

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:03:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008712.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_SRR6008712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:03:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,254,598
Mapped reads	1,047,891 / 83.52%
Unmapped reads	206,707 / 16.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,679 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	16,205 / 1.29%
Duplication rate	1.23%
Clipped reads	462,466 / 36.86%

2.2. ACGT Content

Number/percentage of A's	21,018,300 / 30.12%
Number/percentage of C's	12,280,174 / 17.6%
Number/percentage of T's	20,442,690 / 29.3%
Number/percentage of G's	16,032,115 / 22.98%
Number/percentage of N's	3,699 / 0.01%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.1897
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2.4. Mapping Quality

Mean Mapping Quality	47.01
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2.5. Mismatches and indels

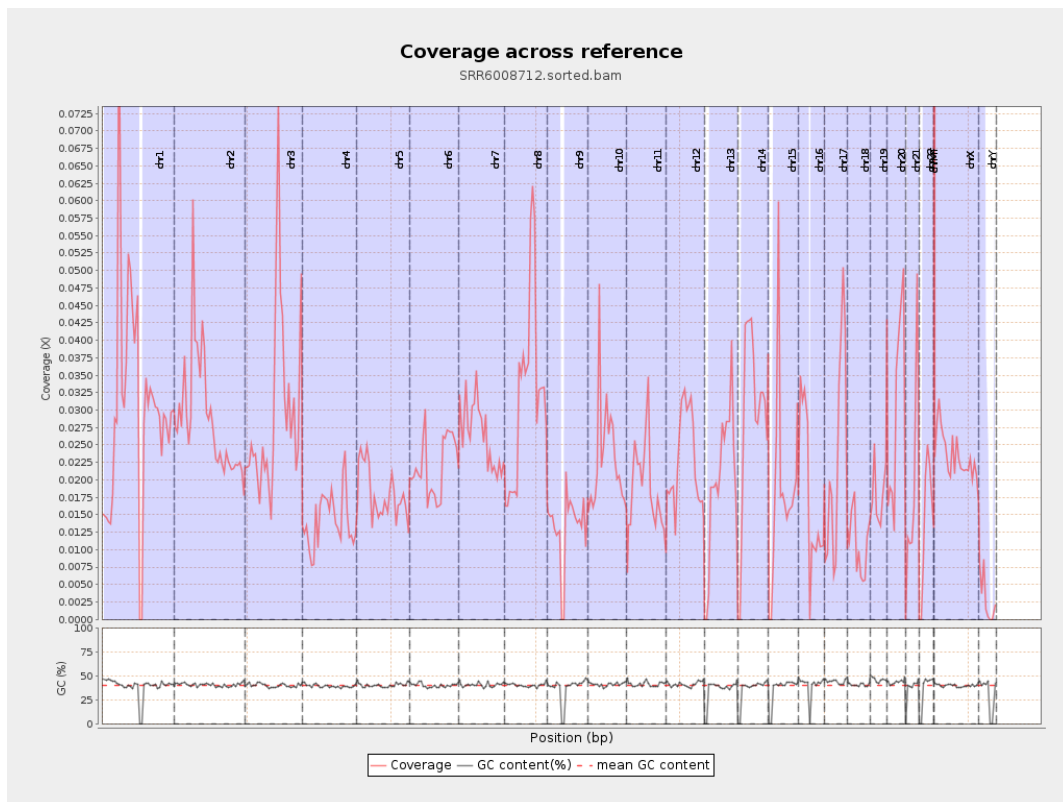
General error rate	0.83%
Mismatches	570,945
Insertions	5,224
Mapped reads with at least one insertion	0.49%
Deletions	19,985
Mapped reads with at least one deletion	1.88%
Homopolymer indels	45.73%

2.6. Chromosome stats

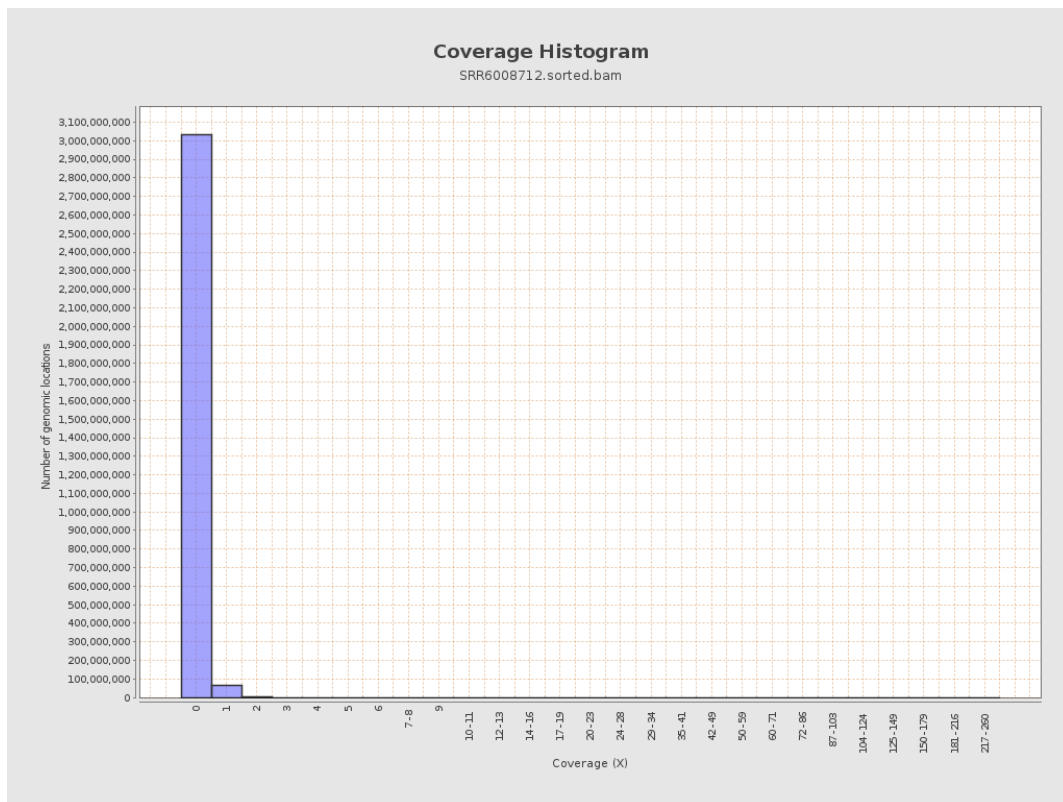
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7537319	0.0302	0.2837
chr2	243199373	6989622	0.0287	0.214
chr3	198022430	5772504	0.0292	0.182
chr4	191154276	2730716	0.0143	0.1268
chr5	180915260	3277205	0.0181	0.1385
chr6	171115067	3758966	0.022	0.1646
chr7	159138663	4219369	0.0265	0.2297

chr8	146364022	4768011	0.0326	0.2166
chr9	141213431	1864433	0.0132	0.1424
chr10	135534747	3134759	0.0231	0.2828
chr11	135006516	2578906	0.0191	0.1666
chr12	133851895	3060573	0.0229	0.156
chr13	115169878	2294911	0.0199	0.1455
chr14	107349540	3155924	0.0294	0.1806
chr15	102531392	1886491	0.0184	0.1414
chr16	90354753	1578142	0.0175	0.1486
chr17	81195210	1869862	0.023	0.1669
chr18	78077248	814930	0.0104	0.2177
chr19	59128983	1098216	0.0186	0.1808
chr20	63025520	1906482	0.0302	0.1816
chr21	48129895	936896	0.0195	0.1484
chr22	51304566	737864	0.0144	0.1239
chrMT	16571	12378	0.747	1.0083
chrX	155270560	3656409	0.0235	0.1645
chrY	59373566	168228	0.0028	0.0767

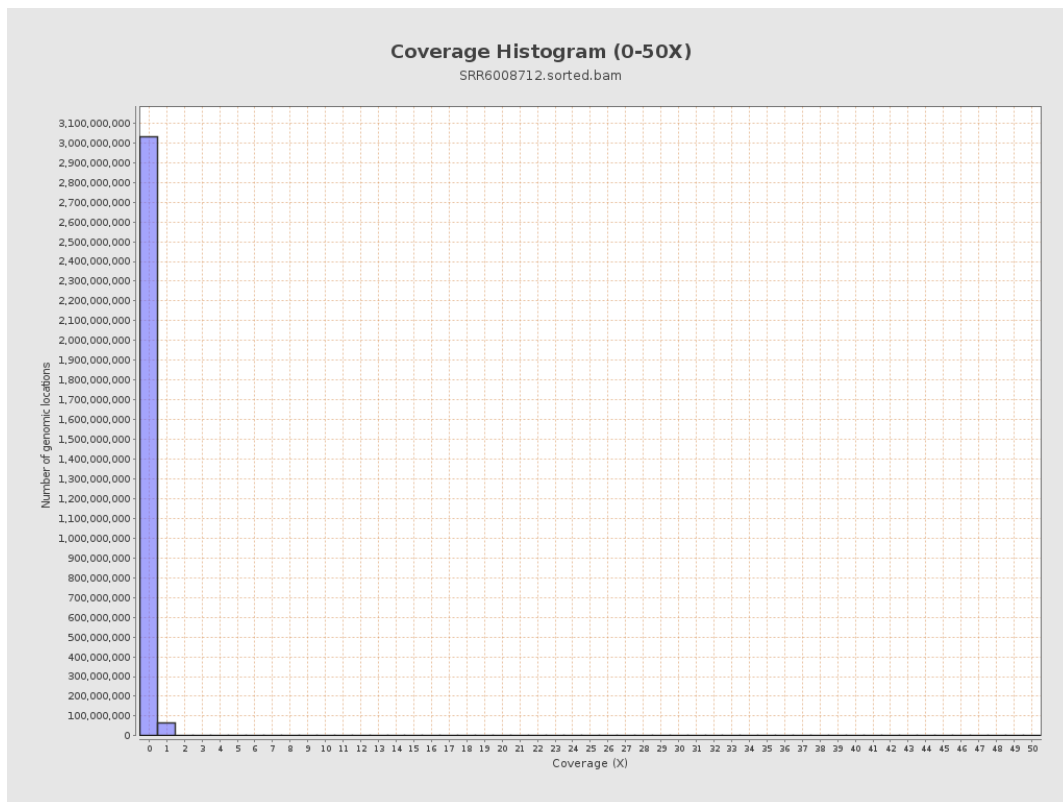
3. Results : Coverage across reference



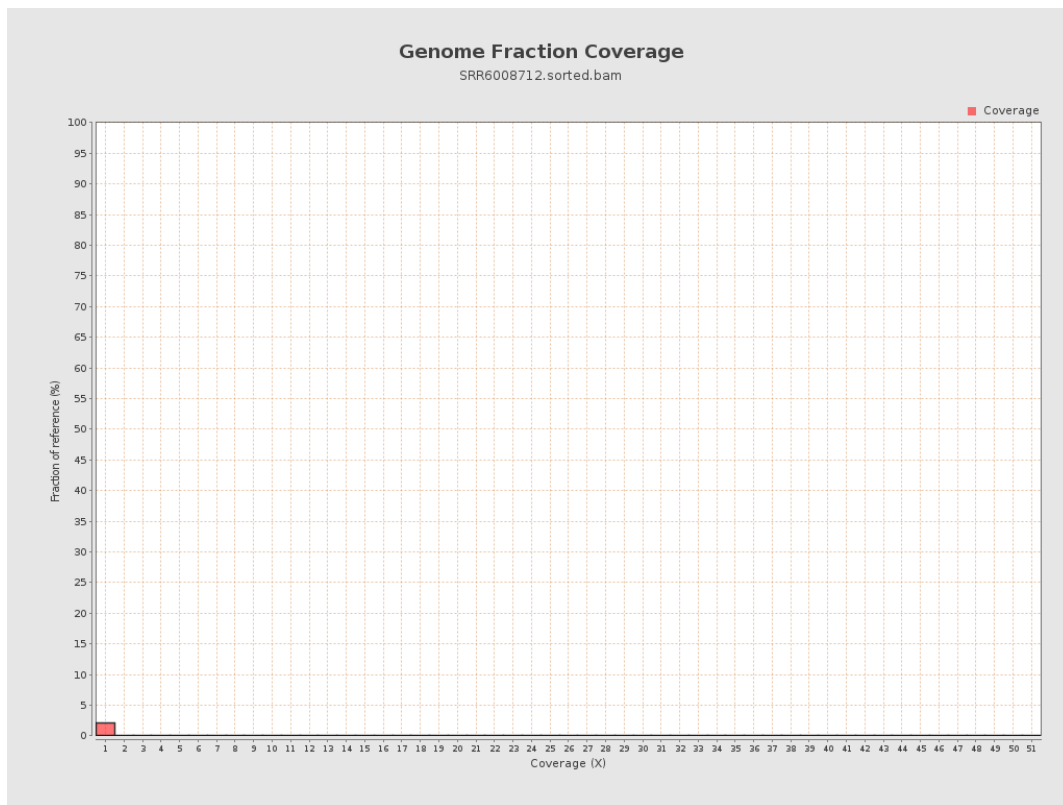
4. Results : Coverage Histogram



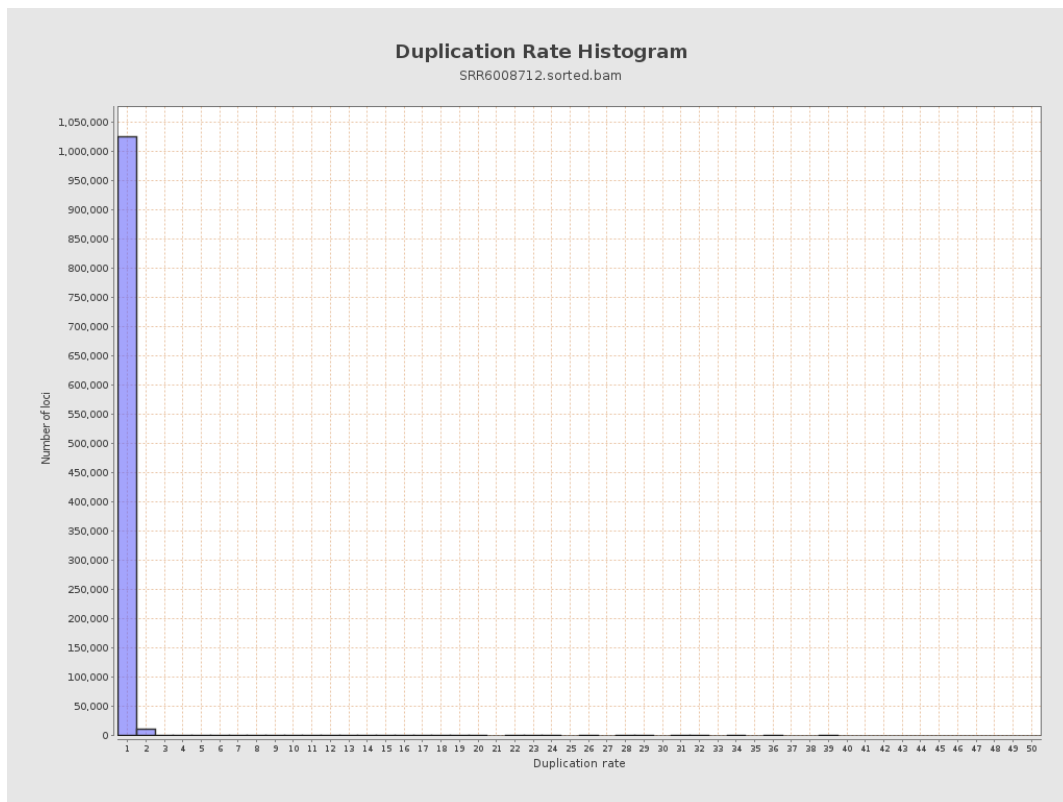
5. Results : Coverage Histogram (0-50X)



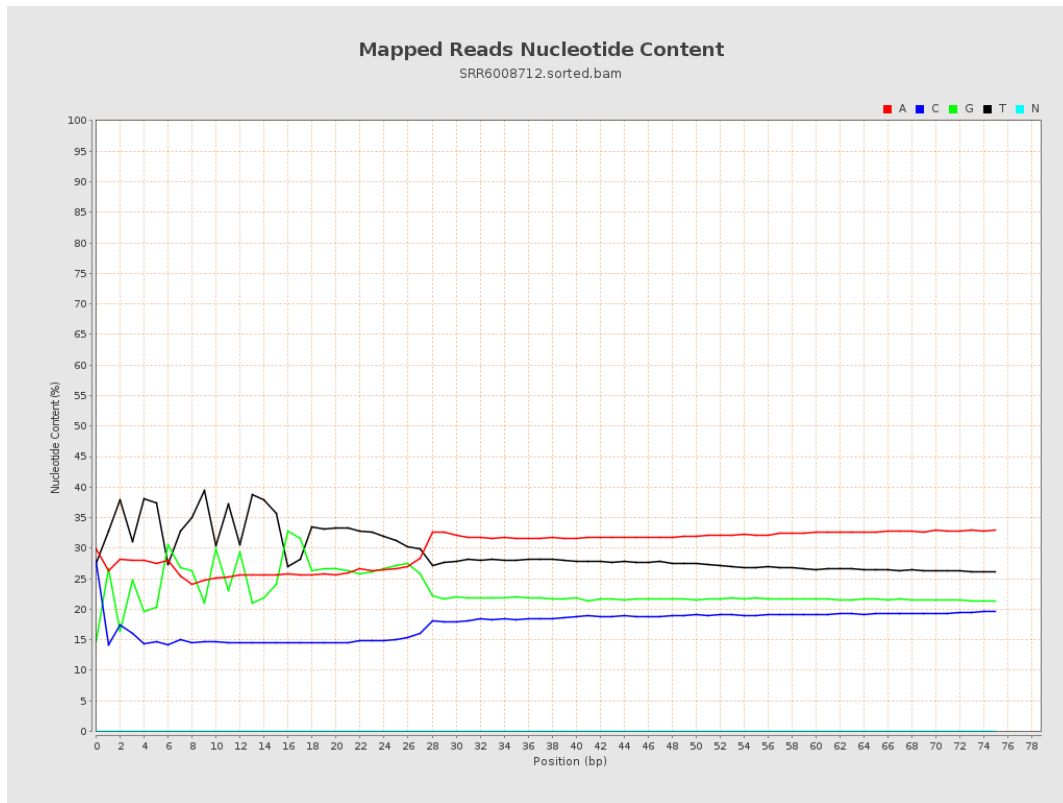
6. Results : Genome Fraction Coverage



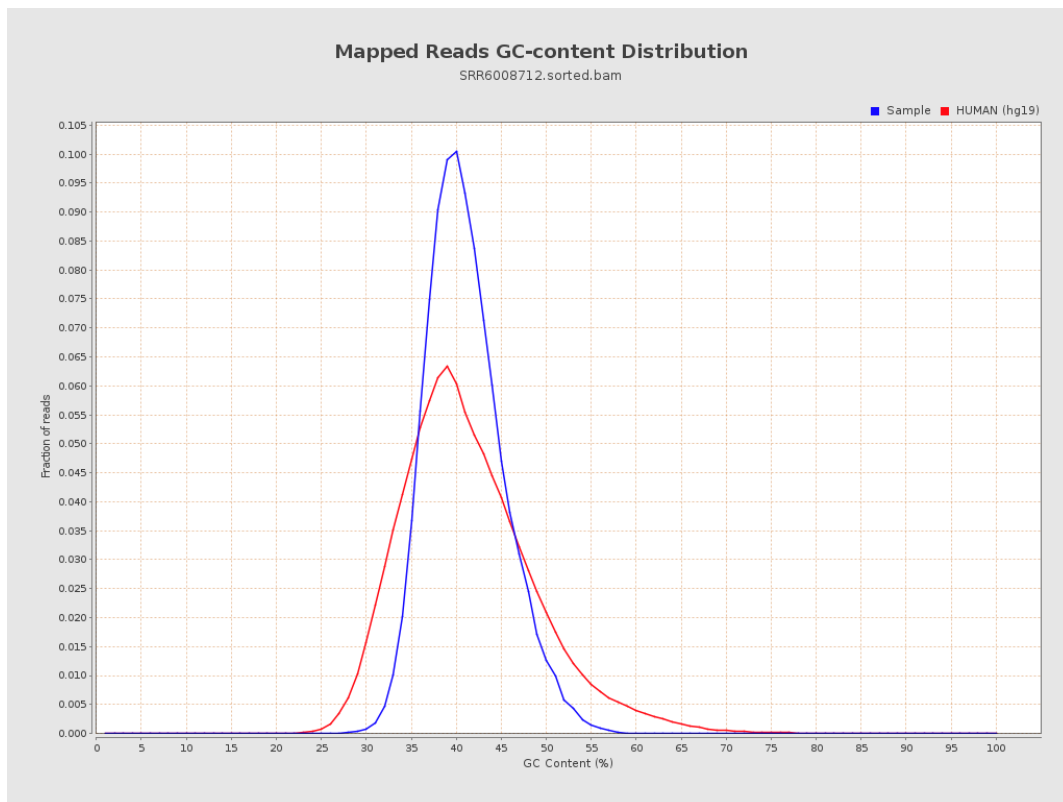
7. Results : Duplication Rate Histogram



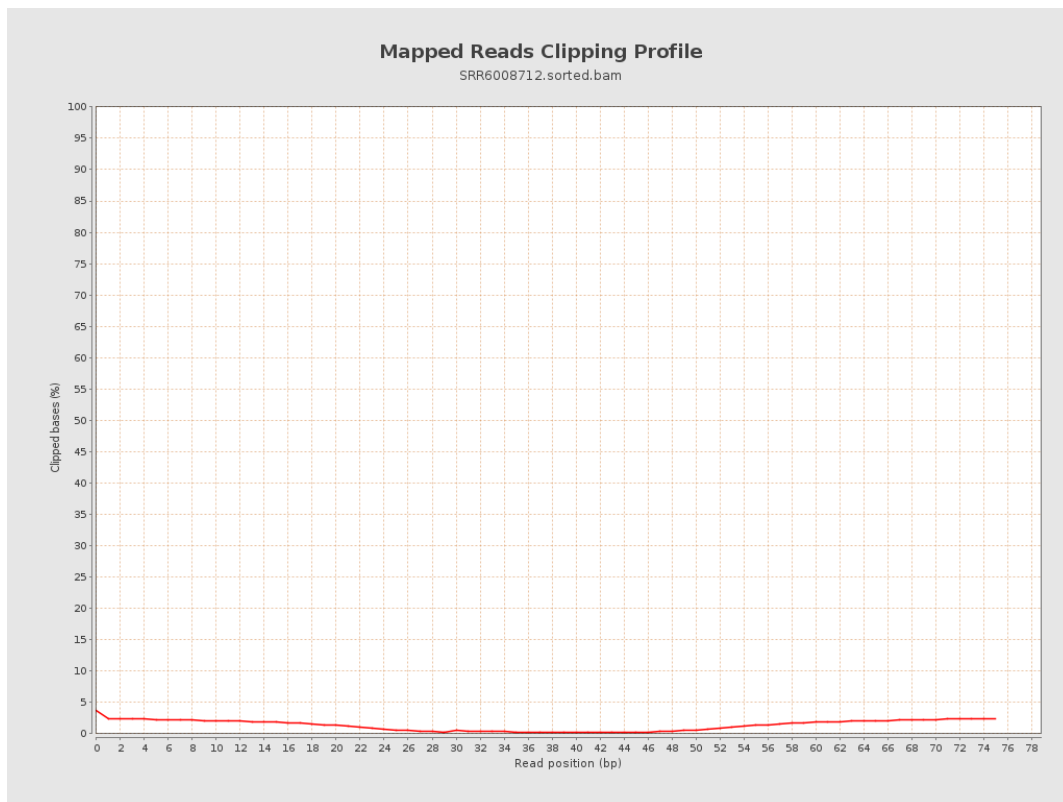
8. Results : Mapped Reads Nucleotide Content



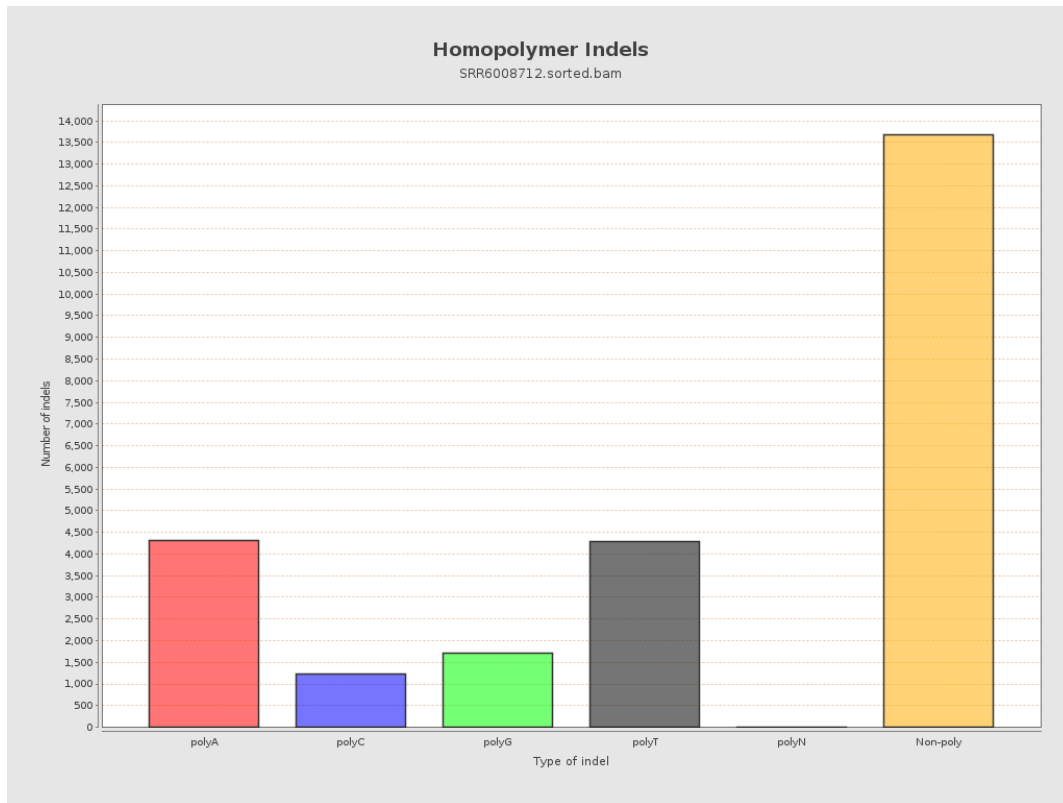
9. Results : Mapped Reads GC-content Distribution



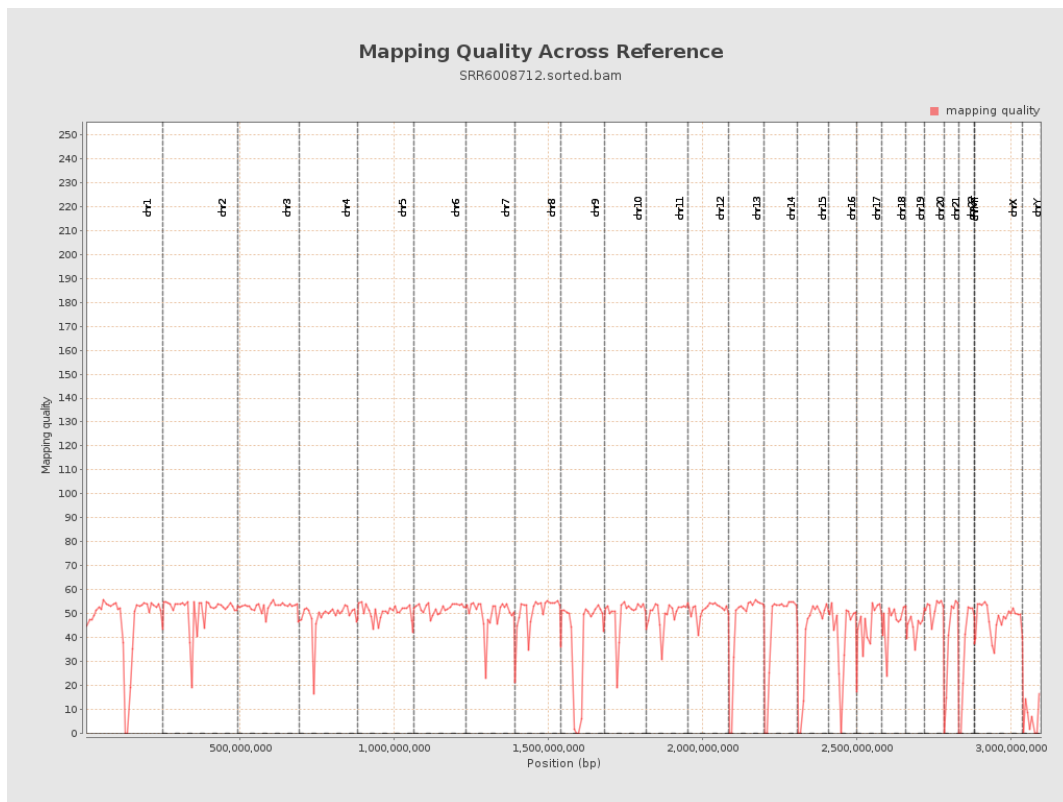
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

