

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:46:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548955.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_SRR1548955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:46:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,973,641
Mapped reads	11,368,790 / 87.63%
Unmapped reads	1,604,851 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	559,328 / 4.31%
Duplication rate	3.52%
Clipped reads	815,834 / 6.29%

2.2. ACGT Content

Number/percentage of A's	128,344,456 / 28.51%
Number/percentage of C's	95,496,460 / 21.22%
Number/percentage of T's	130,530,585 / 29%
Number/percentage of G's	95,756,882 / 21.27%
Number/percentage of N's	672 / 0%
GC Percentage	42.49%

2.3. Coverage

Mean	0.1454
Standard Deviation	1.2693

2.4. Mapping Quality

Mean Mapping Quality	40.38
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2.5. Mismatches and indels

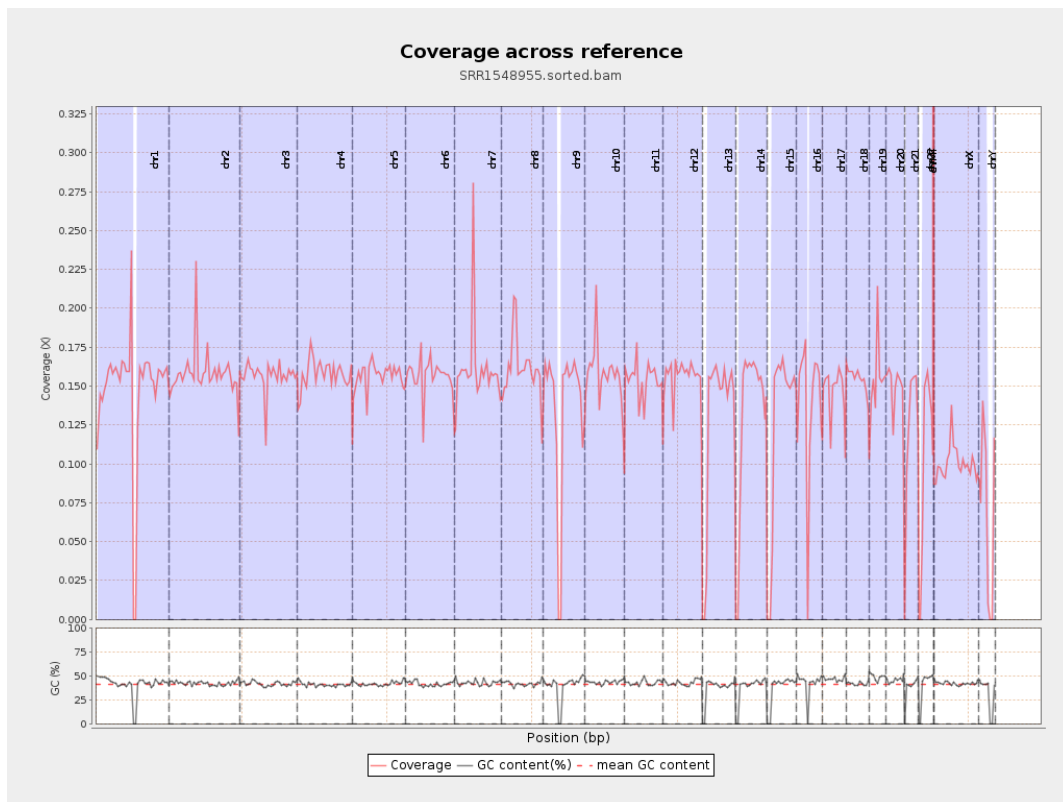
General error rate	0.27%
Mismatches	1,215,217
Insertions	13,791
Mapped reads with at least one insertion	0.12%
Deletions	35,128
Mapped reads with at least one deletion	0.31%
Homopolymer indels	41.05%

2.6. Chromosome stats

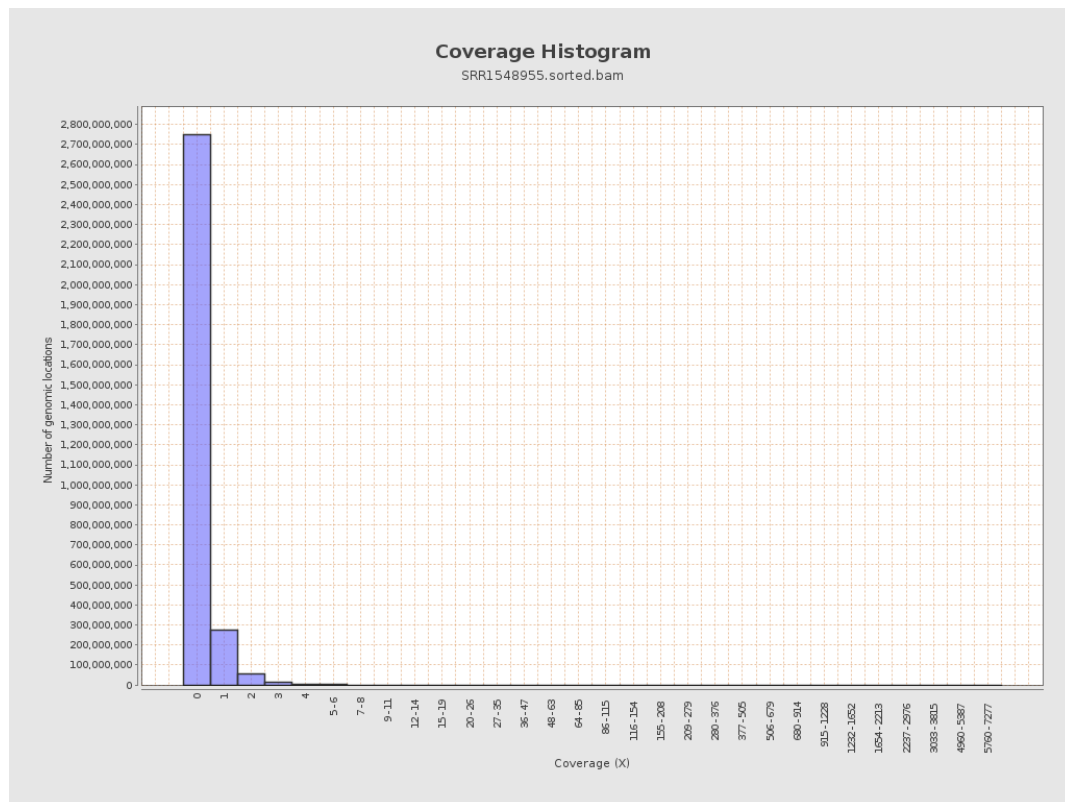
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	36790892	0.1476	2.1849
chr2	243199373	38475126	0.1582	0.9134
chr3	198022430	31021851	0.1567	0.4872
chr4	191154276	30118397	0.1576	0.5347
chr5	180915260	28343133	0.1567	0.5009
chr6	171115067	26751890	0.1563	0.5559
chr7	159138663	25724418	0.1616	1.7015
chr8	146364022	23515921	0.1607	3.5813

chr9	141213431	19148879	0.1356	0.9059
chr10	135534747	21476666	0.1585	0.8494
chr11	135006516	20659901	0.153	0.7436
chr12	133851895	20900205	0.1561	0.5249
chr13	115169878	14728217	0.1279	0.4296
chr14	107349540	14057001	0.1309	0.6135
chr15	102531392	12907284	0.1259	0.4363
chr16	90354753	12559973	0.139	0.5506
chr17	81195210	11815927	0.1455	0.5146
chr18	78077248	12108893	0.1551	1.7545
chr19	59128983	9211179	0.1558	1.9711
chr20	63025520	9286860	0.1474	0.5089
chr21	48129895	5892311	0.1224	0.6086
chr22	51304566	5142538	0.1002	0.6667
chrMT	16571	28182	1.7007	2.2854
chrX	155270560	15562504	0.1002	0.5866
chrY	59373566	3947341	0.0665	0.5782

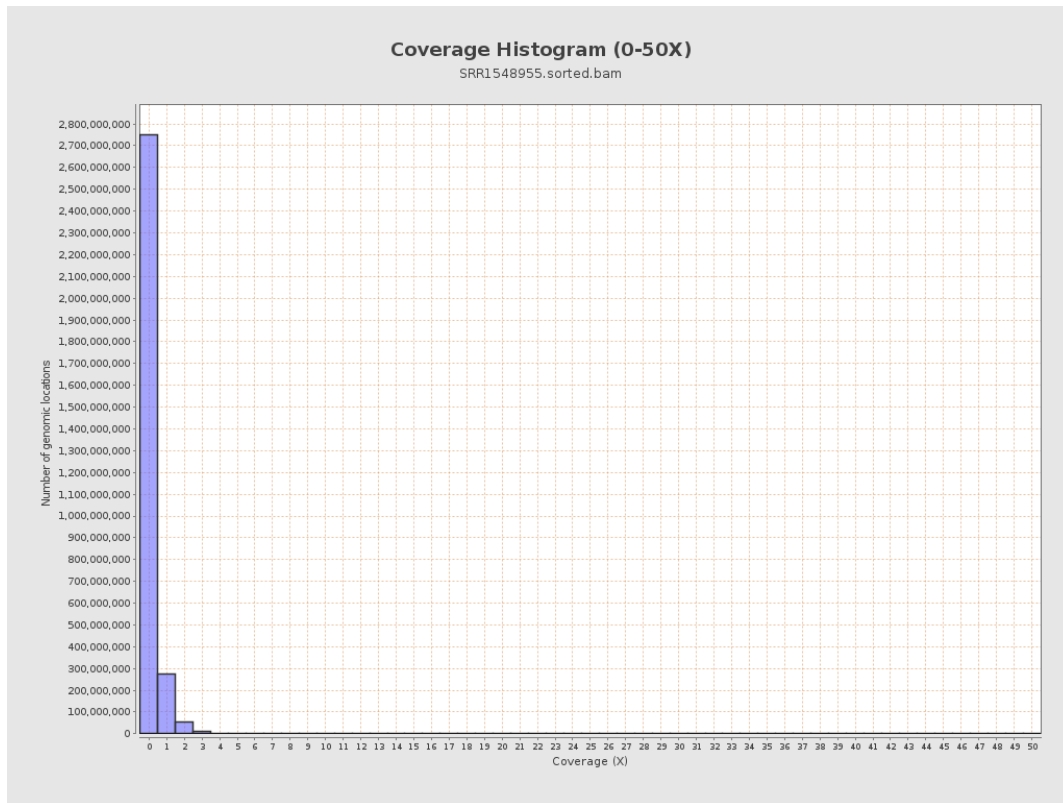
3. Results : Coverage across reference



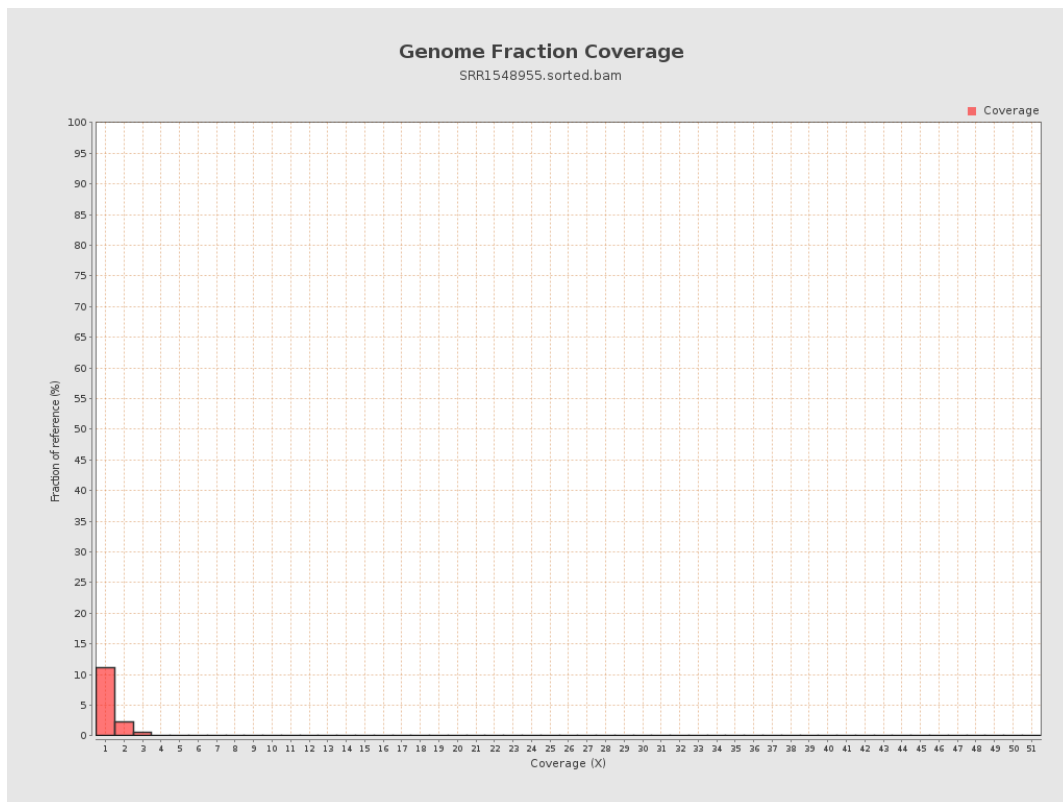
4. Results : Coverage Histogram



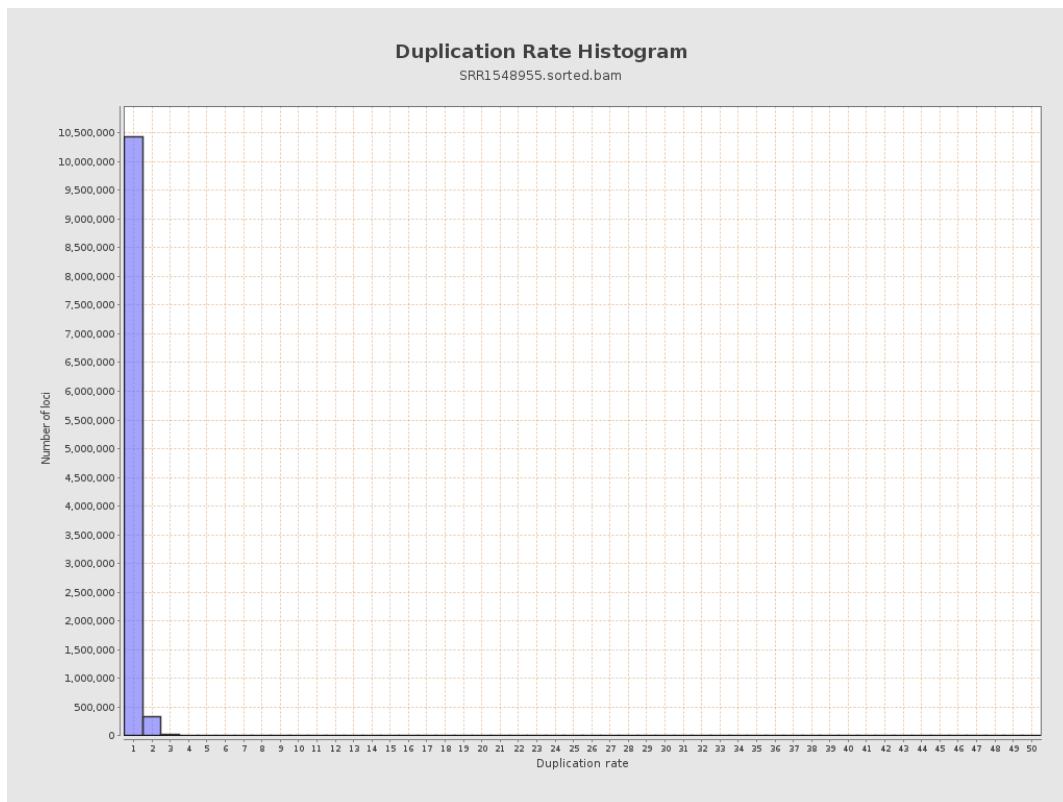
5. Results : Coverage Histogram (0-50X)



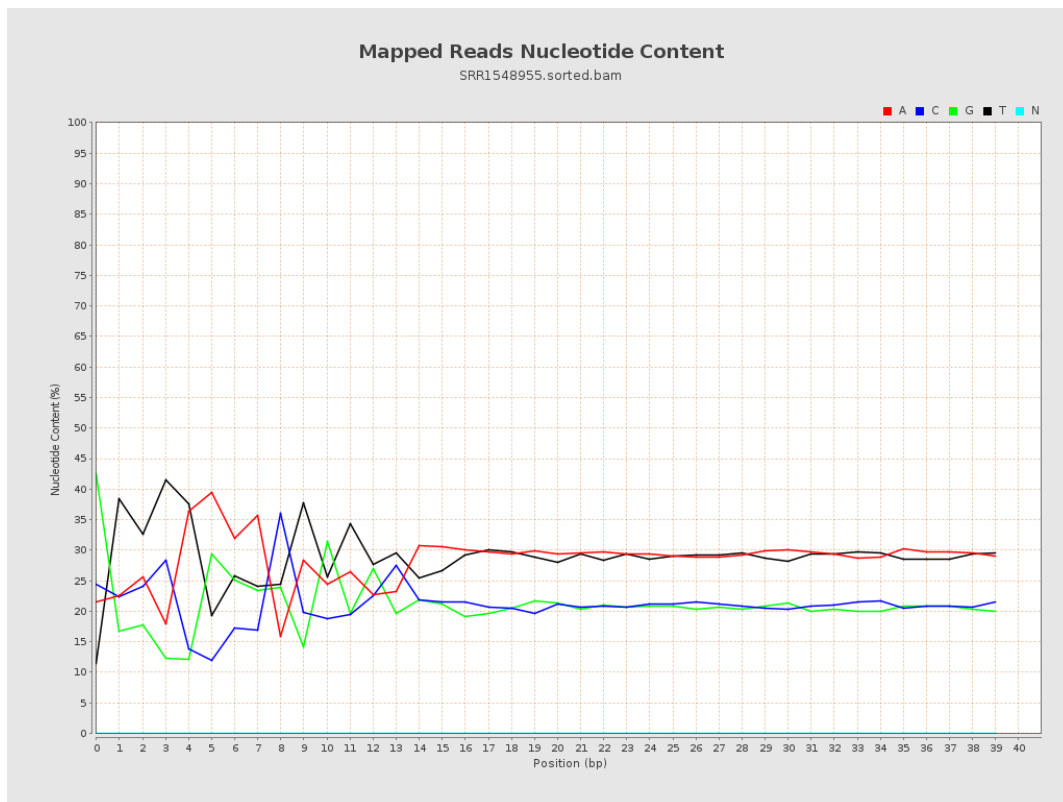
6. Results : Genome Fraction Coverage



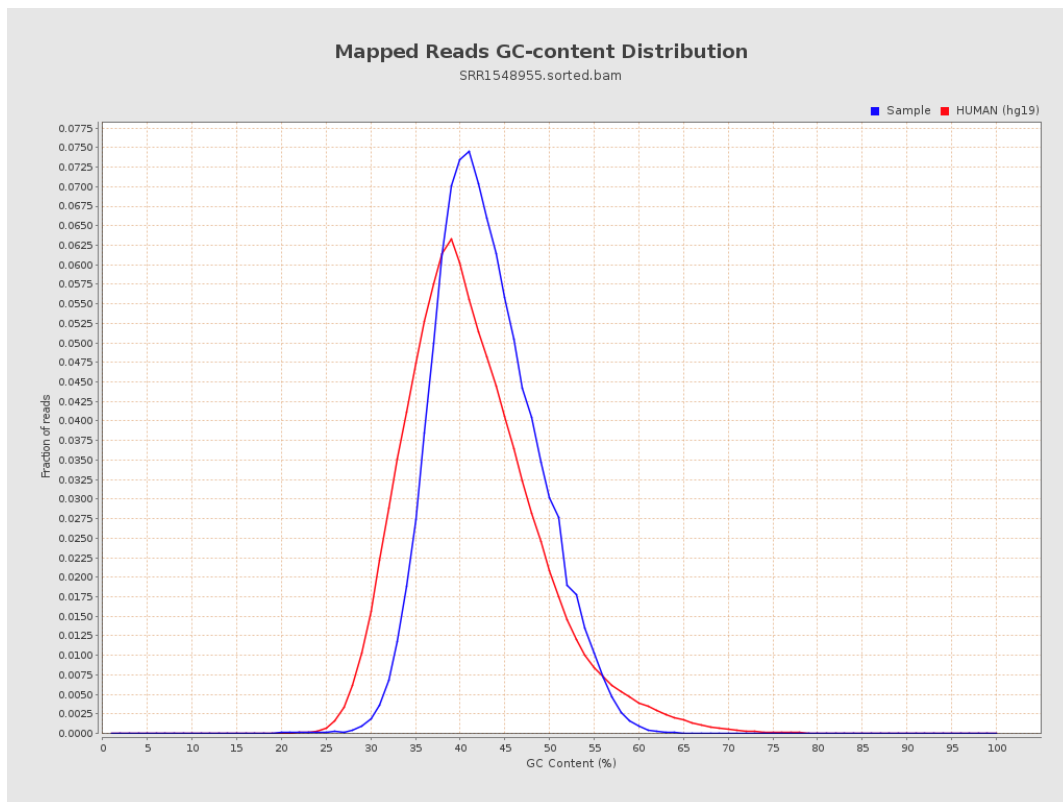
7. Results : Duplication Rate Histogram



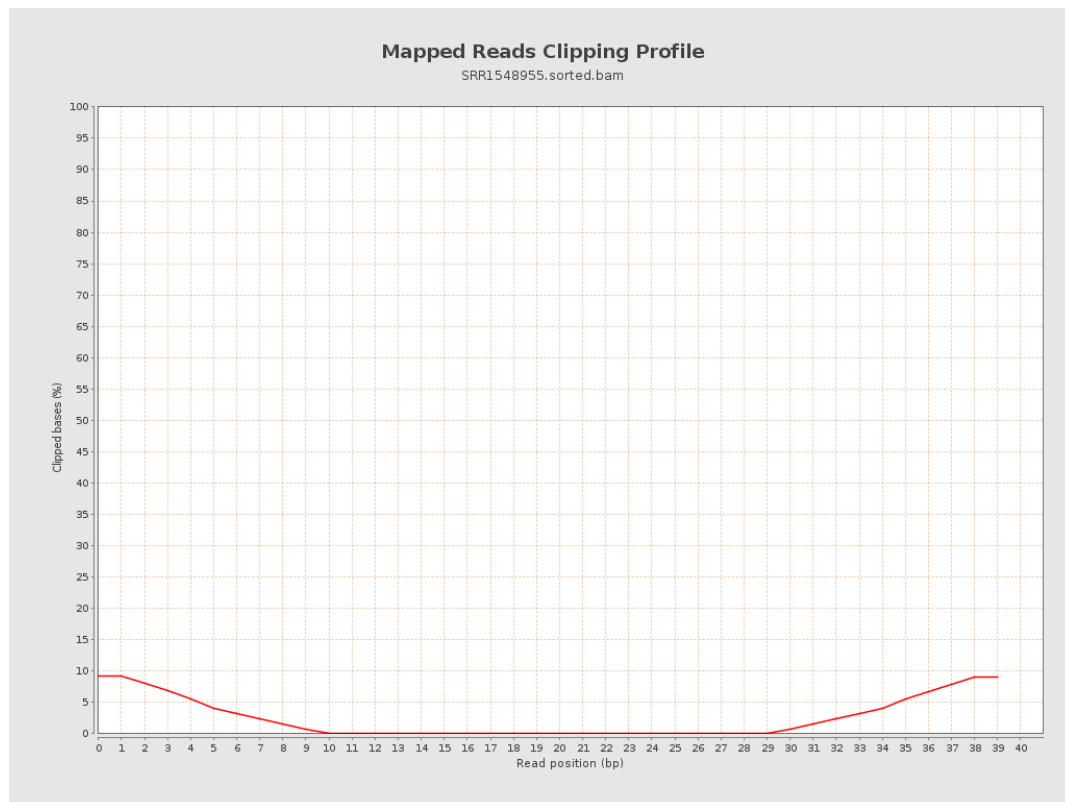
8. Results : Mapped Reads Nucleotide Content



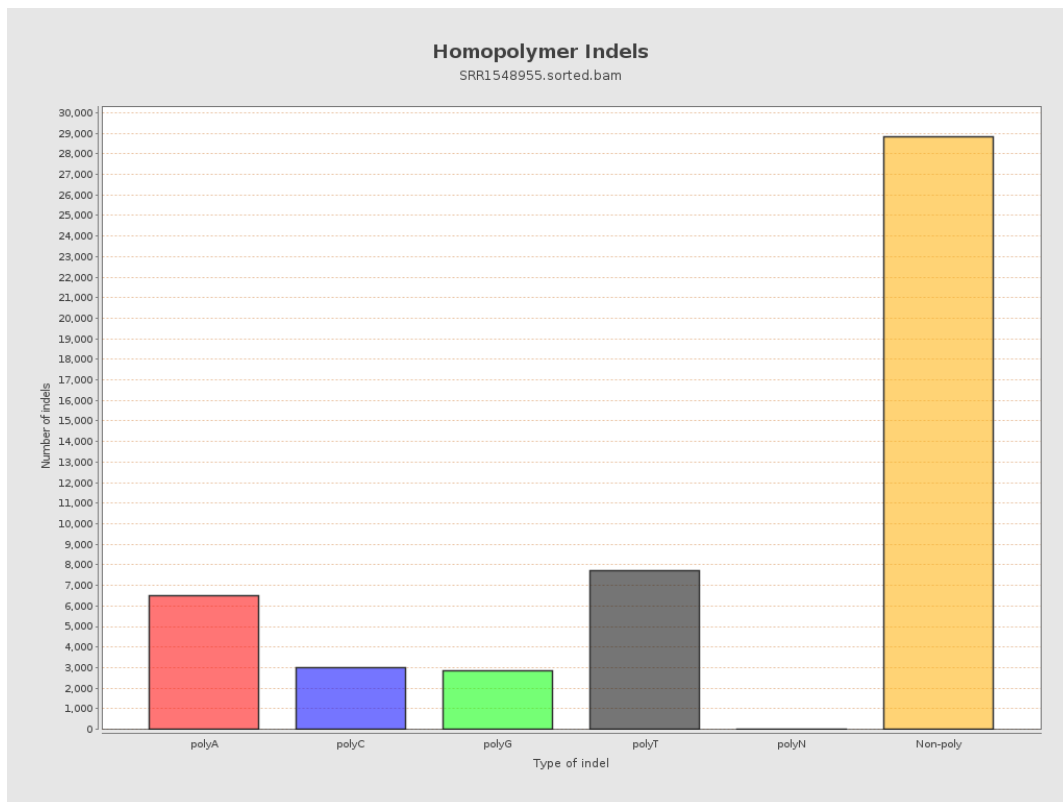
9. Results : Mapped Reads GC-content Distribution



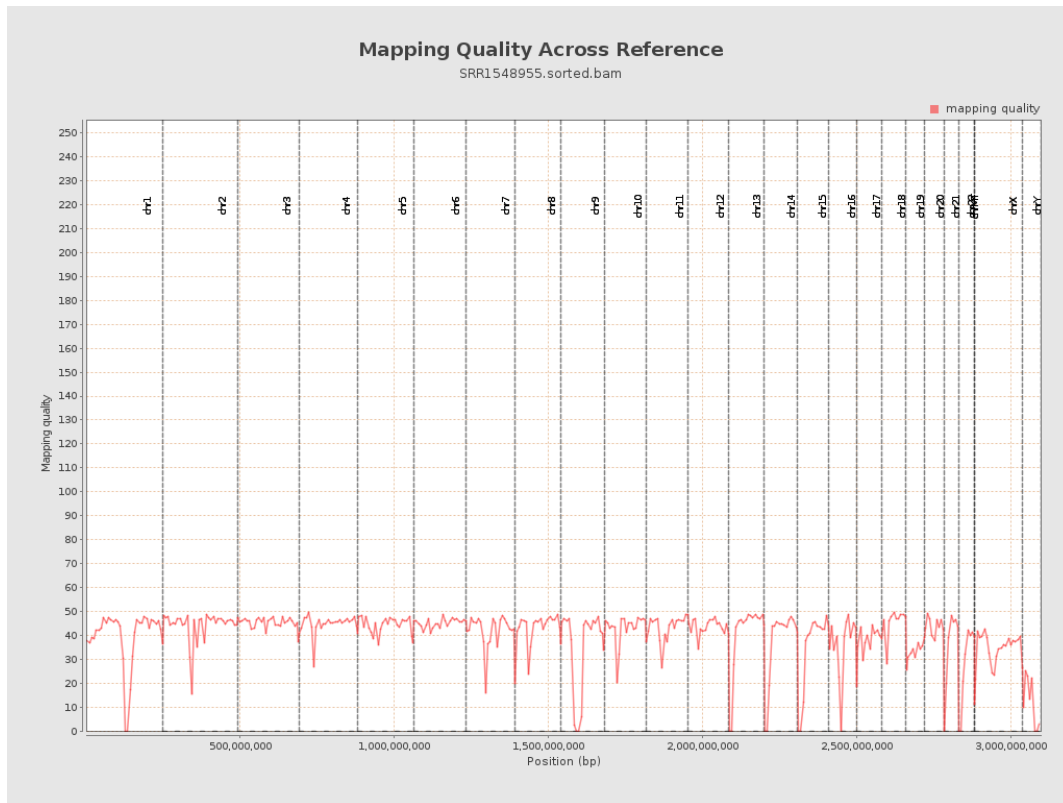
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

