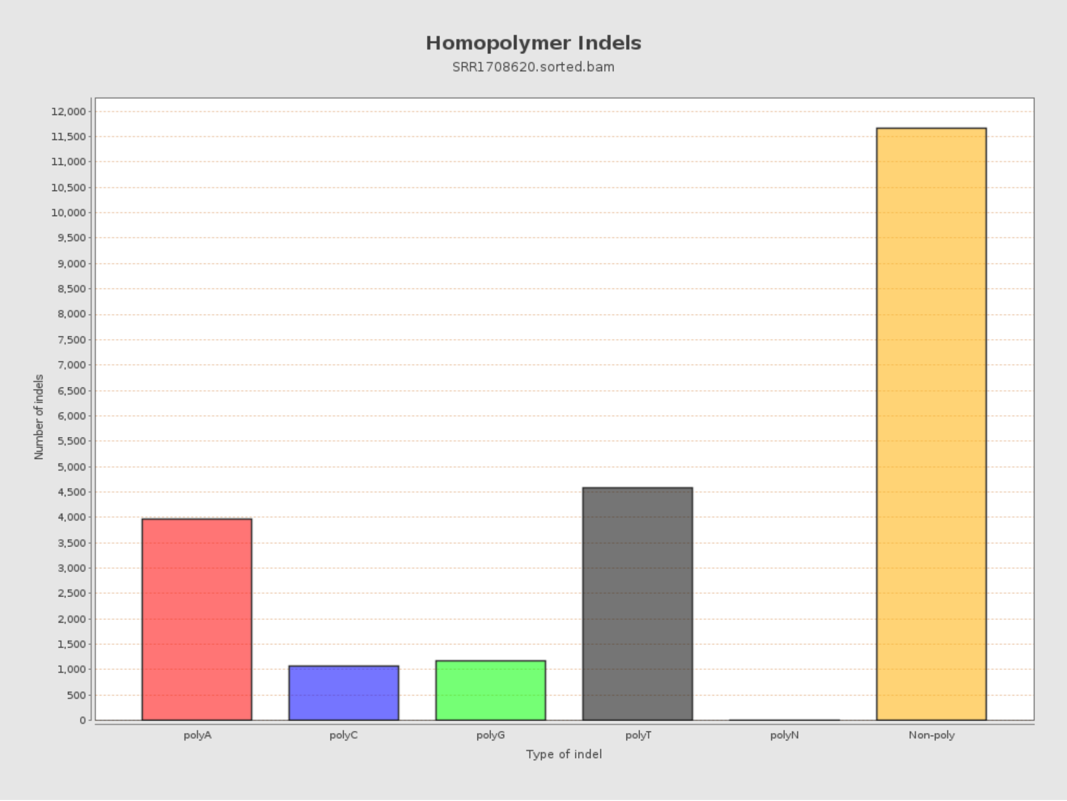
9. Results : Mapped Reads GC-content Distribution



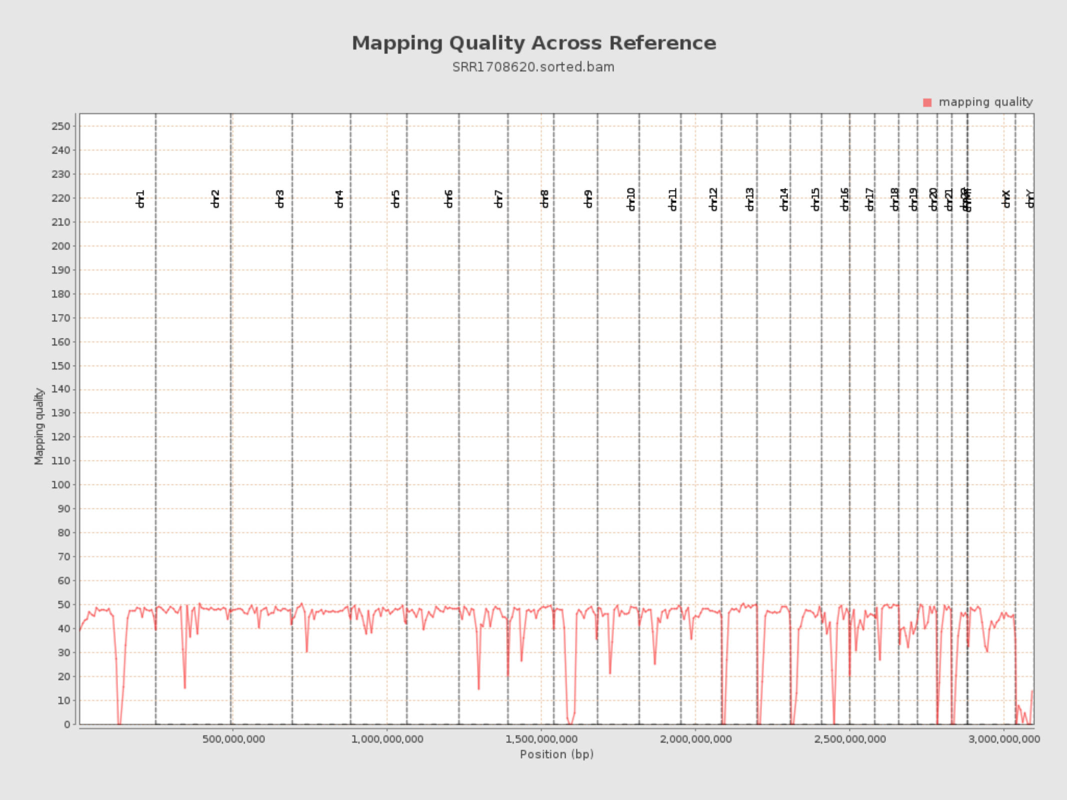
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram