Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:03:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524850.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_SRR10524850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:03:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,104
Mapped reads	6,655 / 65.87%
Unmapped reads	3,449 / 34.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	215 / 2.13%
Duplication rate	3.06%
Clipped reads	6,660 / 65.91%

2.2. ACGT Content

Number/percentage of A's	94,650 / 24.91%
Number/percentage of C's	69,734 / 18.35%
Number/percentage of T's	123,791 / 32.58%
Number/percentage of G's	91,821 / 24.16%
Number/percentage of N's	12 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.012

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

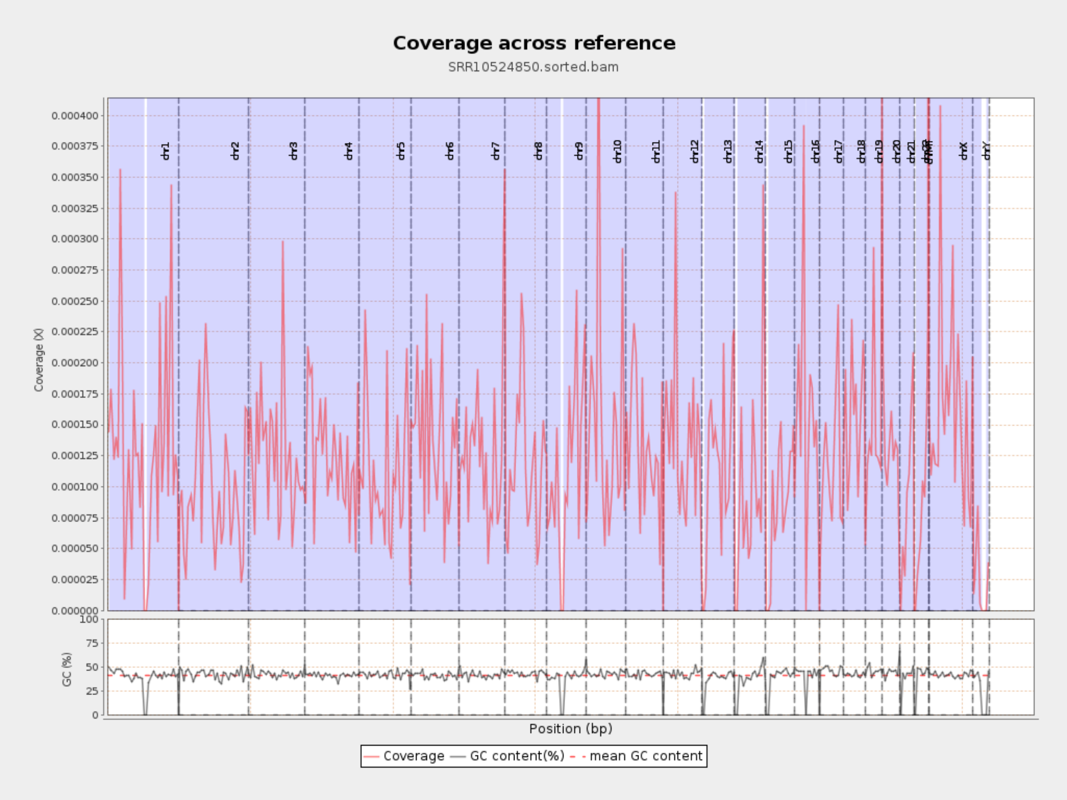
General error rate	0.52%
Mismatches	1,930
Insertions	31
Mapped reads with at least one insertion	0.47%
Deletions	85
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.69%

2.6. Chromosome stats

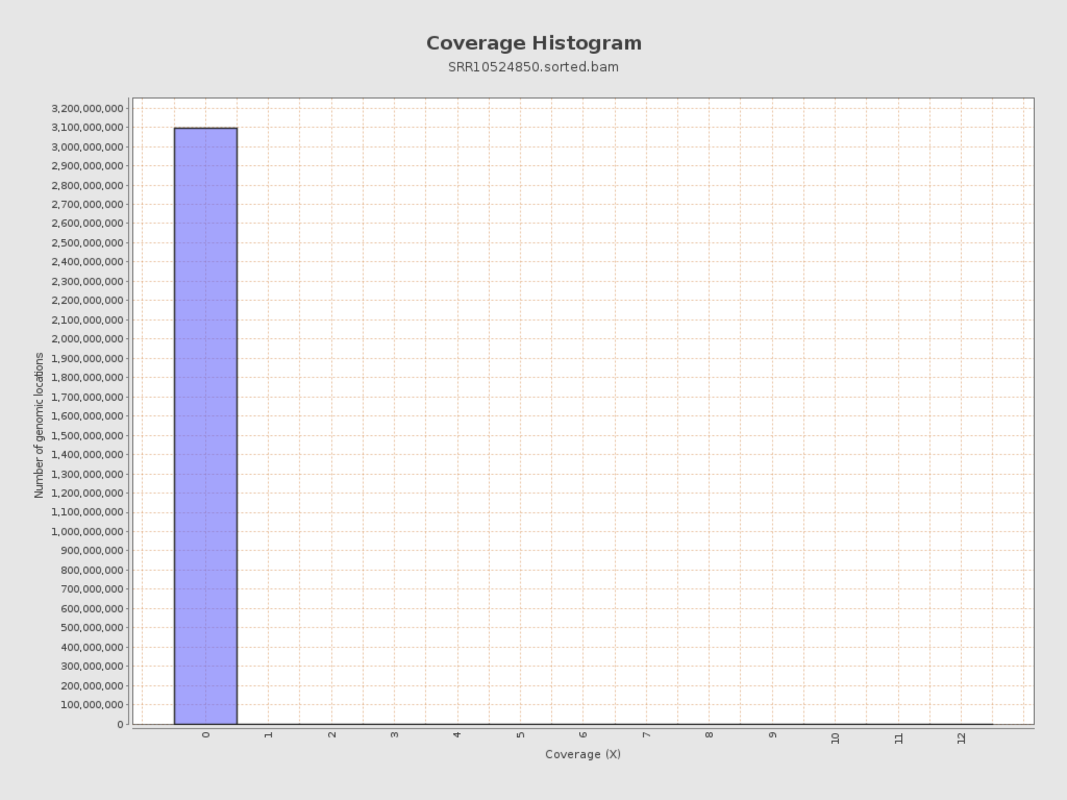
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32181	0.0001	0.0125
chr2	243199373	23676	0.0001	0.0106
chr3	198022430	24669	0.0001	0.0121
chr4	191154276	24033	0.0001	0.0119
chr5	180915260	20272	0.0001	0.0113
chr6	171115067	23526	0.0001	0.0124
chr7	159138663	19977	0.0001	0.0118

chr8	146364022	17232	0.0001	0.0115
chr9	141213431	16203	0.0001	0.0114
chr10	135534747	20973	0.0002	0.0132
chr11	135006516	18033	0.0001	0.0123
chr12	133851895	18608	0.0001	0.0127
chr13	115169878	13414	0.0001	0.0118
chr14	107349540	10576	0.0001	0.0144
chr15	102531392	8399	0.0001	0.0096
chr16	90354753	13780	0.0002	0.0134
chr17	81195210	9927	0.0001	0.0119
chr18	78077248	12434	0.0002	0.0134
chr19	59128983	9062	0.0002	0.0133
chr20	63025520	8176	0.0001	0.0125
chr21	48129895	4510	0.0001	0.0104
chr22	51304566	3921	0.0001	0.0092
chrMT	16571	63	0.0038	0.0615
chrX	155270560	25268	0.0002	0.0139
chrY	59373566	1244	0	0.0049

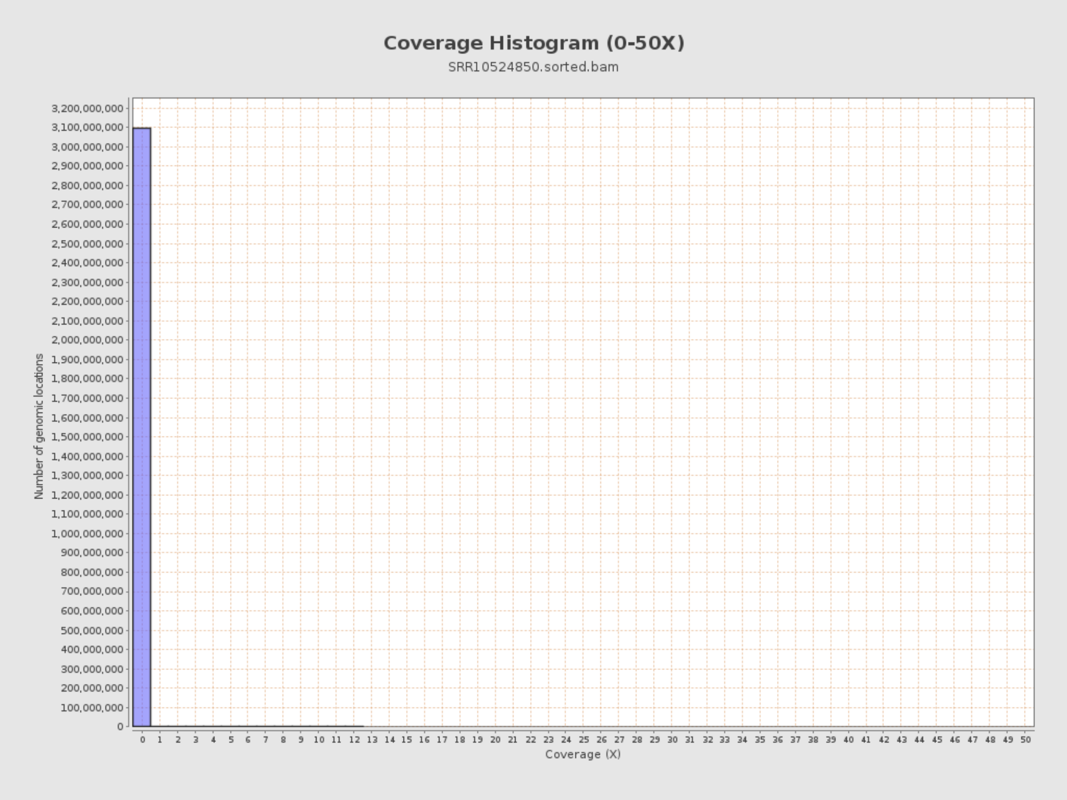
3. Results : Coverage across reference



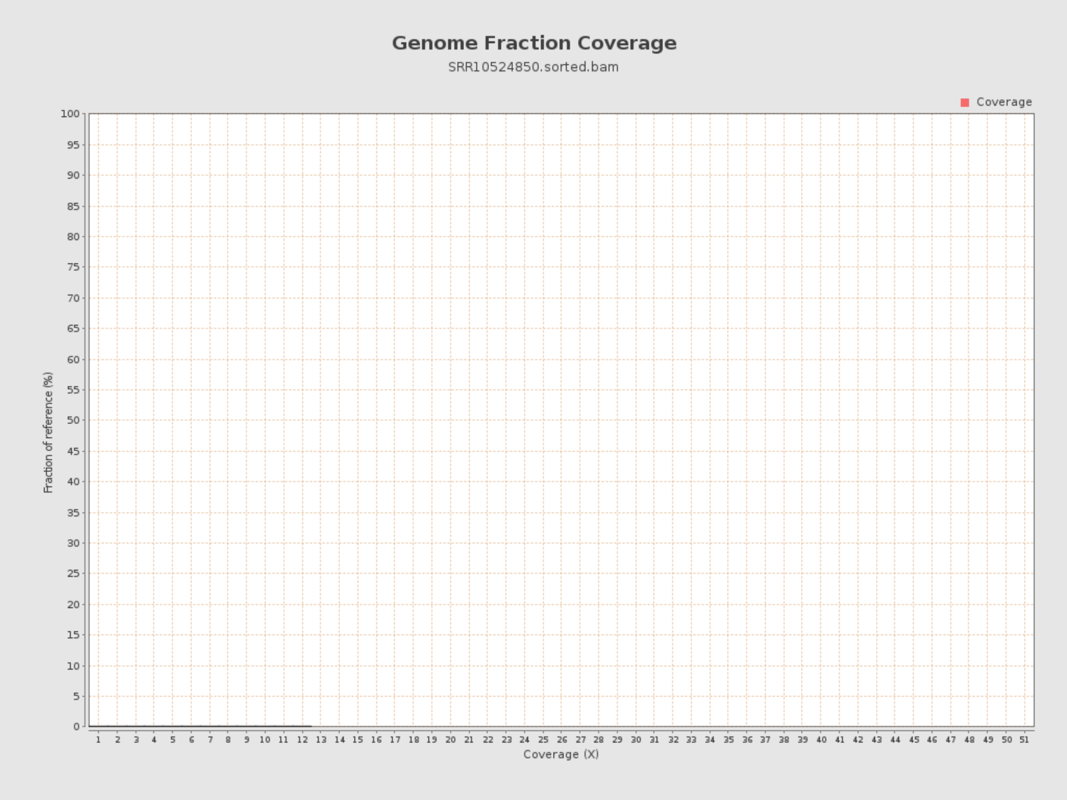
4. Results : Coverage Histogram



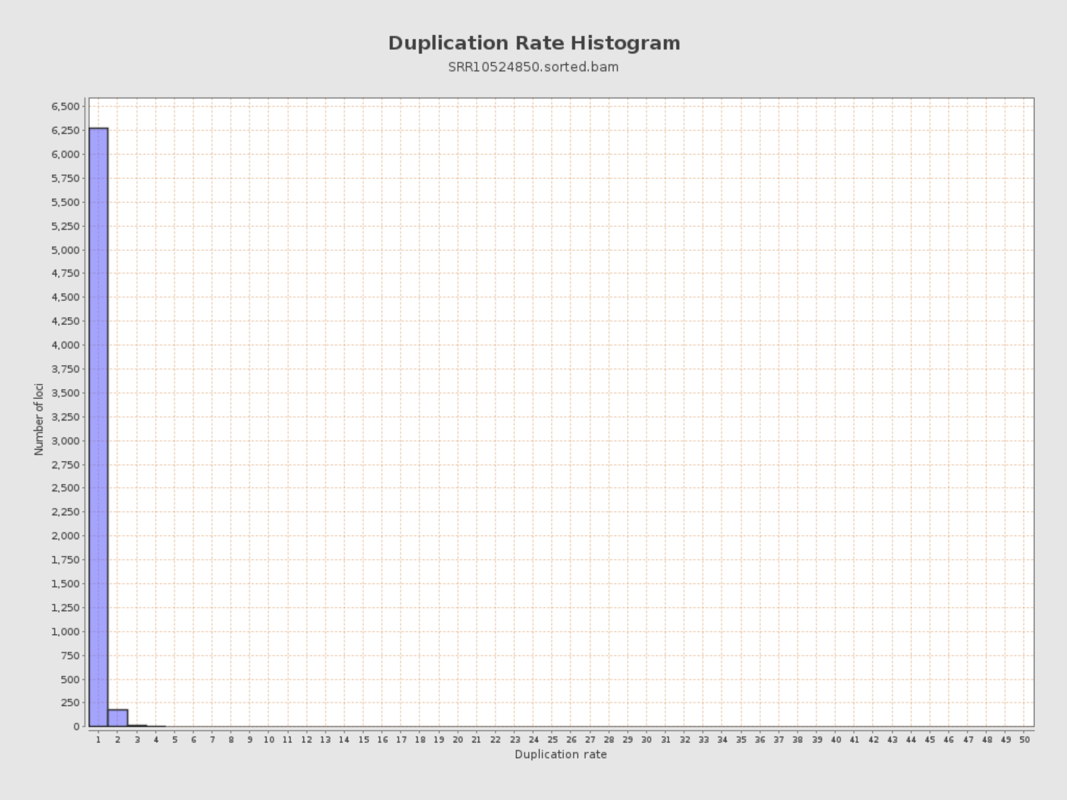
5. Results : Coverage Histogram (0-50X)



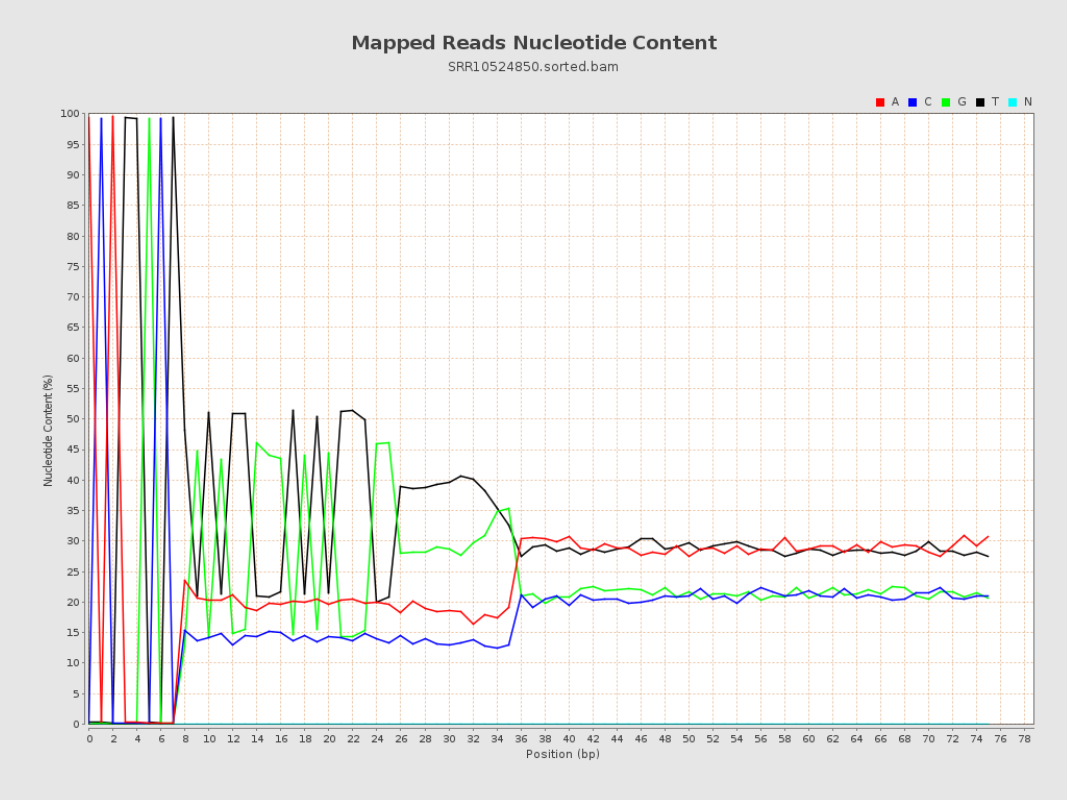
6. Results : Genome Fraction Coverage



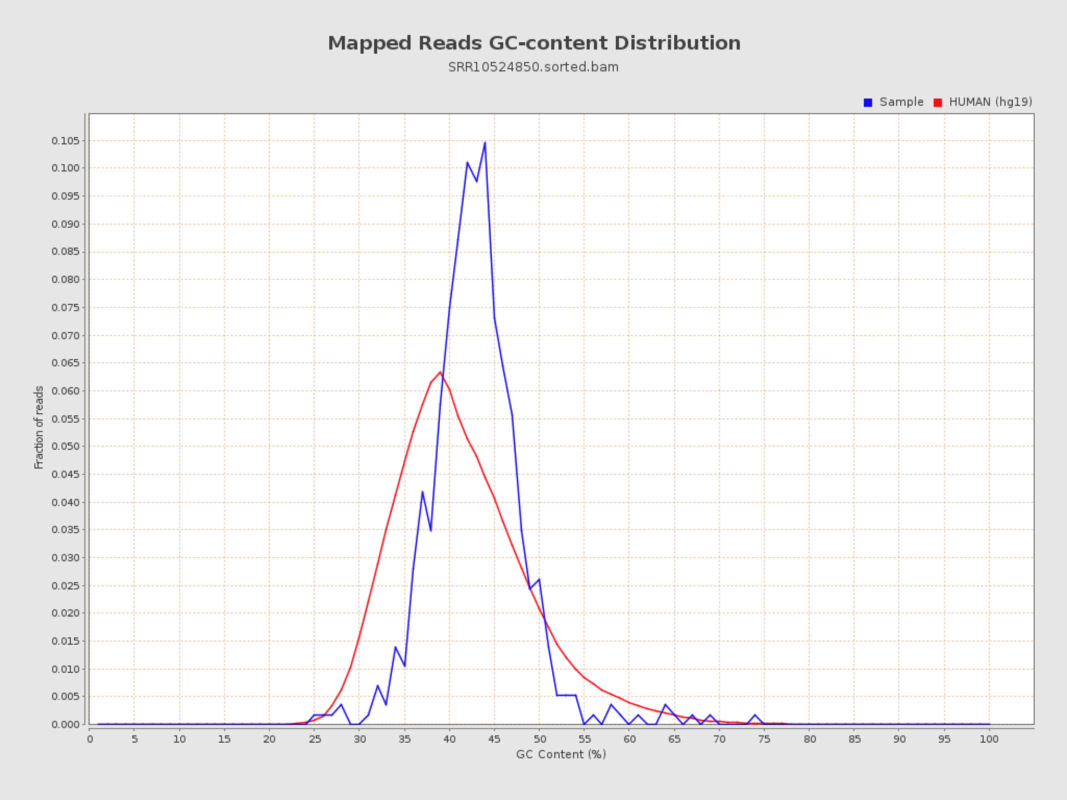
7. Results : Duplication Rate Histogram



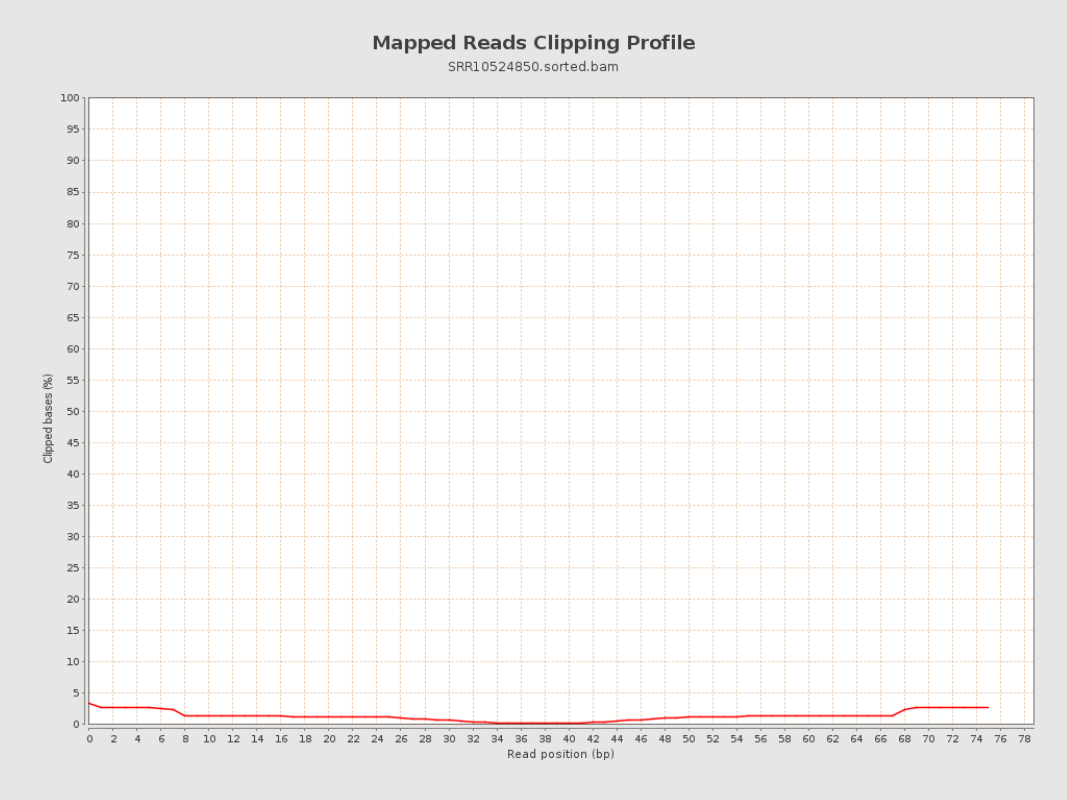
8. Results : Mapped Reads Nucleotide Content



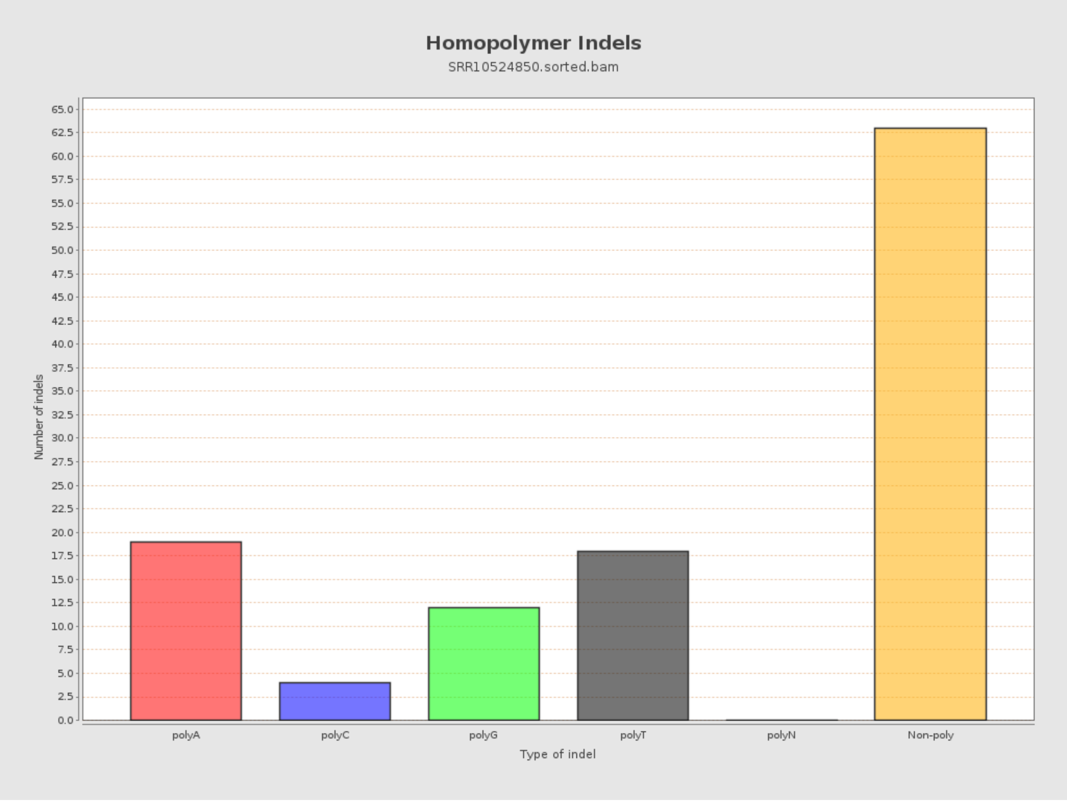
9. Results : Mapped Reads GC-content Distribution



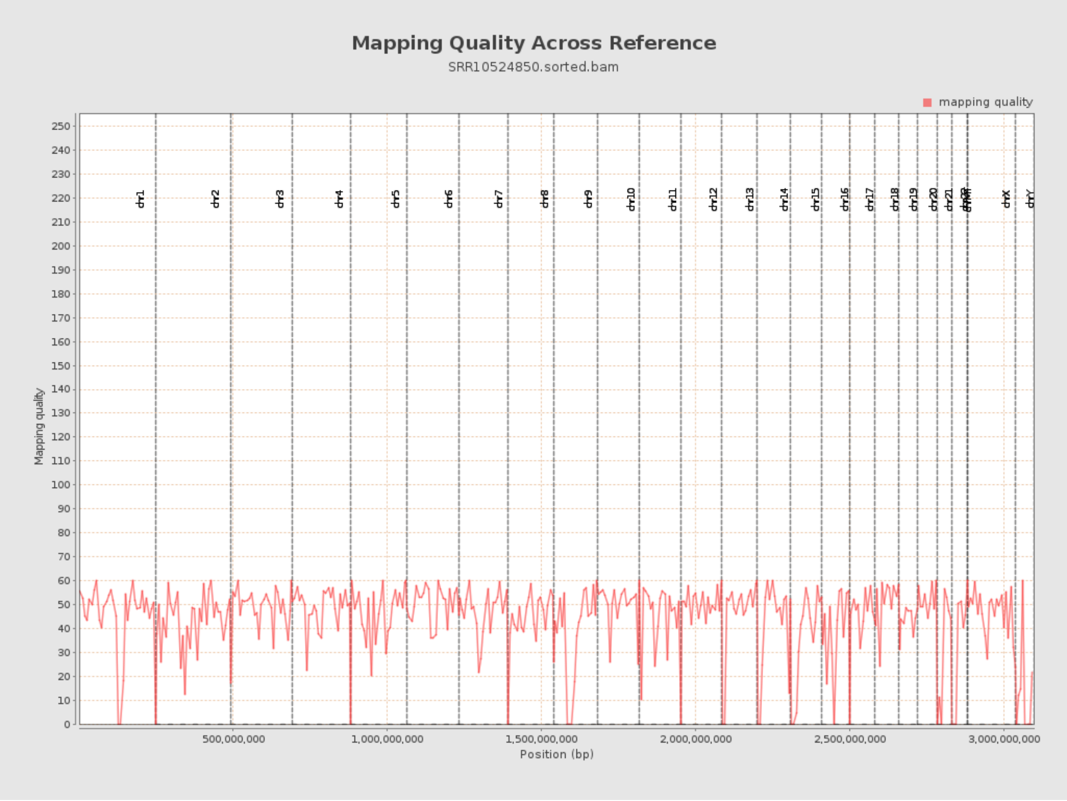
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram