Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:15:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082145.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_SRR3082145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,801,294
Mapped reads	1,640,124 / 91.05%
Unmapped reads	161,170 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,012 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	49,670 / 2.76%
Duplication rate	2.27%
Clipped reads	650,069 / 36.09%

2.2. ACGT Content

Number/percentage of A's	32,523,216 / 28.98%
Number/percentage of C's	21,134,572 / 18.83%
Number/percentage of T's	34,176,705 / 30.45%
Number/percentage of G's	24,394,101 / 21.74%
Number/percentage of N's	2,452 / 0%
GC Percentage	40.57%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.328

2.4. Mapping Quality

Mean Mapping Quality	46.05

2.5. Mismatches and indels

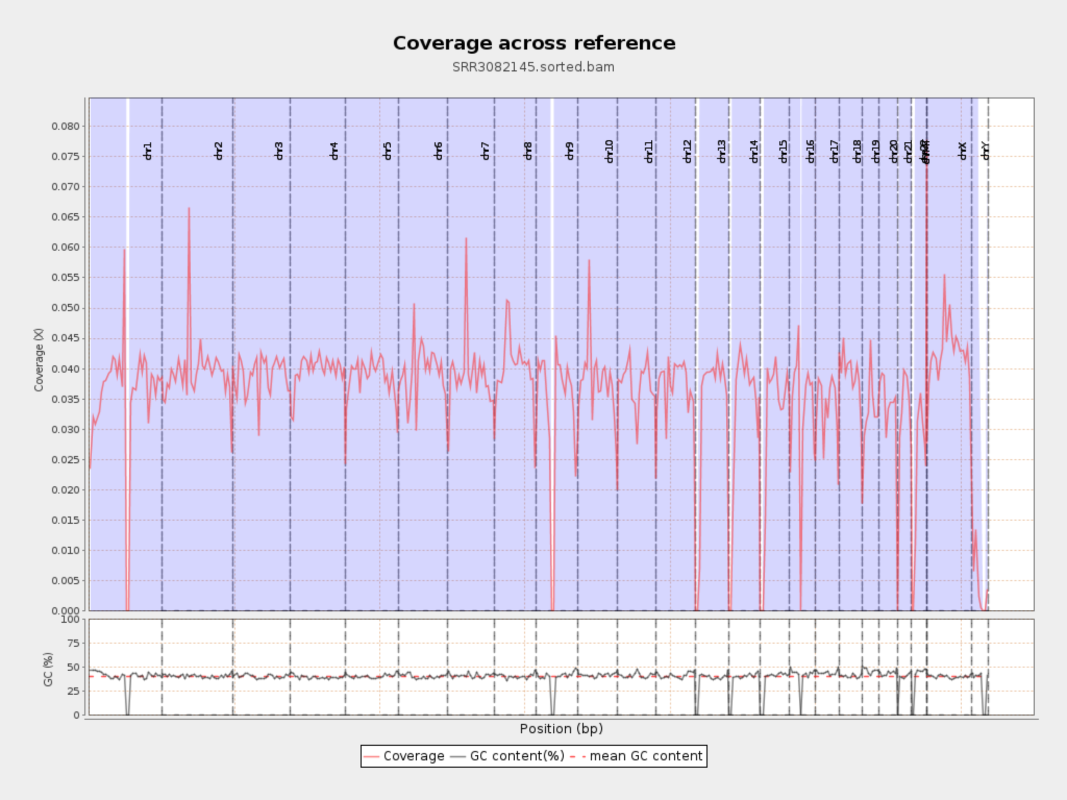
General error rate	0.85%
Mismatches	938,279
Insertions	9,124
Mapped reads with at least one insertion	0.55%
Deletions	24,403
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.27%

2.6. Chromosome stats

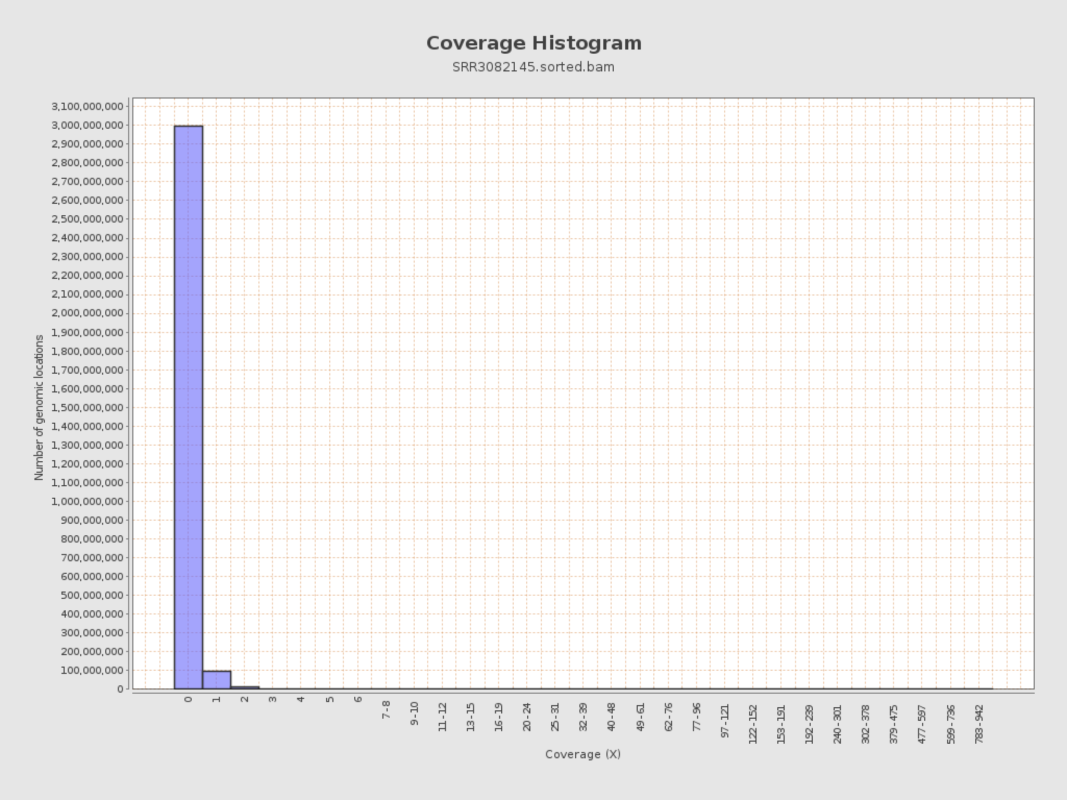
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8849678	0.0355	0.5479
chr2	243199373	9650946	0.0397	0.3693
chr3	198022430	7717325	0.039	0.2137
chr4	191154276	7602242	0.0398	0.221
chr5	180915260	7021448	0.0388	0.2138
chr6	171115067	6730126	0.0393	0.2421
chr7	159138663	6251308	0.0393	0.4201

chr8	146364022	5879514	0.0402	0.6023
chr9	141213431	4704846	0.0333	0.3
chr10	135534747	5197176	0.0383	0.2977
chr11	135006516	5025175	0.0372	0.2643
chr12	133851895	4999457	0.0374	0.2109
chr13	115169878	3724571	0.0323	0.1929
chr14	107349540	3440359	0.032	0.2062
chr15	102531392	3108732	0.0303	0.1918
chr16	90354753	2983194	0.033	0.2183
chr17	81195210	2716381	0.0335	0.2137
chr18	78077248	3074301	0.0394	0.5104
chr19	59128983	1963310	0.0332	0.4211
chr20	63025520	2162380	0.0343	0.2034
chr21	48129895	1485506	0.0309	0.2003
chr22	51304566	1106997	0.0216	0.1578
chrMT	16571	1289	0.0778	0.2882
chrX	155270560	6600052	0.0425	0.24
chrY	59373566	274779	0.0046	0.1052

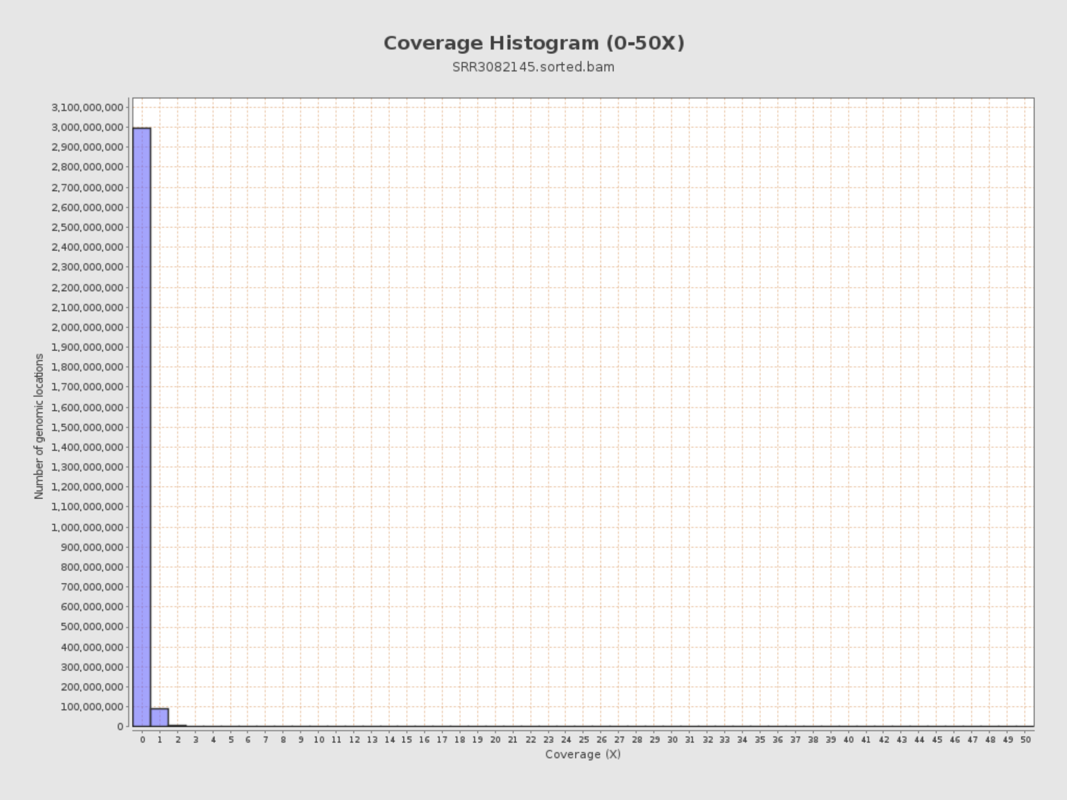
3. Results : Coverage across reference



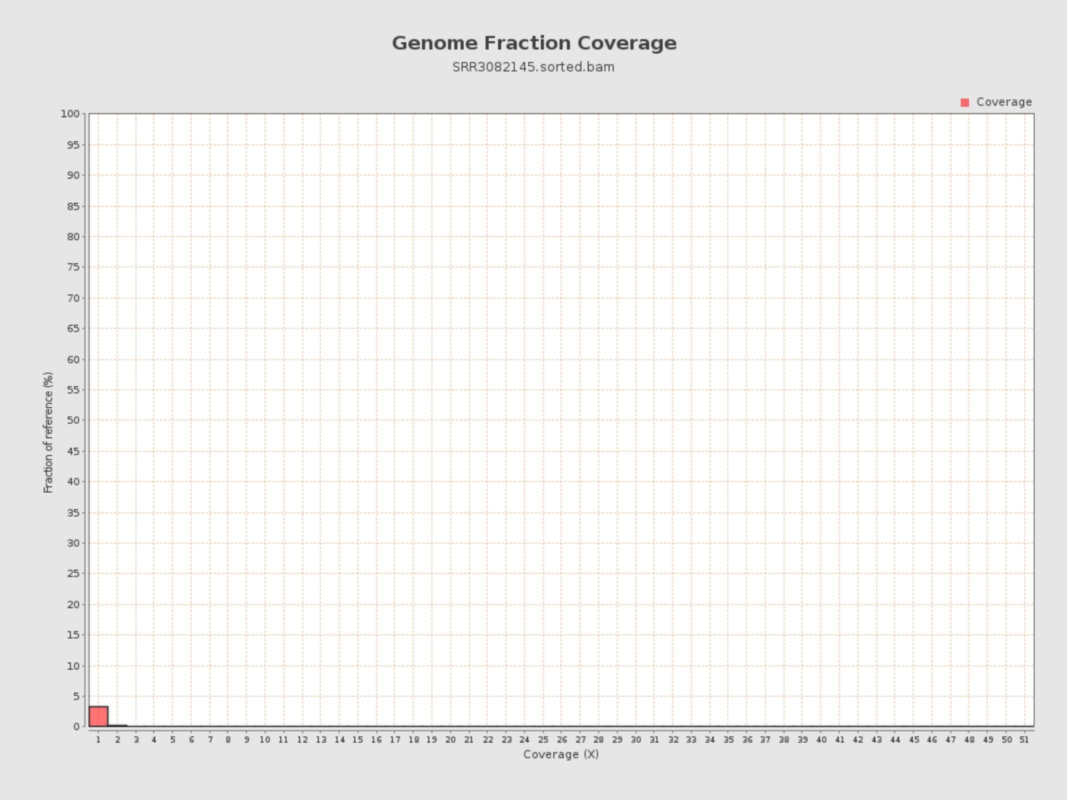
4. Results : Coverage Histogram



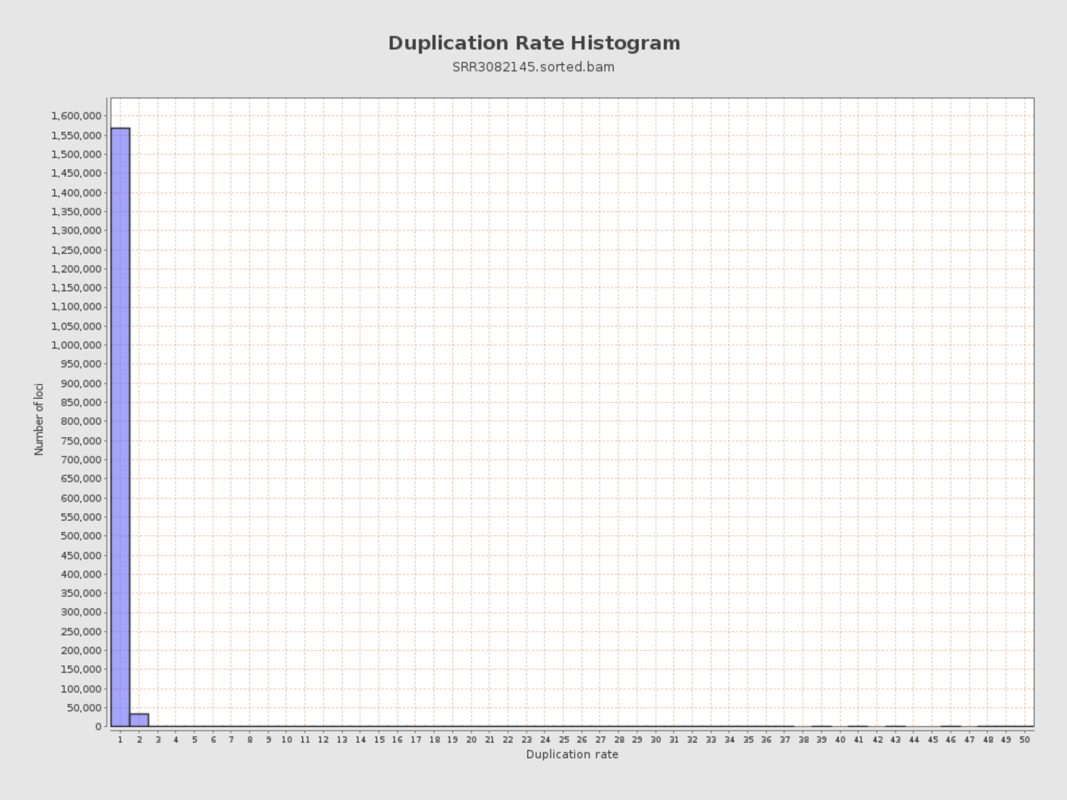
5. Results : Coverage Histogram (0-50X)



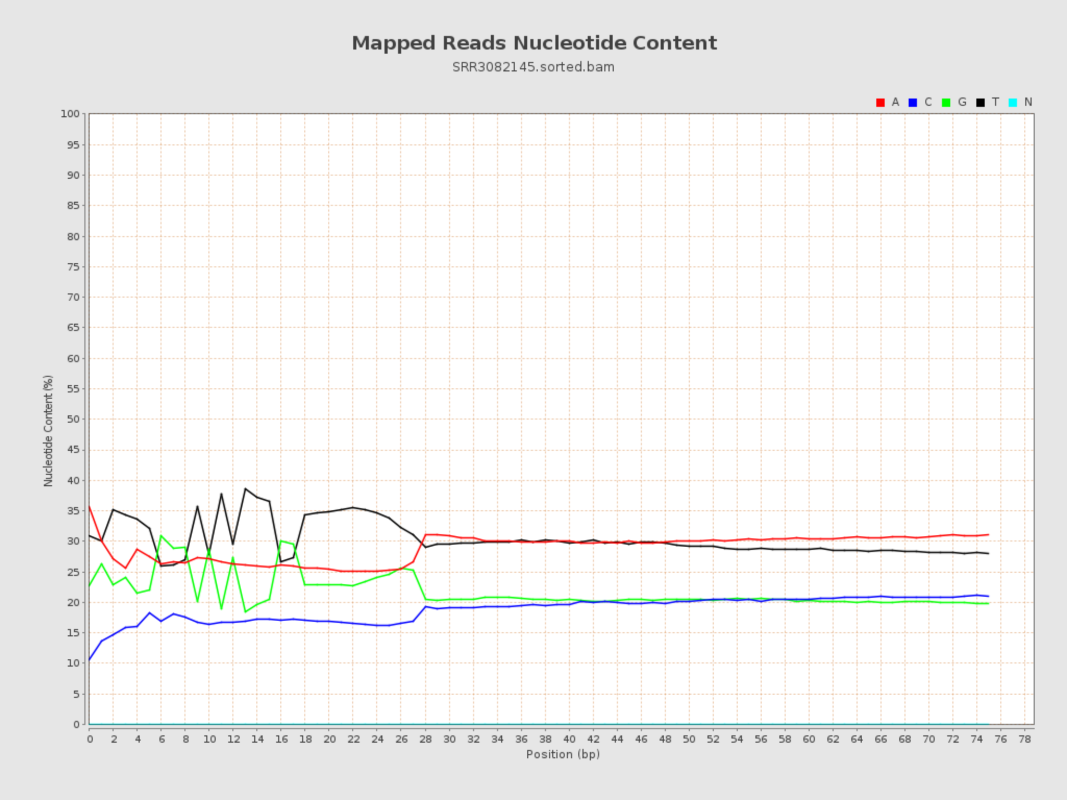
6. Results : Genome Fraction Coverage



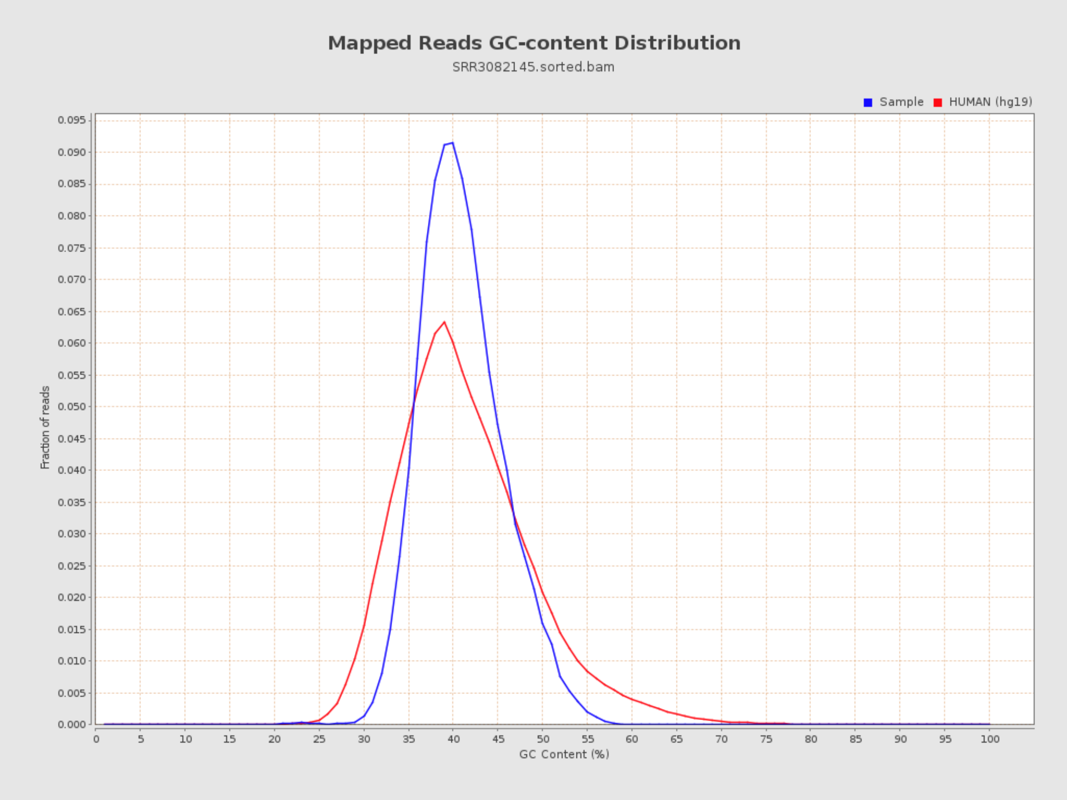
7. Results : Duplication Rate Histogram



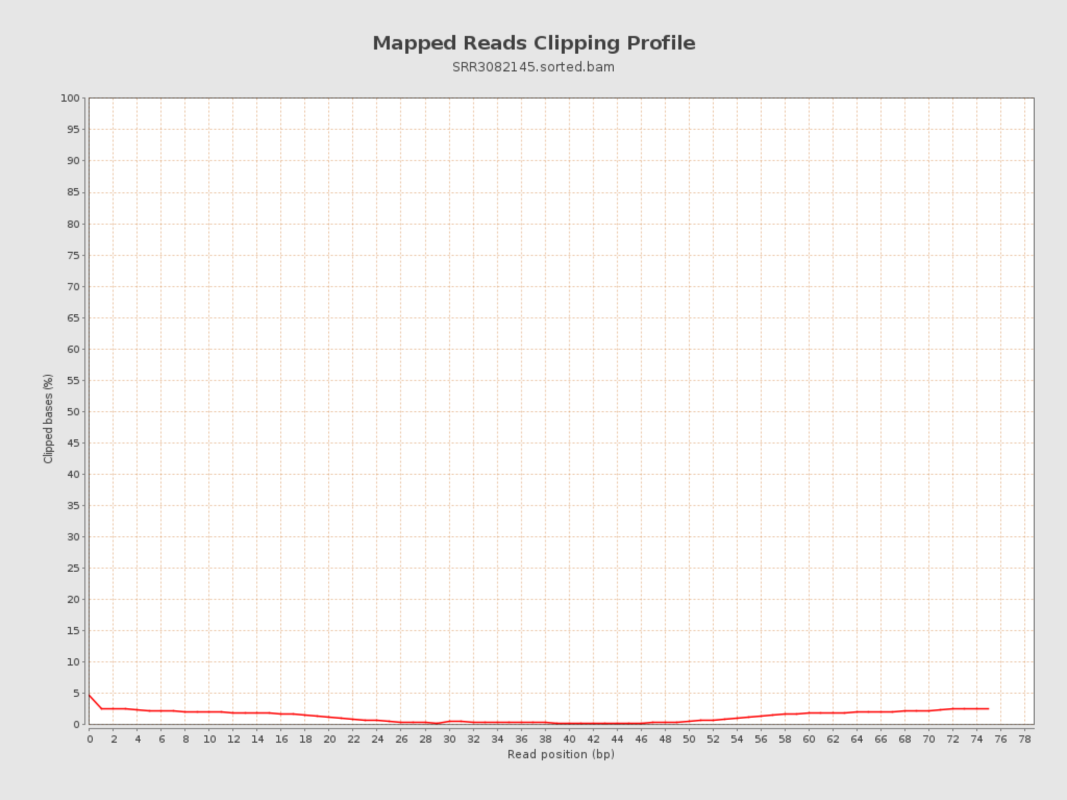
8. Results : Mapped Reads Nucleotide Content



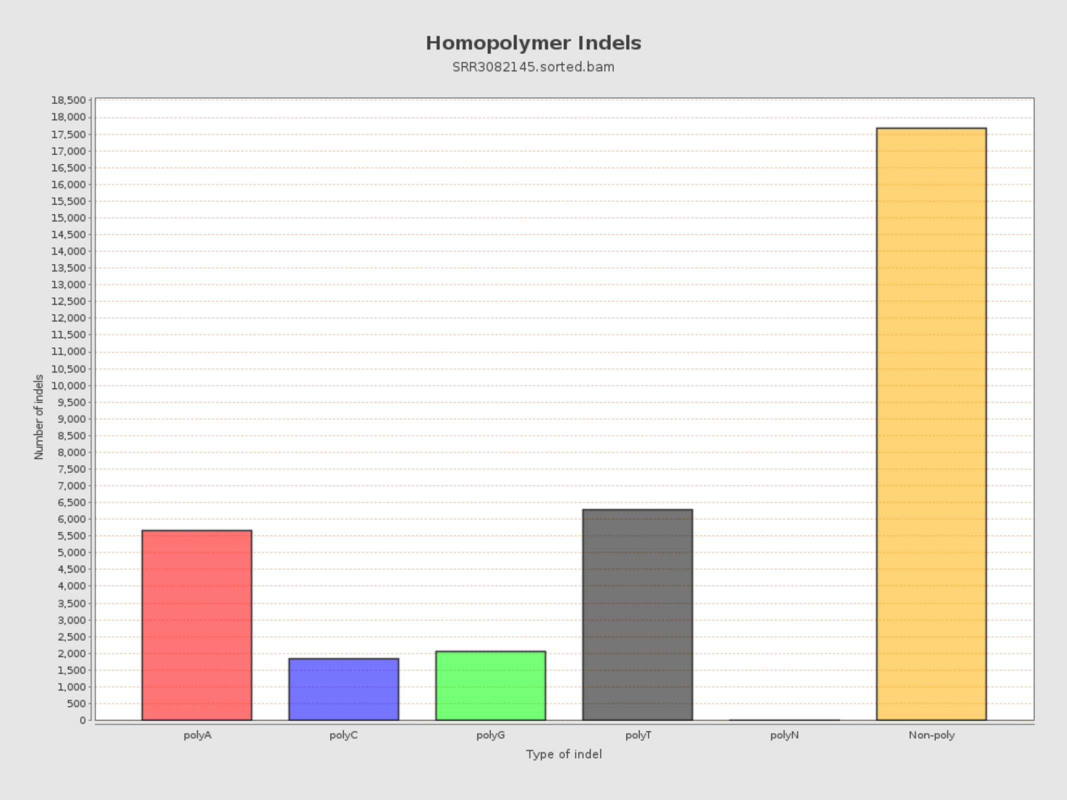
9. Results : Mapped Reads GC-content Distribution



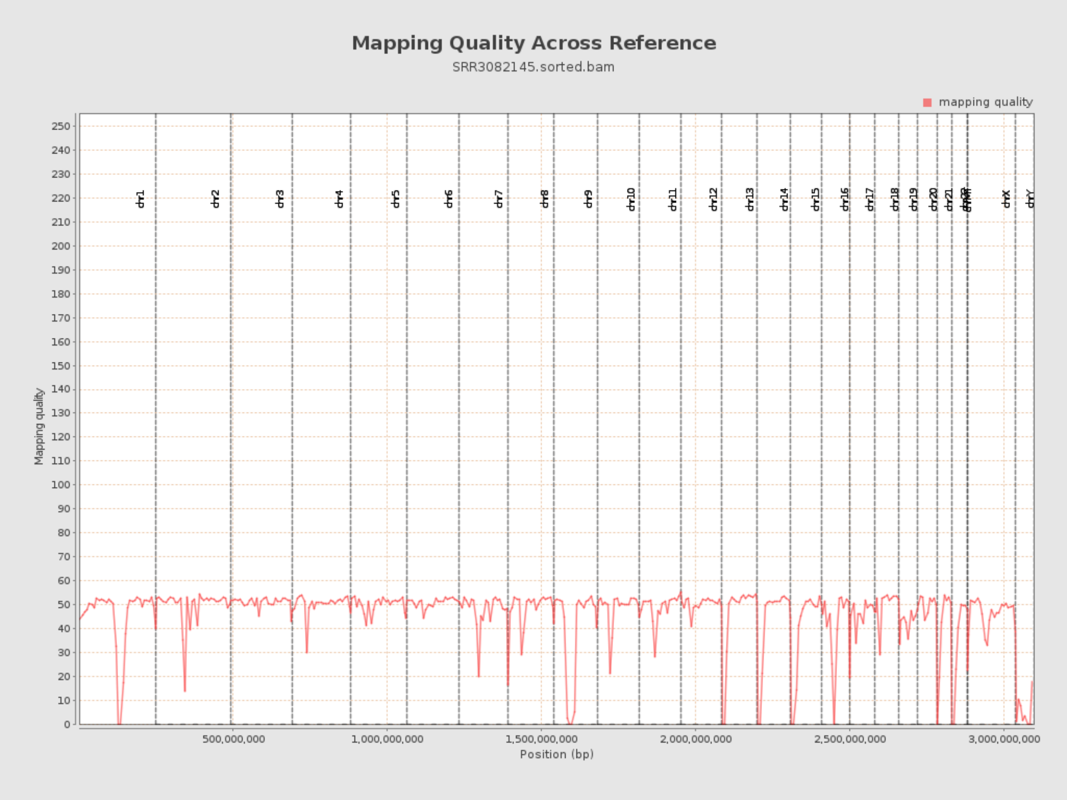
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram