Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:24:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525016.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_SRR10525016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:24:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,146,295
Mapped reads	5,624,555 / 91.51%
Unmapped reads	521,740 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,409 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	476,131 / 7.75%
Duplication rate	6.09%
Clipped reads	5,630,110 / 91.6%

2.2. ACGT Content

Number/percentage of A's	82,077,537 / 25.24%
Number/percentage of C's	63,207,694 / 19.44%
Number/percentage of T's	102,096,739 / 31.4%
Number/percentage of G's	77,776,037 / 23.92%
Number/percentage of N's	3,223 / 0%
GC Percentage	43.36%

2.3. Coverage

Mean	0.1051

Standard Deviation	0.8294

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

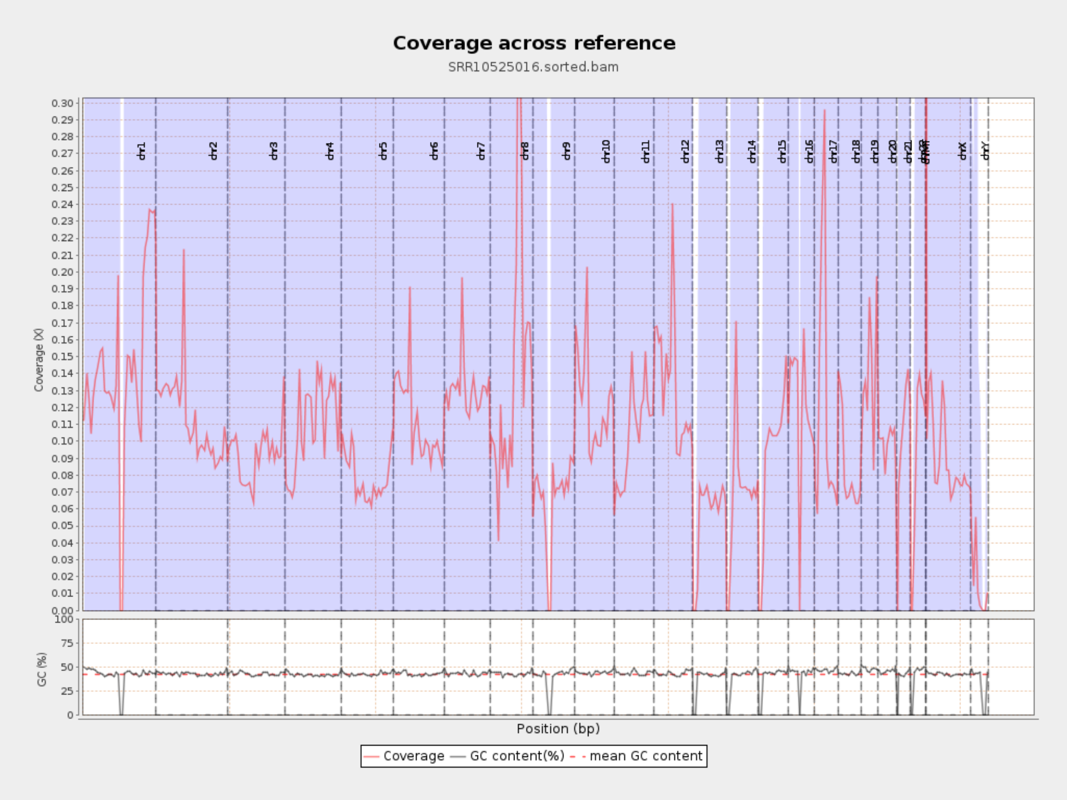
General error rate	0.51%
Mismatches	1,620,656
Insertions	20,845
Mapped reads with at least one insertion	0.37%
Deletions	62,998
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.66%

2.6. Chromosome stats

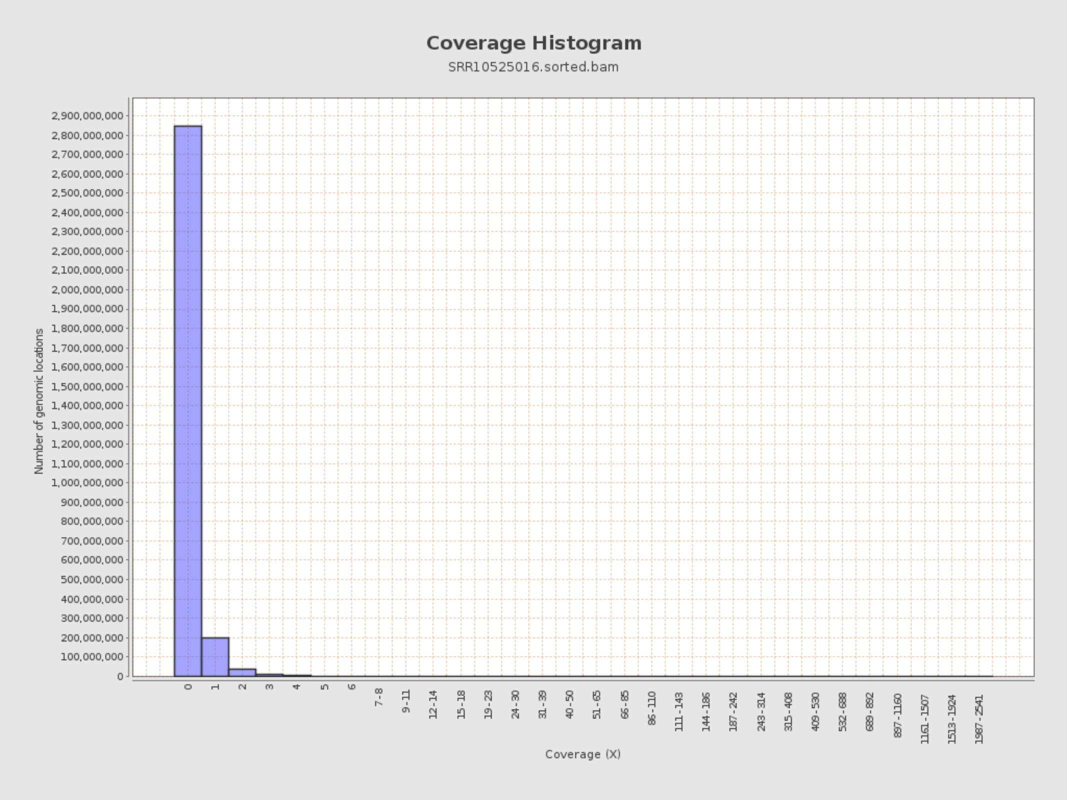
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35530127	0.1425	1.7668
chr2	243199373	27753608	0.1141	0.9956
chr3	198022430	18143045	0.0916	0.3896
chr4	191154276	21207311	0.1109	0.5275
chr5	180915260	14304208	0.0791	0.382
chr6	171115067	19193402	0.1122	0.8418
chr7	159138663	20974375	0.1318	1.1359

chr8	146364022	20593539	0.1407	0.8072
chr9	141213431	9332808	0.0661	0.5888
chr10	135534747	16628487	0.1227	0.7955
chr11	135006516	14224128	0.1054	0.6883
chr12	133851895	18275312	0.1365	0.4829
chr13	115169878	6483117	0.0563	0.3148
chr14	107349540	7582799	0.0706	0.3582
chr15	102531392	9182013	0.0896	0.421
chr16	90354753	10720384	0.1186	0.4862
chr17	81195210	9445212	0.1163	0.8013
chr18	78077248	6518016	0.0835	1.0723
chr19	59128983	8314242	0.1406	0.9949
chr20	63025520	6294222	0.0999	0.4127
chr21	48129895	4934034	0.1025	0.4615
chr22	51304566	4612736	0.0899	0.3751
chrMT	16571	41908	2.529	2.3366
chrX	155270560	14018275	0.0903	0.5311
chrY	59373566	957836	0.0161	0.3905

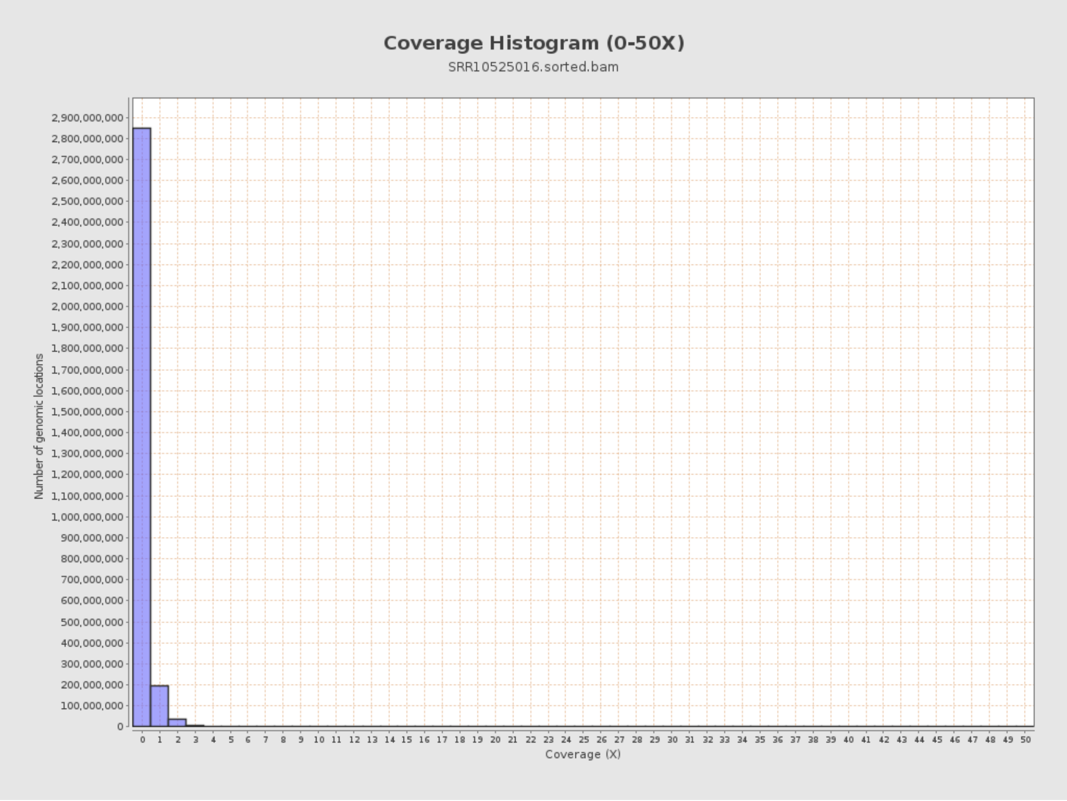
3. Results : Coverage across reference



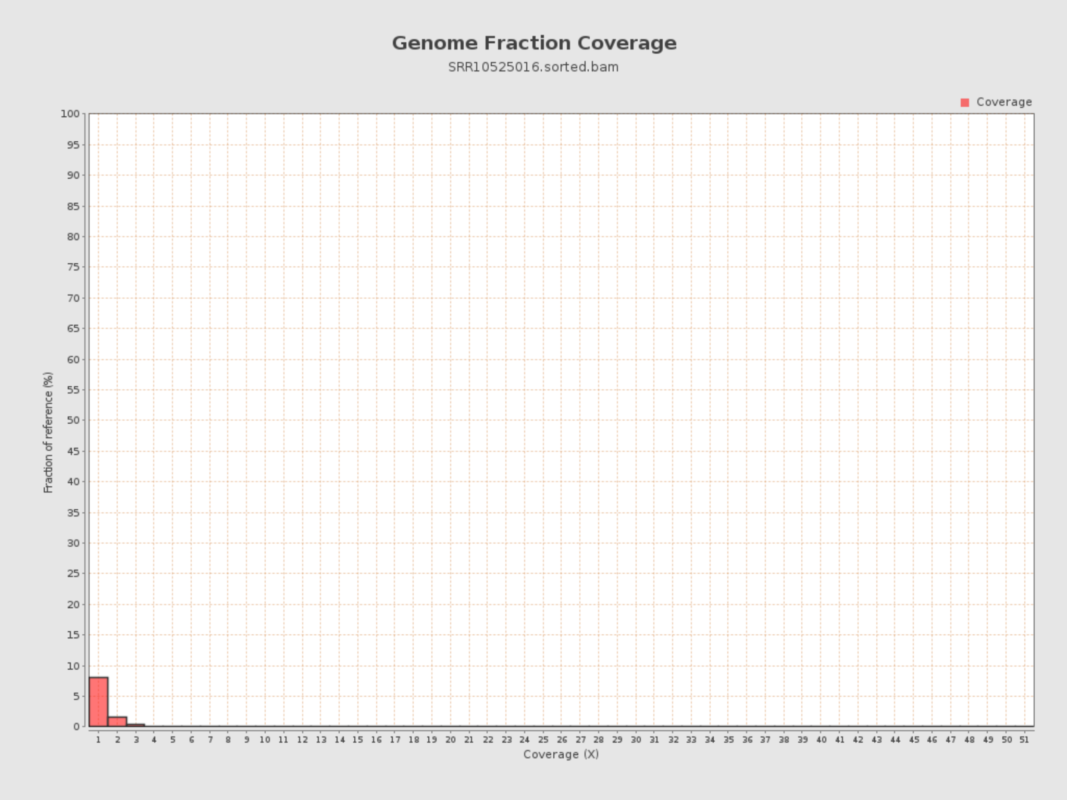
4. Results : Coverage Histogram



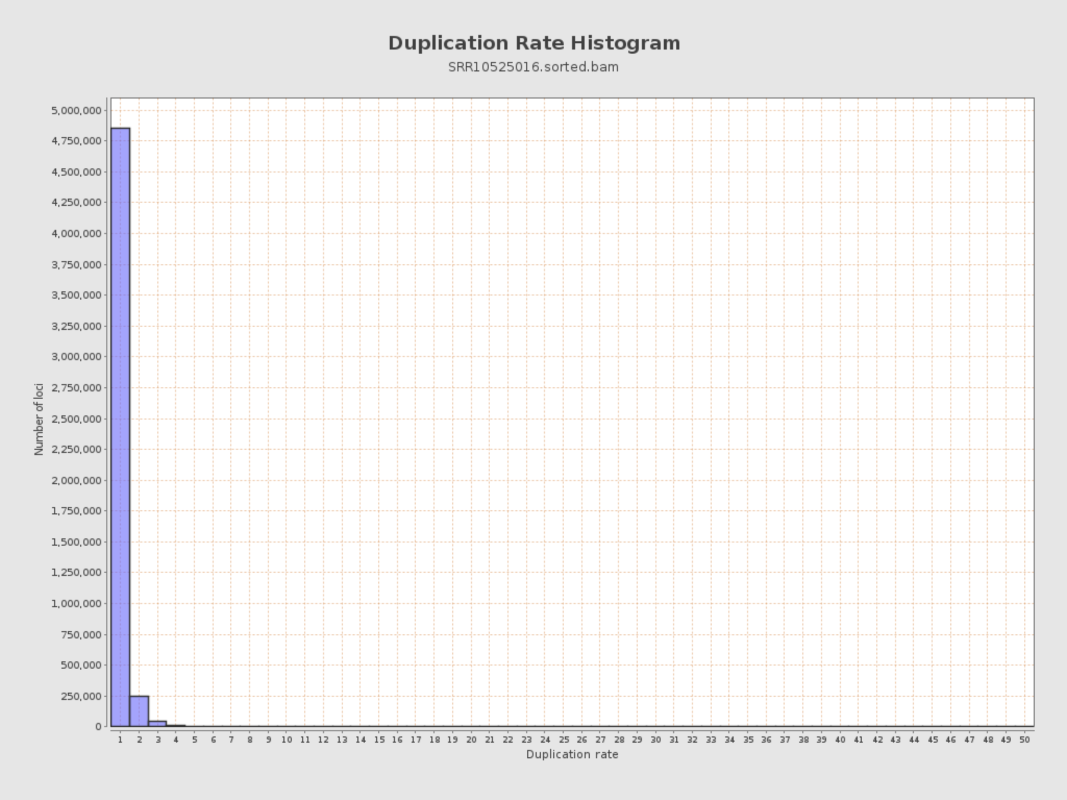
5. Results : Coverage Histogram (0-50X)



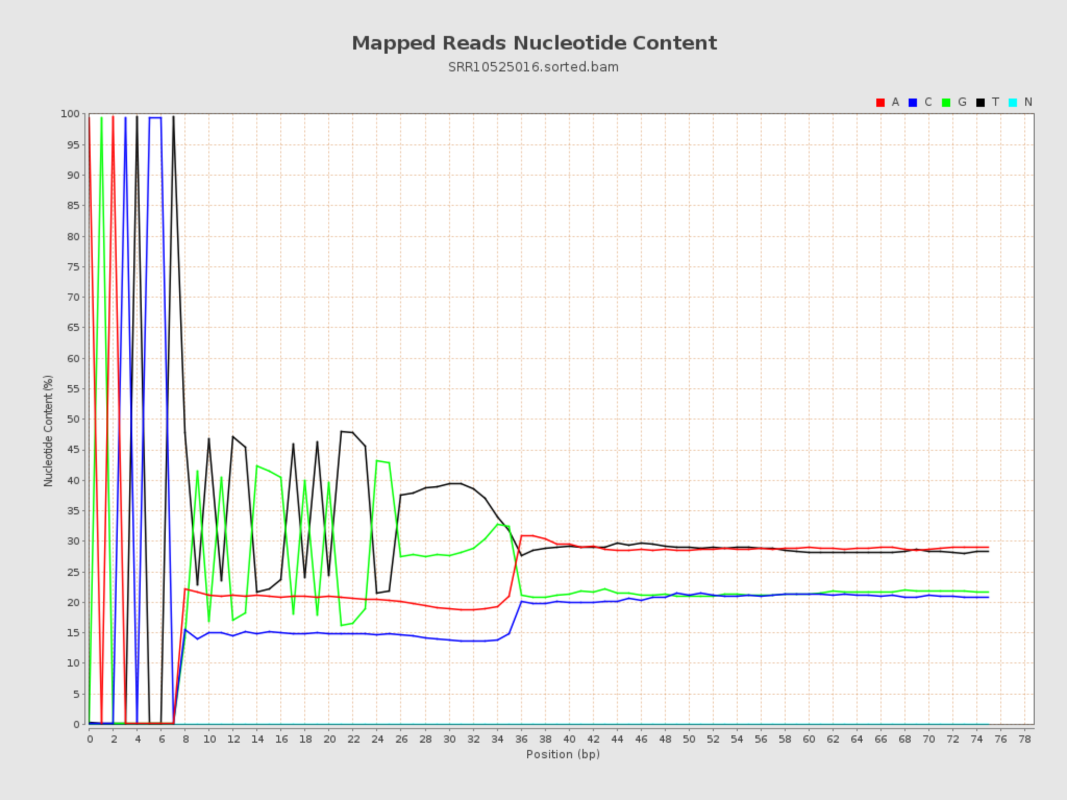
6. Results : Genome Fraction Coverage



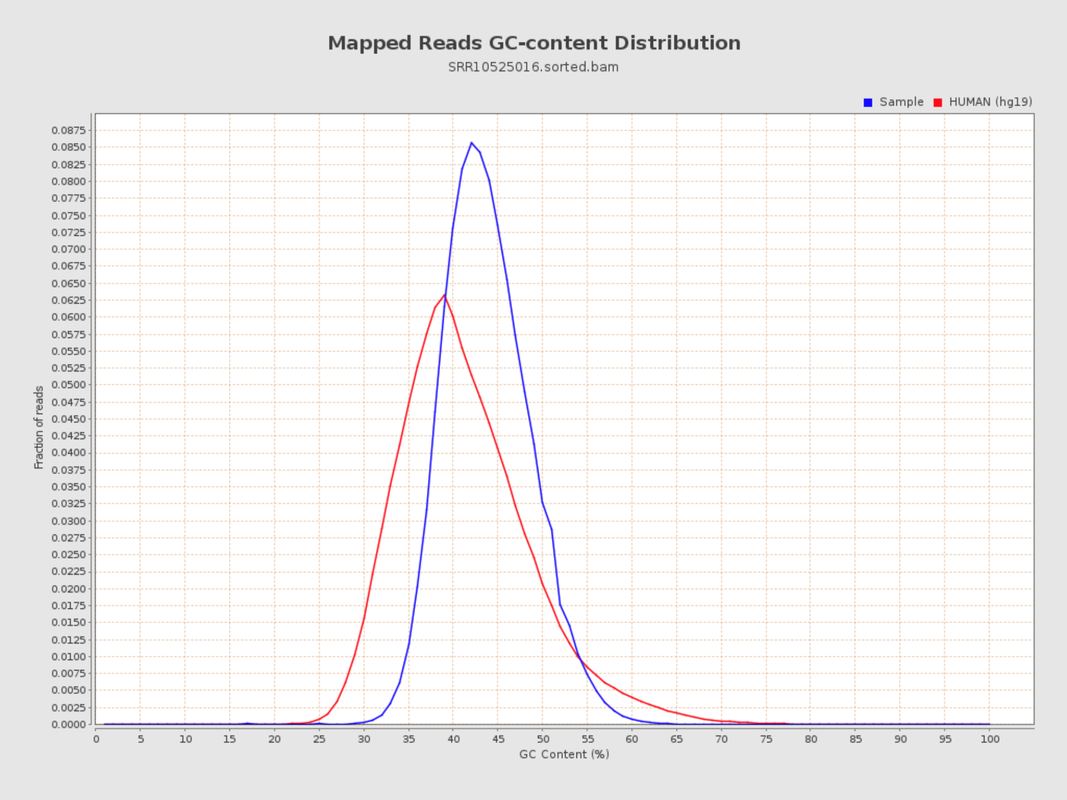
7. Results : Duplication Rate Histogram



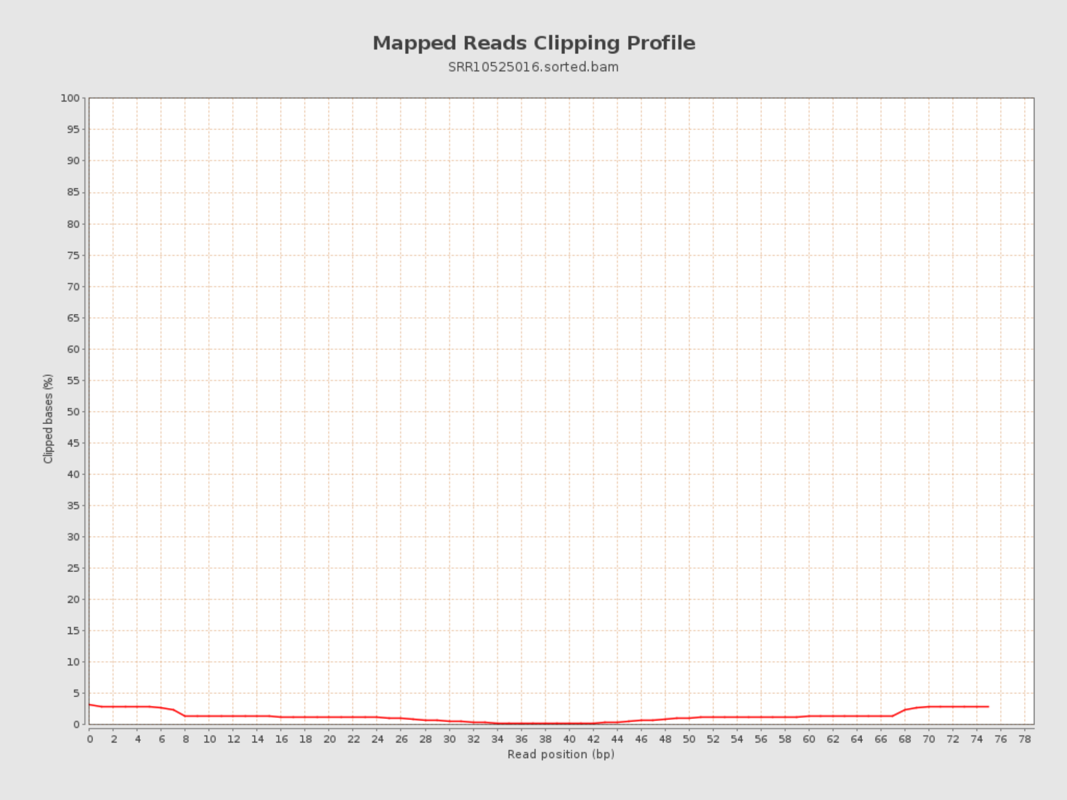
8. Results : Mapped Reads Nucleotide Content



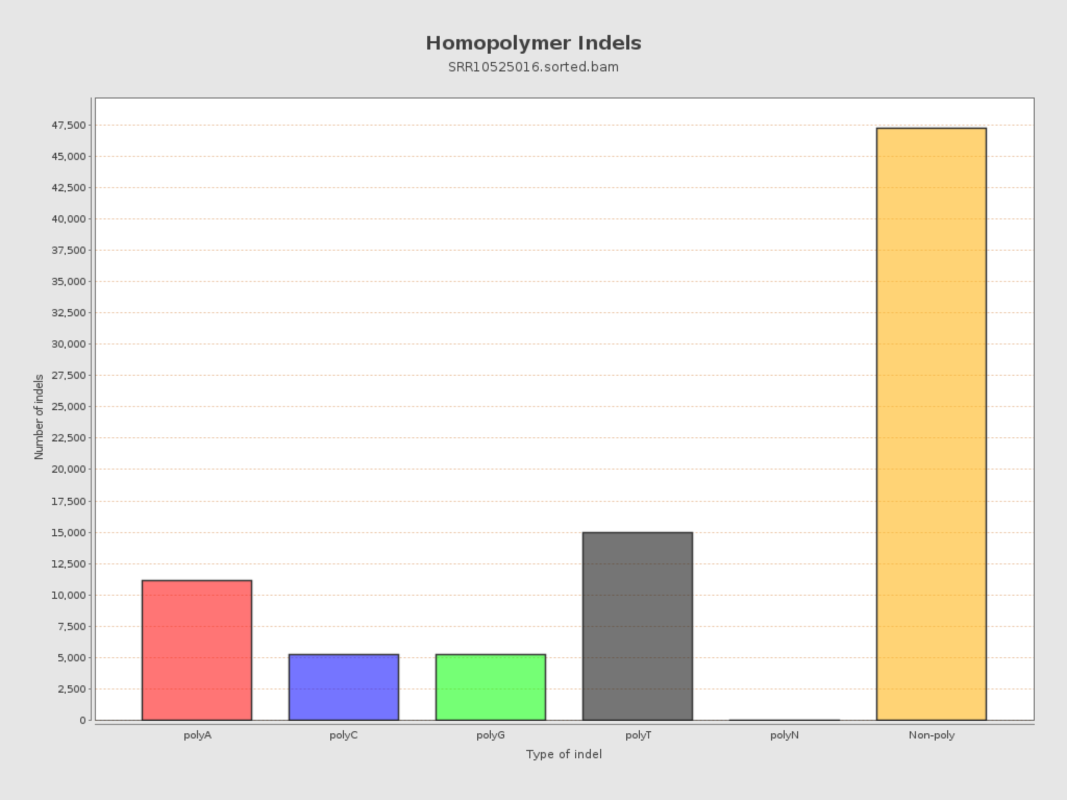
9. Results : Mapped Reads GC-content Distribution



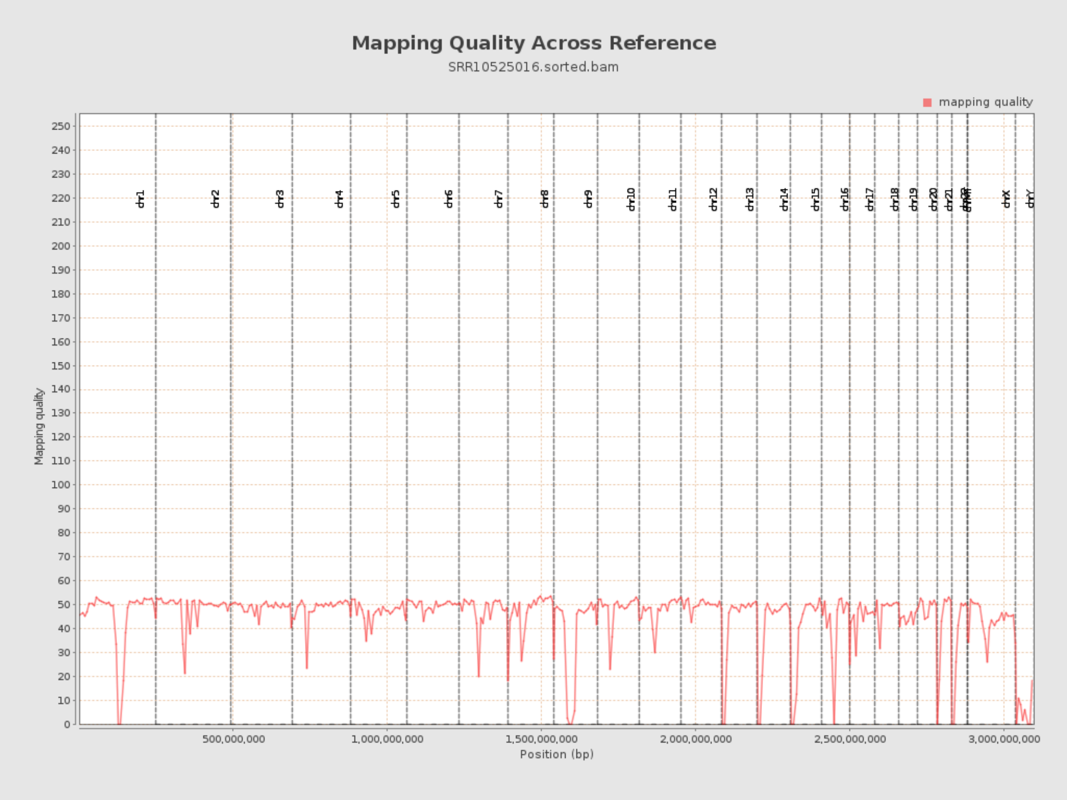
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram