

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708515.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_SRR1708515 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708515.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:27:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708515.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,972,600
Mapped reads	2,071,833 / 69.7%
Unmapped reads	900,767 / 30.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	426 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	91,489 / 3.08%
Duplication rate	3.52%
Clipped reads	398,603 / 13.41%

2.2. ACGT Content

Number/percentage of A's	28,763,564 / 28.92%
Number/percentage of C's	18,468,341 / 18.57%
Number/percentage of T's	31,845,296 / 32.02%
Number/percentage of G's	20,376,234 / 20.49%
Number/percentage of N's	1,314 / 0%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.3127
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2.4. Mapping Quality

Mean Mapping Quality	43.26
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2.5. Mismatches and indels

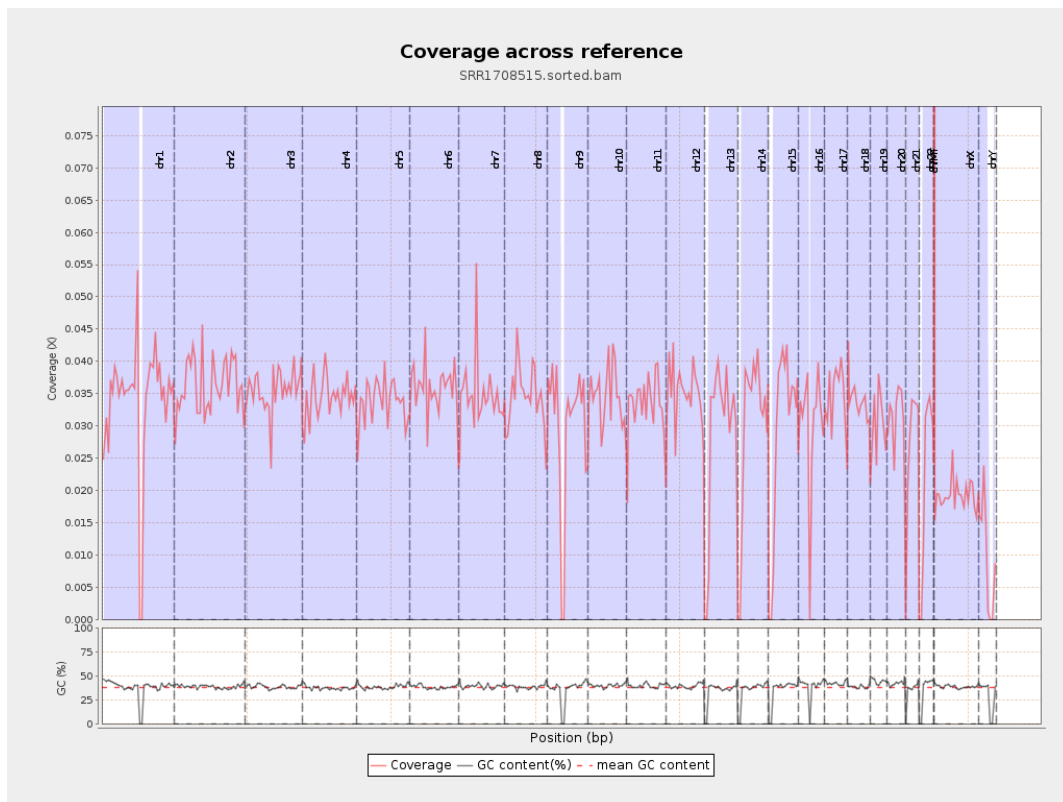
General error rate	0.48%
Mismatches	472,022
Insertions	4,606
Mapped reads with at least one insertion	0.22%
Deletions	11,831
Mapped reads with at least one deletion	0.57%
Homopolymer indels	49.05%

2.6. Chromosome stats

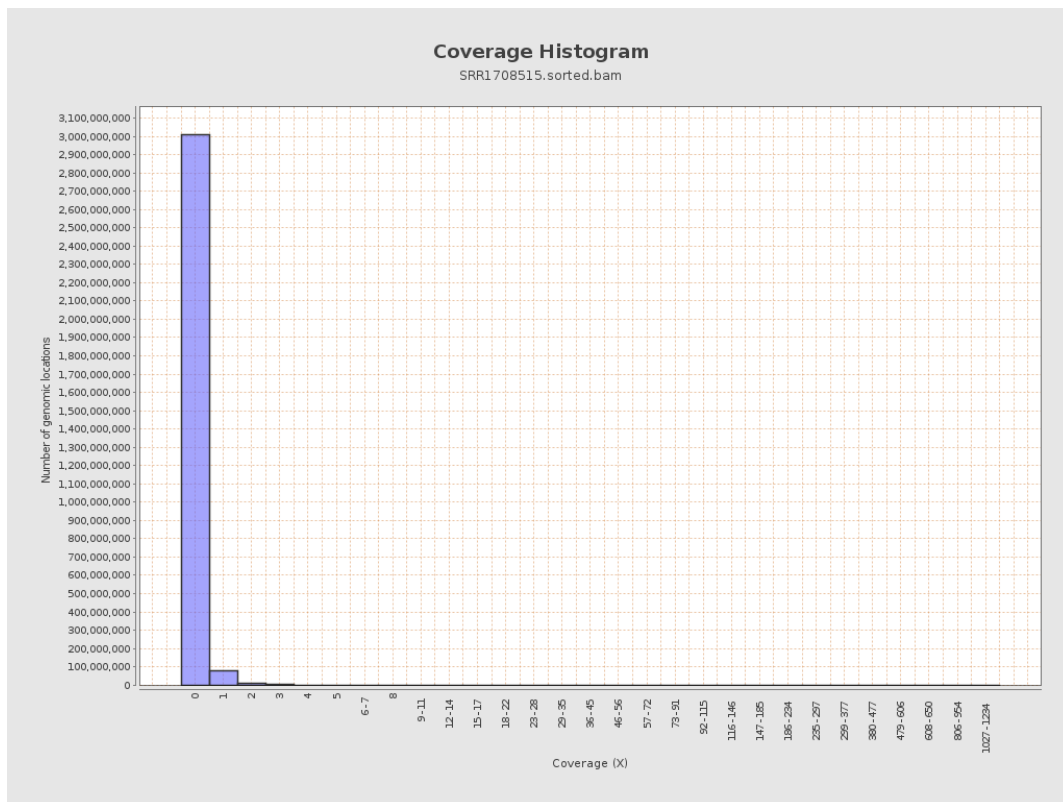
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8410225	0.0337	0.5356
chr2	243199373	8853344	0.0364	0.2763
chr3	198022430	7022090	0.0355	0.2143
chr4	191154276	6584736	0.0344	0.2143
chr5	180915260	6121081	0.0338	0.2089
chr6	171115067	6133872	0.0358	0.2601
chr7	159138663	5532524	0.0348	0.3679

chr8	146364022	5058910	0.0346	0.6892
chr9	141213431	4204094	0.0298	0.2249
chr10	135534747	4695177	0.0346	0.2522
chr11	135006516	4577540	0.0339	0.2809
chr12	133851895	4711584	0.0352	0.2151
chr13	115169878	3293277	0.0286	0.1925
chr14	107349540	3210204	0.0299	0.1988
chr15	102531392	3013427	0.0294	0.1956
chr16	90354753	2694182	0.0298	0.2001
chr17	81195210	2801015	0.0345	0.2414
chr18	78077248	2644017	0.0339	0.3371
chr19	59128983	1798544	0.0304	0.379
chr20	63025520	1960729	0.0311	0.2019
chr21	48129895	1322058	0.0275	0.2063
chr22	51304566	1138894	0.0222	0.1815
chrMT	16571	124019	7.4841	5.6519
chrX	155270560	2989340	0.0193	0.175
chrY	59373566	578021	0.0097	0.1176

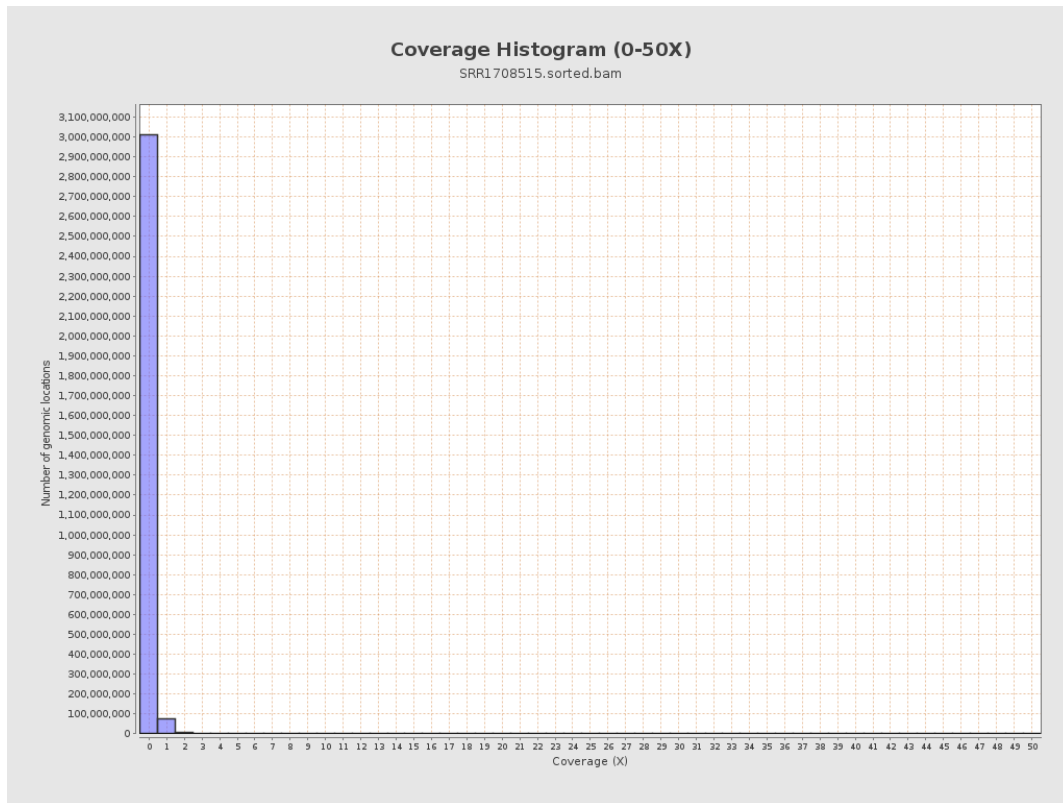
3. Results : Coverage across reference



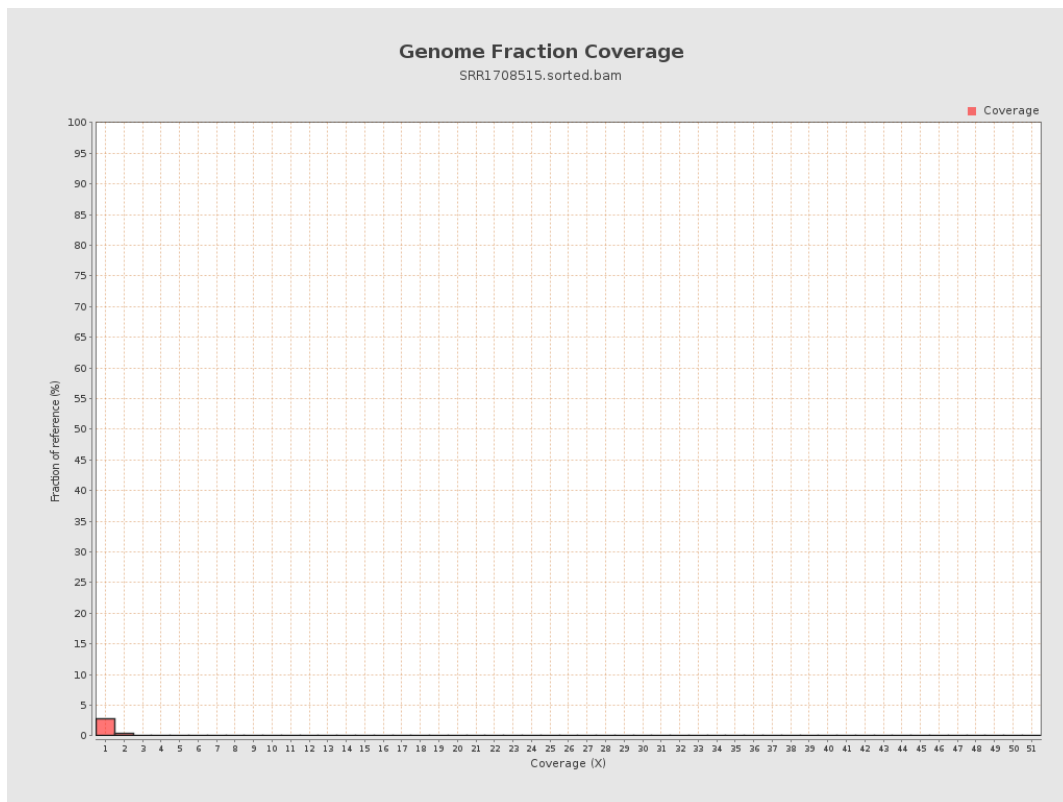
4. Results : Coverage Histogram



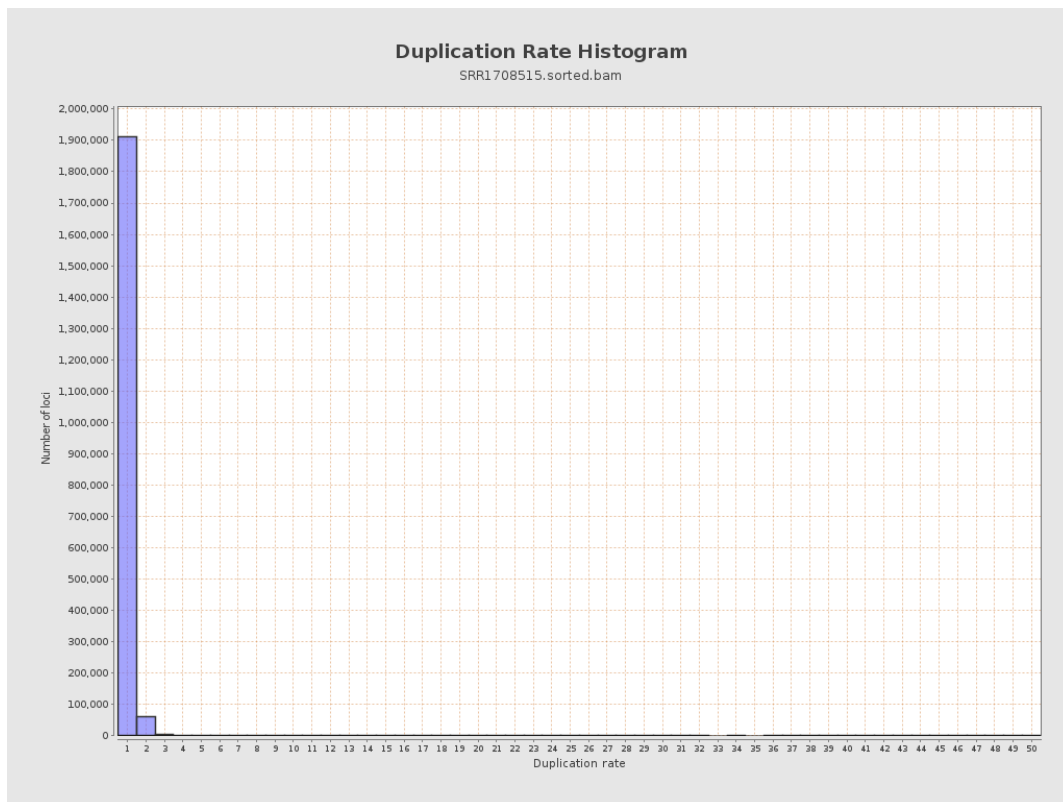
5. Results : Coverage Histogram (0-50X)



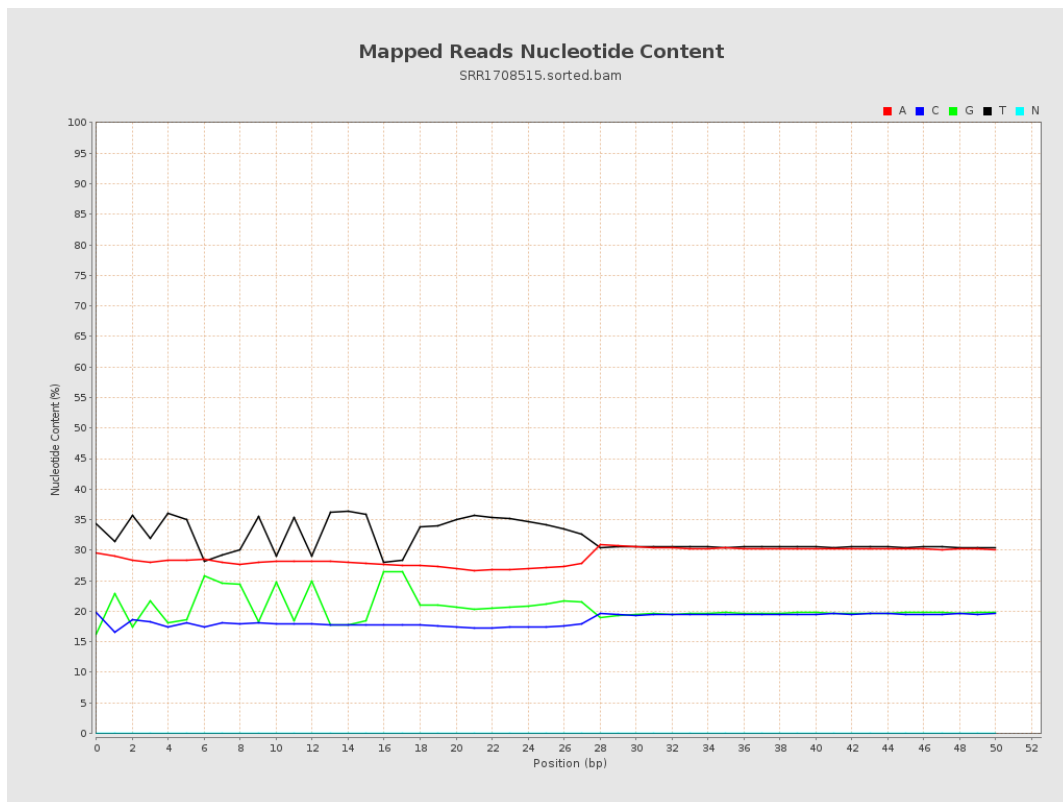
6. Results : Genome Fraction Coverage



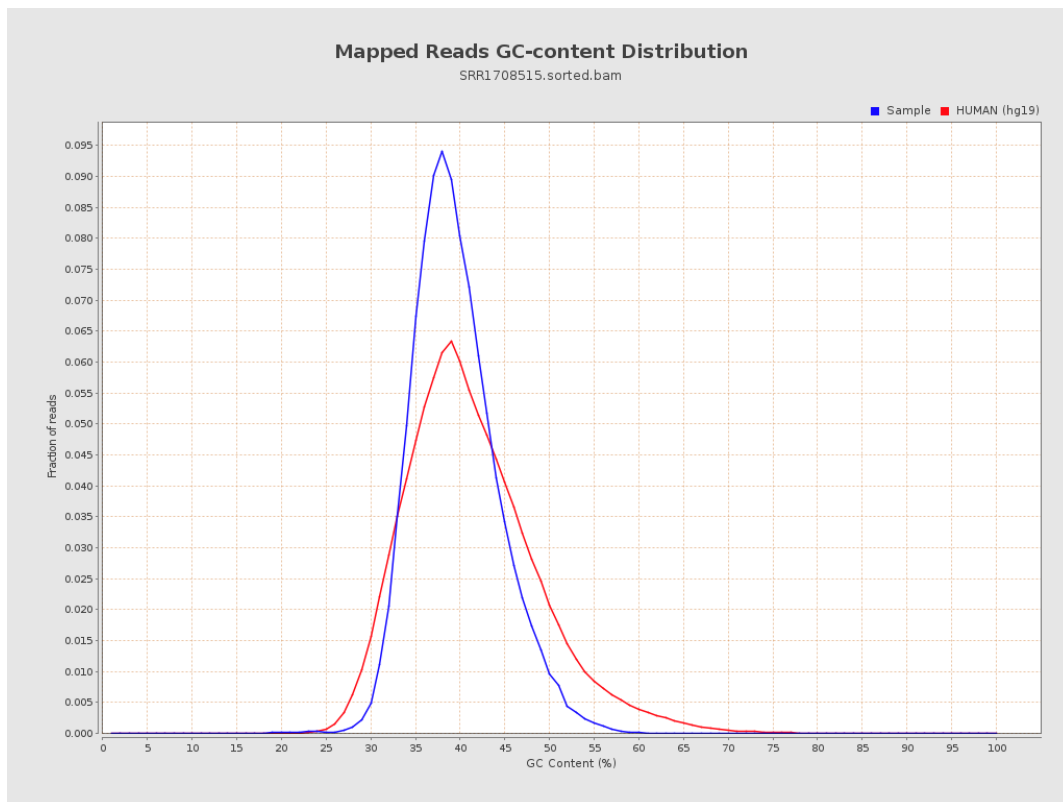
7. Results : Duplication Rate Histogram



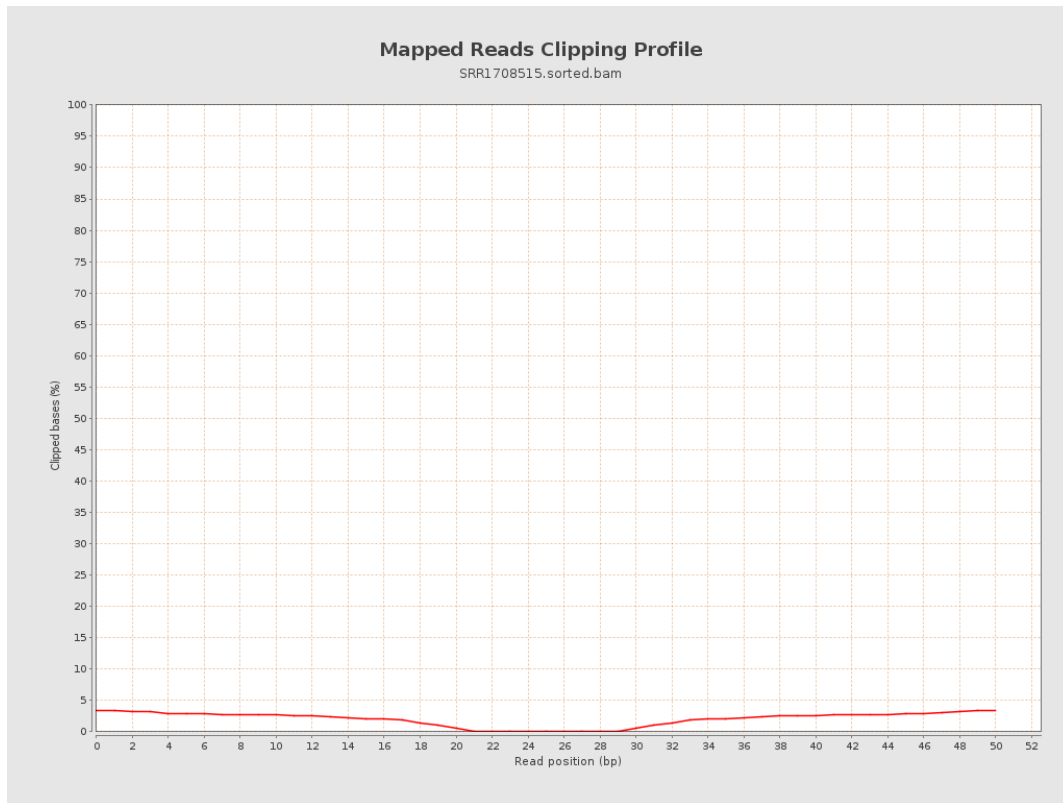
8. Results : Mapped Reads Nucleotide Content



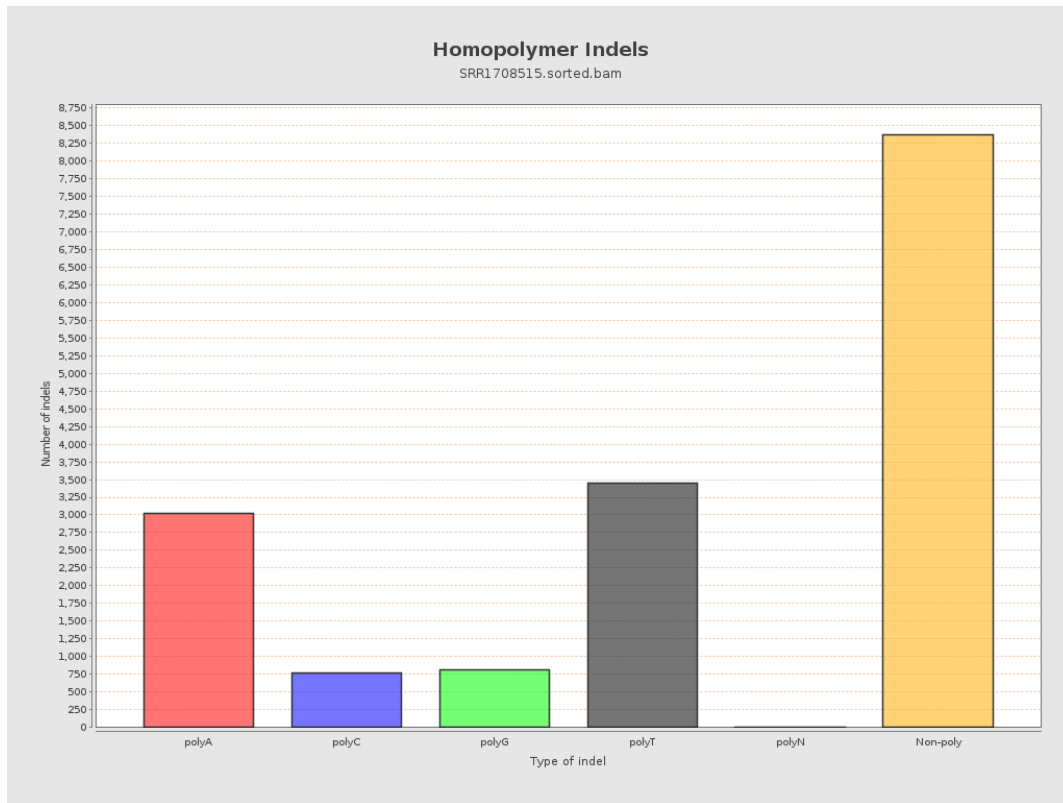
9. Results : Mapped Reads GC-content Distribution



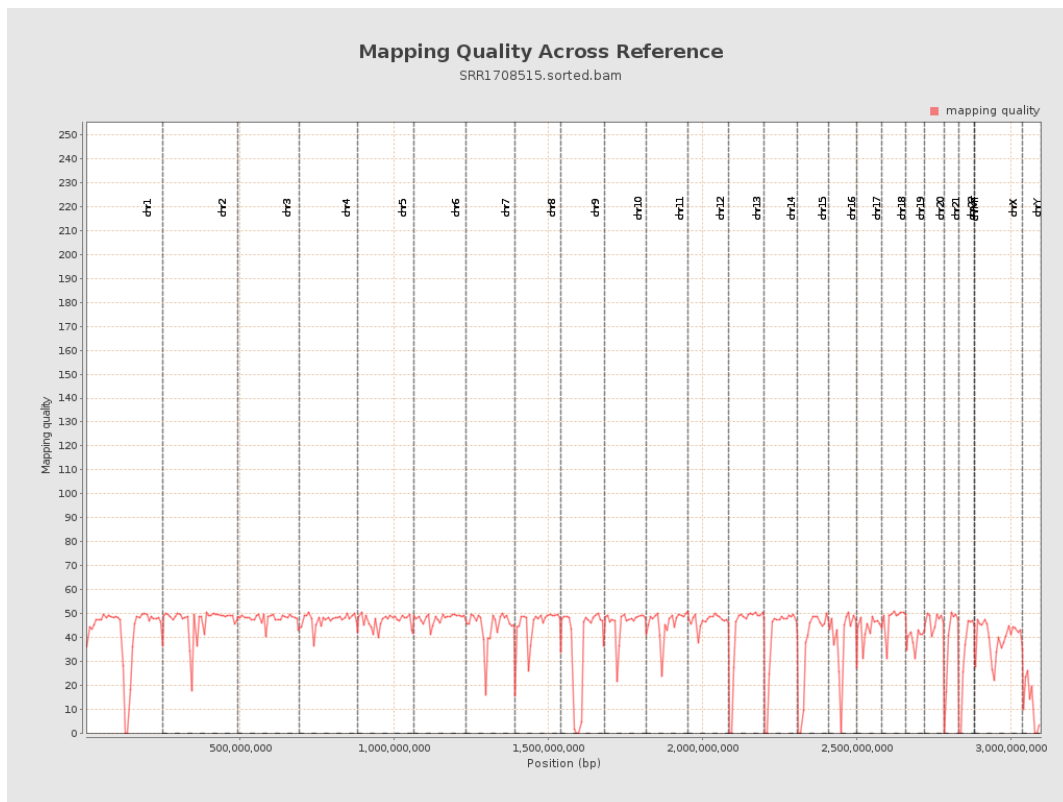
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

