Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:07:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524311.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_SRR10524311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:07:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,533
Mapped reads	1,407,849 / 92.23%
Unmapped reads	118,684 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,464 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	60,755 / 3.98%
Duplication rate	3.27%
Clipped reads	1,408,823 / 92.29%

2.2. ACGT Content

Number/percentage of A's	19,680,786 / 24.07%
Number/percentage of C's	16,349,886 / 19.99%
Number/percentage of T's	26,655,745 / 32.6%
Number/percentage of G's	19,086,254 / 23.34%
Number/percentage of N's	1,797 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2636

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

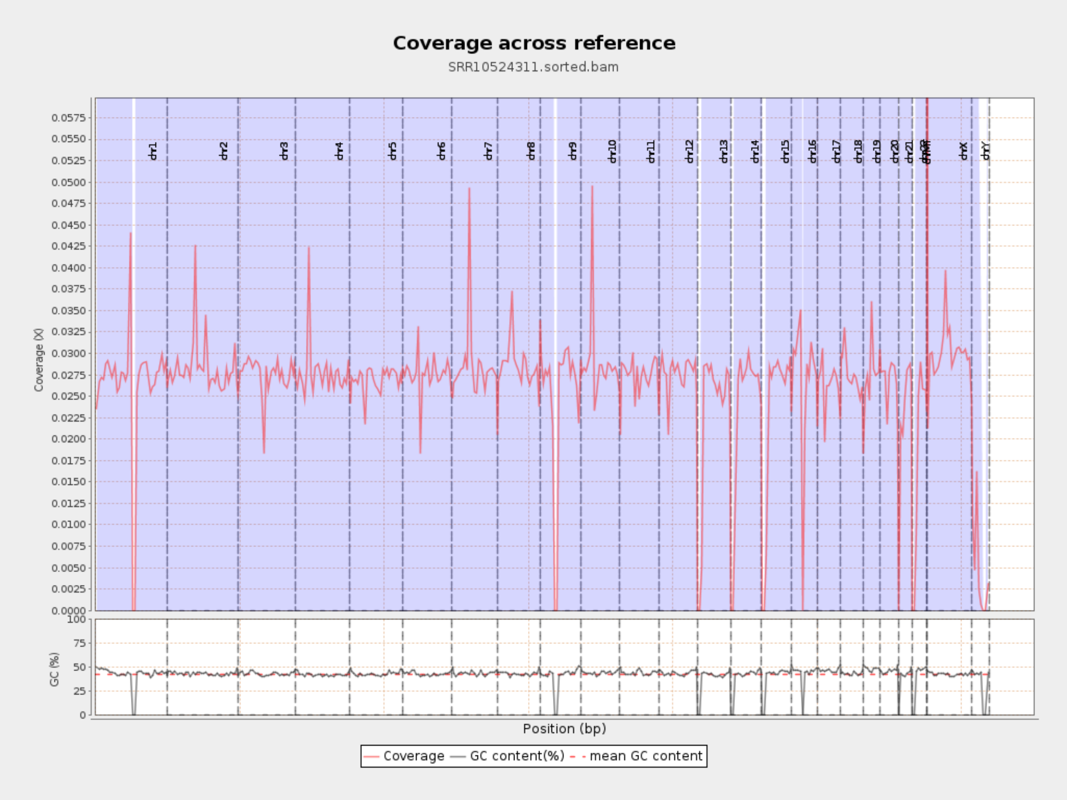
General error rate	0.52%
Mismatches	415,442
Insertions	6,060
Mapped reads with at least one insertion	0.43%
Deletions	17,674
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.06%

2.6. Chromosome stats

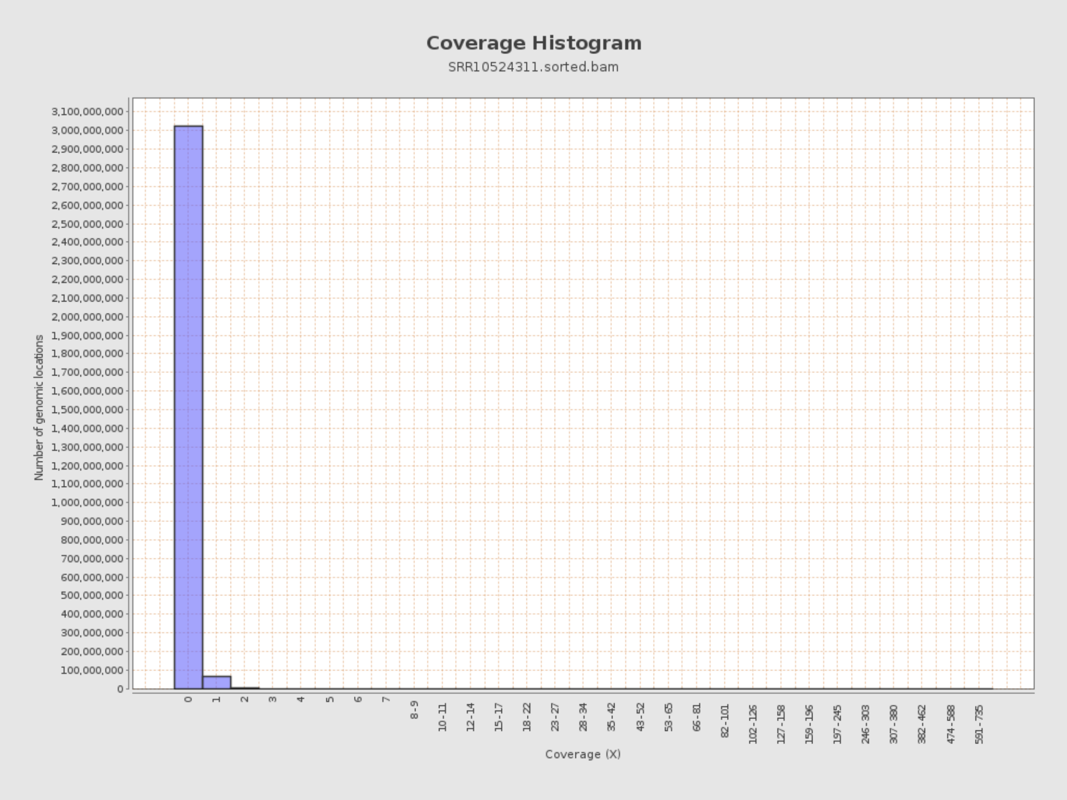
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6540675	0.0262	0.4503
chr2	243199373	6896063	0.0284	0.3616
chr3	198022430	5456030	0.0276	0.1811
chr4	191154276	5313814	0.0278	0.1981
chr5	180915260	4888780	0.027	0.1787
chr6	171115067	4717323	0.0276	0.1999
chr7	159138663	4570302	0.0287	0.3645

chr8	146364022	4201468	0.0287	0.2975
chr9	141213431	3478324	0.0246	0.2198
chr10	135534747	3925187	0.029	0.2544
chr11	135006516	3728061	0.0276	0.2184
chr12	133851895	3708782	0.0277	0.1839
chr13	115169878	2590441	0.0225	0.1647
chr14	107349540	2475777	0.0231	0.1693
chr15	102531392	2308795	0.0225	0.1638
chr16	90354753	2387805	0.0264	0.1901
chr17	81195210	2146429	0.0264	0.1835
chr18	78077248	2154757	0.0276	0.3841
chr19	59128983	1645157	0.0278	0.331
chr20	63025520	1691219	0.0268	0.1807
chr21	48129895	1091455	0.0227	0.1808
chr22	51304566	937678	0.0183	0.1459
chrMT	16571	10389	0.6269	0.961
chrX	155270560	4670927	0.0301	0.2051
chrY	59373566	267257	0.0045	0.1398

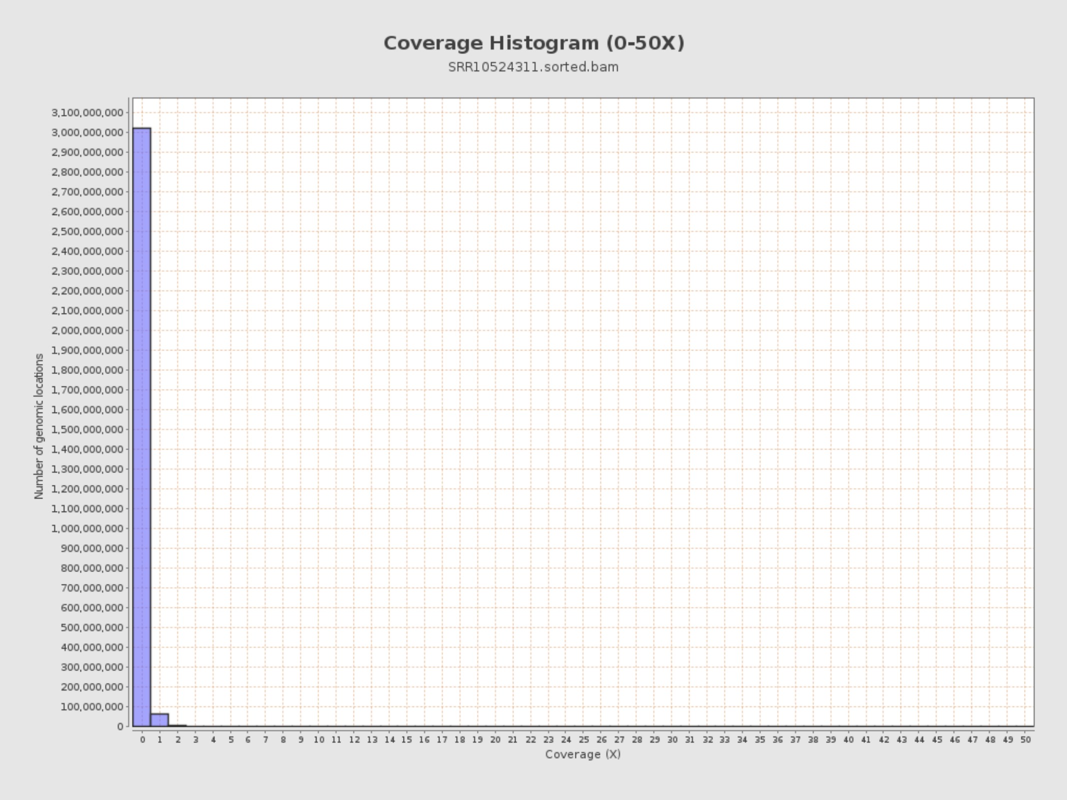
3. Results : Coverage across reference



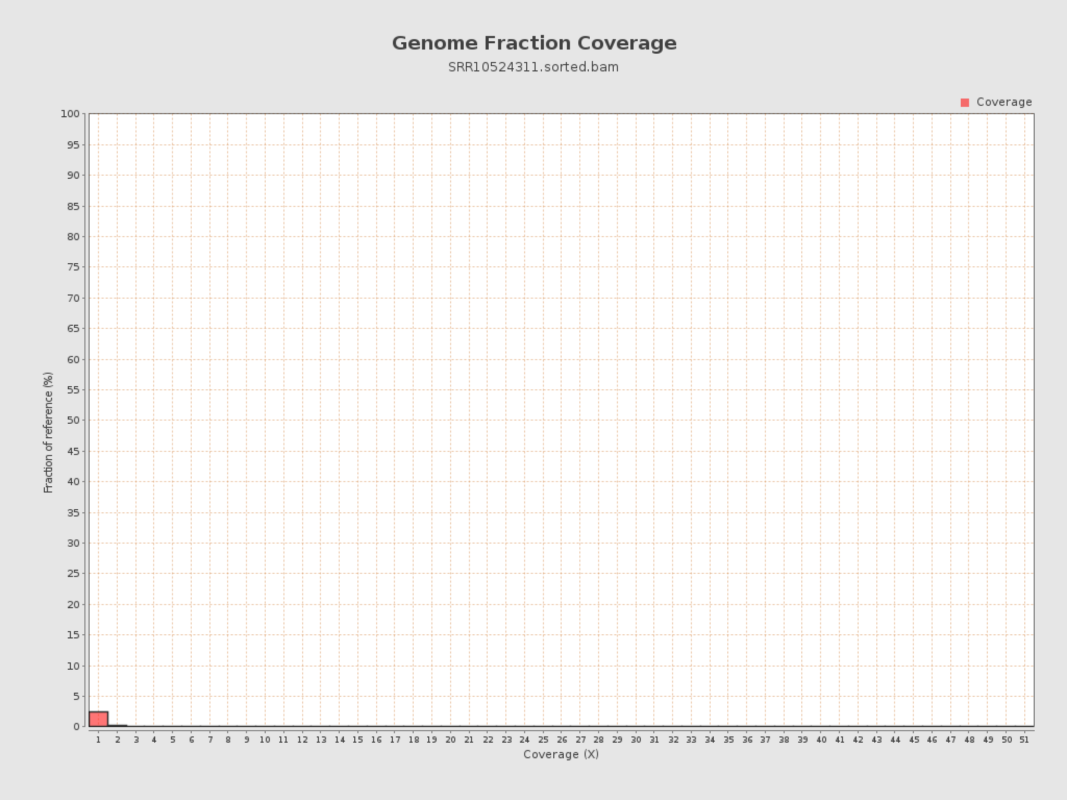
4. Results : Coverage Histogram



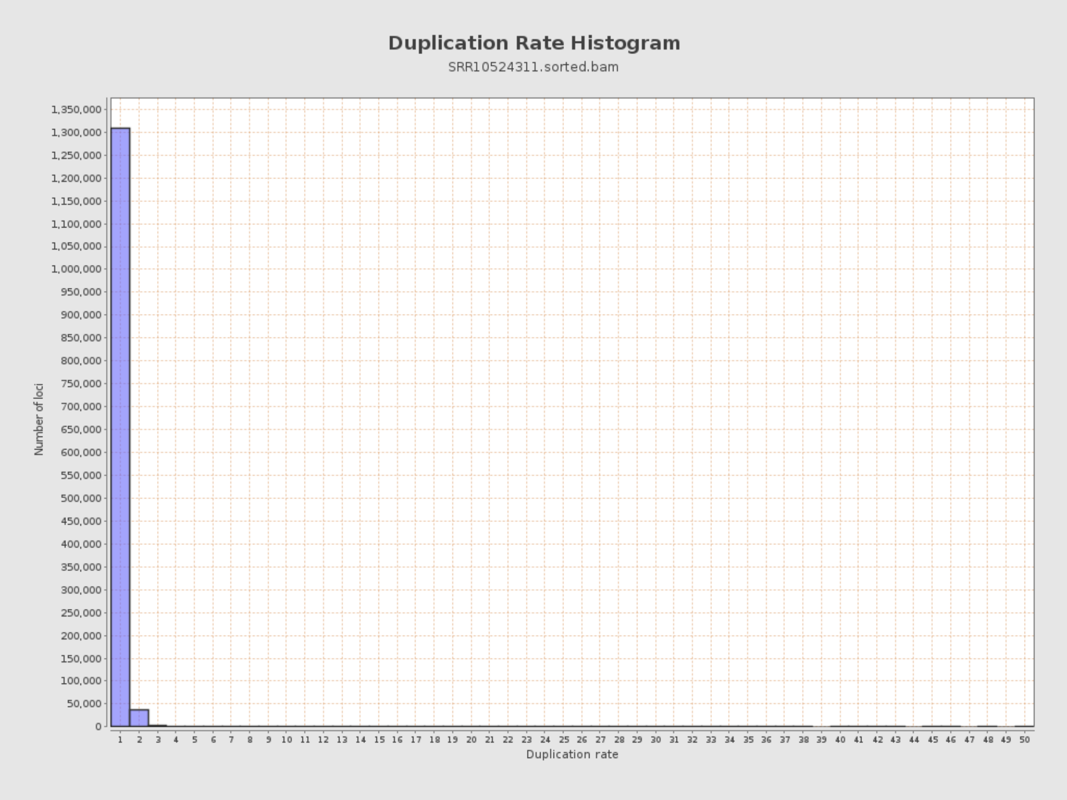
5. Results : Coverage Histogram (0-50X)



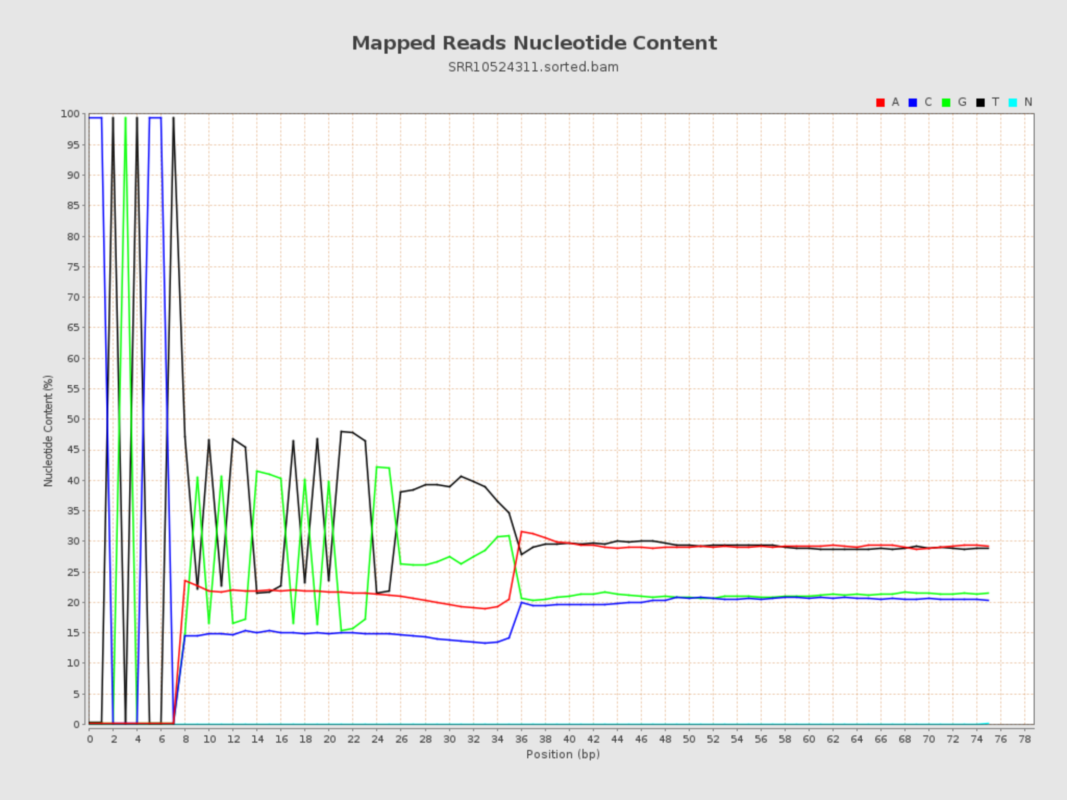
6. Results : Genome Fraction Coverage



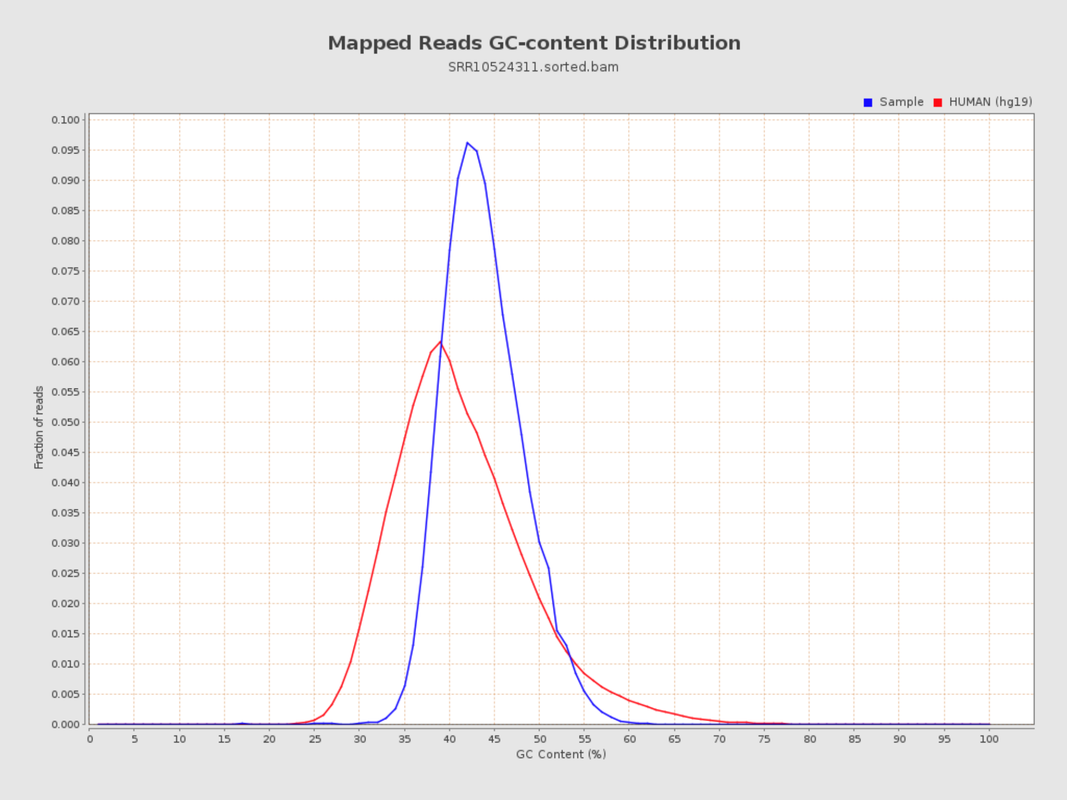
7. Results : Duplication Rate Histogram



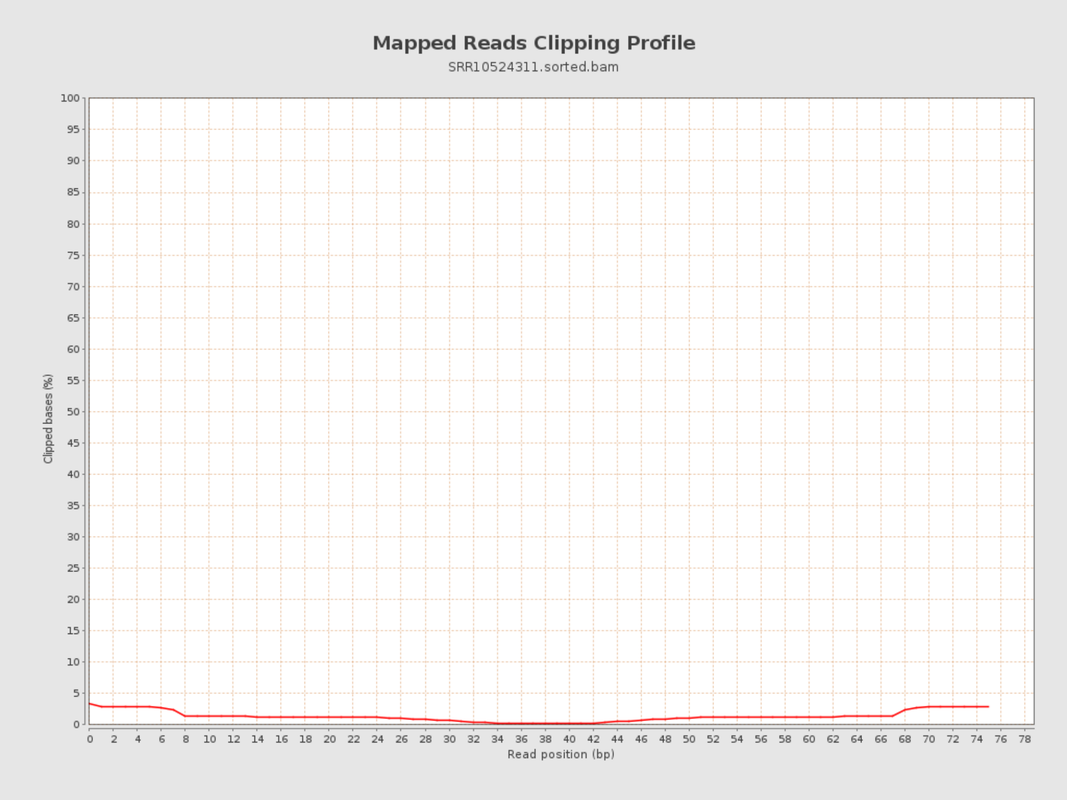
8. Results : Mapped Reads Nucleotide Content



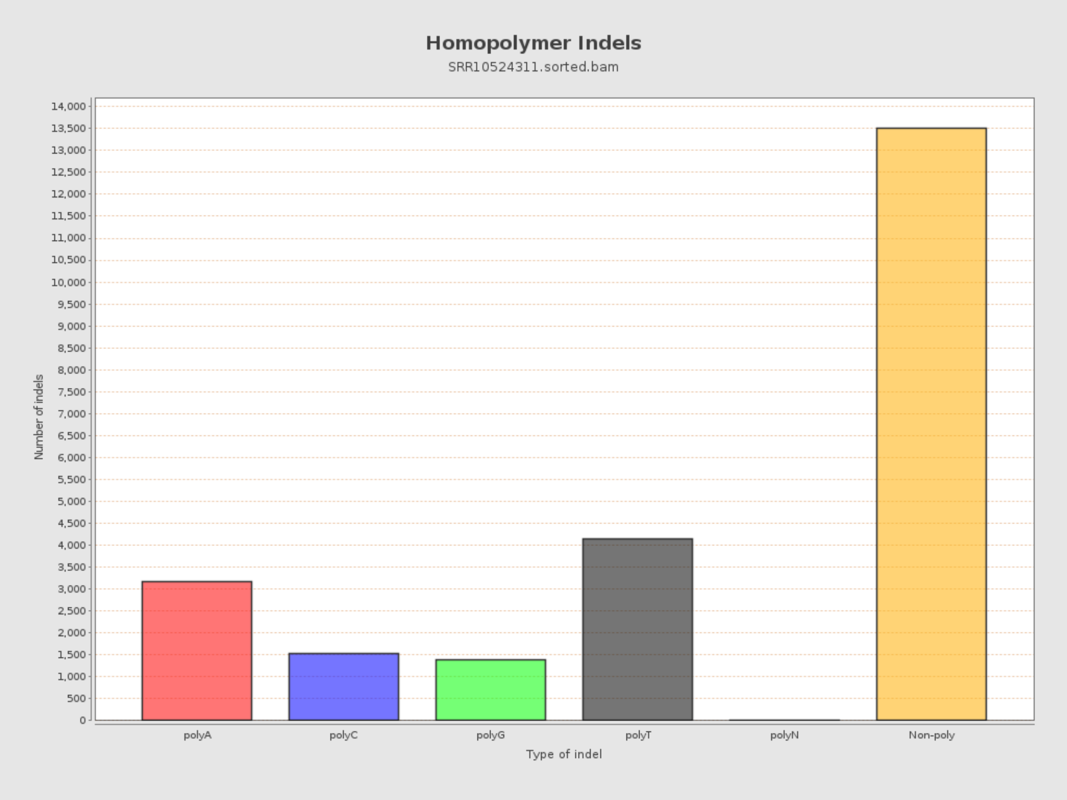
9. Results : Mapped Reads GC-content Distribution



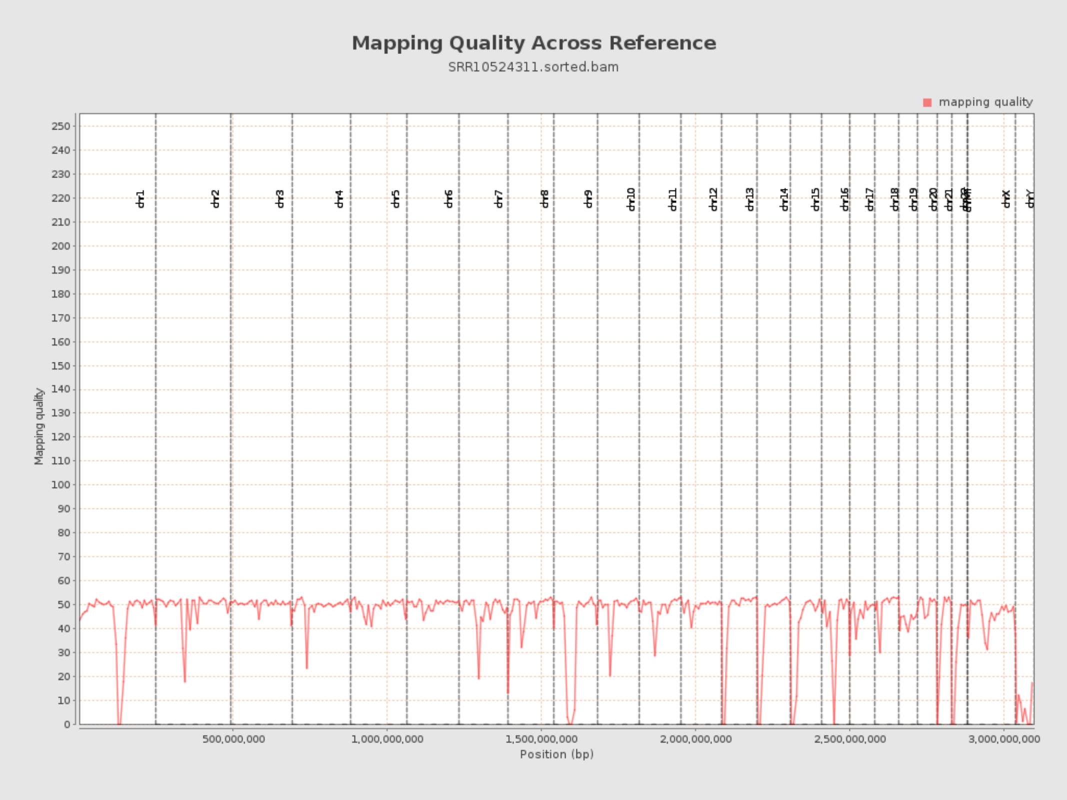
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram