Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:58:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524454.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_SRR10524454 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524454.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:58:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524454.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,660,861
Mapped reads	1,536,204 / 92.49%
Unmapped reads	124,657 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,135 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	75,381 / 4.54%
Duplication rate	3.83%
Clipped reads	1,535,482 / 92.45%

2.2. ACGT Content

Number/percentage of A's	21,813,706 / 24.51%
Number/percentage of C's	16,449,149 / 18.48%
Number/percentage of T's	28,625,531 / 32.17%
Number/percentage of G's	22,102,656 / 24.84%
Number/percentage of N's	1,847 / 0%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2659

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

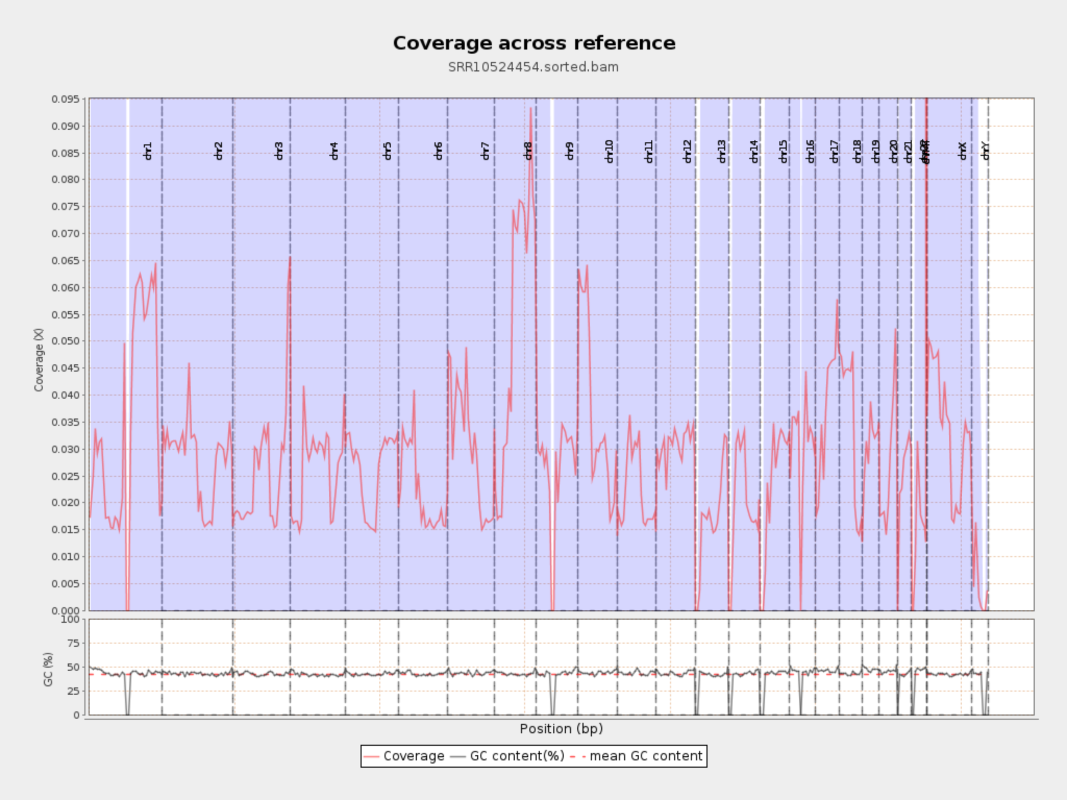
General error rate	0.47%
Mismatches	407,086
Insertions	5,858
Mapped reads with at least one insertion	0.38%
Deletions	15,952
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.67%

2.6. Chromosome stats

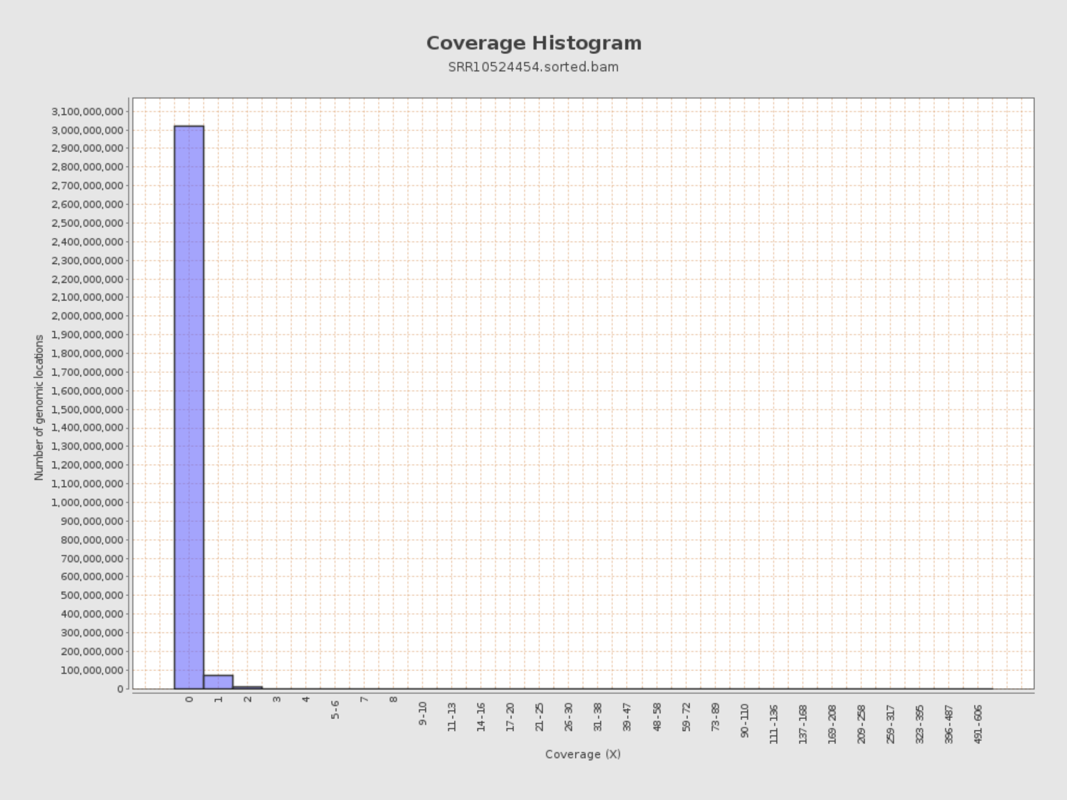
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8644994	0.0347	0.4621
chr2	243199373	6893147	0.0283	0.2942
chr3	198022430	5002256	0.0253	0.1793
chr4	191154276	5025581	0.0263	0.2068
chr5	180915260	4743863	0.0262	0.1819
chr6	171115067	3786866	0.0221	0.2111
chr7	159138663	4796897	0.0301	0.3532

chr8	146364022	7987627	0.0546	0.2942
chr9	141213431	3657671	0.0259	0.2261
chr10	135534747	5068794	0.0374	0.2824
chr11	135006516	3050085	0.0226	0.262
chr12	133851895	4123802	0.0308	0.1984
chr13	115169878	2001440	0.0174	0.1475
chr14	107349540	2138307	0.0199	0.1618
chr15	102531392	2375816	0.0232	0.1808
chr16	90354753	2761702	0.0306	0.2078
chr17	81195210	3097869	0.0382	0.2273
chr18	78077248	2737823	0.0351	0.4165
chr19	59128983	1823435	0.0308	0.3223
chr20	63025520	1716338	0.0272	0.1898
chr21	48129895	1204110	0.025	0.1891
chr22	51304566	728695	0.0142	0.1319
chrMT	16571	85659	5.1692	3.8927
chrX	155270560	5284064	0.034	0.23
chrY	59373566	283608	0.0048	0.1271

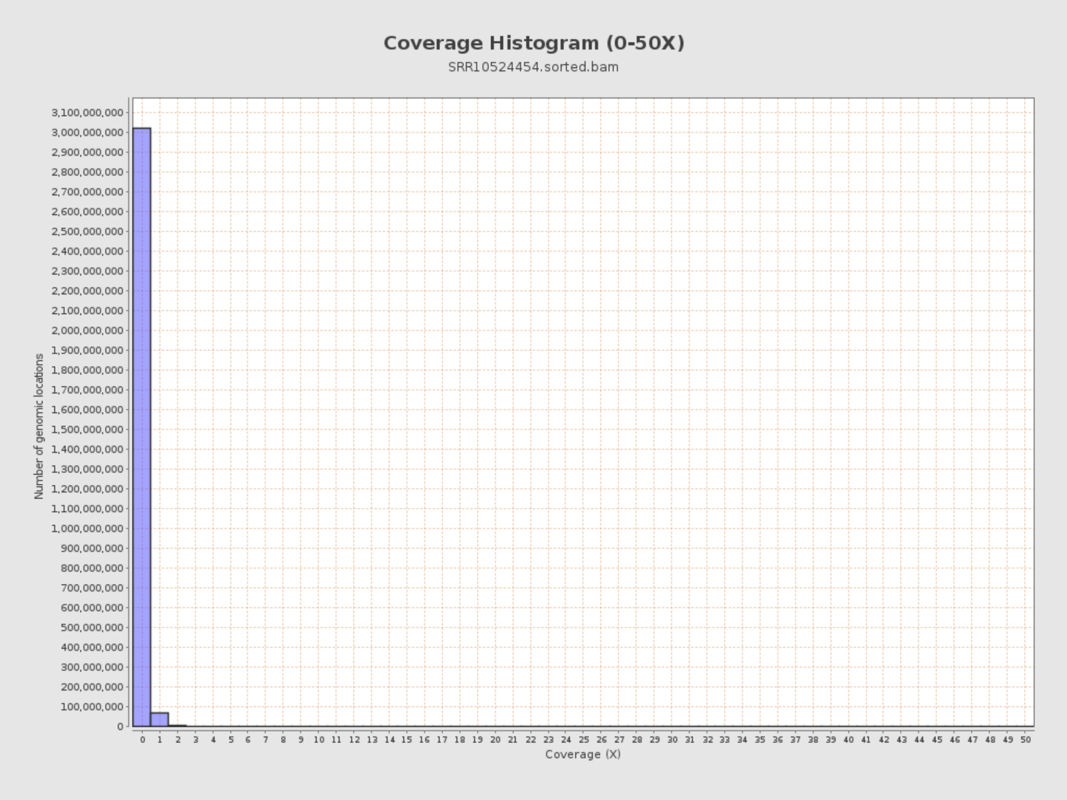
3. Results : Coverage across reference



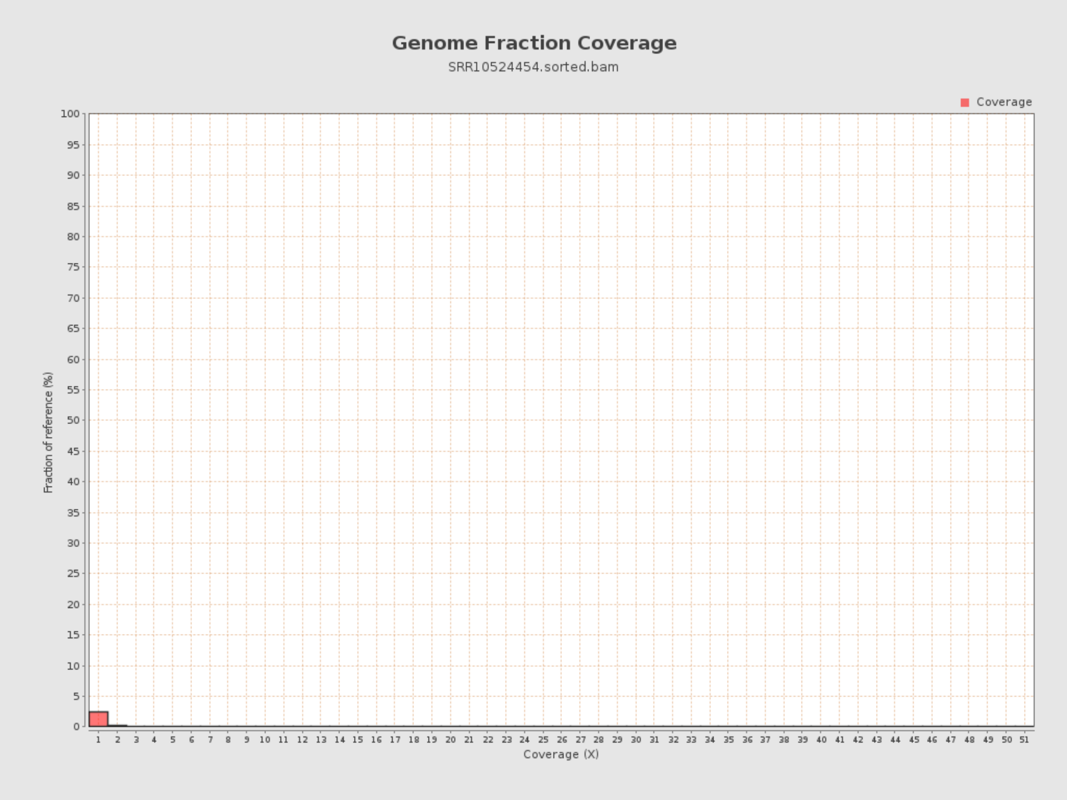
4. Results : Coverage Histogram



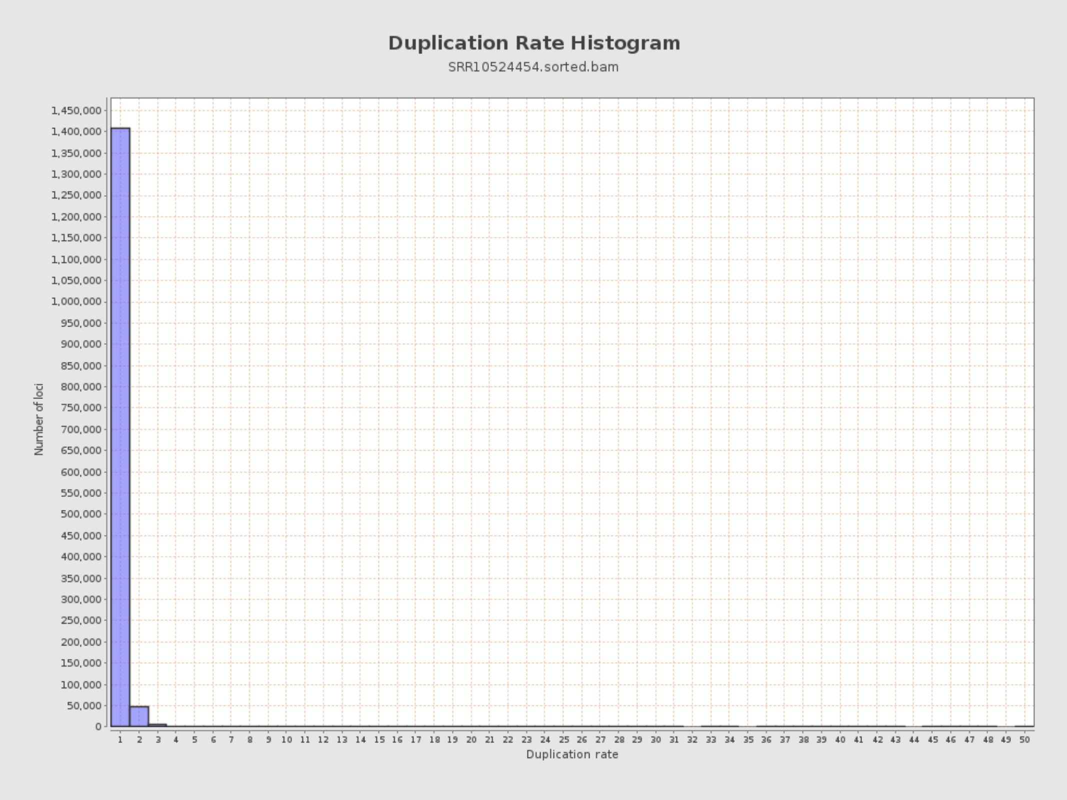
5. Results : Coverage Histogram (0-50X)



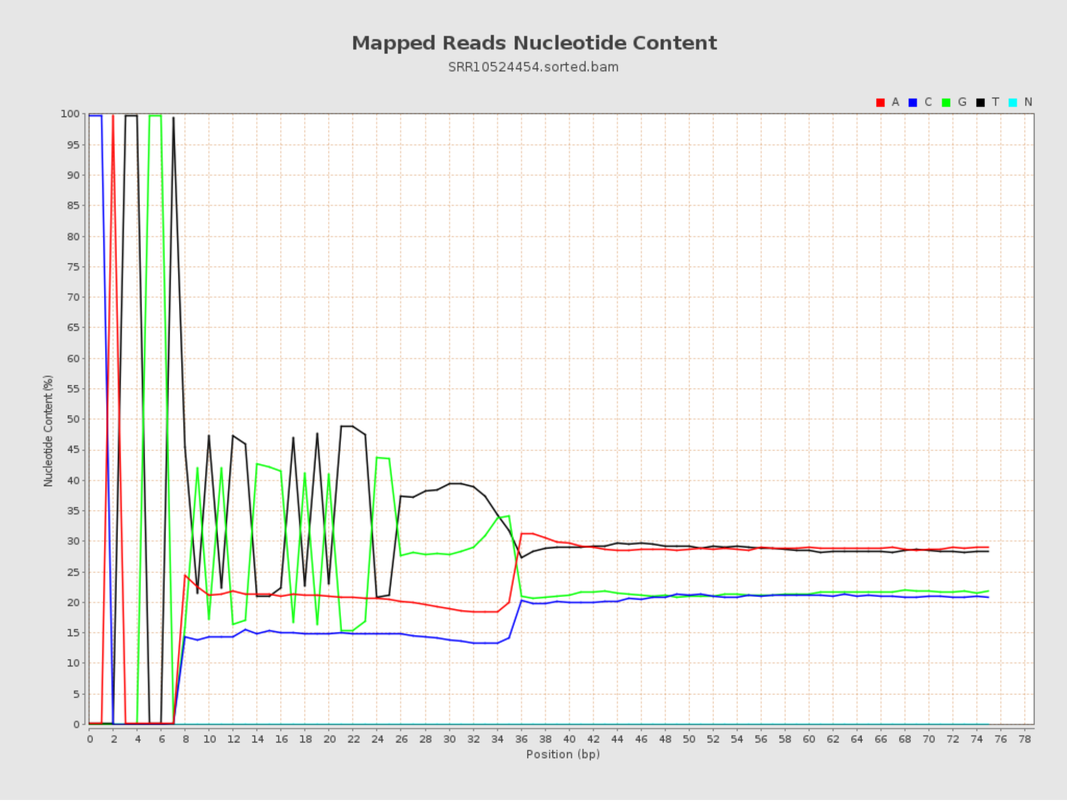
6. Results : Genome Fraction Coverage



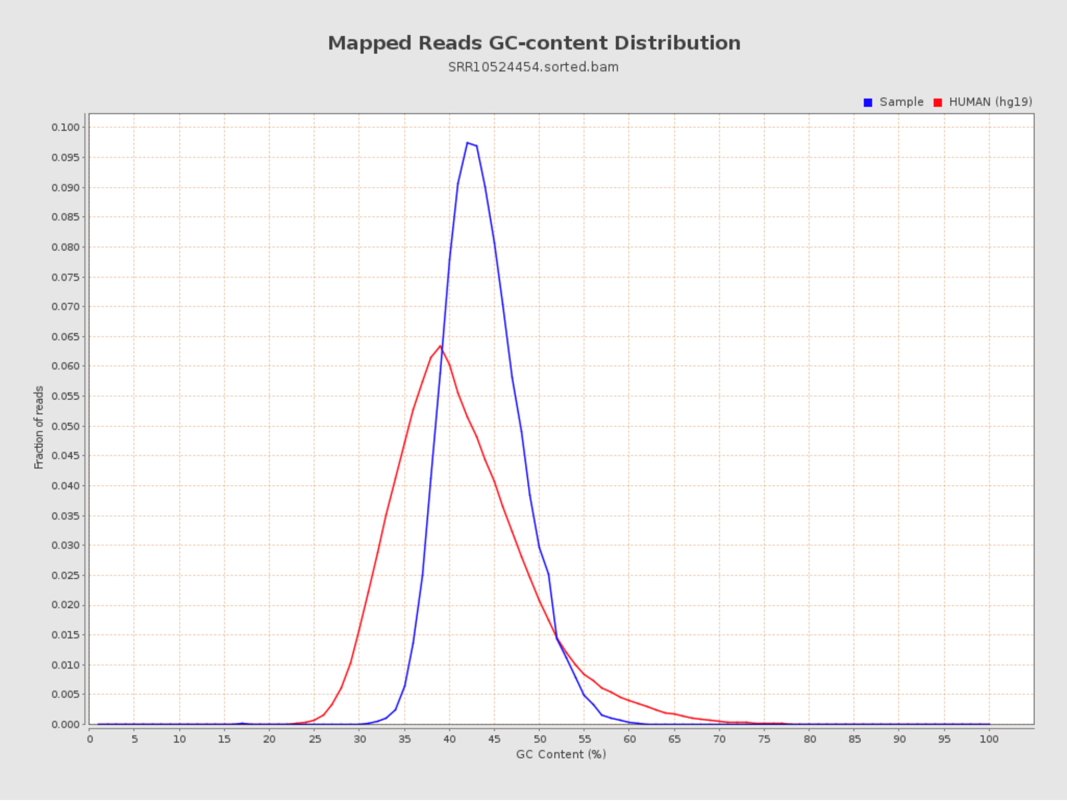
7. Results : Duplication Rate Histogram



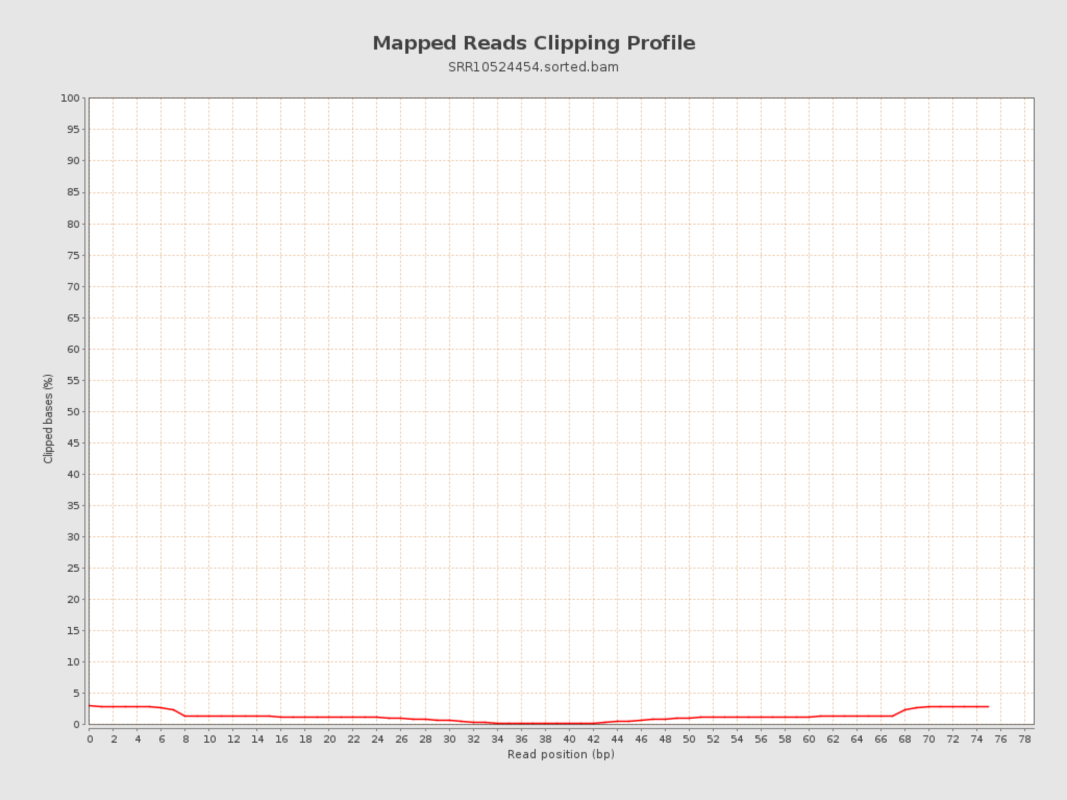
8. Results : Mapped Reads Nucleotide Content



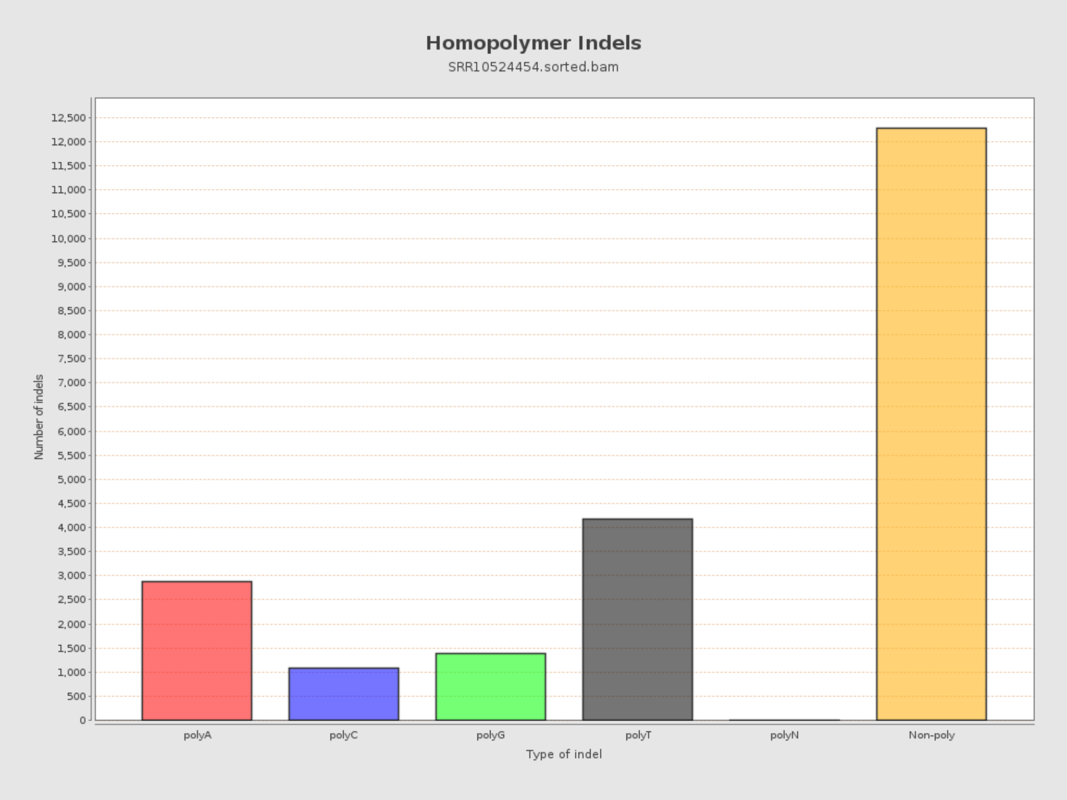
9. Results : Mapped Reads GC-content Distribution



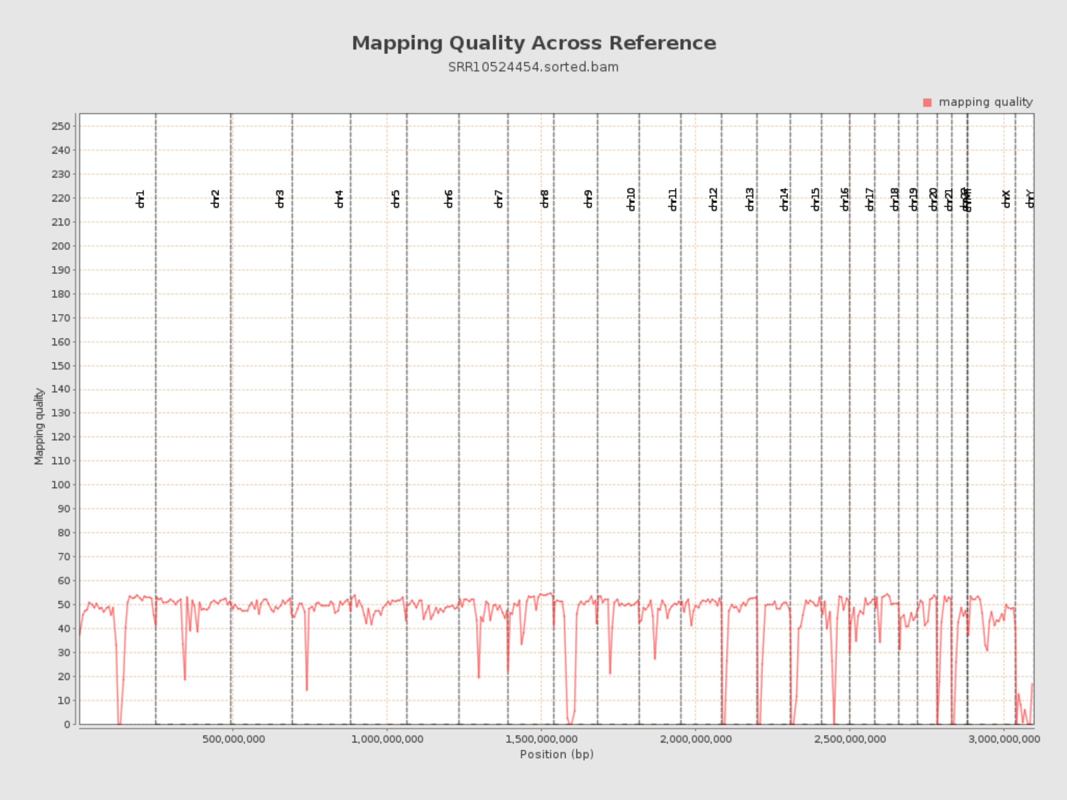
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram