Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:27:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524860.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_SRR10524860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:27:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,374,811
Mapped reads	1,260,976 / 91.72%
Unmapped reads	113,835 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,561 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	32,967 / 2.4%
Duplication rate	1.76%
Clipped reads	1,265,258 / 92.03%

2.2. ACGT Content

Number/percentage of A's	18,504,918 / 25.24%
Number/percentage of C's	12,870,279 / 17.55%
Number/percentage of T's	23,109,509 / 31.51%
Number/percentage of G's	18,834,321 / 25.68%
Number/percentage of N's	9,692 / 0.01%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2454

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

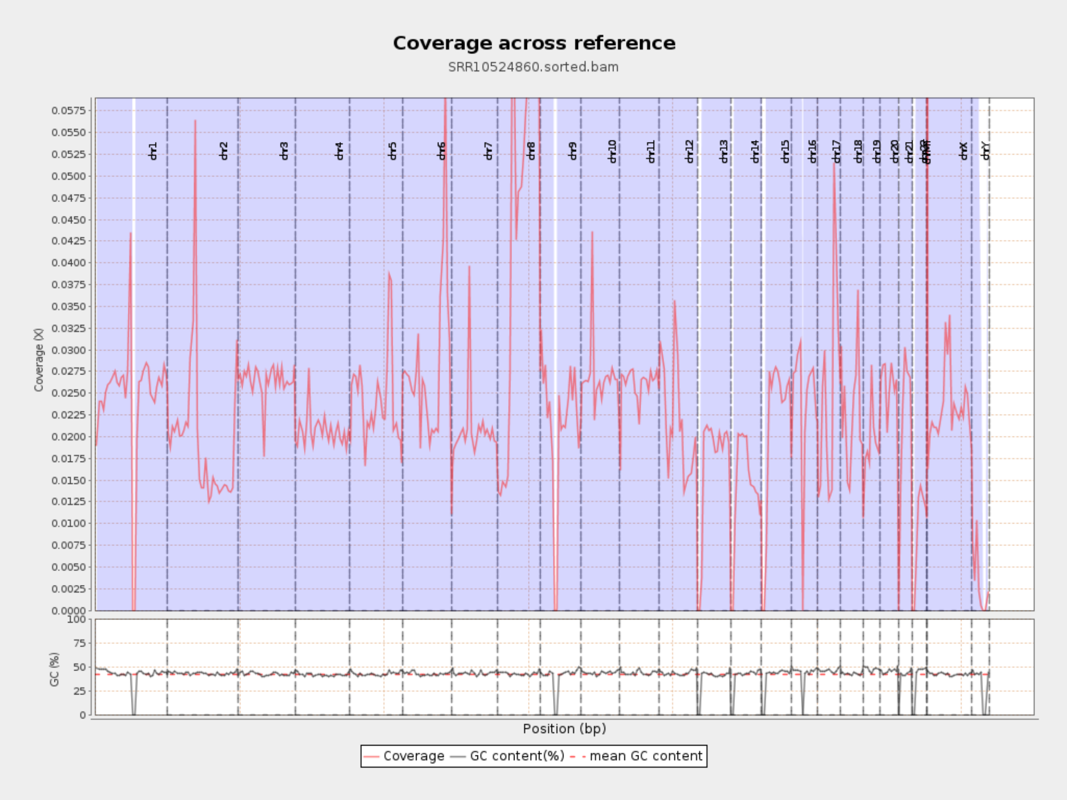
General error rate	0.49%
Mismatches	352,476
Insertions	5,012
Mapped reads with at least one insertion	0.4%
Deletions	13,480
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.76%

2.6. Chromosome stats

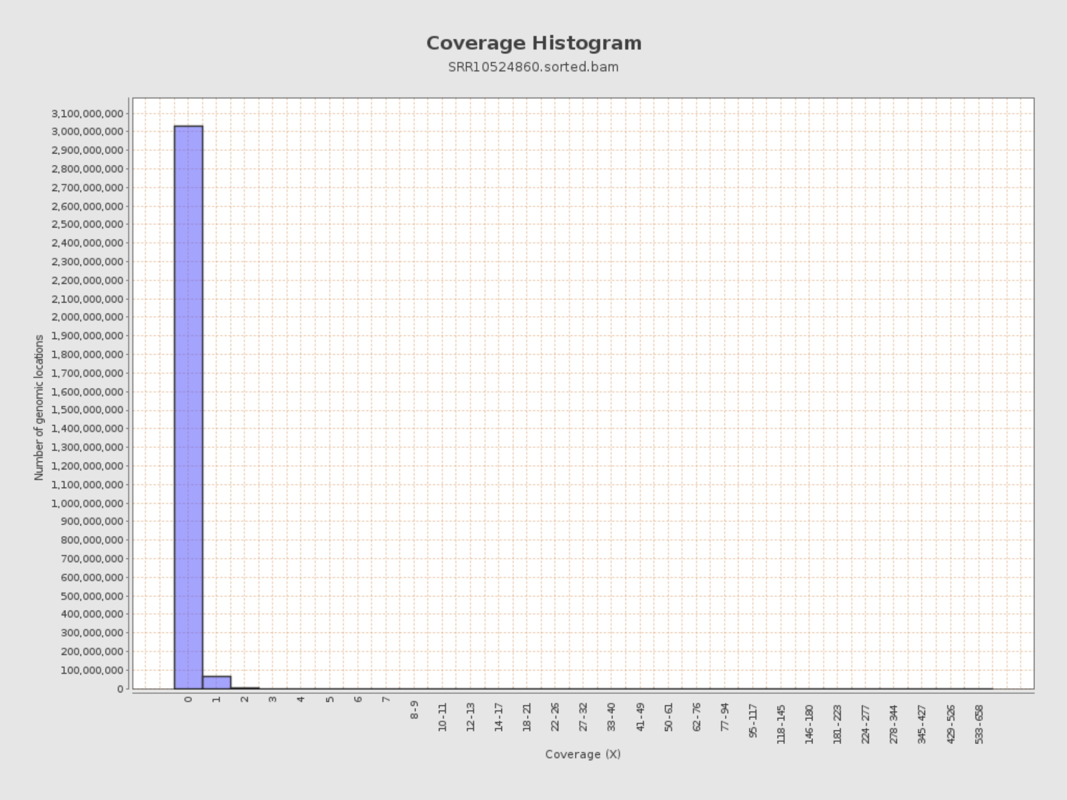
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6135201	0.0246	0.4745
chr2	243199373	4755726	0.0196	0.259
chr3	198022430	5225836	0.0264	0.1716
chr4	191154276	3956262	0.0207	0.1632
chr5	180915260	4436744	0.0245	0.1659
chr6	171115067	4785226	0.028	0.1947
chr7	159138663	3335960	0.021	0.326

chr8	146364022	7859604	0.0537	0.3214
chr9	141213431	3024421	0.0214	0.1992
chr10	135534747	3652425	0.0269	0.2344
chr11	135006516	3522693	0.0261	0.2104
chr12	133851895	2891057	0.0216	0.1579
chr13	115169878	1908403	0.0166	0.1355
chr14	107349540	1517664	0.0141	0.1335
chr15	102531392	2159862	0.0211	0.1537
chr16	90354753	2149468	0.0238	0.1734
chr17	81195210	2075759	0.0256	0.1828
chr18	78077248	1774038	0.0227	0.3584
chr19	59128983	1157043	0.0196	0.313
chr20	63025520	1621924	0.0257	0.1712
chr21	48129895	1058144	0.022	0.1644
chr22	51304566	475240	0.0093	0.1008
chrMT	16571	21937	1.3238	1.4161
chrX	155270560	3662808	0.0236	0.1829
chrY	59373566	186577	0.0031	0.0842

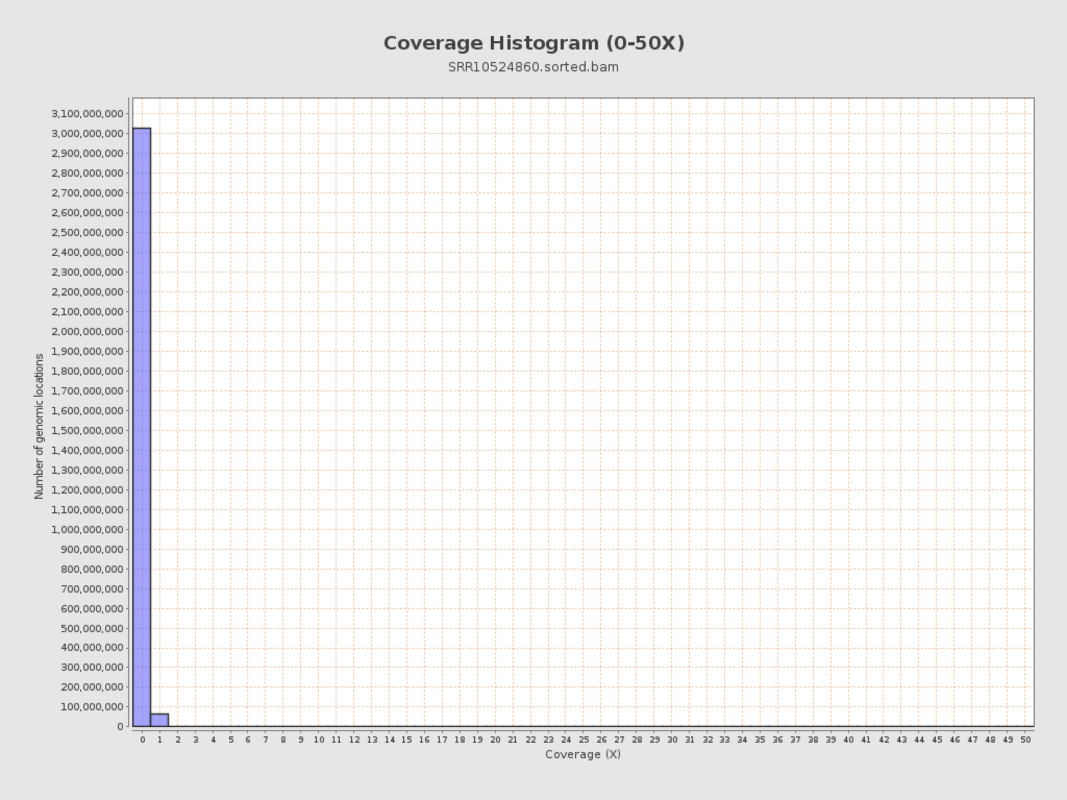
3. Results : Coverage across reference



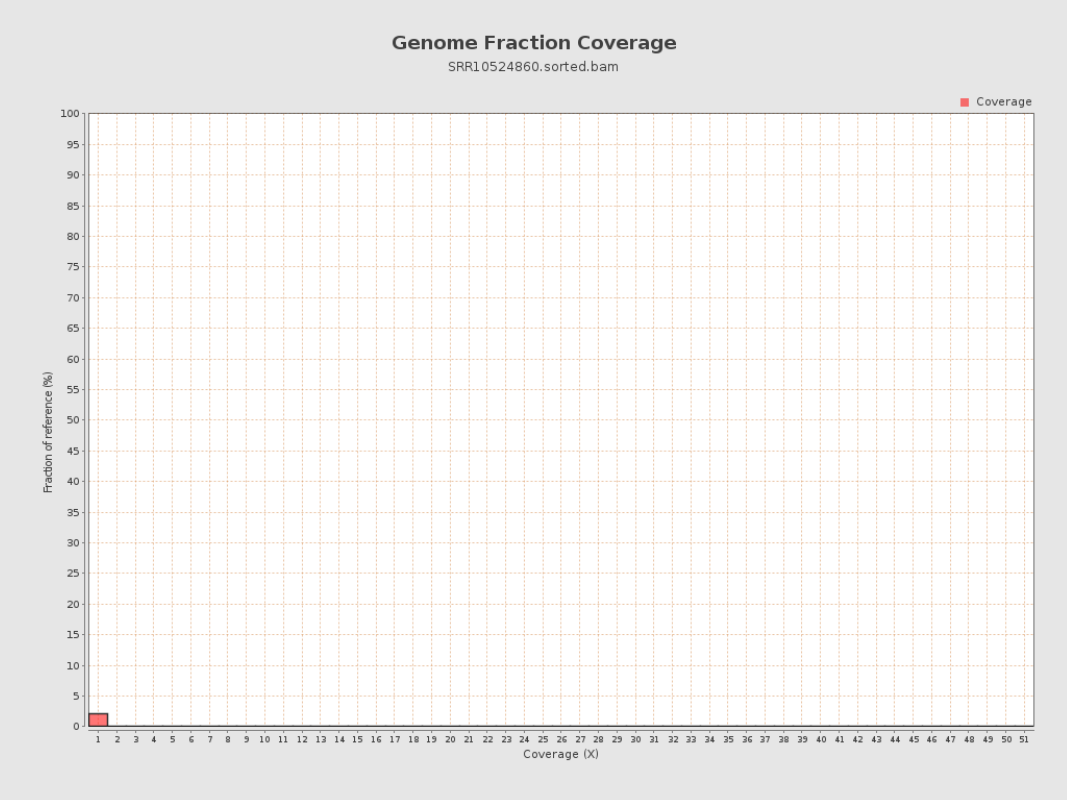
4. Results : Coverage Histogram



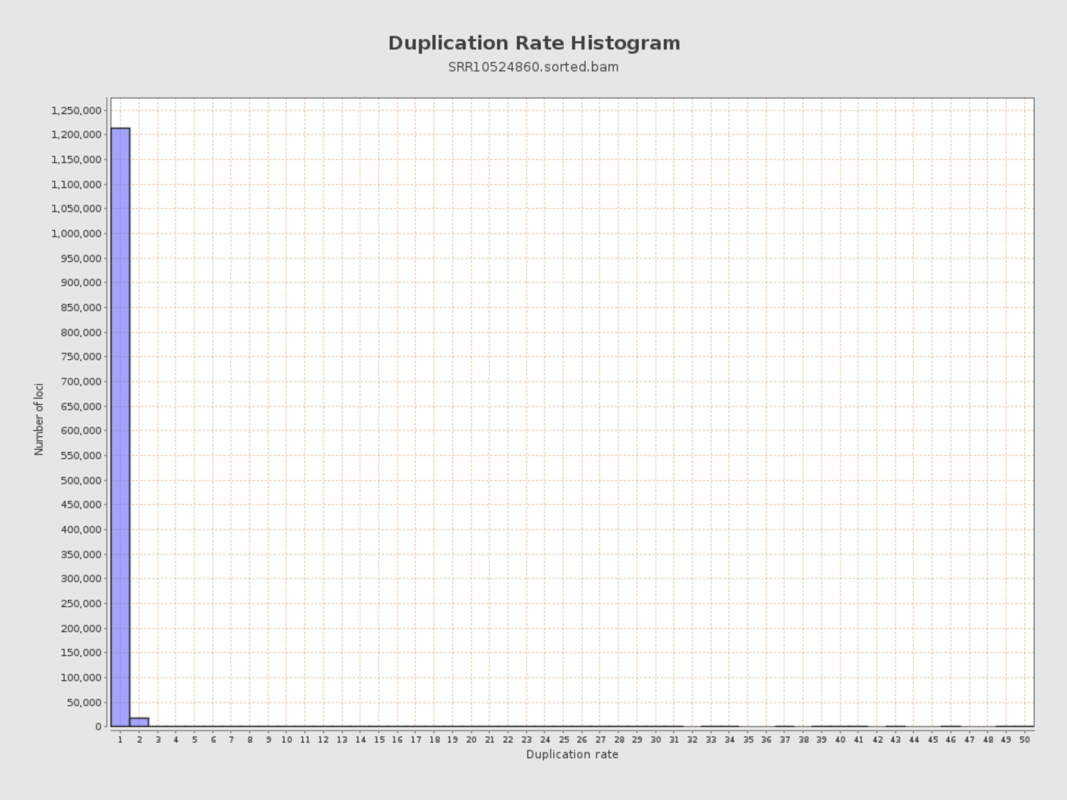
5. Results : Coverage Histogram (0-50X)



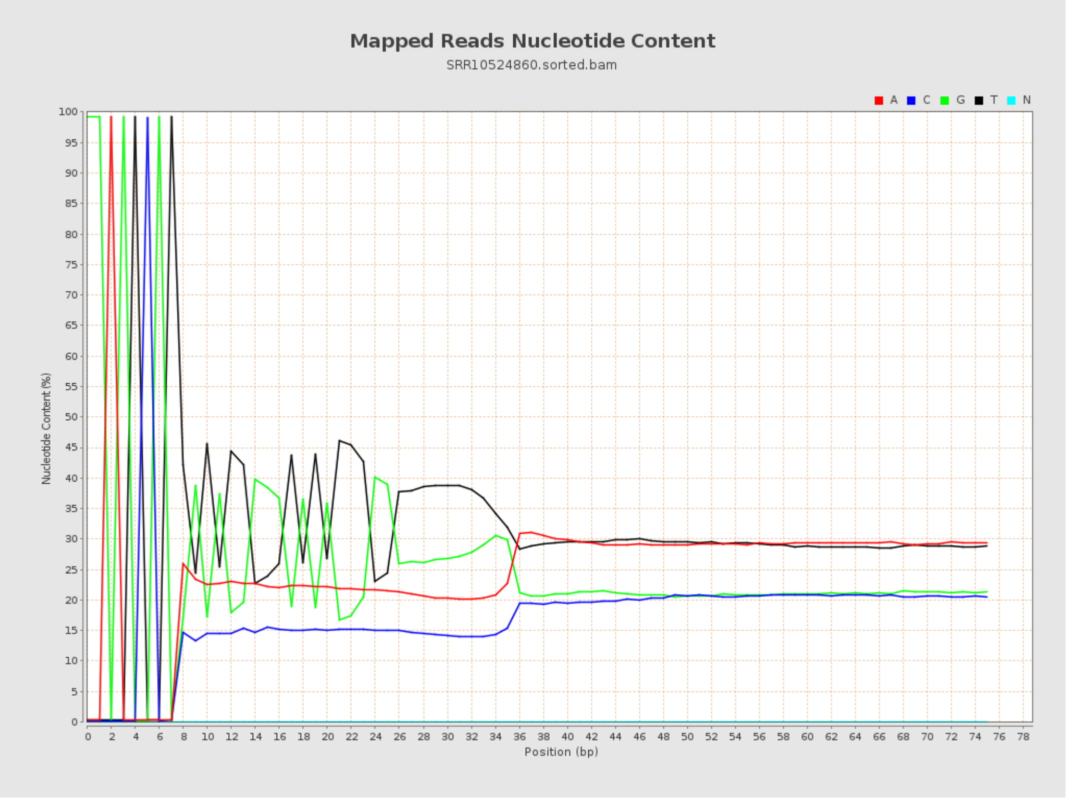
6. Results : Genome Fraction Coverage



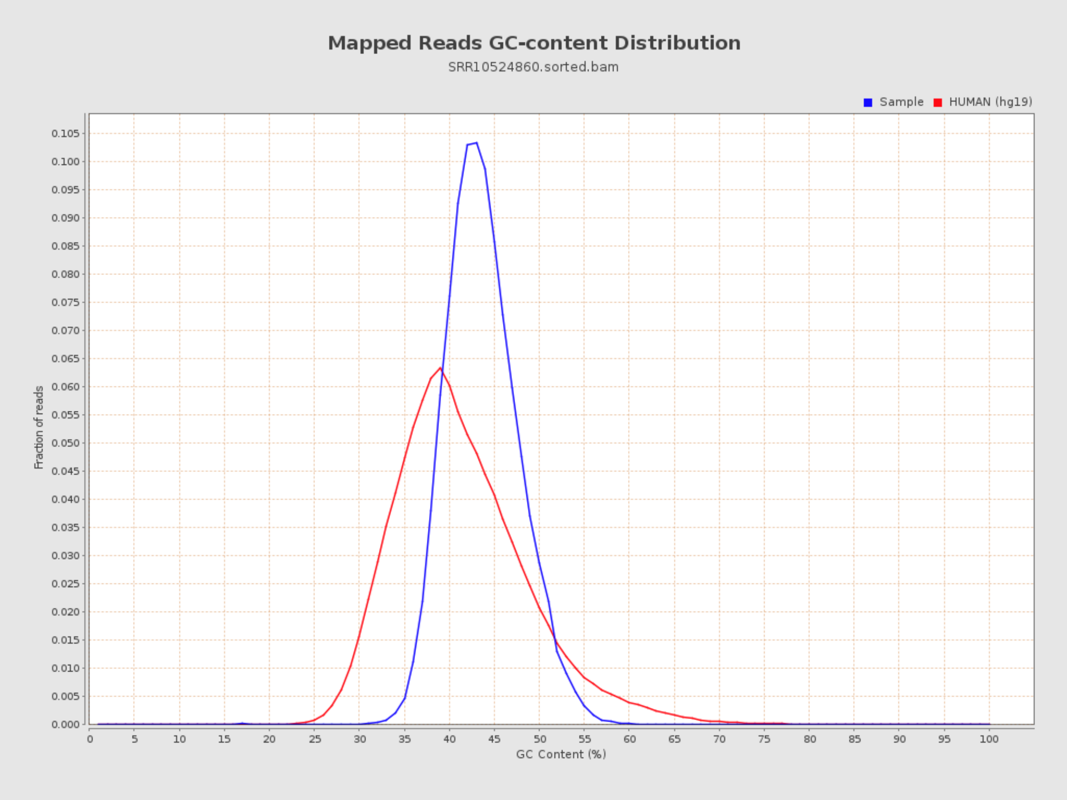
7. Results : Duplication Rate Histogram



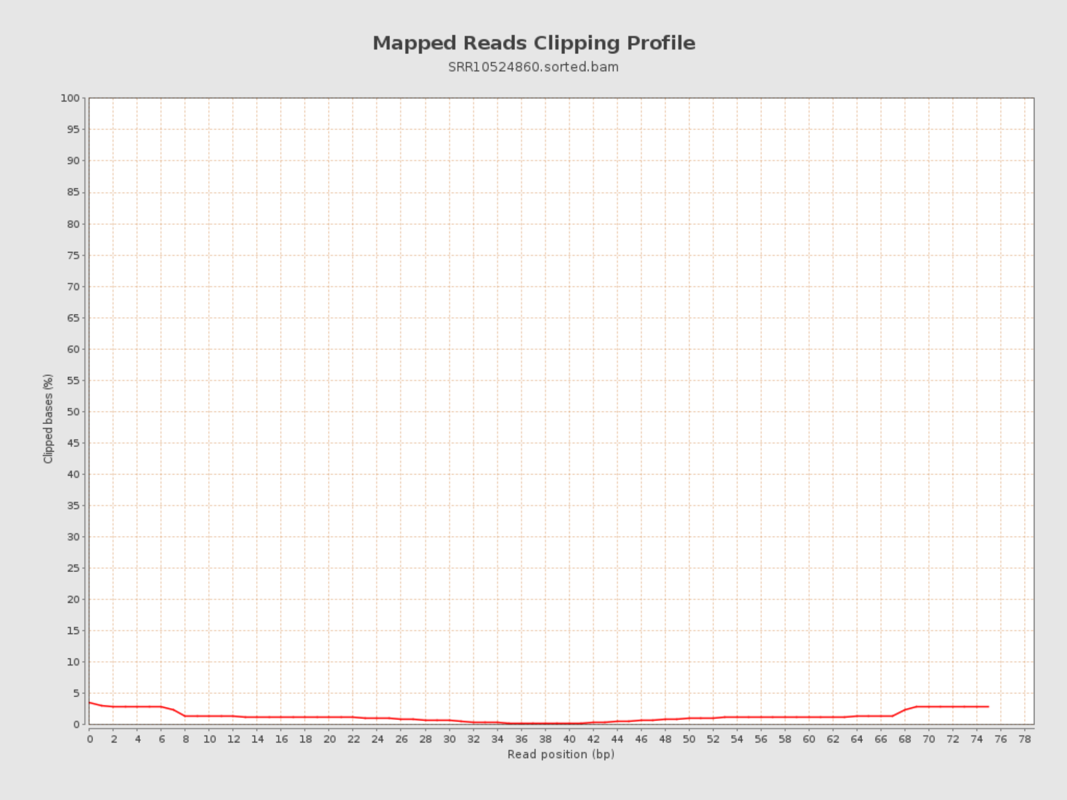
8. Results : Mapped Reads Nucleotide Content



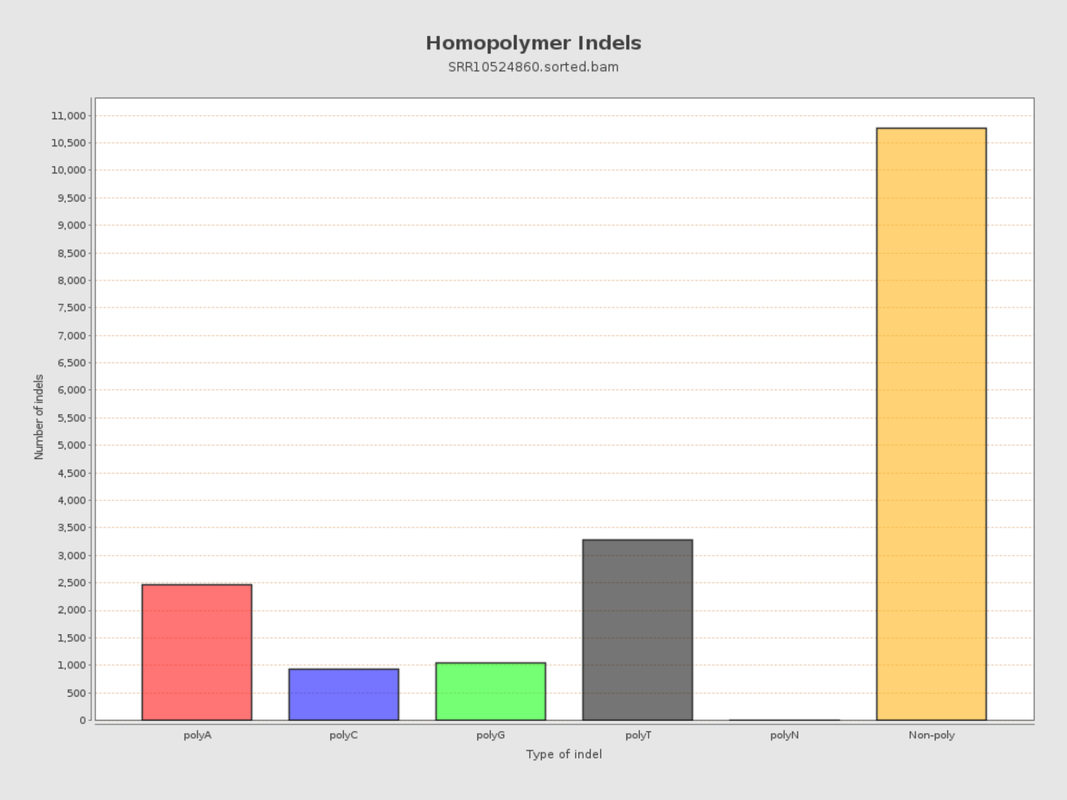
9. Results : Mapped Reads GC-content Distribution



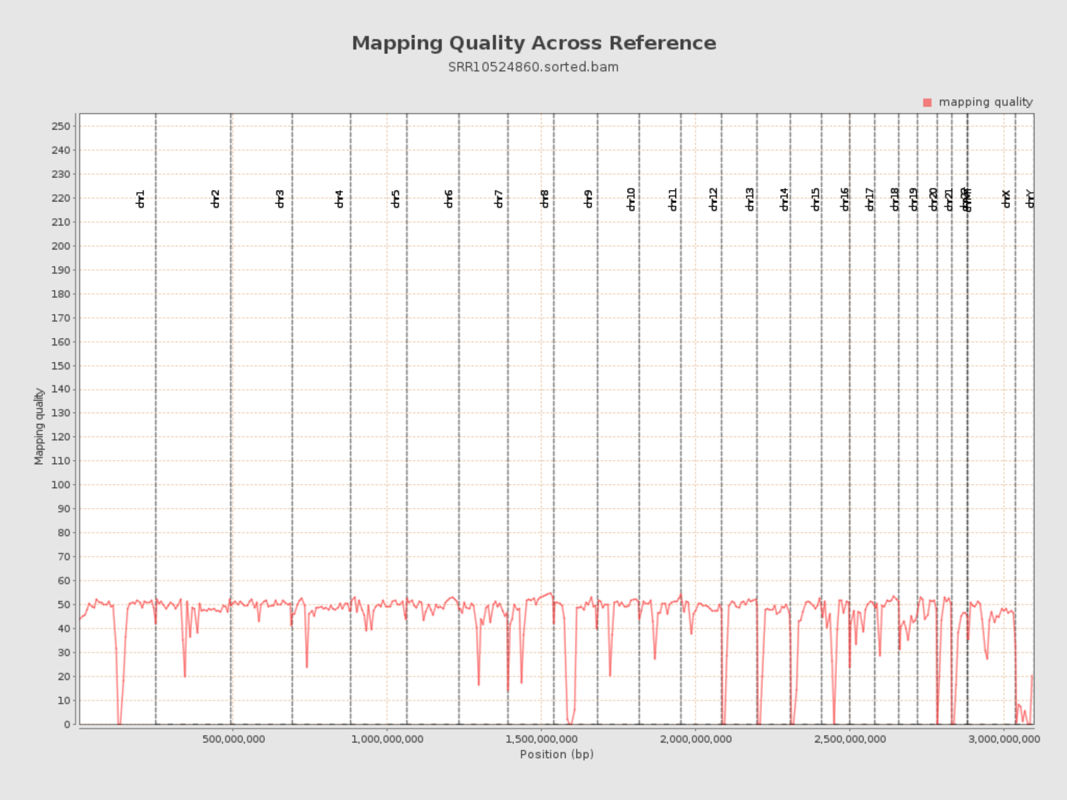
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



Mapping Quality Across Reference

SRR10524860.sorted.bam

13. Results : Mapping Quality Histogram