Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:39:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006435.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_SRR1006435 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006435.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:39:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006435.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,109,374
Mapped reads	1,053,368 / 94.95%
Unmapped reads	56,006 / 5.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,059 / 0.28%
Read min/max/mean length	30 / 59 / 57.72
Duplicated reads (estimated)	22,554 / 2.03%
Duplication rate	1.76%
Clipped reads	132,922 / 11.98%

2.2. ACGT Content

Number/percentage of A's	16,645,167 / 28.05%
Number/percentage of C's	12,697,621 / 21.4%
Number/percentage of T's	16,340,222 / 27.54%
Number/percentage of G's	13,623,342 / 22.96%
Number/percentage of N's	36,132 / 0.06%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0192

Standard Deviation	0.1854

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

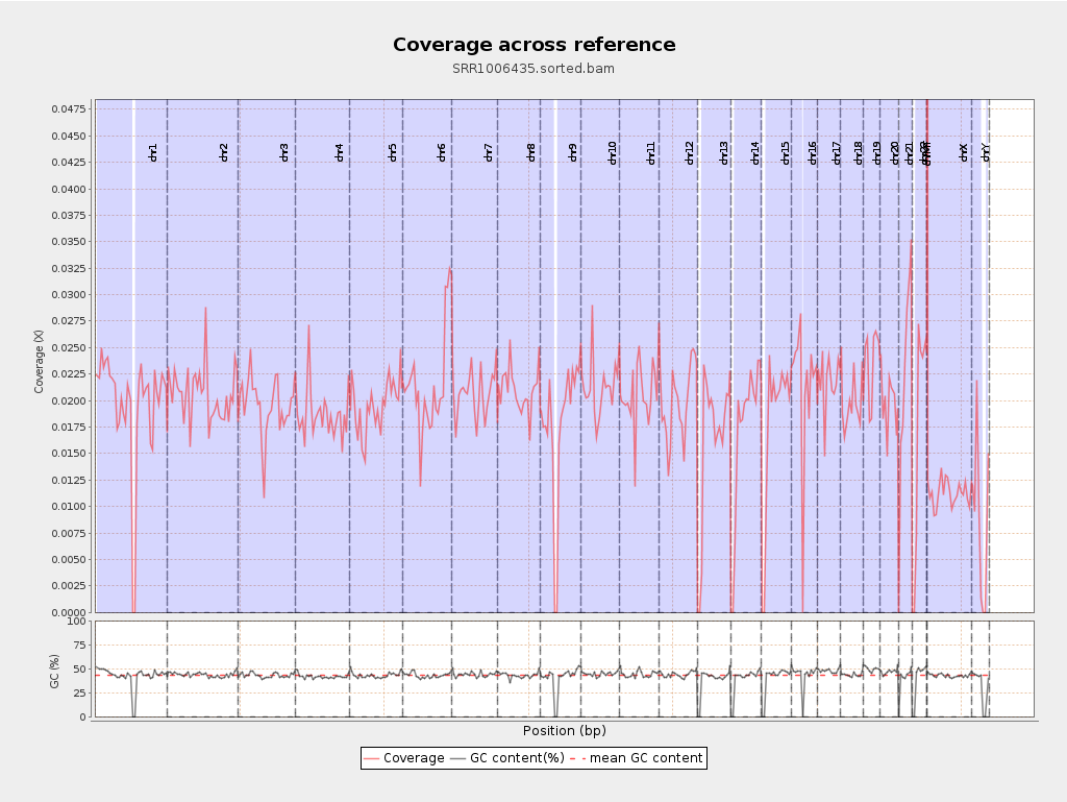
General error rate	0.53%
Mismatches	306,120
Insertions	3,980
Mapped reads with at least one insertion	0.38%
Deletions	10,622
Mapped reads with at least one deletion	1%
Homopolymer indels	41.4%

2.6. Chromosome stats

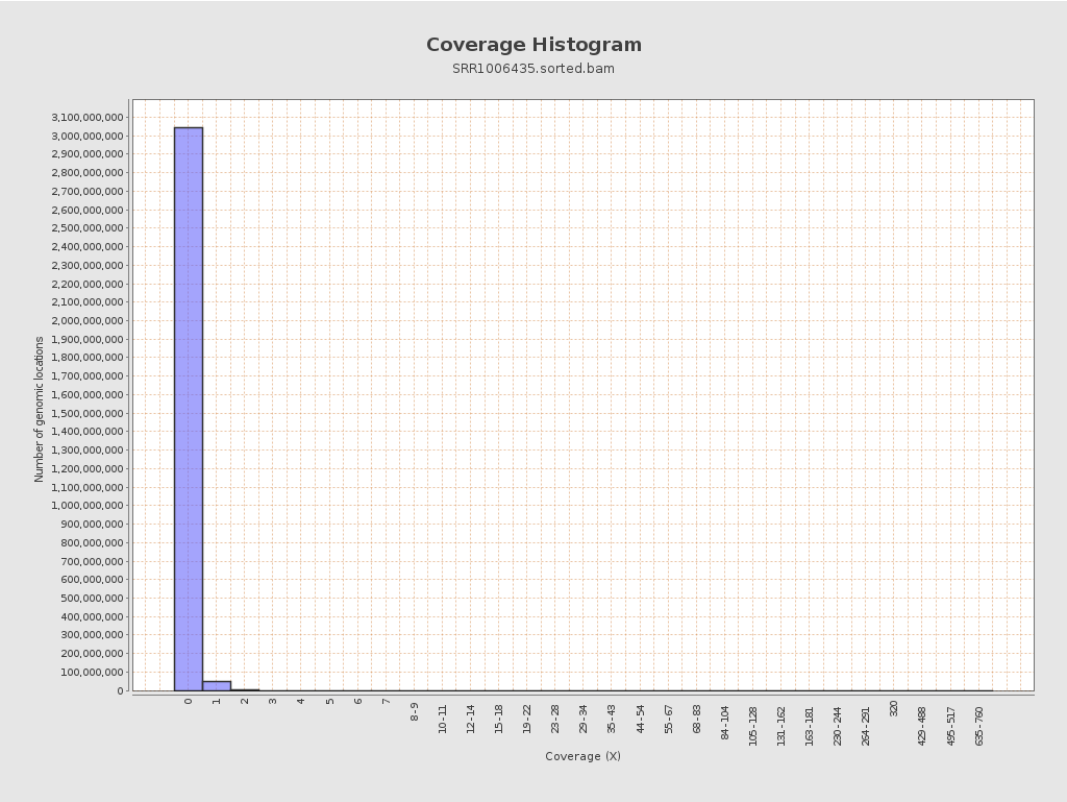
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4881952	0.0196	0.1901
chr2	243199373	5010770	0.0206	0.1774
chr3	198022430	3866542	0.0195	0.1485
chr4	191154276	3599270	0.0188	0.1528
chr5	180915260	3557684	0.0197	0.1497
chr6	171115067	3675660	0.0215	0.1599
chr7	159138663	3303678	0.0208	0.1742

chr8	146364022	3073835	0.021	0.4526
chr9	141213431	2479092	0.0176	0.1495
chr10	135534747	2891646	0.0213	0.1793
chr11	135006516	2763323	0.0205	0.1587
chr12	133851895	2641120	0.0197	0.1512
chr13	115169878	1850392	0.0161	0.1358
chr14	107349540	1833168	0.0171	0.1414
chr15	102531392	1805066	0.0176	0.1418
chr16	90354753	1922442	0.0213	0.1812
chr17	81195210	1767466	0.0218	0.1627
chr18	78077248	1538819	0.0197	0.1814
chr19	59128983	1388699	0.0235	0.1915
chr20	63025520	1238762	0.0197	0.1524
chr21	48129895	1091287	0.0227	0.1711
chr22	51304566	893177	0.0174	0.1545
chrMT	16571	32239	1.9455	1.8211
chrX	155270560	1745463	0.0112	0.114
chrY	59373566	509515	0.0086	0.1429

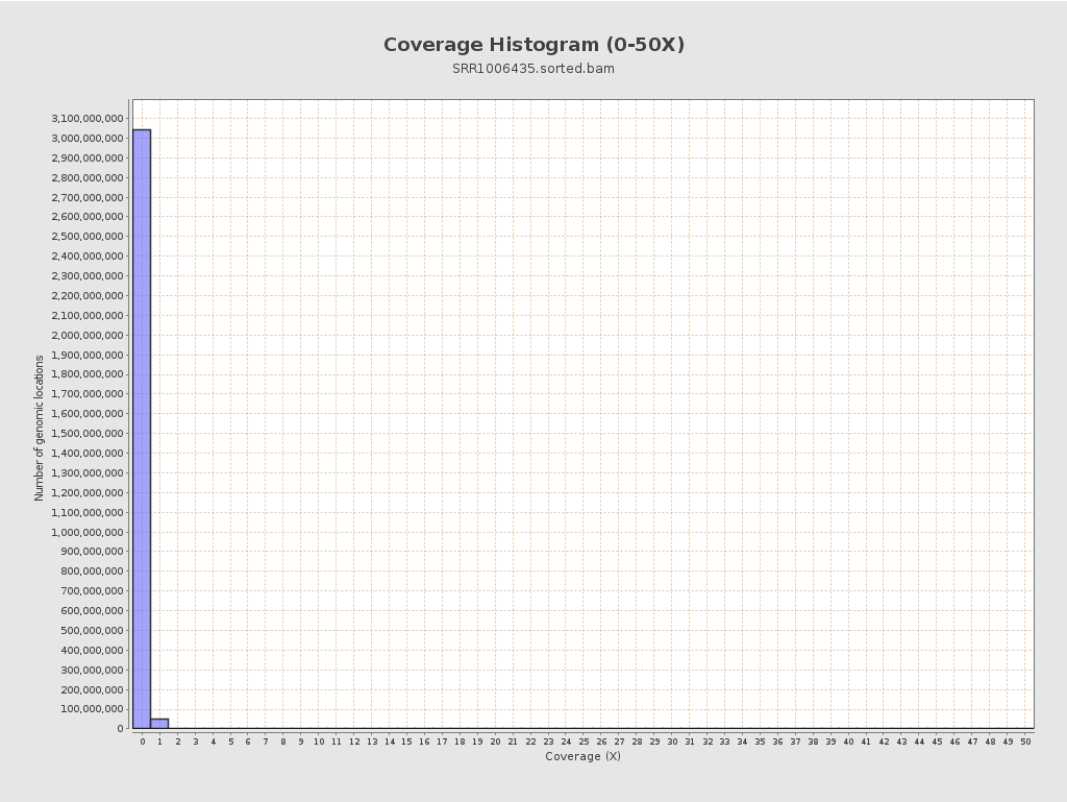
3. Results : Coverage across reference



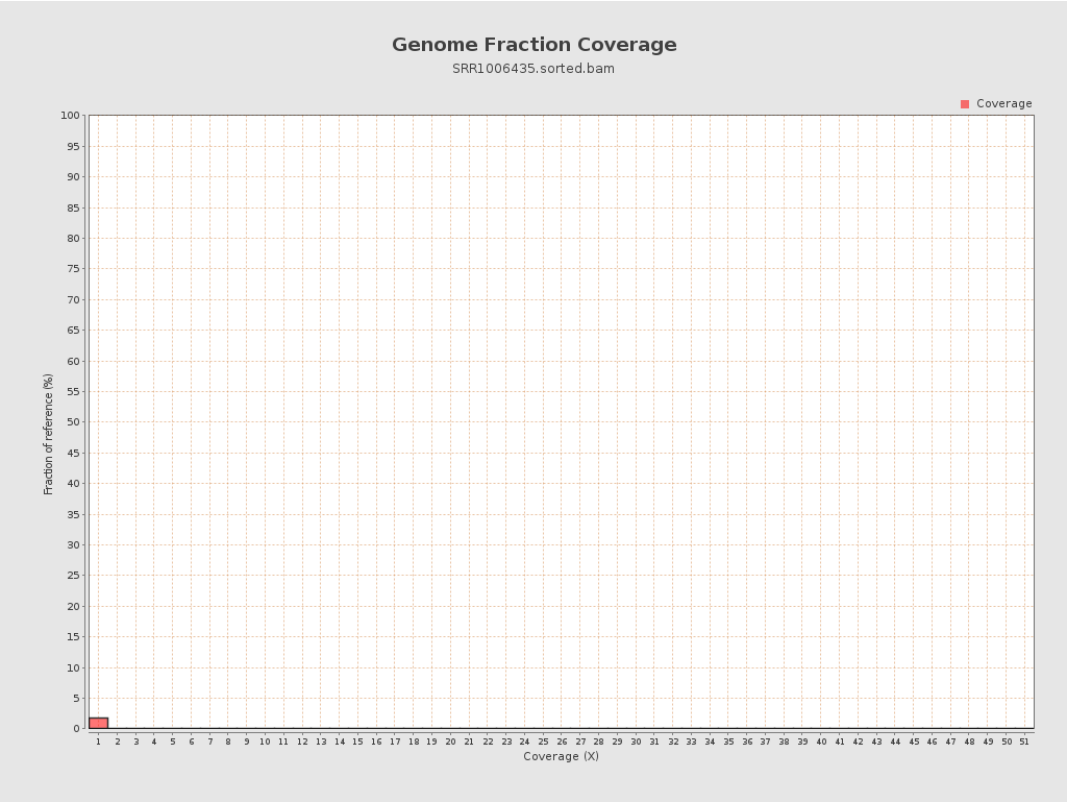
4. Results : Coverage Histogram



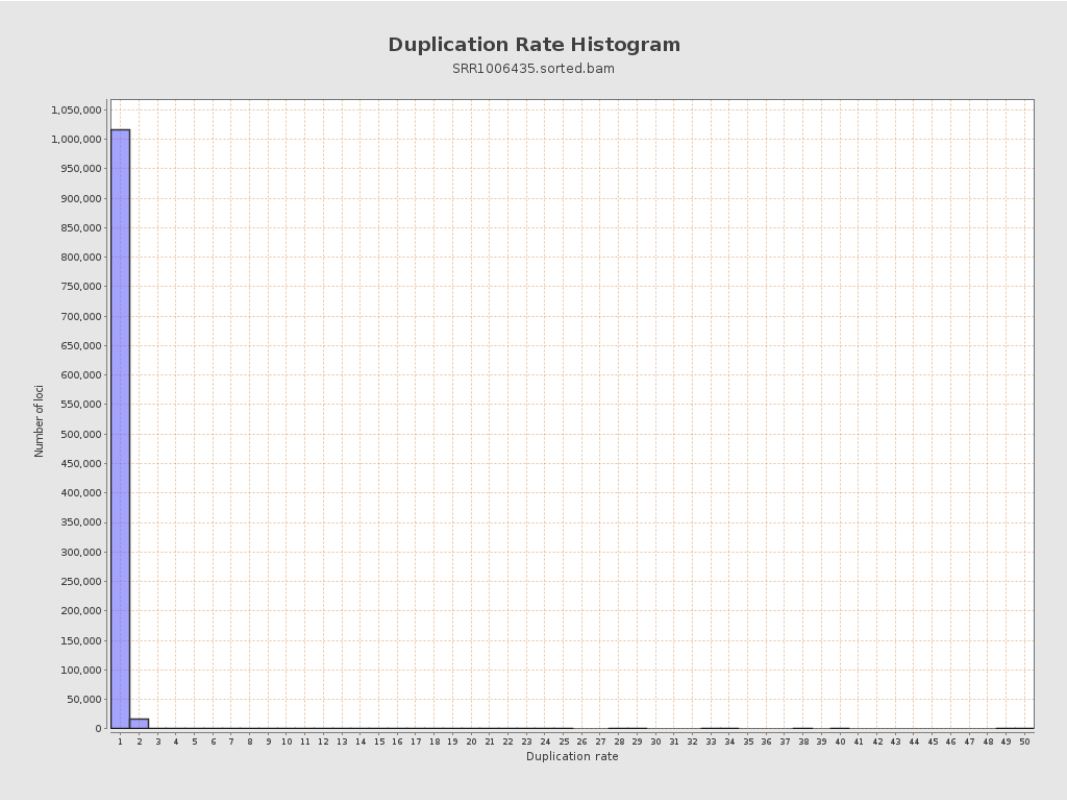
5. Results : Coverage Histogram (0-50X)



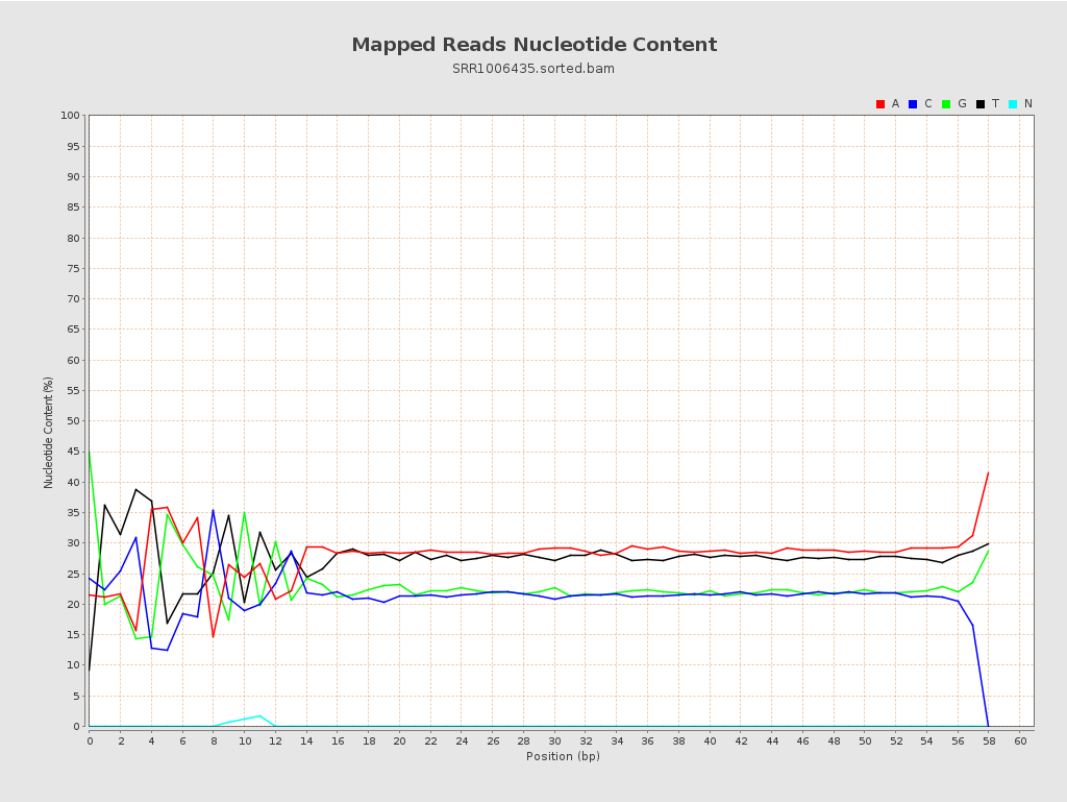
6. Results : Genome Fraction Coverage



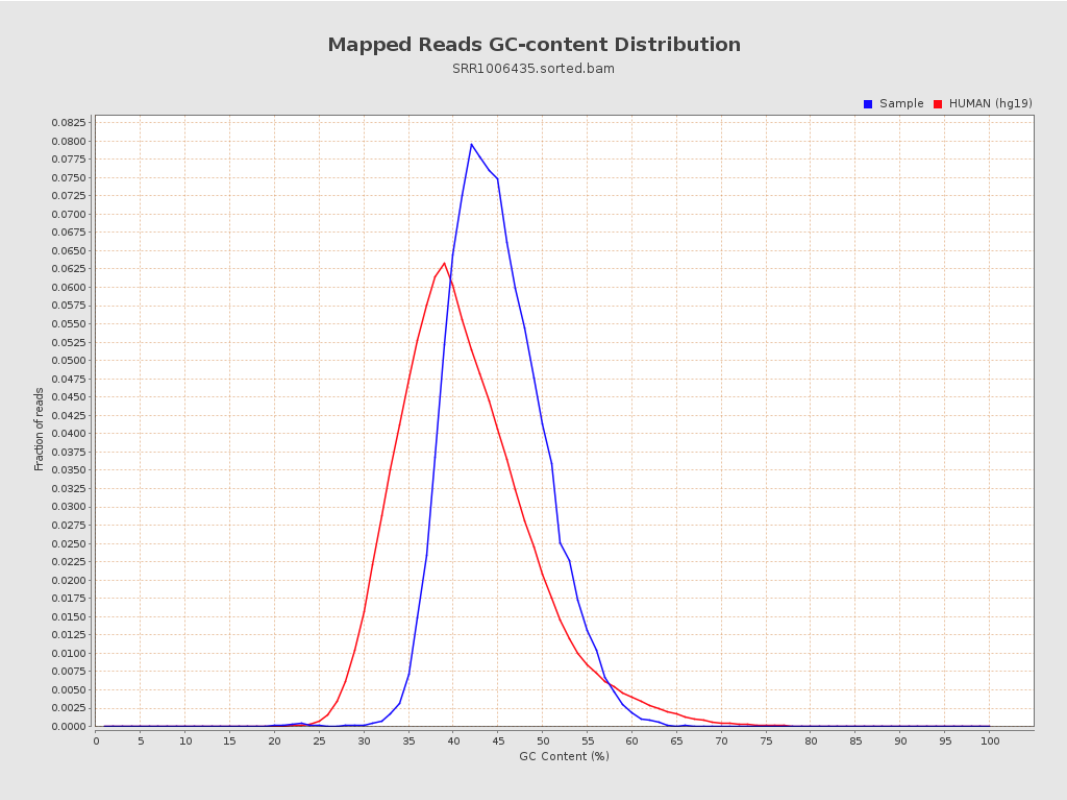
7. Results : Duplication Rate Histogram



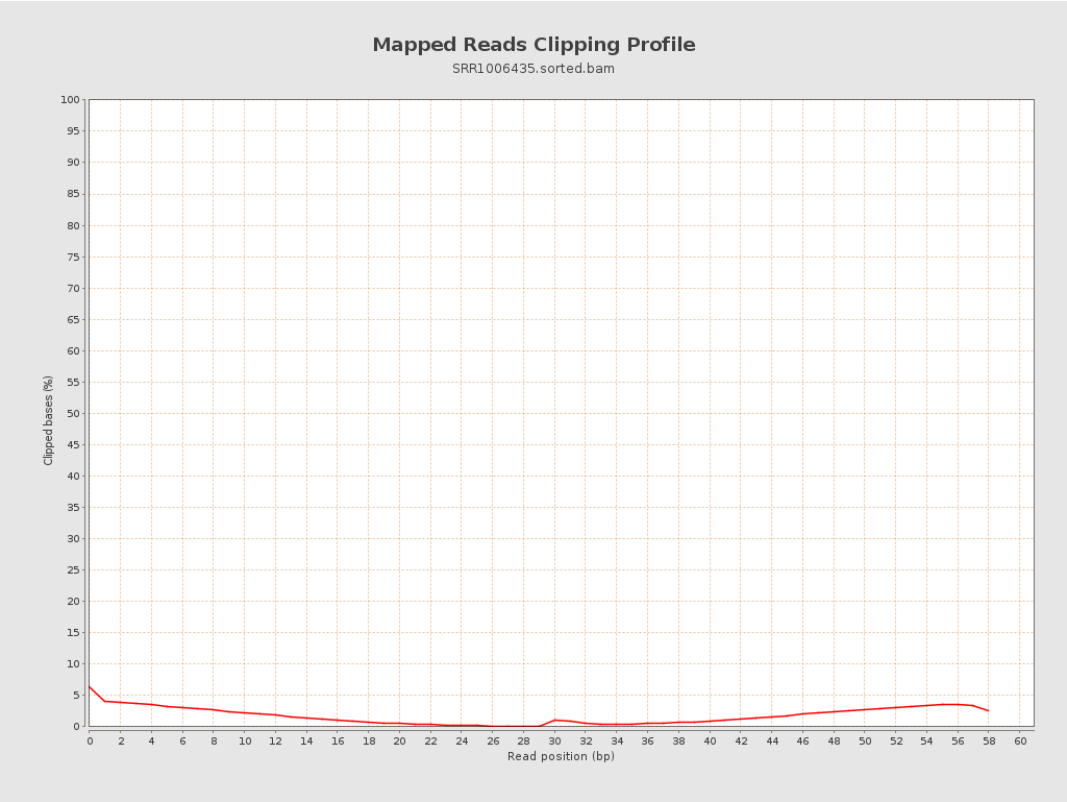
8. Results : Mapped Reads Nucleotide Content



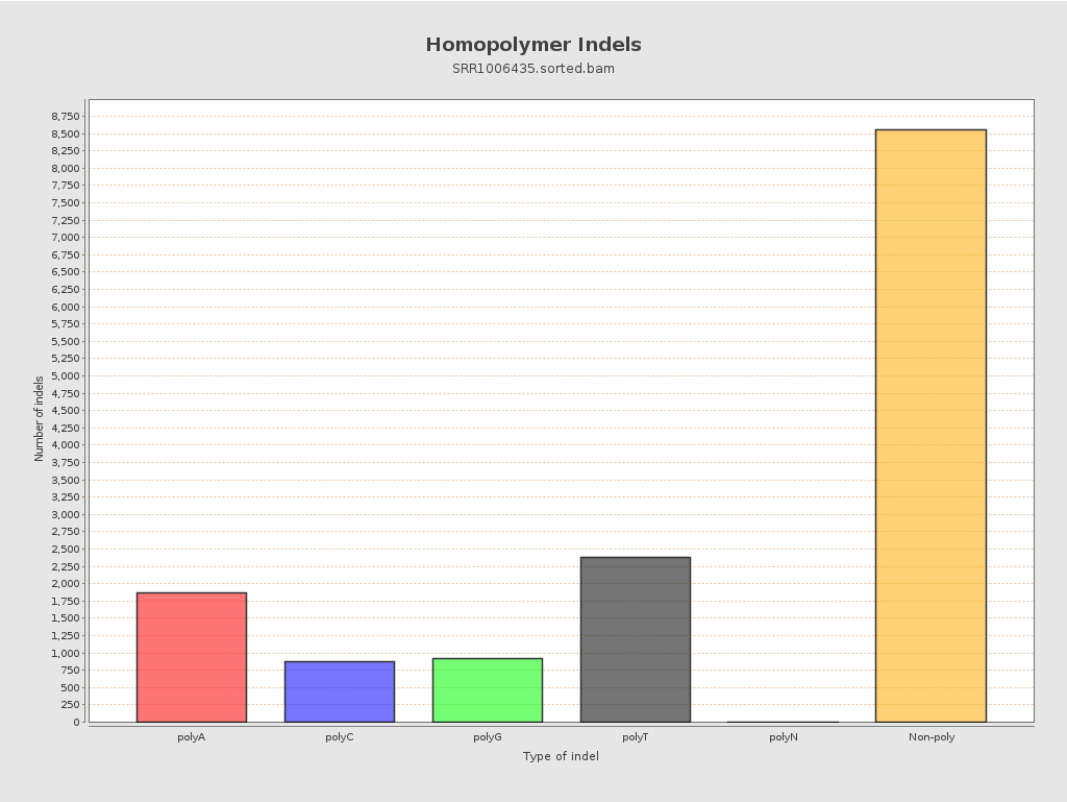
9. Results : Mapped Reads GC-content Distribution



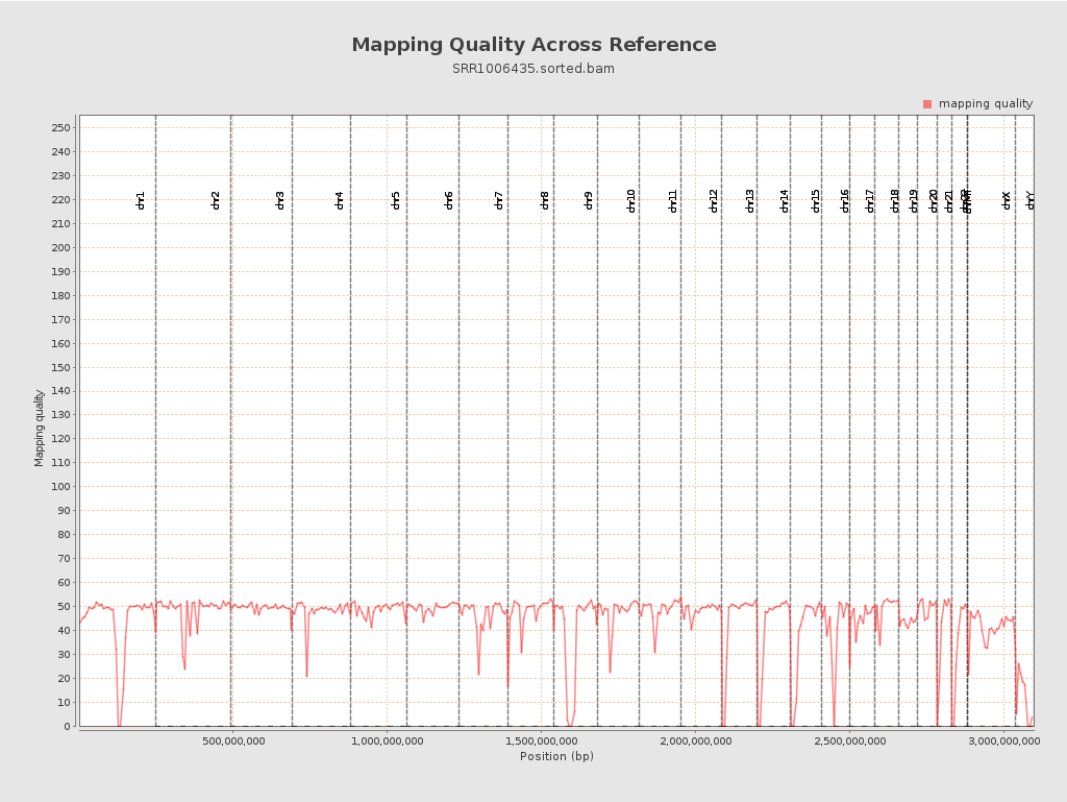
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram