Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:49:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524613.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_SRR10524613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:49:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,006,211
Mapped reads	1,868,577 / 93.14%
Unmapped reads	137,634 / 6.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,283 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	94,317 / 4.7%
Duplication rate	3.92%
Clipped reads	1,867,719 / 93.1%

2.2. ACGT Content

Number/percentage of A's	27,036,367 / 24.81%
Number/percentage of C's	19,211,996 / 17.63%
Number/percentage of T's	36,086,518 / 33.11%
Number/percentage of G's	26,657,170 / 24.46%
Number/percentage of N's	653 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0352

Standard Deviation	0.3059

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

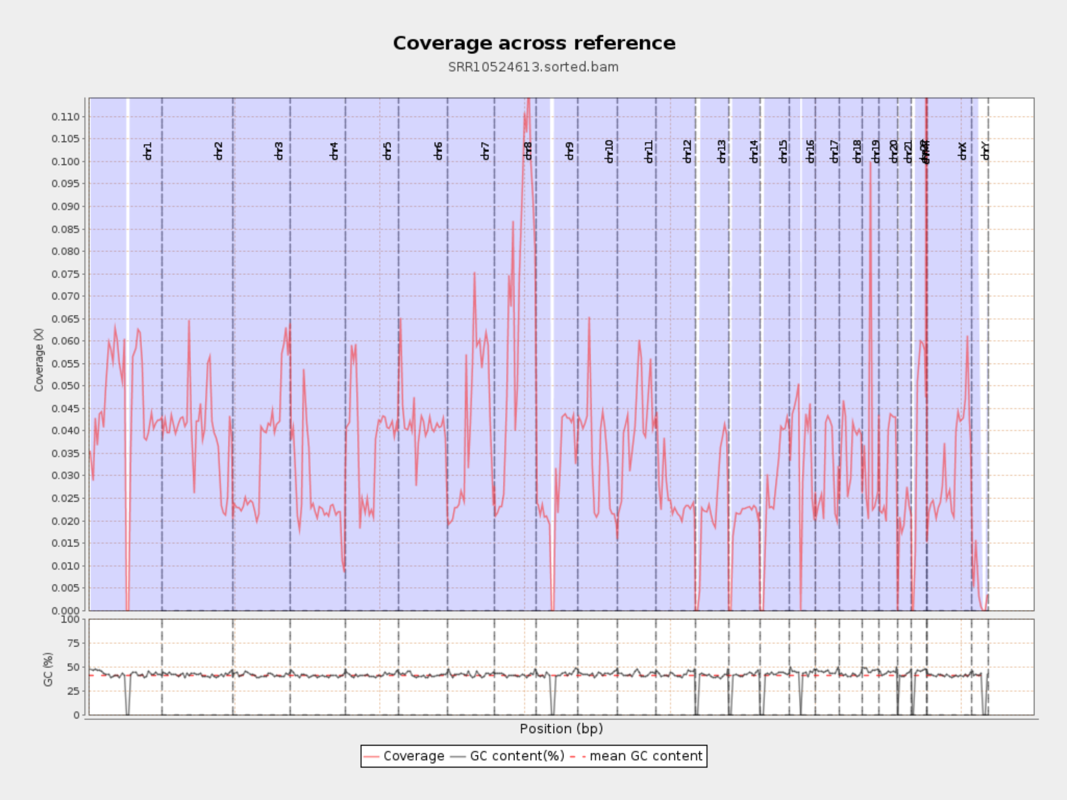
General error rate	0.49%
Mismatches	515,189
Insertions	7,234
Mapped reads with at least one insertion	0.39%
Deletions	20,293
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.77%

2.6. Chromosome stats

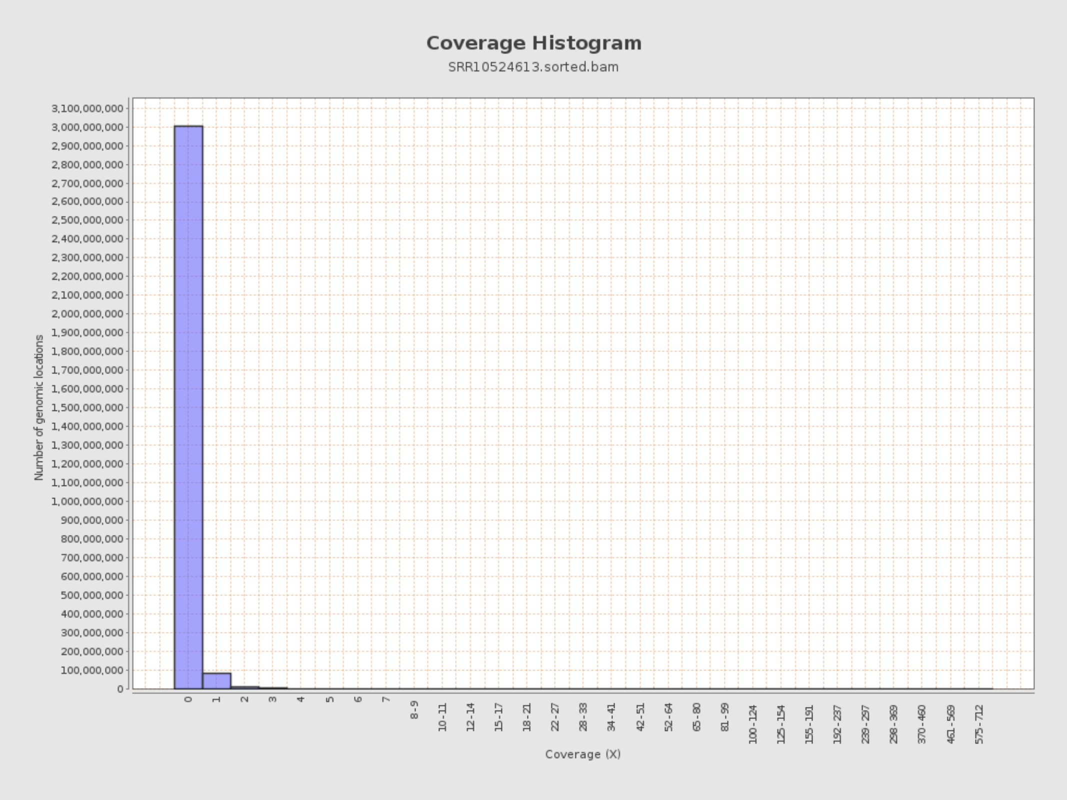
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11238629	0.0451	0.5405
chr2	243199373	9737059	0.04	0.3557
chr3	198022430	7009191	0.0354	0.2136
chr4	191154276	4849207	0.0254	0.2119
chr5	180915260	6819019	0.0377	0.2194
chr6	171115067	7149187	0.0418	0.2515
chr7	159138663	6579181	0.0413	0.3955

chr8	146364022	9678692	0.0661	0.4126
chr9	141213431	3964379	0.0281	0.2678
chr10	135534747	4673587	0.0345	0.3104
chr11	135006516	5553786	0.0411	0.2955
chr12	133851895	3396033	0.0254	0.1856
chr13	115169878	2657098	0.0231	0.1736
chr14	107349540	2055370	0.0191	0.1645
chr15	102531392	2749473	0.0268	0.1938
chr16	90354753	3200046	0.0354	0.2258
chr17	81195210	2455821	0.0302	0.2051
chr18	78077248	2937681	0.0376	0.4646
chr19	59128983	2133947	0.0361	0.37
chr20	63025520	2042380	0.0324	0.2081
chr21	48129895	939969	0.0195	0.1726
chr22	51304566	1964648	0.0383	0.22
chrMT	16571	15683	0.9464	1.2976
chrX	155270560	4963550	0.032	0.2316
chrY	59373566	263813	0.0044	0.1242

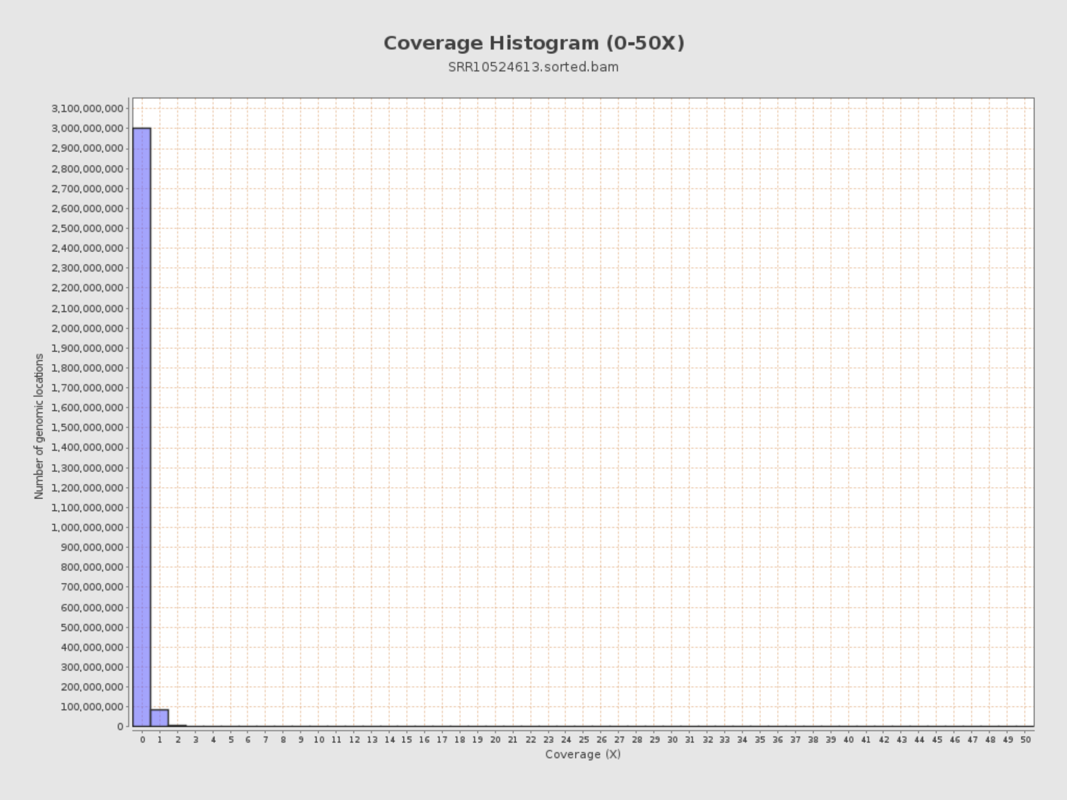
3. Results : Coverage across reference



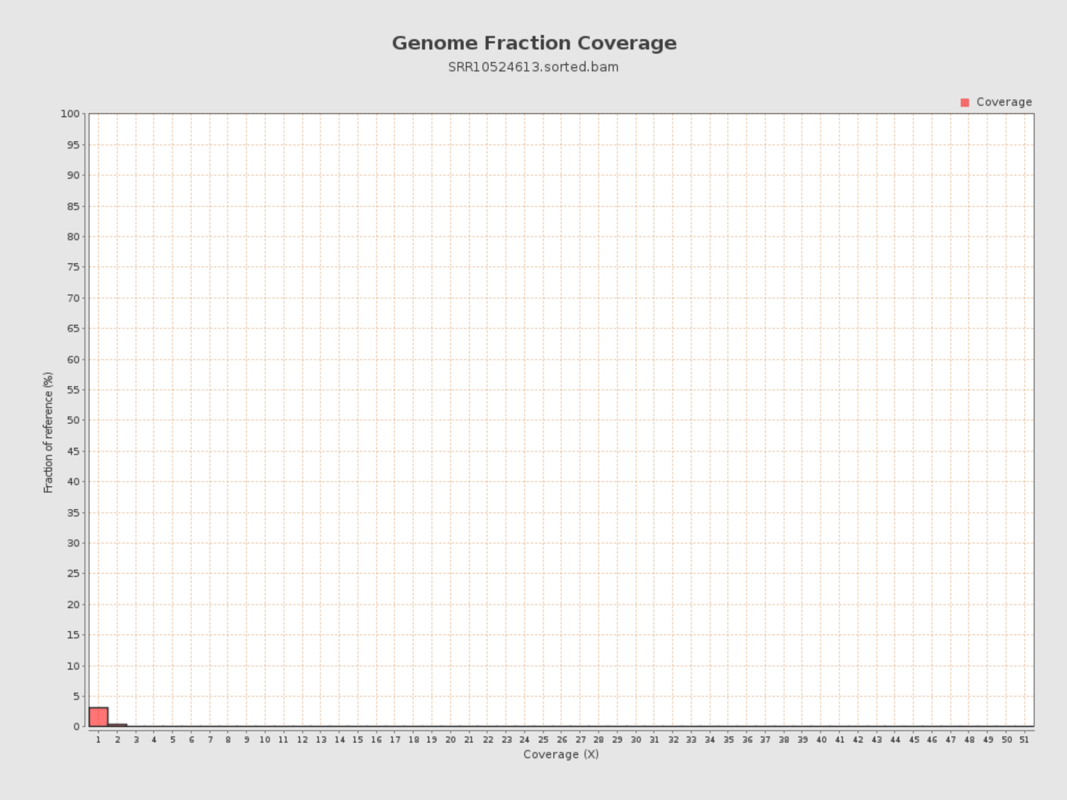
4. Results : Coverage Histogram



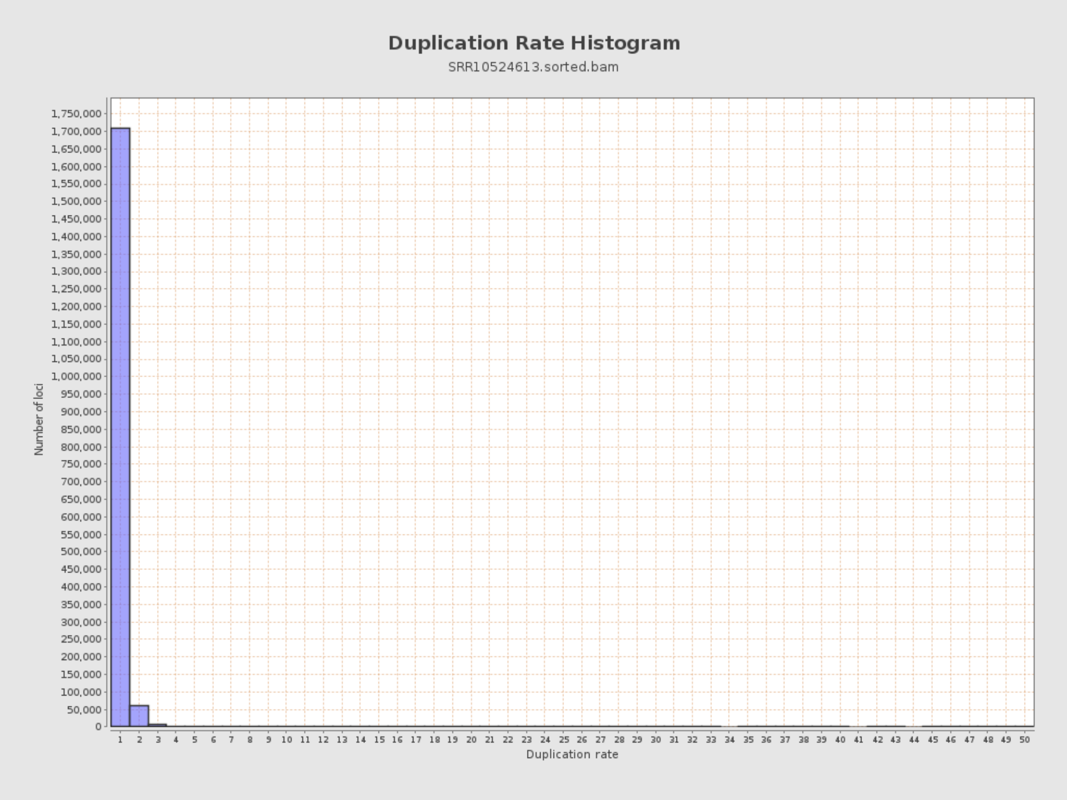
5. Results : Coverage Histogram (0-50X)



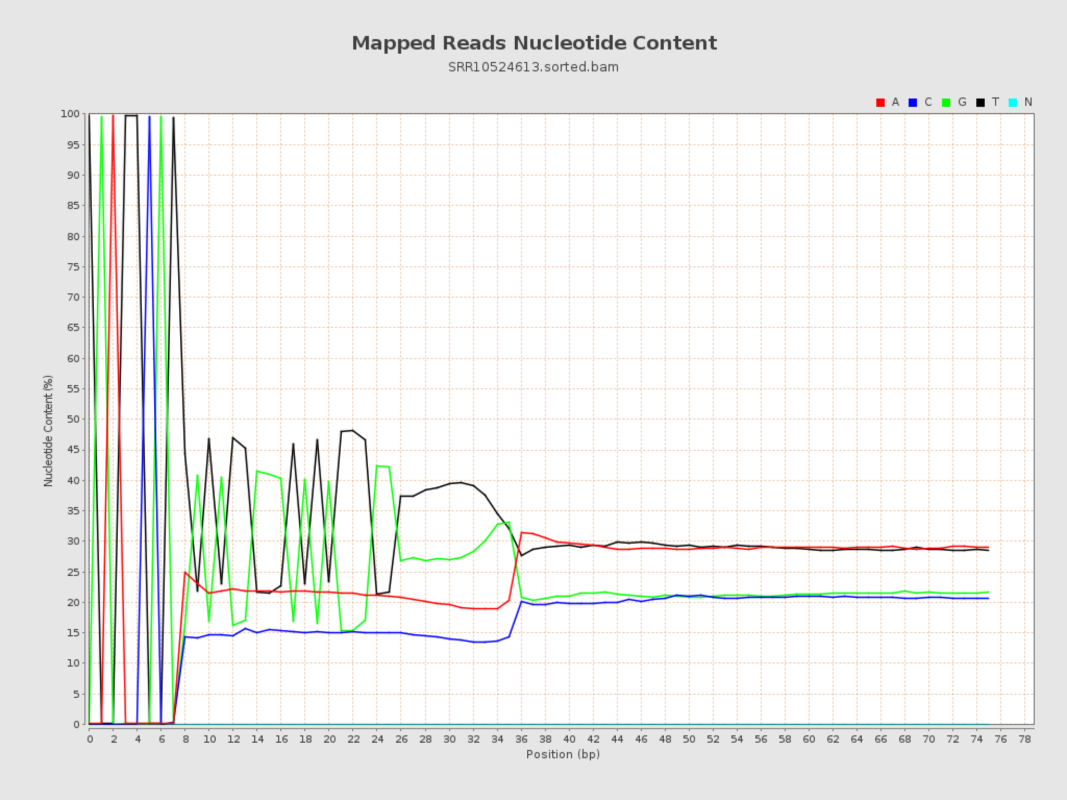
6. Results : Genome Fraction Coverage



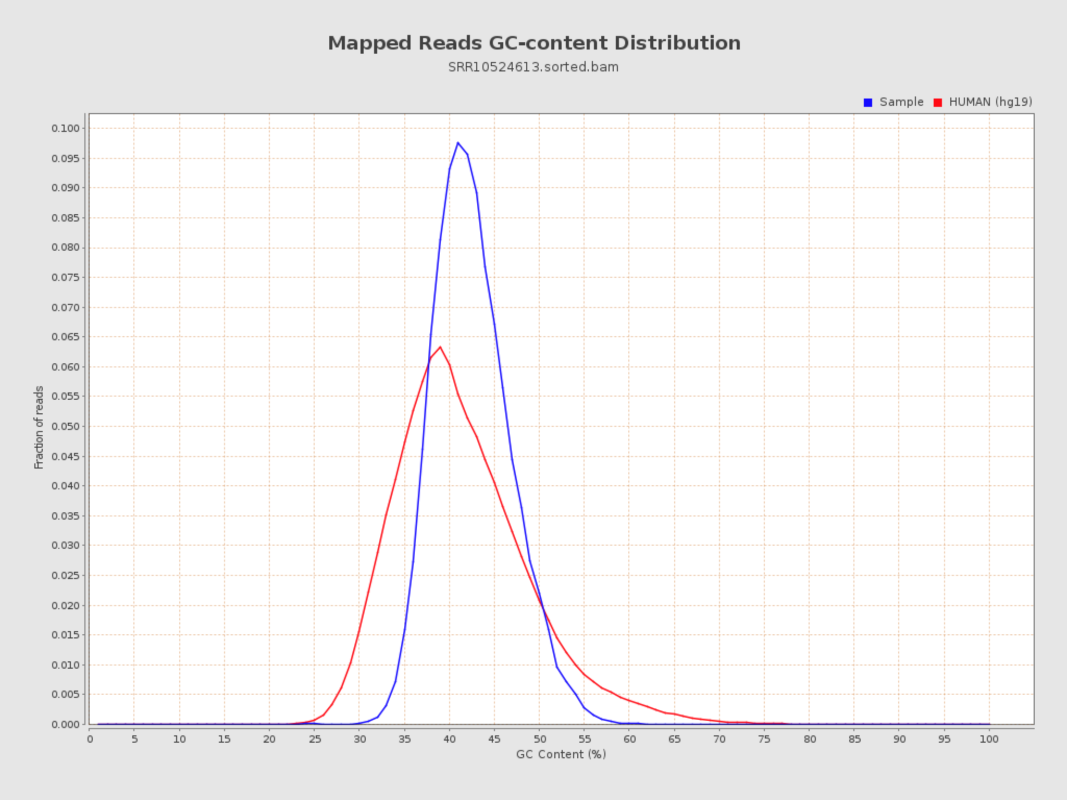
7. Results : Duplication Rate Histogram



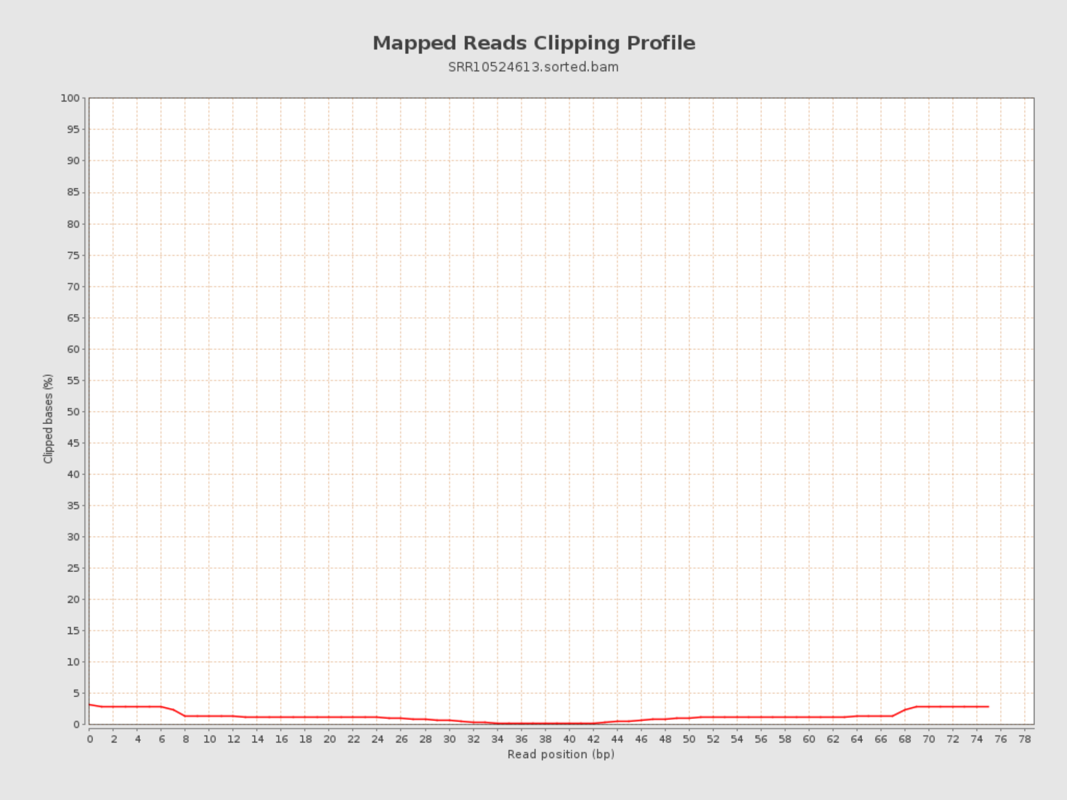
8. Results : Mapped Reads Nucleotide Content



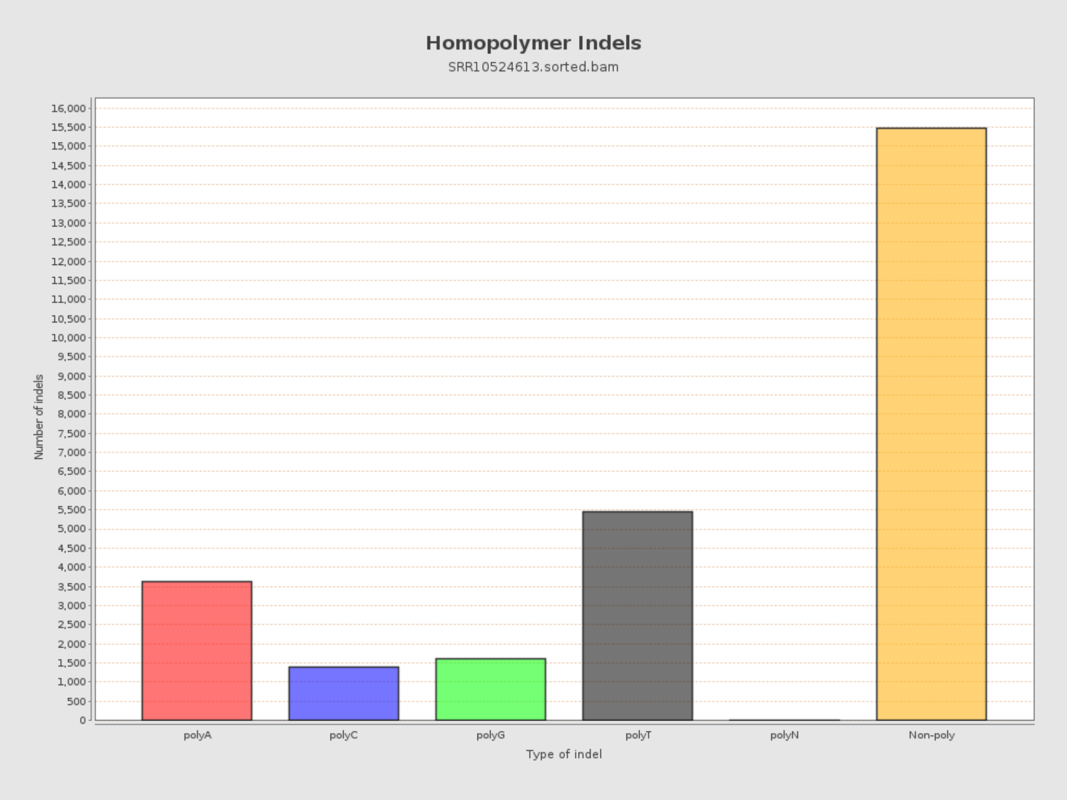
9. Results : Mapped Reads GC-content Distribution



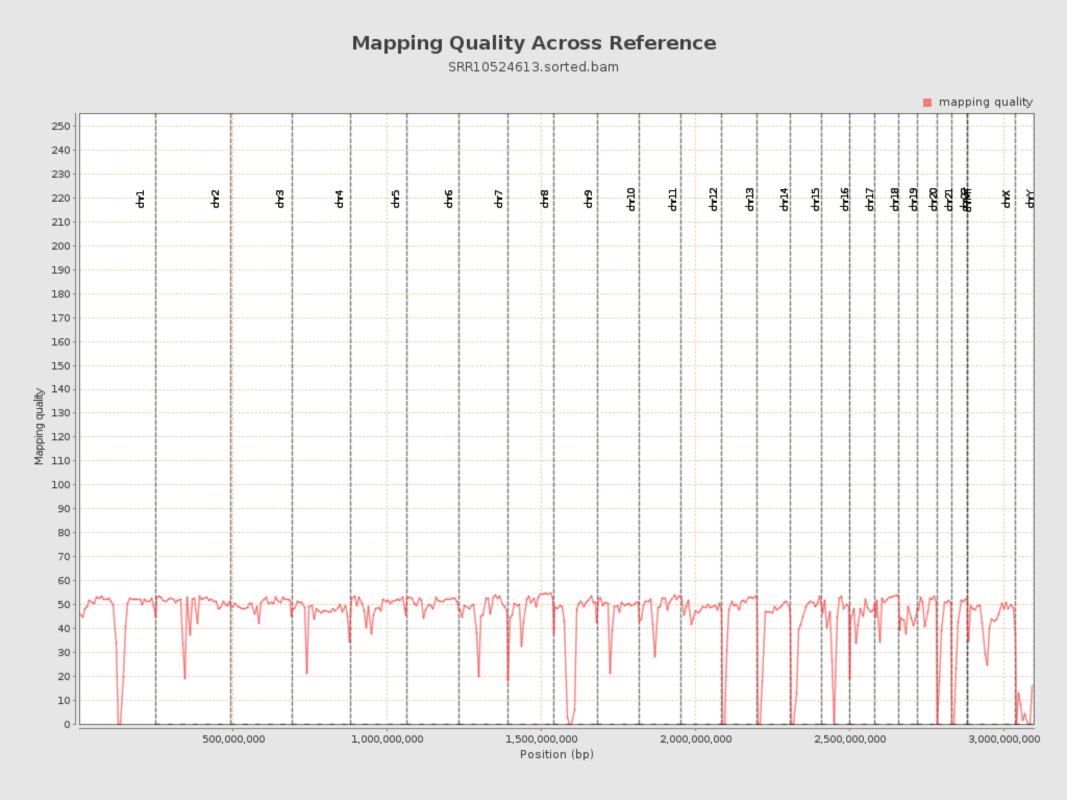
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram