Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:24:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524808.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_SRR10524808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:24:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,479,883
Mapped reads	1,353,754 / 91.48%
Unmapped reads	126,129 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,269 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	55,195 / 3.73%
Duplication rate	3.14%
Clipped reads	1,356,364 / 91.65%

2.2. ACGT Content

Number/percentage of A's	18,788,875 / 24.16%
Number/percentage of C's	13,835,135 / 17.79%
Number/percentage of T's	24,493,821 / 31.49%
Number/percentage of G's	20,650,125 / 26.55%
Number/percentage of N's	9,068 / 0.01%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2307

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

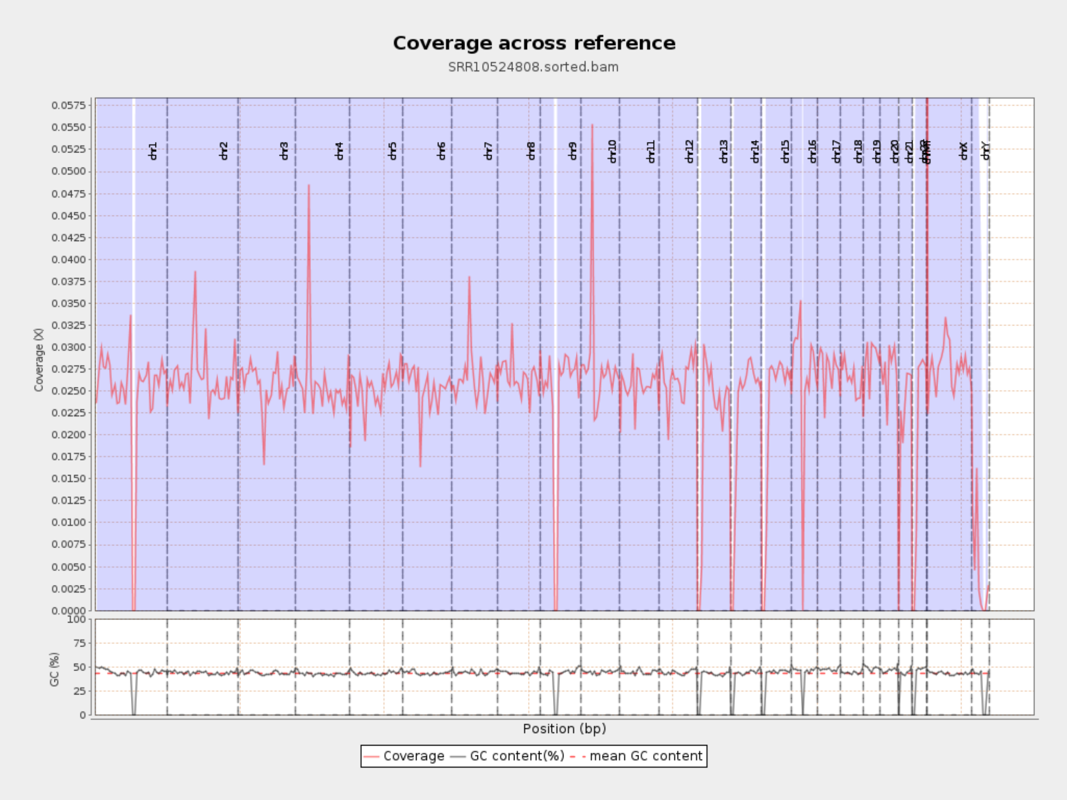
General error rate	0.52%
Mismatches	397,159
Insertions	5,319
Mapped reads with at least one insertion	0.39%
Deletions	15,634
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.93%

2.6. Chromosome stats

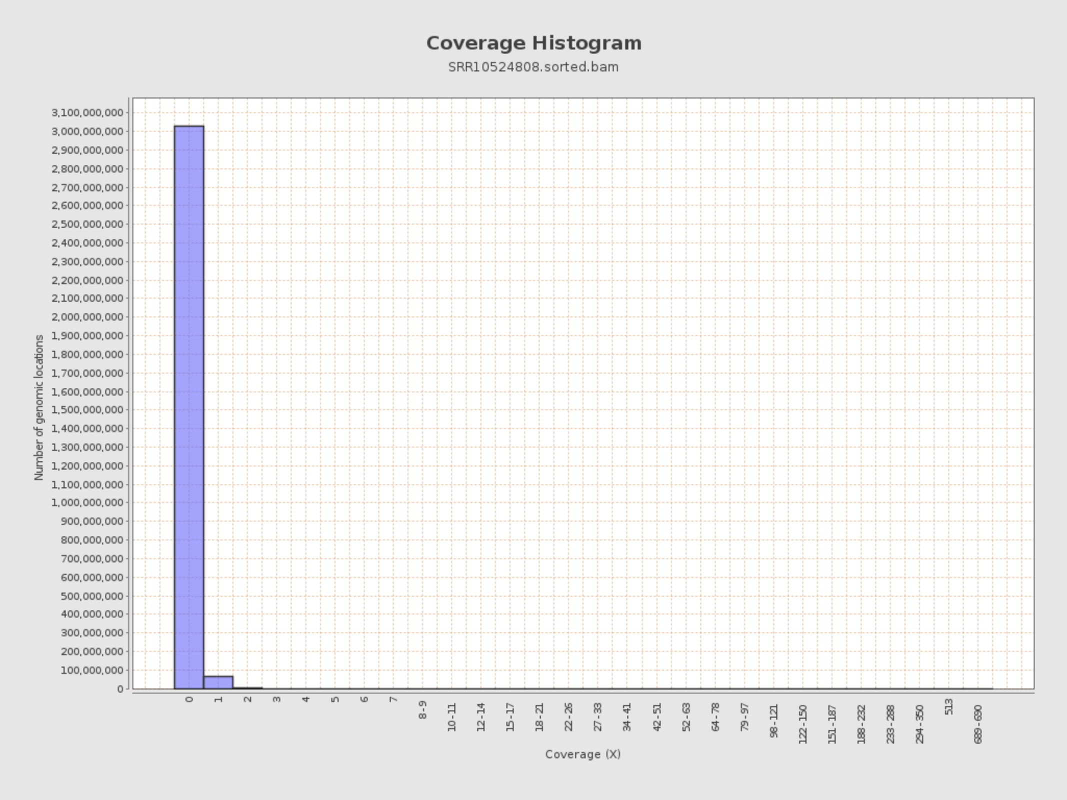
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6173078	0.0248	0.3144
chr2	243199373	6472074	0.0266	0.3508
chr3	198022430	5088171	0.0257	0.1788
chr4	191154276	4978433	0.026	0.2033
chr5	180915260	4625142	0.0256	0.1757
chr6	171115067	4328479	0.0253	0.1934
chr7	159138663	4236015	0.0266	0.2751

chr8	146364022	3901713	0.0267	0.2208
chr9	141213431	3387668	0.024	0.198
chr10	135534747	3816473	0.0282	0.2778
chr11	135006516	3488563	0.0258	0.2029
chr12	133851895	3555396	0.0266	0.1826
chr13	115169878	2424740	0.0211	0.1601
chr14	107349540	2361591	0.022	0.1665
chr15	102531392	2257178	0.022	0.1637
chr16	90354753	2373205	0.0263	0.1972
chr17	81195210	2234180	0.0275	0.1912
chr18	78077248	2060024	0.0264	0.3065
chr19	59128983	1686954	0.0285	0.2655
chr20	63025520	1705648	0.0271	0.1903
chr21	48129895	1054270	0.0219	0.1816
chr22	51304566	984116	0.0192	0.1532
chrMT	16571	20086	1.2121	1.2813
chrX	155270560	4323115	0.0278	0.1948
chrY	59373566	266563	0.0045	0.1322

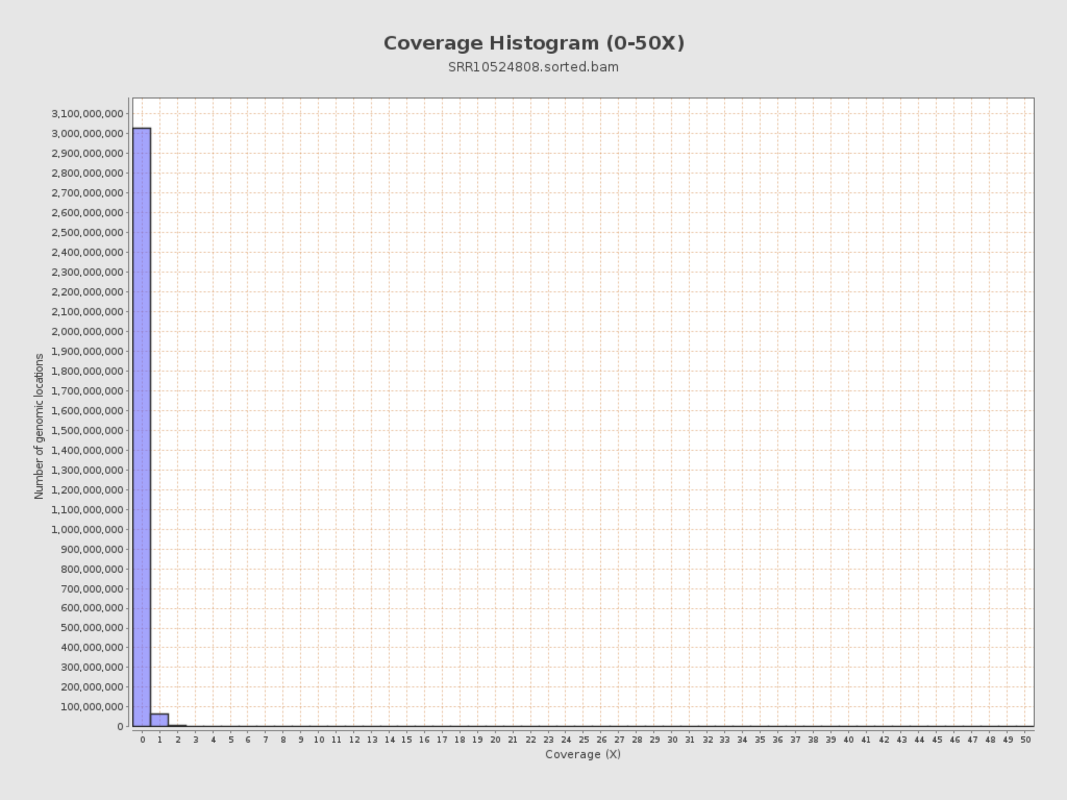
3. Results : Coverage across reference



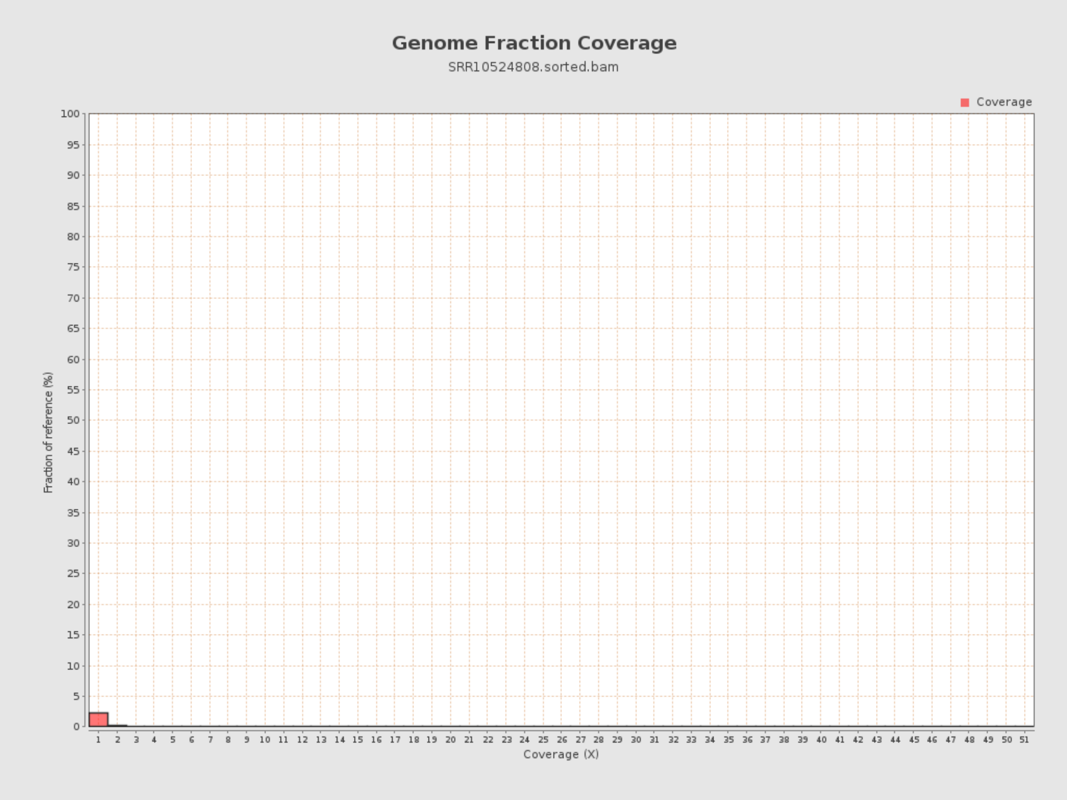
4. Results : Coverage Histogram



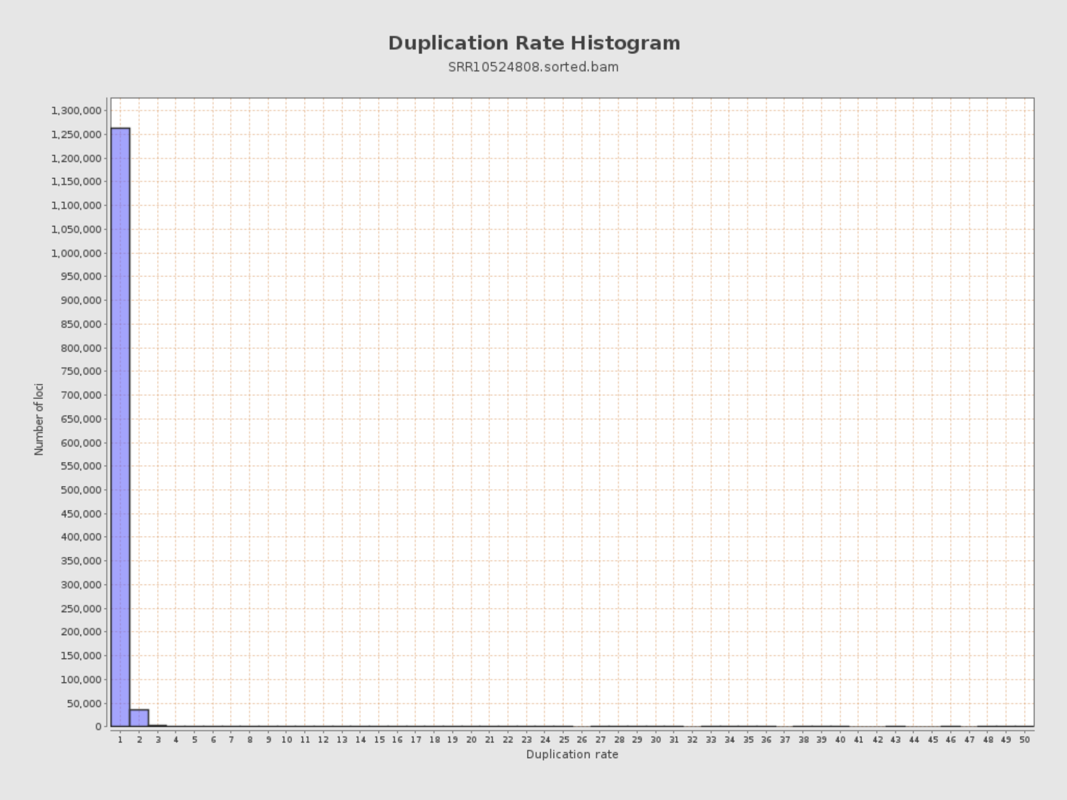
5. Results : Coverage Histogram (0-50X)



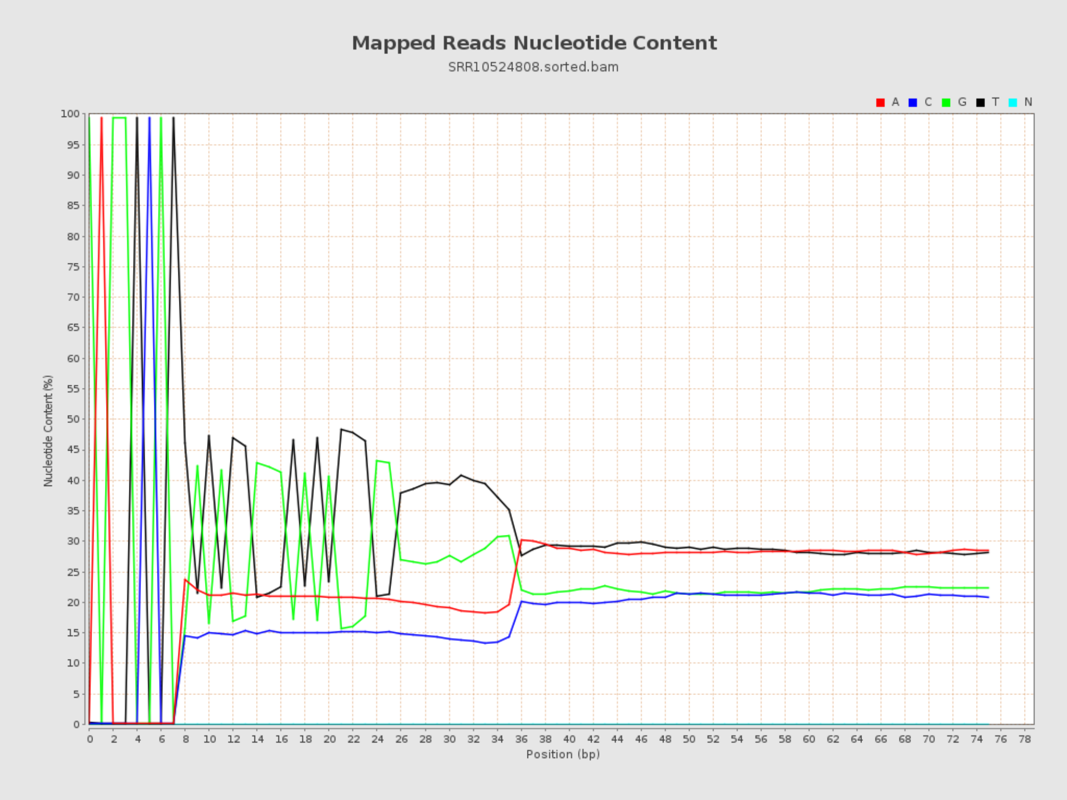
6. Results : Genome Fraction Coverage



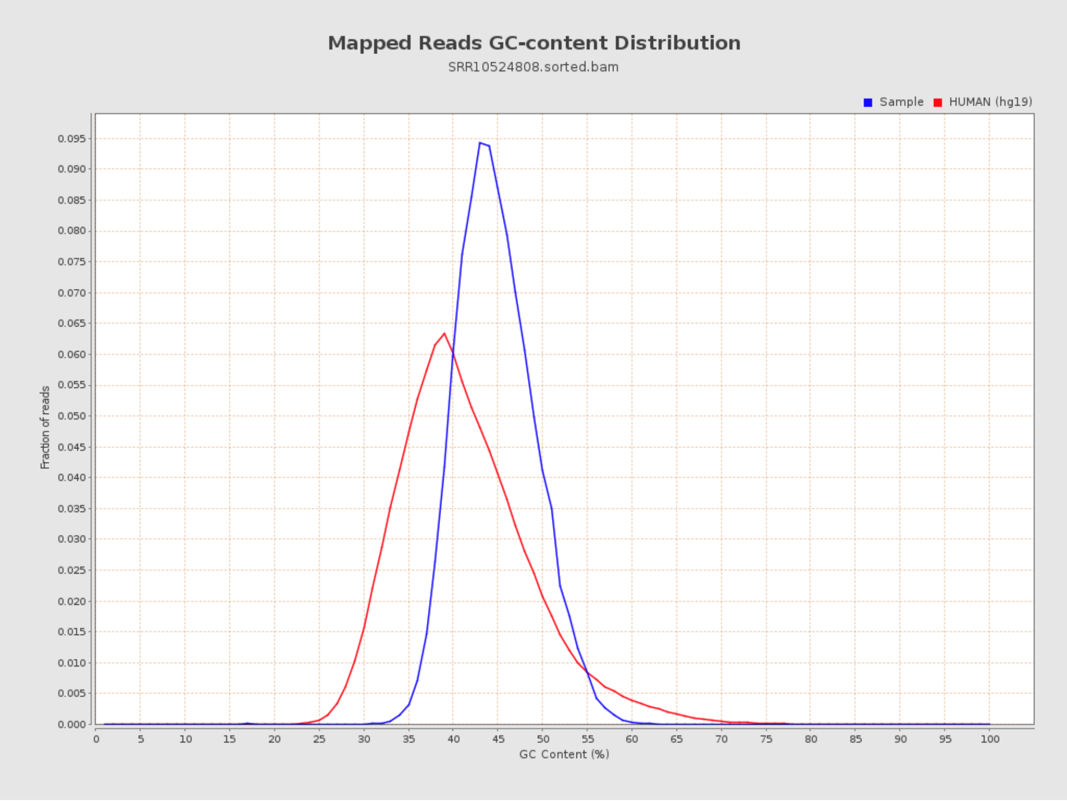
7. Results : Duplication Rate Histogram



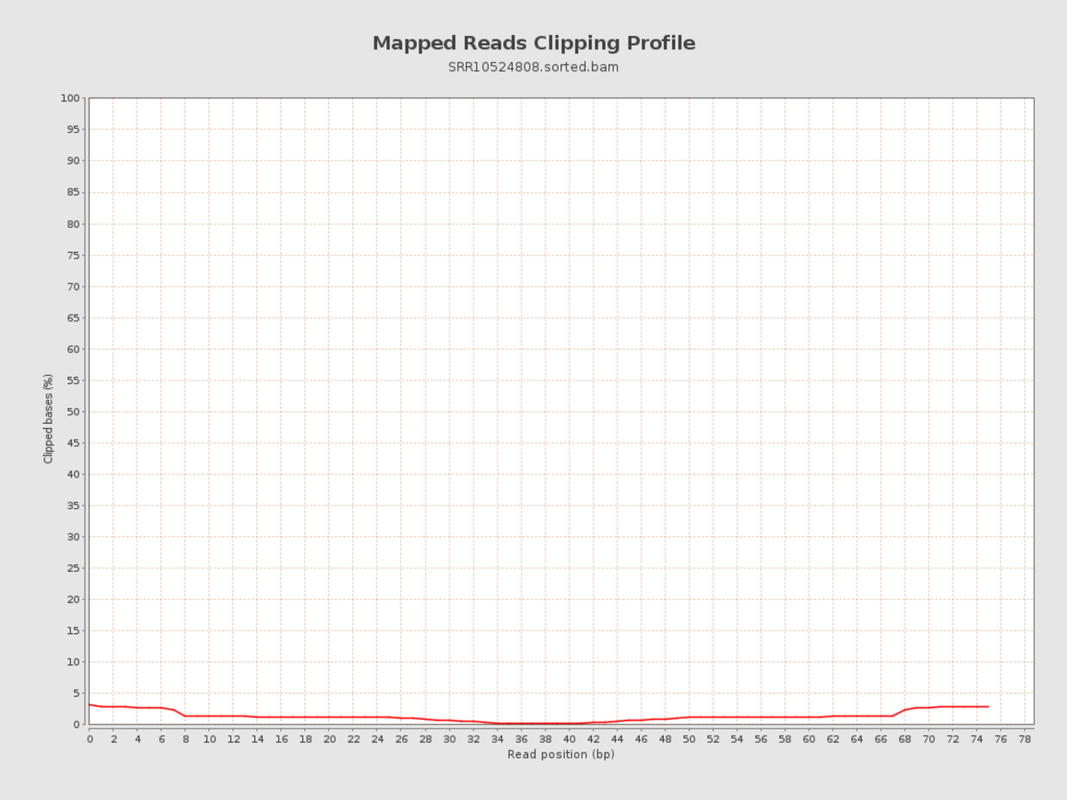
8. Results : Mapped Reads Nucleotide Content



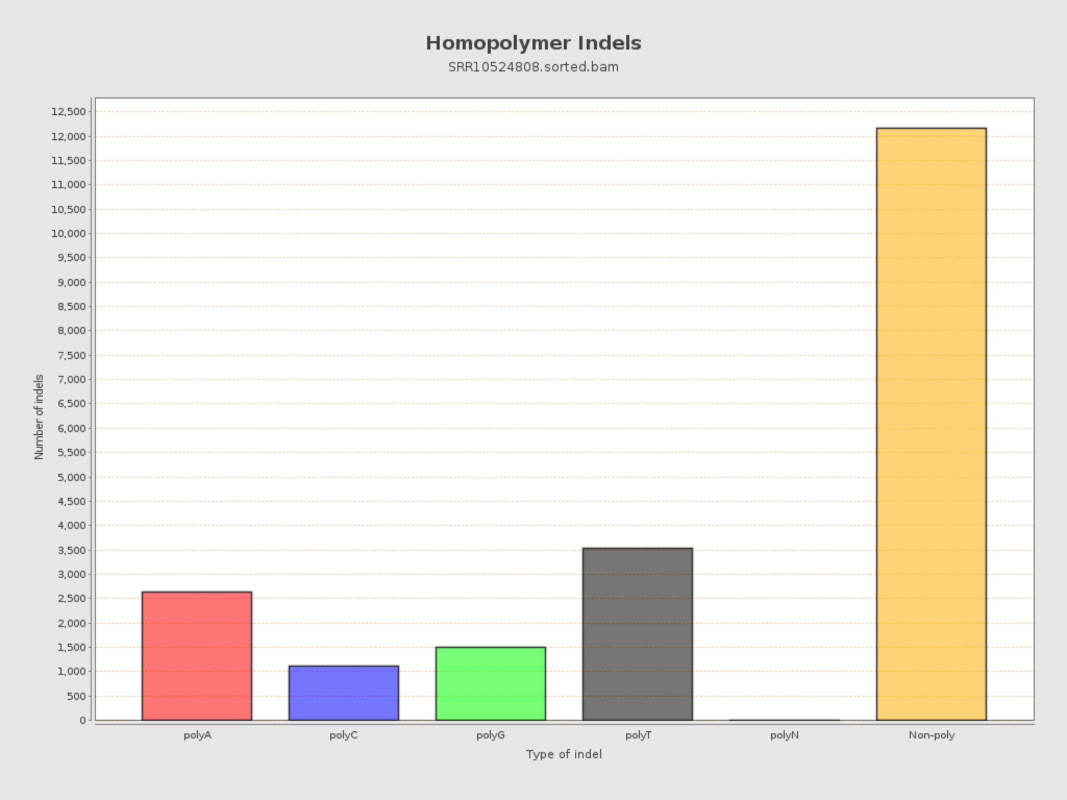
9. Results : Mapped Reads GC-content Distribution



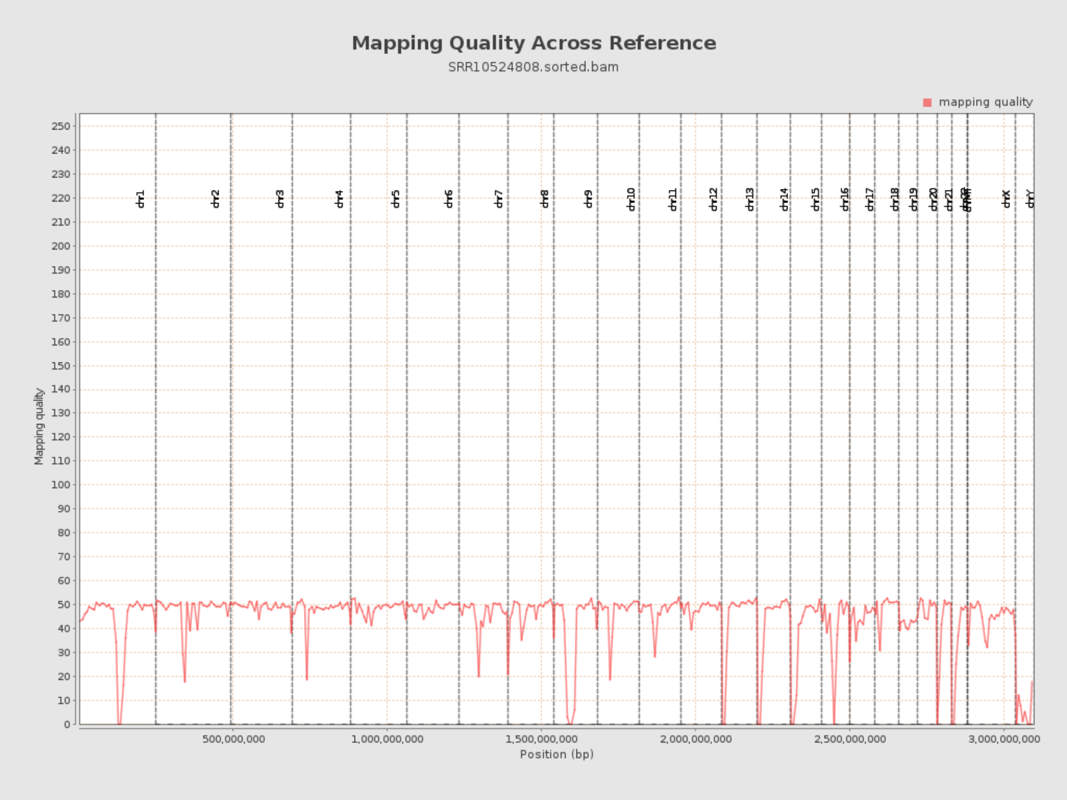
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram