Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:51:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524868.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_SRR10524868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:51:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,104,374
Mapped reads	1,015,664 / 91.97%
Unmapped reads	88,710 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,304 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	24,316 / 2.2%
Duplication rate	1.61%
Clipped reads	1,017,651 / 92.15%

2.2. ACGT Content

Number/percentage of A's	14,721,655 / 24.79%
Number/percentage of C's	11,335,421 / 19.09%
Number/percentage of T's	19,639,293 / 33.07%
Number/percentage of G's	13,686,654 / 23.05%
Number/percentage of N's	7,824 / 0.01%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0192

Standard Deviation	0.2094

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

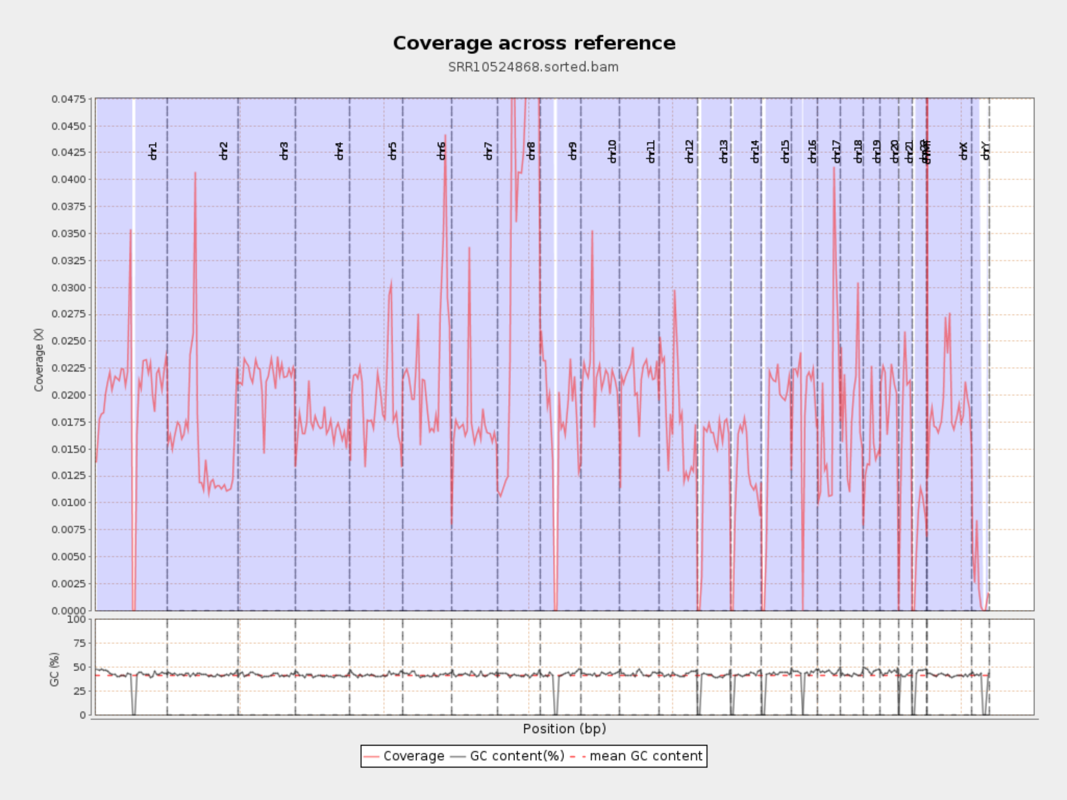
General error rate	0.49%
Mismatches	286,420
Insertions	4,291
Mapped reads with at least one insertion	0.42%
Deletions	11,168
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.5%

2.6. Chromosome stats

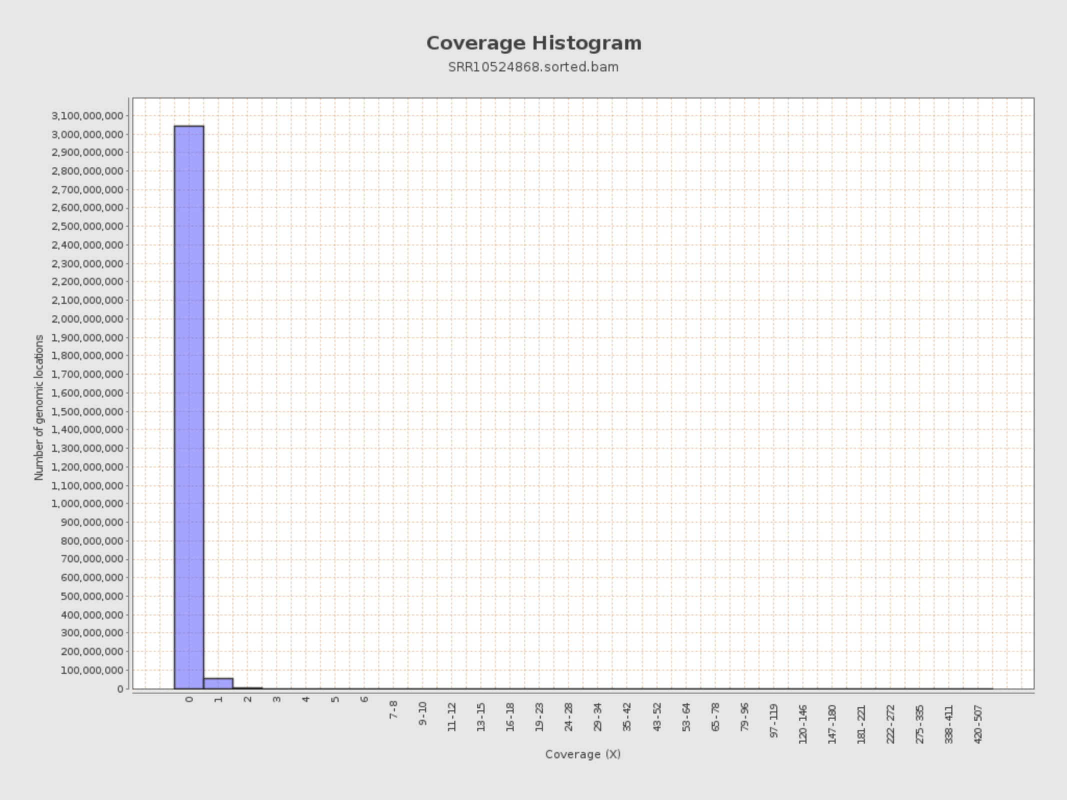
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4982623	0.02	0.3837
chr2	243199373	3776179	0.0155	0.2127
chr3	198022430	4314064	0.0218	0.1547
chr4	191154276	3252545	0.017	0.144
chr5	180915260	3595401	0.0199	0.148
chr6	171115067	3848387	0.0225	0.168
chr7	159138663	2759772	0.0173	0.2784

chr8	146364022	6399443	0.0437	0.2776
chr9	141213431	2445473	0.0173	0.1804
chr10	135534747	2982631	0.022	0.204
chr11	135006516	2896648	0.0215	0.1883
chr12	133851895	2392752	0.0179	0.1414
chr13	115169878	1591351	0.0138	0.1229
chr14	107349540	1250095	0.0116	0.1212
chr15	102531392	1737498	0.0169	0.138
chr16	90354753	1724237	0.0191	0.1532
chr17	81195210	1528675	0.0188	0.1567
chr18	78077248	1455693	0.0186	0.3207
chr19	59128983	878918	0.0149	0.2782
chr20	63025520	1273124	0.0202	0.1505
chr21	48129895	843008	0.0175	0.1425
chr22	51304566	362894	0.0071	0.0874
chrMT	16571	2655	0.1602	0.4158
chrX	155270560	2969160	0.0191	0.1605
chrY	59373566	144874	0.0024	0.0657

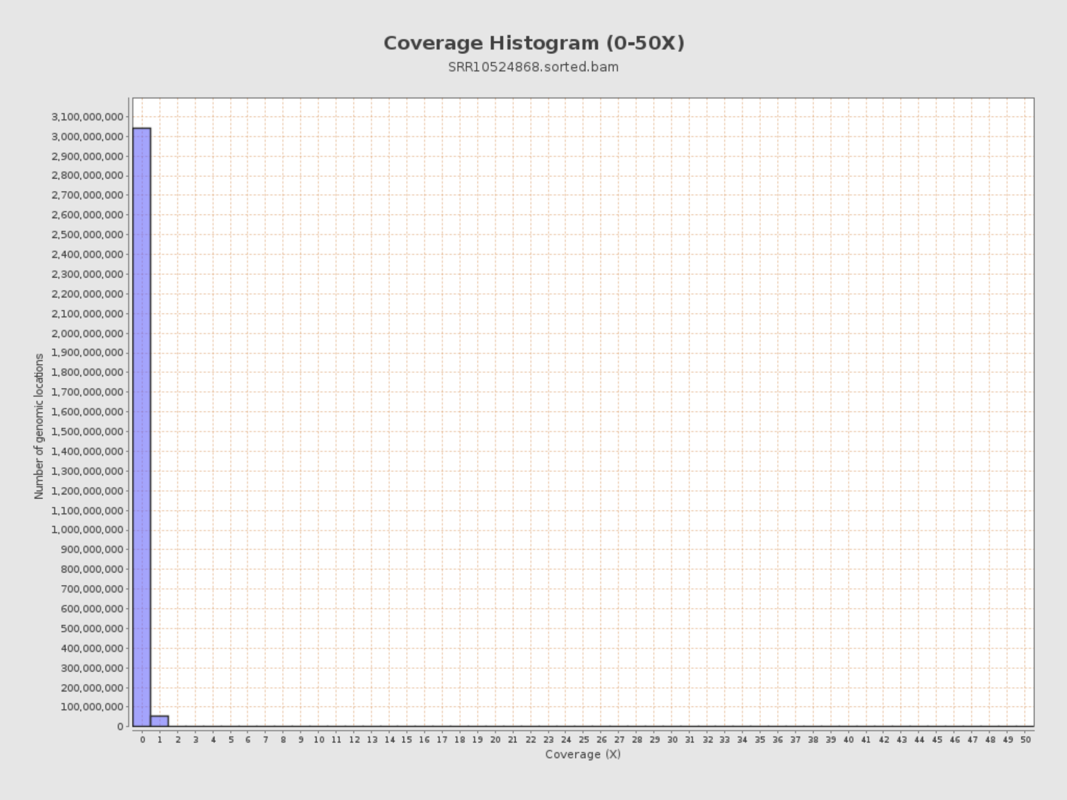
3. Results : Coverage across reference



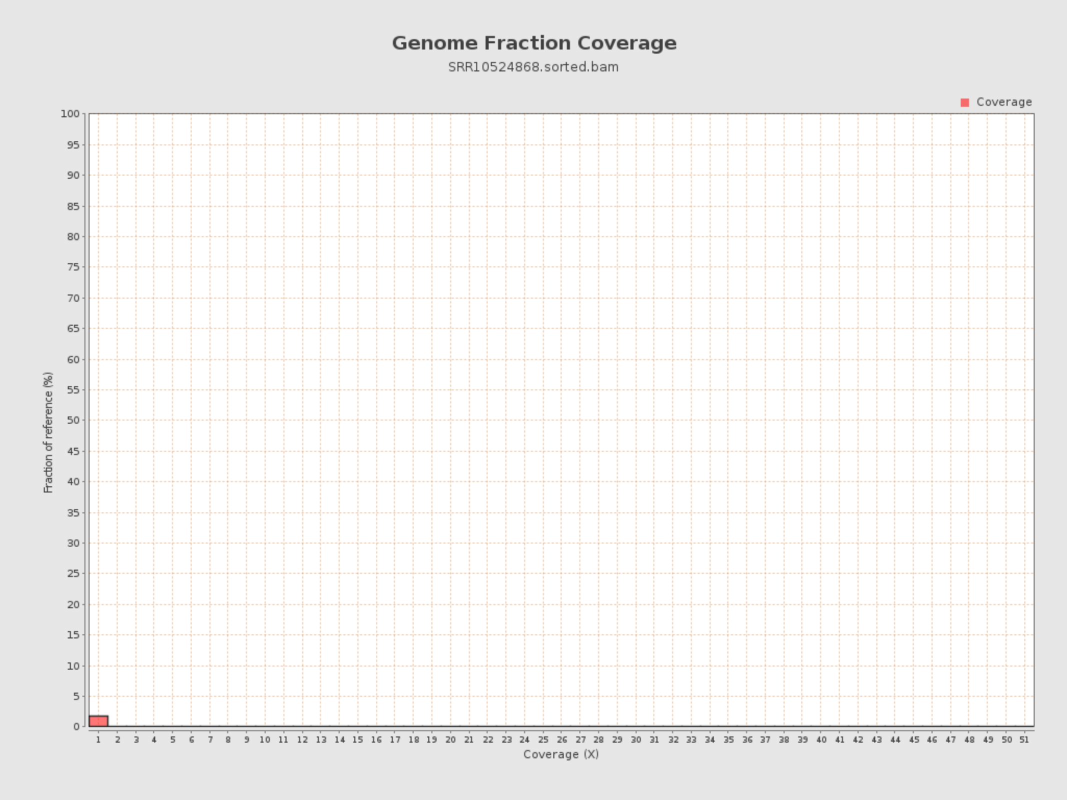
4. Results : Coverage Histogram



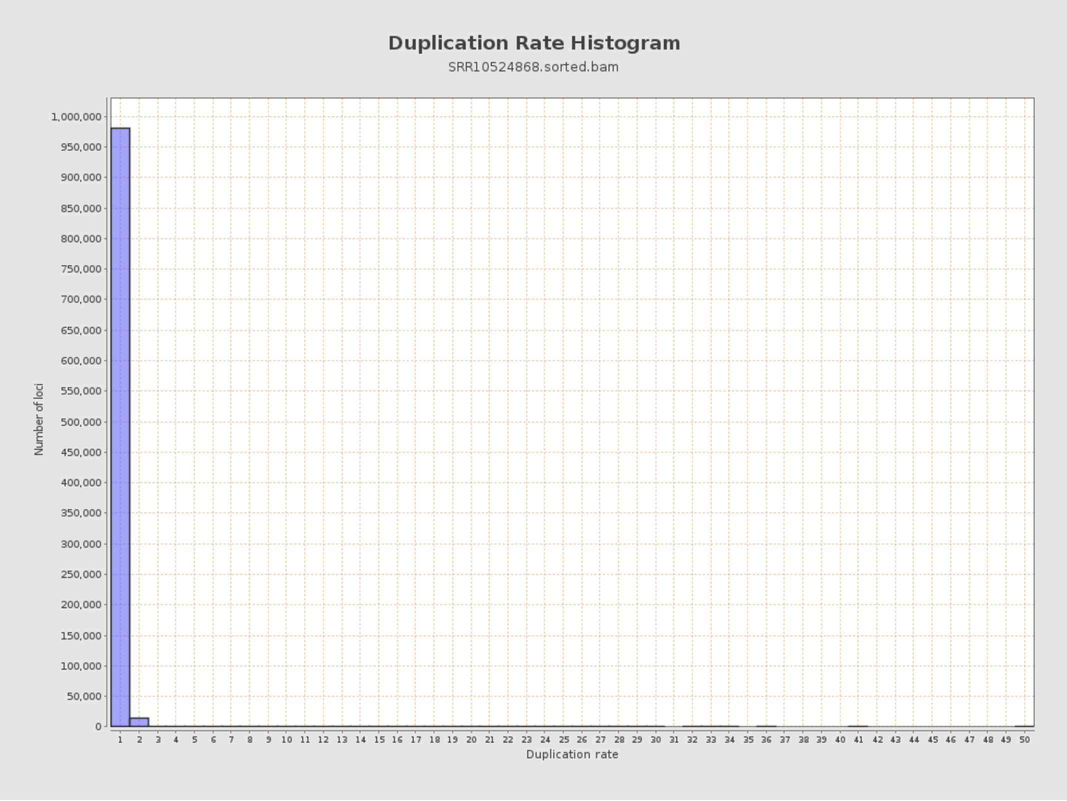
5. Results : Coverage Histogram (0-50X)



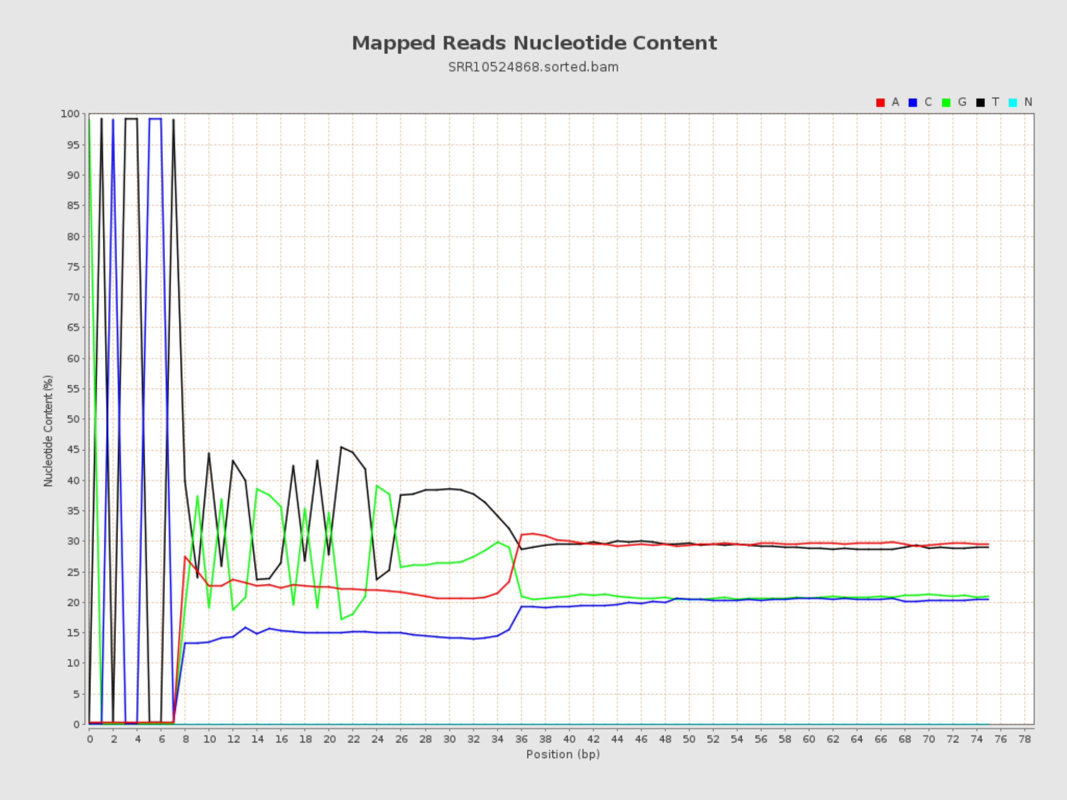
6. Results : Genome Fraction Coverage



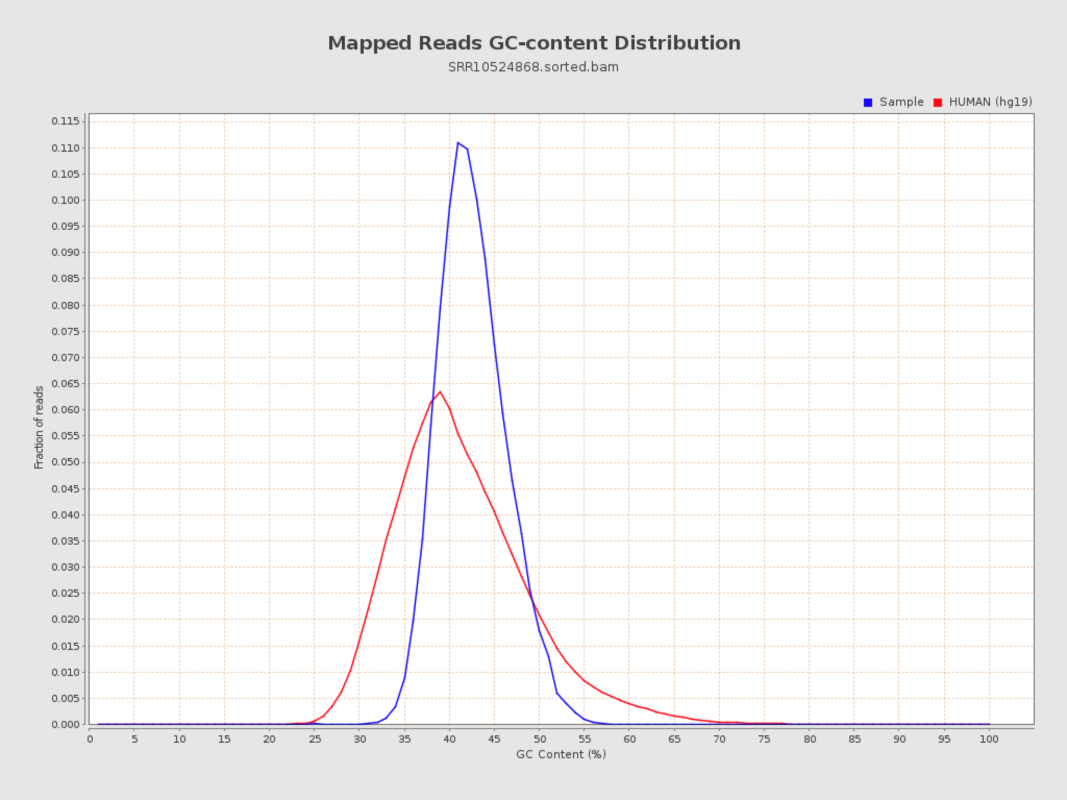
7. Results : Duplication Rate Histogram



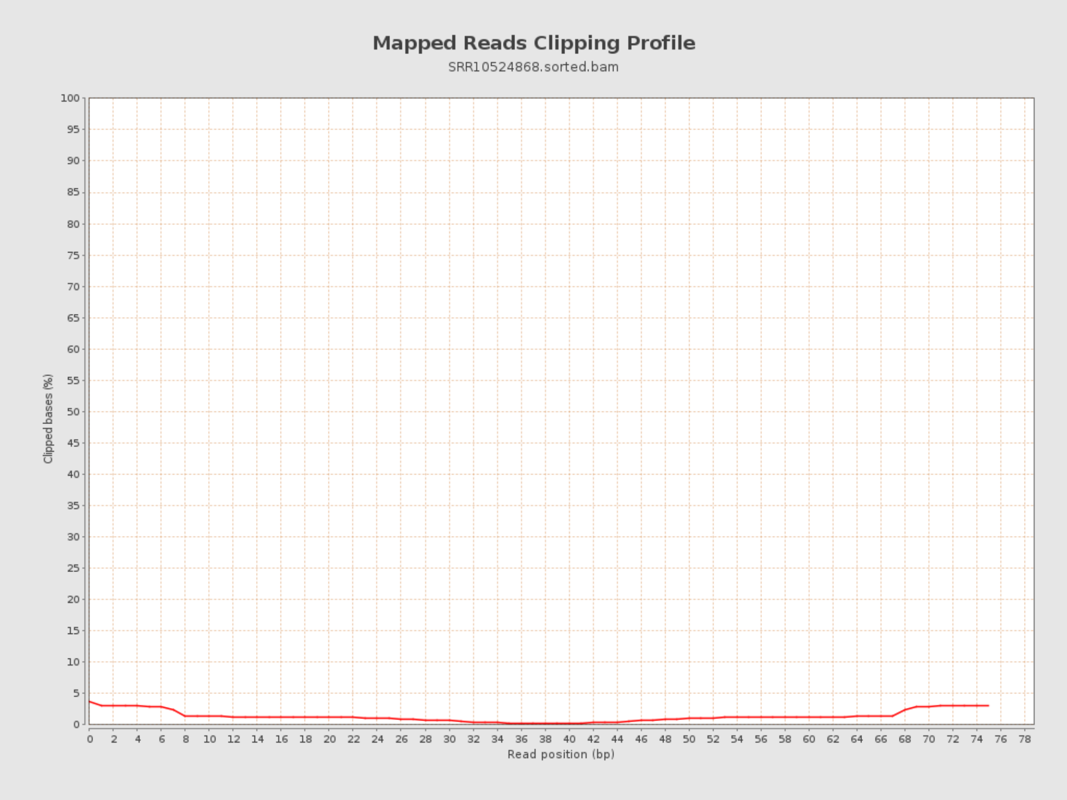
8. Results : Mapped Reads Nucleotide Content



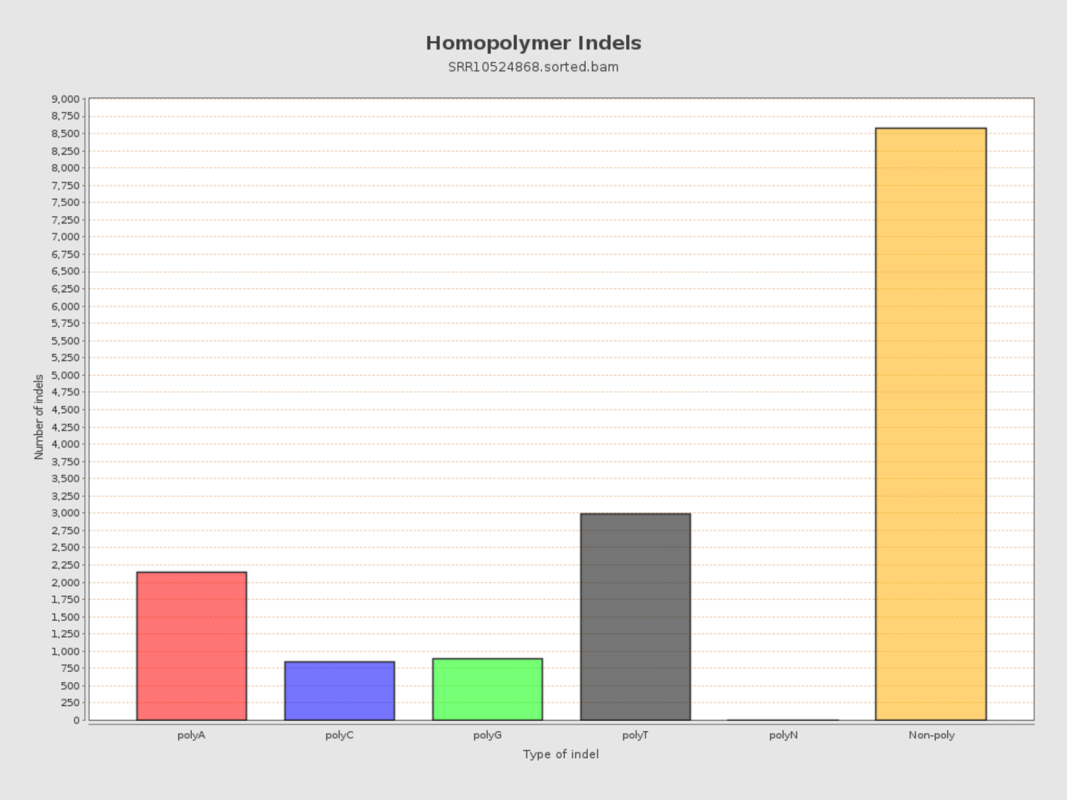
9. Results : Mapped Reads GC-content Distribution



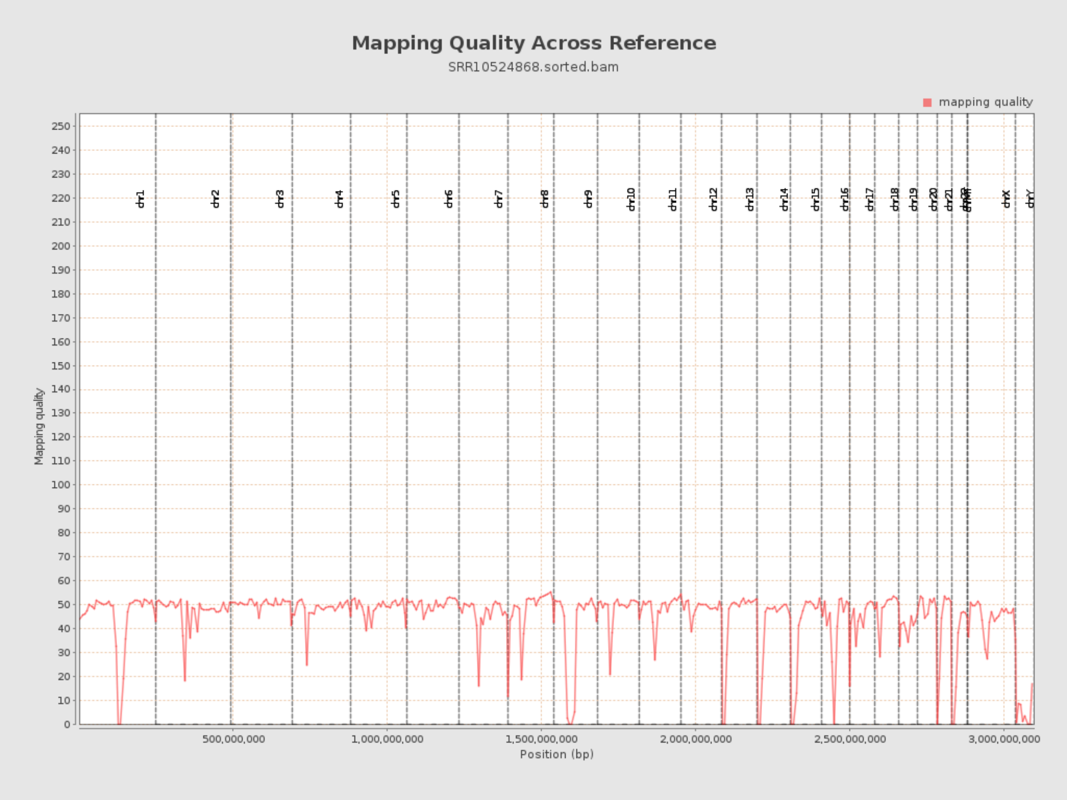
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram