Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:43:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524574.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_SRR10524574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:43:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,588,778
Mapped reads	1,431,662 / 90.11%
Unmapped reads	157,116 / 9.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,620 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	40,528 / 2.55%
Duplication rate	2%
Clipped reads	1,434,546 / 90.29%

2.2. ACGT Content

Number/percentage of A's	19,346,725 / 23.57%
Number/percentage of C's	14,643,708 / 17.84%
Number/percentage of T's	26,916,755 / 32.79%
Number/percentage of G's	21,181,276 / 25.8%
Number/percentage of N's	1,227 / 0%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2397

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

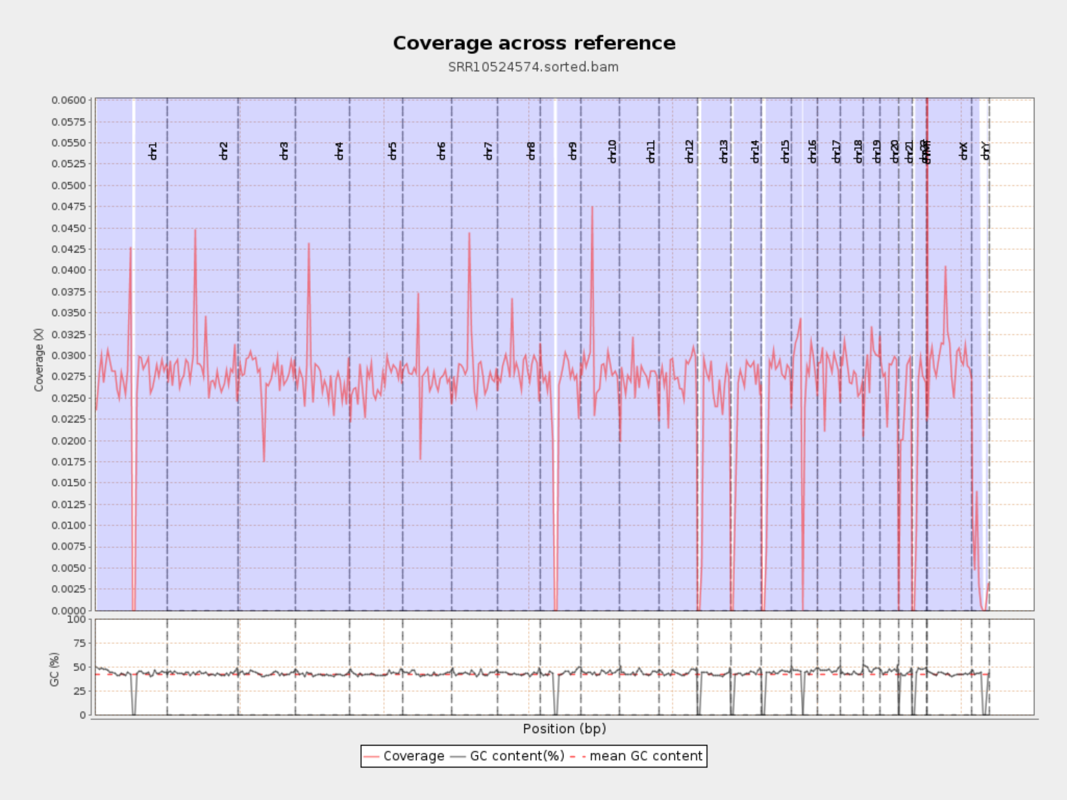
General error rate	0.52%
Mismatches	419,570
Insertions	5,280
Mapped reads with at least one insertion	0.37%
Deletions	15,351
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.66%

2.6. Chromosome stats

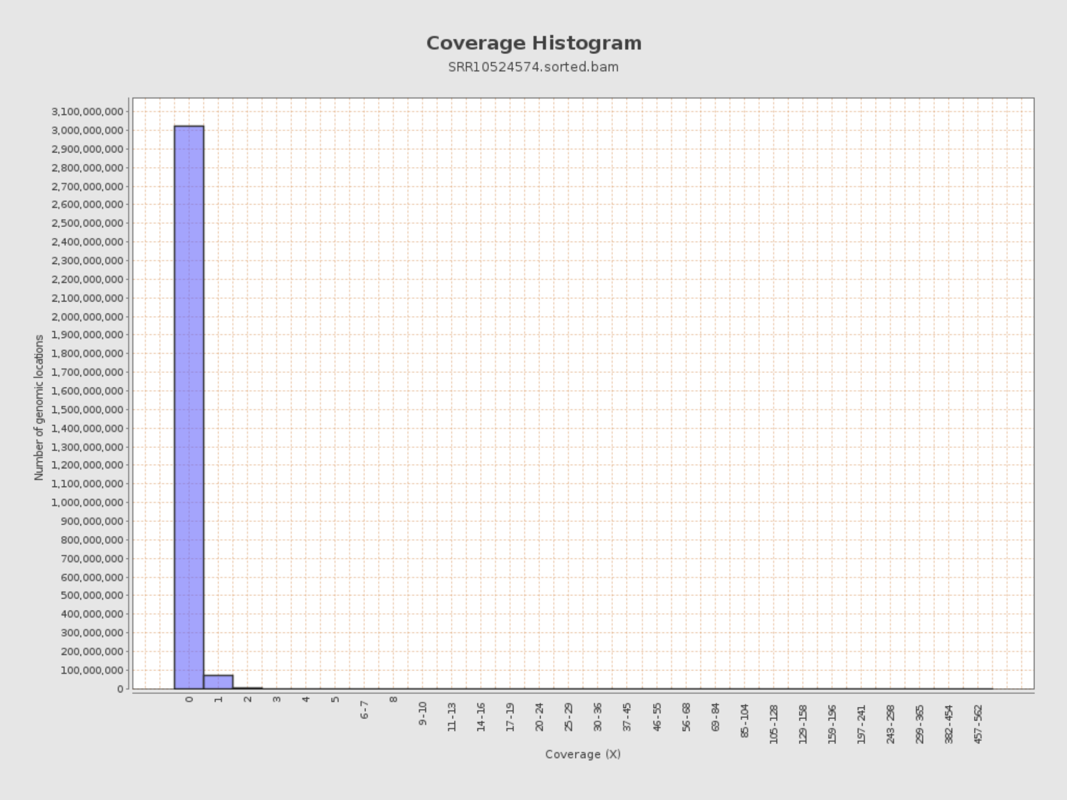
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6632638	0.0266	0.4101
chr2	243199373	6939887	0.0285	0.2744
chr3	198022430	5476109	0.0277	0.1802
chr4	191154276	5247578	0.0275	0.1941
chr5	180915260	4888666	0.027	0.177
chr6	171115067	4710548	0.0275	0.2064
chr7	159138663	4528564	0.0285	0.3157

chr8	146364022	4201376	0.0287	0.2159
chr9	141213431	3413973	0.0242	0.2094
chr10	135534747	3935943	0.029	0.2477
chr11	135006516	3716588	0.0275	0.2208
chr12	133851895	3705264	0.0277	0.1796
chr13	115169878	2566479	0.0223	0.1607
chr14	107349540	2480390	0.0231	0.1668
chr15	102531392	2360988	0.023	0.1697
chr16	90354753	2421404	0.0268	0.1891
chr17	81195210	2304923	0.0284	0.1915
chr18	78077248	2168014	0.0278	0.3659
chr19	59128983	1730870	0.0293	0.2978
chr20	63025520	1738919	0.0276	0.1818
chr21	48129895	1072930	0.0223	0.1695
chr22	51304566	978587	0.0191	0.1478
chrMT	16571	3060	0.1847	0.4896
chrX	155270560	4639746	0.0299	0.2091
chrY	59373566	251897	0.0042	0.1115

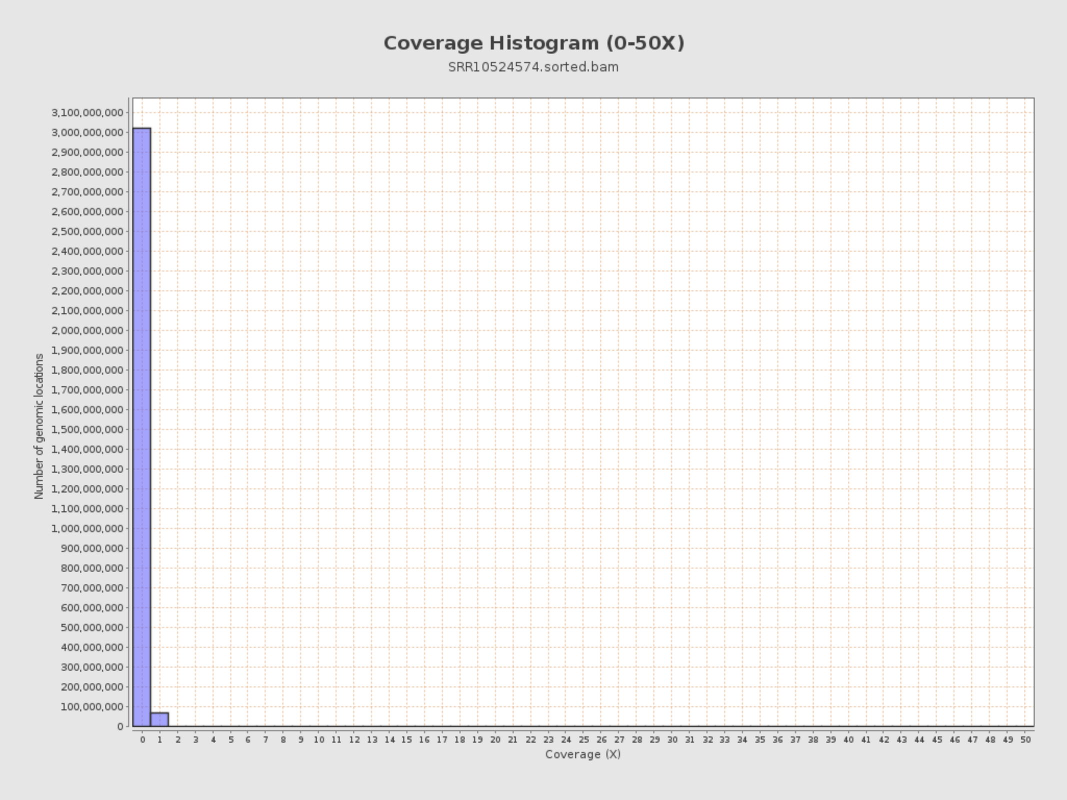
3. Results : Coverage across reference



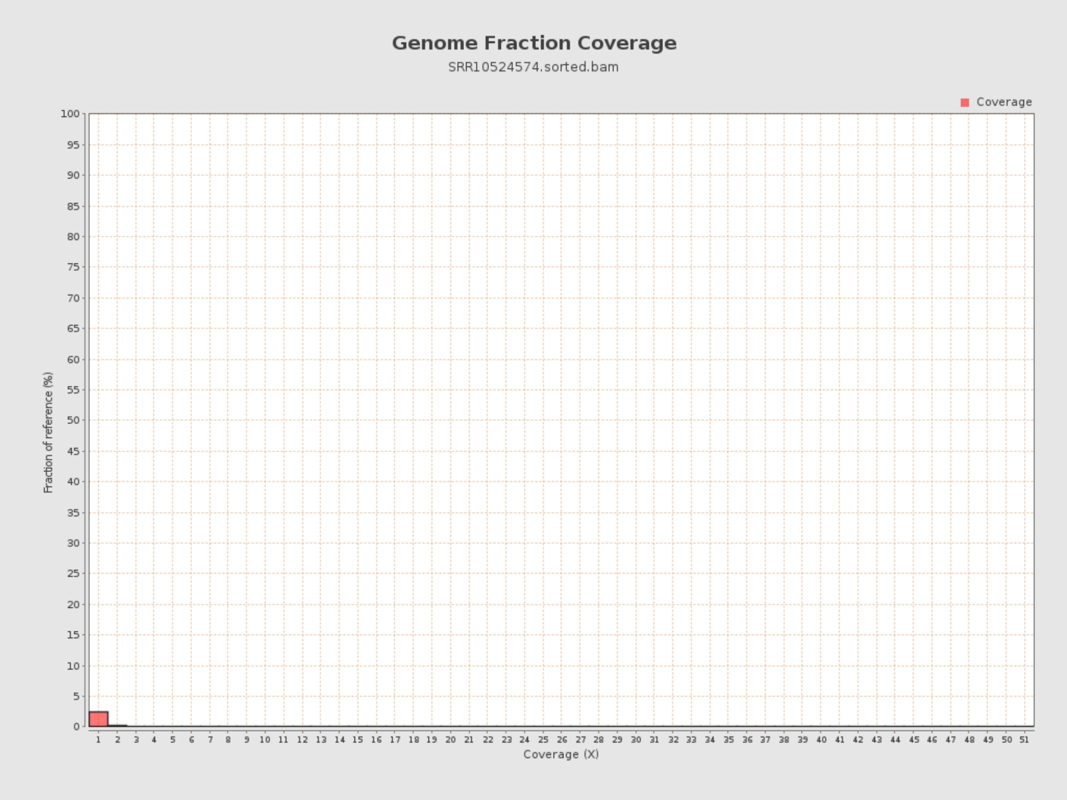
4. Results : Coverage Histogram



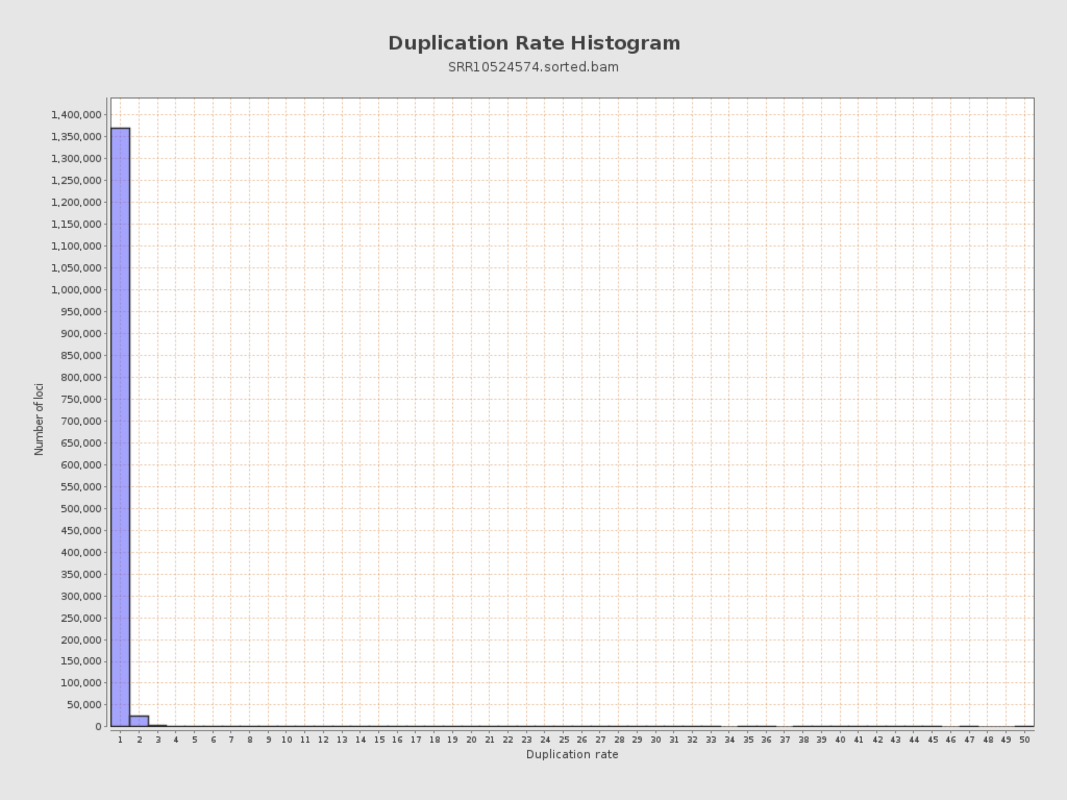
5. Results : Coverage Histogram (0-50X)



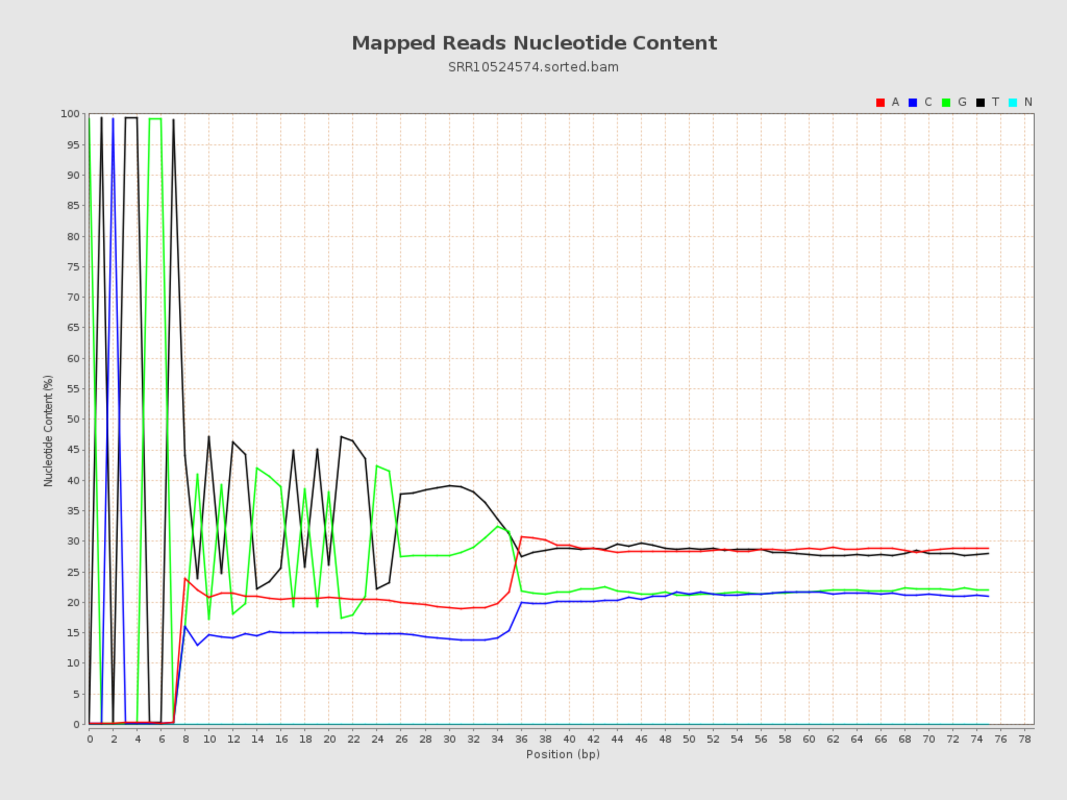
6. Results : Genome Fraction Coverage



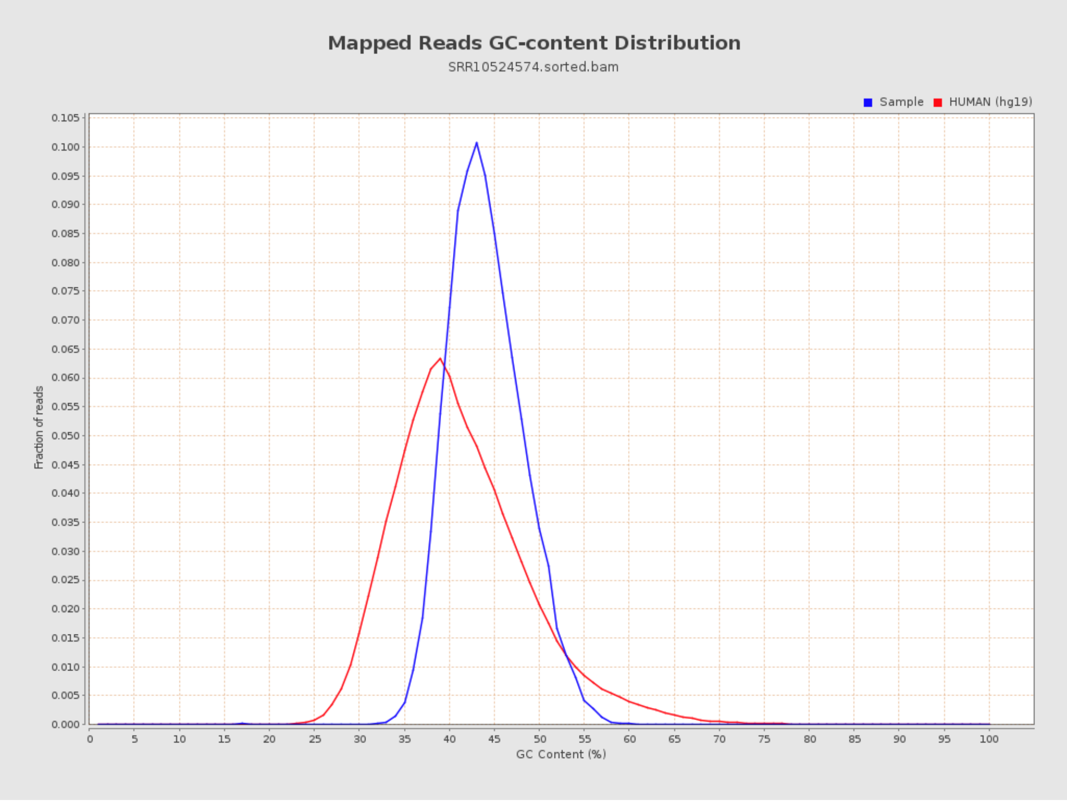
7. Results : Duplication Rate Histogram



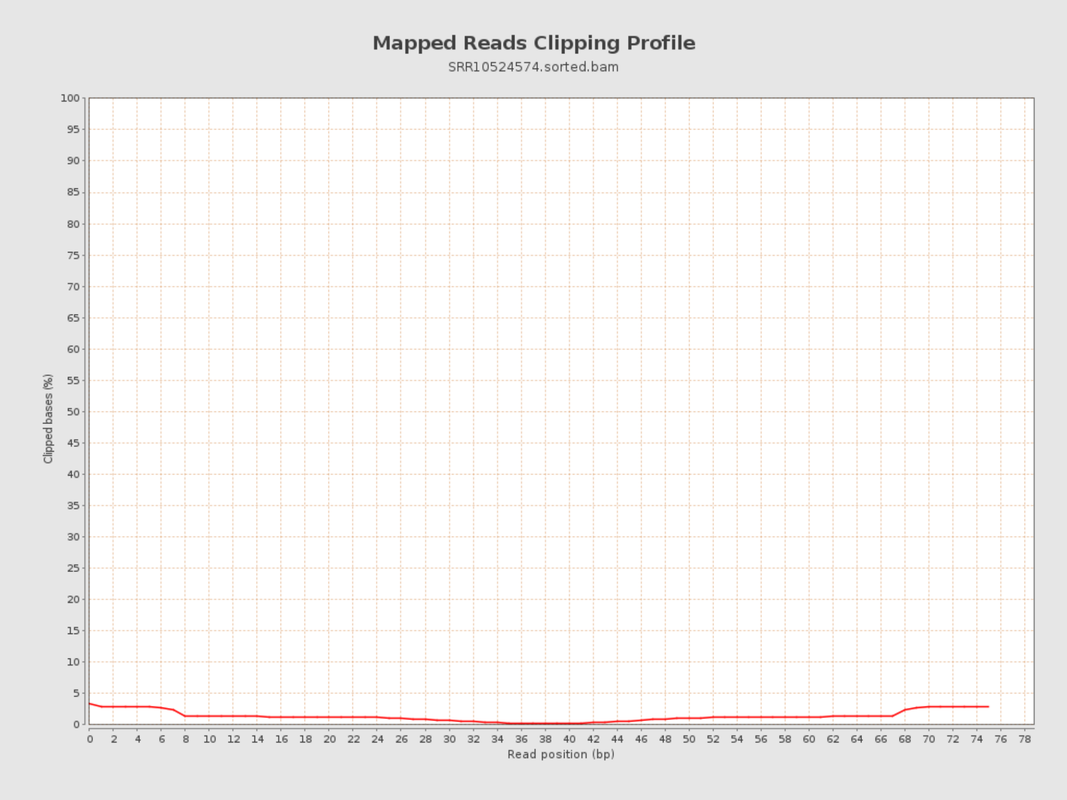
8. Results : Mapped Reads Nucleotide Content



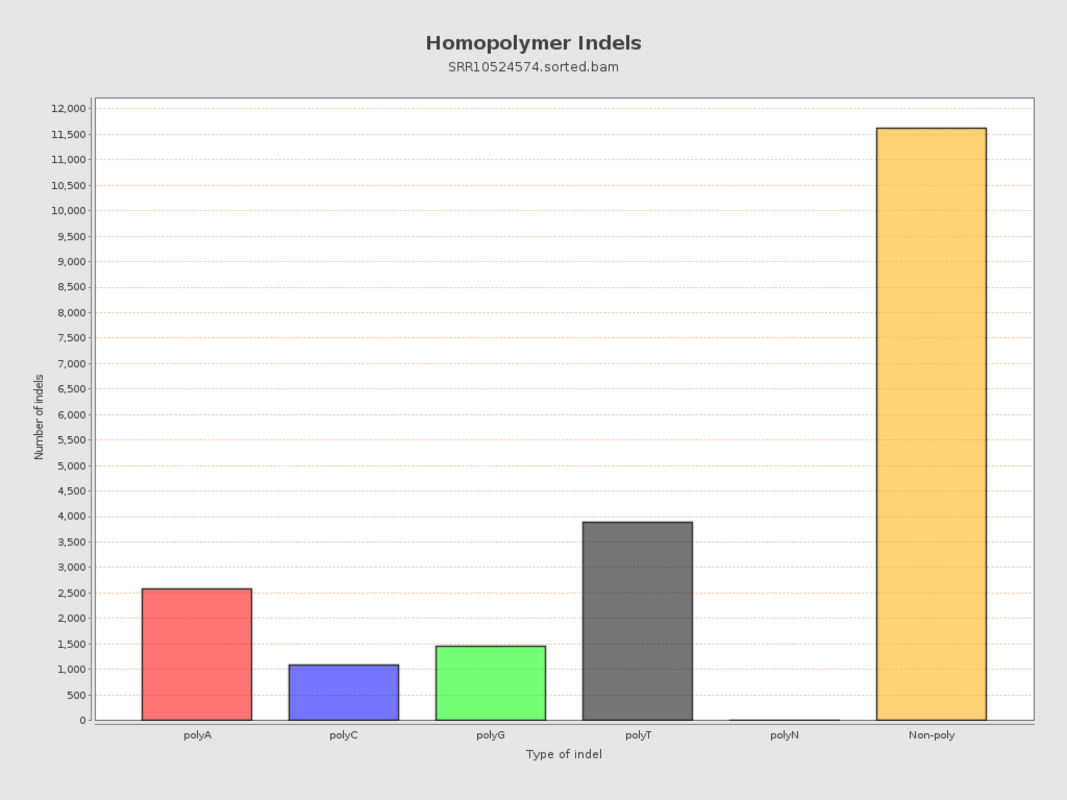
9. Results : Mapped Reads GC-content Distribution



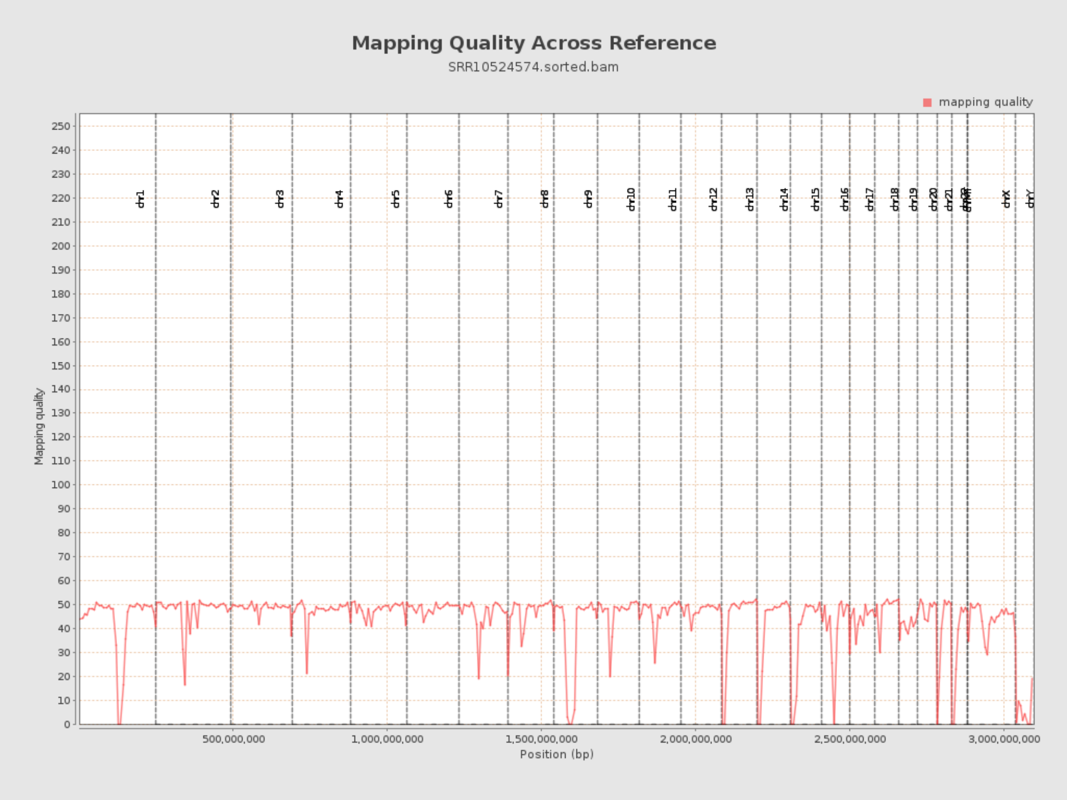
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram