Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004035.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_SRR6004035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	468,757
Mapped reads	386,345 / 82.42%
Unmapped reads	82,412 / 17.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,445 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	6,352 / 1.36%
Duplication rate	1.23%
Clipped reads	162,011 / 34.56%

2.2. ACGT Content

Number/percentage of A's	7,729,402 / 29.62%
Number/percentage of C's	4,616,805 / 17.69%
Number/percentage of T's	7,995,819 / 30.64%
Number/percentage of G's	5,749,430 / 22.03%
Number/percentage of N's	5,412 / 0.02%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1204

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

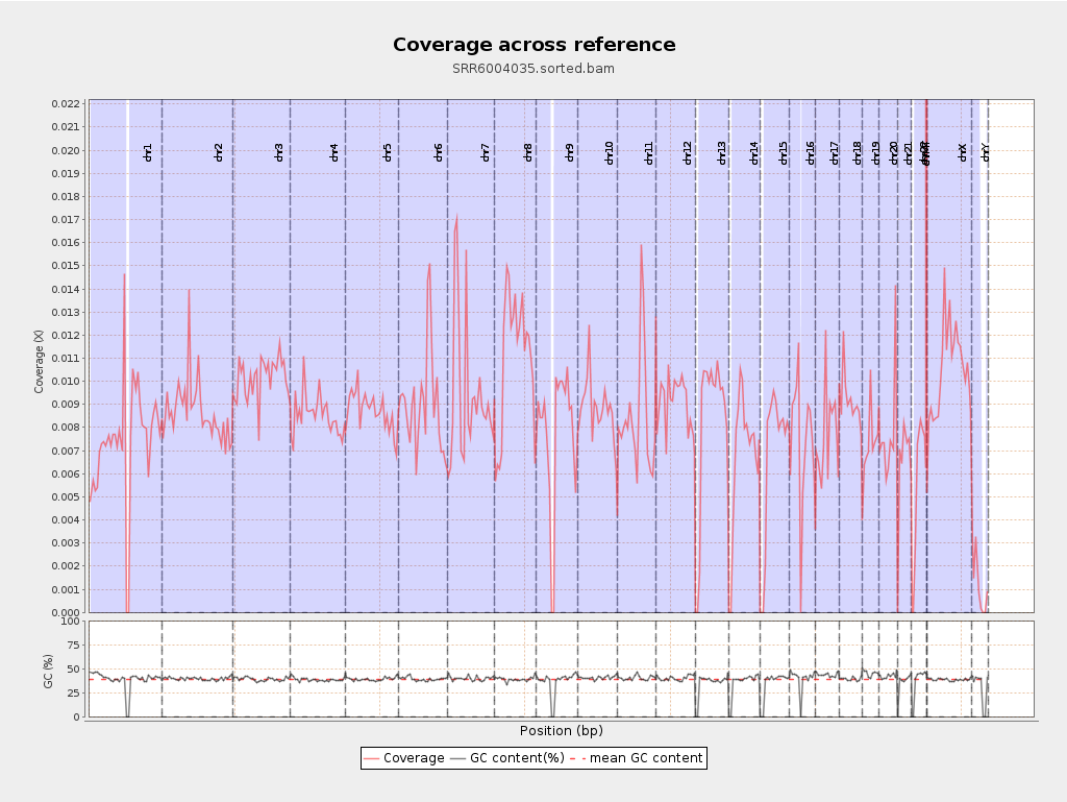
General error rate	0.95%
Mismatches	242,566
Insertions	2,268
Mapped reads with at least one insertion	0.58%
Deletions	6,809
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.58%

2.6. Chromosome stats

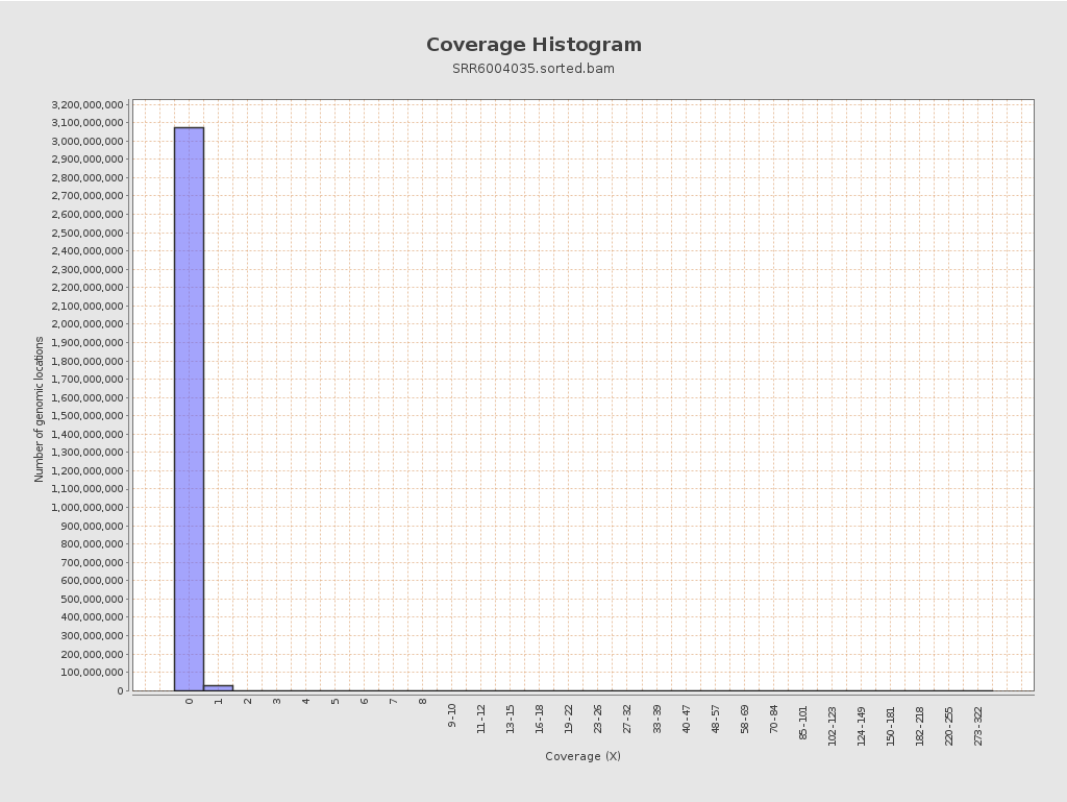
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1842439	0.0074	0.1731
chr2	243199373	2116137	0.0087	0.1127
chr3	198022430	2012400	0.0102	0.103
chr4	191154276	1629083	0.0085	0.0961
chr5	180915260	1579914	0.0087	0.0953
chr6	171115067	1541863	0.009	0.0995
chr7	159138663	1524892	0.0096	0.1378

chr8	146364022	1598949	0.0109	0.222
chr9	141213431	1085563	0.0077	0.105
chr10	135534747	1199052	0.0088	0.1091
chr11	135006516	1149142	0.0085	0.1121
chr12	133851895	1214897	0.0091	0.0978
chr13	115169878	938418	0.0081	0.0923
chr14	107349540	723663	0.0067	0.0865
chr15	102531392	698895	0.0068	0.0842
chr16	90354753	676189	0.0075	0.0932
chr17	81195210	625836	0.0077	0.093
chr18	78077248	720585	0.0092	0.1837
chr19	59128983	437581	0.0074	0.1264
chr20	63025520	494036	0.0078	0.0913
chr21	48129895	311862	0.0065	0.0844
chr22	51304566	276436	0.0054	0.0748
chrMT	16571	22020	1.3288	1.4845
chrX	155270560	1621490	0.0104	0.1084
chrY	59373566	67220	0.0011	0.0373

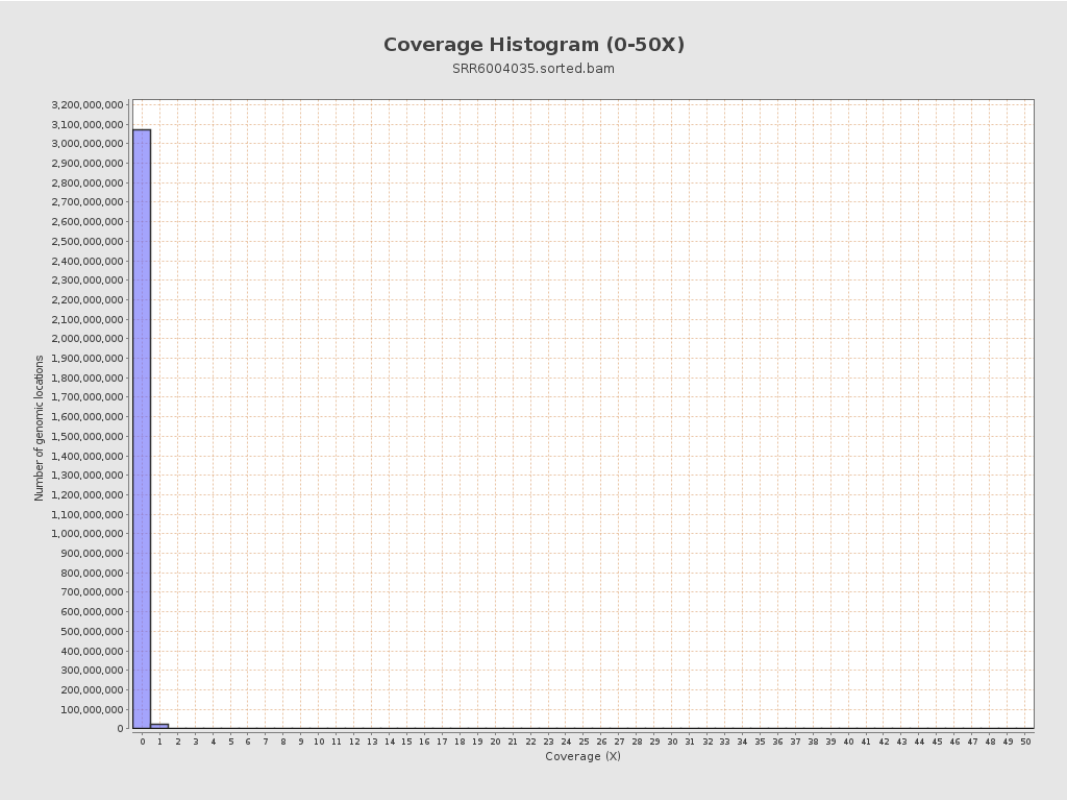
3. Results : Coverage across reference



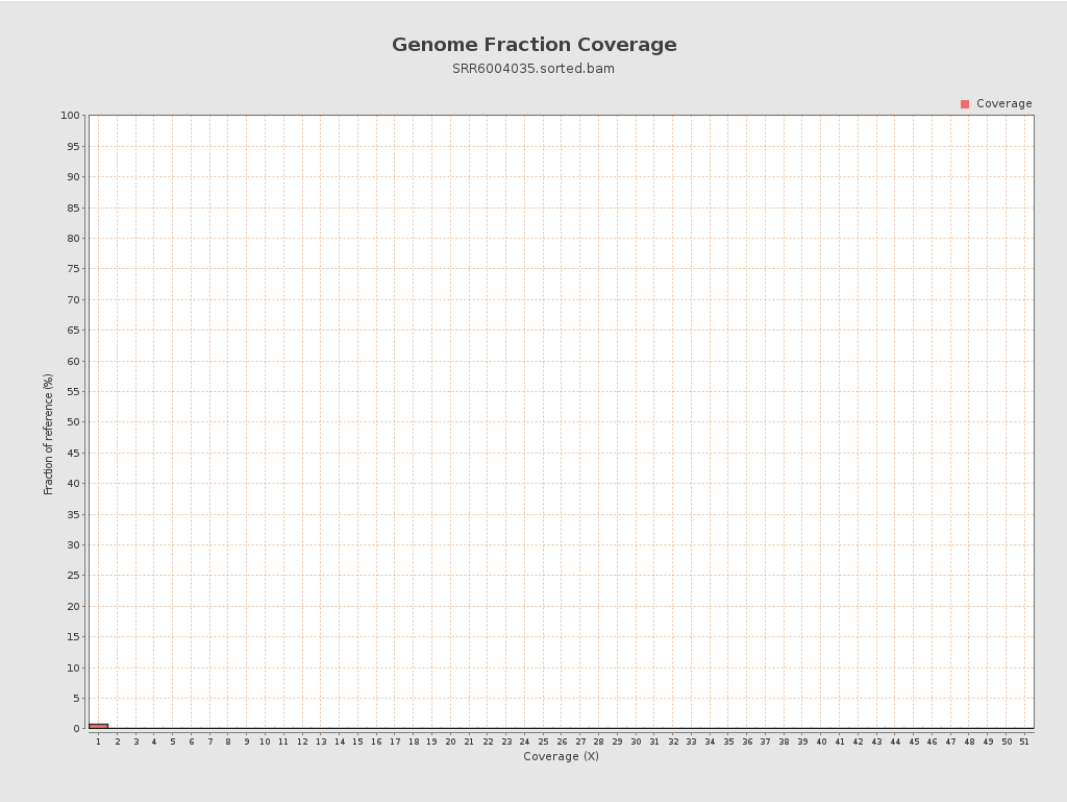
4. Results : Coverage Histogram



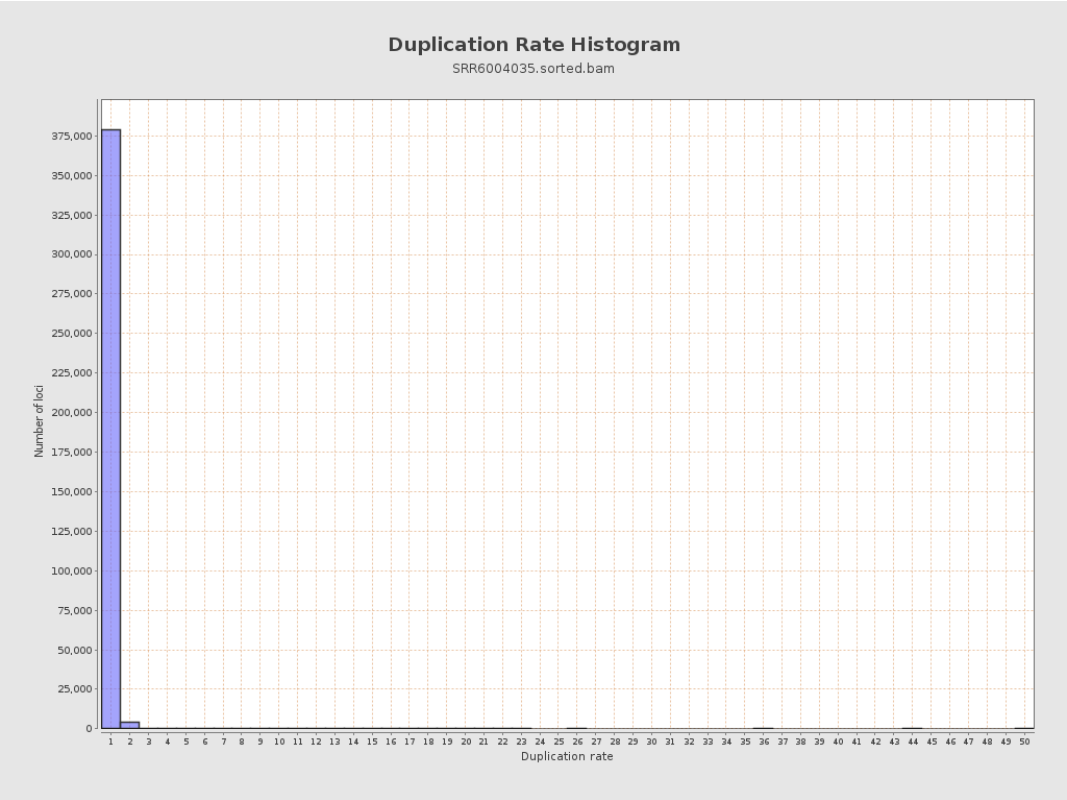
5. Results : Coverage Histogram (0-50X)



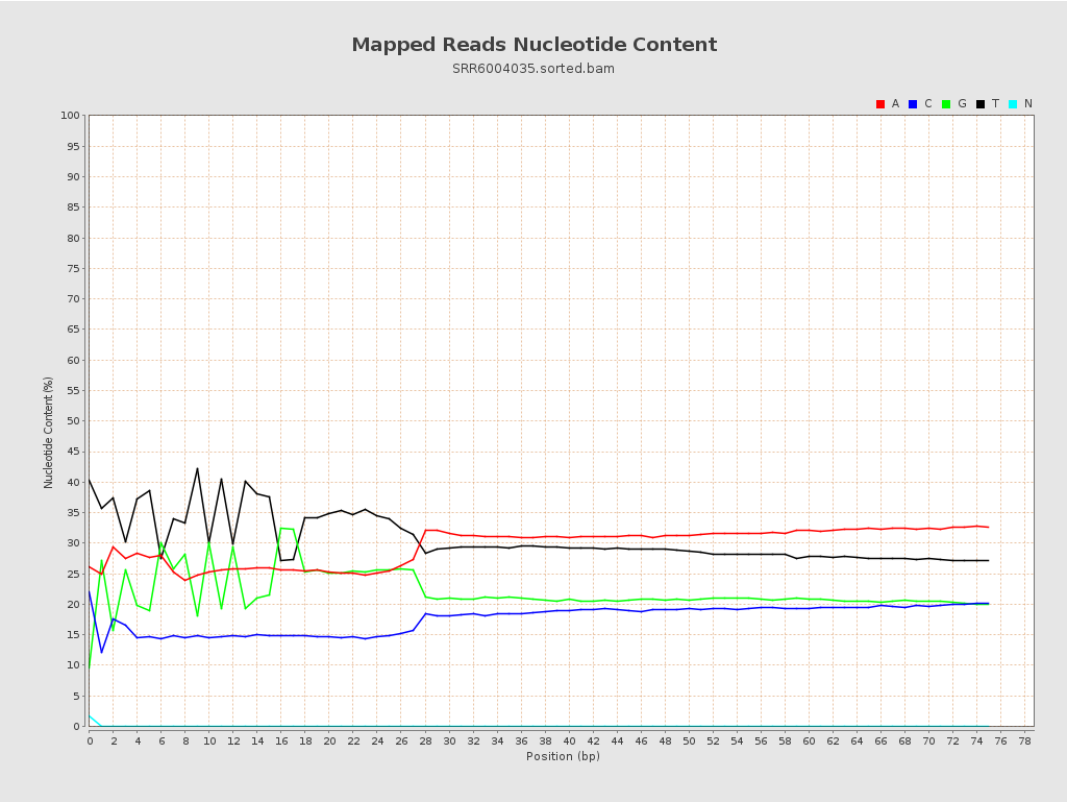
6. Results : Genome Fraction Coverage



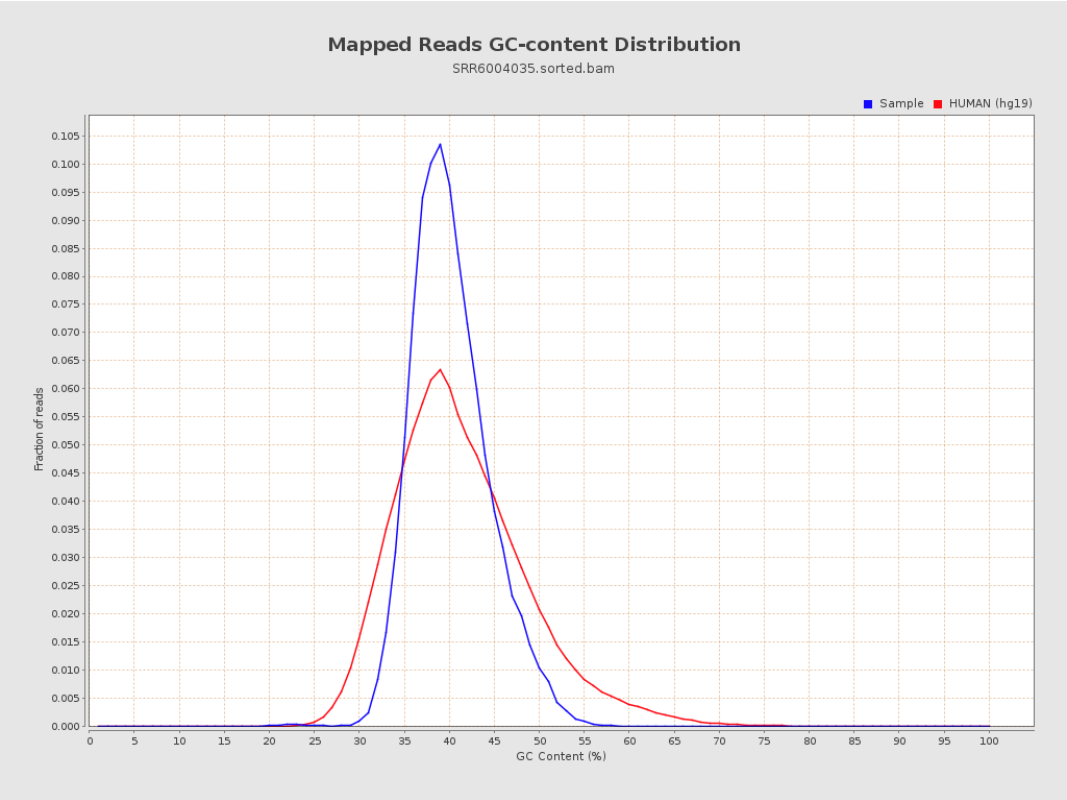
7. Results : Duplication Rate Histogram



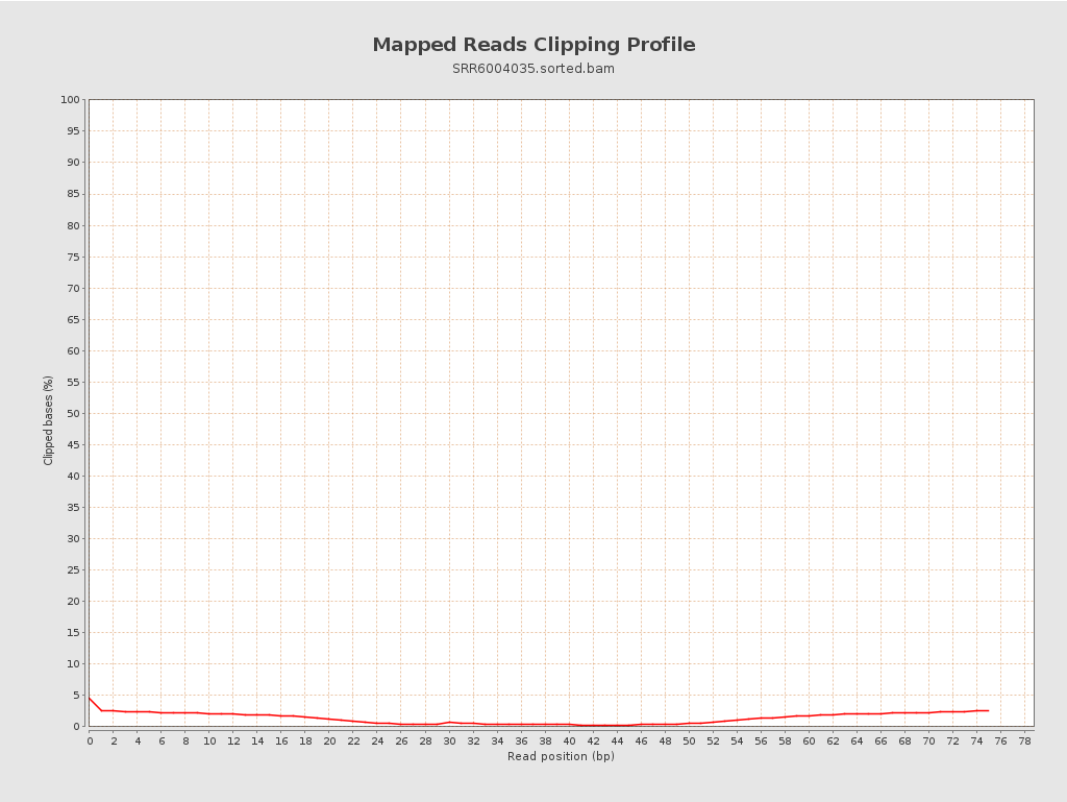
8. Results : Mapped Reads Nucleotide Content



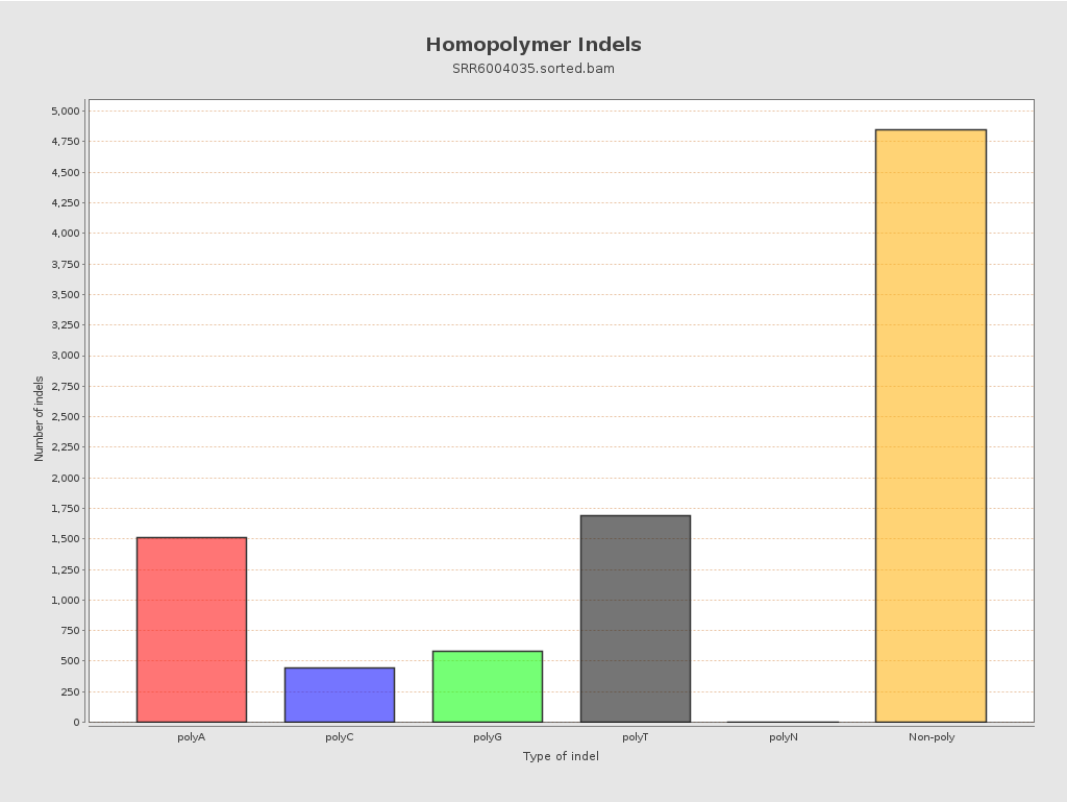
9. Results : Mapped Reads GC-content Distribution



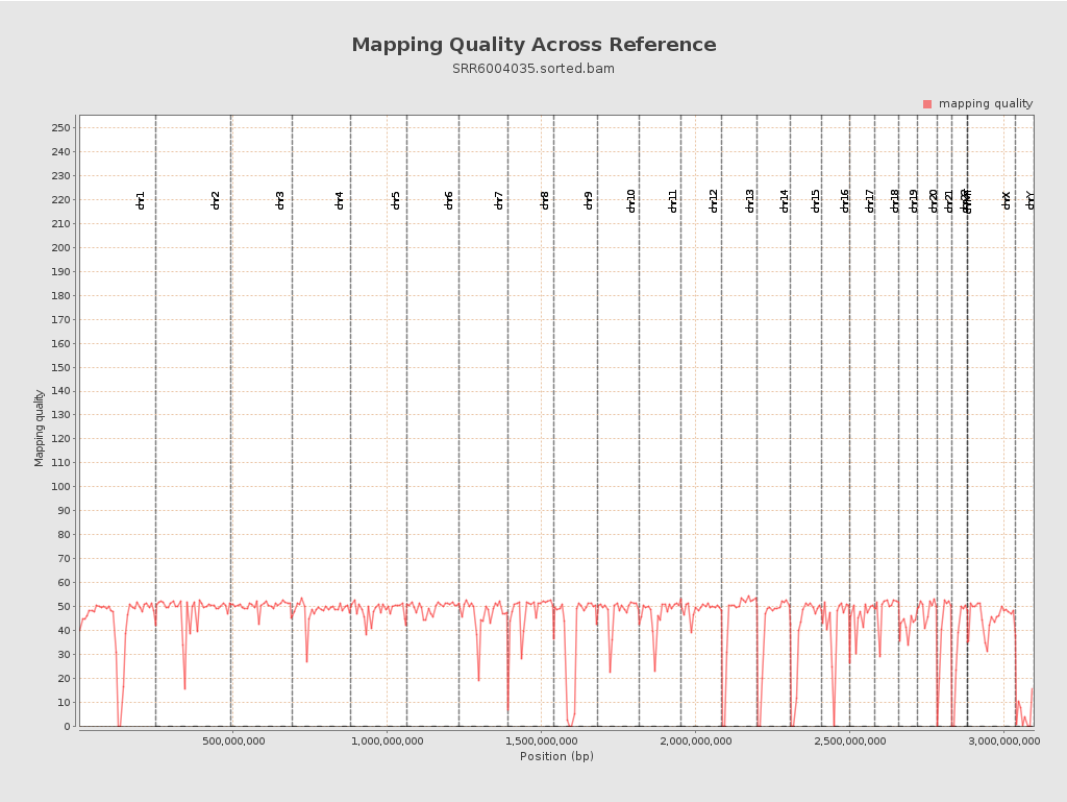
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram