

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:16:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549148.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_SRR1549148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:16:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,931,689
Mapped reads	14,922,385 / 88.13%
Unmapped reads	2,009,304 / 11.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,300,588 / 7.68%
Duplication rate	7.29%
Clipped reads	1,127,595 / 6.66%

2.2. ACGT Content

Number/percentage of A's	159,838,714 / 27.08%
Number/percentage of C's	133,965,924 / 22.7%
Number/percentage of T's	162,272,953 / 27.49%
Number/percentage of G's	134,028,637 / 22.71%
Number/percentage of N's	116,041 / 0.02%
GC Percentage	45.41%

2.3. Coverage

Mean	0.1907
Standard Deviation	0.981

2.4. Mapping Quality

Mean Mapping Quality	39.93
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2.5. Mismatches and indels

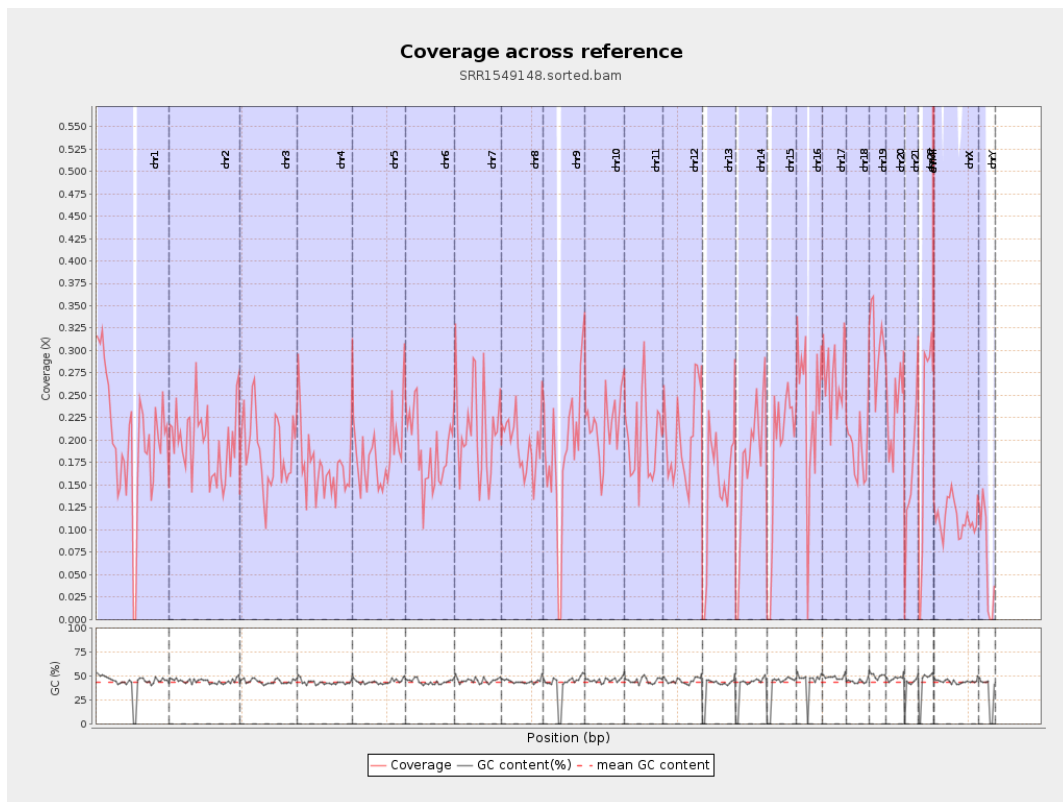
General error rate	0.34%
Mismatches	1,982,001
Insertions	18,790
Mapped reads with at least one insertion	0.13%
Deletions	50,948
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.1%

2.6. Chromosome stats

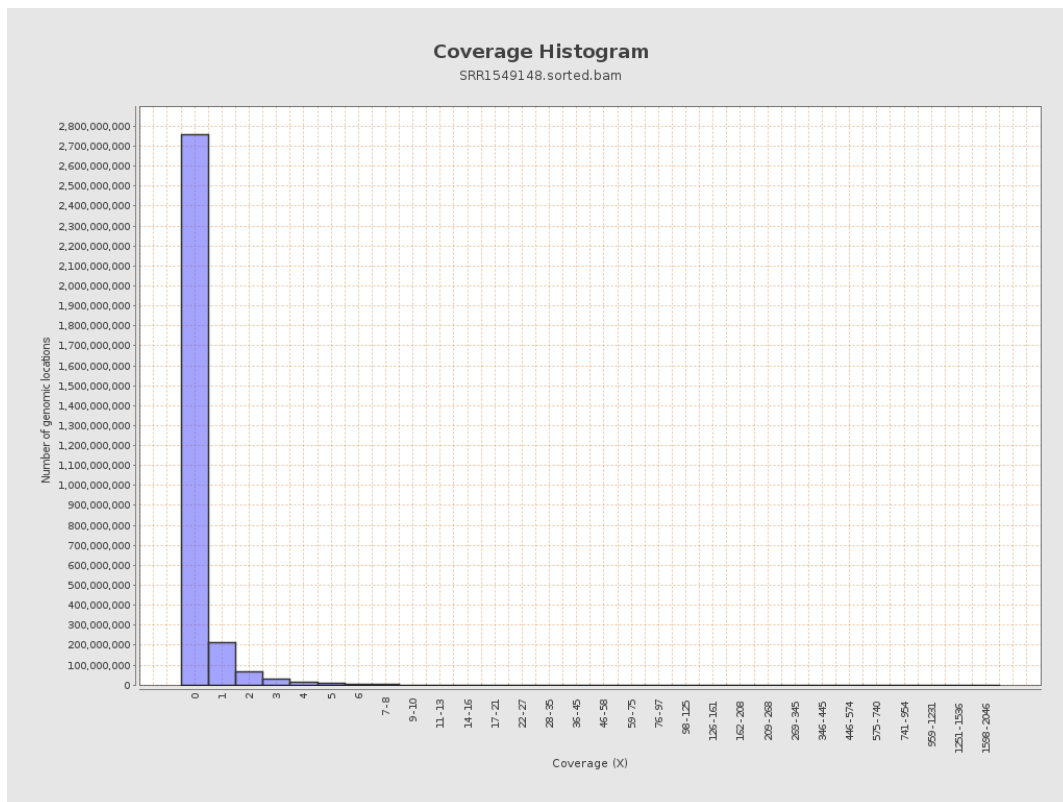
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	49915162	0.2003	1.443
chr2	243199373	48038401	0.1975	1.005
chr3	198022430	37142766	0.1876	0.7188
chr4	191154276	32376269	0.1694	0.685
chr5	180915260	33382228	0.1845	0.7264
chr6	171115067	32304649	0.1888	0.7645
chr7	159138663	33352832	0.2096	1.2793
chr8	146364022	28676537	0.1959	1.2906

chr9	141213431	25515189	0.1807	0.9525
chr10	135534747	29261055	0.2159	0.9098
chr11	135006516	27187577	0.2014	0.8678
chr12	133851895	27306370	0.204	0.7652
chr13	115169878	17029690	0.1479	0.6375
chr14	107349540	18632037	0.1736	0.9222
chr15	102531392	18962598	0.1849	0.7012
chr16	90354753	21380965	0.2366	0.8696
chr17	81195210	22106162	0.2723	0.9009
chr18	78077248	14731485	0.1887	1.6943
chr19	59128983	18242533	0.3085	1.5956
chr20	63025520	14628212	0.2321	0.8265
chr21	48129895	7946207	0.1651	0.7747
chr22	51304566	10421348	0.2031	0.7779
chrMT	16571	347900	20.9945	28.2464
chrX	155270560	17601858	0.1134	0.6562
chrY	59373566	3796408	0.0639	0.4264

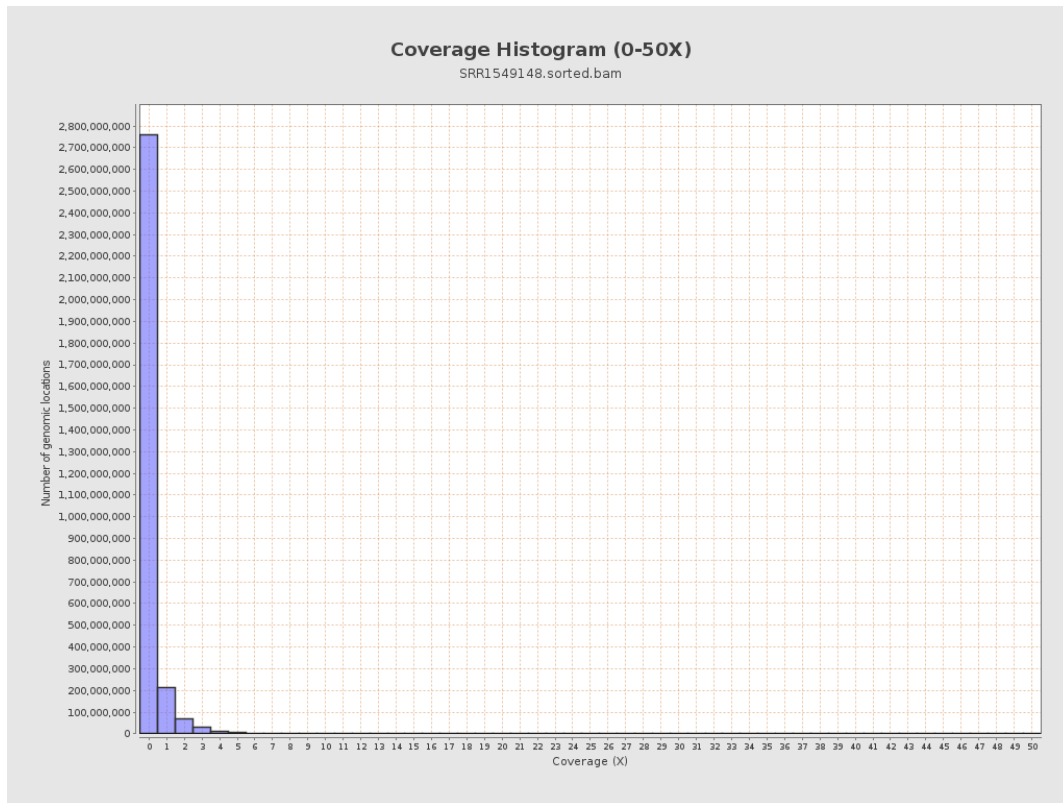
3. Results : Coverage across reference



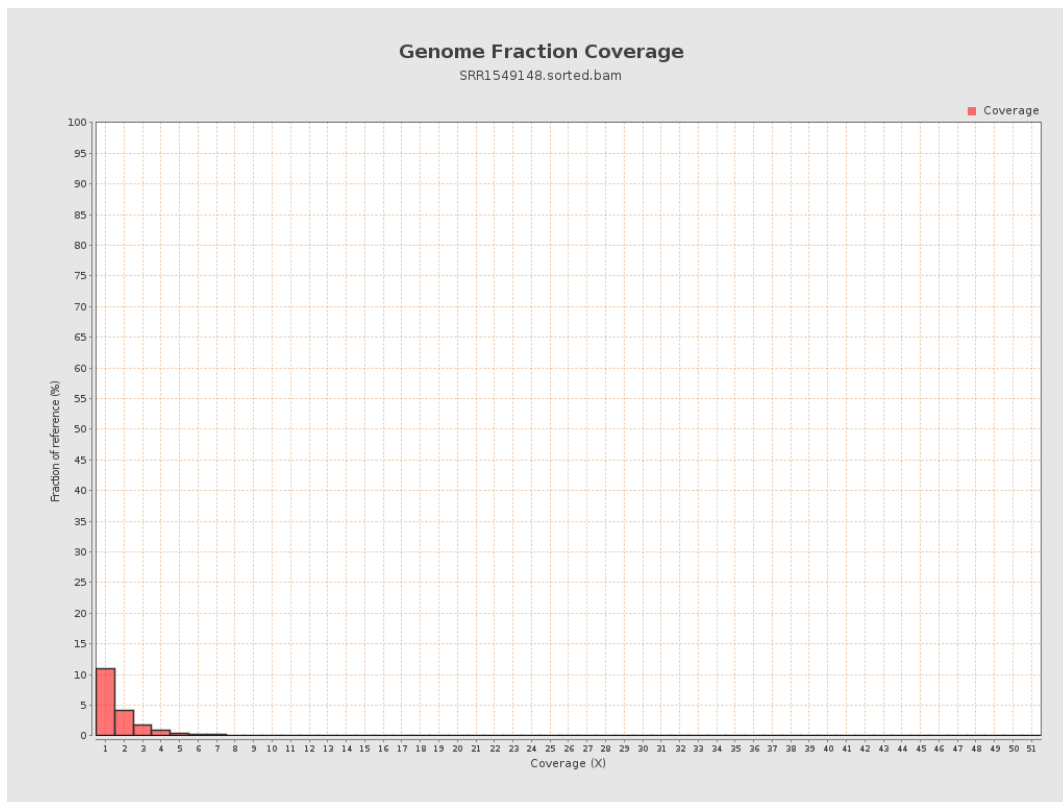
4. Results : Coverage Histogram



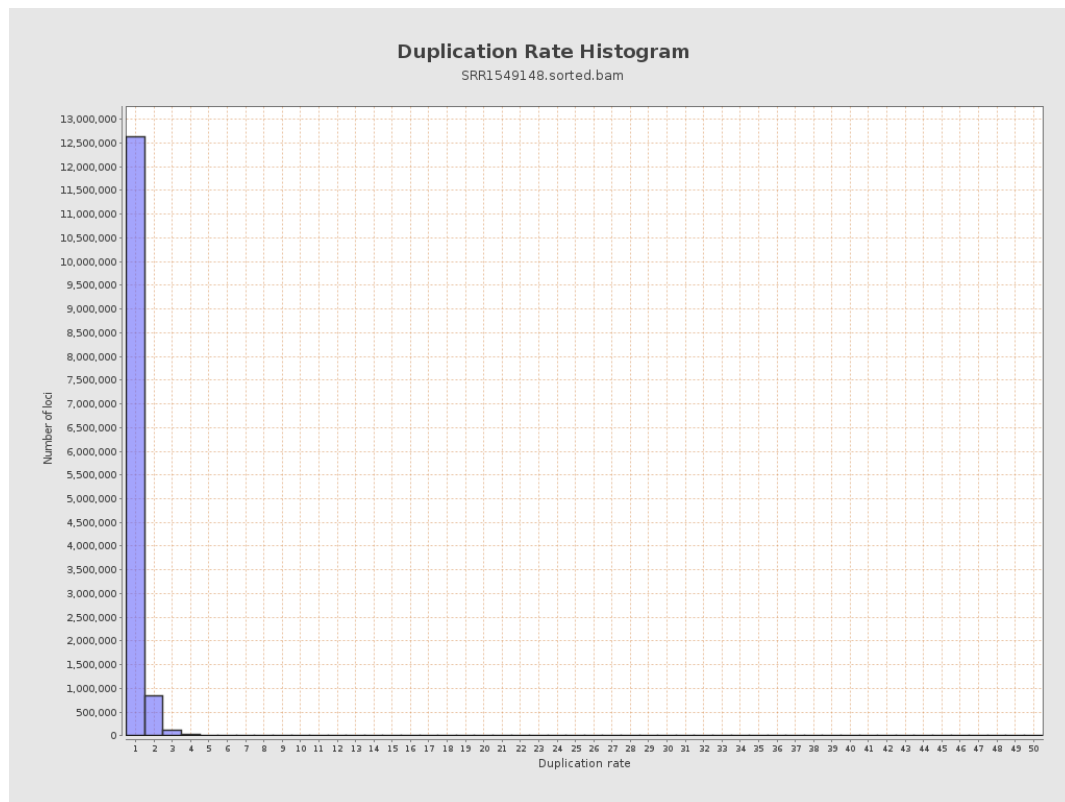
5. Results : Coverage Histogram (0-50X)



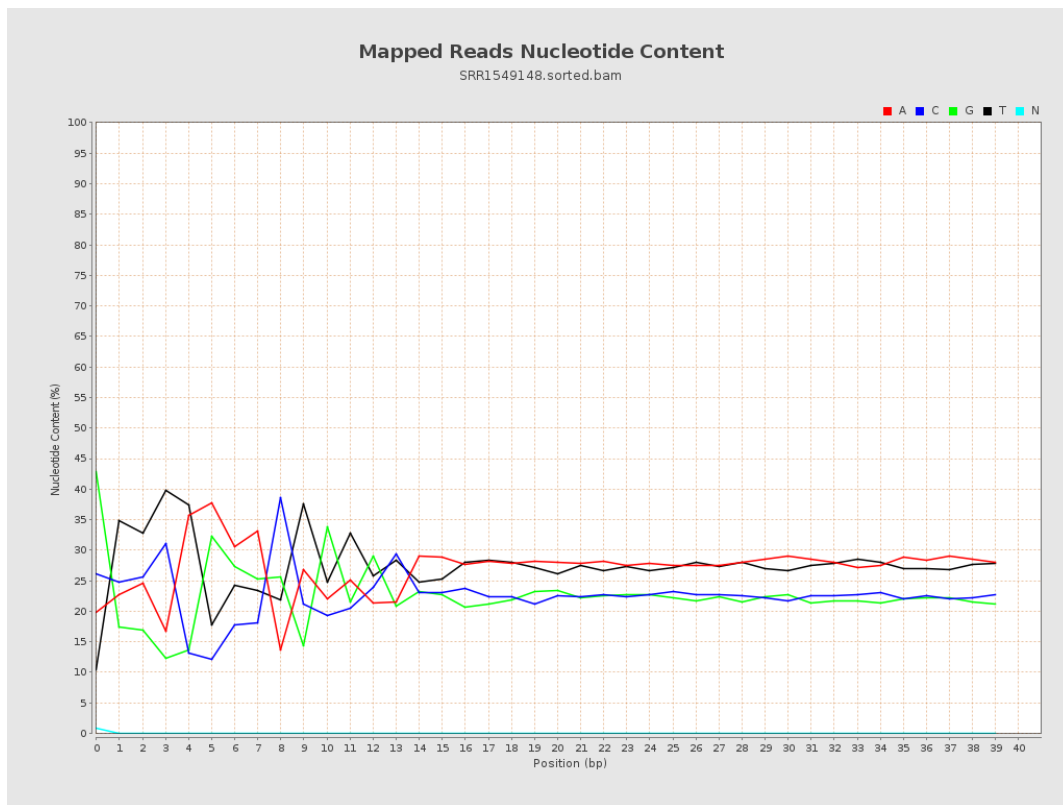
6. Results : Genome Fraction Coverage



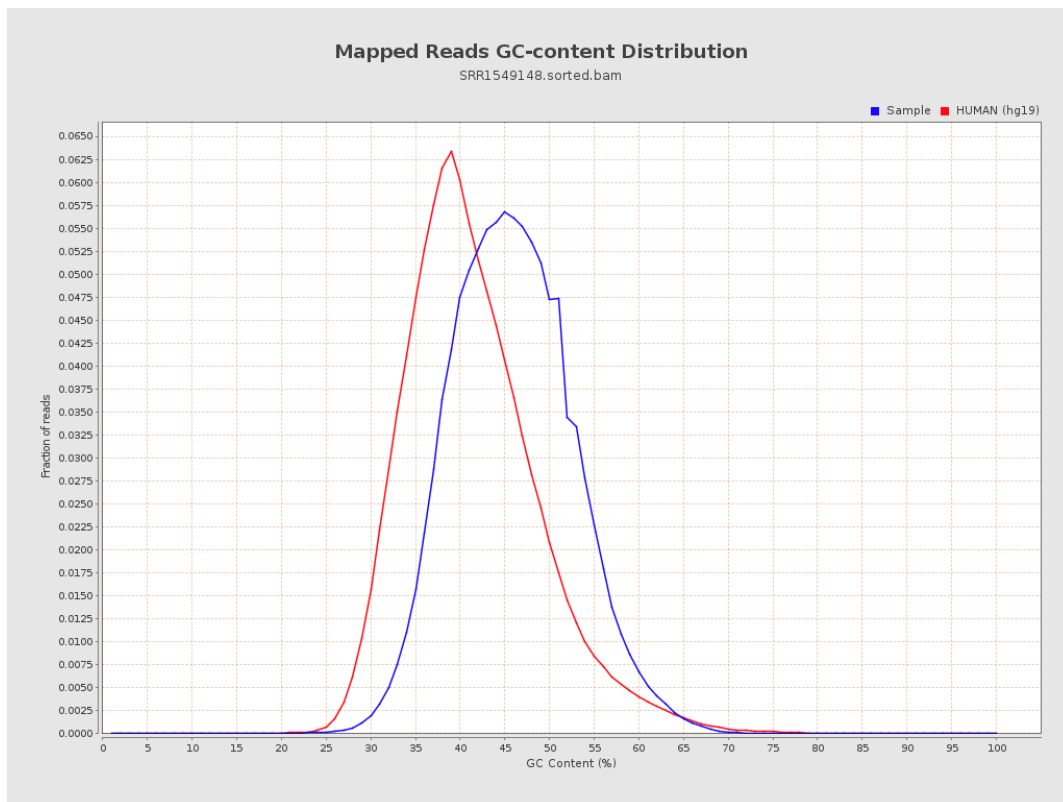
7. Results : Duplication Rate Histogram



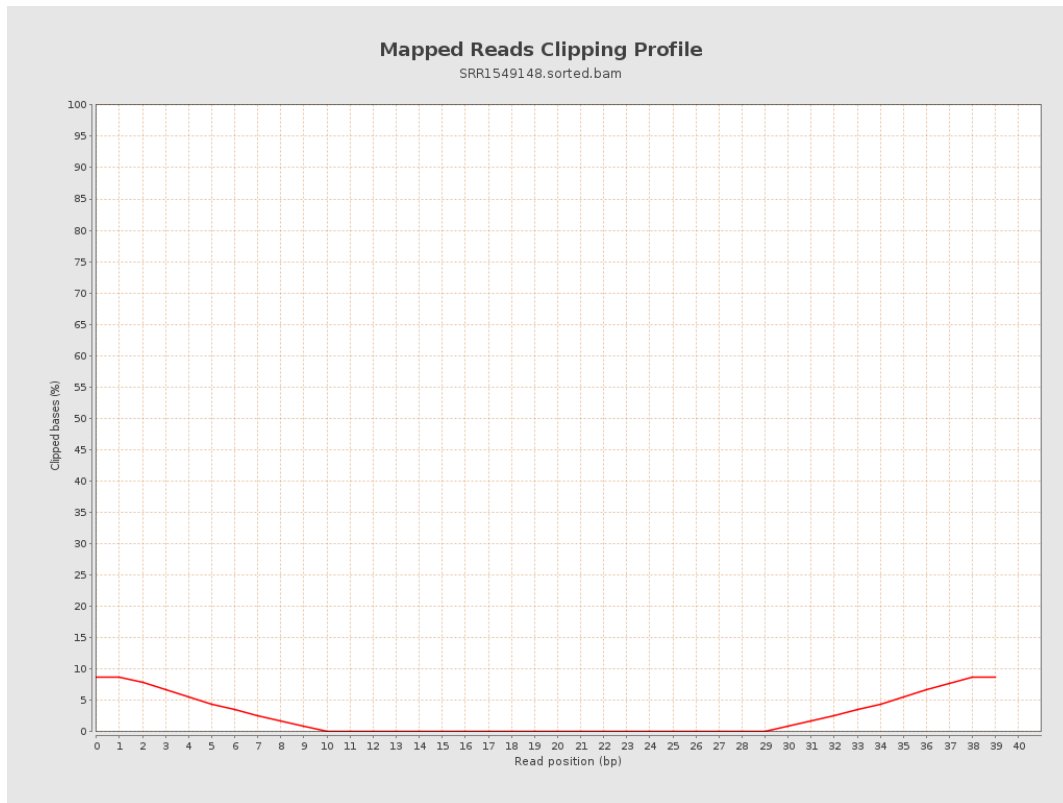
8. Results : Mapped Reads Nucleotide Content



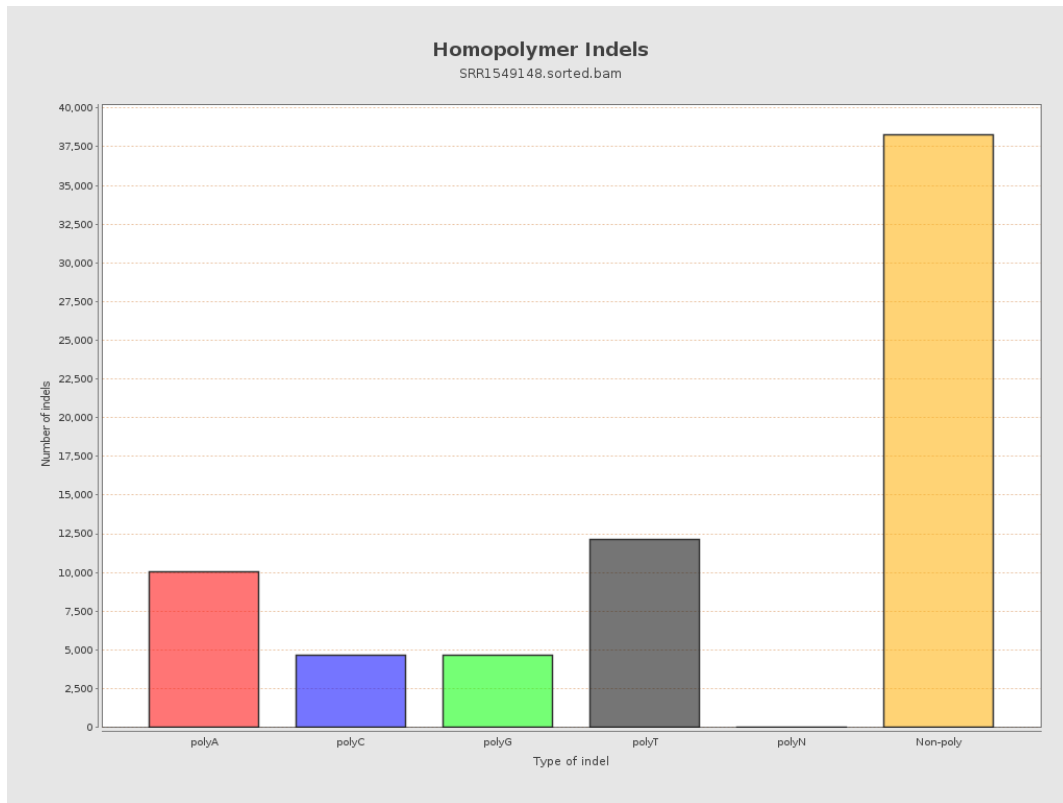
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

