Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:23:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524780.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_SRR10524780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,322,867
Mapped reads	1,201,761 / 90.85%
Unmapped reads	121,106 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,090 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,775 / 3.16%
Duplication rate	2.62%
Clipped reads	1,202,175 / 90.88%

2.2. ACGT Content

Number/percentage of A's	16,348,753 / 23.92%
Number/percentage of C's	13,694,391 / 20.03%
Number/percentage of T's	22,258,067 / 32.56%
Number/percentage of G's	16,046,736 / 23.48%
Number/percentage of N's	8,034 / 0.01%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2105

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

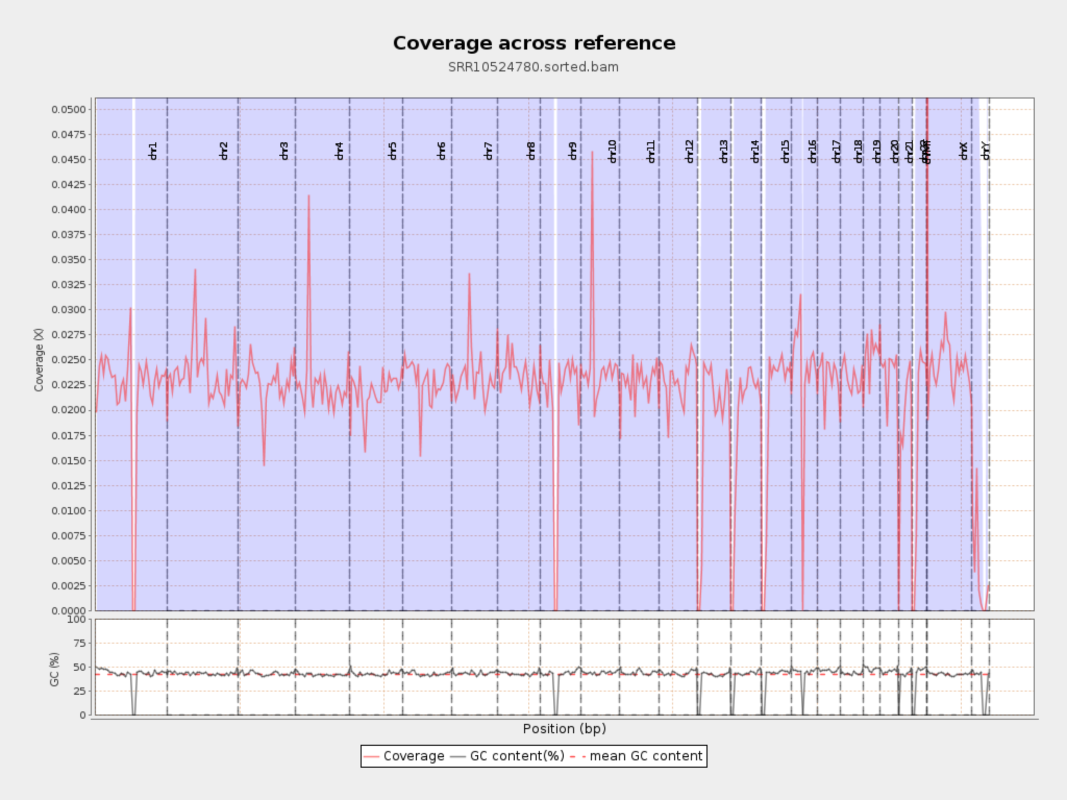
General error rate	0.52%
Mismatches	346,644
Insertions	5,266
Mapped reads with at least one insertion	0.44%
Deletions	13,239
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.12%

2.6. Chromosome stats

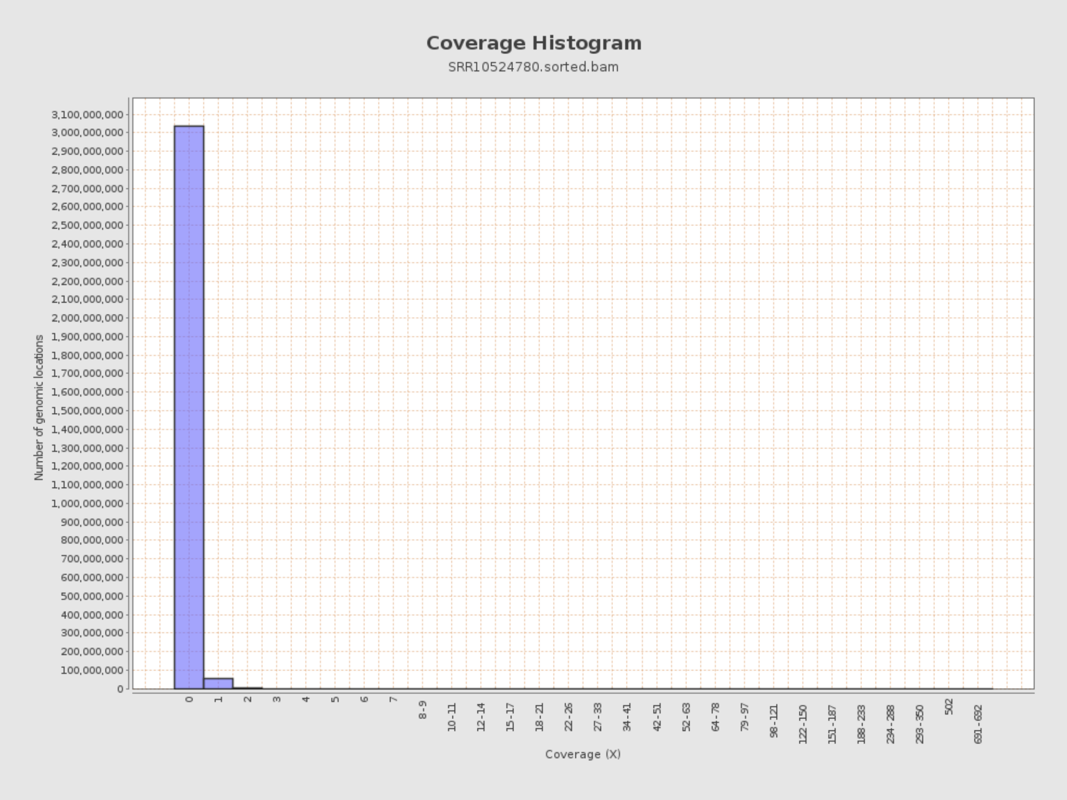
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5435035	0.0218	0.2773
chr2	243199373	5803033	0.0239	0.3352
chr3	198022430	4470561	0.0226	0.1655
chr4	191154276	4367243	0.0228	0.1844
chr5	180915260	3982274	0.022	0.1612
chr6	171115067	3924532	0.0229	0.1805
chr7	159138663	3741900	0.0235	0.2408

chr8	146364022	3448753	0.0236	0.1926
chr9	141213431	2894273	0.0205	0.1857
chr10	135534747	3327163	0.0245	0.2415
chr11	135006516	3107183	0.023	0.1928
chr12	133851895	3095458	0.0231	0.1663
chr13	115169878	2133174	0.0185	0.1482
chr14	107349540	2008984	0.0187	0.1525
chr15	102531392	2002504	0.0195	0.1526
chr16	90354753	2106716	0.0233	0.1826
chr17	81195210	1894397	0.0233	0.1707
chr18	78077248	1809351	0.0232	0.2773
chr19	59128983	1516745	0.0257	0.2351
chr20	63025520	1495149	0.0237	0.1739
chr21	48129895	895982	0.0186	0.161
chr22	51304566	873855	0.017	0.1429
chrMT	16571	18838	1.1368	1.2094
chrX	155270560	3794202	0.0244	0.1827
chrY	59373566	229768	0.0039	0.1149

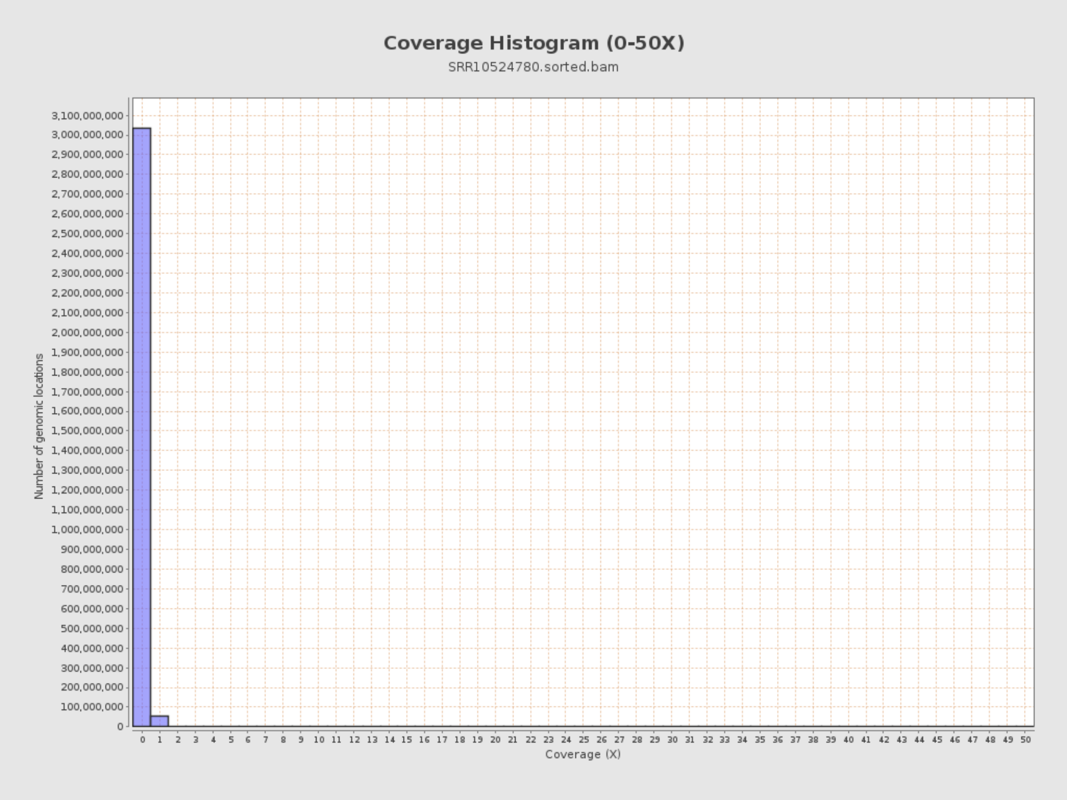
3. Results : Coverage across reference



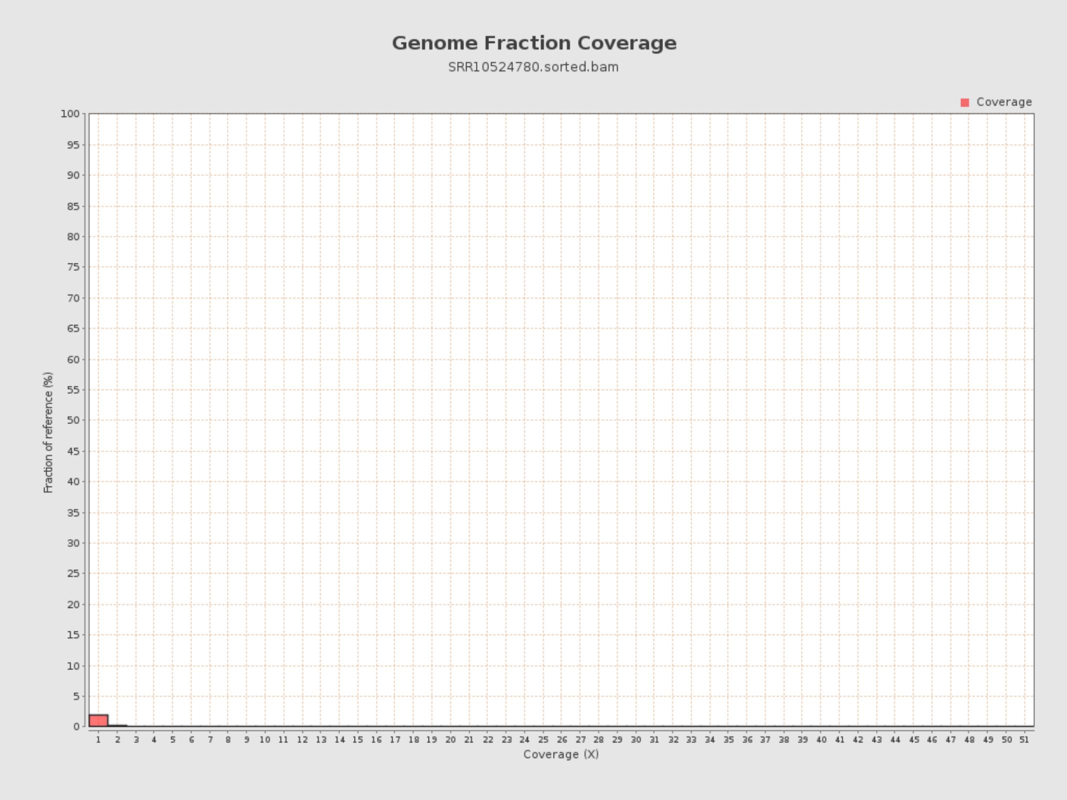
4. Results : Coverage Histogram



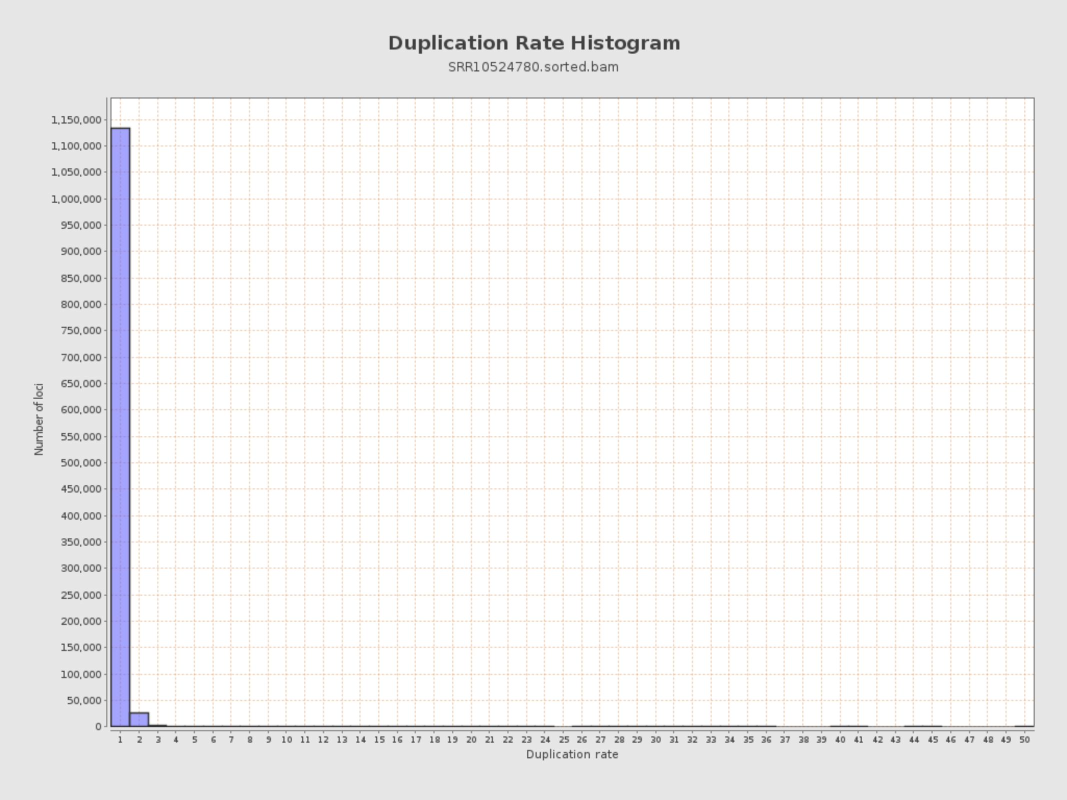
5. Results : Coverage Histogram (0-50X)



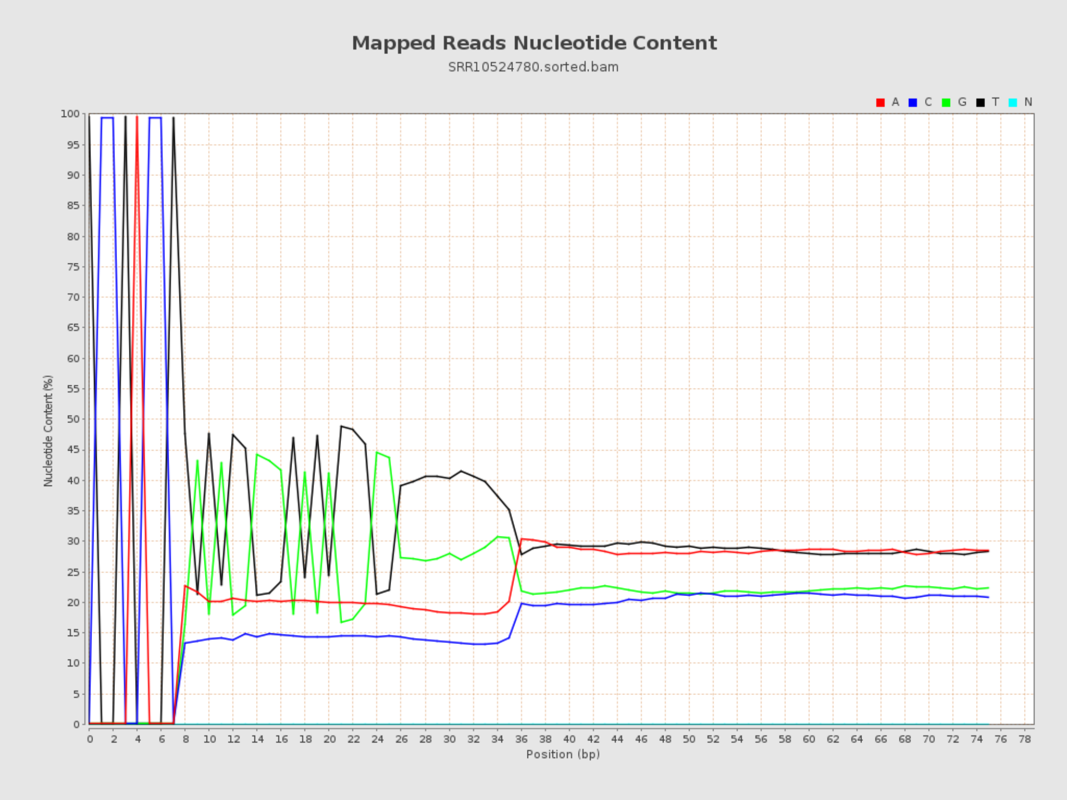
6. Results : Genome Fraction Coverage



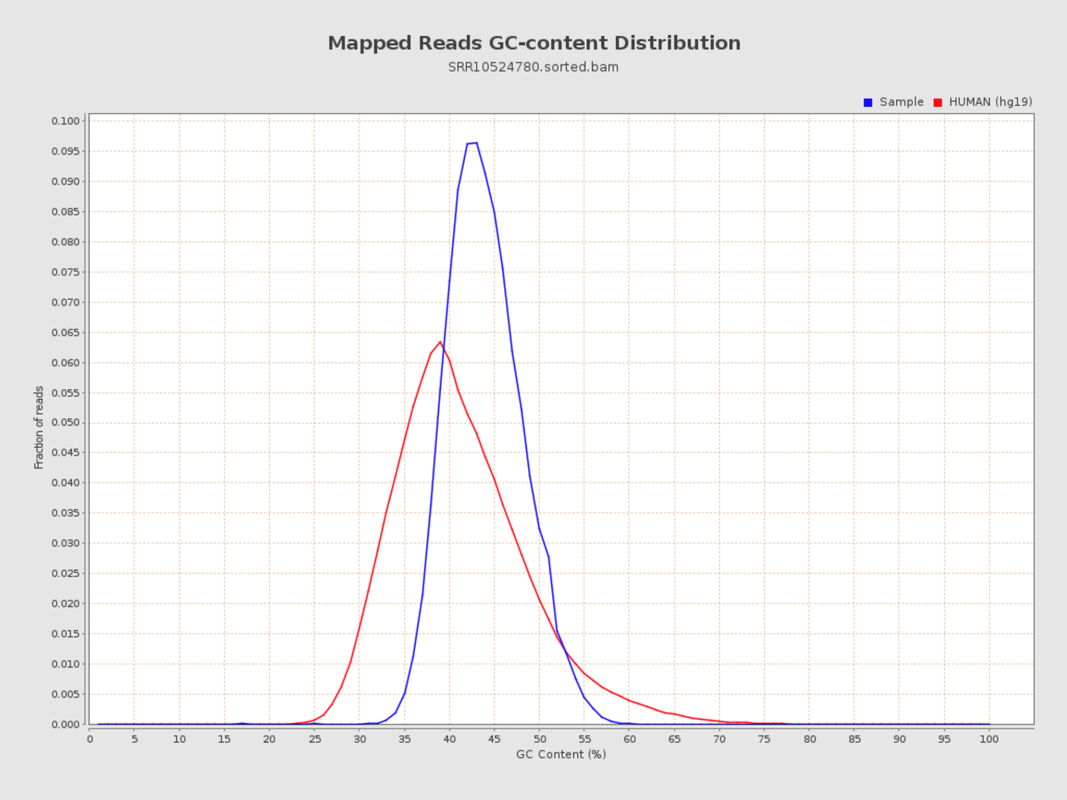
7. Results : Duplication Rate Histogram



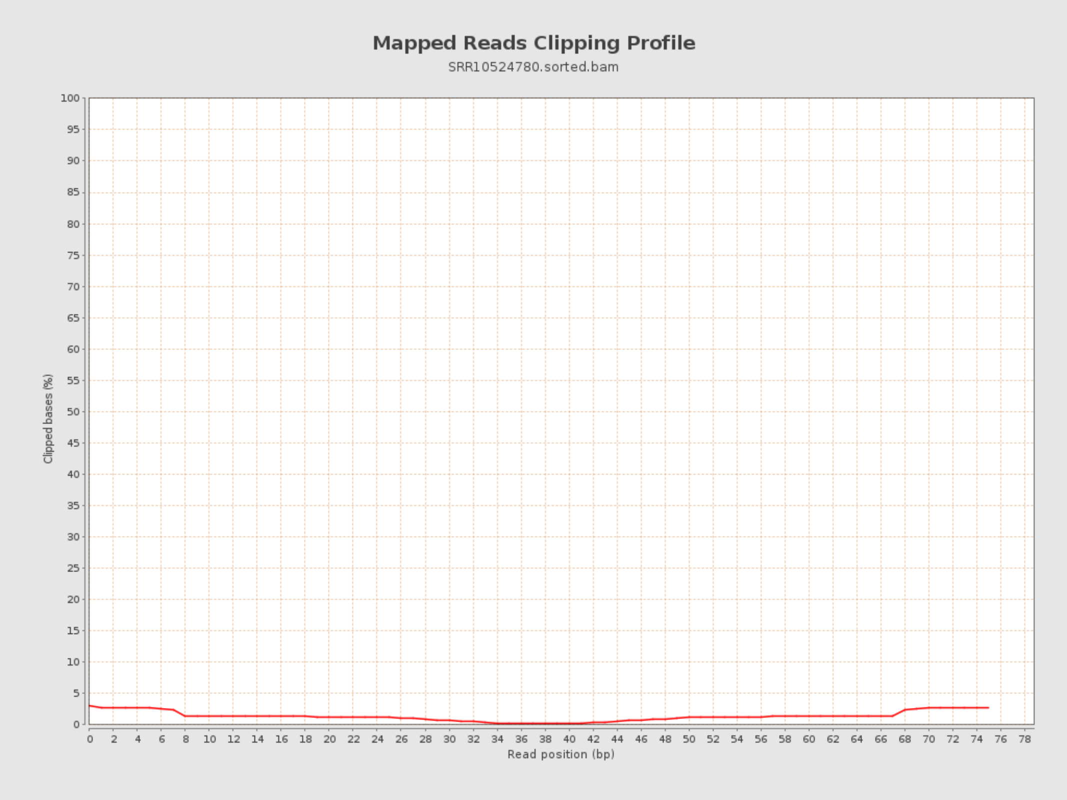
8. Results : Mapped Reads Nucleotide Content



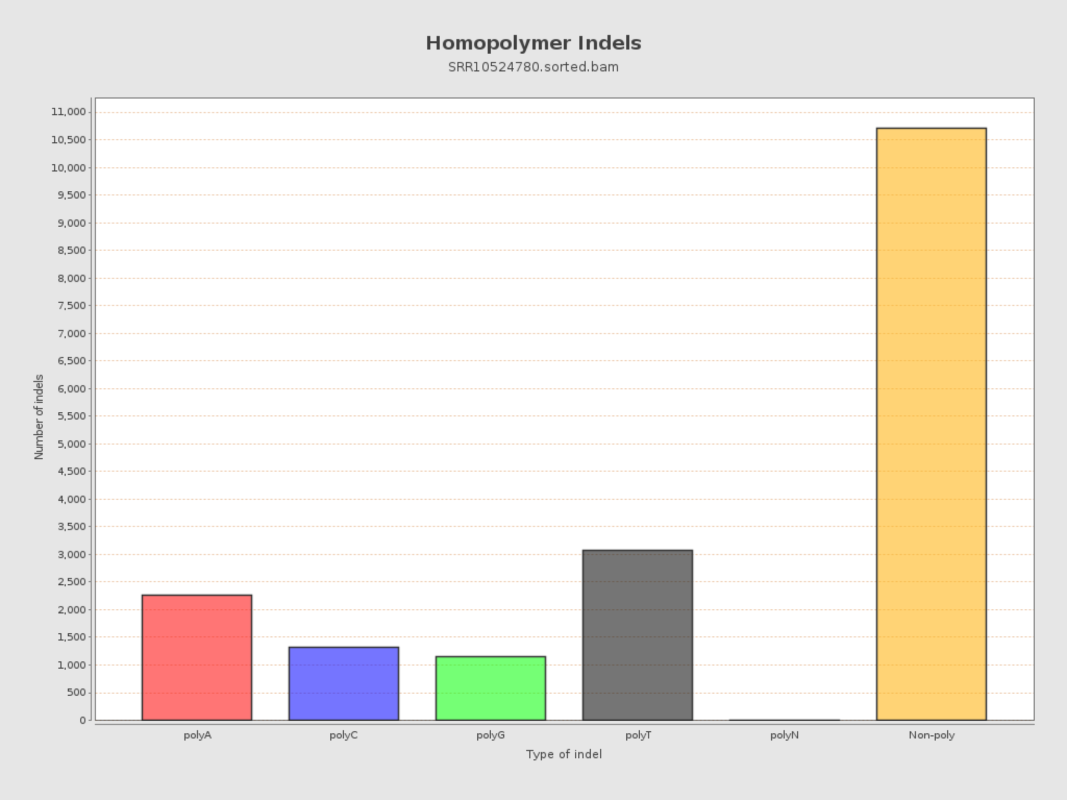
9. Results : Mapped Reads GC-content Distribution



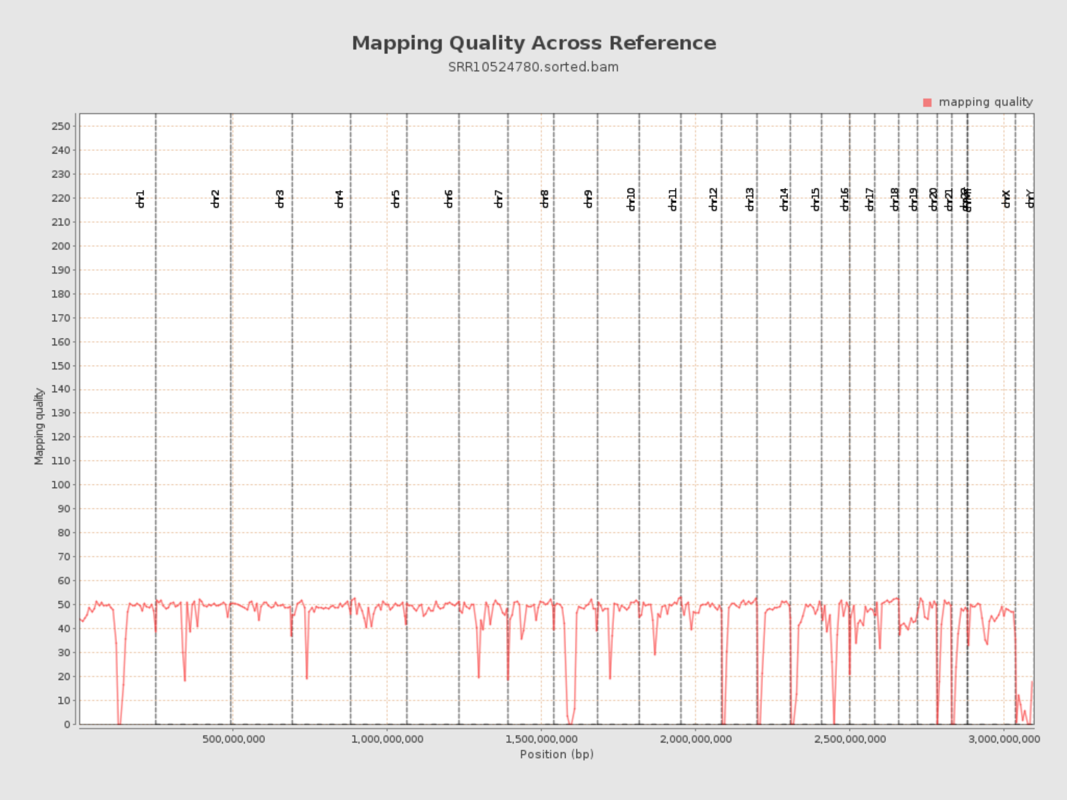
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram