Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:14:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524354.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_SRR10524354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524354.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:14:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	442,006
Mapped reads	408,094 / 92.33%
Unmapped reads	33,912 / 7.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,905 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	7,527 / 1.7%
Duplication rate	1.37%
Clipped reads	409,766 / 92.71%

2.2. ACGT Content

Number/percentage of A's	6,099,985 / 25.04%
Number/percentage of C's	4,952,295 / 20.33%
Number/percentage of T's	7,380,713 / 30.3%
Number/percentage of G's	5,925,419 / 24.32%
Number/percentage of N's	3,655 / 0.02%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1096

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

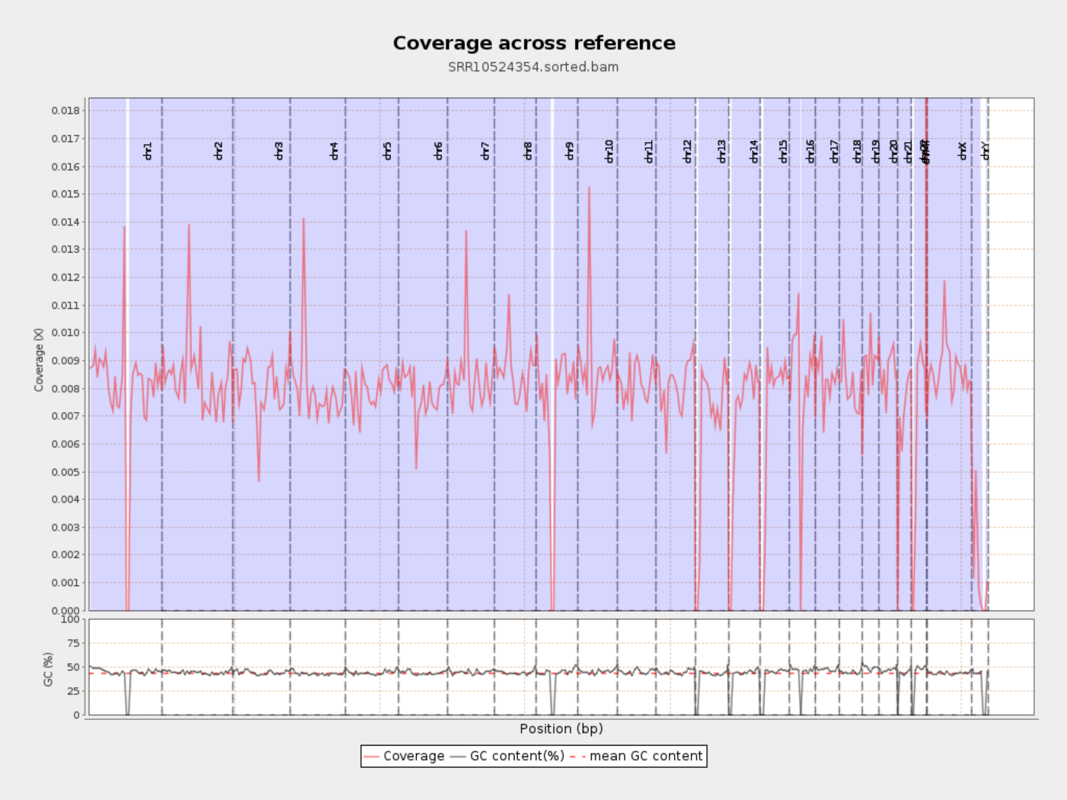
General error rate	0.52%
Mismatches	122,944
Insertions	1,476
Mapped reads with at least one insertion	0.36%
Deletions	4,414
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.68%

2.6. Chromosome stats

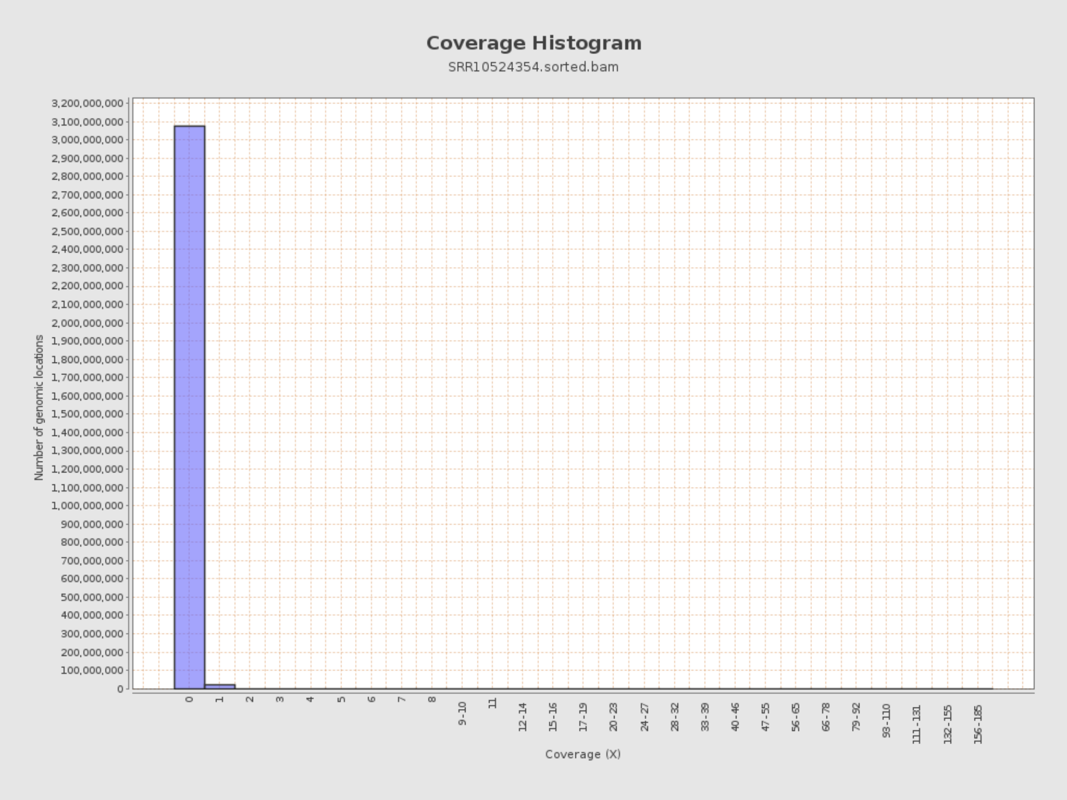
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1972771	0.0079	0.1698
chr2	243199373	2060639	0.0085	0.1257
chr3	198022430	1595562	0.0081	0.0925
chr4	191154276	1524584	0.008	0.0965
chr5	180915260	1448584	0.008	0.0922
chr6	171115067	1346289	0.0079	0.0931
chr7	159138663	1336574	0.0084	0.1272

chr8	146364022	1259381	0.0086	0.1053
chr9	141213431	1033188	0.0073	0.1014
chr10	135534747	1196636	0.0088	0.1099
chr11	135006516	1107389	0.0082	0.1057
chr12	133851895	1089428	0.0081	0.0935
chr13	115169878	752973	0.0065	0.0832
chr14	107349540	729697	0.0068	0.0862
chr15	102531392	707766	0.0069	0.0858
chr16	90354753	749263	0.0083	0.0964
chr17	81195210	681280	0.0084	0.098
chr18	78077248	634386	0.0081	0.15
chr19	59128983	525003	0.0089	0.1291
chr20	63025520	541691	0.0086	0.0968
chr21	48129895	324835	0.0067	0.0896
chr22	51304566	318102	0.0062	0.0813
chrMT	16571	5294	0.3195	0.5988
chrX	155270560	1346138	0.0087	0.0993
chrY	59373566	81782	0.0014	0.0518

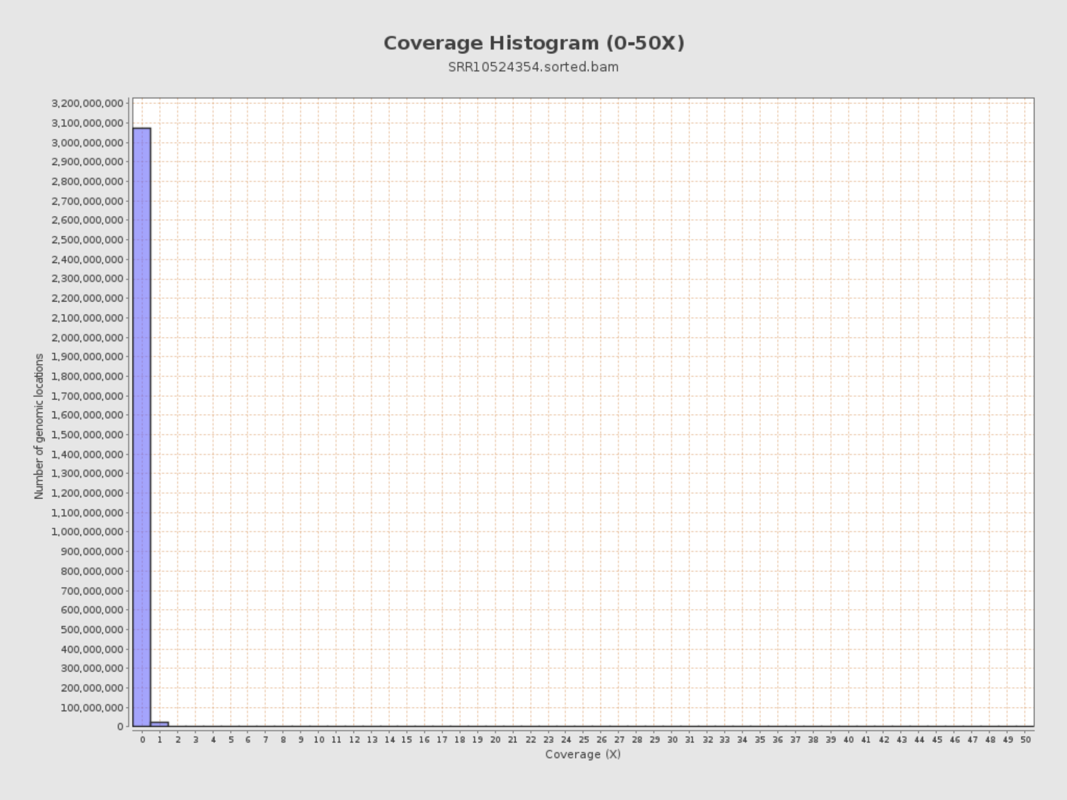
3. Results : Coverage across reference



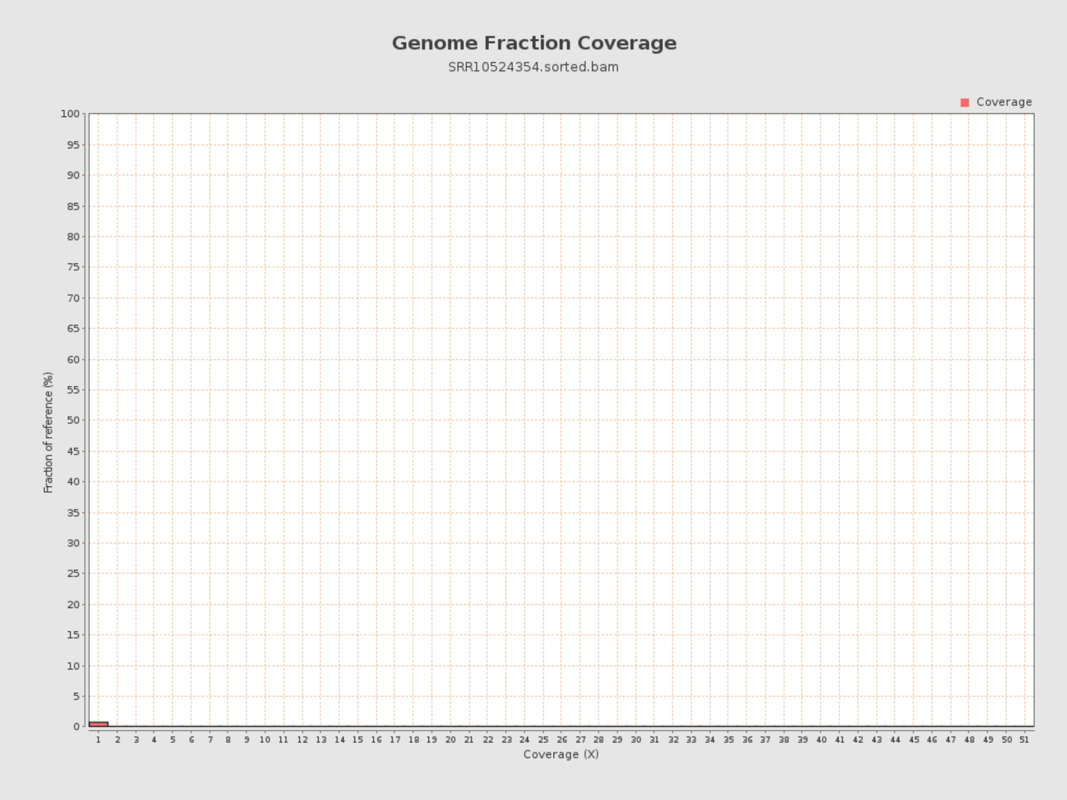
4. Results : Coverage Histogram



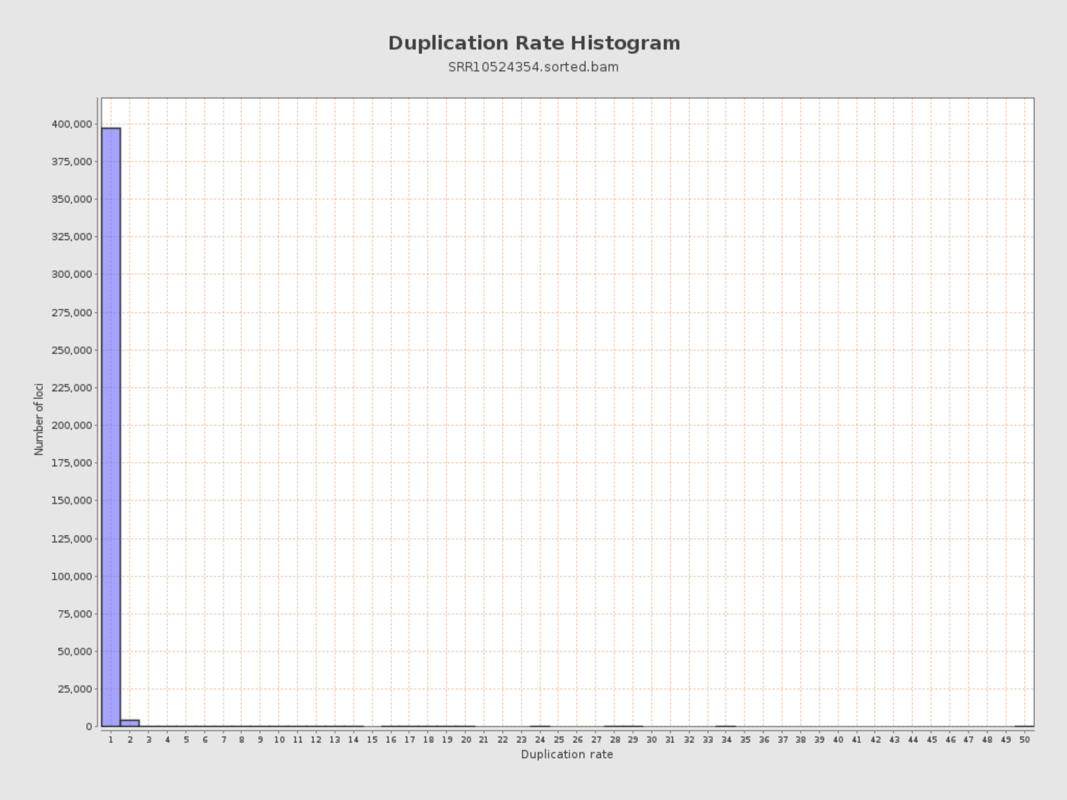
5. Results : Coverage Histogram (0-50X)



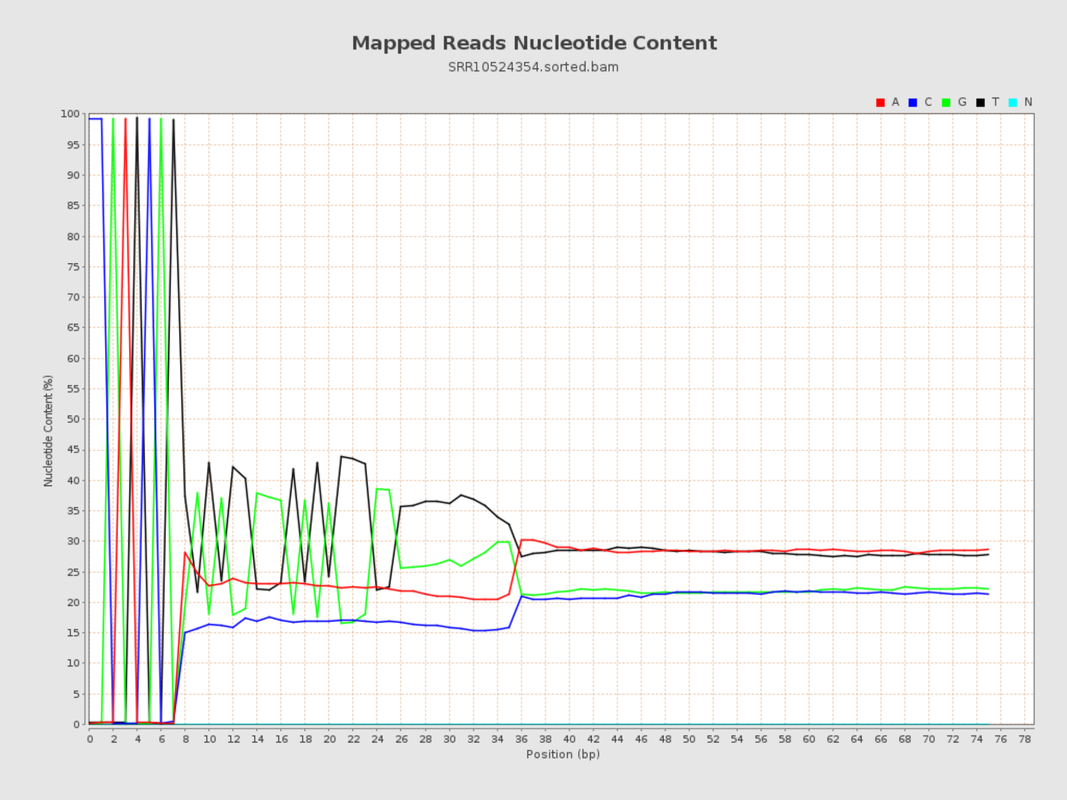
6. Results : Genome Fraction Coverage



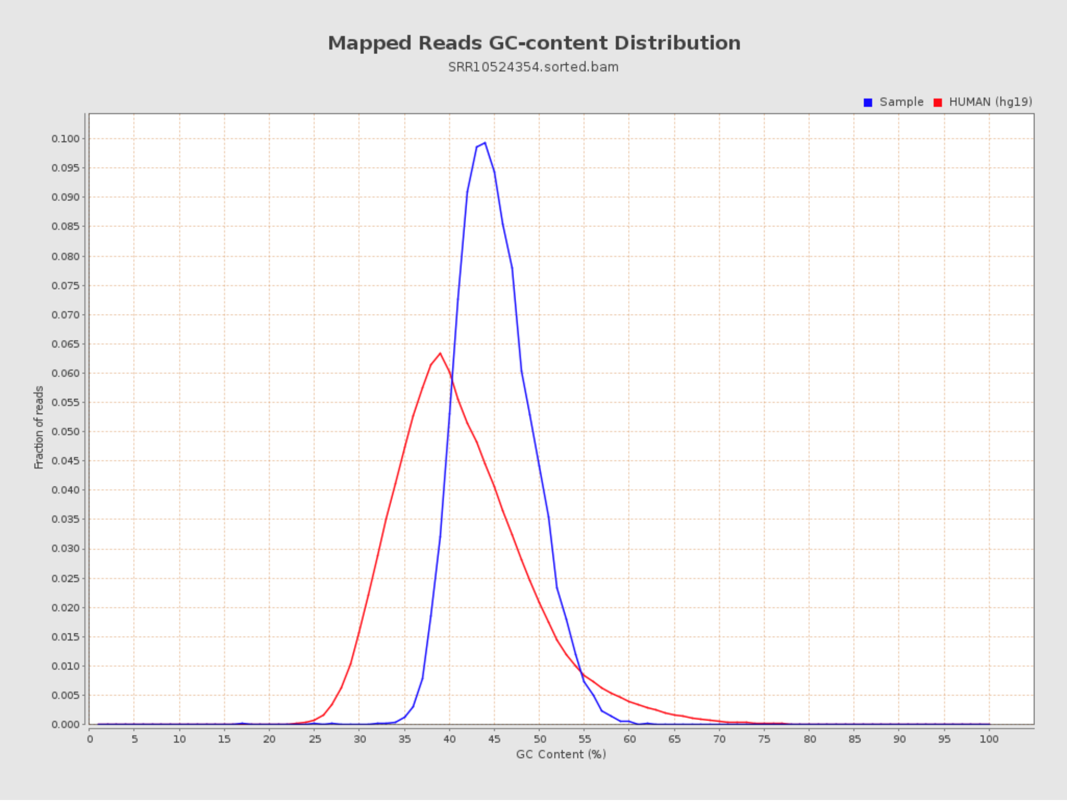
7. Results : Duplication Rate Histogram



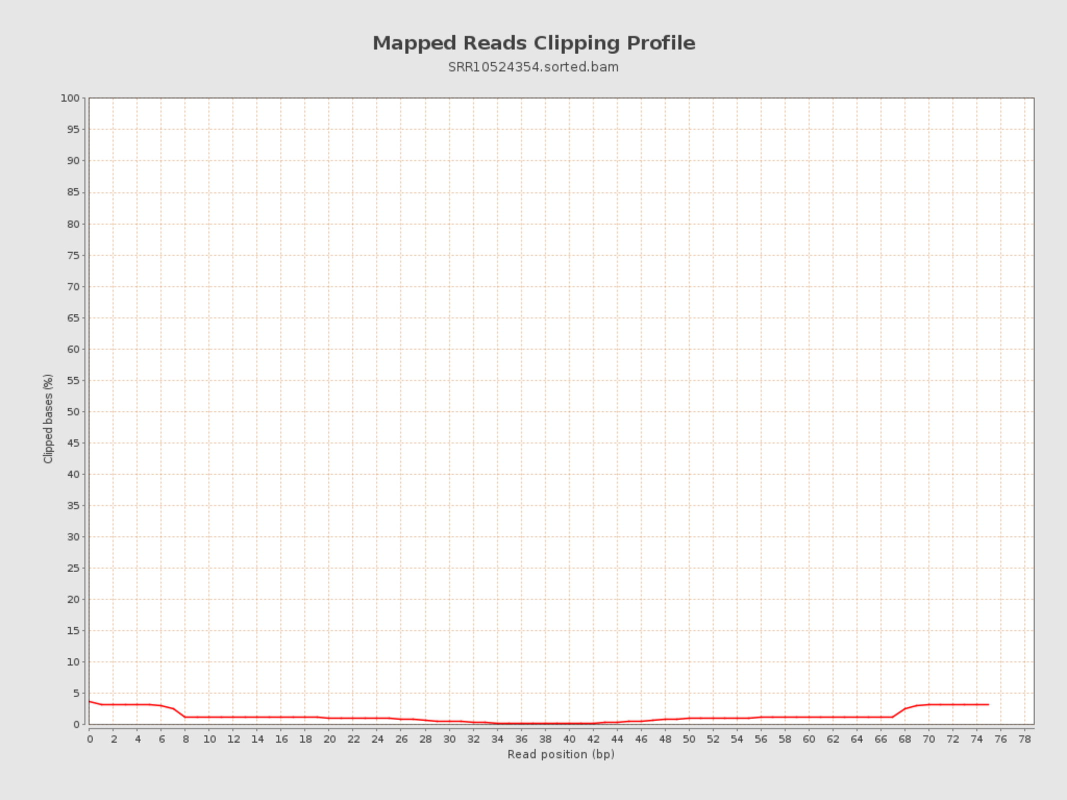
8. Results : Mapped Reads Nucleotide Content



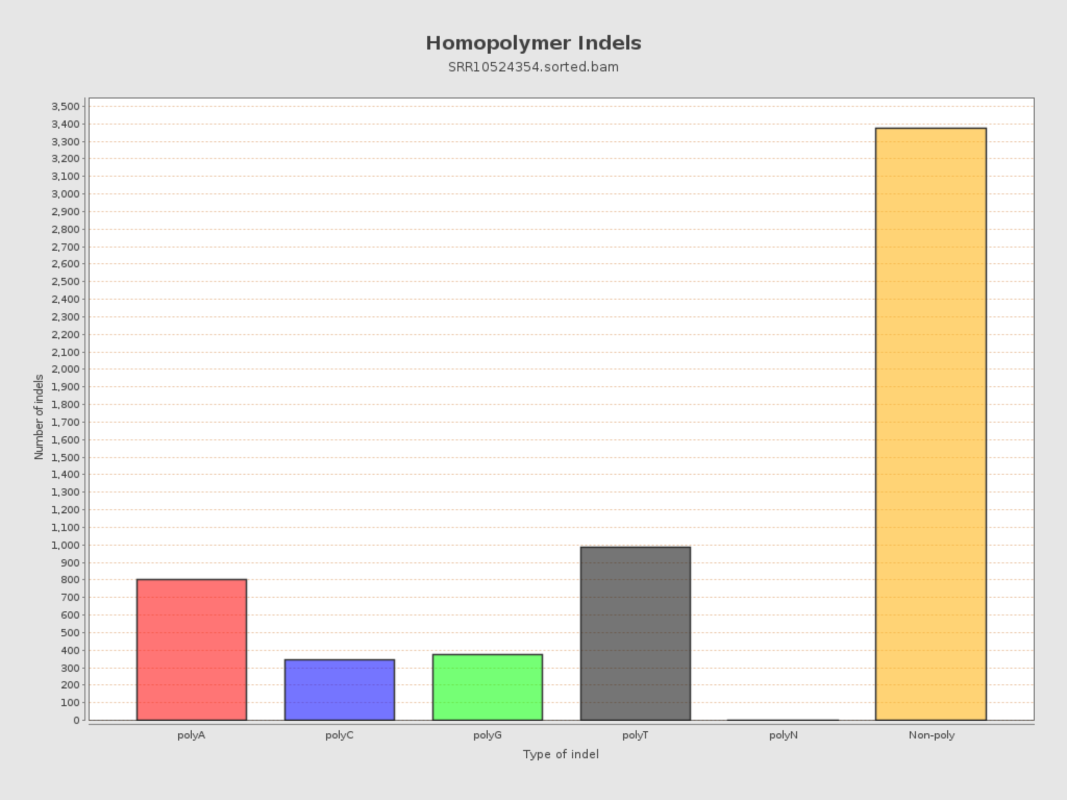
9. Results : Mapped Reads GC-content Distribution



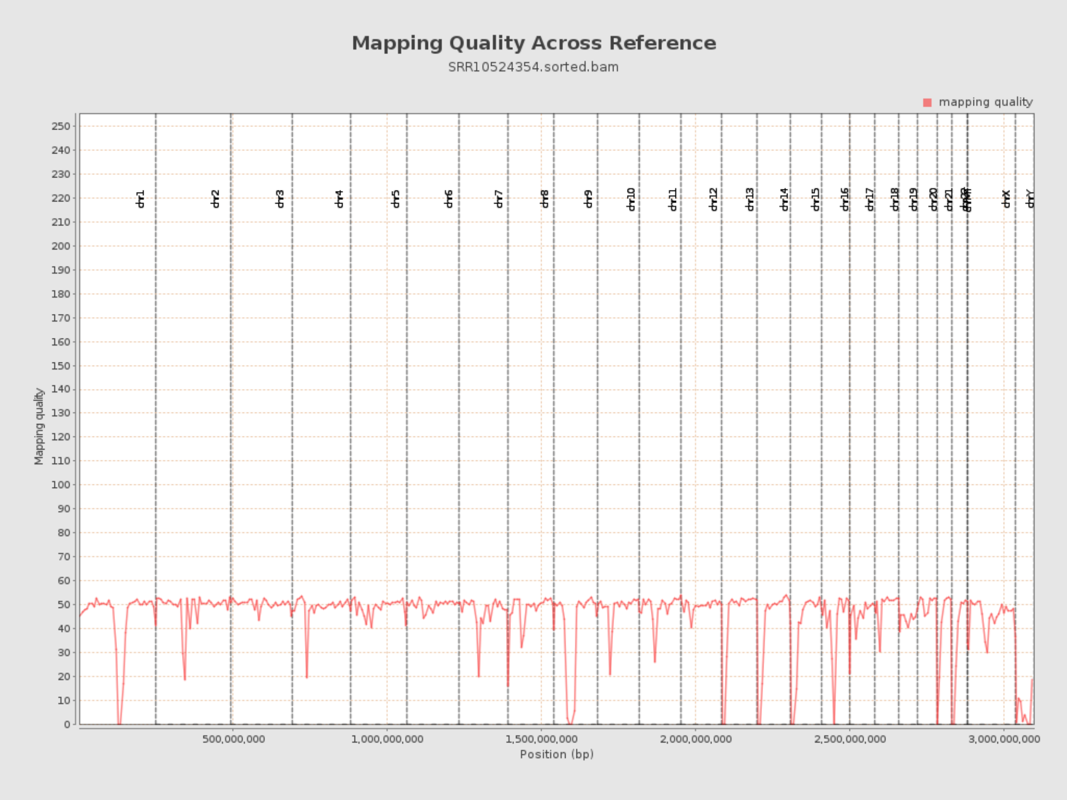
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram