Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:11:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524854.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_SRR10524854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:11:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,372,279
Mapped reads	1,257,685 / 91.65%
Unmapped reads	114,594 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,506 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	34,332 / 2.5%
Duplication rate	1.85%
Clipped reads	1,262,984 / 92.04%

2.2. ACGT Content

Number/percentage of A's	19,237,992 / 26.26%
Number/percentage of C's	13,951,939 / 19.04%
Number/percentage of T's	23,169,266 / 31.62%
Number/percentage of G's	16,897,838 / 23.06%
Number/percentage of N's	9,729 / 0.01%
GC Percentage	42.11%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.248

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

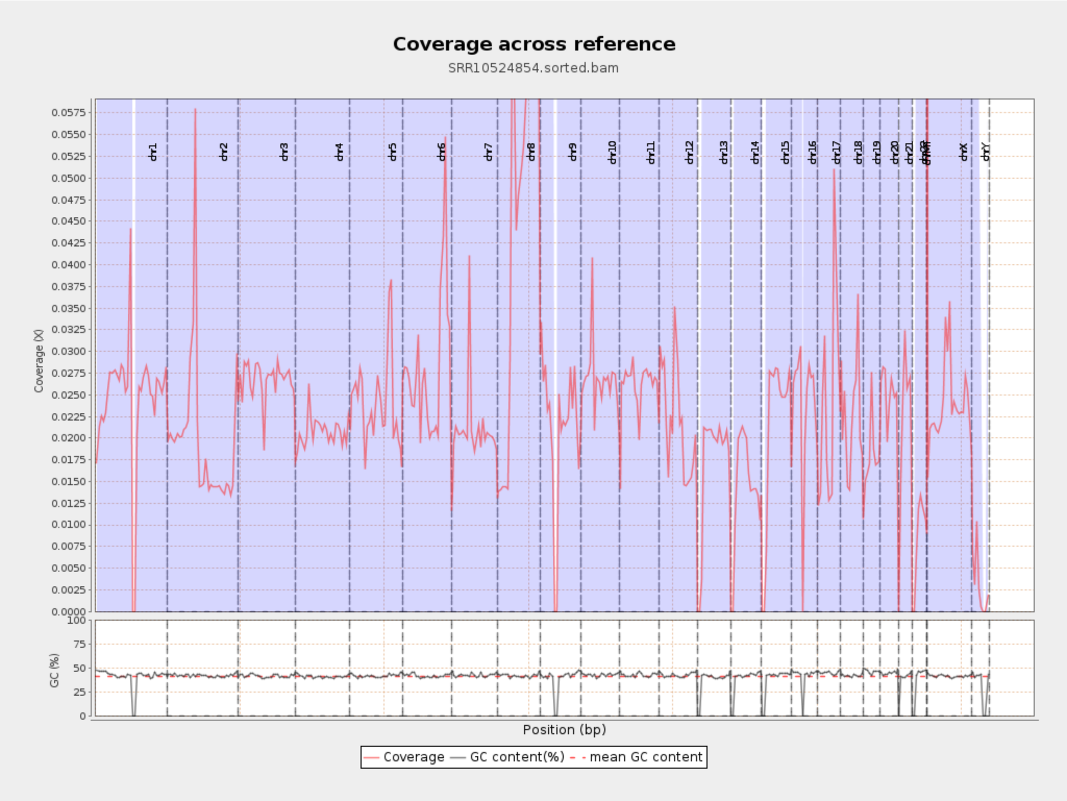
General error rate	0.49%
Mismatches	352,859
Insertions	4,291
Mapped reads with at least one insertion	0.34%
Deletions	13,479
Mapped reads with at least one deletion	1.06%
Homopolymer indels	45.13%

2.6. Chromosome stats

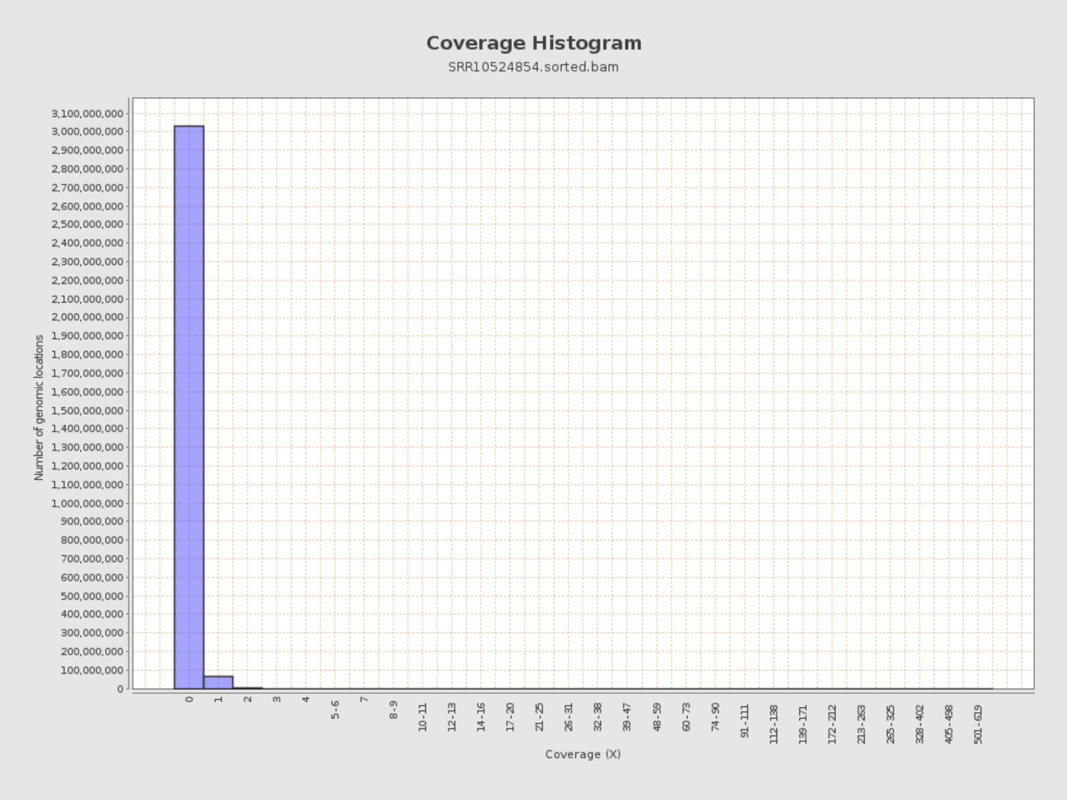
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6077735	0.0244	0.4789
chr2	243199373	4772218	0.0196	0.2473
chr3	198022430	5294828	0.0267	0.1731
chr4	191154276	3955404	0.0207	0.1633
chr5	180915260	4401672	0.0243	0.1653
chr6	171115067	4763356	0.0278	0.1906
chr7	159138663	3352700	0.0211	0.3366

chr8	146364022	7964681	0.0544	0.3374
chr9	141213431	3016760	0.0214	0.2063
chr10	135534747	3632157	0.0268	0.2249
chr11	135006516	3536133	0.0262	0.2198
chr12	133851895	2912684	0.0218	0.1595
chr13	115169878	1939983	0.0168	0.1368
chr14	107349540	1522809	0.0142	0.1348
chr15	102531392	2195288	0.0214	0.1568
chr16	90354753	2109437	0.0233	0.1735
chr17	81195210	2015067	0.0248	0.1849
chr18	78077248	1764442	0.0226	0.3719
chr19	59128983	1066476	0.018	0.3204
chr20	63025520	1562000	0.0248	0.1679
chr21	48129895	1057646	0.022	0.1658
chr22	51304566	438289	0.0085	0.0971
chrMT	16571	9119	0.5503	0.8281
chrX	155270560	3746884	0.0241	0.1856
chrY	59373566	180060	0.003	0.0874

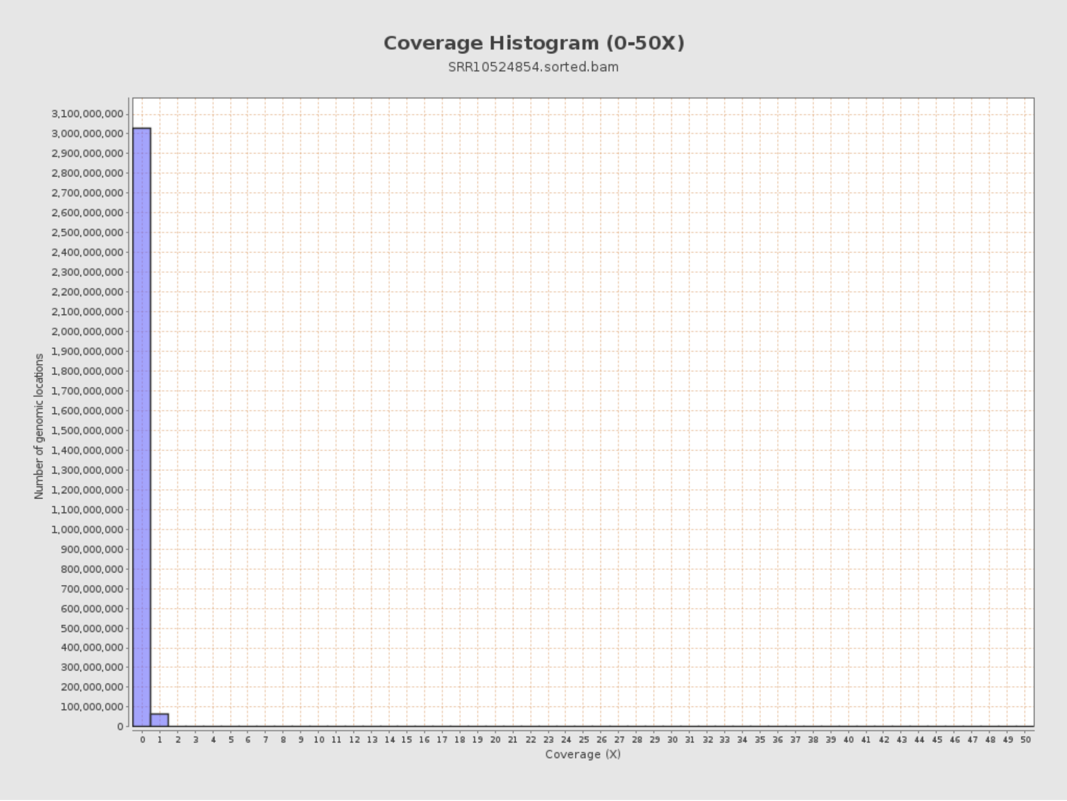
3. Results : Coverage across reference



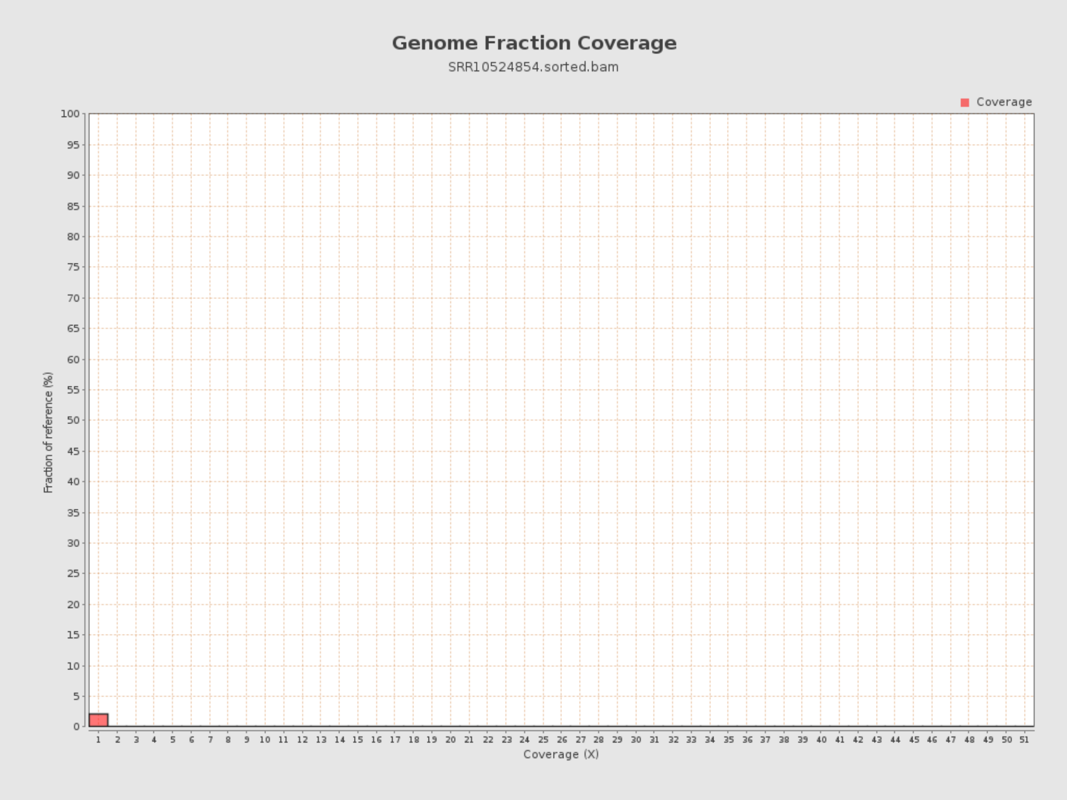
4. Results : Coverage Histogram



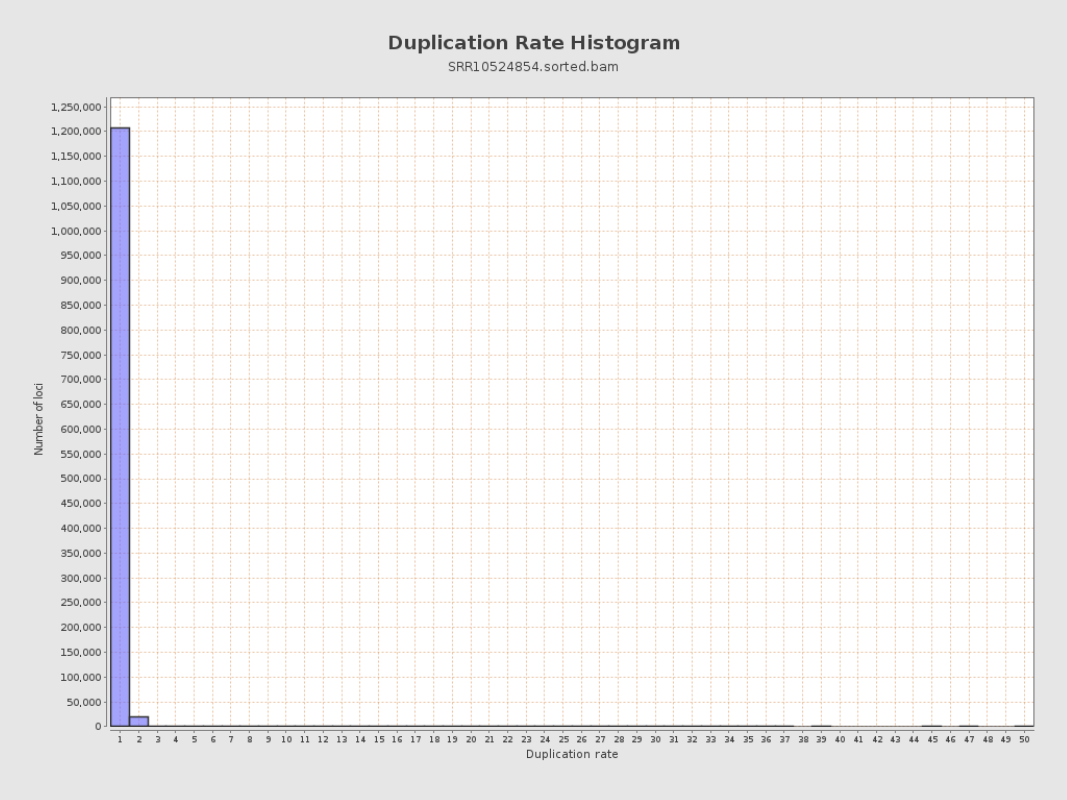
5. Results : Coverage Histogram (0-50X)



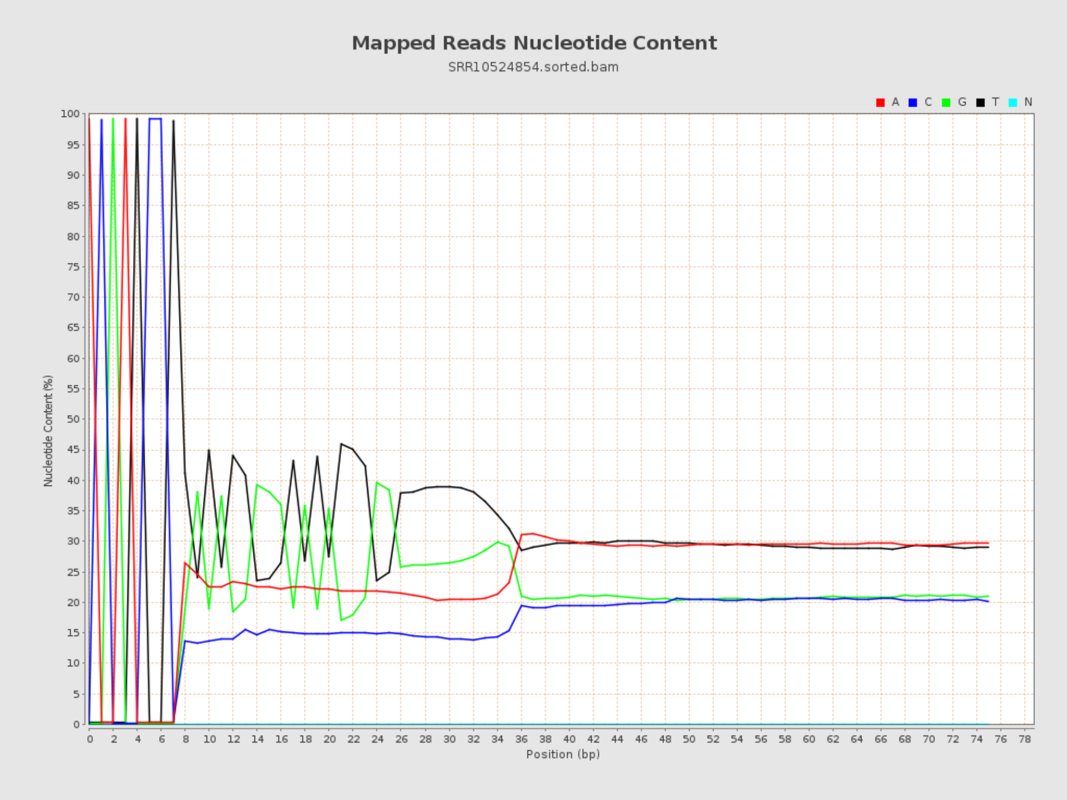
6. Results : Genome Fraction Coverage



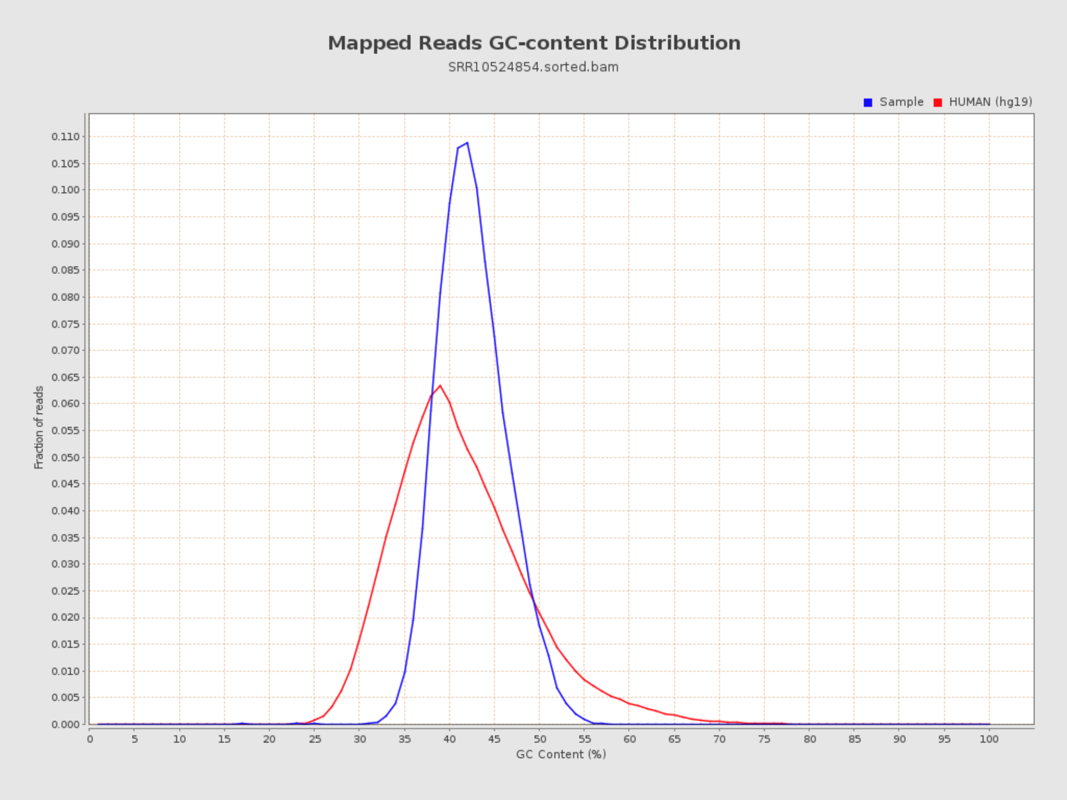
7. Results : Duplication Rate Histogram



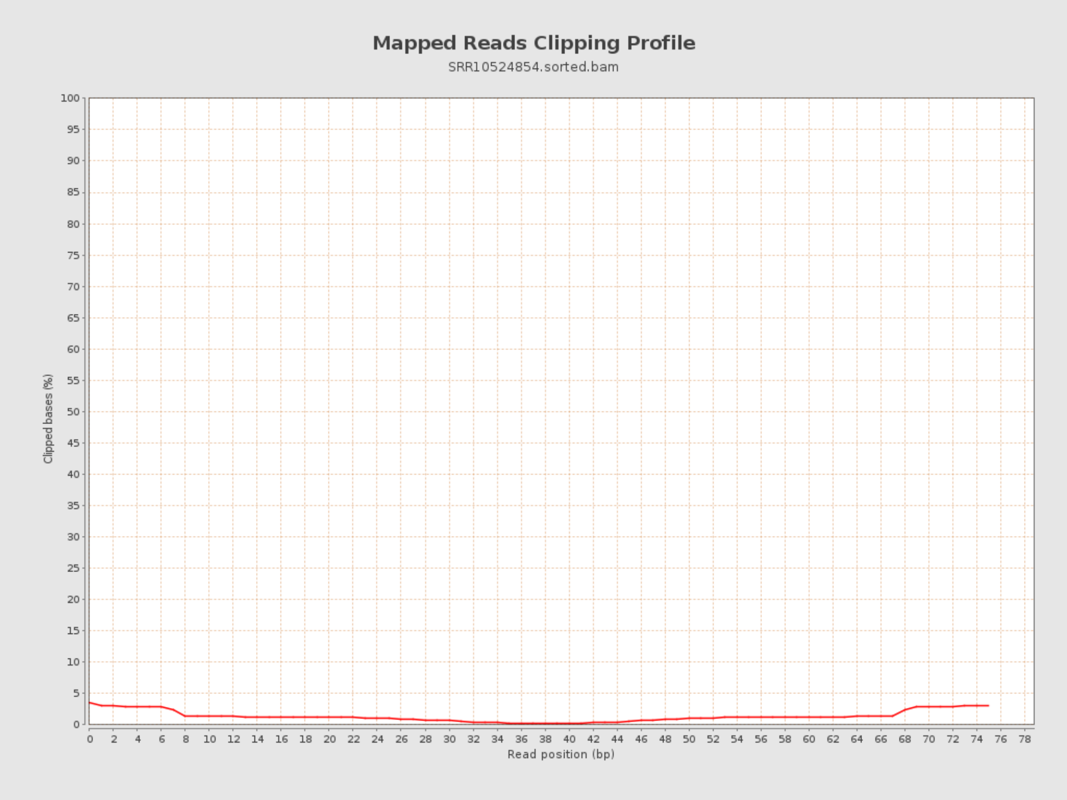
8. Results : Mapped Reads Nucleotide Content



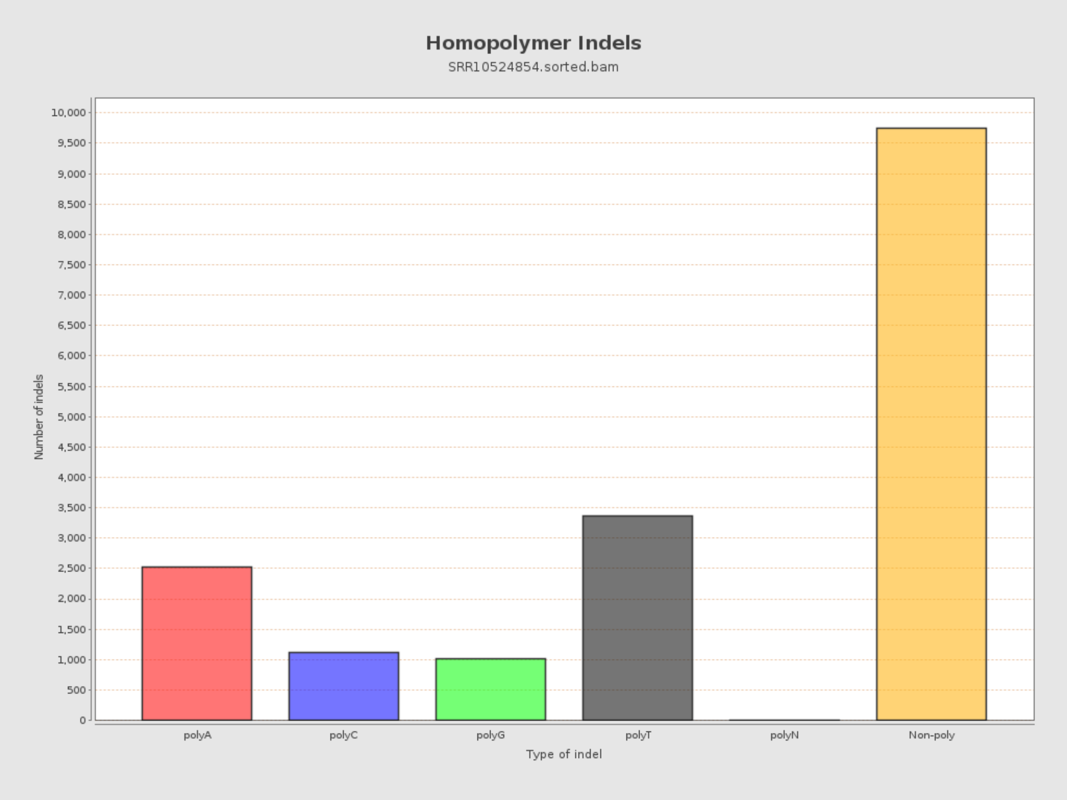
9. Results : Mapped Reads GC-content Distribution



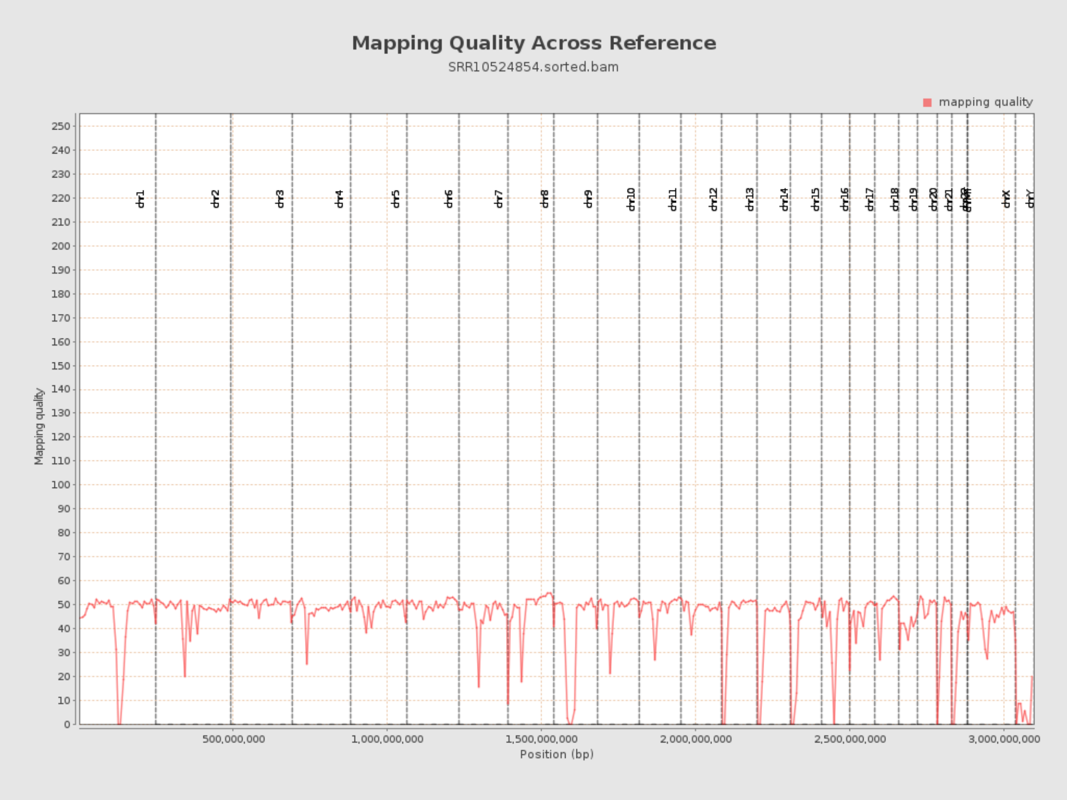
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram