Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:46:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524980.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_SRR10524980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:46:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	978,367
Mapped reads	905,835 / 92.59%
Unmapped reads	72,532 / 7.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,253 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	23,780 / 2.43%
Duplication rate	1.98%
Clipped reads	905,117 / 92.51%

2.2. ACGT Content

Number/percentage of A's	12,814,087 / 24.21%
Number/percentage of C's	10,708,922 / 20.23%
Number/percentage of T's	16,933,694 / 31.99%
Number/percentage of G's	12,474,320 / 23.57%
Number/percentage of N's	604 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1755

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

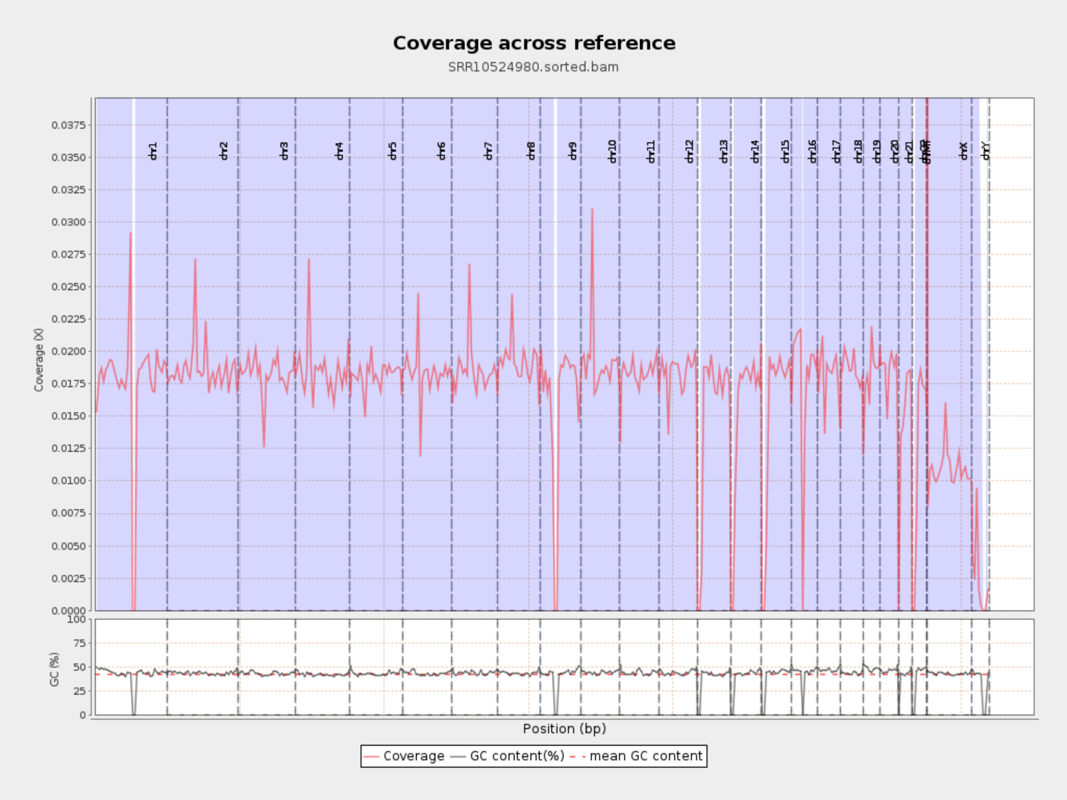
General error rate	0.5%
Mismatches	259,127
Insertions	3,577
Mapped reads with at least one insertion	0.39%
Deletions	10,435
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.81%

2.6. Chromosome stats

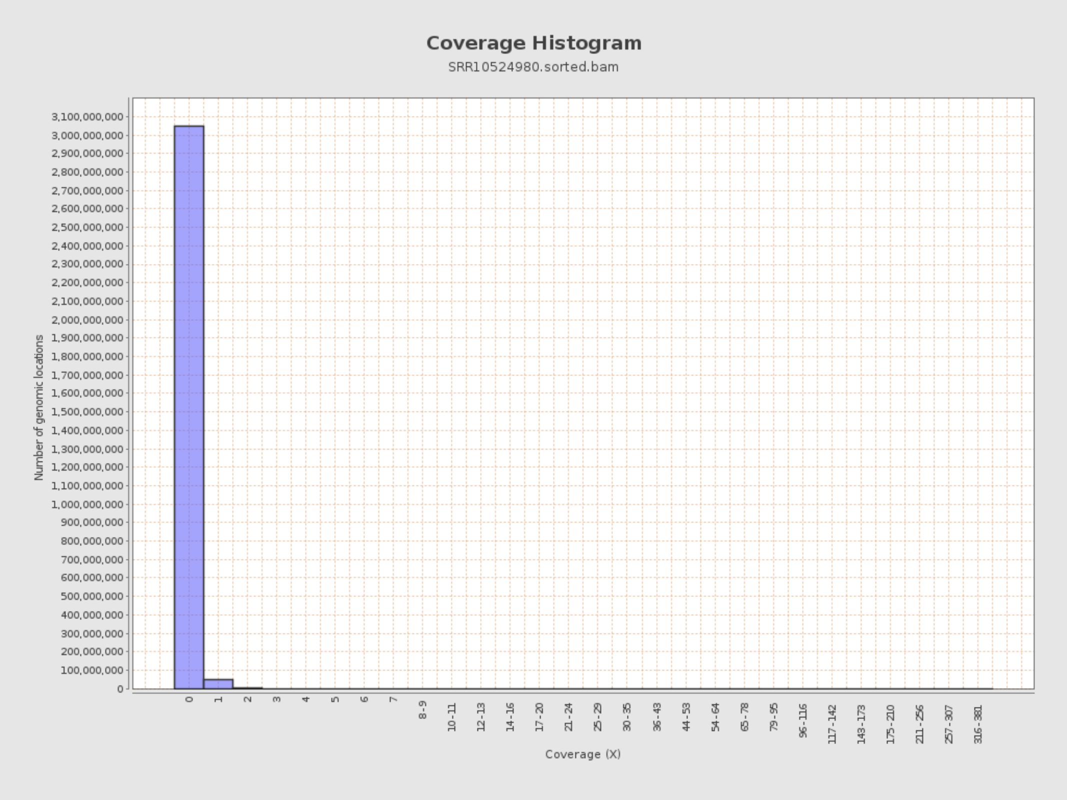
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4364104	0.0175	0.2943
chr2	243199373	4544765	0.0187	0.1941
chr3	198022430	3610685	0.0182	0.1427
chr4	191154276	3548705	0.0186	0.1528
chr5	180915260	3305455	0.0183	0.1428
chr6	171115067	3141917	0.0184	0.1632
chr7	159138663	2962721	0.0186	0.2016

chr8	146364022	2811884	0.0192	0.1849
chr9	141213431	2247020	0.0159	0.1541
chr10	135534747	2615364	0.0193	0.1825
chr11	135006516	2480532	0.0184	0.1718
chr12	133851895	2457314	0.0184	0.144
chr13	115169878	1736677	0.0151	0.1305
chr14	107349540	1626371	0.0152	0.1342
chr15	102531392	1551558	0.0151	0.1343
chr16	90354753	1587107	0.0176	0.1452
chr17	81195210	1468652	0.0181	0.1523
chr18	78077248	1460199	0.0187	0.2287
chr19	59128983	1083642	0.0183	0.2082
chr20	63025520	1159607	0.0184	0.1482
chr21	48129895	705268	0.0147	0.1344
chr22	51304566	623291	0.0121	0.1154
chrMT	16571	7170	0.4327	0.6855
chrX	155270560	1706825	0.011	0.121
chrY	59373566	142574	0.0024	0.081

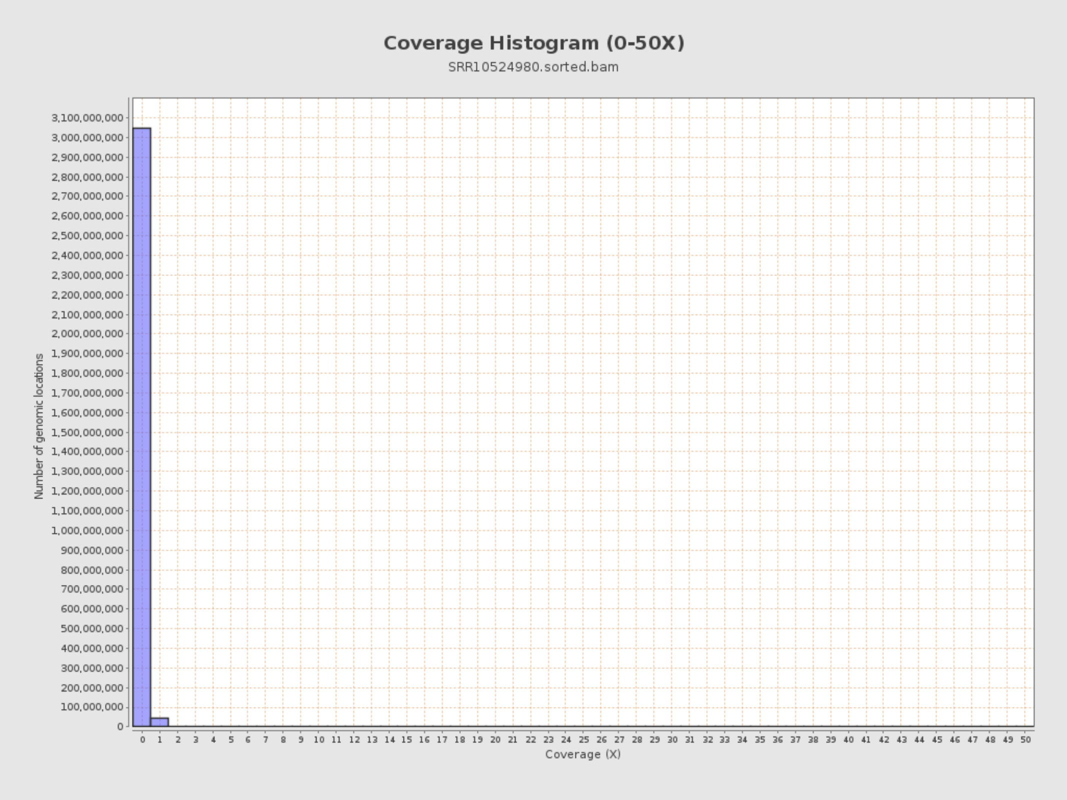
3. Results : Coverage across reference



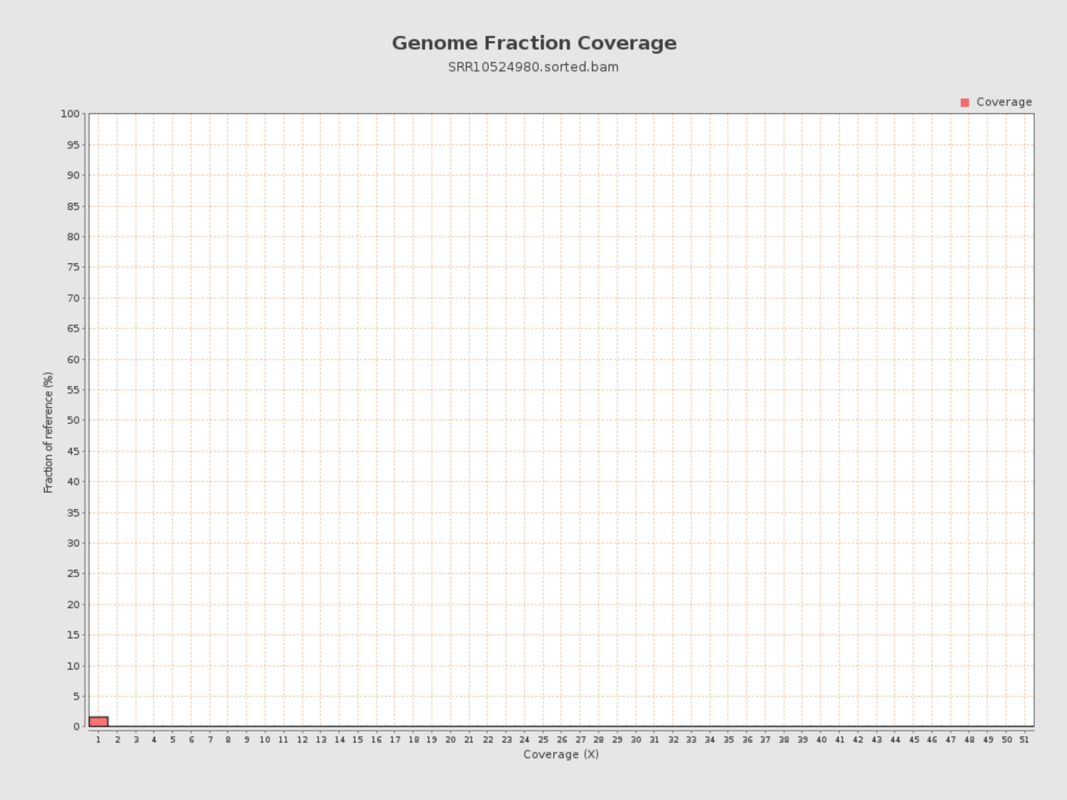
4. Results : Coverage Histogram



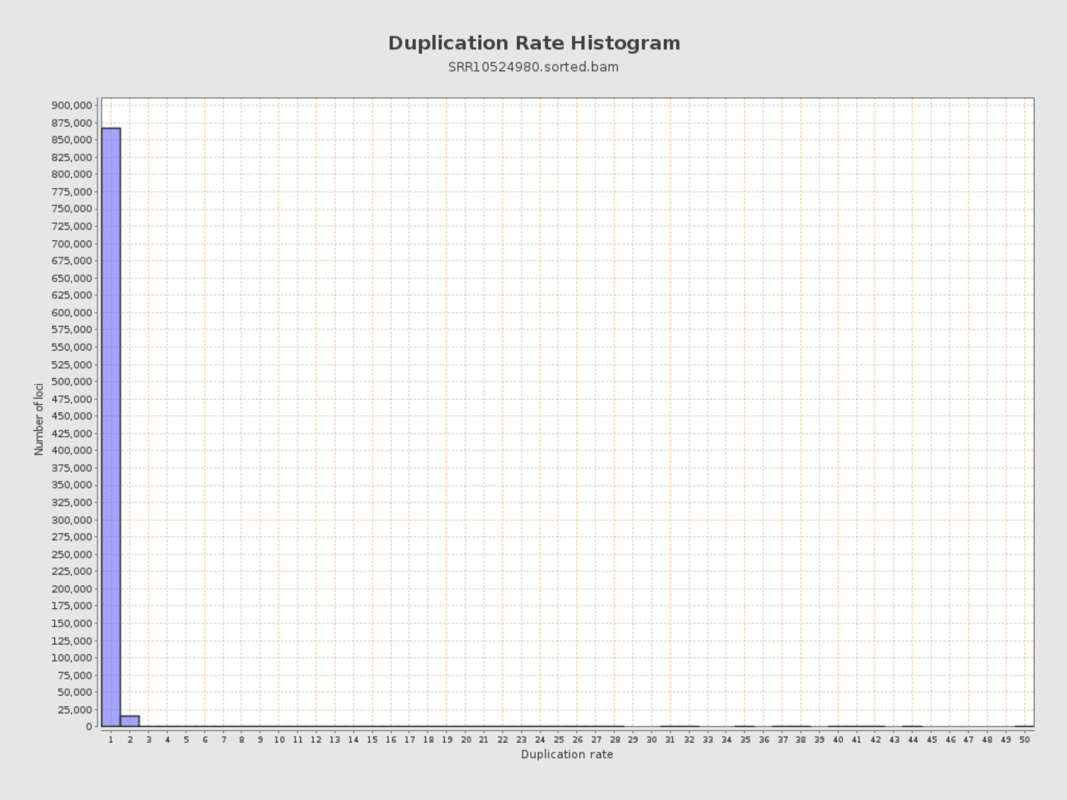
5. Results : Coverage Histogram (0-50X)



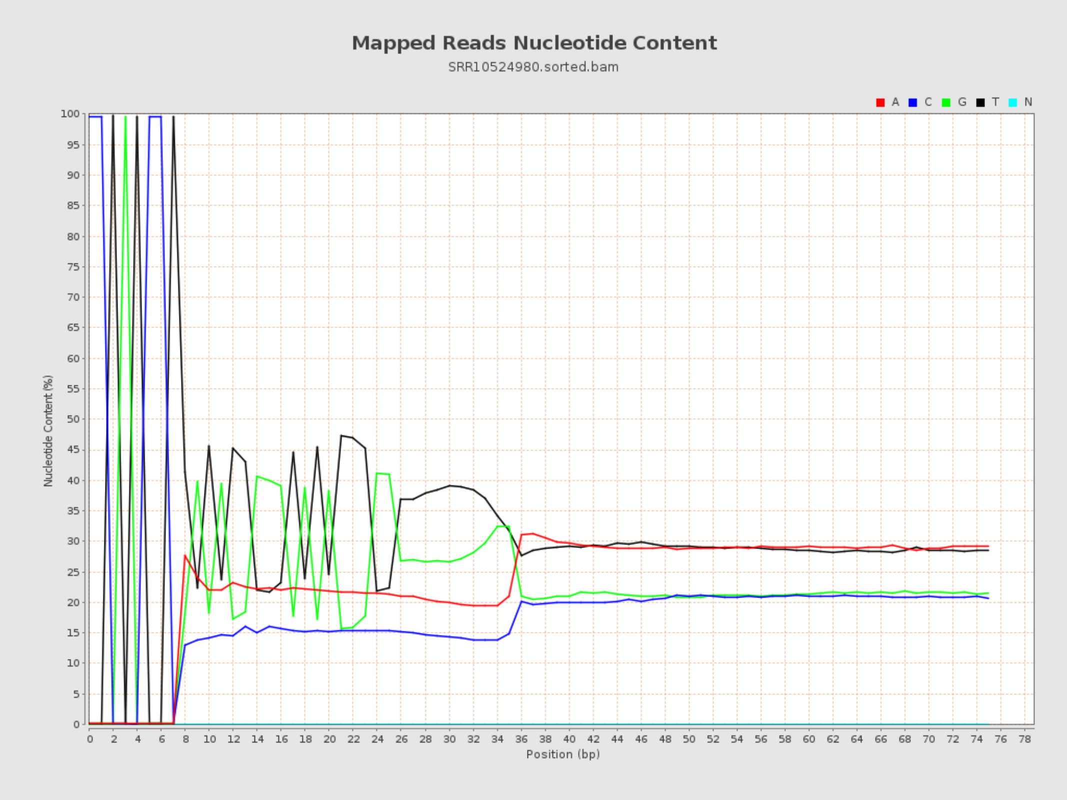
6. Results : Genome Fraction Coverage



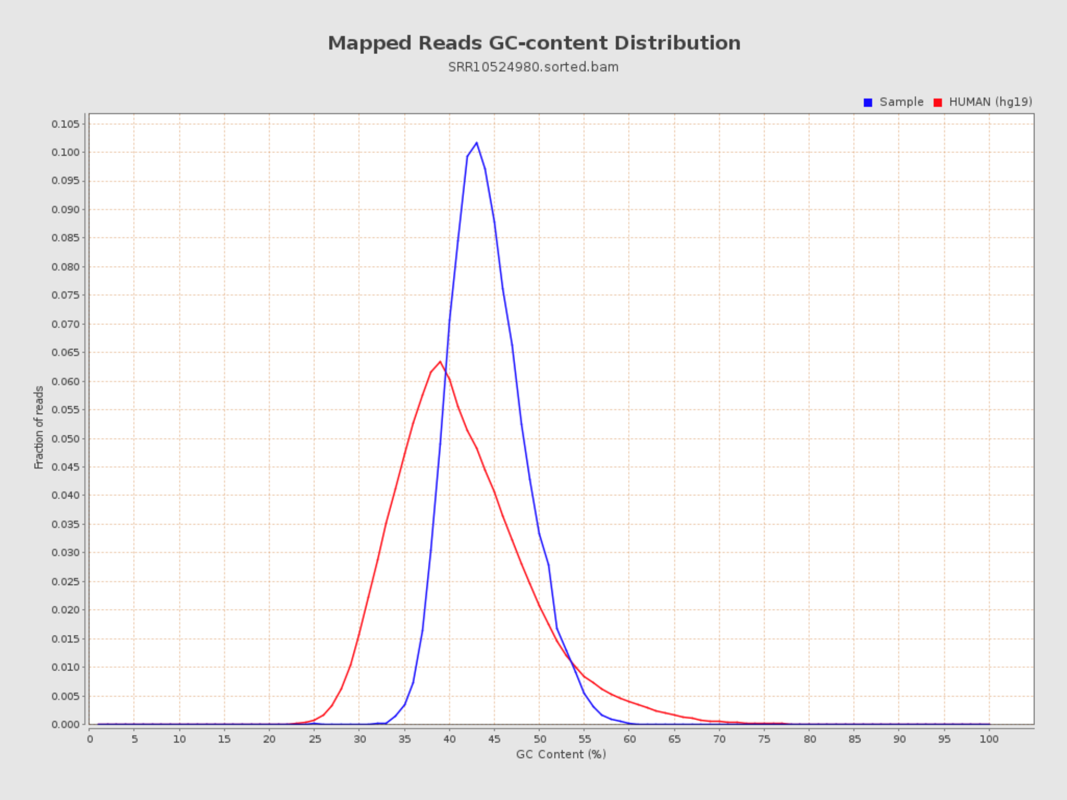
7. Results : Duplication Rate Histogram



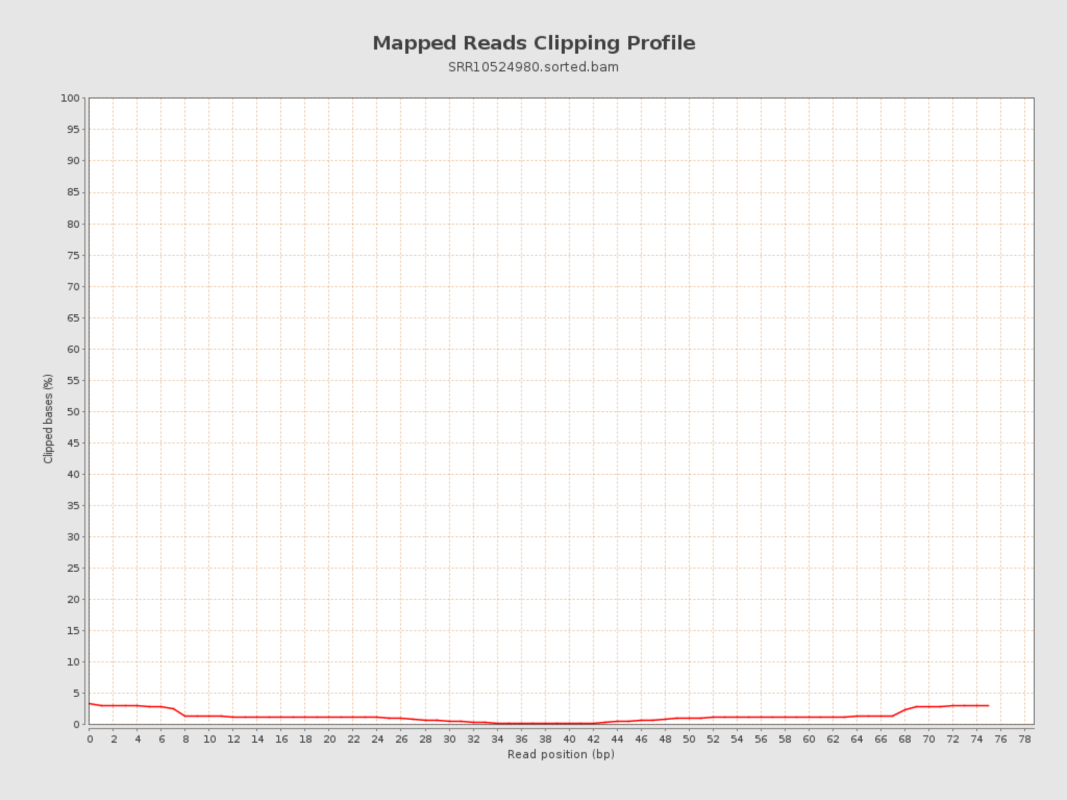
8. Results : Mapped Reads Nucleotide Content



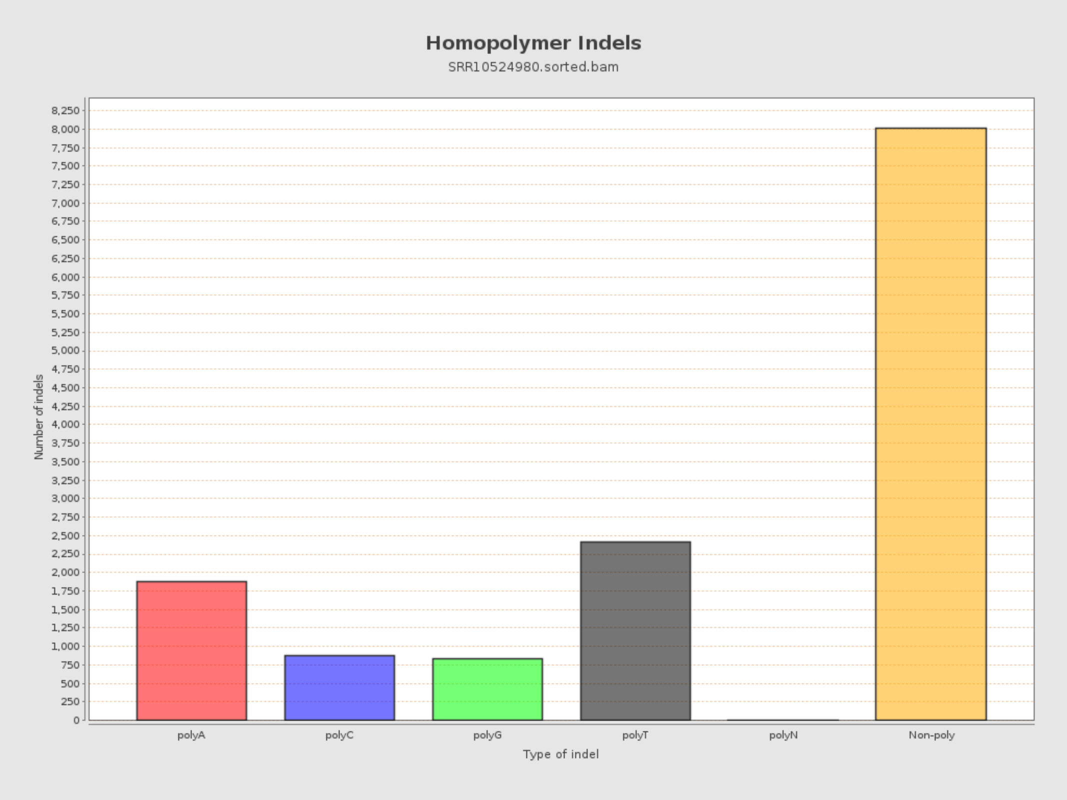
9. Results : Mapped Reads GC-content Distribution



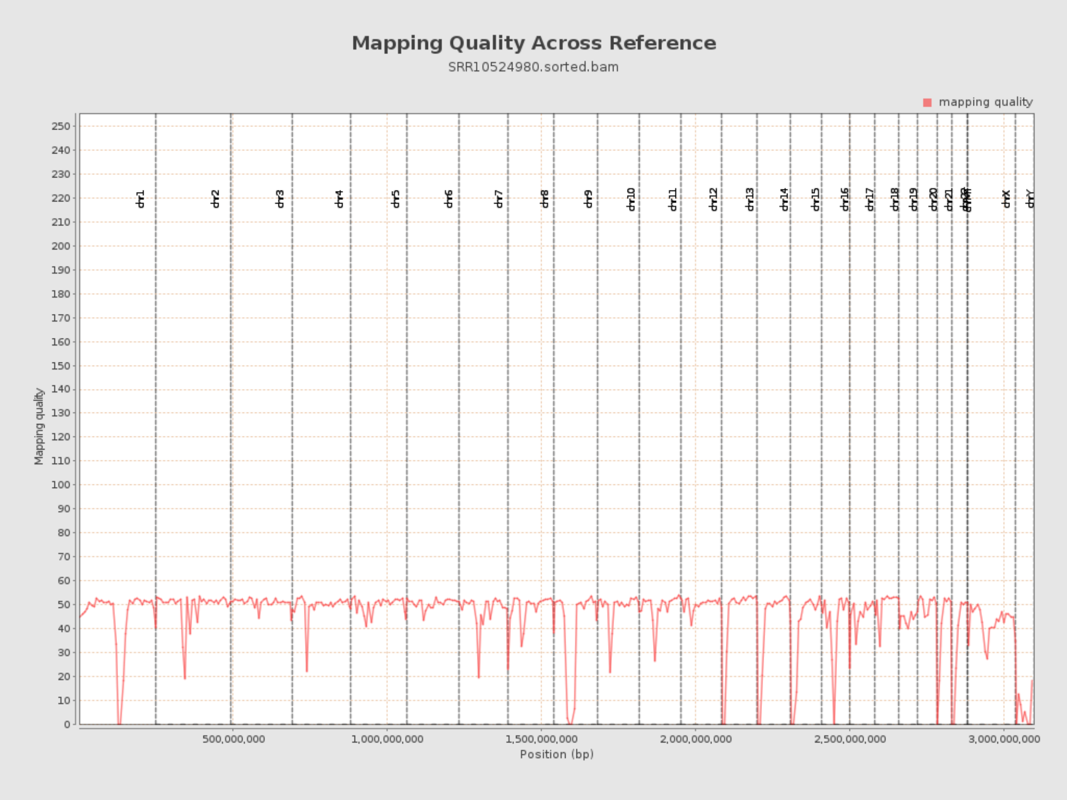
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram