Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:43:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708616.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_SRR1708616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:43:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,059,607
Mapped reads	2,245,773 / 73.4%
Unmapped reads	813,834 / 26.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	791 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	77,805 / 2.54%
Duplication rate	2.4%
Clipped reads	341,865 / 11.17%

2.2. ACGT Content

Number/percentage of A's	32,372,701 / 29.57%
Number/percentage of C's	20,652,689 / 18.87%
Number/percentage of T's	34,486,445 / 31.5%
Number/percentage of G's	21,949,169 / 20.05%
Number/percentage of N's	9,613 / 0.01%
GC Percentage	38.92%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.3682

2.4. Mapping Quality

Mean Mapping Quality	43.14

2.5. Mismatches and indels

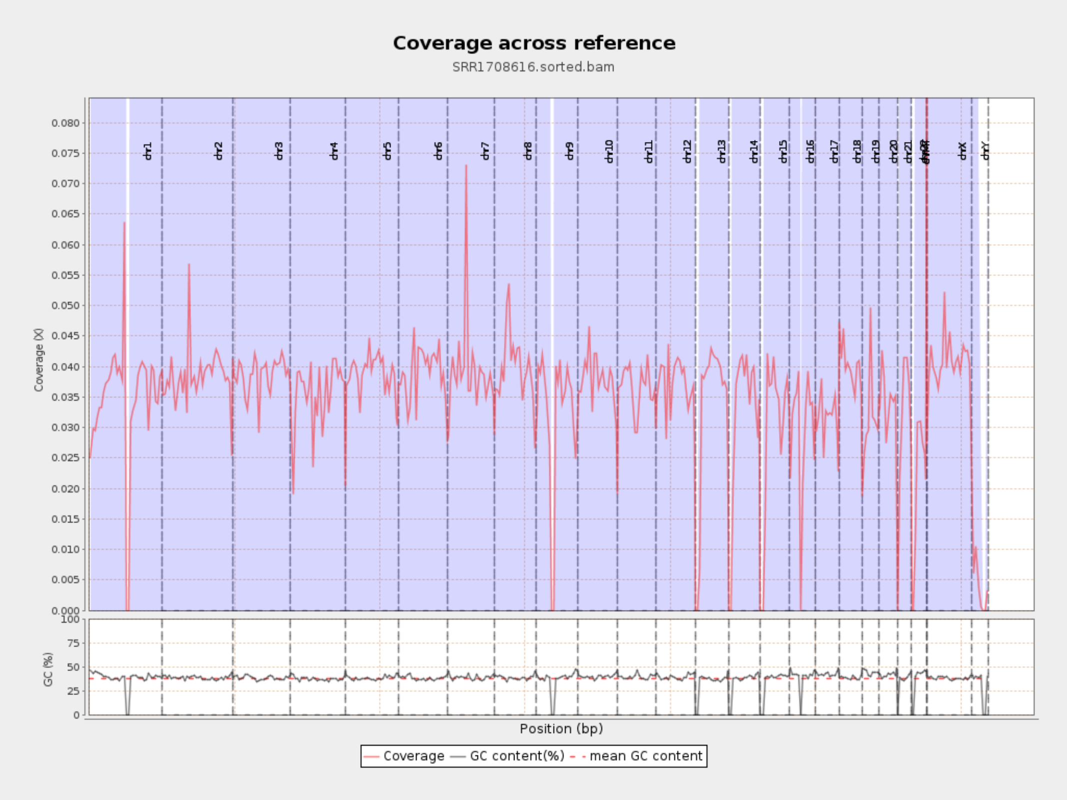
General error rate	0.64%
Mismatches	695,290
Insertions	5,278
Mapped reads with at least one insertion	0.23%
Deletions	13,656
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.98%

2.6. Chromosome stats

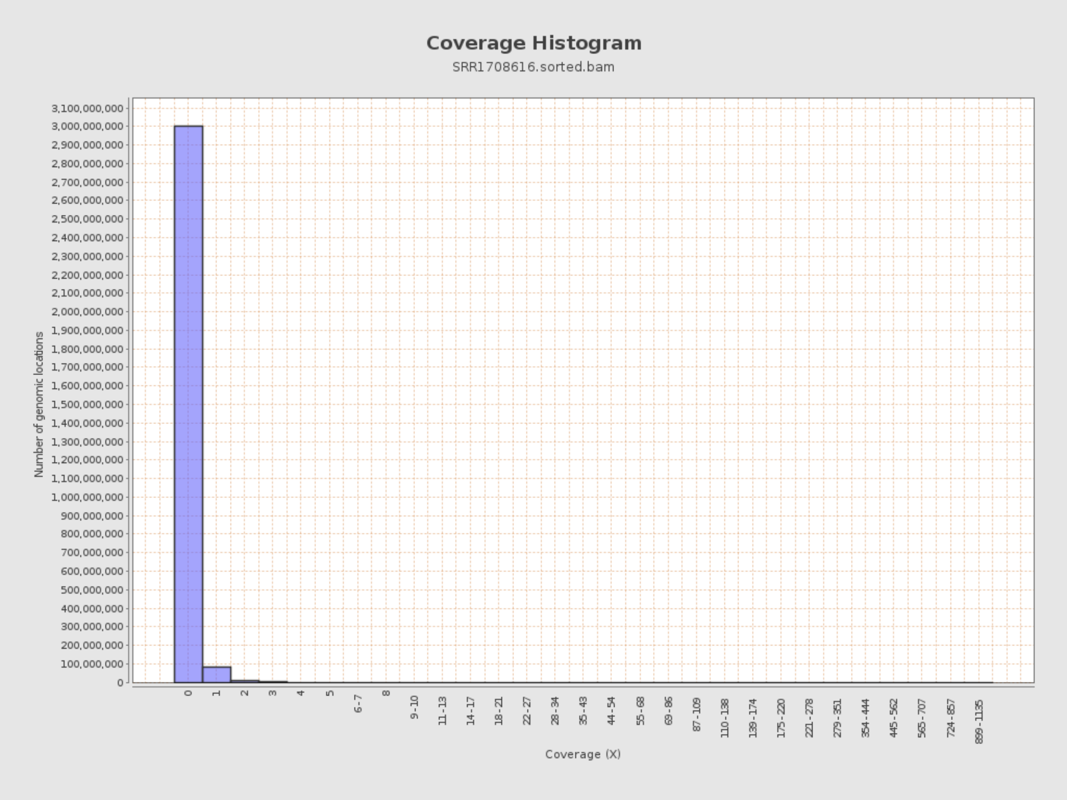
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8651656	0.0347	0.6646
chr2	243199373	9370667	0.0385	0.3818
chr3	198022430	7669789	0.0387	0.2235
chr4	191154276	6764994	0.0354	0.2172
chr5	180915260	7023155	0.0388	0.2296
chr6	171115067	6686375	0.0391	0.2923
chr7	159138663	6331602	0.0398	0.5352

chr8	146364022	5823277	0.0398	0.6657
chr9	141213431	4544020	0.0322	0.2844
chr10	135534747	5166784	0.0381	0.2901
chr11	135006516	4900749	0.0363	0.2848
chr12	133851895	4976034	0.0372	0.2272
chr13	115169878	3776116	0.0328	0.2069
chr14	107349540	3393198	0.0316	0.224
chr15	102531392	2998581	0.0292	0.194
chr16	90354753	2660109	0.0294	0.2097
chr17	81195210	2539645	0.0313	0.2314
chr18	78077248	3132445	0.0401	0.58
chr19	59128983	1878814	0.0318	0.4888
chr20	63025520	2144286	0.034	0.2156
chr21	48129895	1467057	0.0305	0.2106
chr22	51304566	1024072	0.02	0.1586
chrMT	16571	1846	0.1114	0.3254
chrX	155270560	6306820	0.0406	0.2561
chrY	59373566	259238	0.0044	0.0847

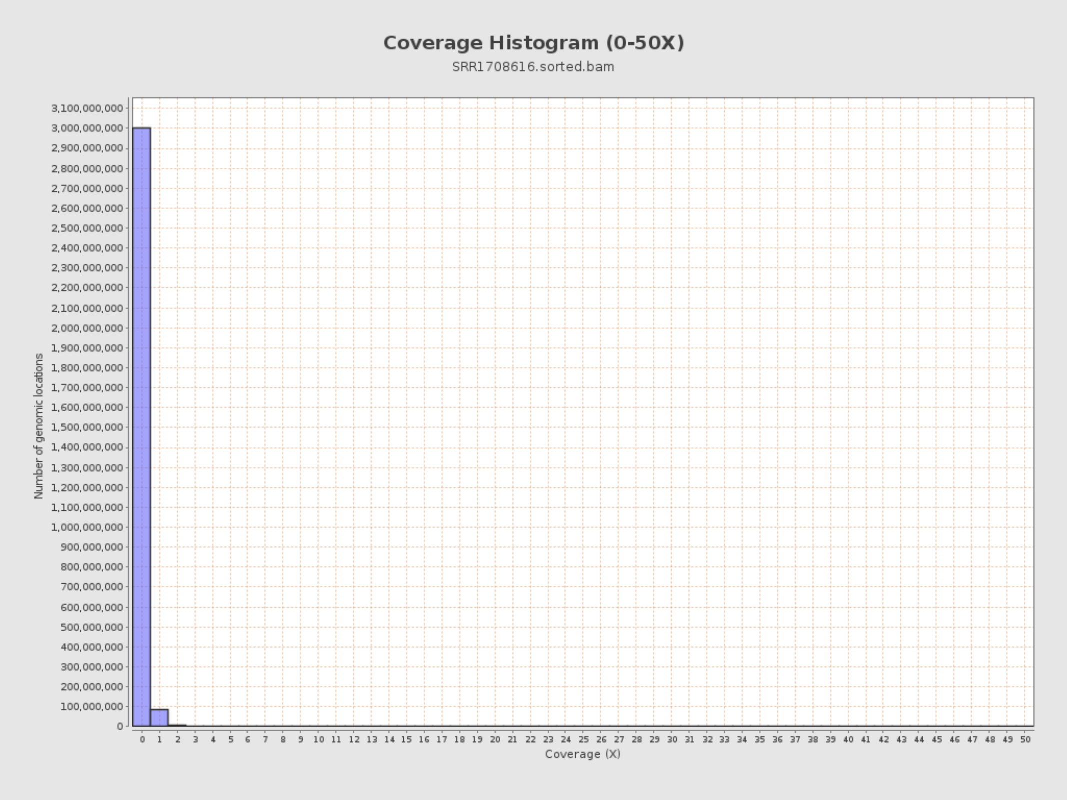
3. Results : Coverage across reference



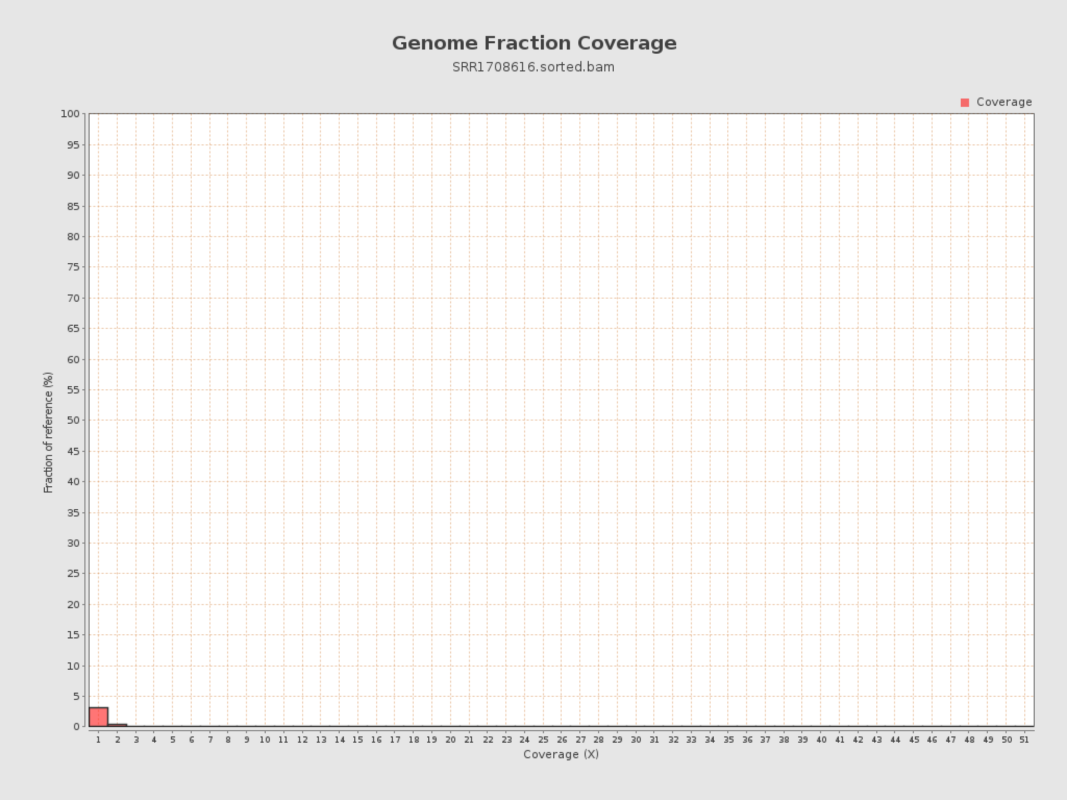
4. Results : Coverage Histogram



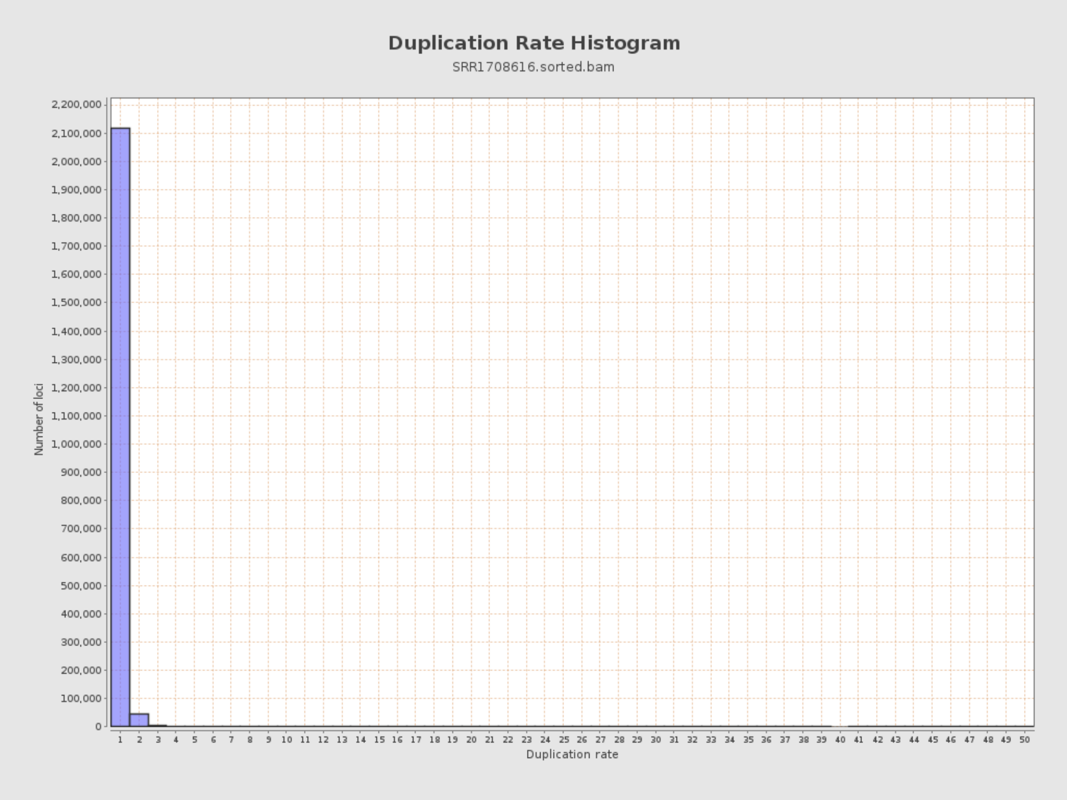
5. Results : Coverage Histogram (0-50X)



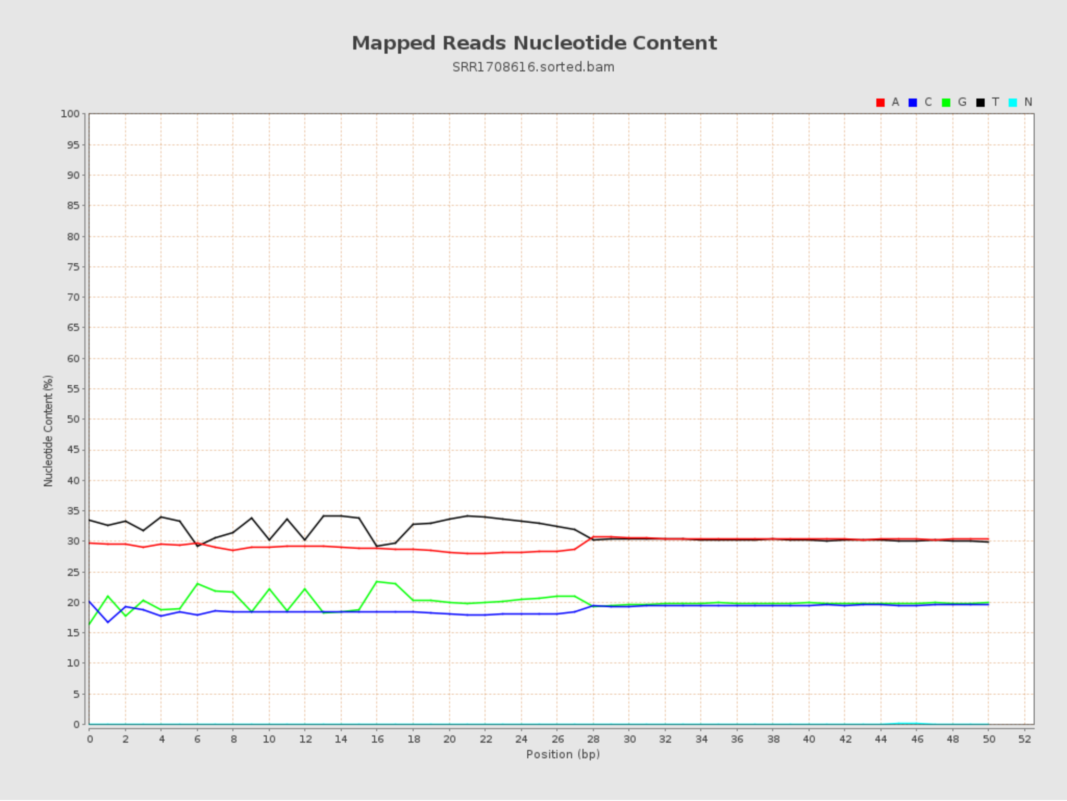
6. Results : Genome Fraction Coverage



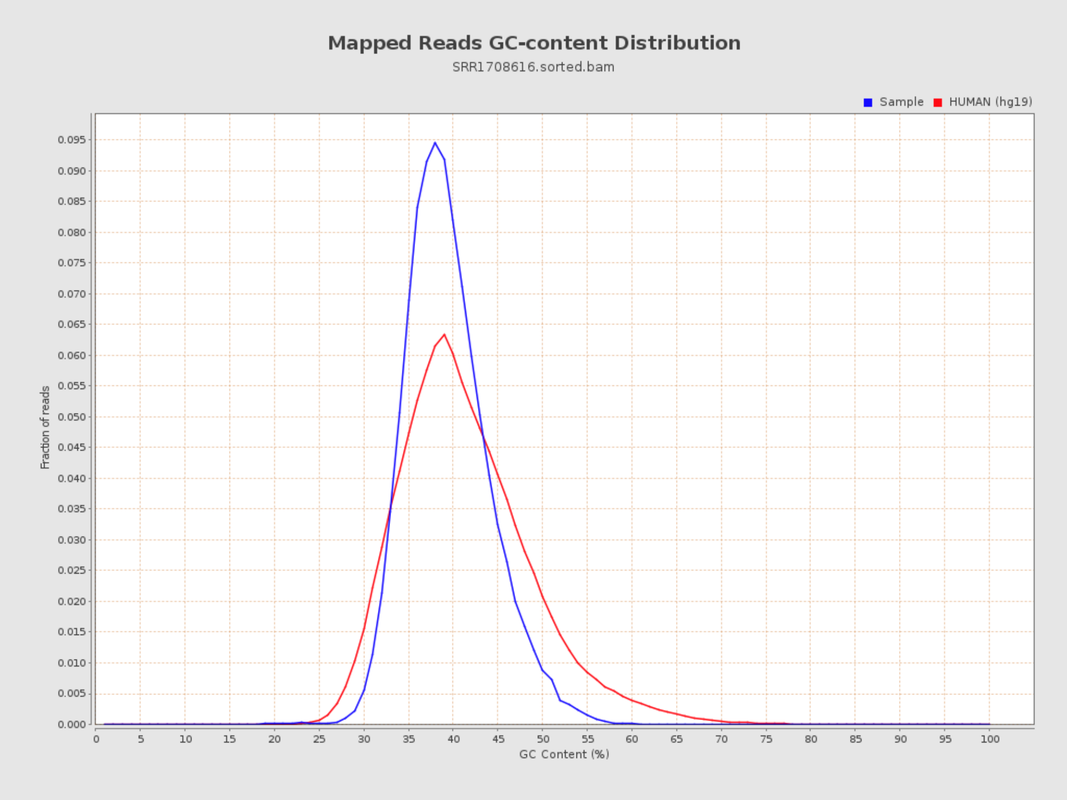
7. Results : Duplication Rate Histogram



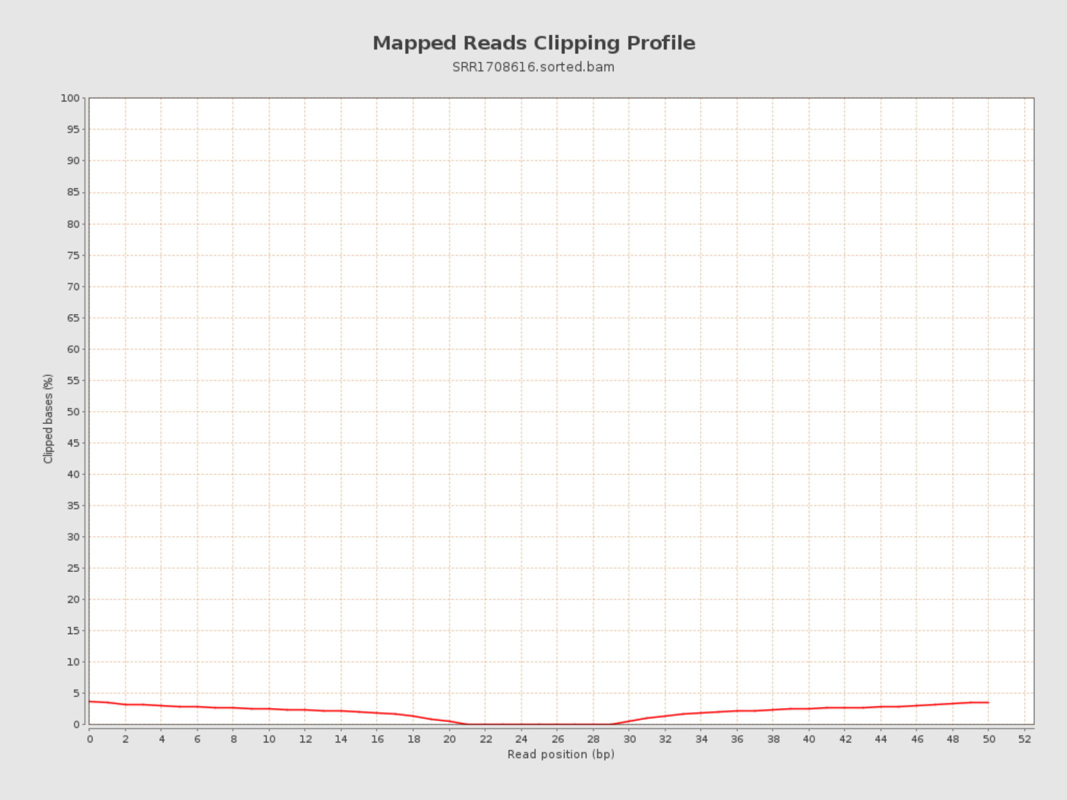
8. Results : Mapped Reads Nucleotide Content



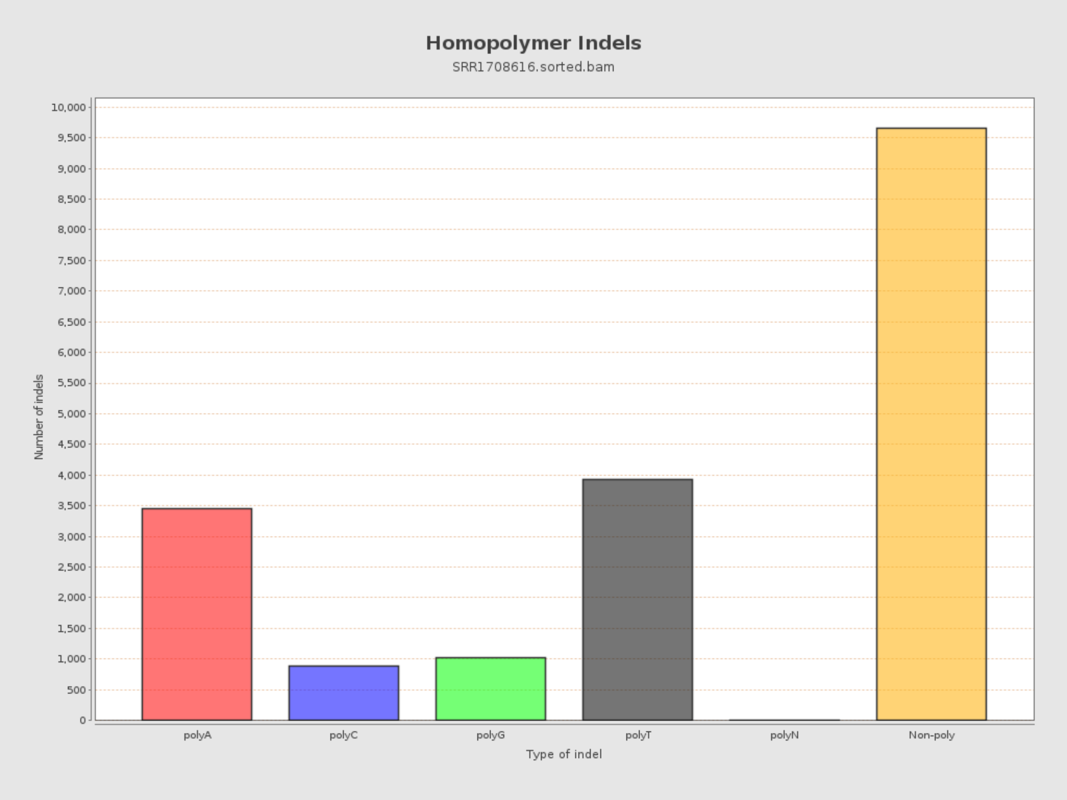
9. Results : Mapped Reads GC-content Distribution



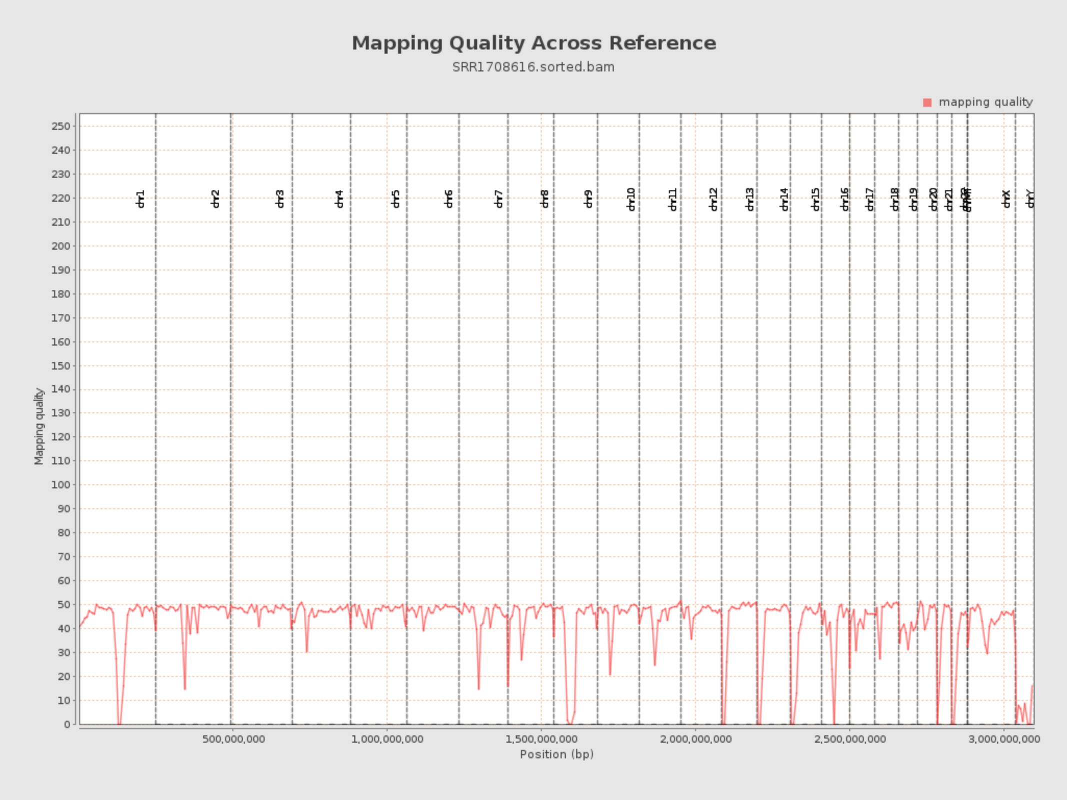
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram