

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:06:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708581.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_SRR1708581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708581.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:06:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,451,402
Mapped reads	6,320,976 / 97.98%
Unmapped reads	130,426 / 2.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	165 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	63,866 / 0.99%
Duplication rate	1.01%
Clipped reads	84,267 / 1.31%

2.2. ACGT Content

Number/percentage of A's	97,704,940 / 30.99%
Number/percentage of C's	59,775,518 / 18.96%
Number/percentage of T's	97,027,980 / 30.78%
Number/percentage of G's	60,735,580 / 19.27%
Number/percentage of N's	10,696 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	0.1018

Standard Deviation	0.336
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2.4. Mapping Quality

Mean Mapping Quality	46.76
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2.5. Mismatches and indels

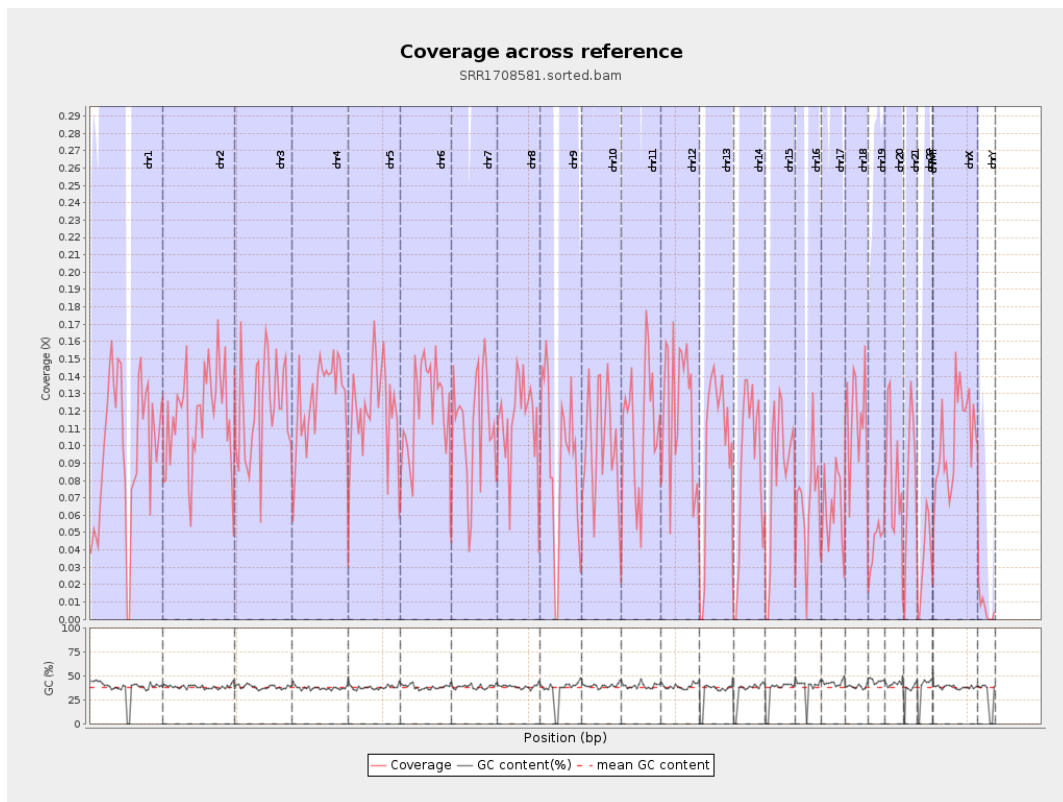
General error rate	0.16%
Mismatches	465,985
Insertions	19,923
Mapped reads with at least one insertion	0.31%
Deletions	16,107
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.21%

2.6. Chromosome stats

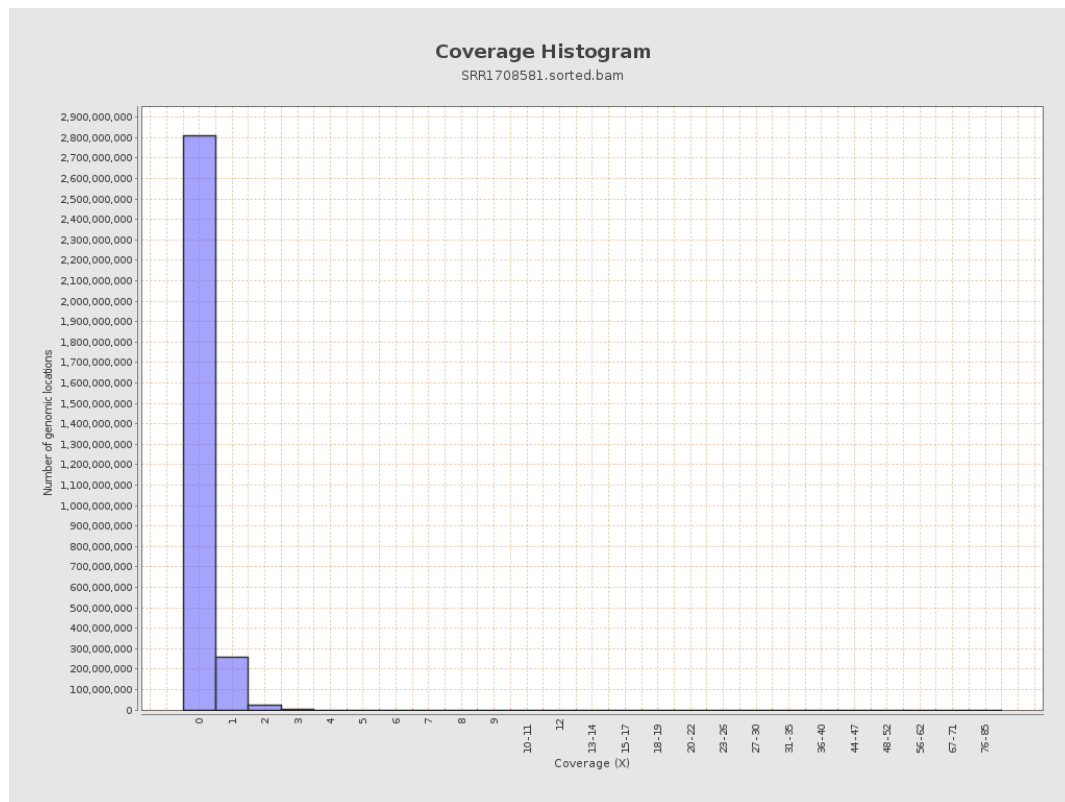
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24451195	0.0981	0.3328
chr2	243199373	28395137	0.1168	0.3605
chr3	198022430	24074266	0.1216	0.3644
chr4	191154276	24278677	0.127	0.372
chr5	180915260	21685108	0.1199	0.3618
chr6	171115067	20881724	0.122	0.365
chr7	159138663	17477997	0.1098	0.3481

chr8	146364022	16686581	0.114	0.3526
chr9	141213431	13112588	0.0929	0.3218
chr10	135534747	13772132	0.1016	0.3336
chr11	135006516	14892820	0.1103	0.3509
chr12	133851895	15826705	0.1182	0.3618
chr13	115169878	11506259	0.0999	0.3321
chr14	107349540	9473573	0.0882	0.3134
chr15	102531392	8602663	0.0839	0.3062
chr16	90354753	5863761	0.0649	0.2677
chr17	81195210	5214183	0.0642	0.2655
chr18	78077248	9005777	0.1153	0.3545
chr19	59128983	2648691	0.0448	0.2199
chr20	63025520	5233845	0.083	0.3035
chr21	48129895	3773302	0.0784	0.2973
chr22	51304566	1839961	0.0359	0.1979
chrMT	16571	337	0.0203	0.1566
chrX	155270560	16211197	0.1044	0.3377
chrY	59373566	373342	0.0063	0.0844

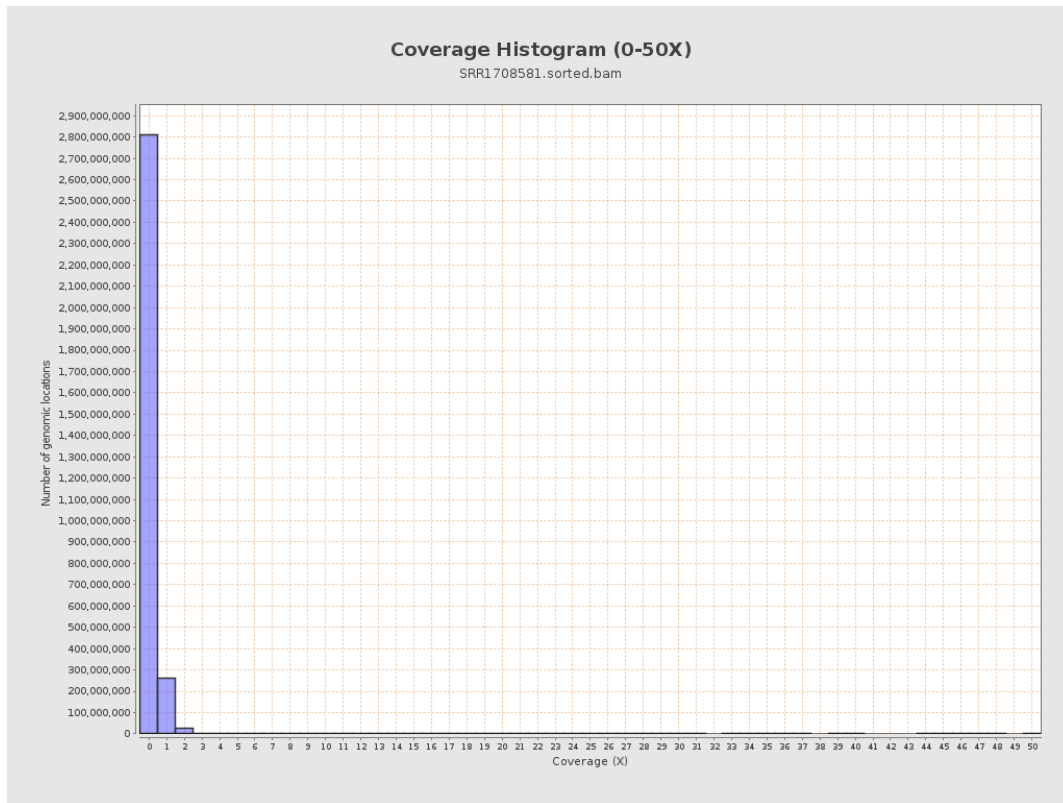
3. Results : Coverage across reference



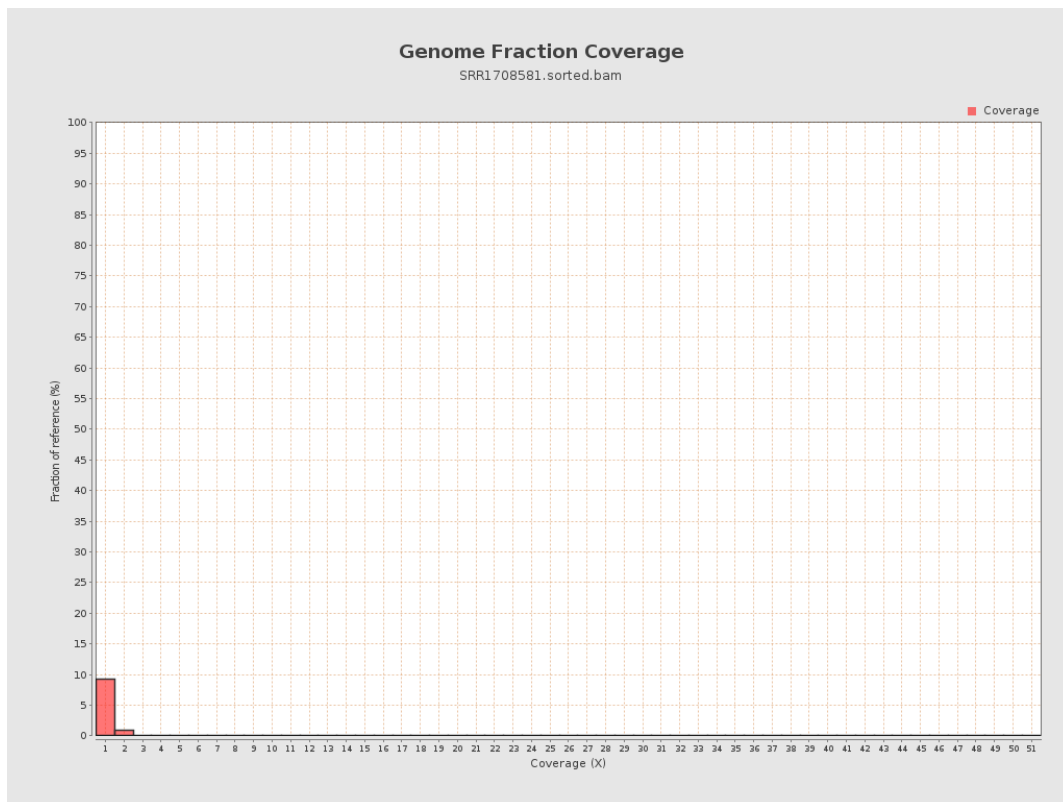
4. Results : Coverage Histogram



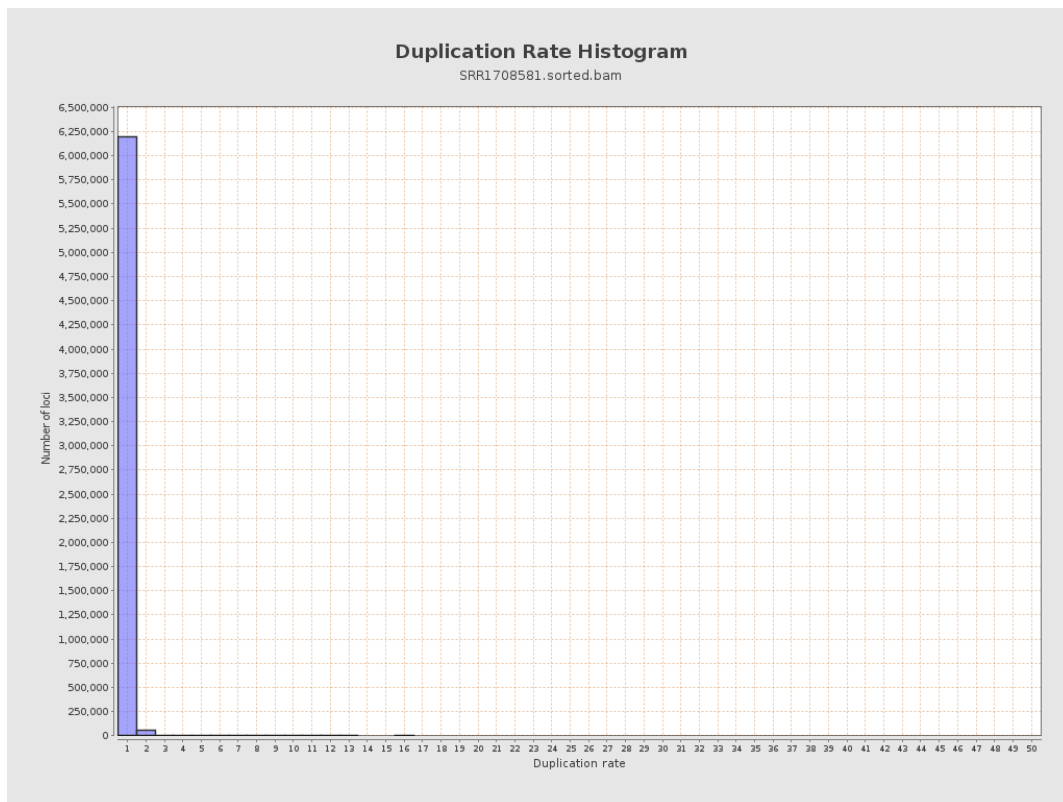
5. Results : Coverage Histogram (0-50X)



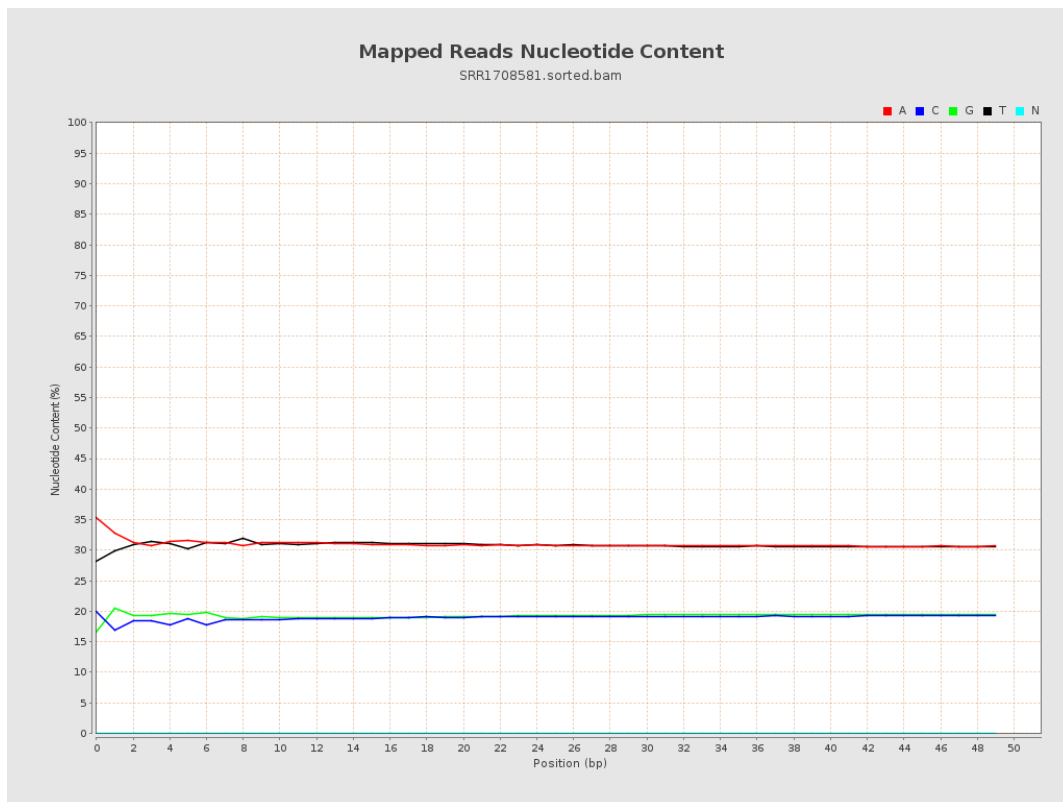
6. Results : Genome Fraction Coverage



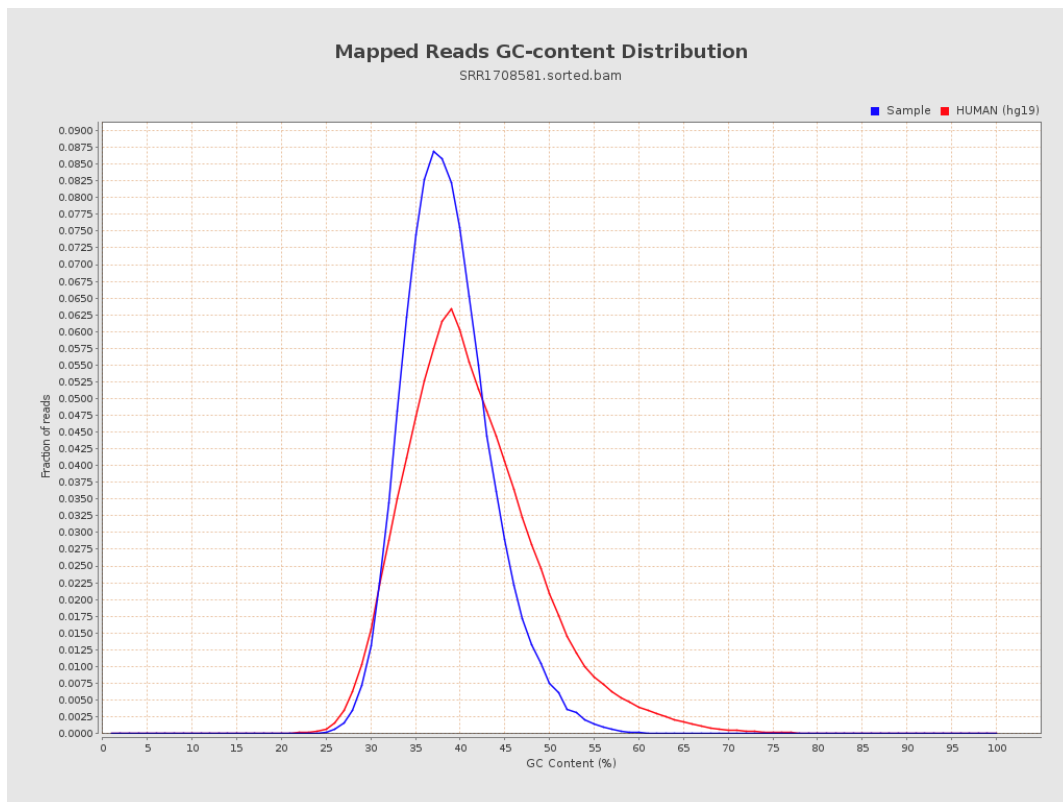
7. Results : Duplication Rate Histogram



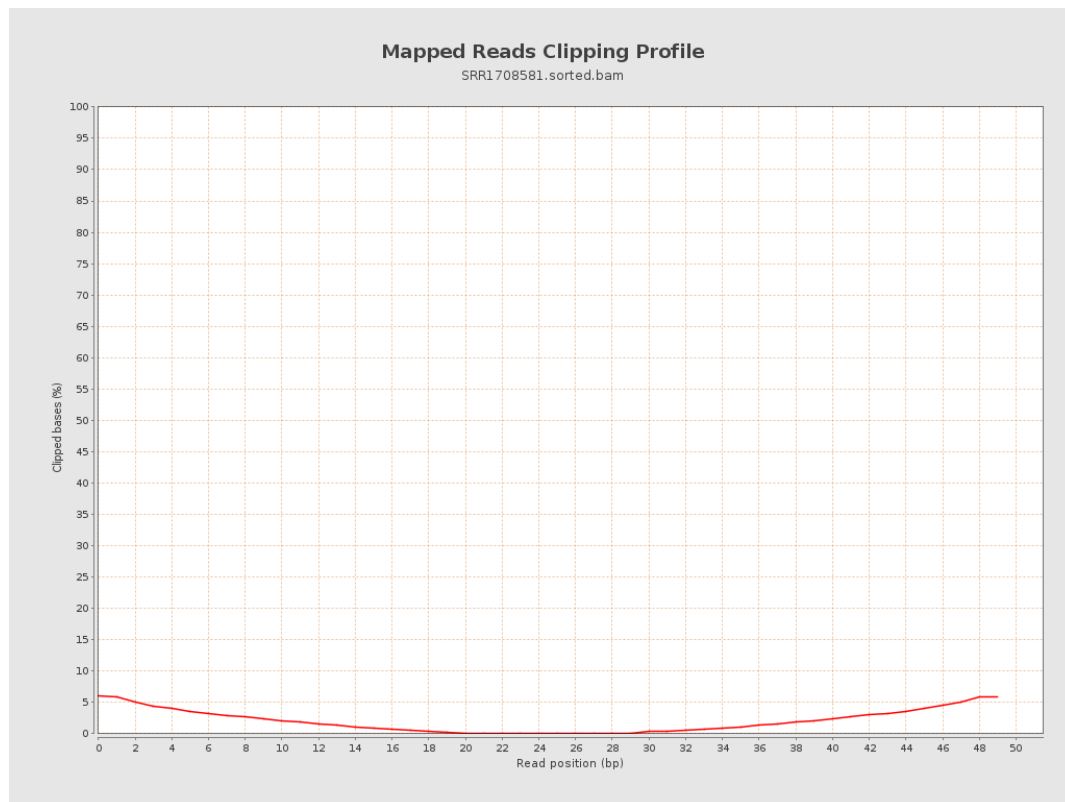
8. Results : Mapped Reads Nucleotide Content



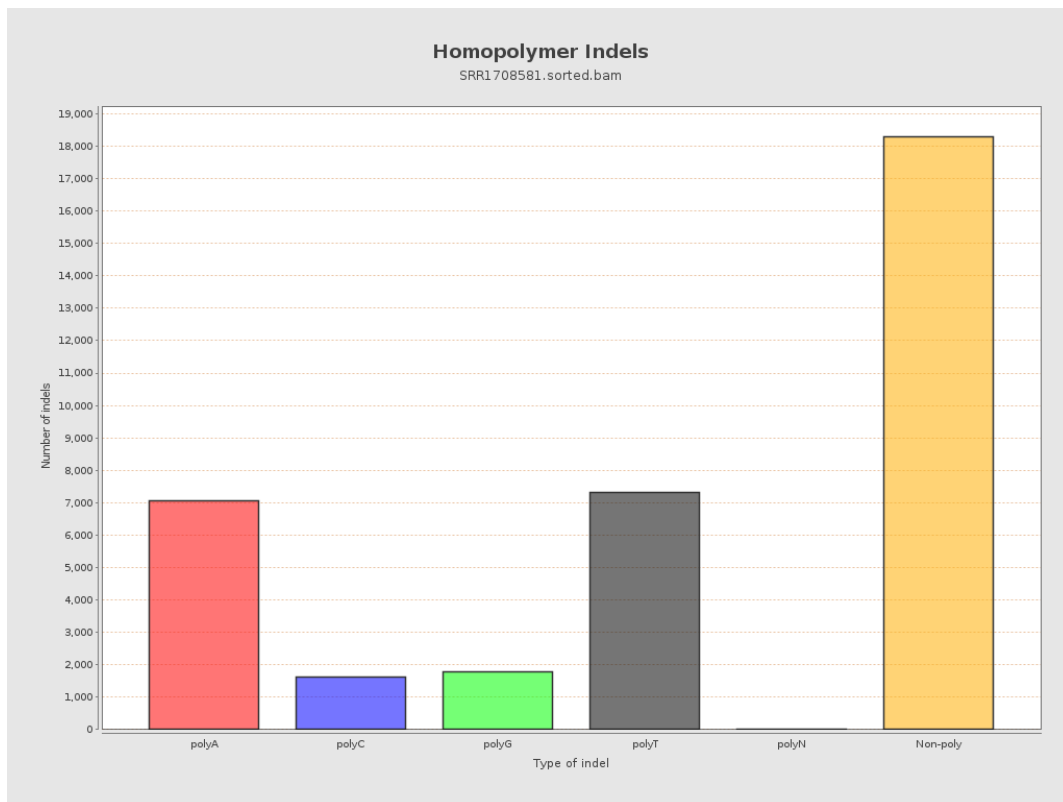
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

