Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:11:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524880.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_SRR10524880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524880.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:11:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,206,890
Mapped reads	1,113,508 / 92.26%
Unmapped reads	93,382 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,263 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	35,253 / 2.92%
Duplication rate	2.29%
Clipped reads	1,114,607 / 92.35%

2.2. ACGT Content

Number/percentage of A's	17,042,805 / 26.08%
Number/percentage of C's	11,528,885 / 17.64%
Number/percentage of T's	20,511,932 / 31.39%
Number/percentage of G's	16,254,996 / 24.87%
Number/percentage of N's	8,685 / 0.01%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.2281

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

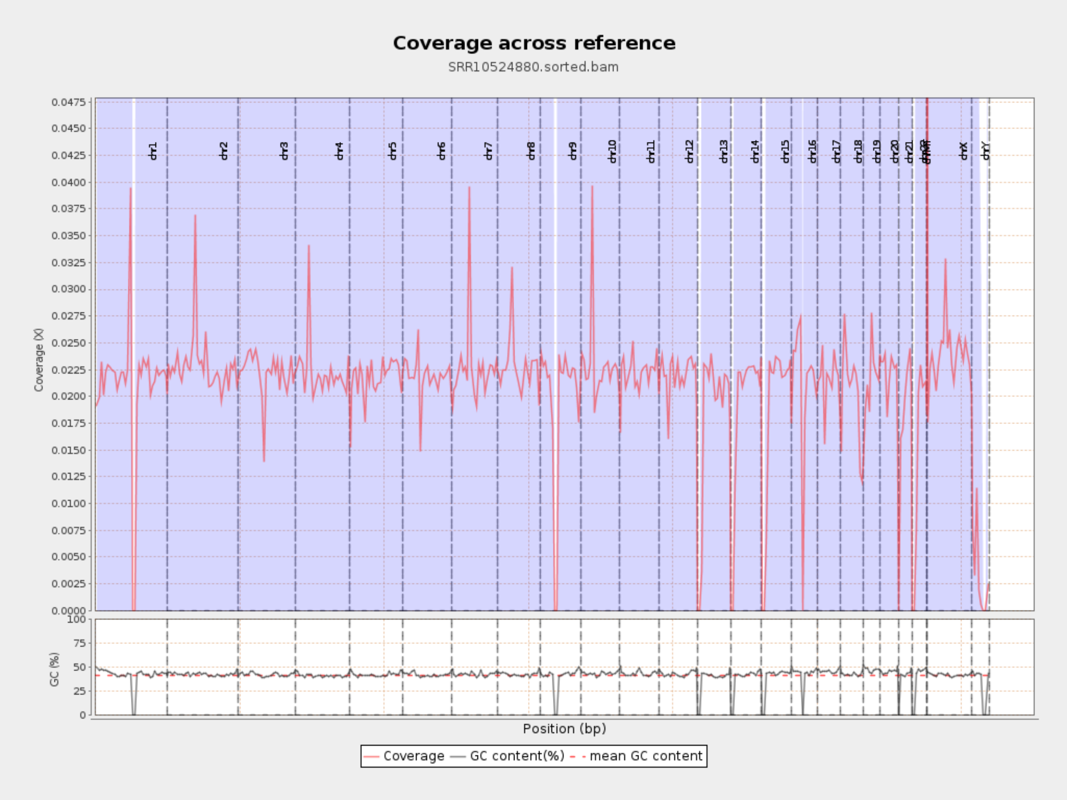
General error rate	0.5%
Mismatches	319,251
Insertions	4,298
Mapped reads with at least one insertion	0.38%
Deletions	12,235
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.39%

2.6. Chromosome stats

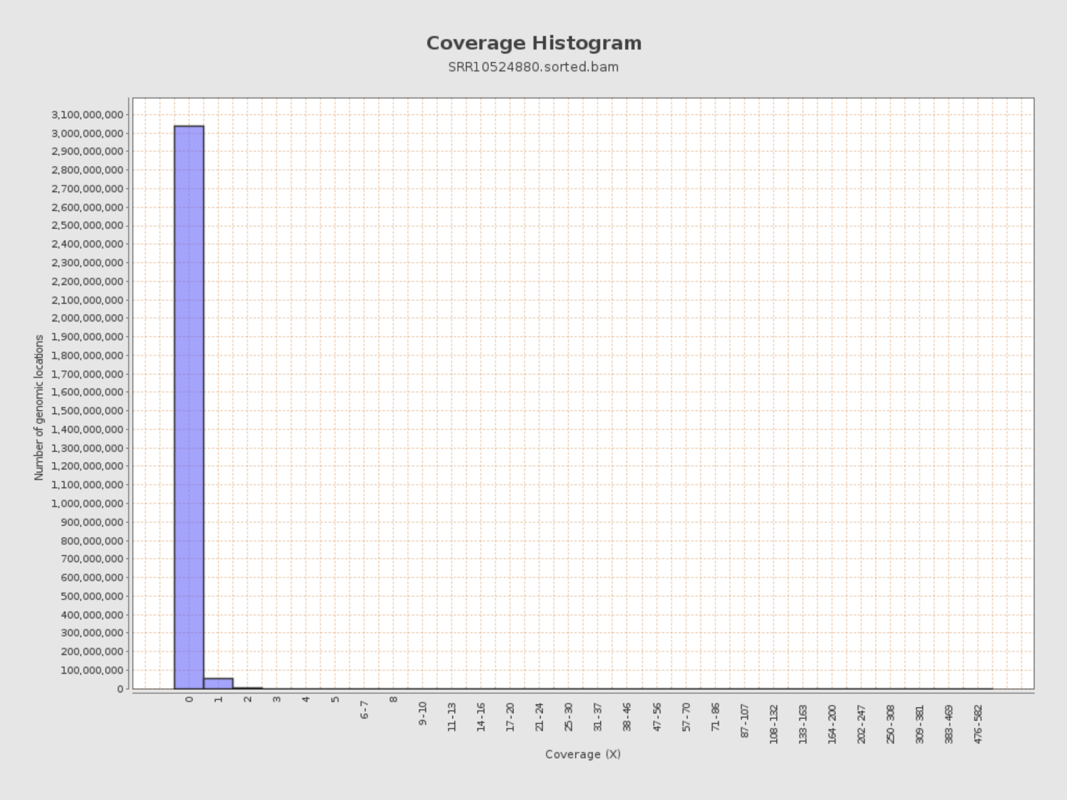
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5240589	0.021	0.4429
chr2	243199373	5582106	0.023	0.2392
chr3	198022430	4396610	0.0222	0.1573
chr4	191154276	4257778	0.0223	0.1706
chr5	180915260	3963480	0.0219	0.1573
chr6	171115067	3741593	0.0219	0.1686
chr7	159138663	3618862	0.0227	0.3019

chr8	146364022	3351976	0.0229	0.2209
chr9	141213431	2754496	0.0195	0.1997
chr10	135534747	3120160	0.023	0.2111
chr11	135006516	3008401	0.0223	0.2062
chr12	133851895	2948531	0.022	0.16
chr13	115169878	2065136	0.0179	0.1418
chr14	107349540	1999913	0.0186	0.1493
chr15	102531392	1878530	0.0183	0.1426
chr16	90354753	1874761	0.0207	0.1643
chr17	81195210	1749873	0.0216	0.165
chr18	78077248	1599772	0.0205	0.366
chr19	59128983	1273858	0.0215	0.2804
chr20	63025520	1390343	0.0221	0.159
chr21	48129895	874997	0.0182	0.1536
chr22	51304566	758181	0.0148	0.1291
chrMT	16571	7612	0.4594	0.7076
chrX	155270560	3716914	0.0239	0.1834
chrY	59373566	192066	0.0032	0.0952

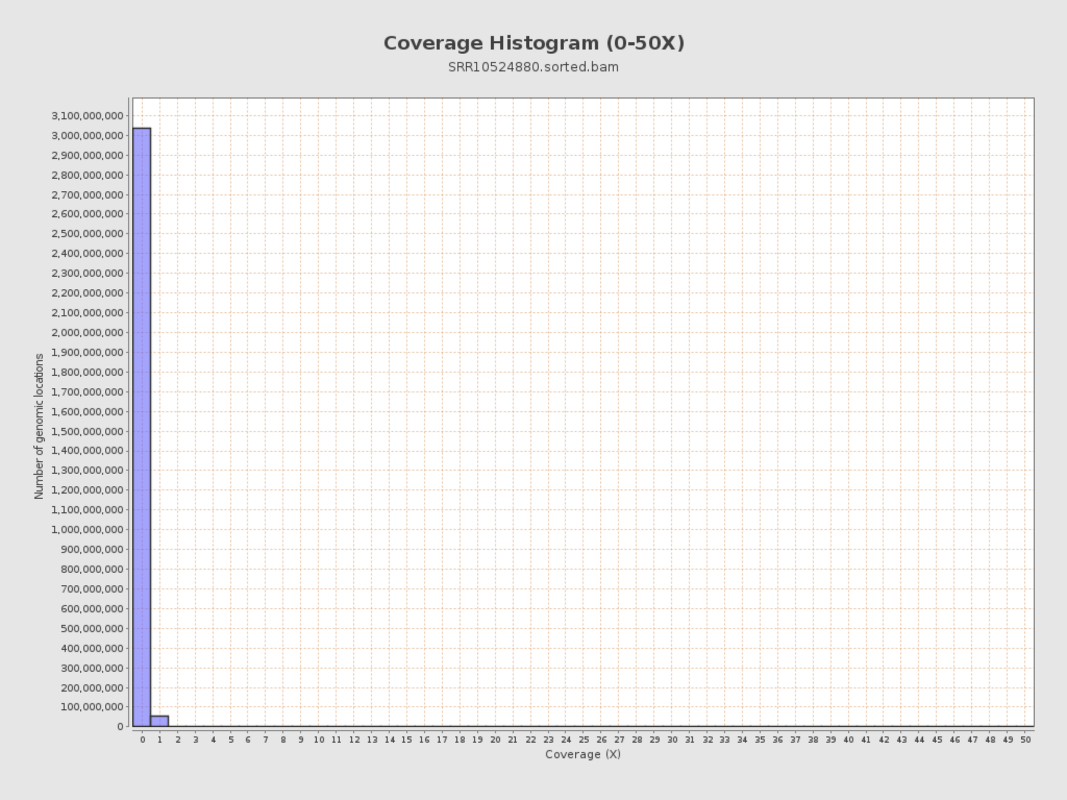
3. Results : Coverage across reference



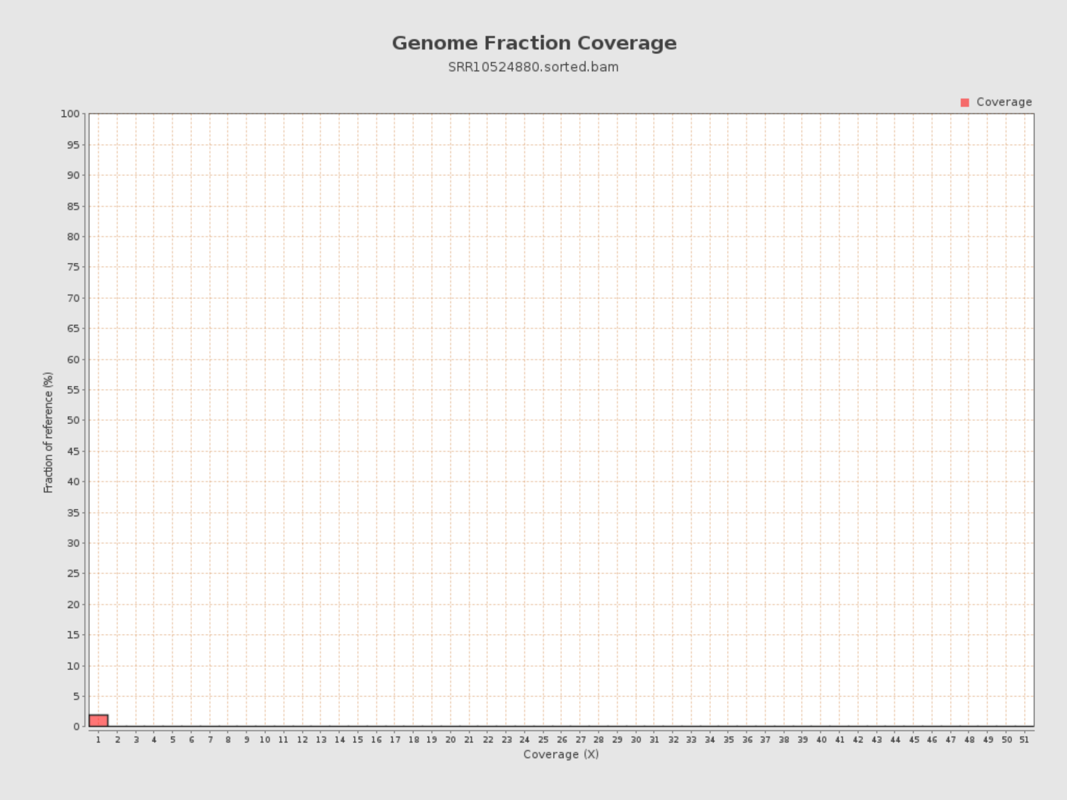
4. Results : Coverage Histogram



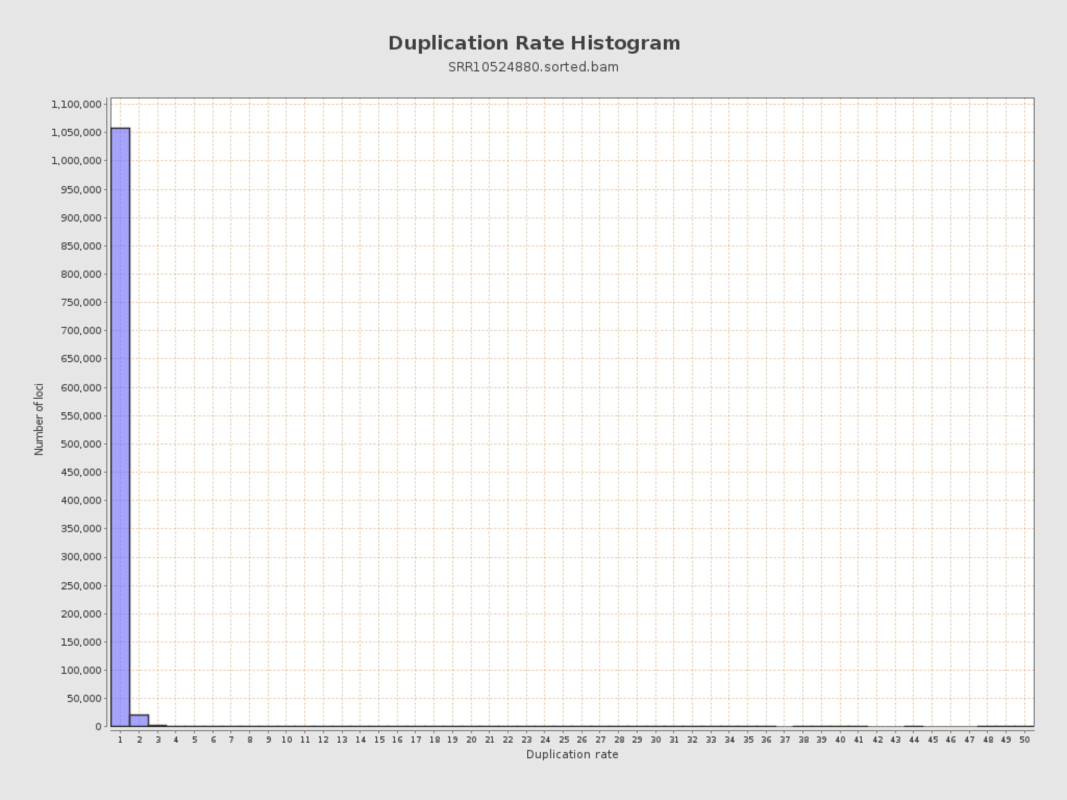
5. Results : Coverage Histogram (0-50X)



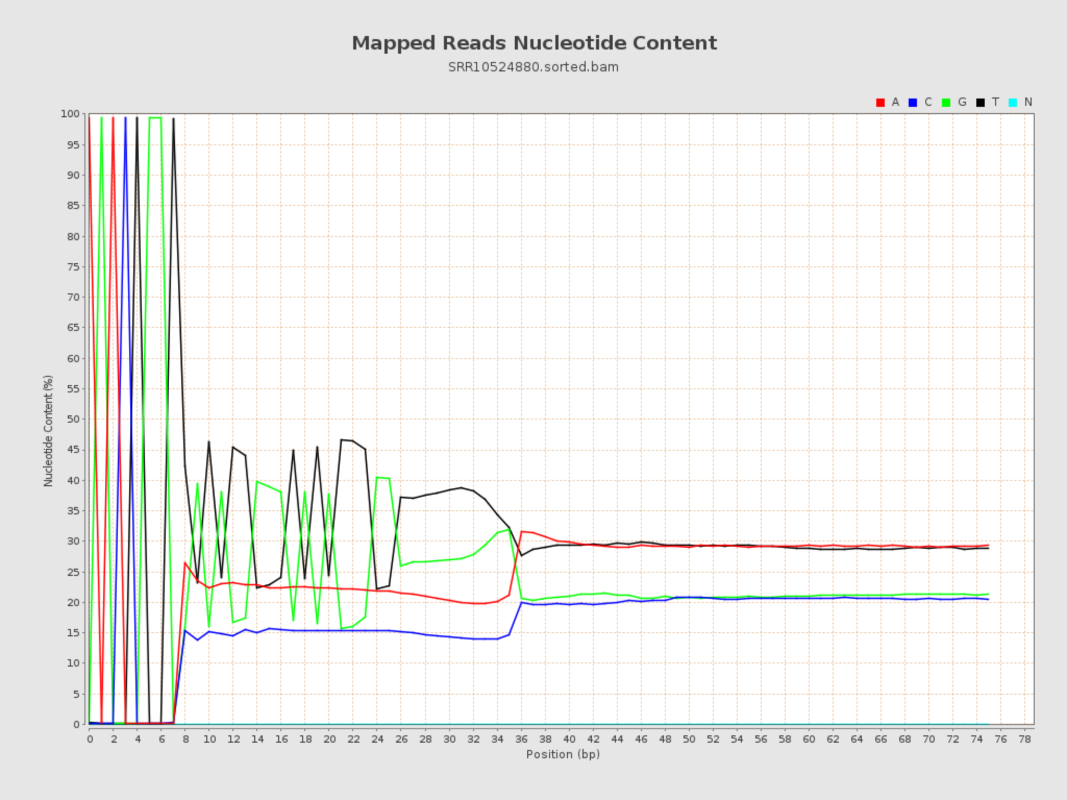
6. Results : Genome Fraction Coverage



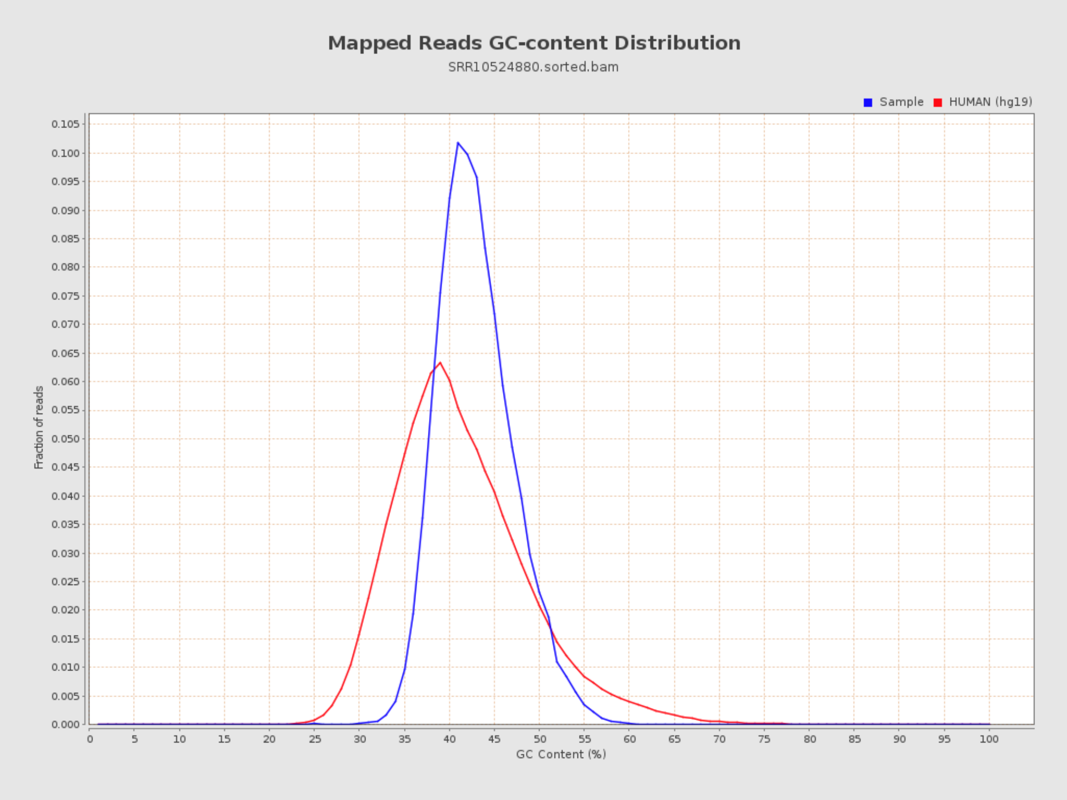
7. Results : Duplication Rate Histogram



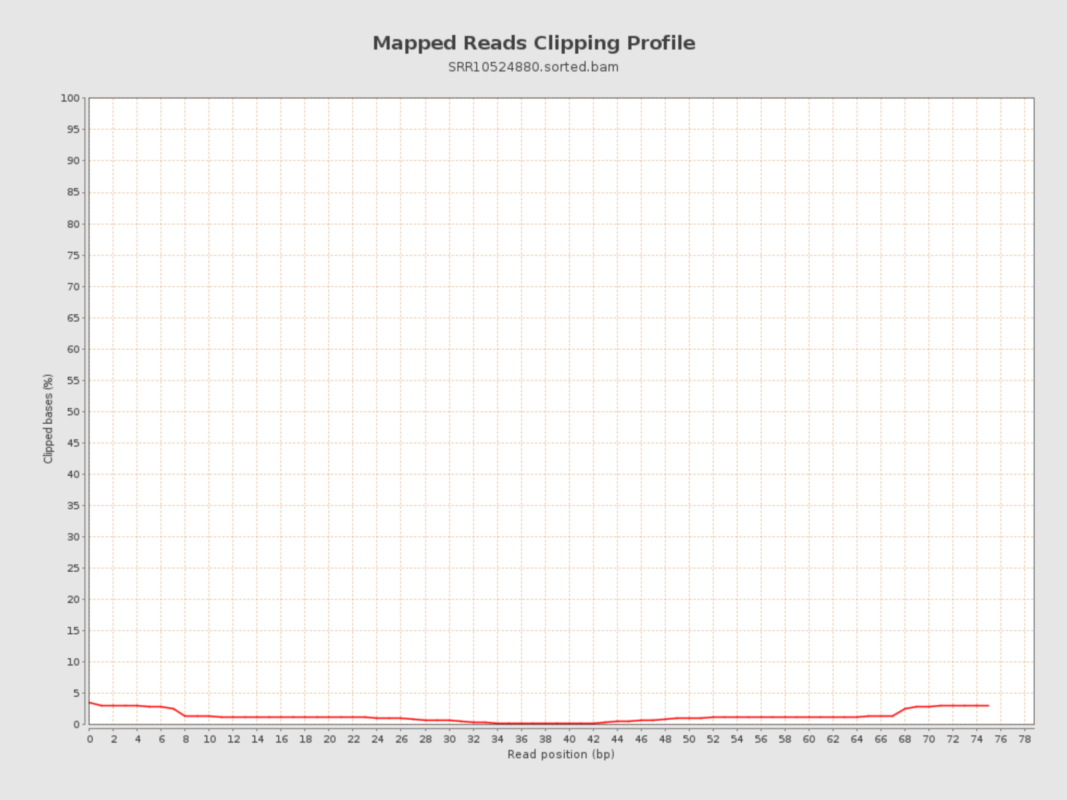
8. Results : Mapped Reads Nucleotide Content



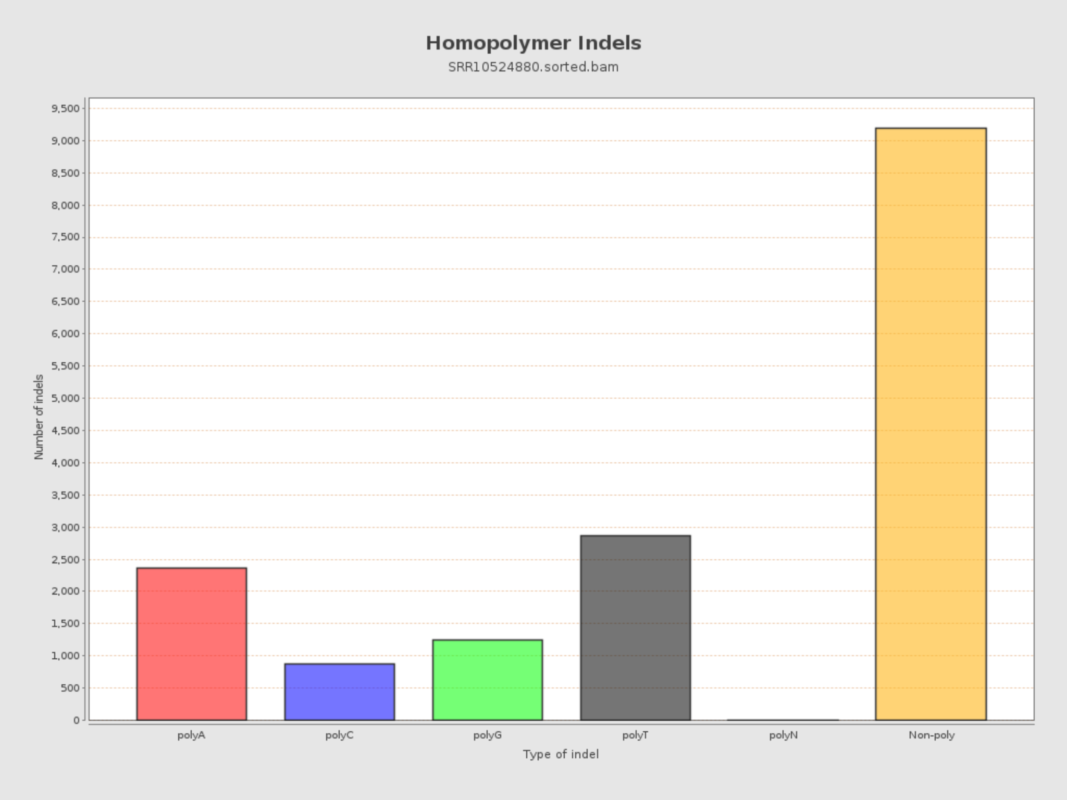
9. Results : Mapped Reads GC-content Distribution



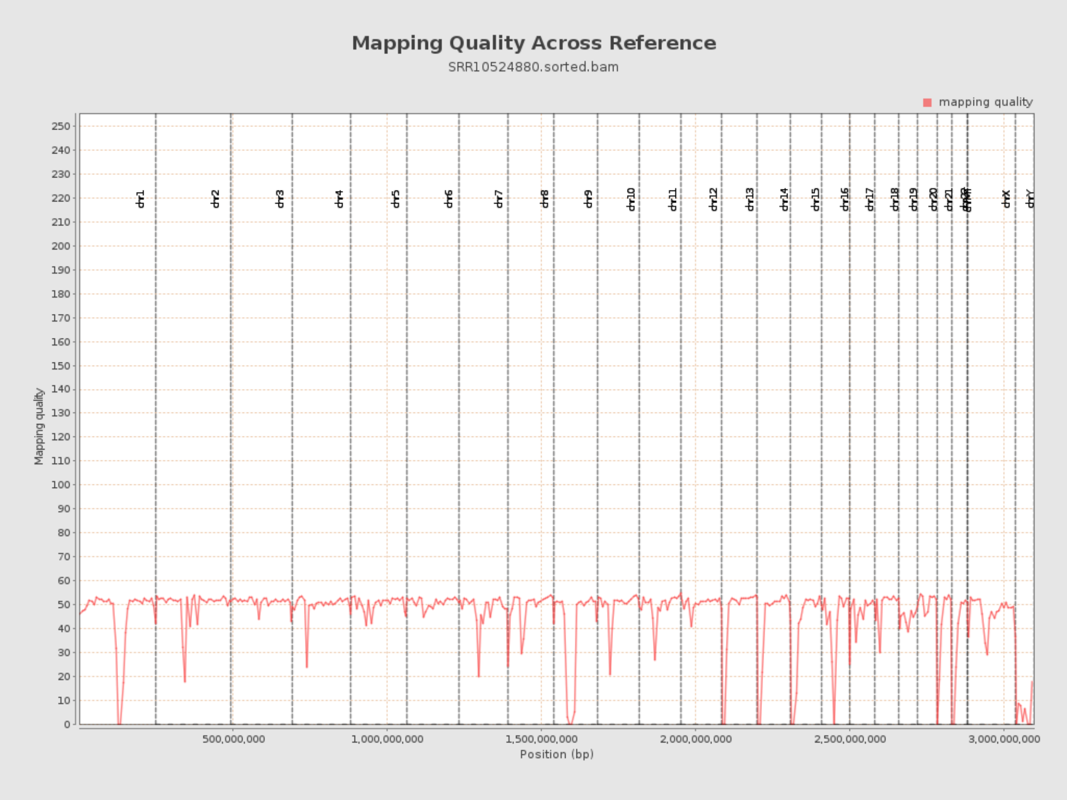
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram