Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:11:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524900.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_SRR10524900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524900.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:11:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,141,201
Mapped reads	1,033,775 / 90.59%
Unmapped reads	107,426 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,189 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	29,454 / 2.58%
Duplication rate	2.04%
Clipped reads	1,034,276 / 90.63%

2.2. ACGT Content

Number/percentage of A's	14,155,484 / 23.9%
Number/percentage of C's	10,095,011 / 17.04%
Number/percentage of T's	20,035,473 / 33.82%
Number/percentage of G's	14,949,122 / 25.24%
Number/percentage of N's	1,193 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.207

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

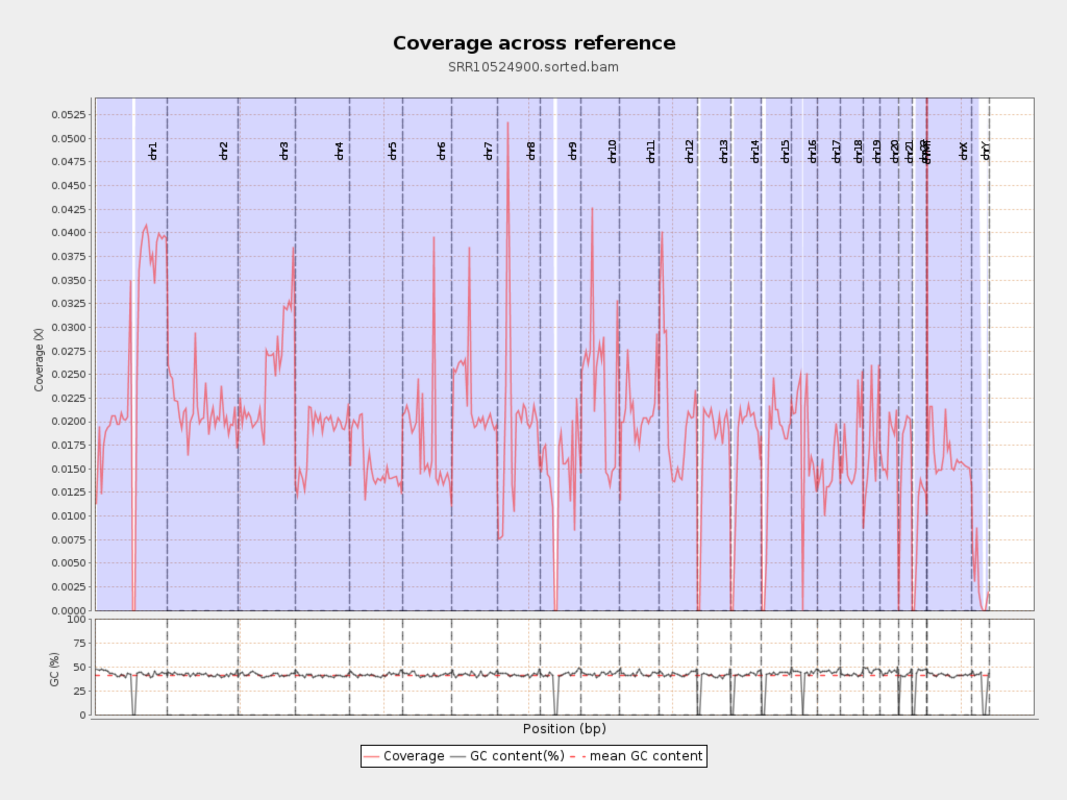
General error rate	0.53%
Mismatches	305,462
Insertions	4,069
Mapped reads with at least one insertion	0.39%
Deletions	11,874
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.68%

2.6. Chromosome stats

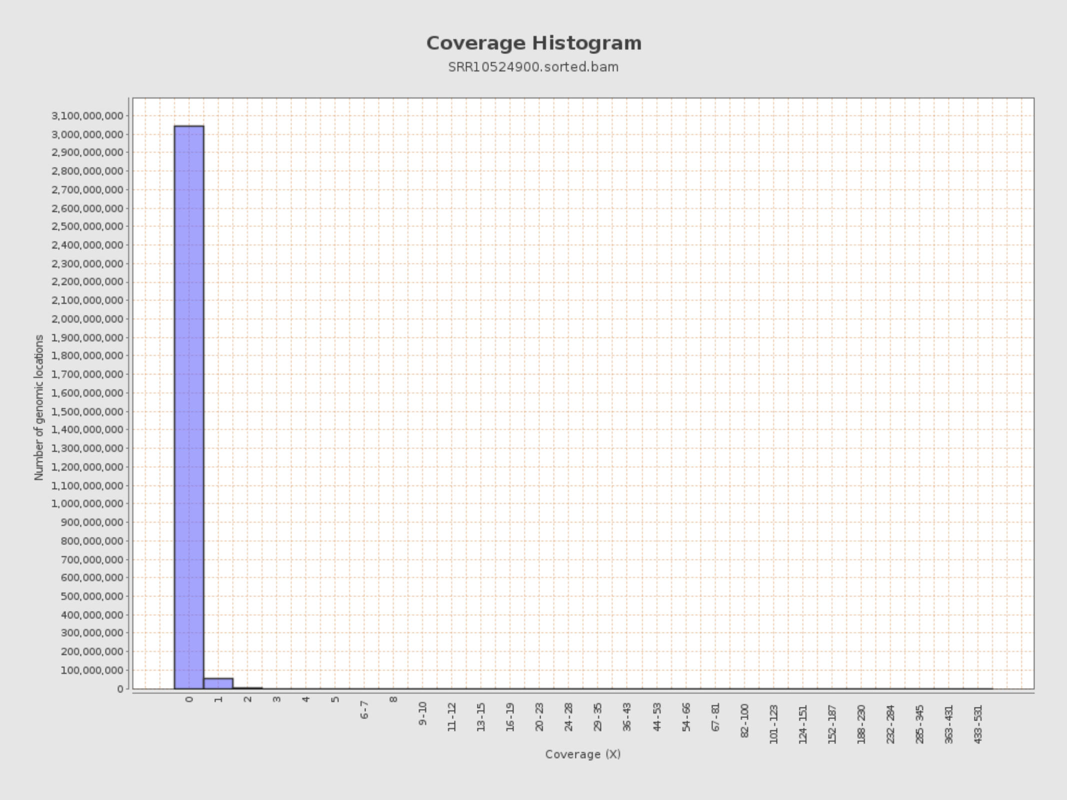
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6573769	0.0264	0.3612
chr2	243199373	5145440	0.0212	0.2673
chr3	198022430	4948469	0.025	0.1692
chr4	191154276	3566228	0.0187	0.1488
chr5	180915260	2820885	0.0156	0.1322
chr6	171115067	3097833	0.0181	0.1603
chr7	159138663	3612428	0.0227	0.3099

chr8	146364022	2901160	0.0198	0.204
chr9	141213431	1988074	0.0141	0.1518
chr10	135534747	3260036	0.0241	0.2383
chr11	135006516	2824330	0.0209	0.1769
chr12	133851895	2812933	0.021	0.1557
chr13	115169878	1981042	0.0172	0.1414
chr14	107349540	1778675	0.0166	0.1389
chr15	102531392	1673083	0.0163	0.1397
chr16	90354753	1625358	0.018	0.1559
chr17	81195210	1201328	0.0148	0.1329
chr18	78077248	1332806	0.0171	0.2588
chr19	59128983	1041681	0.0176	0.2513
chr20	63025520	1093957	0.0174	0.1414
chr21	48129895	798210	0.0166	0.1403
chr22	51304566	457461	0.0089	0.0989
chrMT	16571	1142	0.0689	0.2741
chrX	155270560	2558020	0.0165	0.1467
chrY	59373566	160372	0.0027	0.0843

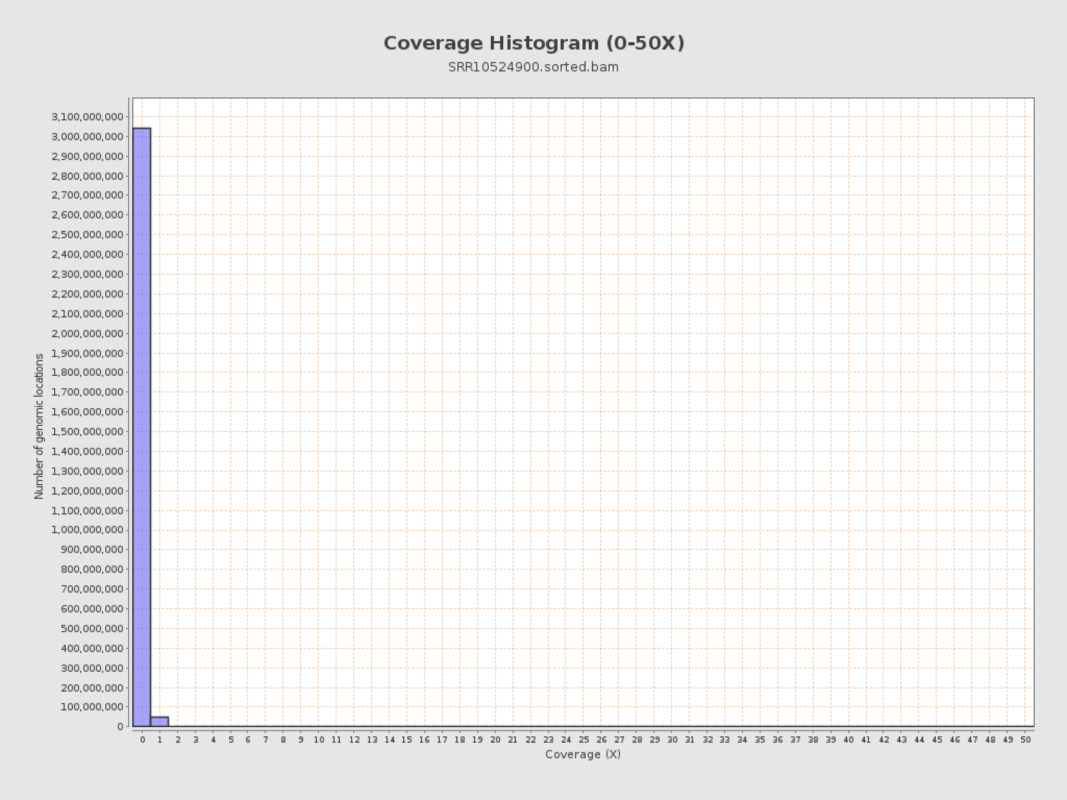
3. Results : Coverage across reference



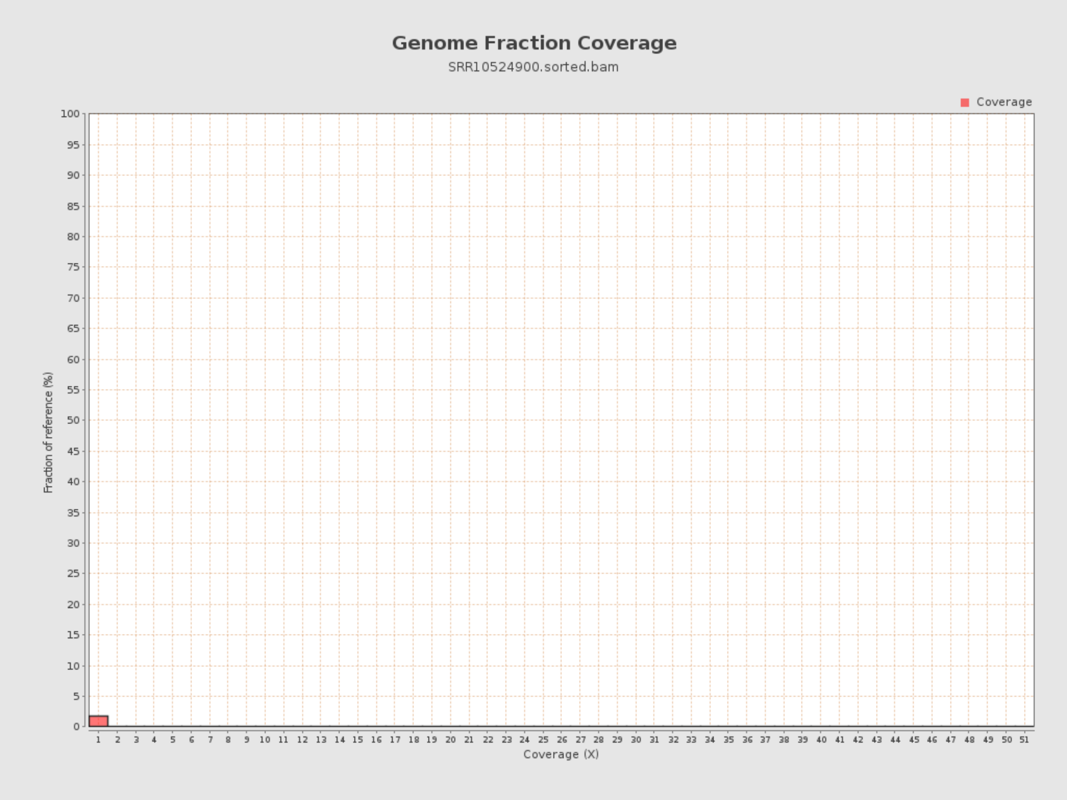
4. Results : Coverage Histogram



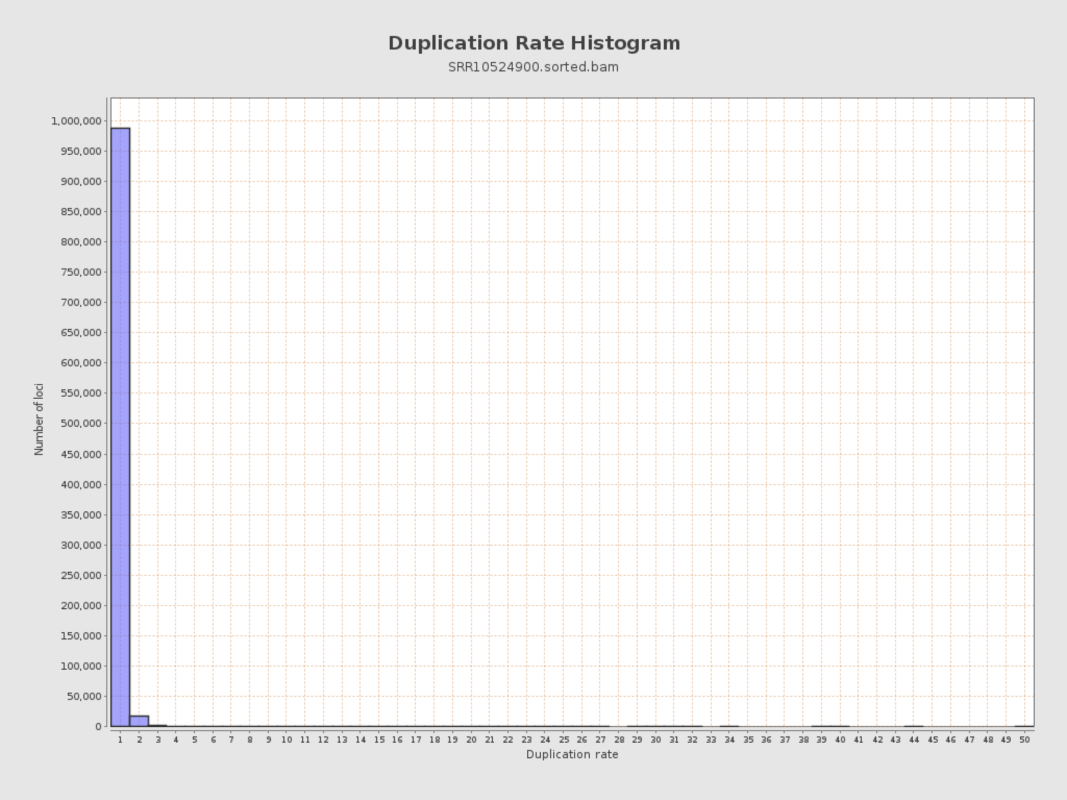
5. Results : Coverage Histogram (0-50X)



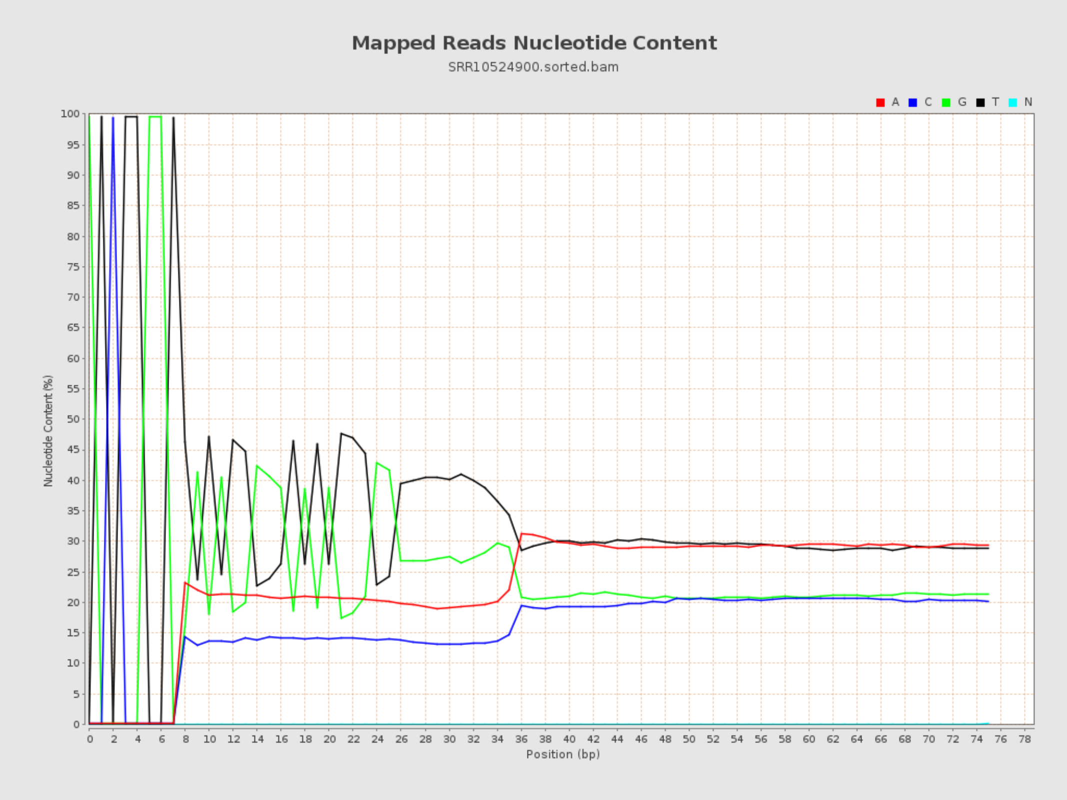
6. Results : Genome Fraction Coverage



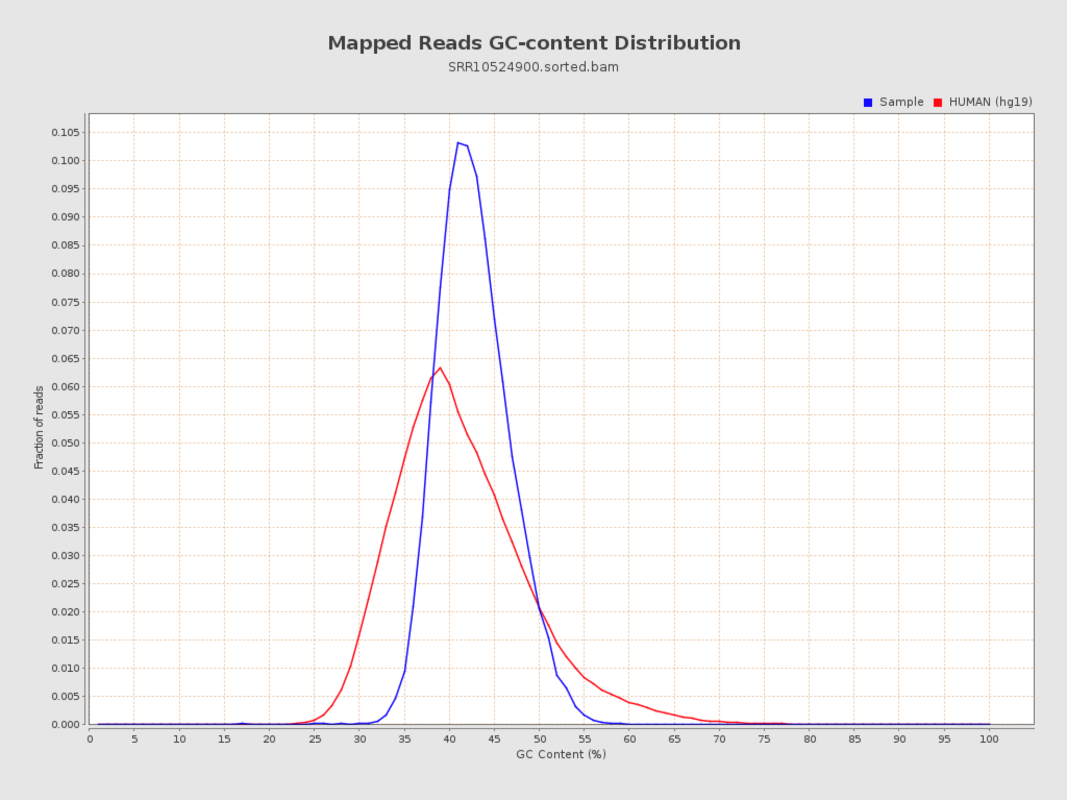
7. Results : Duplication Rate Histogram



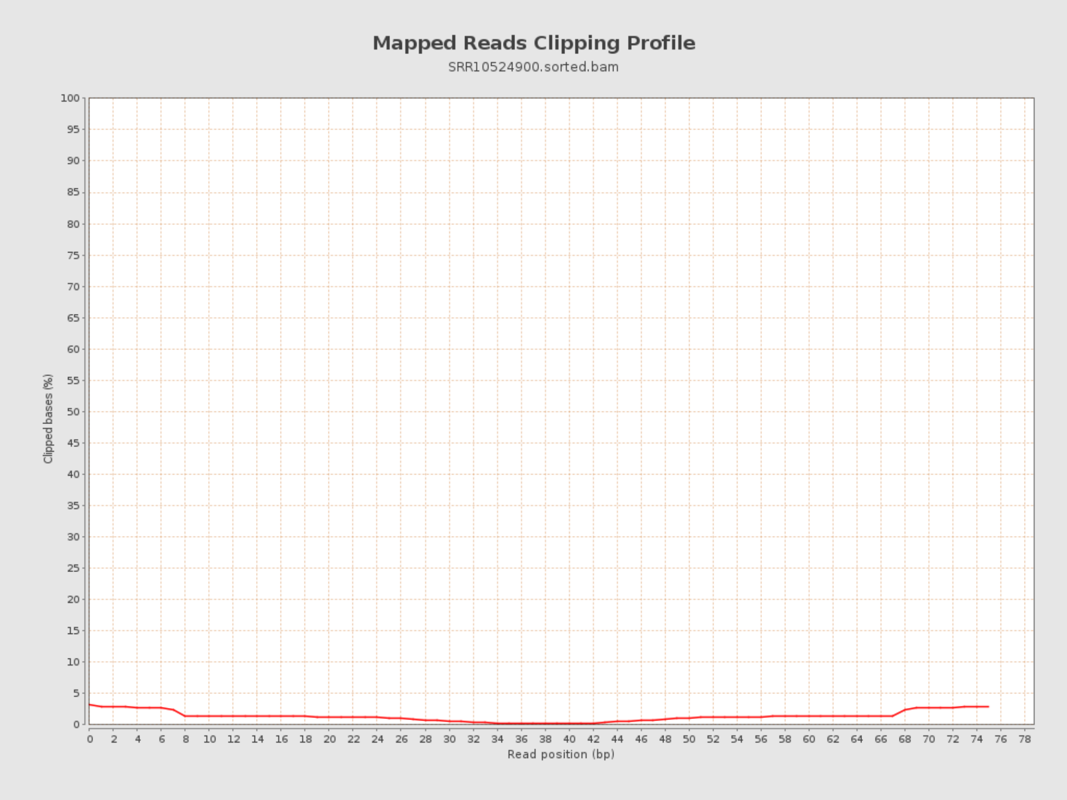
8. Results : Mapped Reads Nucleotide Content



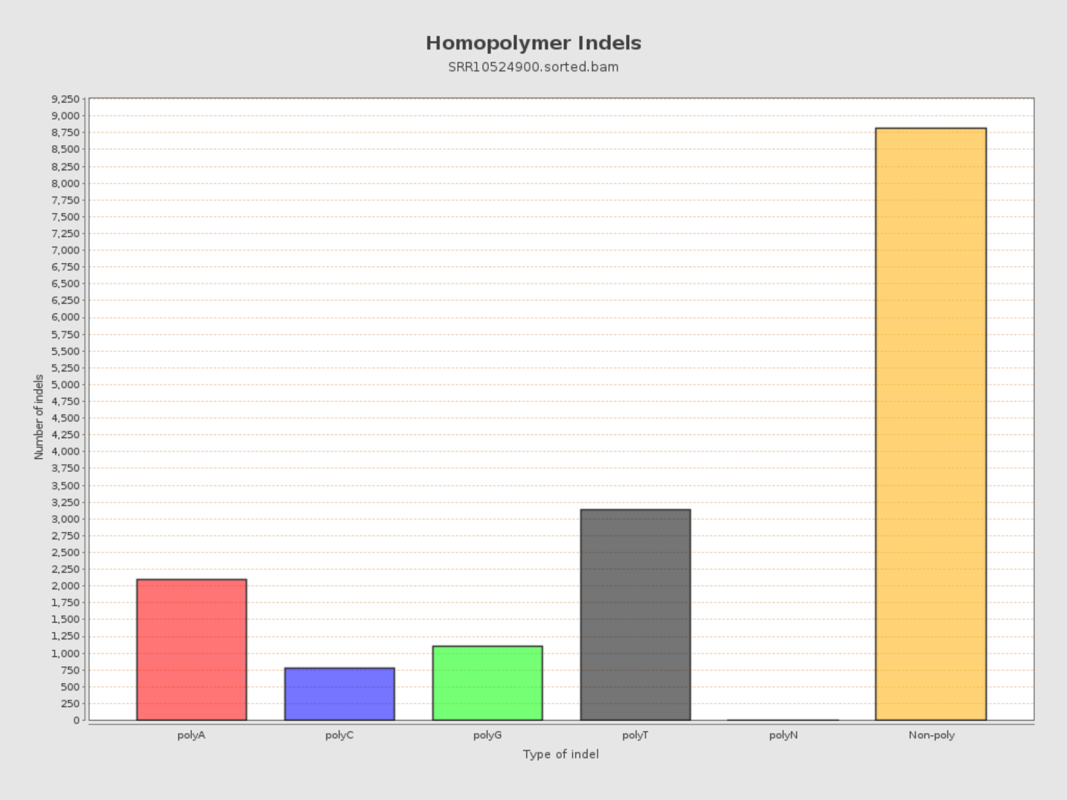
9. Results : Mapped Reads GC-content Distribution



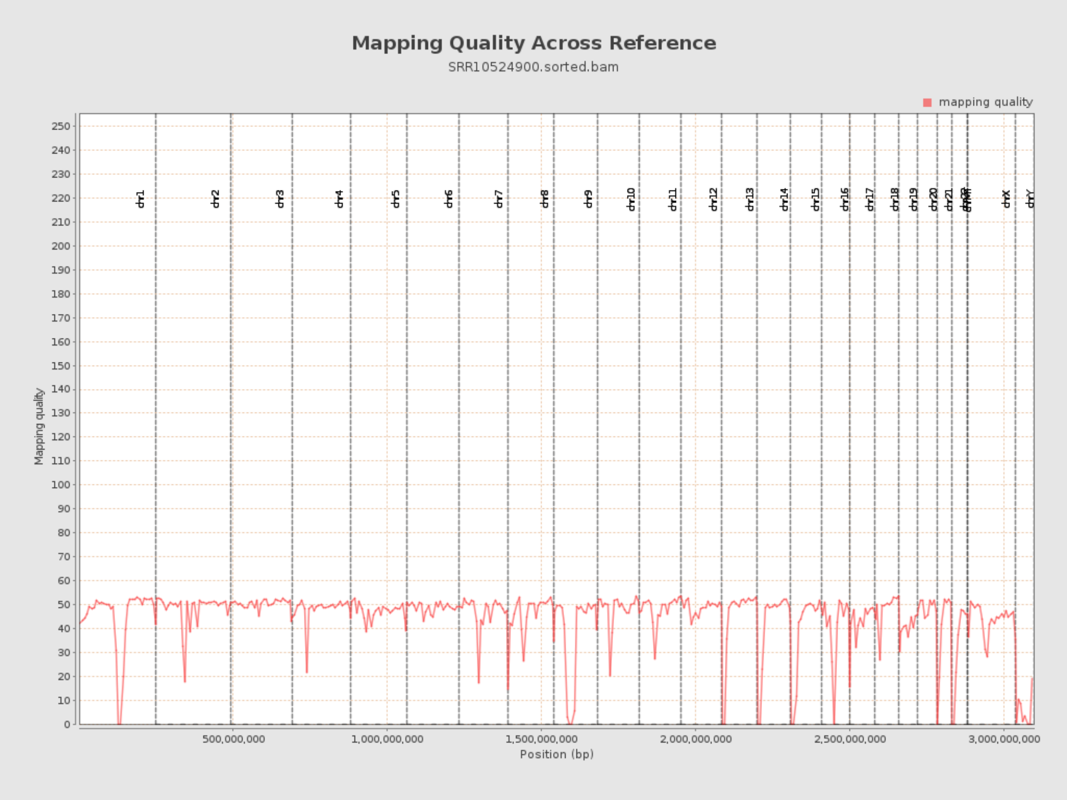
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram