Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:49:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524817.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_SRR10524817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:49:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,468,322
Mapped reads	1,340,700 / 91.31%
Unmapped reads	127,622 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,959 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	51,419 / 3.5%
Duplication rate	2.98%
Clipped reads	1,343,304 / 91.49%

2.2. ACGT Content

Number/percentage of A's	18,599,672 / 24.18%
Number/percentage of C's	14,318,964 / 18.61%
Number/percentage of T's	24,752,225 / 32.17%
Number/percentage of G's	19,254,429 / 25.03%
Number/percentage of N's	9,427 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2243

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

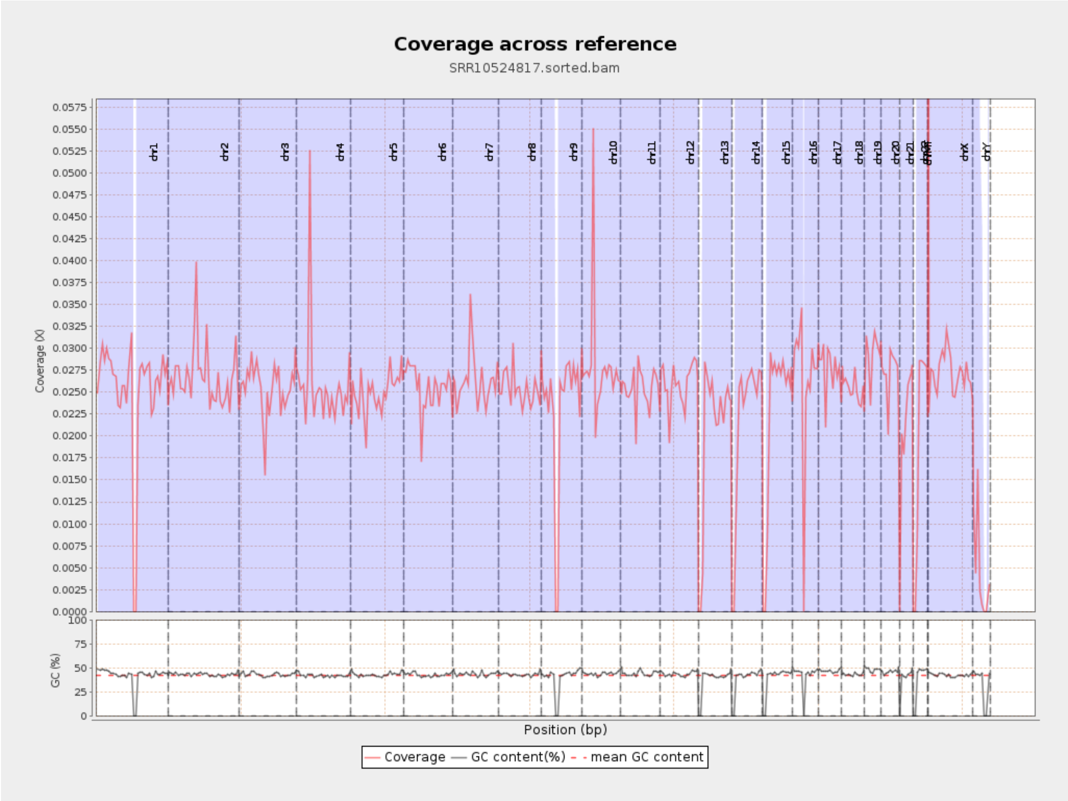
General error rate	0.51%
Mismatches	382,449
Insertions	5,308
Mapped reads with at least one insertion	0.39%
Deletions	14,431
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41%

2.6. Chromosome stats

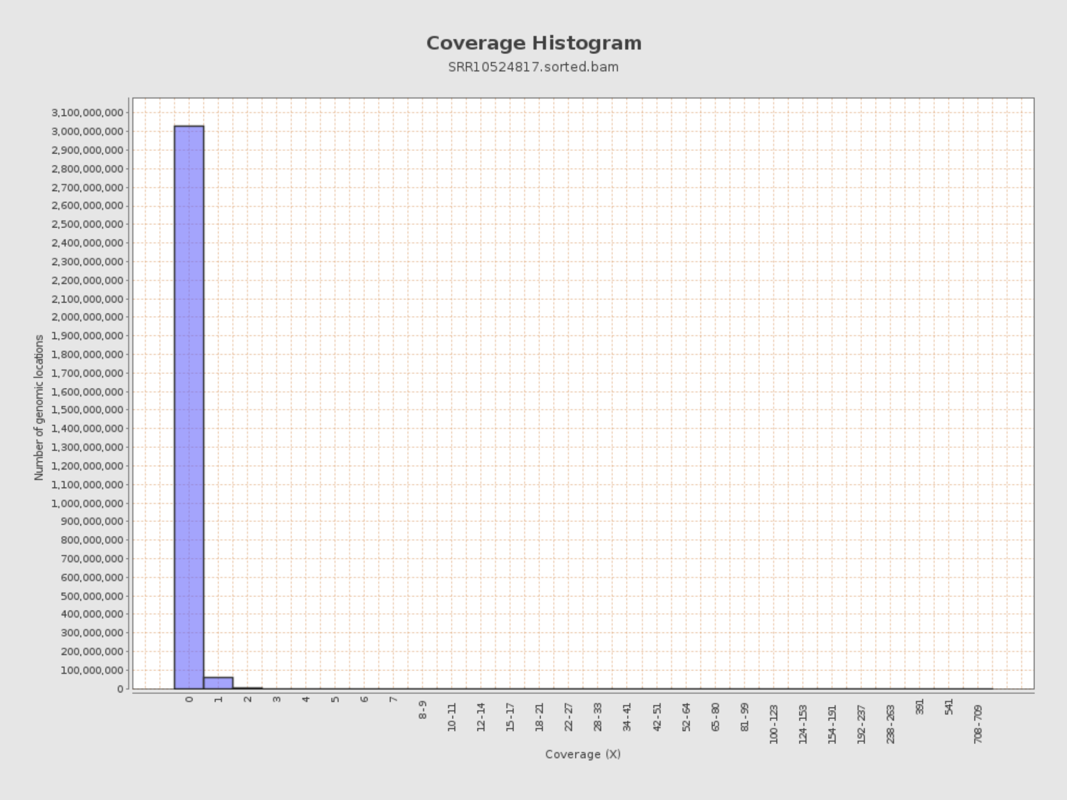
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6279229	0.0252	0.2662
chr2	243199373	6505493	0.0267	0.3598
chr3	198022430	5026889	0.0254	0.1779
chr4	191154276	4937131	0.0258	0.2103
chr5	180915260	4536220	0.0251	0.1744
chr6	171115067	4373192	0.0256	0.1926
chr7	159138663	4196954	0.0264	0.2576

chr8	146364022	3703483	0.0253	0.2067
chr9	141213431	3230667	0.0229	0.1953
chr10	135534747	3798805	0.028	0.2855
chr11	135006516	3444557	0.0255	0.2037
chr12	133851895	3475006	0.026	0.1788
chr13	115169878	2340361	0.0203	0.1573
chr14	107349540	2328625	0.0217	0.1673
chr15	102531392	2274960	0.0222	0.1656
chr16	90354753	2348125	0.026	0.1962
chr17	81195210	2235620	0.0275	0.1898
chr18	78077248	1986315	0.0254	0.2866
chr19	59128983	1725218	0.0292	0.2392
chr20	63025520	1701055	0.027	0.1904
chr21	48129895	1017221	0.0211	0.183
chr22	51304566	991564	0.0193	0.1551
chrMT	16571	8311	0.5015	0.7556
chrX	155270560	4227015	0.0272	0.1923
chrY	59373566	266098	0.0045	0.1335

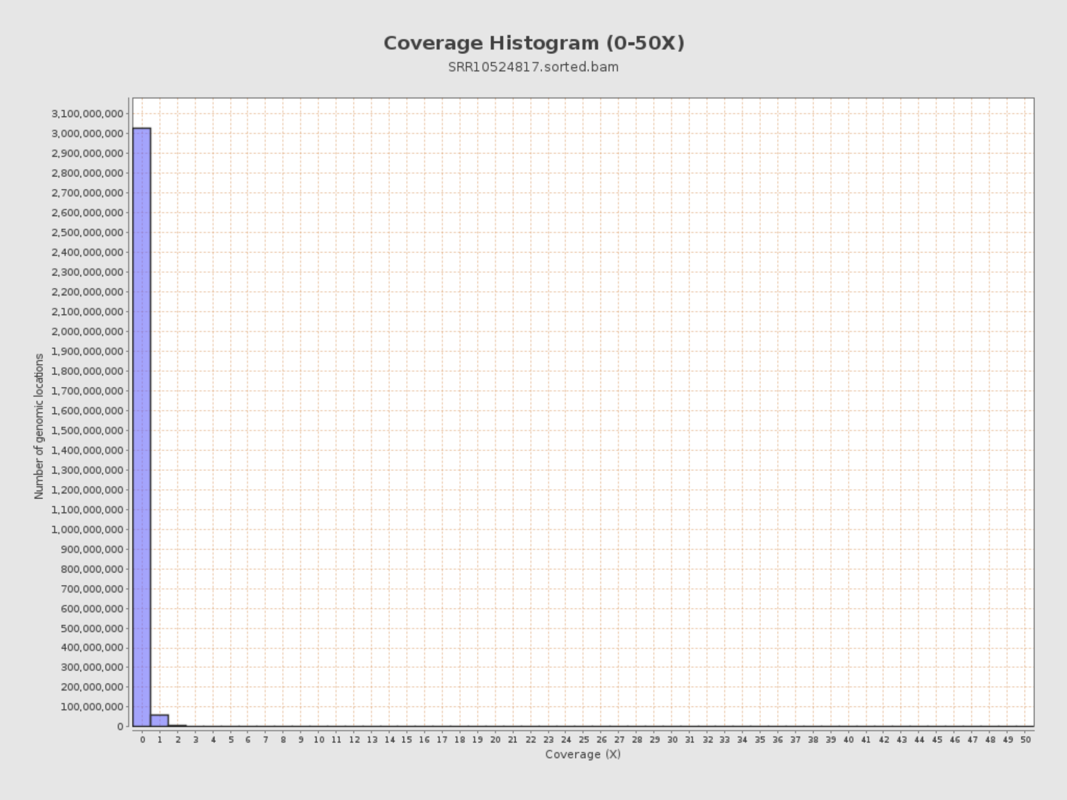
3. Results : Coverage across reference



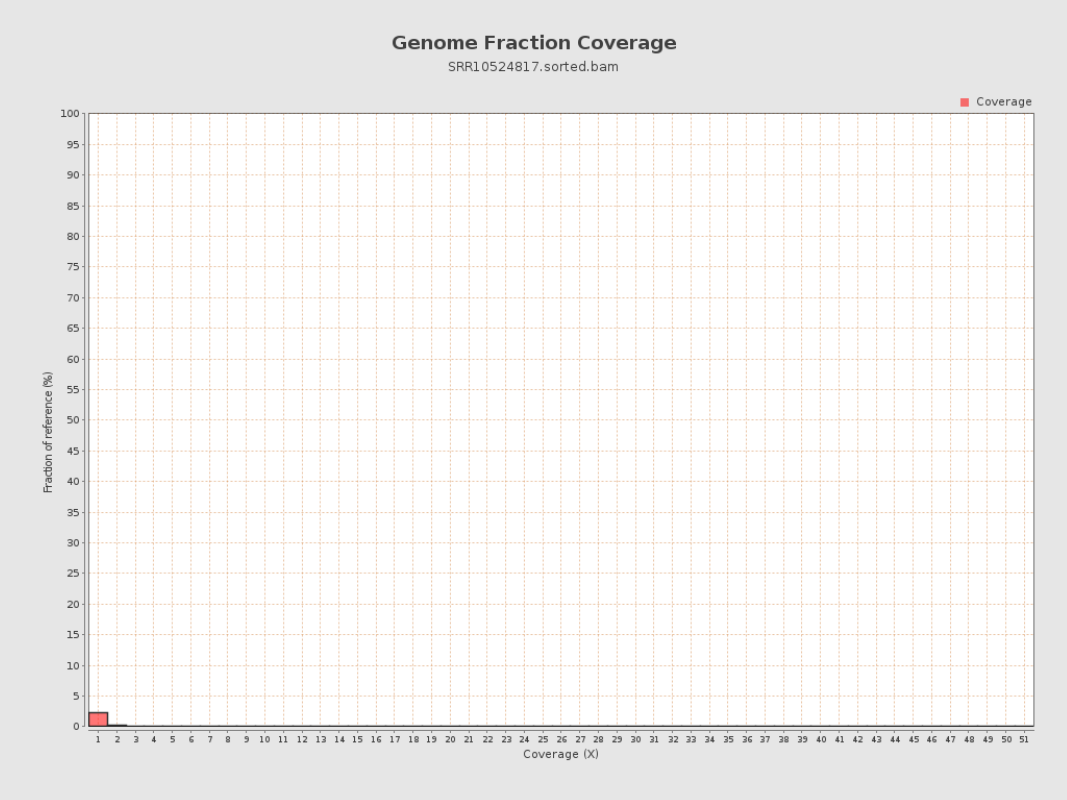
4. Results : Coverage Histogram



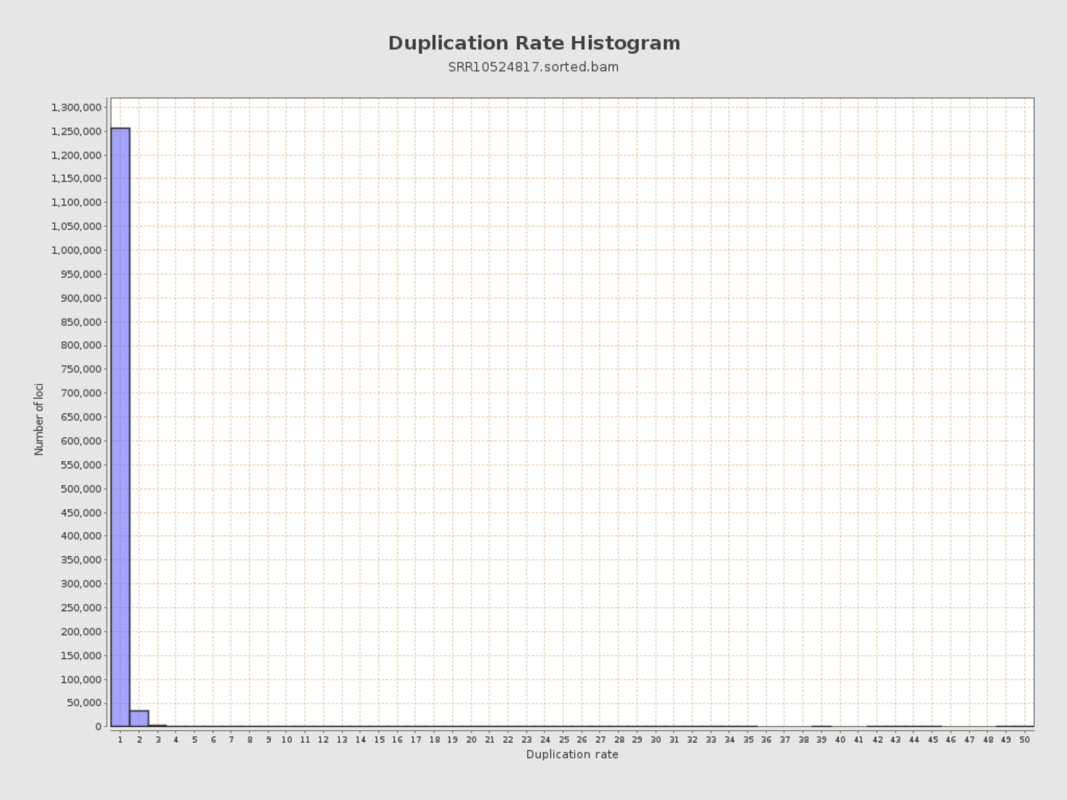
5. Results : Coverage Histogram (0-50X)



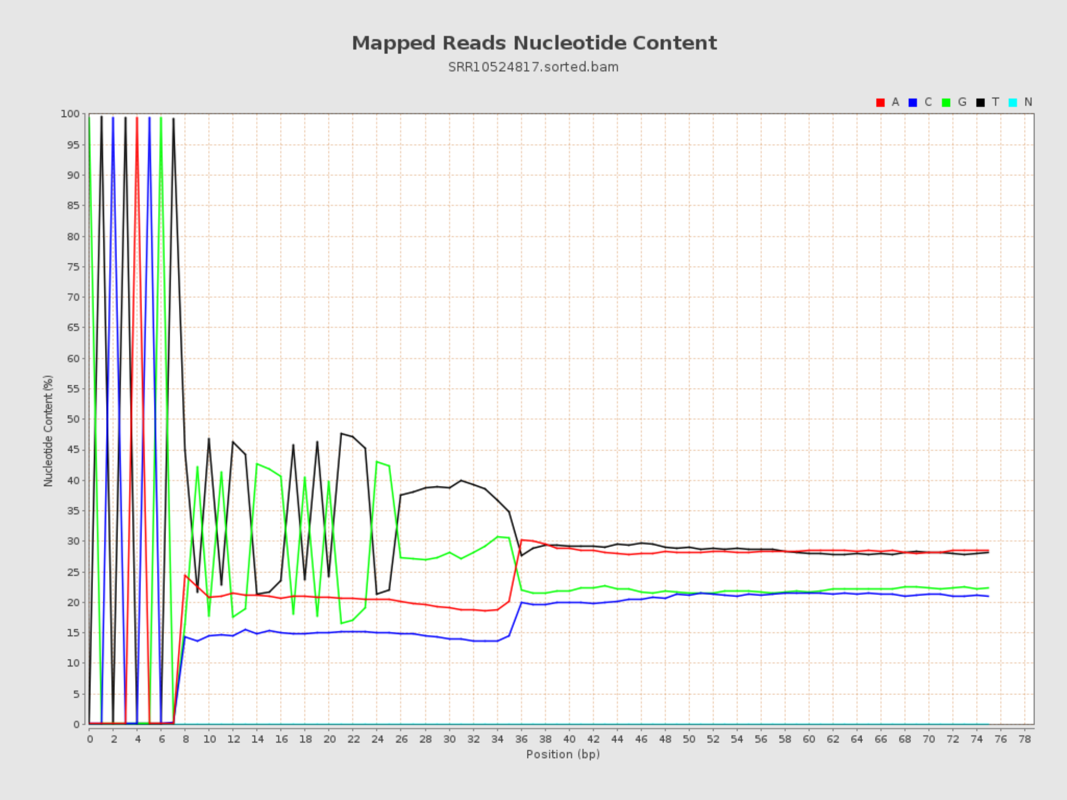
6. Results : Genome Fraction Coverage



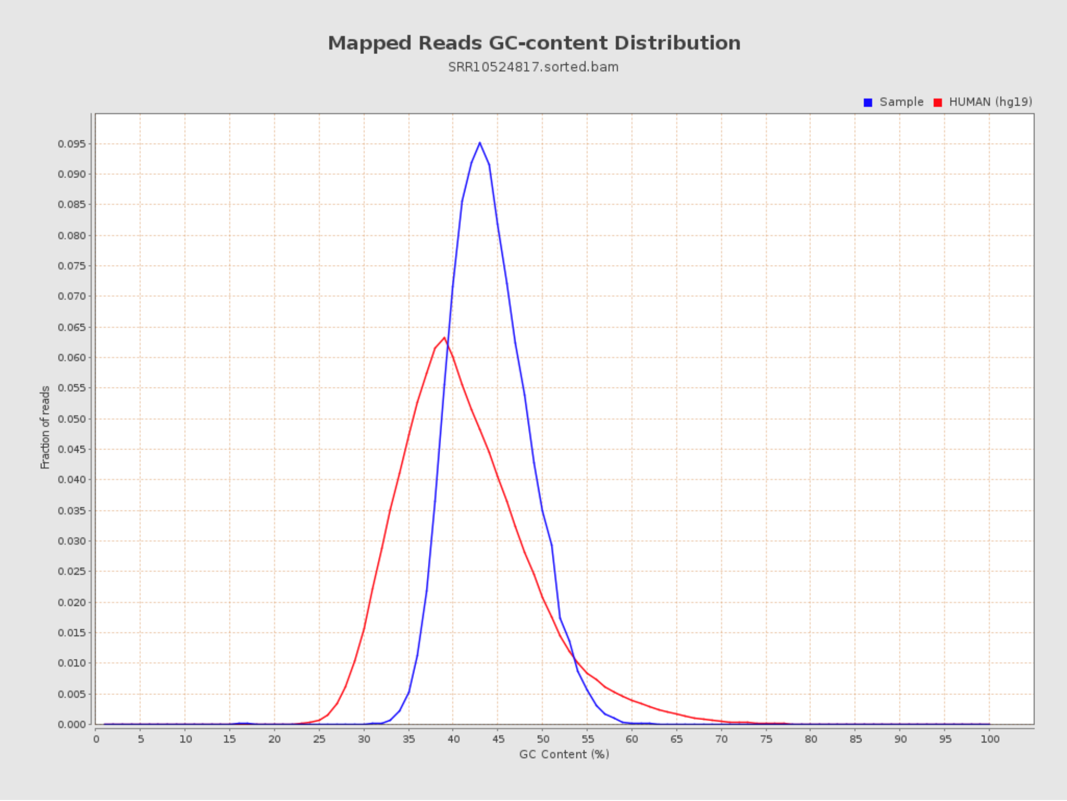
7. Results : Duplication Rate Histogram



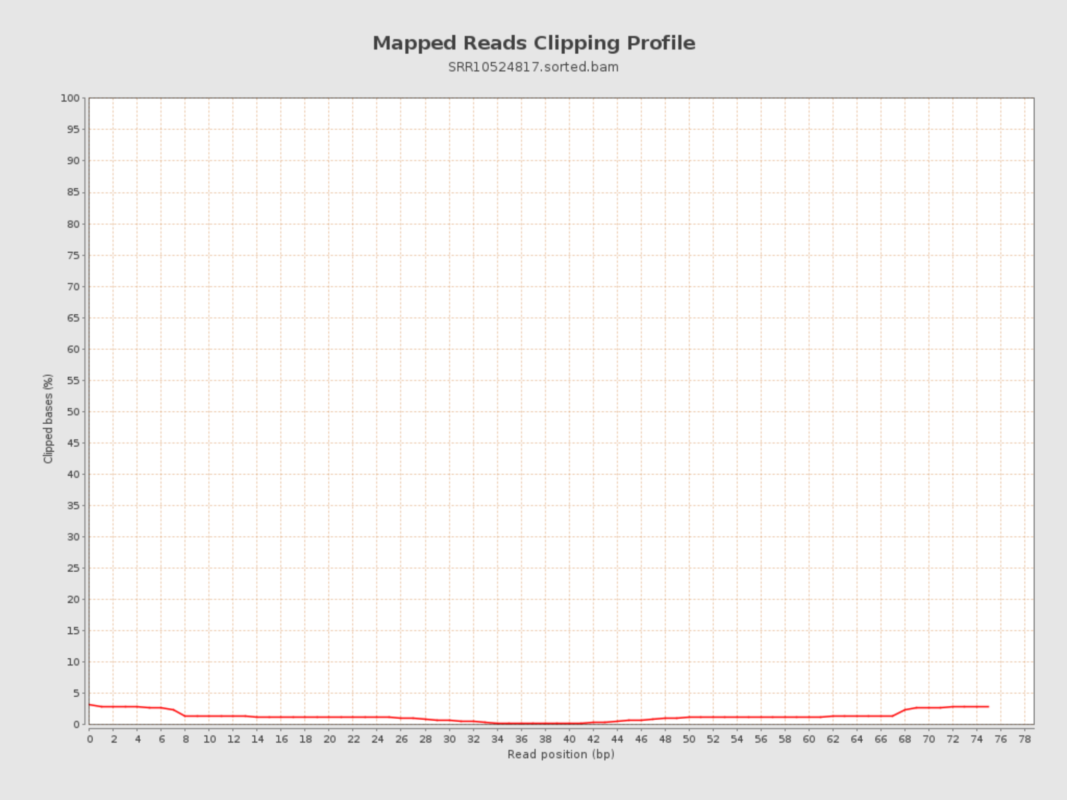
8. Results : Mapped Reads Nucleotide Content



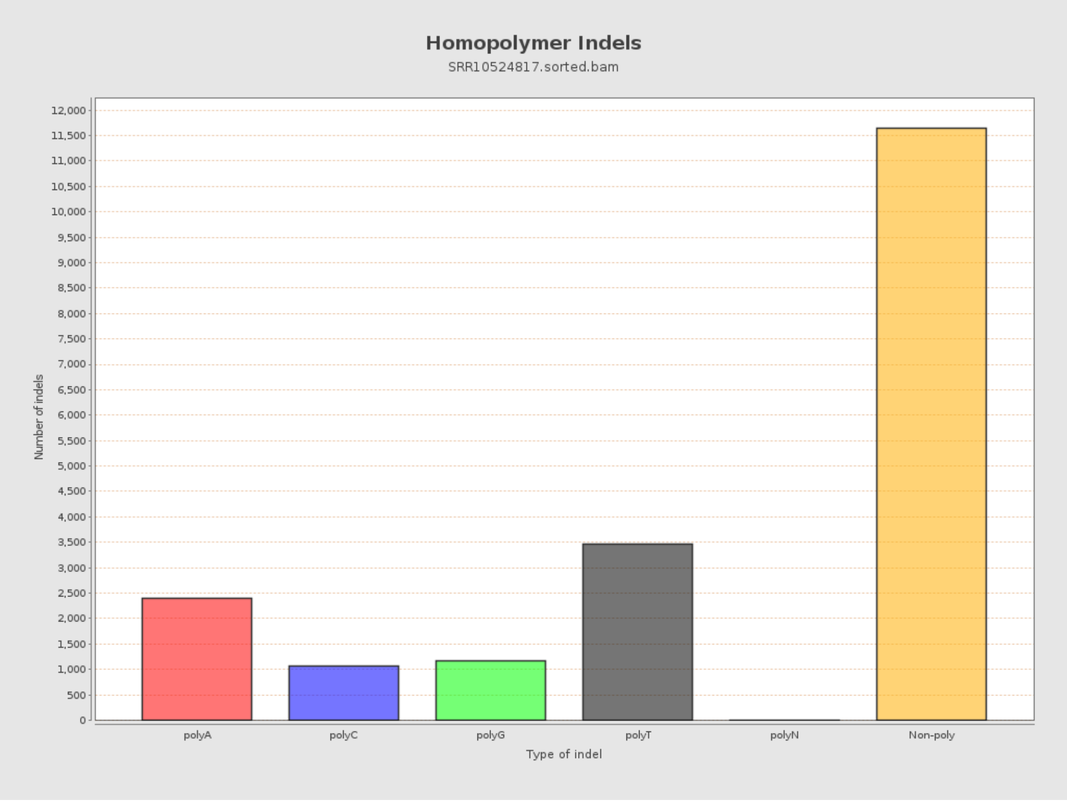
9. Results : Mapped Reads GC-content Distribution



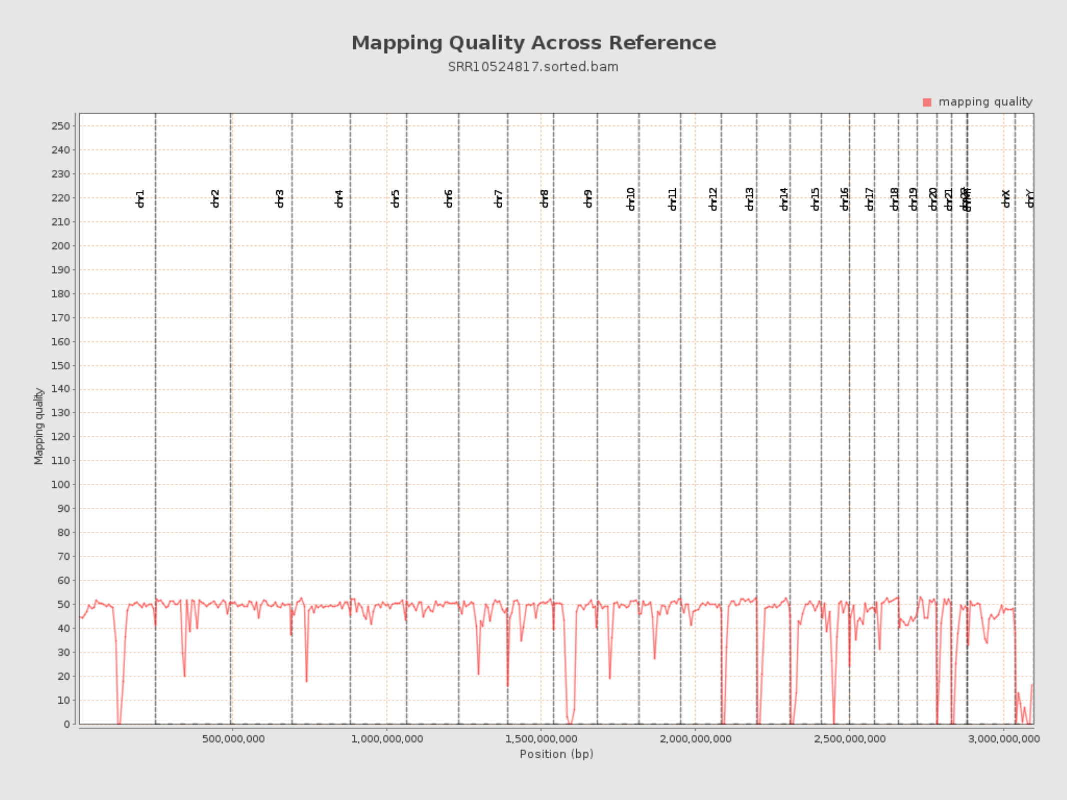
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram