Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 20:51:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524280.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_SRR10524280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 20:51:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,358,908
Mapped reads	1,255,261 / 92.37%
Unmapped reads	103,647 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,526 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	40,584 / 2.99%
Duplication rate	2.29%
Clipped reads	1,259,495 / 92.68%

2.2. ACGT Content

Number/percentage of A's	18,095,550 / 24.55%
Number/percentage of C's	14,236,872 / 19.31%
Number/percentage of T's	23,072,971 / 31.3%
Number/percentage of G's	18,299,319 / 24.82%
Number/percentage of N's	9,122 / 0.01%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2563

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

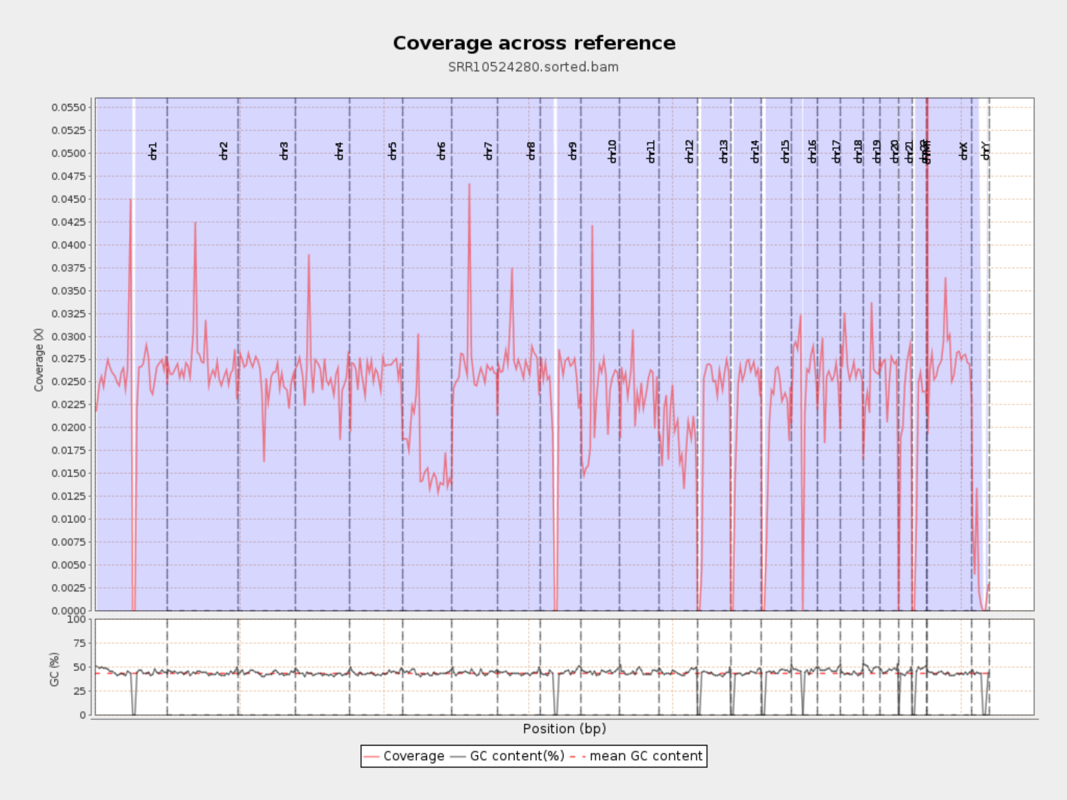
General error rate	0.5%
Mismatches	359,692
Insertions	4,332
Mapped reads with at least one insertion	0.34%
Deletions	13,703
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.1%

2.6. Chromosome stats

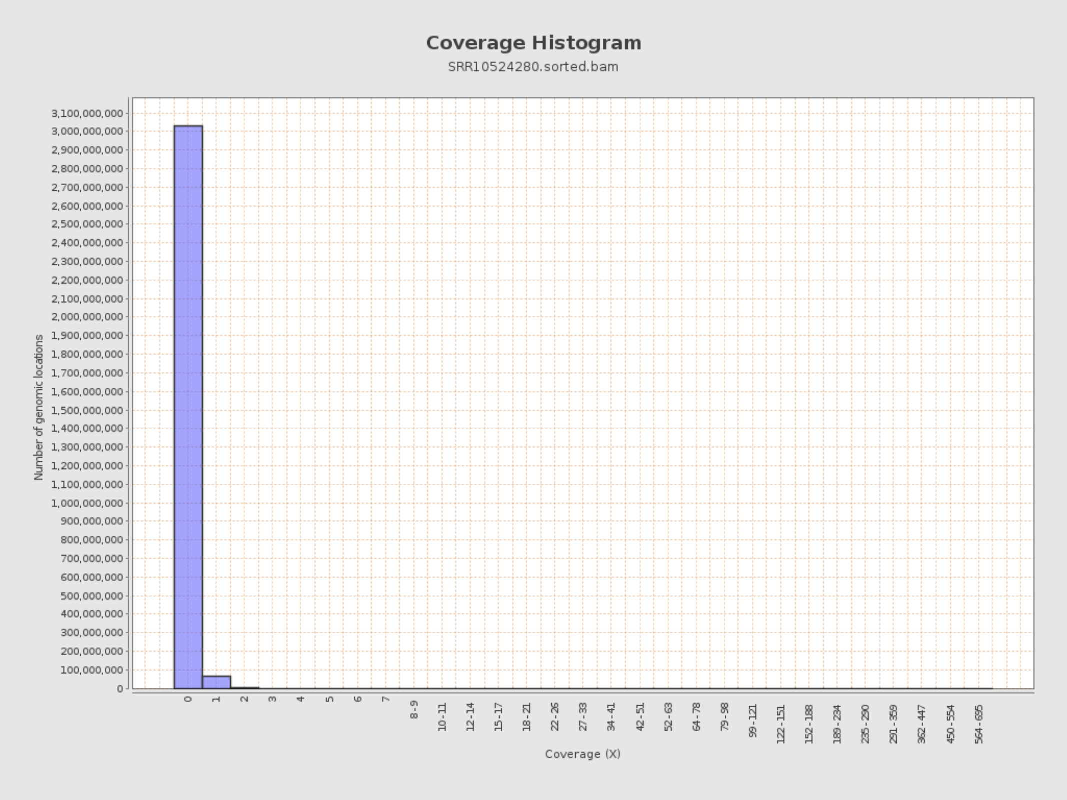
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6185918	0.0248	0.5116
chr2	243199373	6574917	0.027	0.2649
chr3	198022430	5046142	0.0255	0.1697
chr4	191154276	4969513	0.026	0.1872
chr5	180915260	4751356	0.0263	0.1725
chr6	171115067	2896558	0.0169	0.1573
chr7	159138663	4291178	0.027	0.3484

chr8	146364022	4040508	0.0276	0.2376
chr9	141213431	3266847	0.0231	0.2208
chr10	135534747	3140101	0.0232	0.2327
chr11	135006516	3303364	0.0245	0.2261
chr12	133851895	2567173	0.0192	0.1531
chr13	115169878	2473990	0.0215	0.1562
chr14	107349540	2353294	0.0219	0.1668
chr15	102531392	1942869	0.0189	0.1461
chr16	90354753	2235843	0.0247	0.1821
chr17	81195210	2038564	0.0251	0.1811
chr18	78077248	2104066	0.0269	0.438
chr19	59128983	1497657	0.0253	0.3508
chr20	63025520	1621395	0.0257	0.1738
chr21	48129895	1047001	0.0218	0.17
chr22	51304566	882941	0.0172	0.1391
chrMT	16571	7555	0.4559	0.7414
chrX	155270560	4270067	0.0275	0.1997
chrY	59373566	226752	0.0038	0.1094

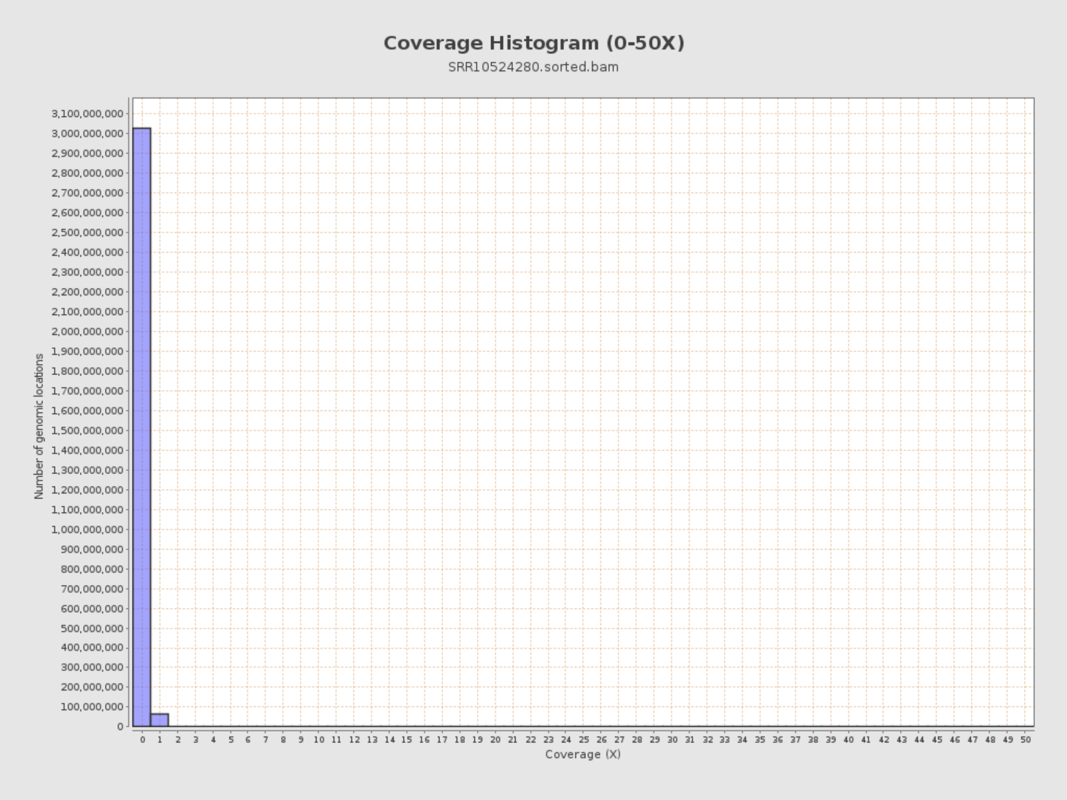
3. Results : Coverage across reference



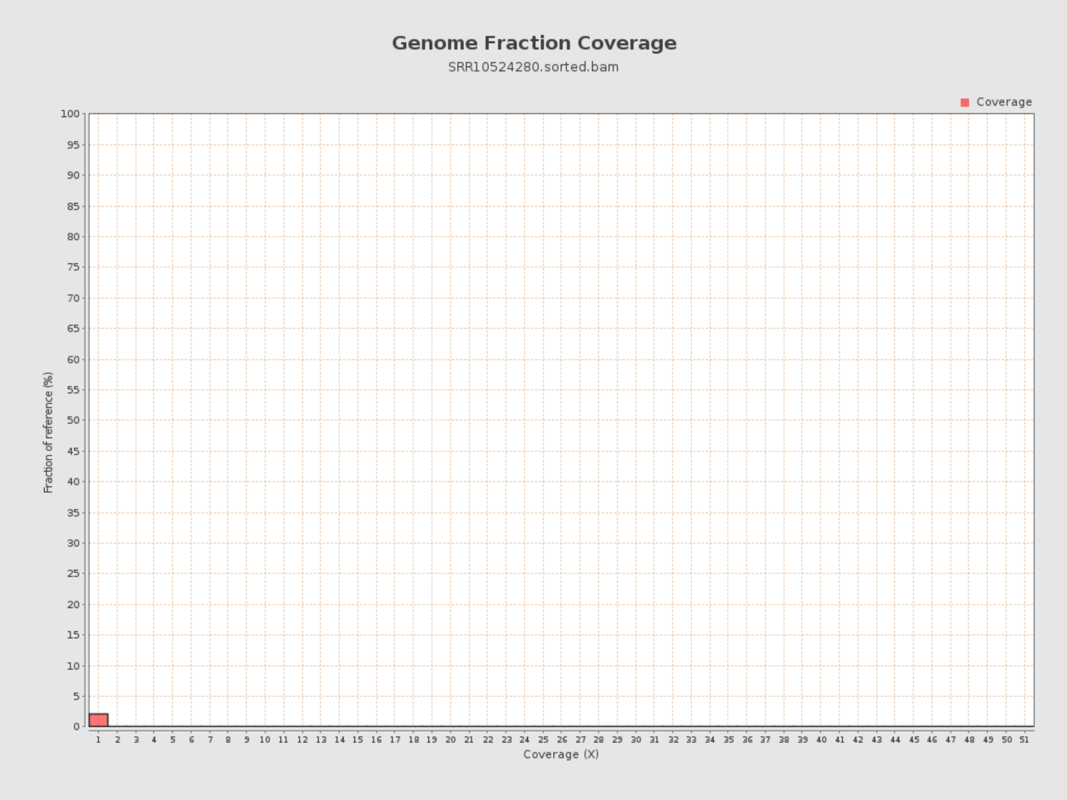
4. Results : Coverage Histogram



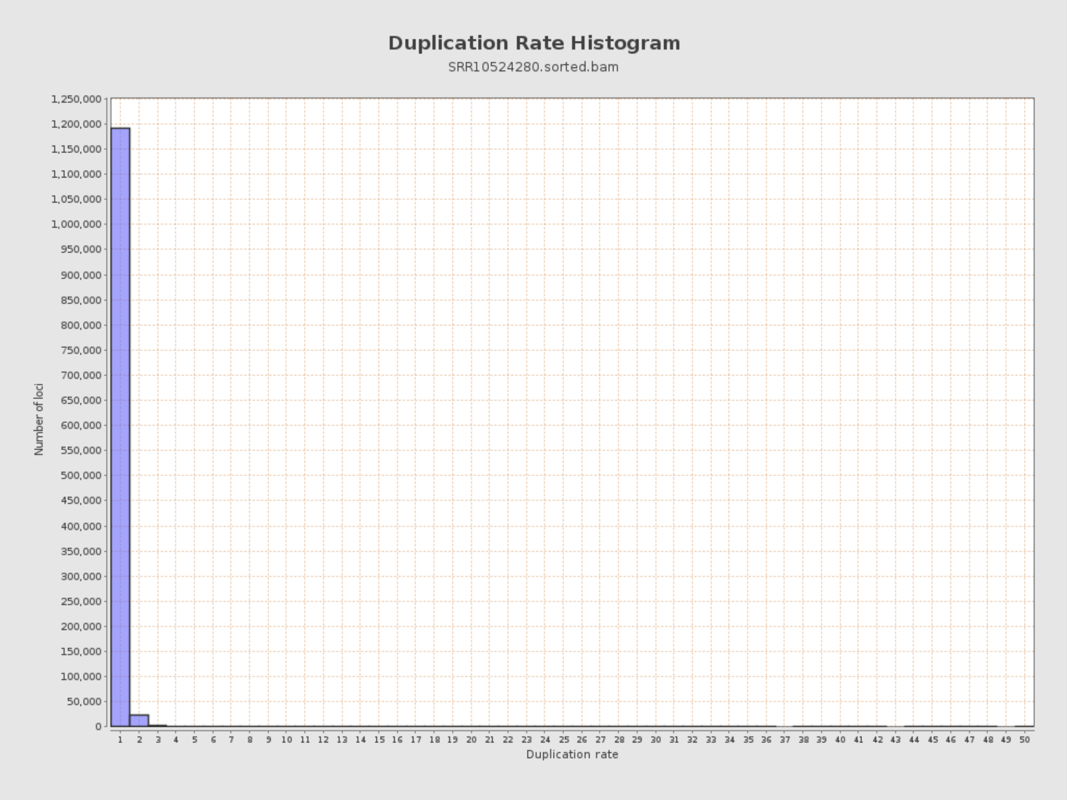
5. Results : Coverage Histogram (0-50X)



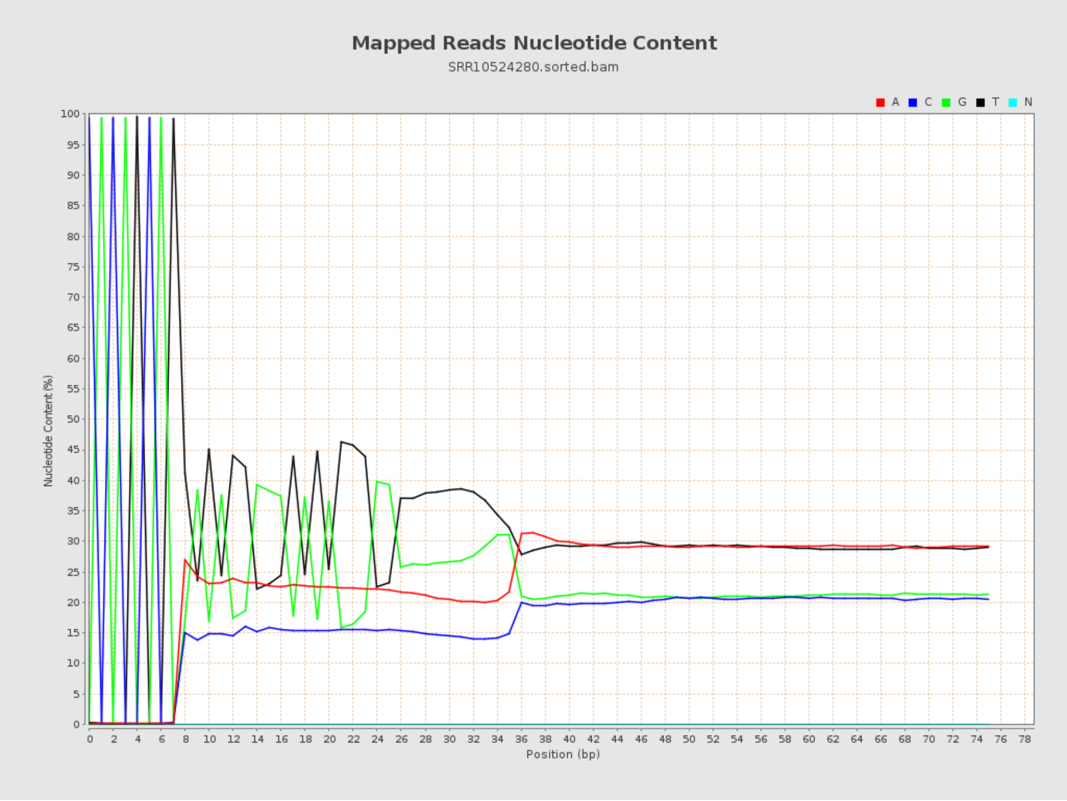
6. Results : Genome Fraction Coverage



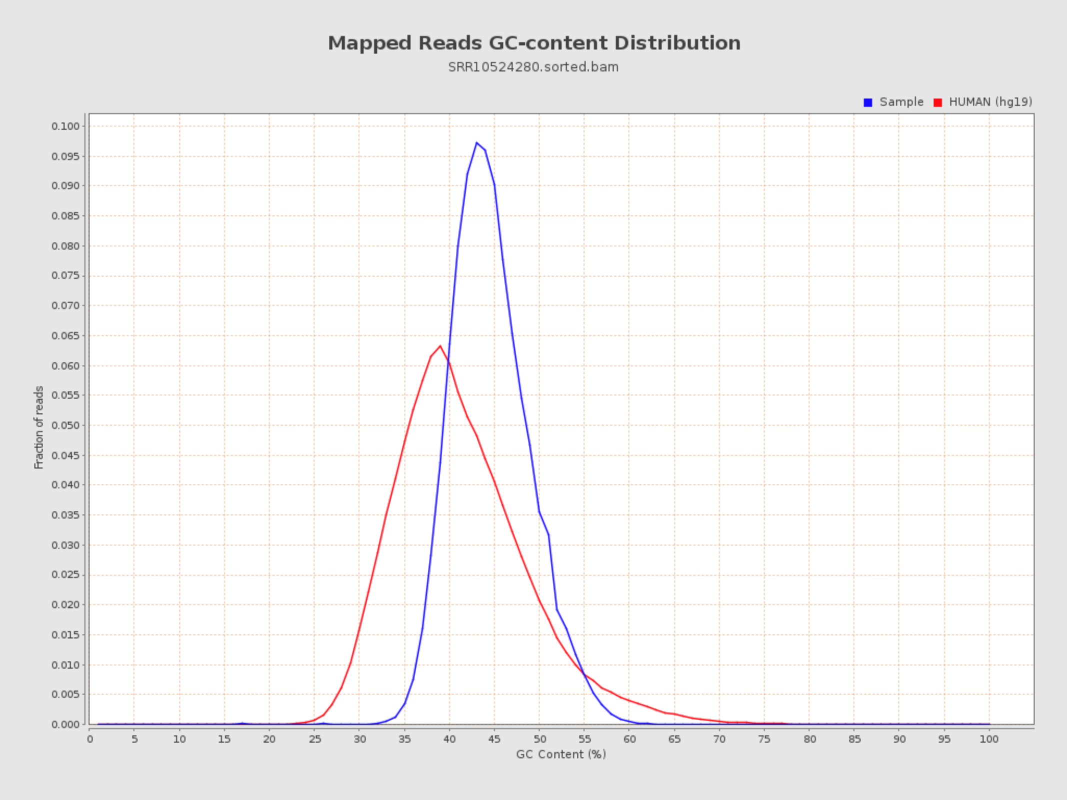
7. Results : Duplication Rate Histogram



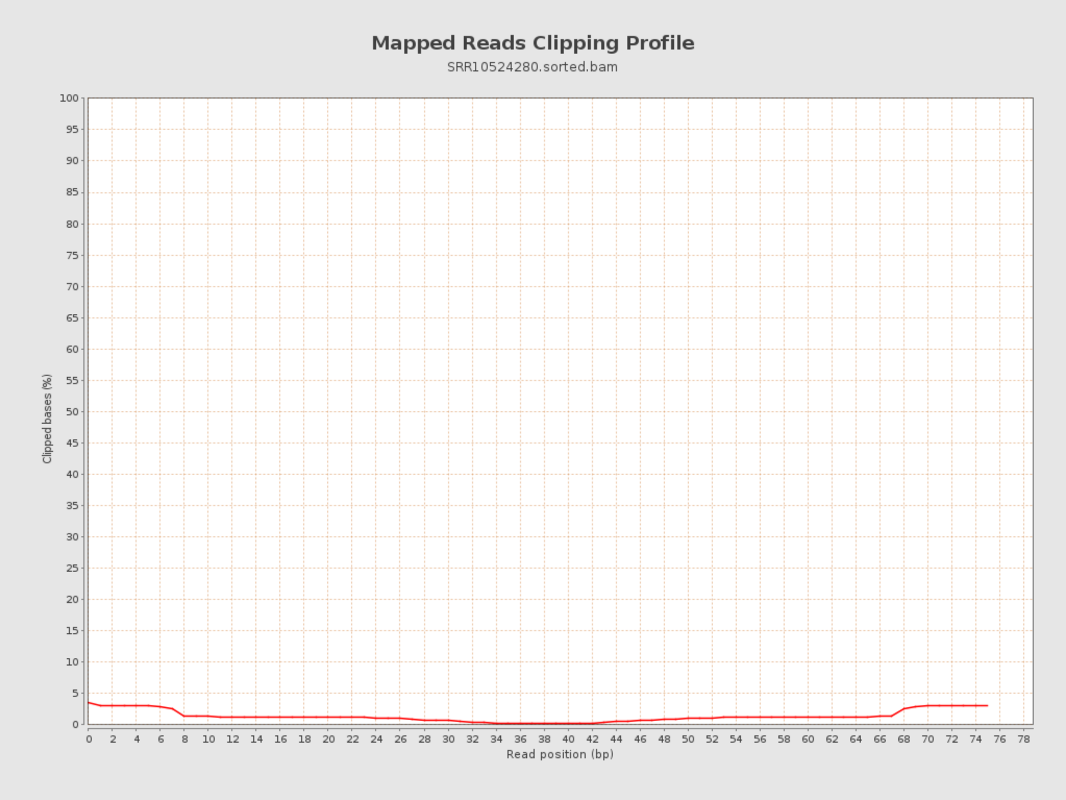
8. Results : Mapped Reads Nucleotide Content



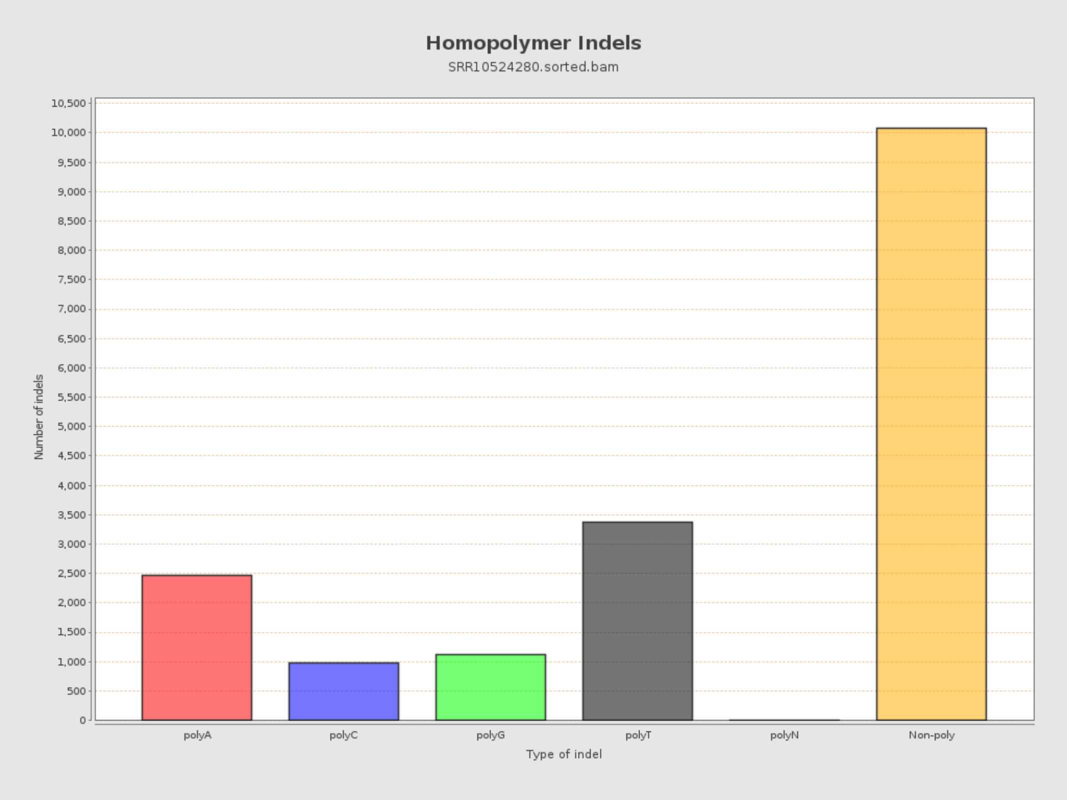
9. Results : Mapped Reads GC-content Distribution



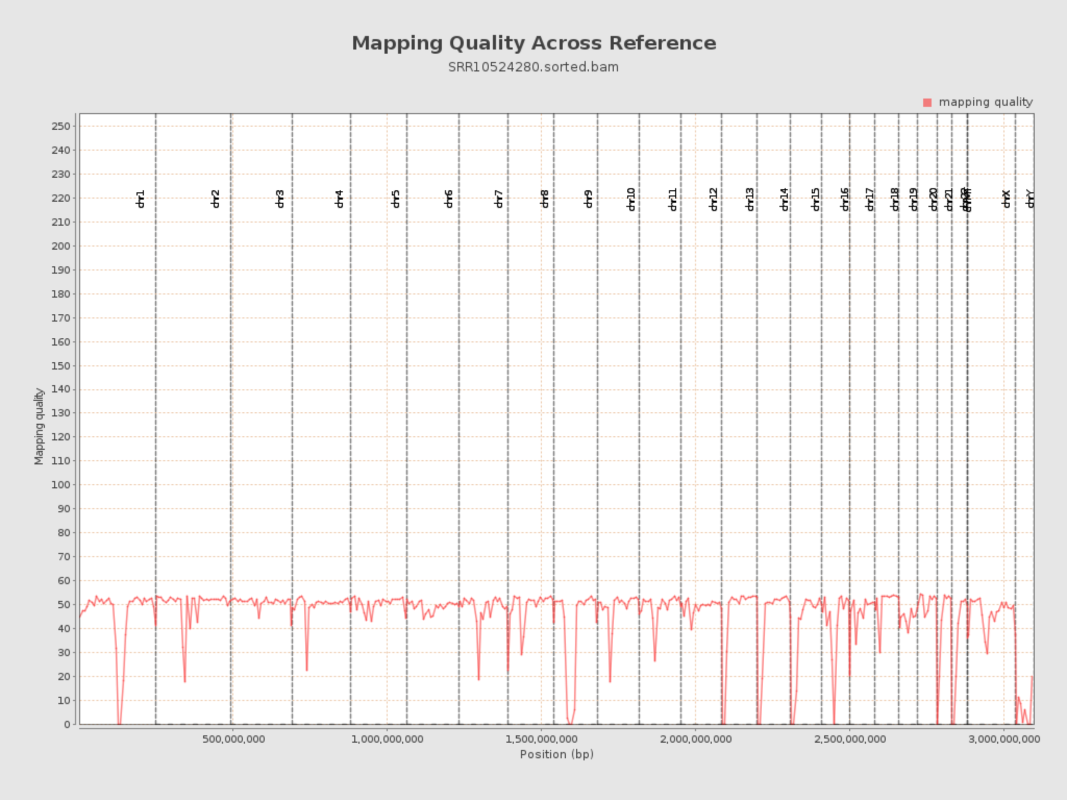
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram