

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:48:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708590.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_SRR1708590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708590.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:48:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,194,549
Mapped reads	5,064,096 / 97.49%
Unmapped reads	130,453 / 2.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	137 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	52,557 / 1.01%
Duplication rate	1.03%
Clipped reads	68,236 / 1.31%

2.2. ACGT Content

Number/percentage of A's	78,558,386 / 31.1%
Number/percentage of C's	47,619,518 / 18.85%
Number/percentage of T's	78,130,850 / 30.94%
Number/percentage of G's	48,245,875 / 19.1%
Number/percentage of N's	7,970 / 0%
GC Percentage	37.96%

2.3. Coverage

Mean	0.0816

Standard Deviation	0.3063
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2.4. Mapping Quality

Mean Mapping Quality	46.73
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2.5. Mismatches and indels

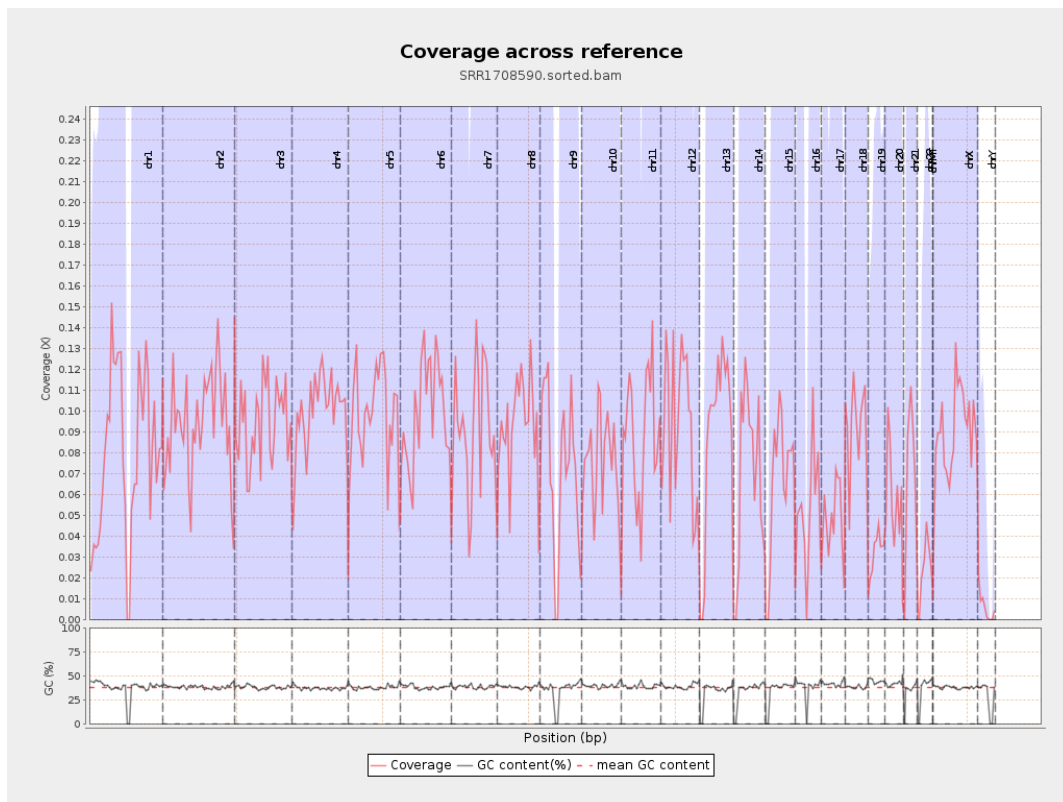
General error rate	0.16%
Mismatches	375,186
Insertions	15,923
Mapped reads with at least one insertion	0.31%
Deletions	12,881
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.24%

2.6. Chromosome stats

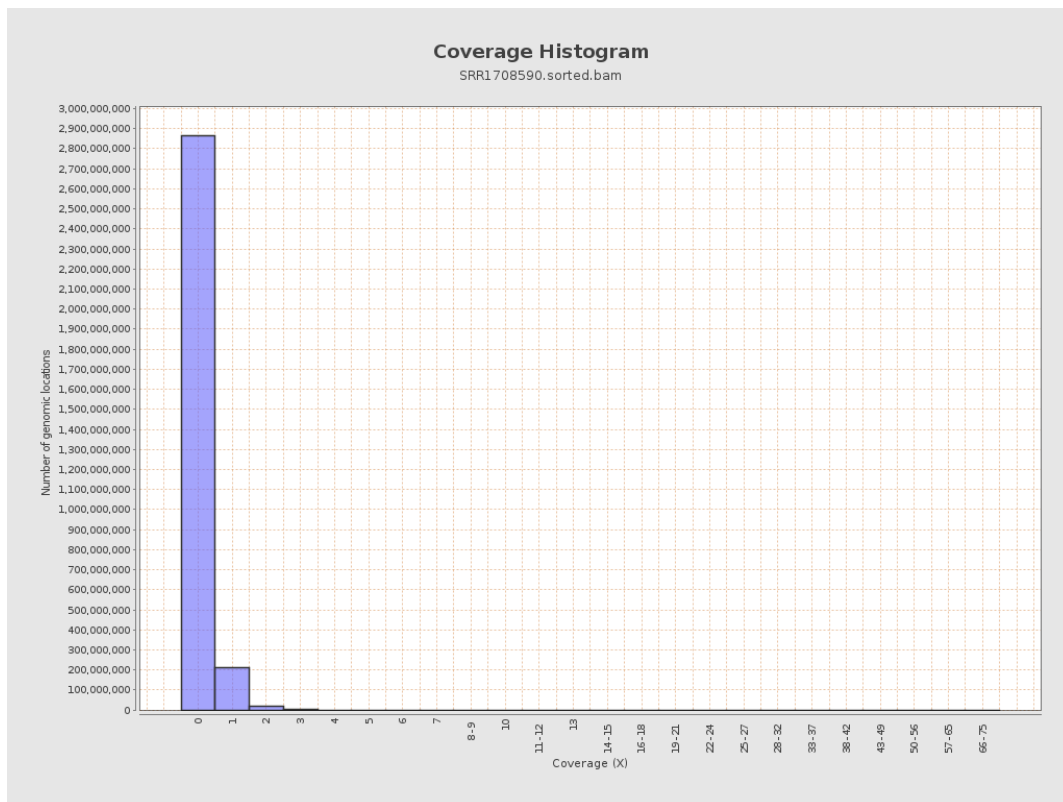
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19732651	0.0792	0.2986
chr2	243199373	22753557	0.0936	0.3795
chr3	198022430	18832841	0.0951	0.3276
chr4	191154276	19068488	0.0998	0.3301
chr5	180915260	17473052	0.0966	0.3248
chr6	171115067	17028083	0.0995	0.3307
chr7	159138663	14354814	0.0902	0.3153

chr8	146364022	13758319	0.094	0.321
chr9	141213431	10310759	0.073	0.2847
chr10	135534747	10346094	0.0763	0.2884
chr11	135006516	11858174	0.0878	0.3132
chr12	133851895	12313644	0.092	0.32
chr13	115169878	10232952	0.0889	0.3143
chr14	107349540	7665486	0.0714	0.2819
chr15	102531392	6659418	0.065	0.2693
chr16	90354753	4593675	0.0508	0.236
chr17	81195210	3982498	0.049	0.2327
chr18	78077248	7218972	0.0925	0.318
chr19	59128983	1929800	0.0326	0.1874
chr20	63025520	3715730	0.059	0.2554
chr21	48129895	3152298	0.0655	0.2725
chr22	51304566	1256948	0.0245	0.163
chrMT	16571	150	0.0091	0.0947
chrX	155270560	14004176	0.0902	0.3143
chrY	59373566	341897	0.0058	0.08

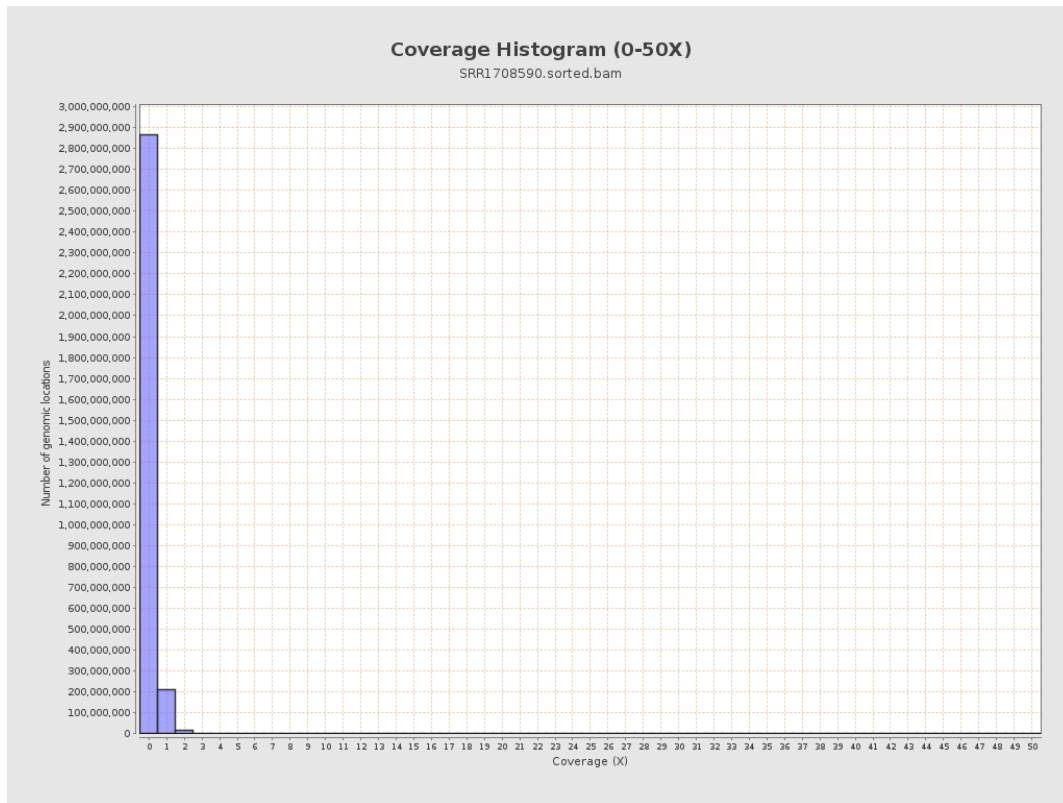
3. Results : Coverage across reference



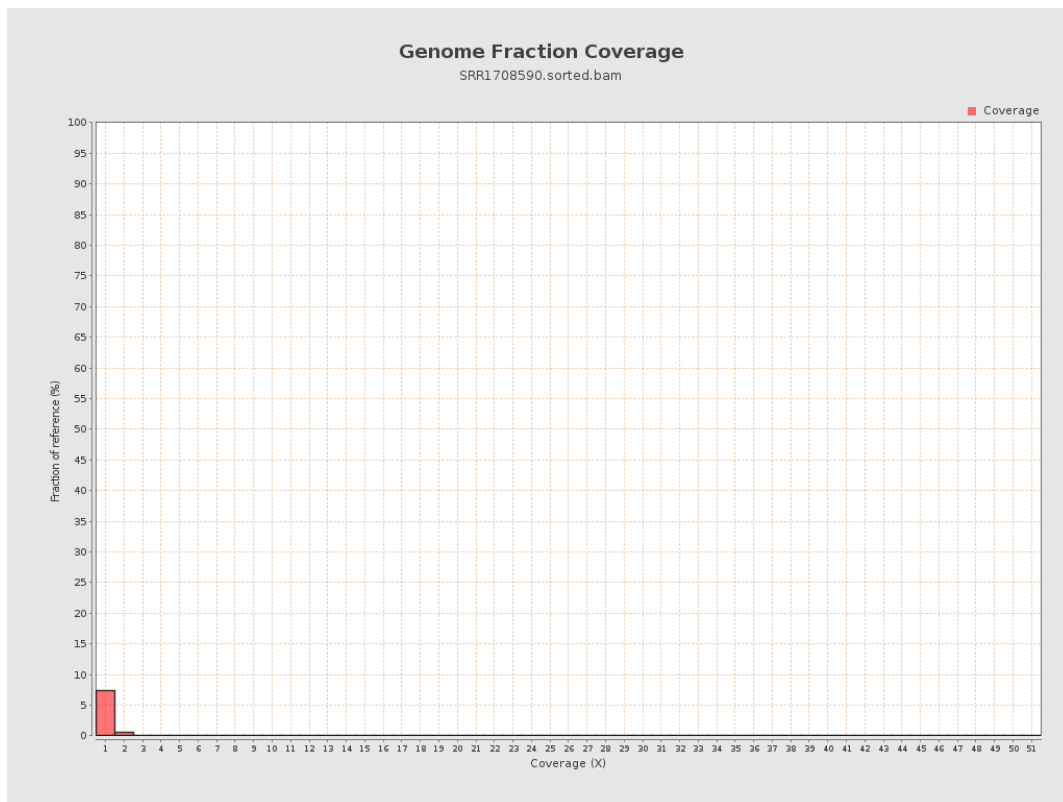
4. Results : Coverage Histogram



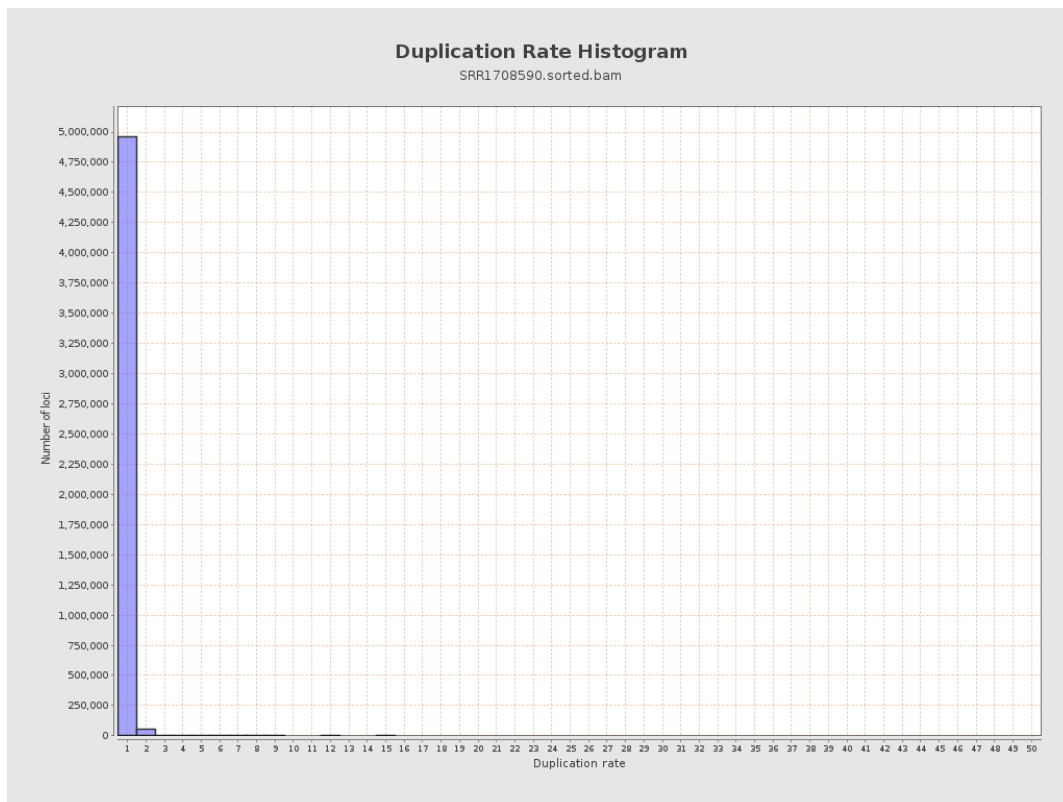
5. Results : Coverage Histogram (0-50X)



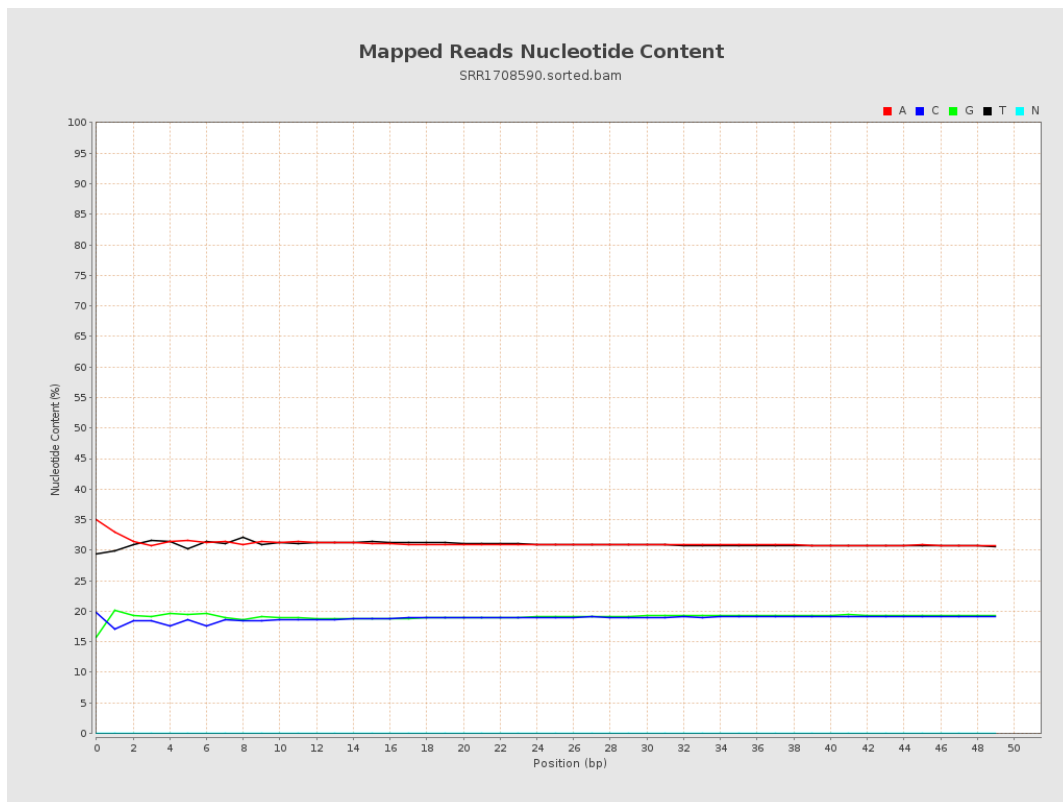
6. Results : Genome Fraction Coverage



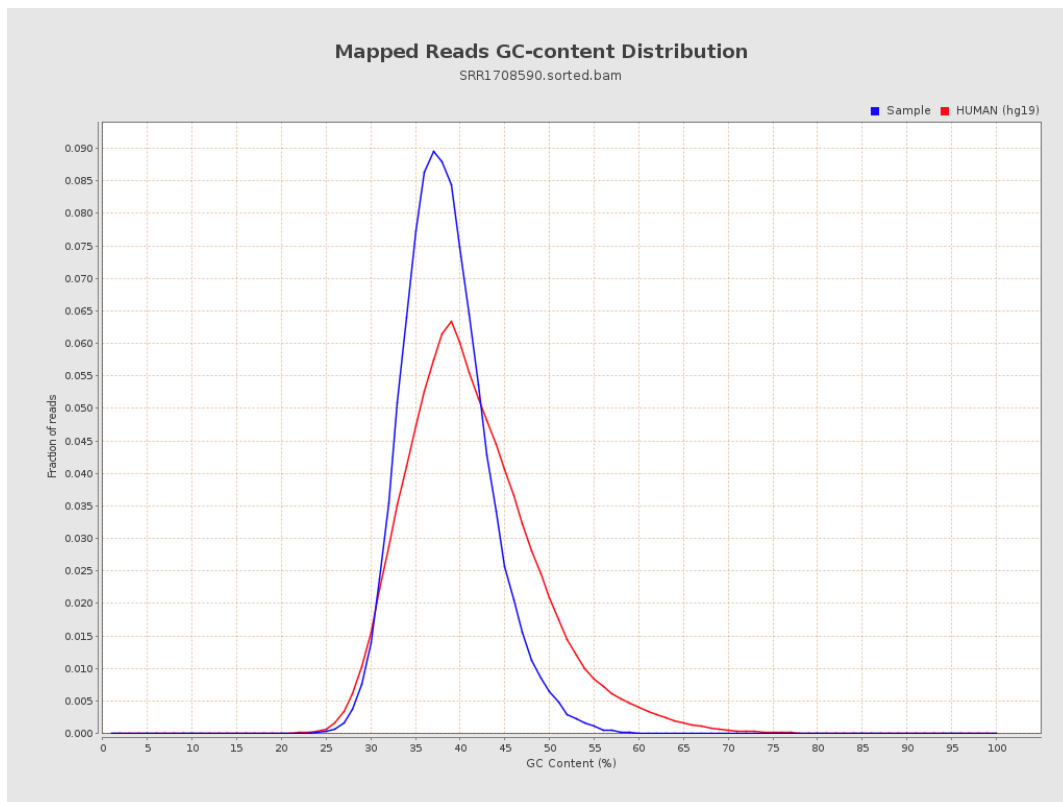
7. Results : Duplication Rate Histogram



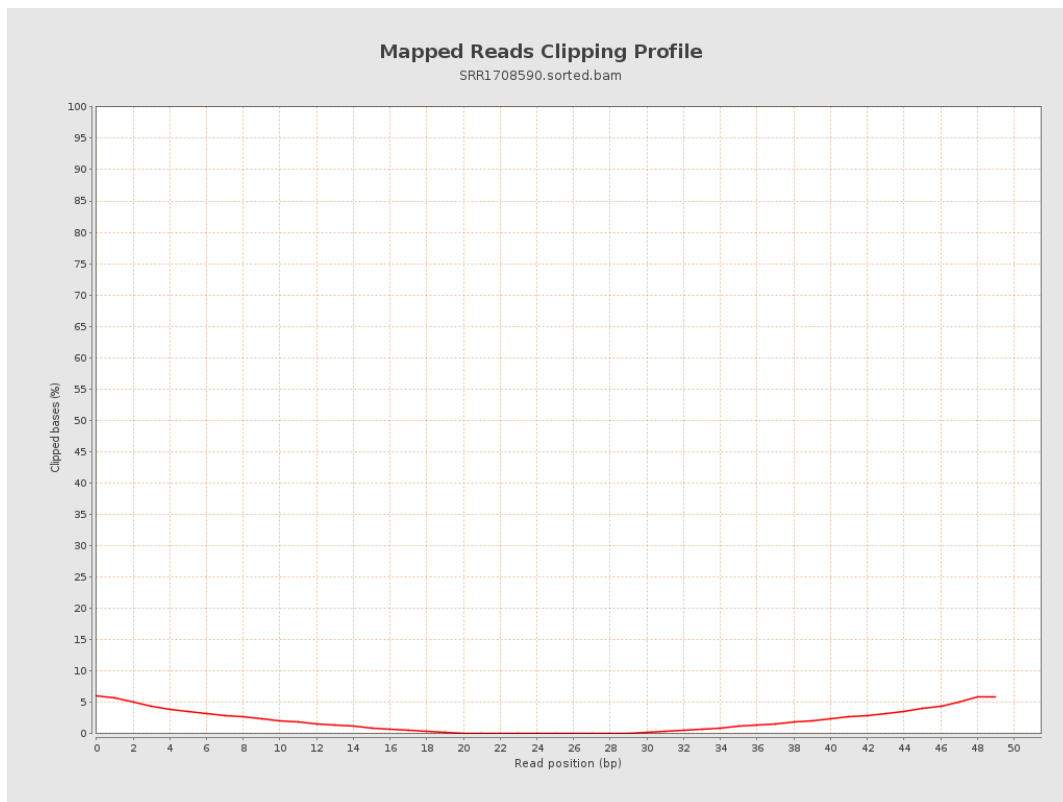
8. Results : Mapped Reads Nucleotide Content



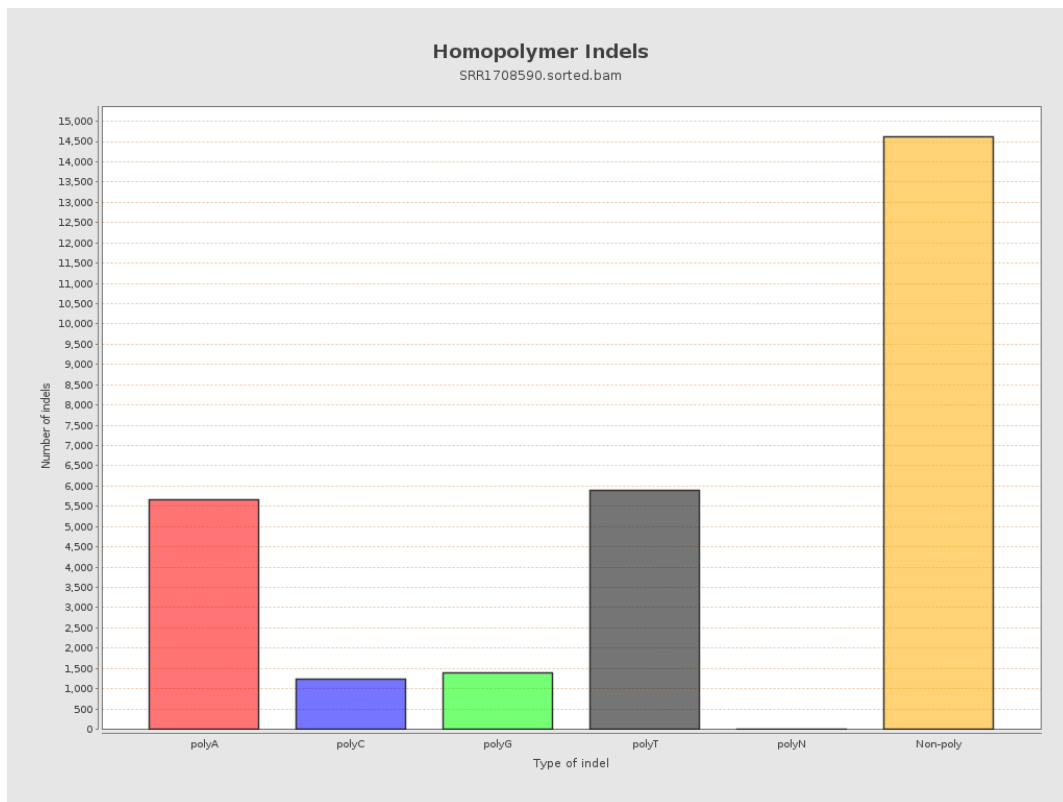
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

