Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:20:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524830.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_SRR10524830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:20:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,055,653
Mapped reads	982,825 / 93.1%
Unmapped reads	72,828 / 6.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,690 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	23,504 / 2.23%
Duplication rate	1.64%
Clipped reads	987,267 / 93.52%

2.2. ACGT Content

Number/percentage of A's	15,459,779 / 26.65%
Number/percentage of C's	11,551,764 / 19.91%
Number/percentage of T's	17,876,064 / 30.81%
Number/percentage of G's	13,125,604 / 22.62%
Number/percentage of N's	7,681 / 0.01%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.2066

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

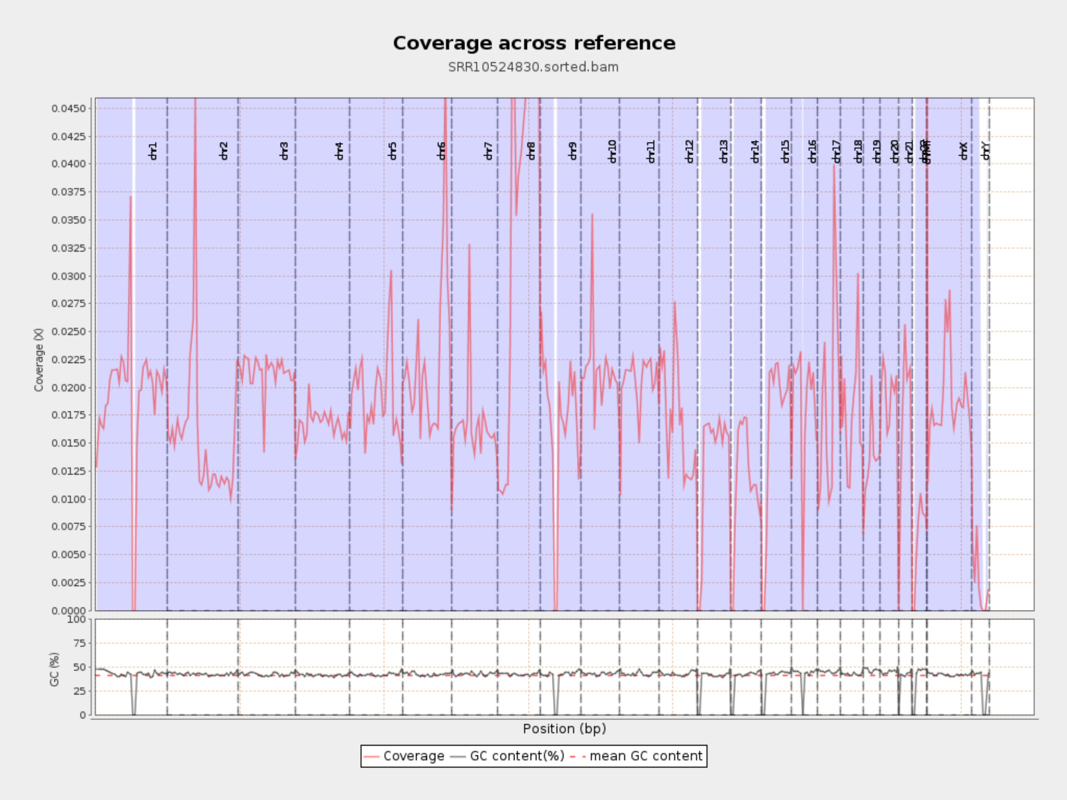
General error rate	0.48%
Mismatches	272,040
Insertions	3,521
Mapped reads with at least one insertion	0.36%
Deletions	10,275
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.38%

2.6. Chromosome stats

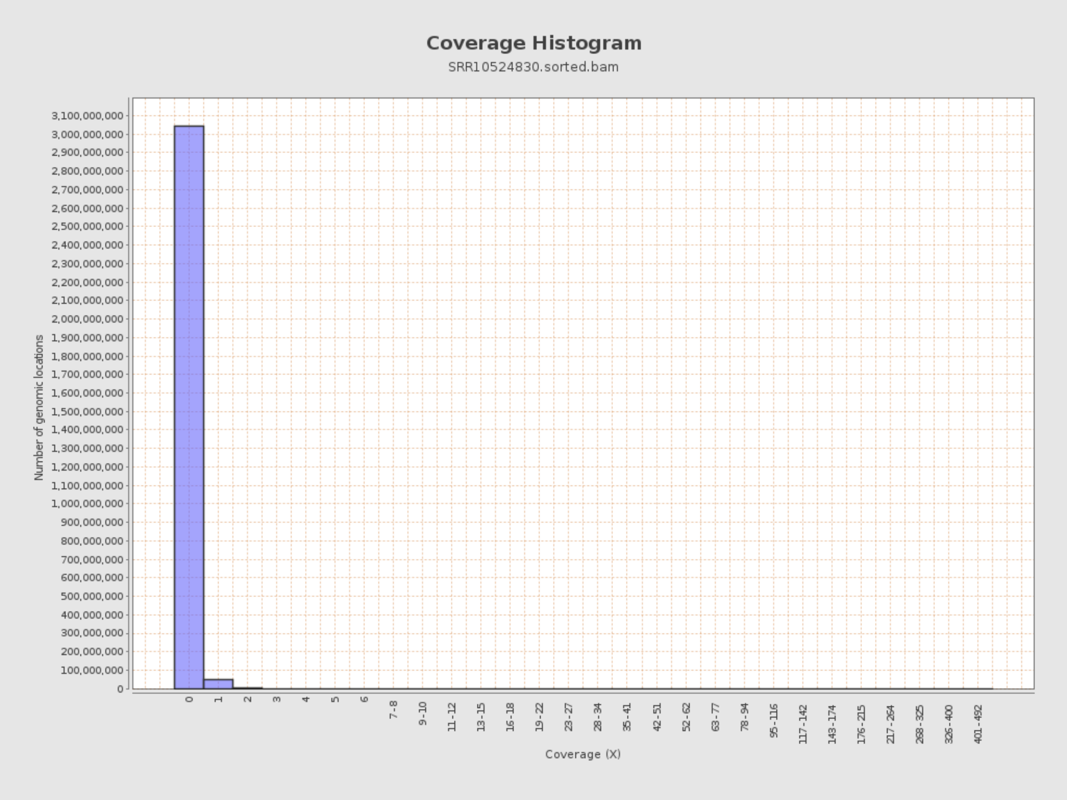
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4776043	0.0192	0.3907
chr2	243199373	3773818	0.0155	0.1969
chr3	198022430	4236575	0.0214	0.1533
chr4	191154276	3192901	0.0167	0.1422
chr5	180915260	3533321	0.0195	0.1465
chr6	171115067	3806552	0.0222	0.1666
chr7	159138663	2663547	0.0167	0.2726

chr8	146364022	6350214	0.0434	0.2843
chr9	141213431	2380536	0.0169	0.1665
chr10	135534747	2919655	0.0215	0.1989
chr11	135006516	2780092	0.0206	0.1847
chr12	133851895	2267442	0.0169	0.1378
chr13	115169878	1539187	0.0134	0.1204
chr14	107349540	1226013	0.0114	0.1168
chr15	102531392	1702058	0.0166	0.1348
chr16	90354753	1632512	0.0181	0.1478
chr17	81195210	1556067	0.0192	0.1593
chr18	78077248	1409042	0.018	0.3085
chr19	59128983	808329	0.0137	0.2577
chr20	63025520	1211990	0.0192	0.1455
chr21	48129895	835847	0.0174	0.1451
chr22	51304566	330949	0.0065	0.0835
chrMT	16571	866	0.0523	0.2376
chrX	155270560	2962901	0.0191	0.1595
chrY	59373566	140568	0.0024	0.0665

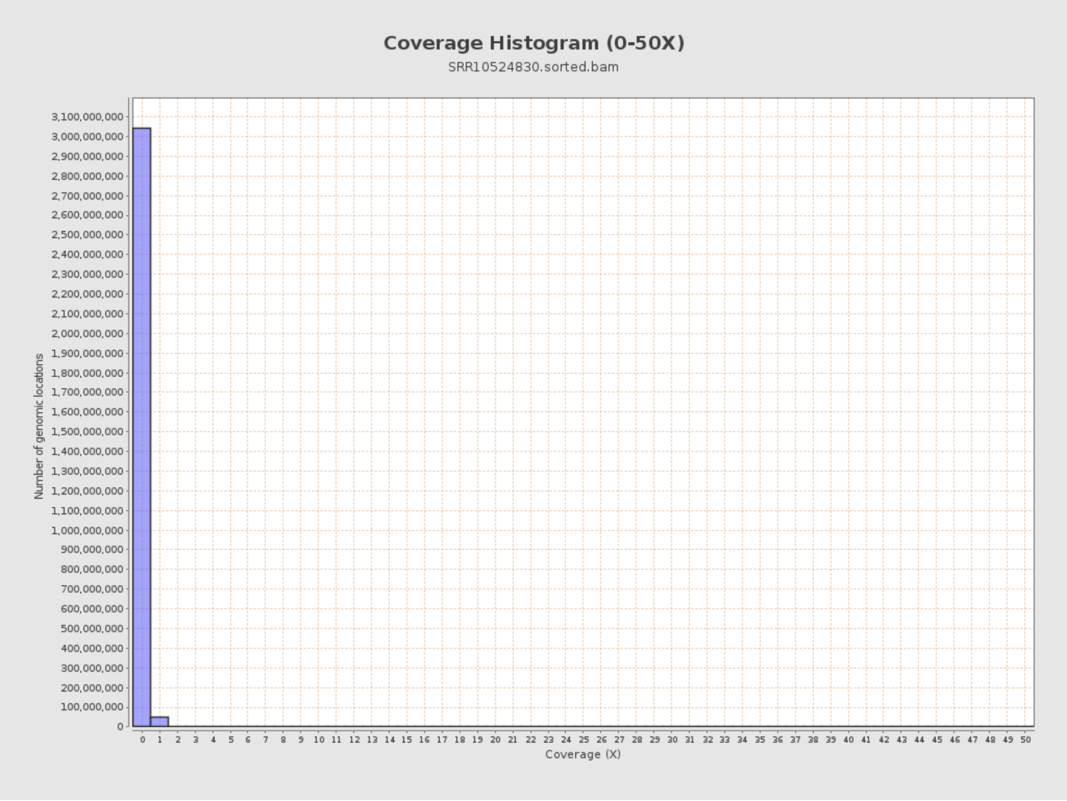
3. Results : Coverage across reference



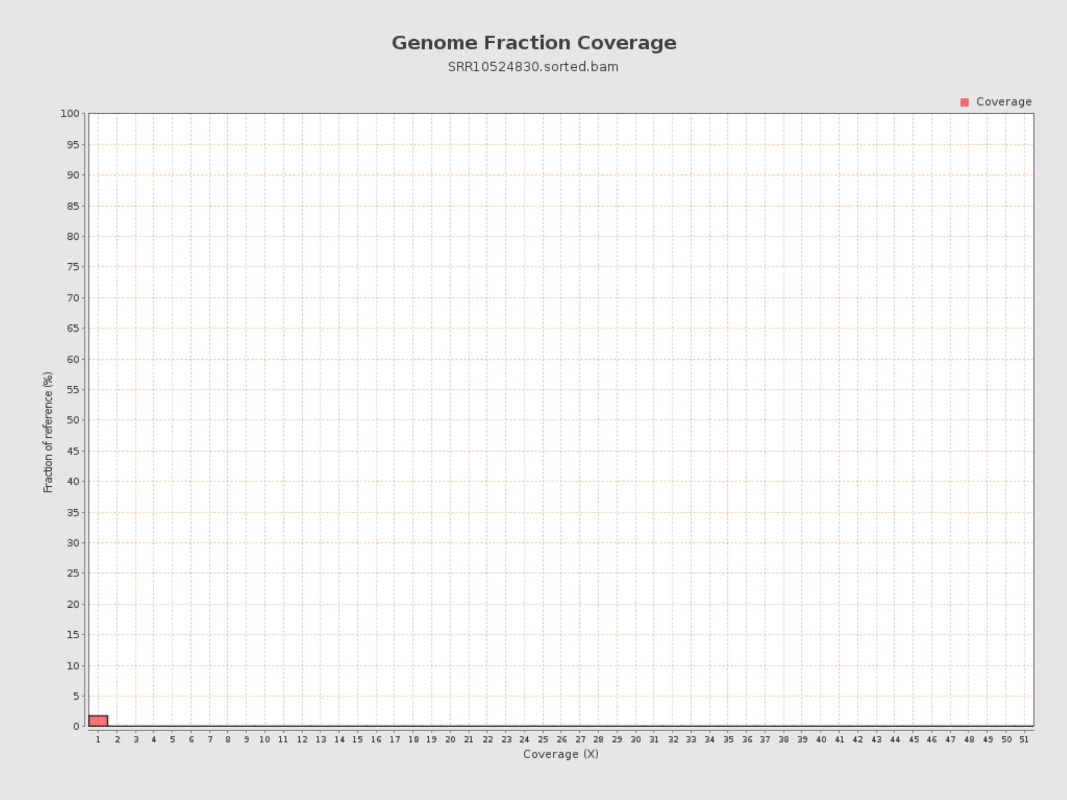
4. Results : Coverage Histogram



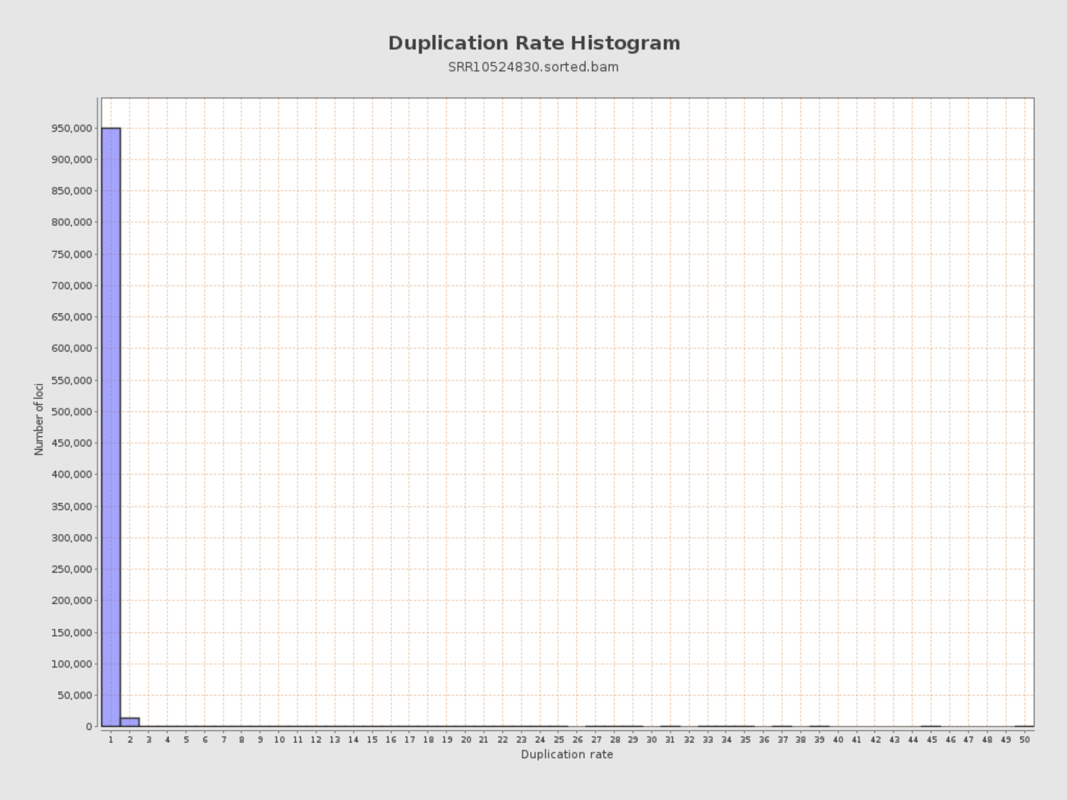
5. Results : Coverage Histogram (0-50X)



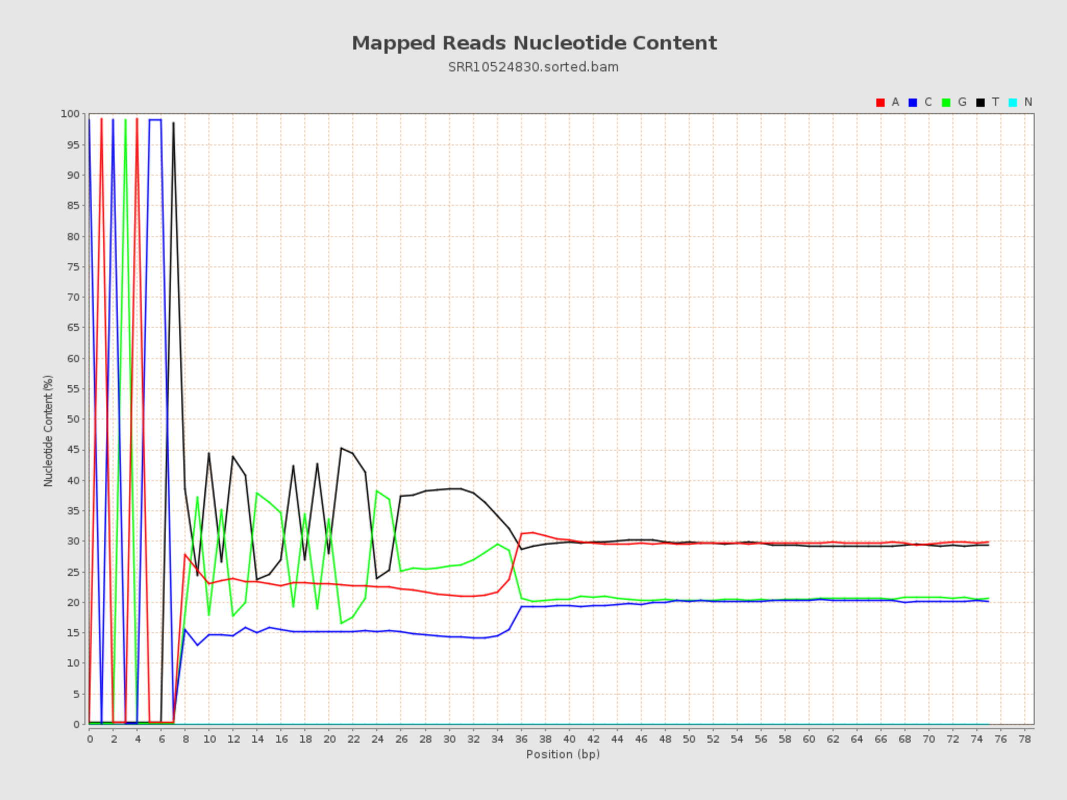
6. Results : Genome Fraction Coverage



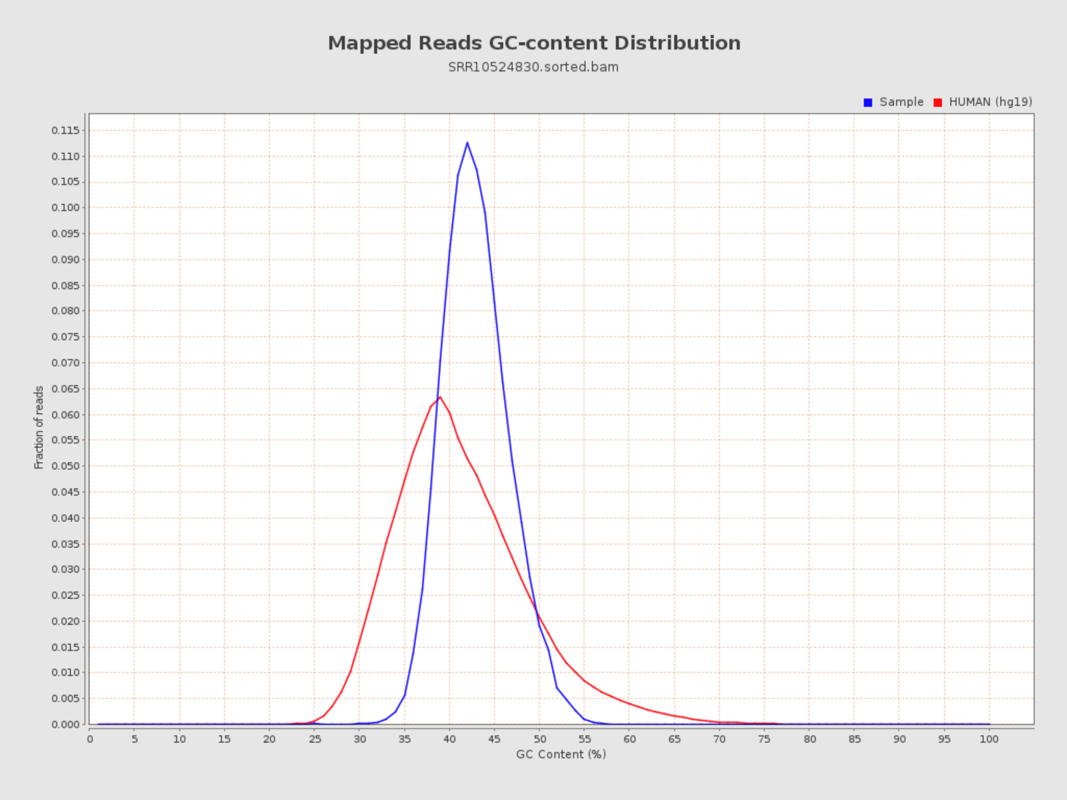
7. Results : Duplication Rate Histogram



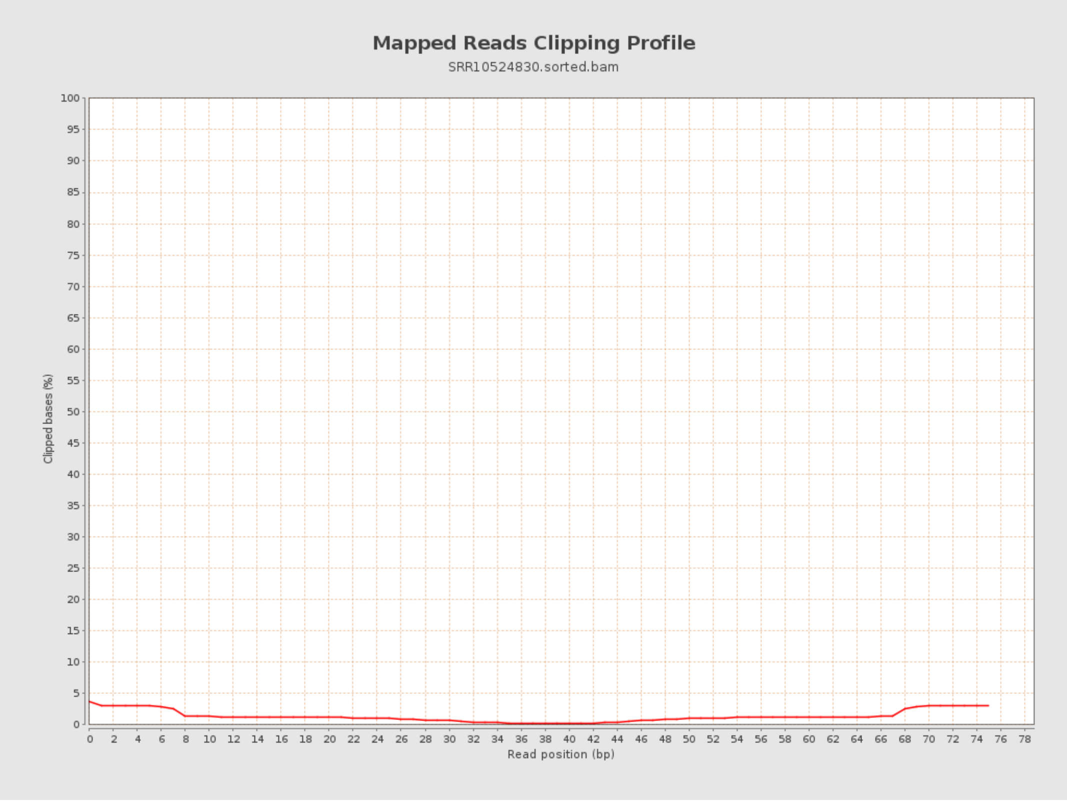
8. Results : Mapped Reads Nucleotide Content



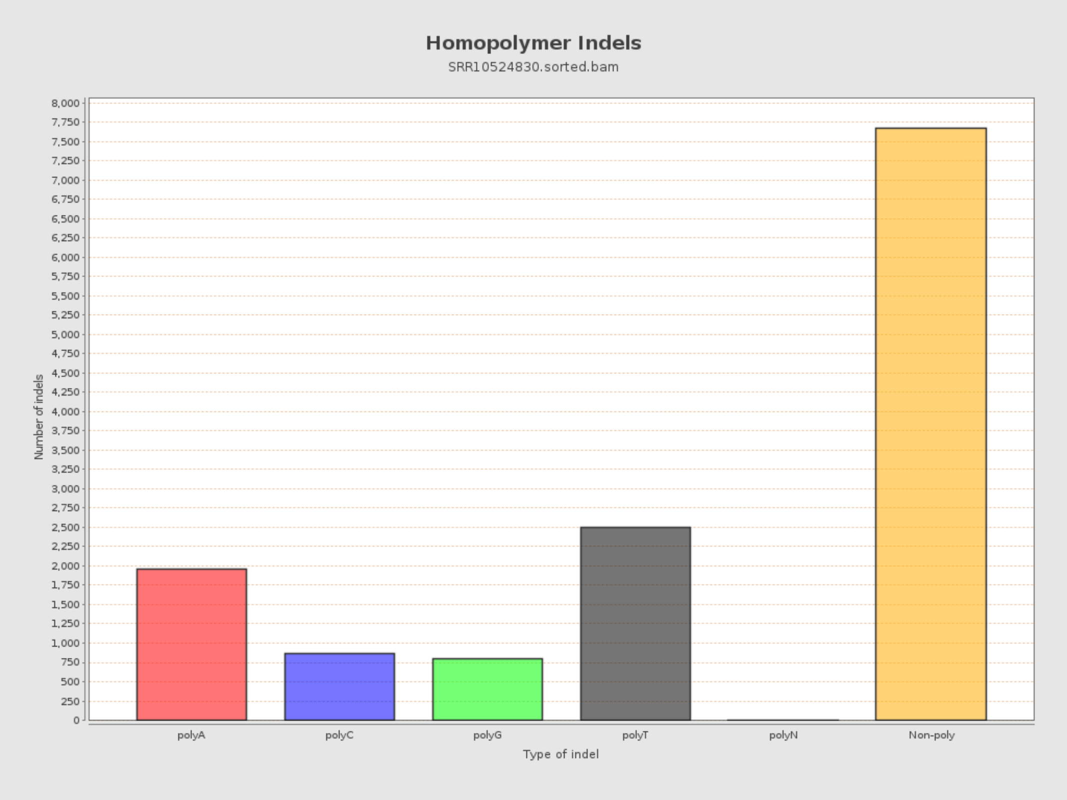
9. Results : Mapped Reads GC-content Distribution



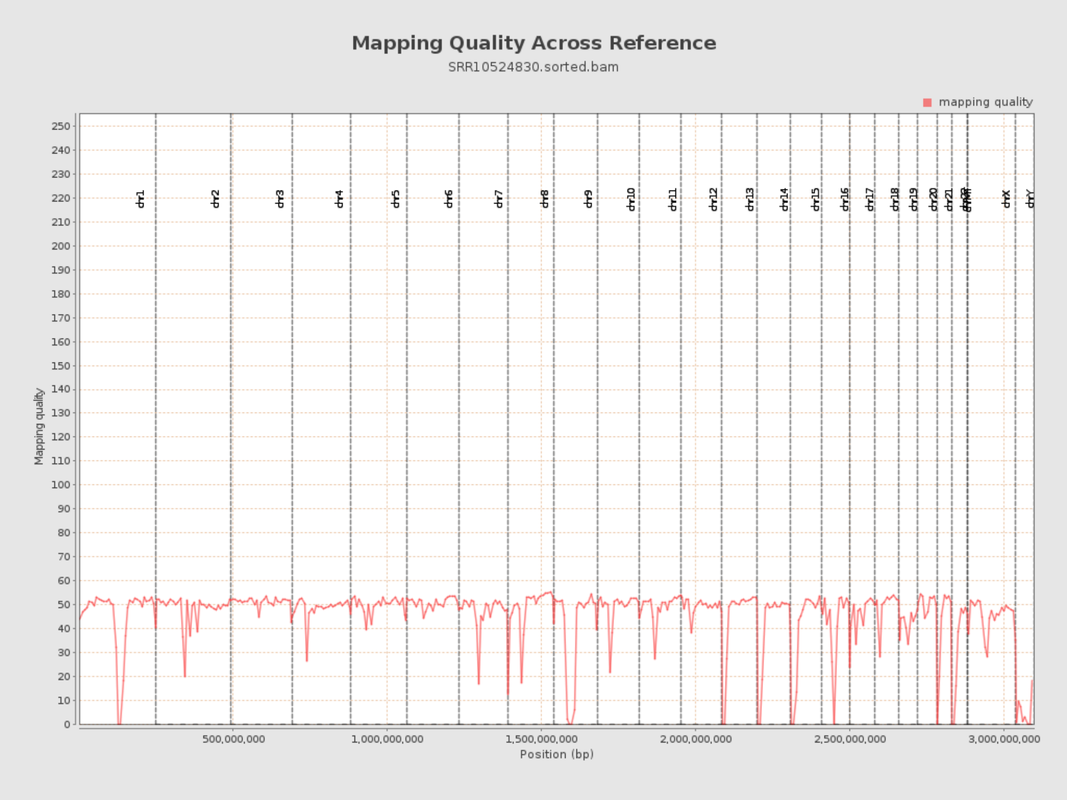
10. Results : Mapped Reads Clipping Profile



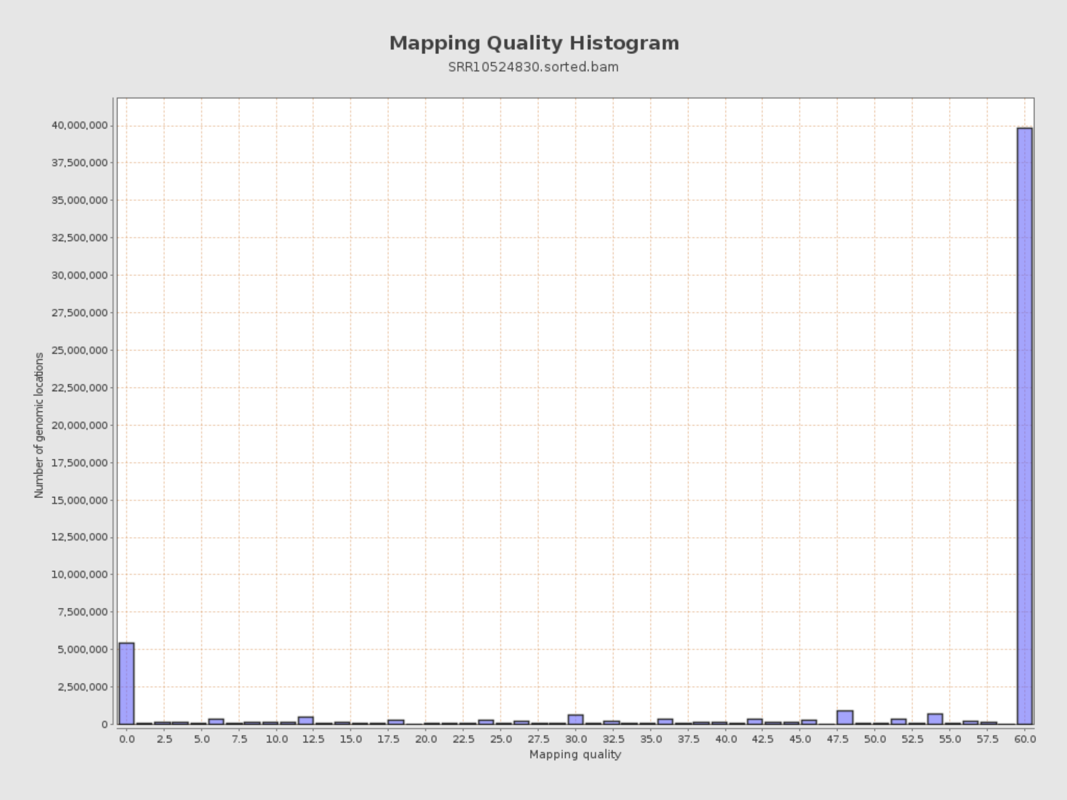
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



]