

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:42:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549066.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_SRR1549066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:42:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,592,533
Mapped reads	8,256,776 / 86.08%
Unmapped reads	1,335,757 / 13.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	355,703 / 3.71%
Duplication rate	3.13%
Clipped reads	356,391 / 3.72%

2.2. ACGT Content

Number/percentage of A's	96,683,075 / 29.46%
Number/percentage of C's	67,385,234 / 20.54%
Number/percentage of T's	96,804,620 / 29.5%
Number/percentage of G's	67,252,261 / 20.5%
Number/percentage of N's	6,254 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.106
Standard Deviation	1.0234

2.4. Mapping Quality

Mean Mapping Quality	44.5
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2.5. Mismatches and indels

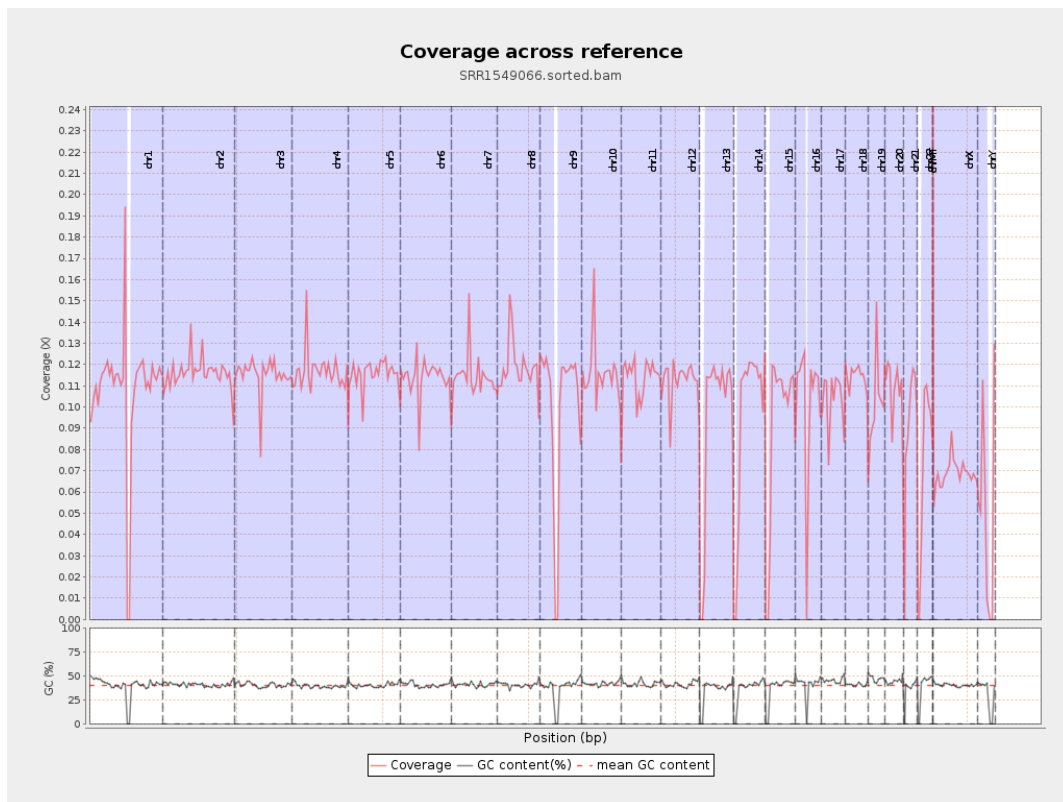
General error rate	0.31%
Mismatches	1,009,172
Insertions	7,821
Mapped reads with at least one insertion	0.09%
Deletions	27,726
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.79%

2.6. Chromosome stats

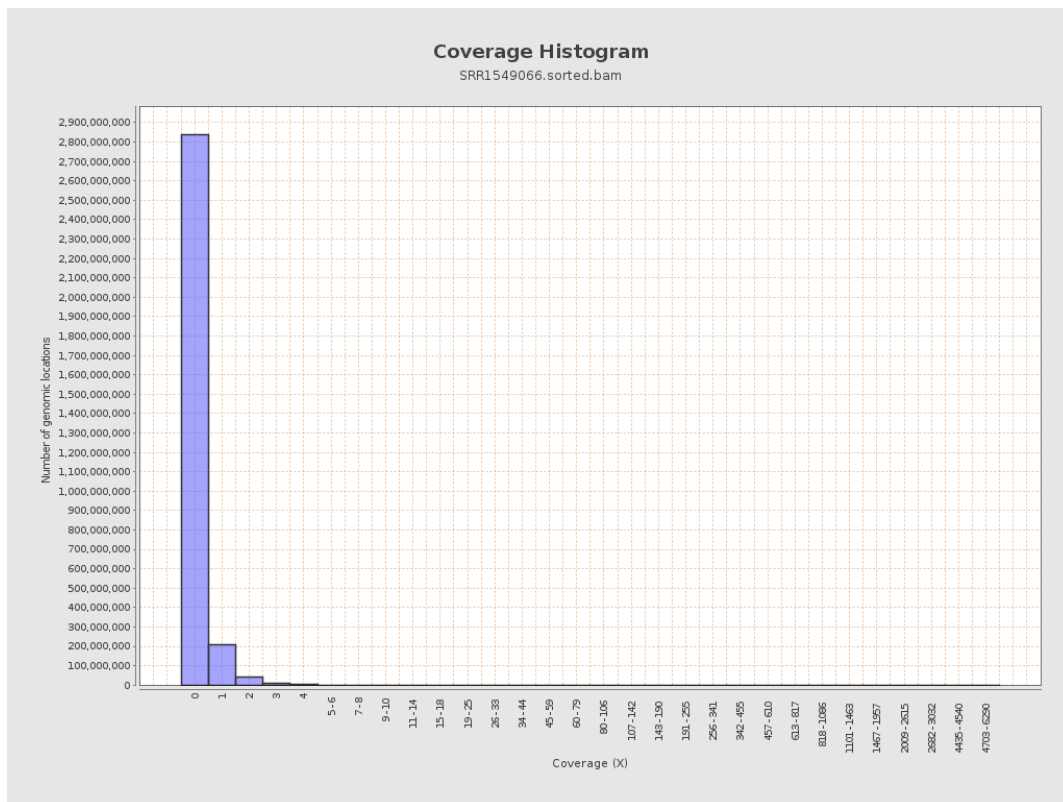
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26948937	0.1081	1.9974
chr2	243199373	28200162	0.116	0.584
chr3	198022430	22819367	0.1152	0.4106
chr4	191154276	22355248	0.1169	0.4779
chr5	180915260	20863372	0.1153	0.4173
chr6	171115067	19496462	0.1139	0.4731
chr7	159138663	18212667	0.1144	0.789
chr8	146364022	17372040	0.1187	3.0849

chr9	141213431	14161313	0.1003	0.549
chr10	135534747	15695108	0.1158	0.6759
chr11	135006516	15347998	0.1137	0.5605
chr12	133851895	15088269	0.1127	0.4228
chr13	115169878	10866927	0.0944	0.3658
chr14	107349540	10291223	0.0959	0.4135
chr15	102531392	9257114	0.0903	0.3588
chr16	90354753	9031925	0.1	0.4338
chr17	81195210	8438845	0.1039	0.4241
chr18	78077248	8931167	0.1144	1.0417
chr19	59128983	6084224	0.1029	1.3979
chr20	63025520	6825188	0.1083	0.4184
chr21	48129895	4385254	0.0911	0.4526
chr22	51304566	3664896	0.0714	0.3534
chrMT	16571	4050	0.2444	0.579
chrX	155270560	10676423	0.0688	0.3913
chrY	59373566	3148921	0.053	0.6409

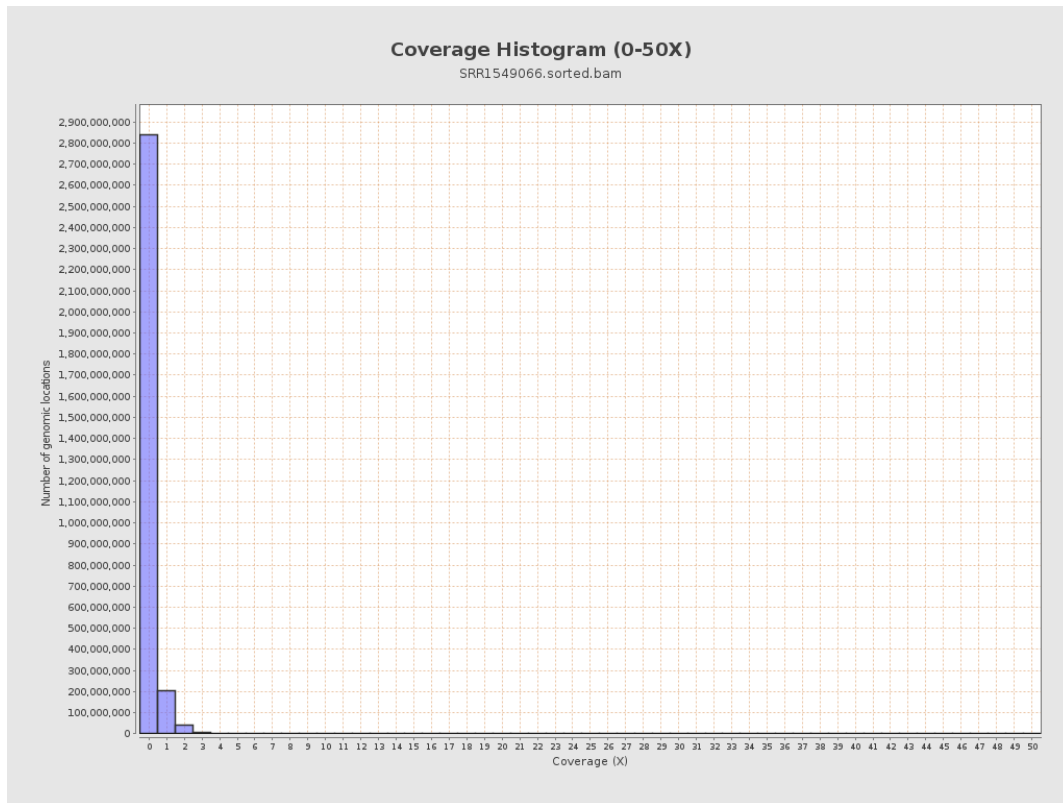
3. Results : Coverage across reference



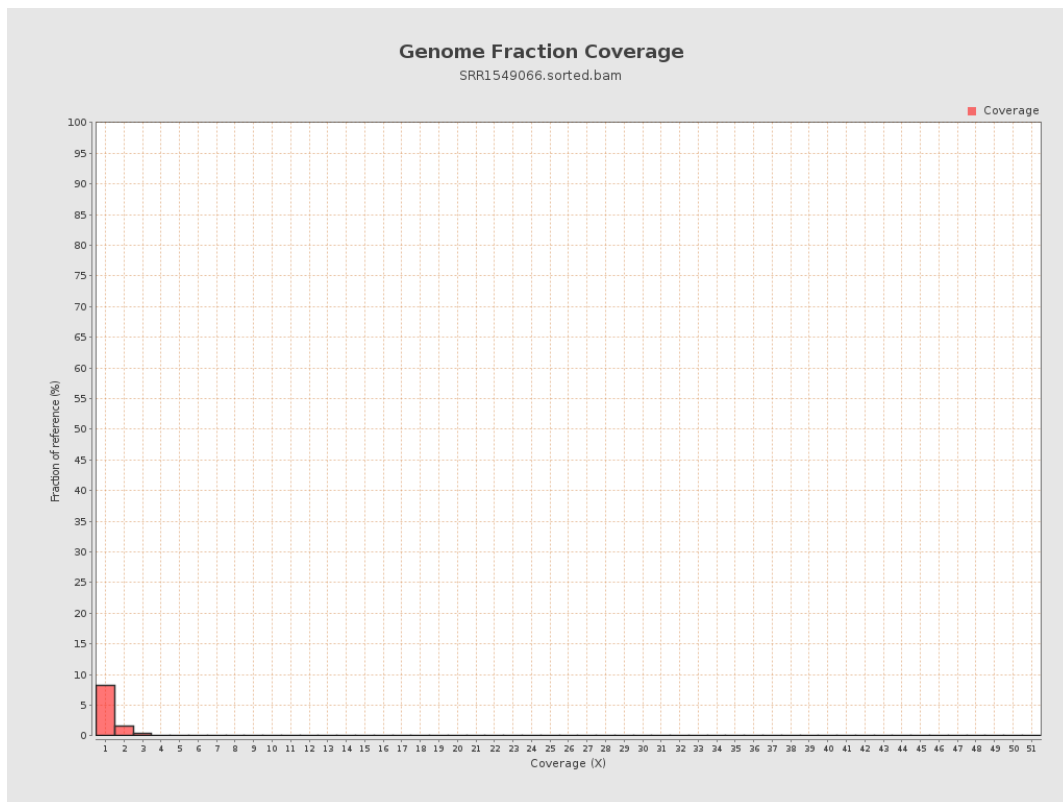
4. Results : Coverage Histogram



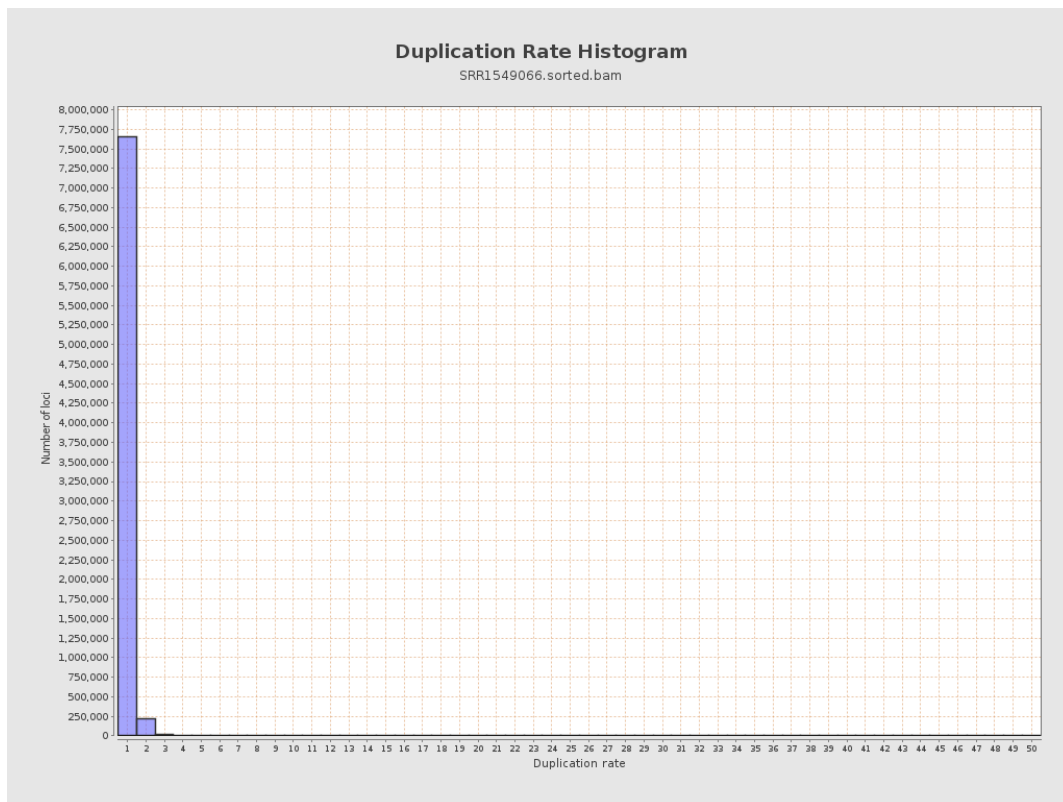
5. Results : Coverage Histogram (0-50X)



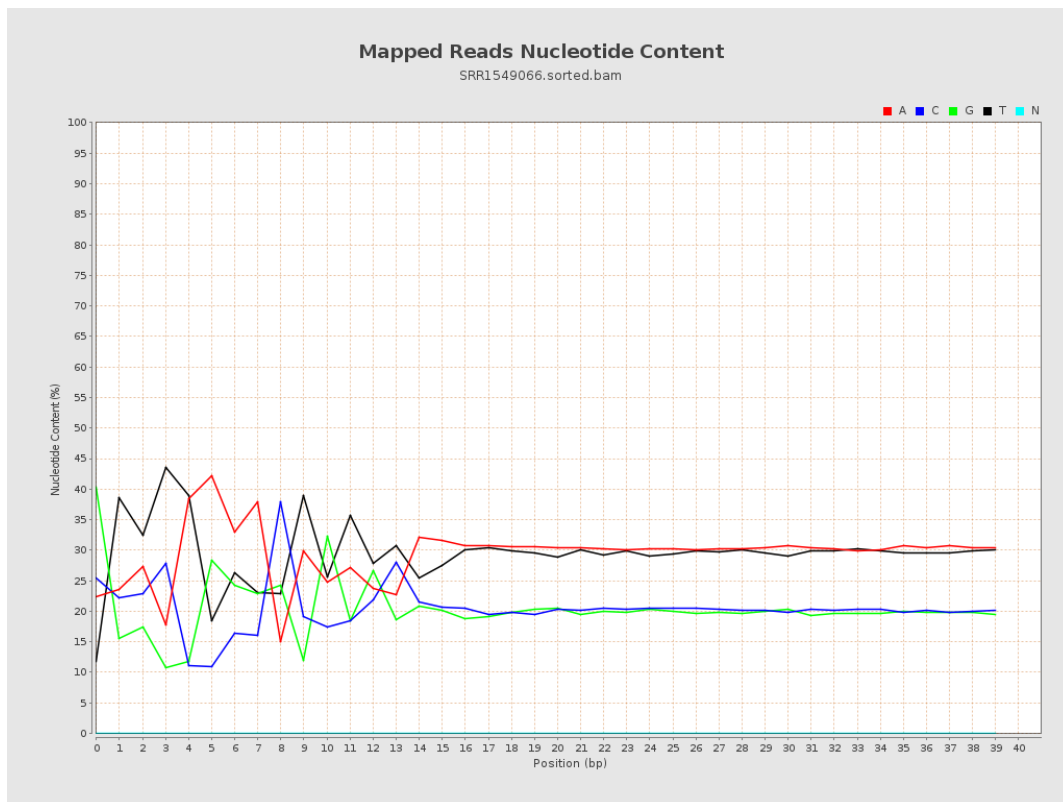
6. Results : Genome Fraction Coverage



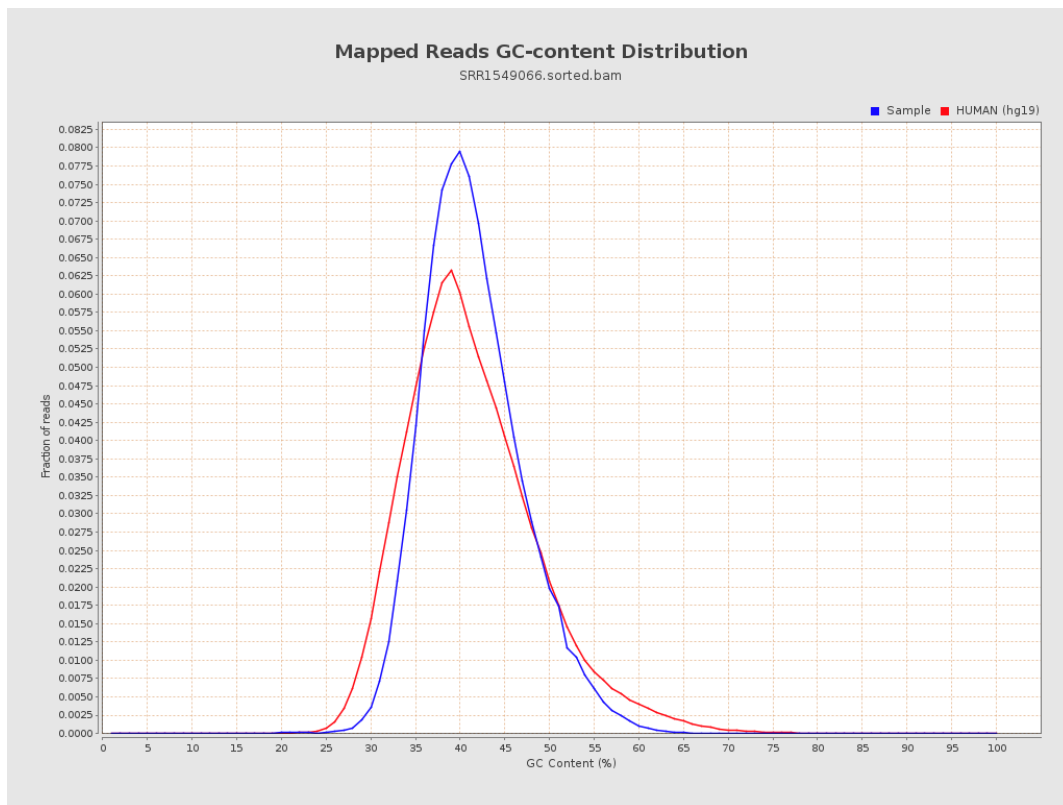
7. Results : Duplication Rate Histogram



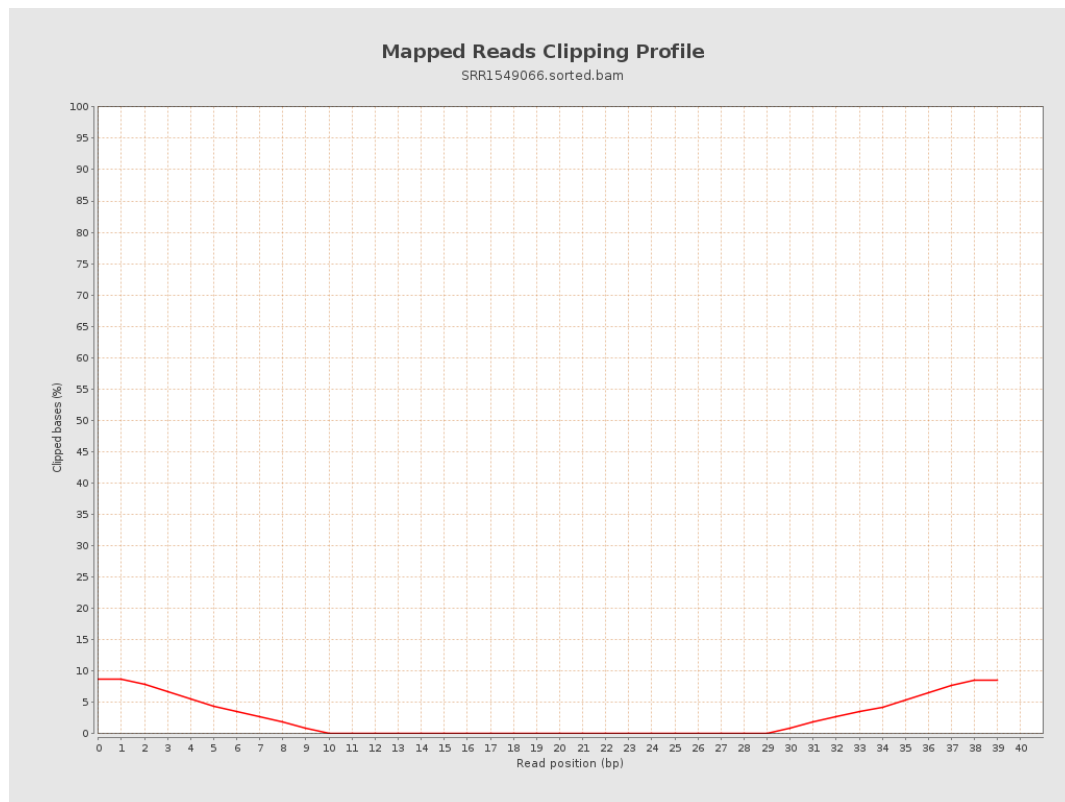
8. Results : Mapped Reads Nucleotide Content



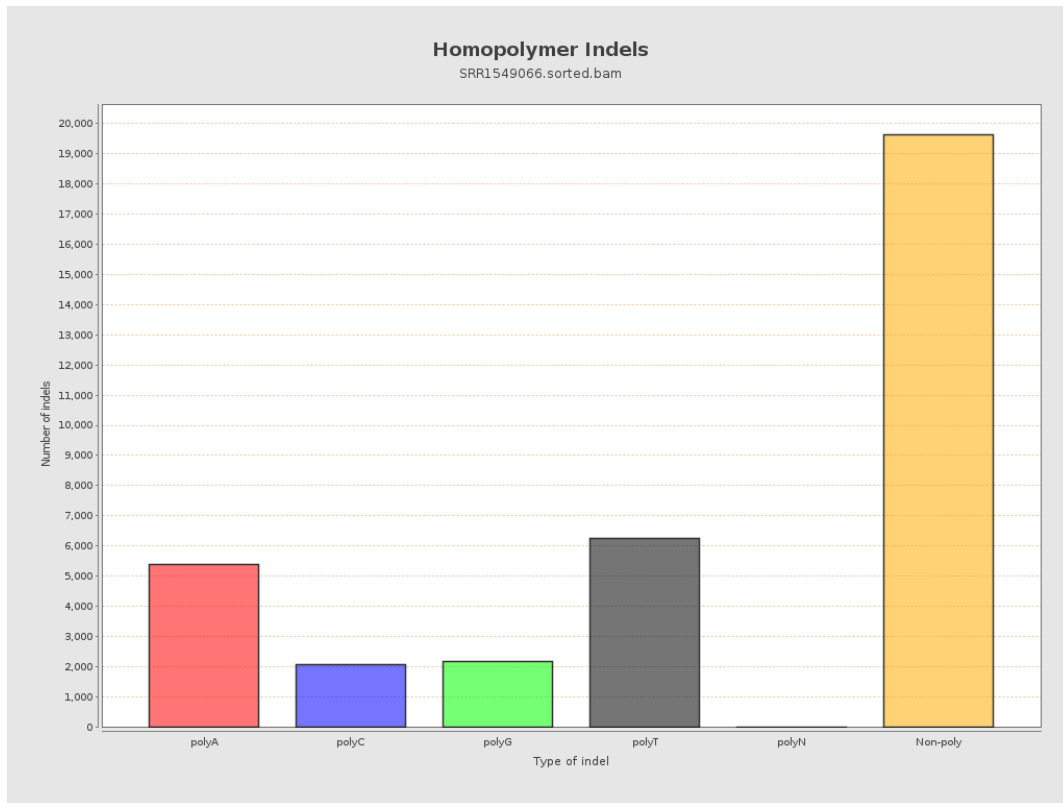
9. Results : Mapped Reads GC-content Distribution



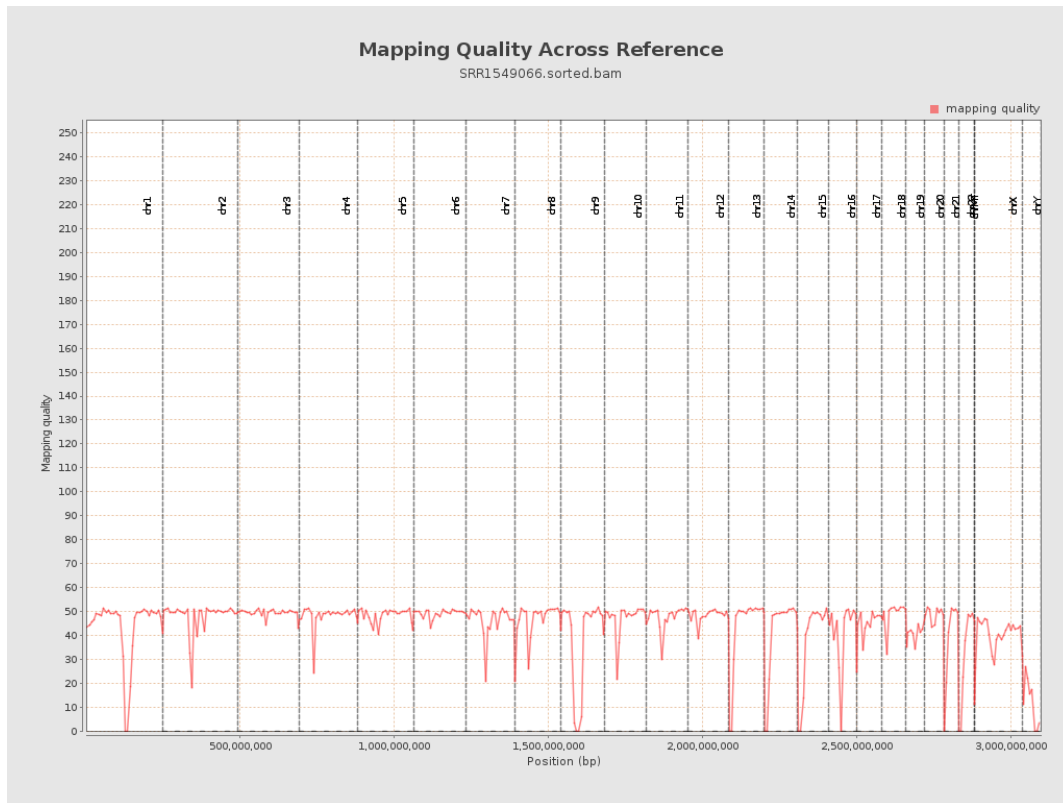
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

