Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 07:45:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524517.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_SRR10524517 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524517.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 07:45:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524517.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,258,149
Mapped reads	1,134,220 / 90.15%
Unmapped reads	123,929 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,028 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	60,237 / 4.79%
Duplication rate	4.21%
Clipped reads	1,135,979 / 90.29%

2.2. ACGT Content

Number/percentage of A's	16,156,492 / 24.48%
Number/percentage of C's	13,536,160 / 20.51%
Number/percentage of T's	21,169,857 / 32.08%
Number/percentage of G's	15,129,070 / 22.93%
Number/percentage of N's	887 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2259

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

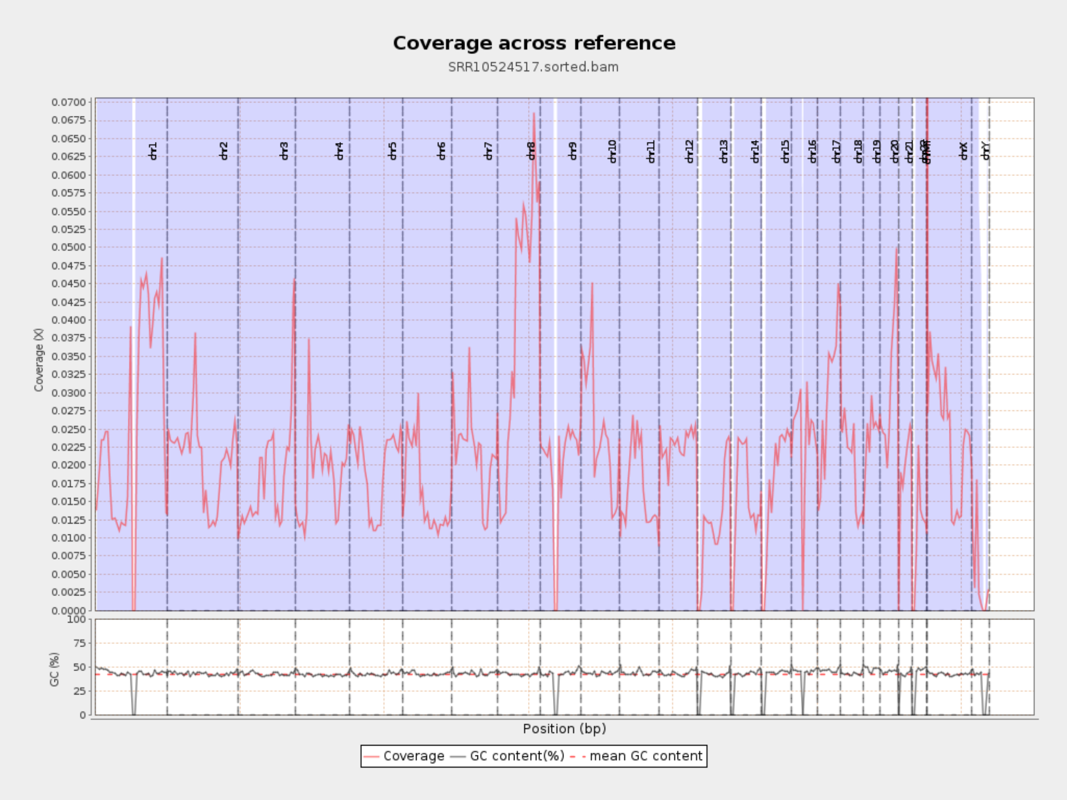
General error rate	0.54%
Mismatches	346,273
Insertions	4,414
Mapped reads with at least one insertion	0.39%
Deletions	12,279
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.88%

2.6. Chromosome stats

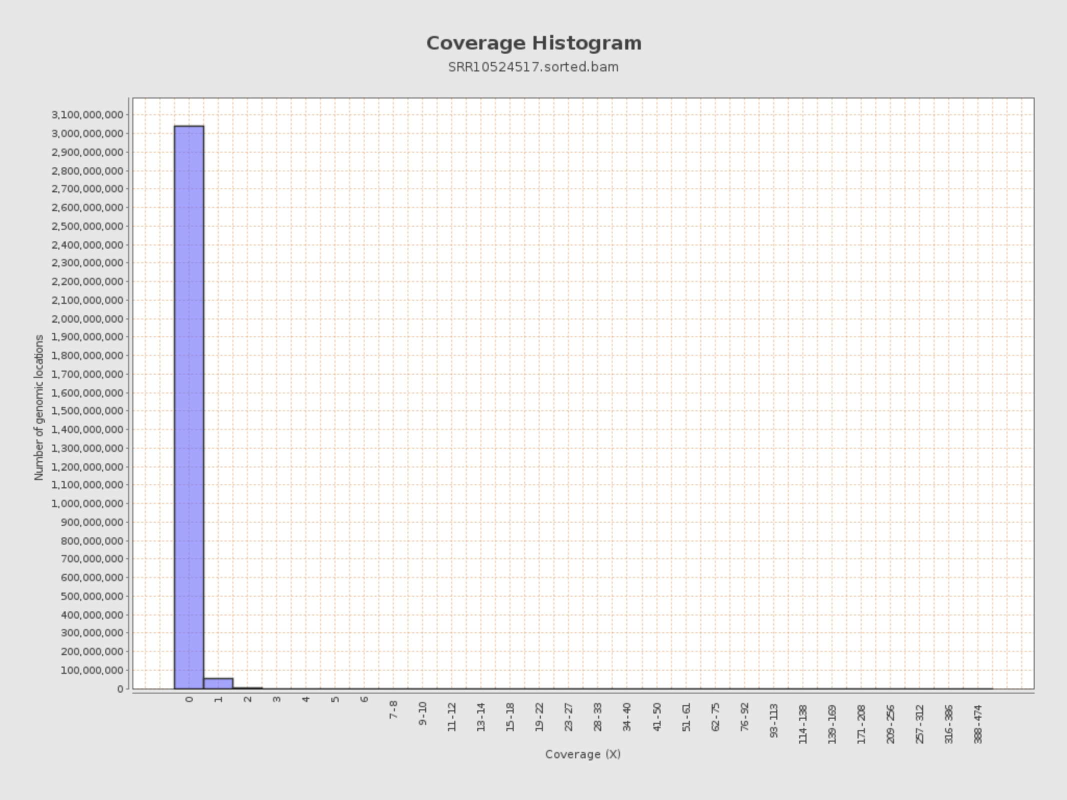
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6394496	0.0257	0.4016
chr2	243199373	5136707	0.0211	0.2716
chr3	198022430	3608066	0.0182	0.1503
chr4	191154276	3609763	0.0189	0.1852
chr5	180915260	3562153	0.0197	0.1555
chr6	171115067	2773365	0.0162	0.1716
chr7	159138663	3522616	0.0221	0.2566

chr8	146364022	5928206	0.0405	0.2613
chr9	141213431	2784751	0.0197	0.1869
chr10	135534747	3464616	0.0256	0.2473
chr11	135006516	2288407	0.017	0.1885
chr12	133851895	3066486	0.0229	0.169
chr13	115169878	1390243	0.0121	0.1226
chr14	107349540	1595728	0.0149	0.1379
chr15	102531392	1766866	0.0172	0.1456
chr16	90354753	2110611	0.0234	0.1782
chr17	81195210	2395826	0.0295	0.2008
chr18	78077248	1567027	0.0201	0.3256
chr19	59128983	1424705	0.0241	0.2844
chr20	63025520	1985757	0.0315	0.2026
chr21	48129895	926221	0.0192	0.1768
chr22	51304566	559839	0.0109	0.1172
chrMT	16571	10531	0.6355	0.9501
chrX	155270560	3873643	0.0249	0.1848
chrY	59373566	266307	0.0045	0.1676

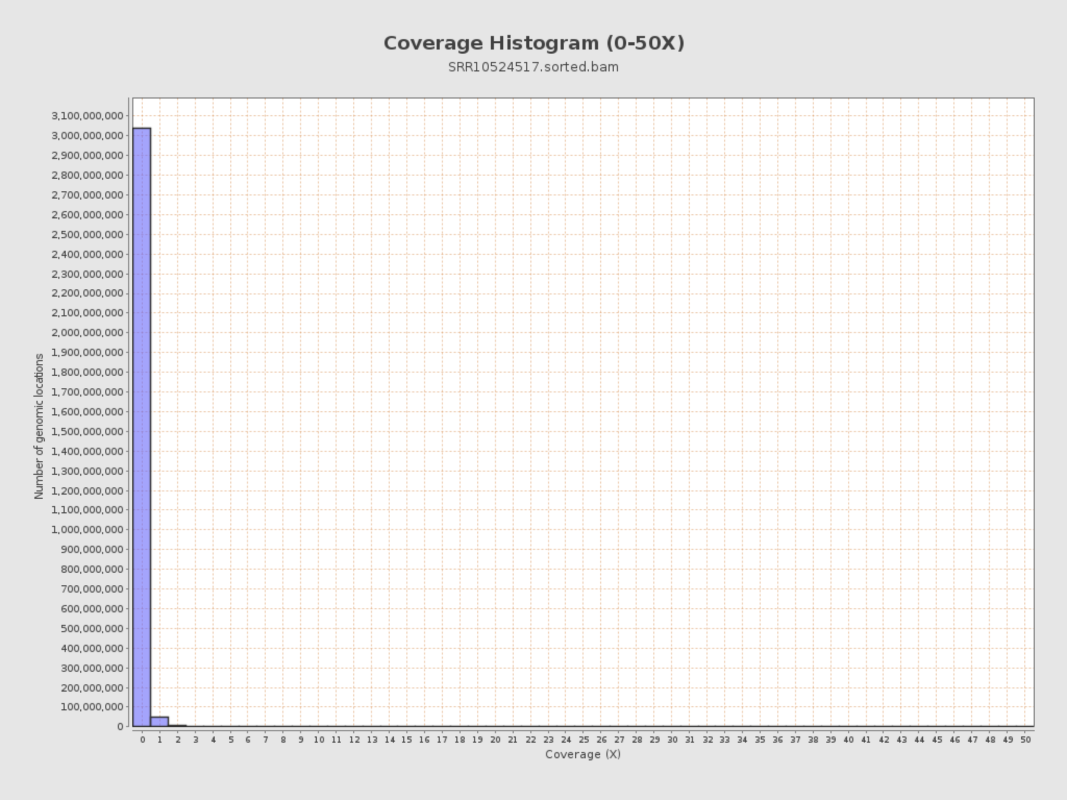
3. Results : Coverage across reference



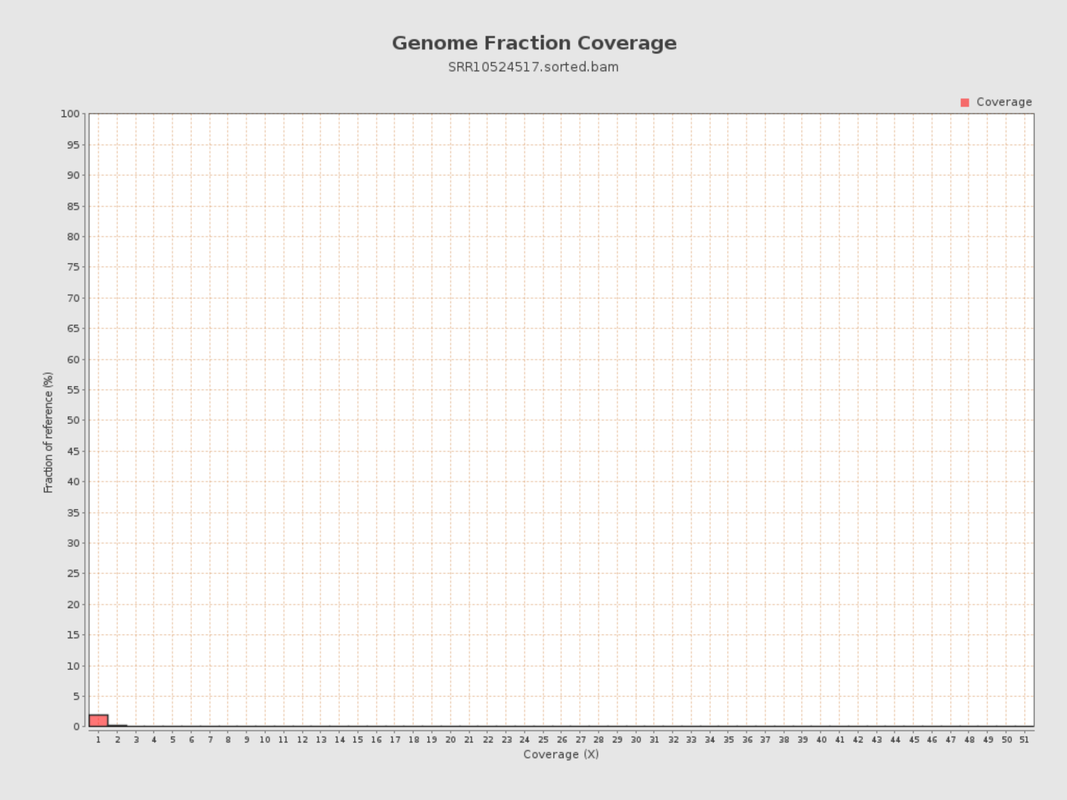
4. Results : Coverage Histogram



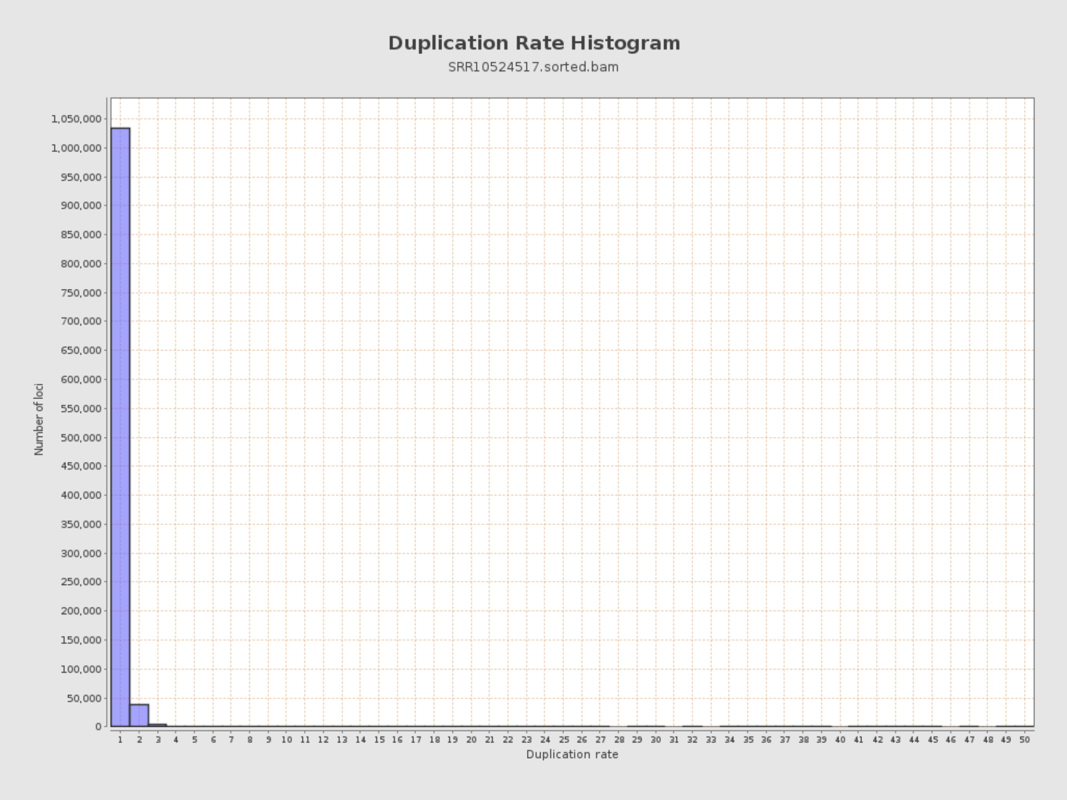
5. Results : Coverage Histogram (0-50X)



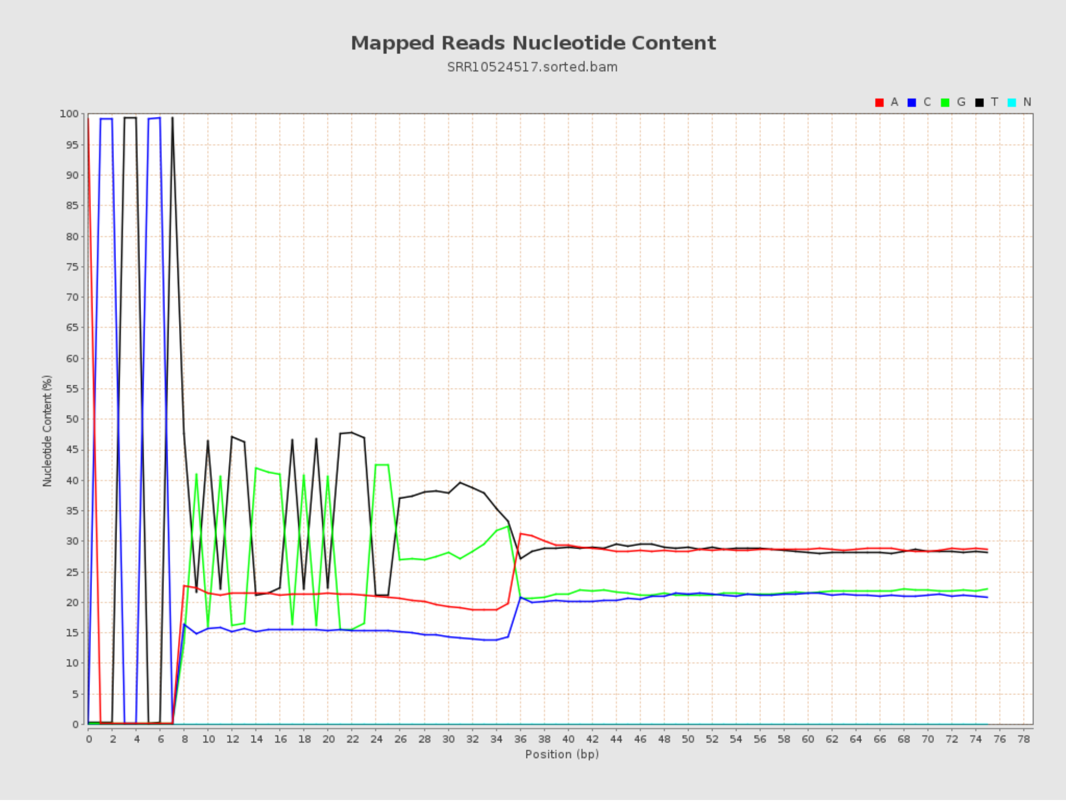
6. Results : Genome Fraction Coverage



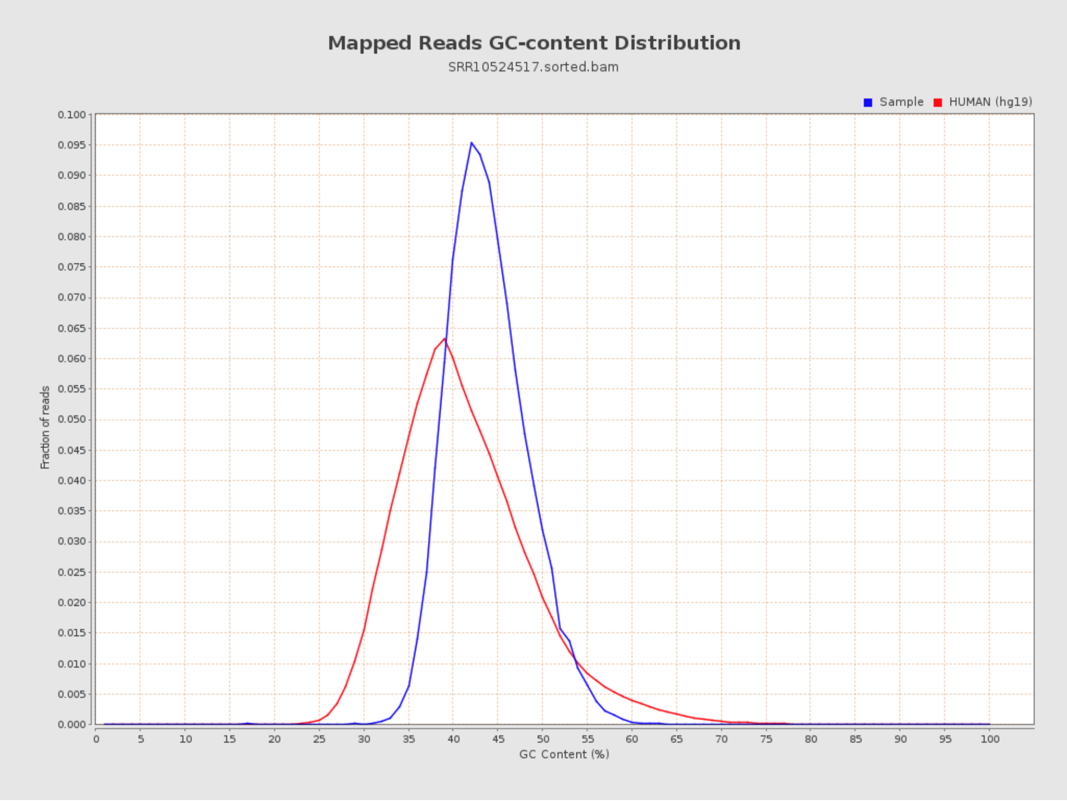
7. Results : Duplication Rate Histogram



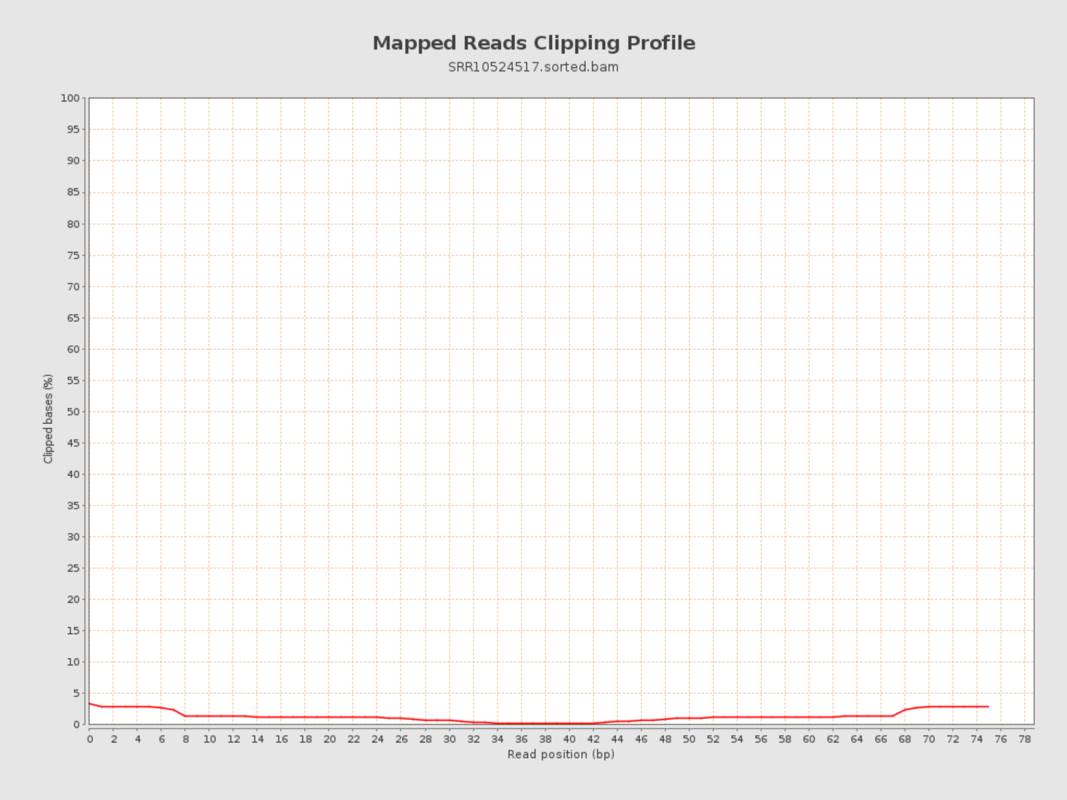
8. Results : Mapped Reads Nucleotide Content



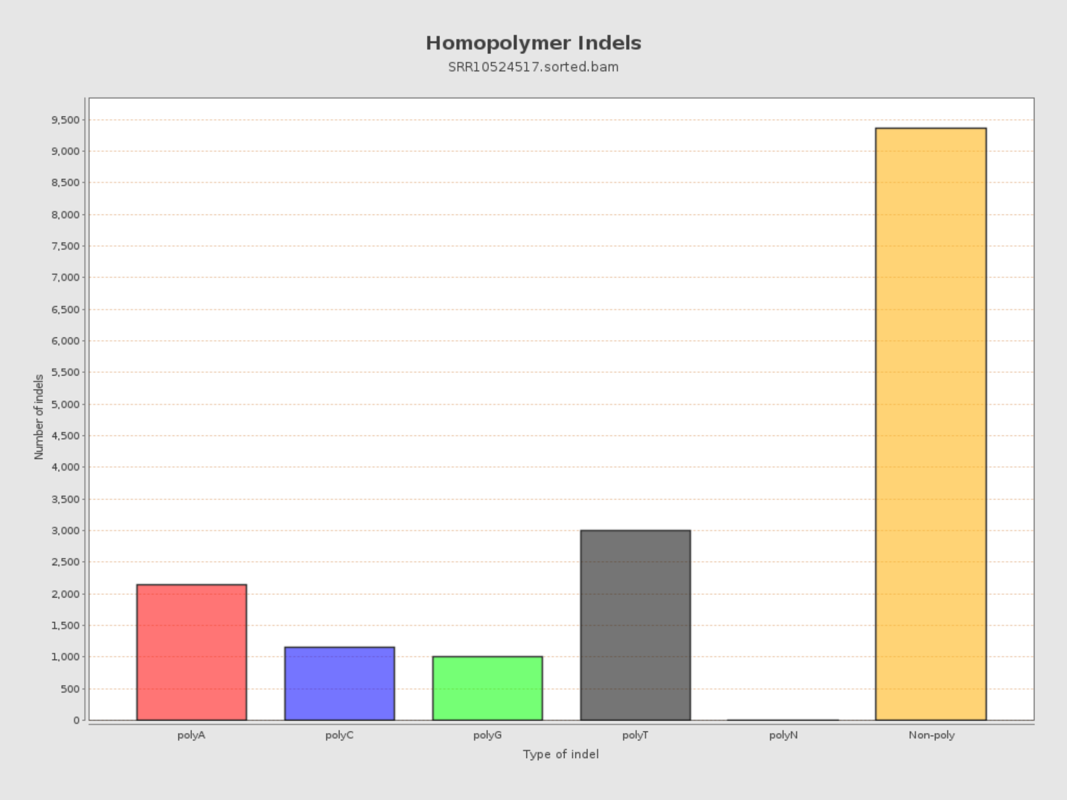
9. Results : Mapped Reads GC-content Distribution



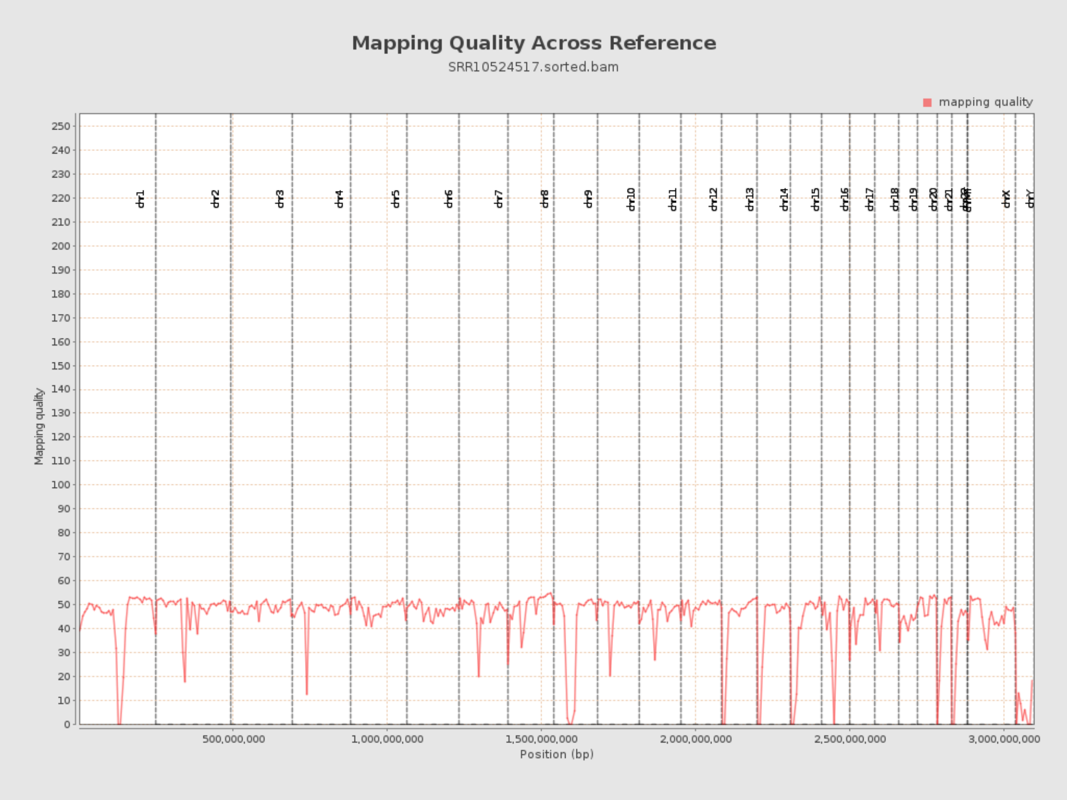
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram