Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 22:37:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR052148.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_SRR052148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR052148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 22:37:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR052148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,305,884
Mapped reads	7,093,758 / 62.74%
Unmapped reads	4,212,126 / 37.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	148 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,831,239 / 16.2%
Duplication rate	18.42%
Clipped reads	1,545,132 / 13.67%

2.2. ACGT Content

Number/percentage of A's	96,557,870 / 29.6%
Number/percentage of C's	66,812,672 / 20.48%
Number/percentage of T's	96,086,992 / 29.45%
Number/percentage of G's	66,644,053 / 20.43%
Number/percentage of N's	162,317 / 0.05%
GC Percentage	40.9%

2.3. Coverage

Mean	0.1054

Standard Deviation	0.8911

2.4. Mapping Quality

Mean Mapping Quality	42.14

2.5. Mismatches and indels

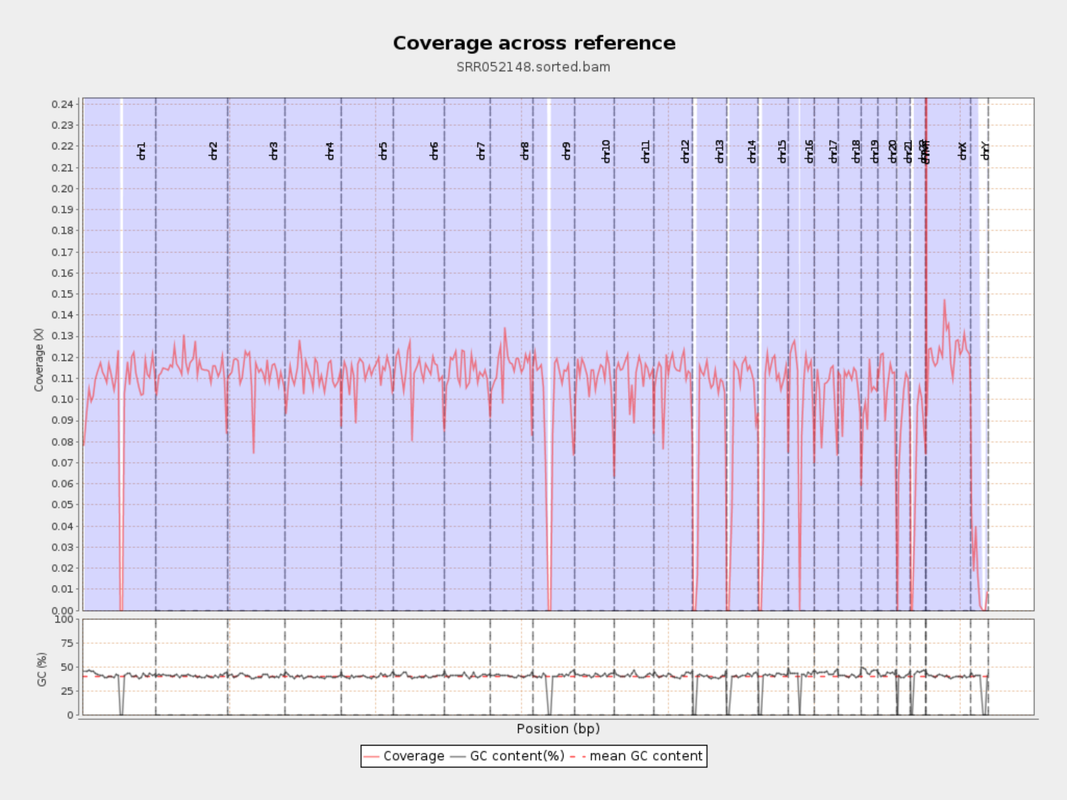
General error rate	1.49%
Mismatches	4,831,769
Insertions	18,299
Mapped reads with at least one insertion	0.26%
Deletions	42,356
Mapped reads with at least one deletion	0.59%
Homopolymer indels	37.7%

2.6. Chromosome stats

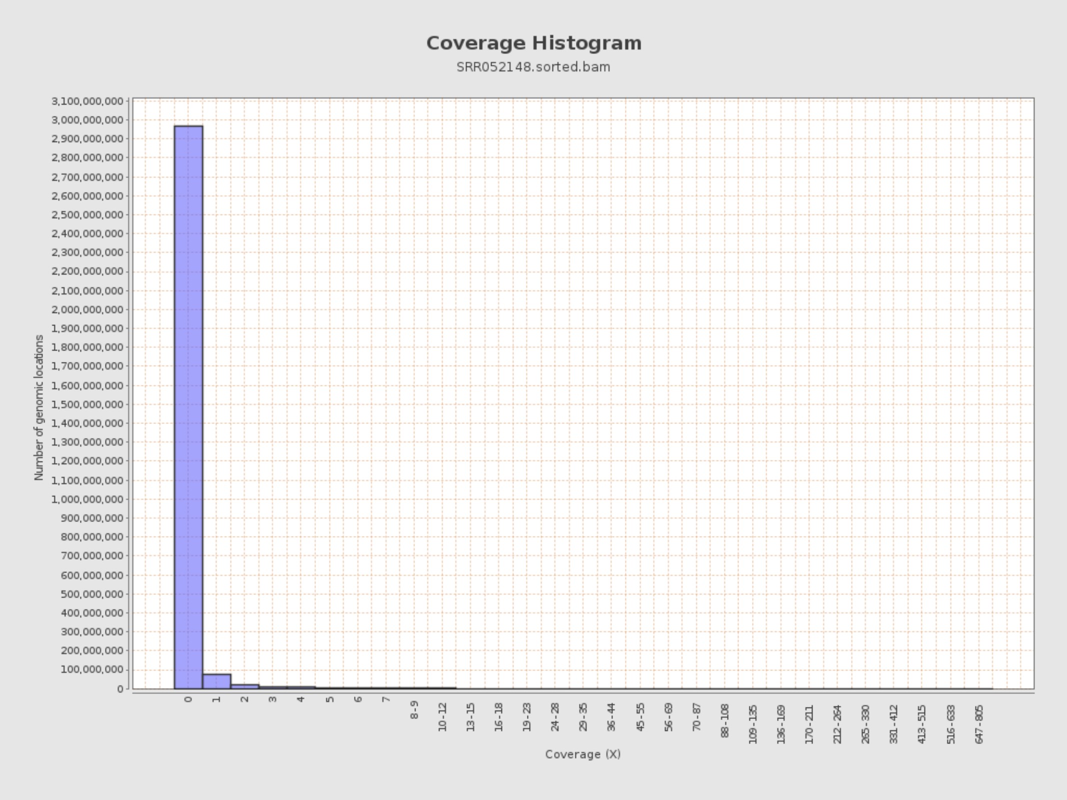
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25608001	0.1027	0.9598
chr2	243199373	27926179	0.1148	0.9706
chr3	198022430	22246455	0.1123	0.8592
chr4	191154276	21343284	0.1117	0.8795
chr5	180915260	20347146	0.1125	0.8571
chr6	171115067	19430543	0.1136	0.9502
chr7	159138663	17881611	0.1124	0.9976

chr8	146364022	16808365	0.1148	0.9676
chr9	141213431	13392211	0.0948	0.812
chr10	135534747	15078496	0.1113	0.9001
chr11	135006516	14936541	0.1106	0.9739
chr12	133851895	15053709	0.1125	0.8633
chr13	115169878	10497057	0.0911	0.7761
chr14	107349540	9988749	0.093	0.8514
chr15	102531392	9384679	0.0915	0.7532
chr16	90354753	9107319	0.1008	0.8147
chr17	81195210	8336601	0.1027	0.7961
chr18	78077248	8403345	0.1076	0.9263
chr19	59128983	5910751	0.1	0.9494
chr20	63025520	6883284	0.1092	0.8457
chr21	48129895	4130590	0.0858	0.7719
chr22	51304566	3434676	0.0669	0.6307
chrMT	16571	208221	12.5654	20.3278
chrX	155270560	19088367	0.1229	0.9675
chrY	59373566	897973	0.0151	0.2953

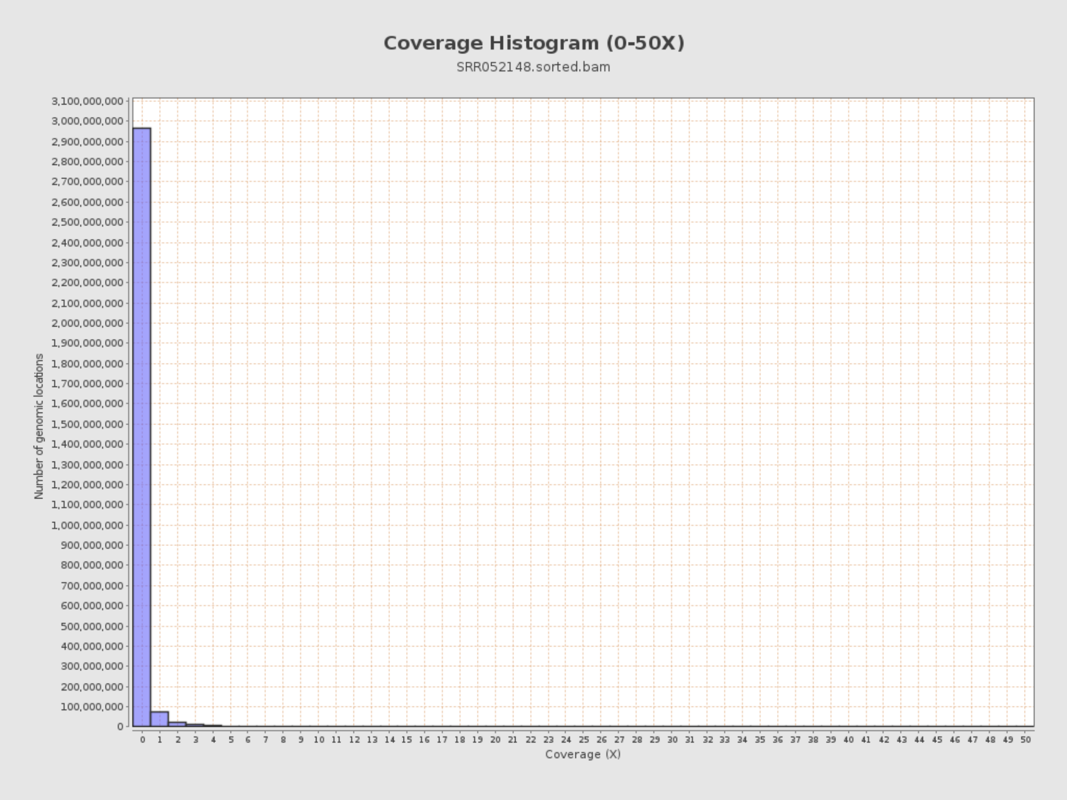
3. Results : Coverage across reference



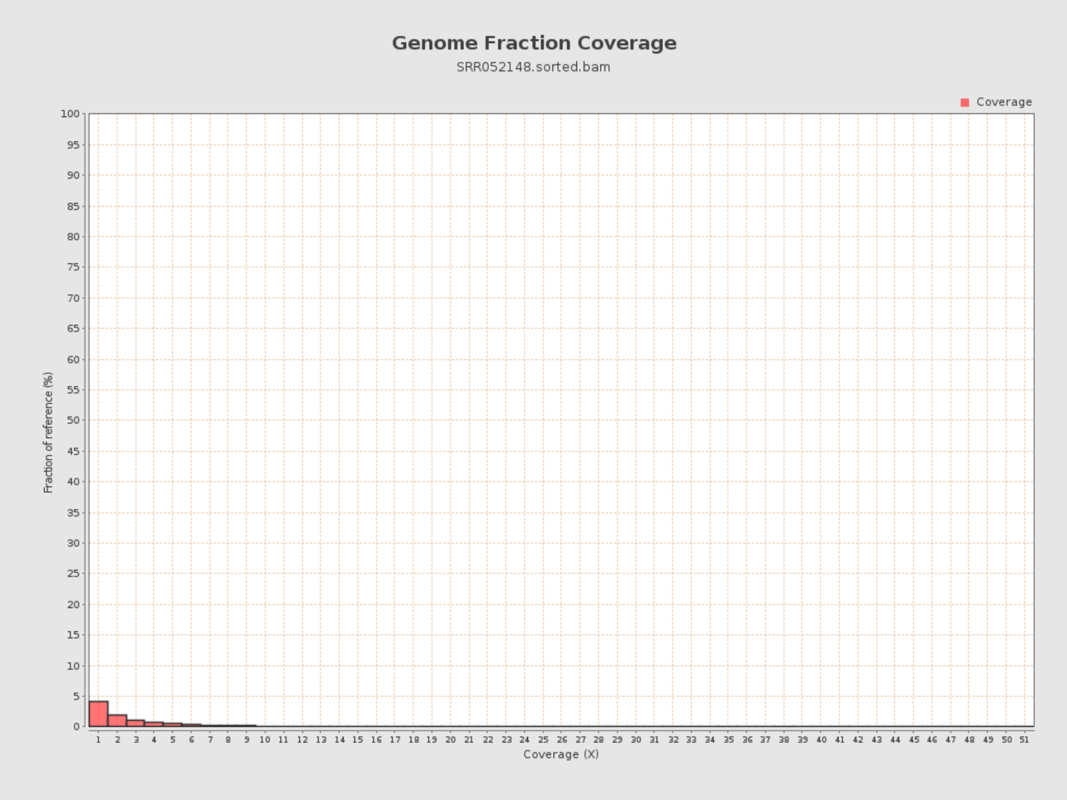
4. Results : Coverage Histogram



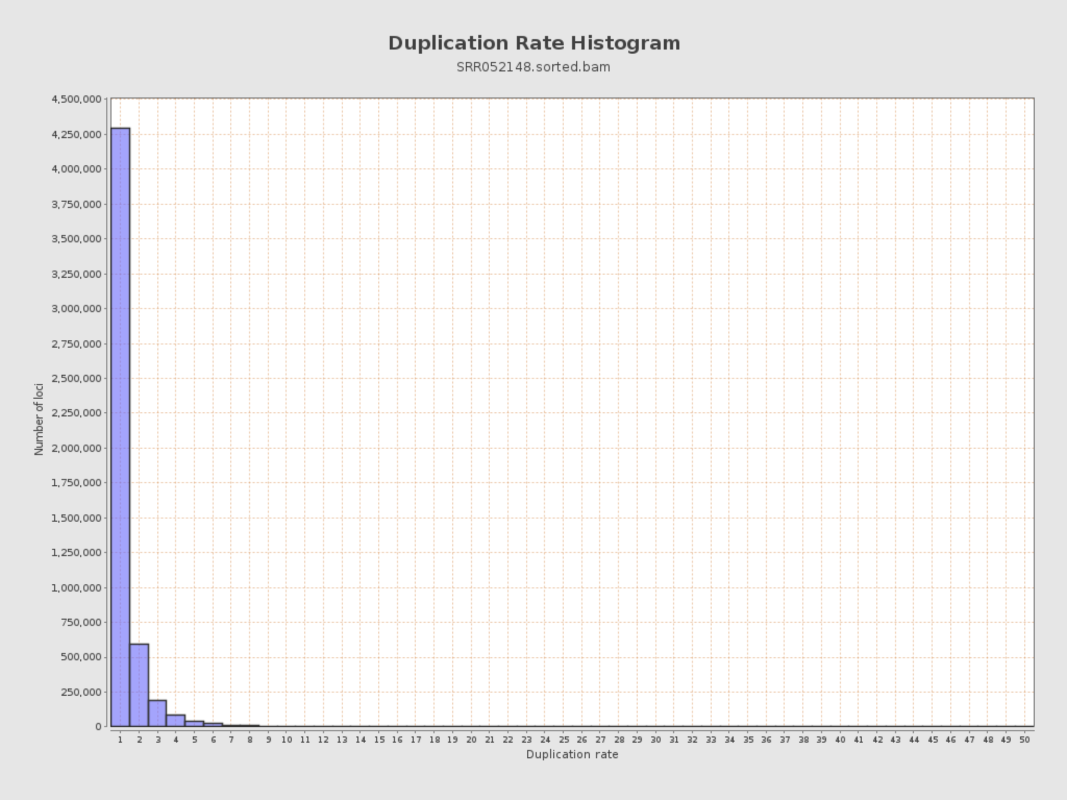
5. Results : Coverage Histogram (0-50X)



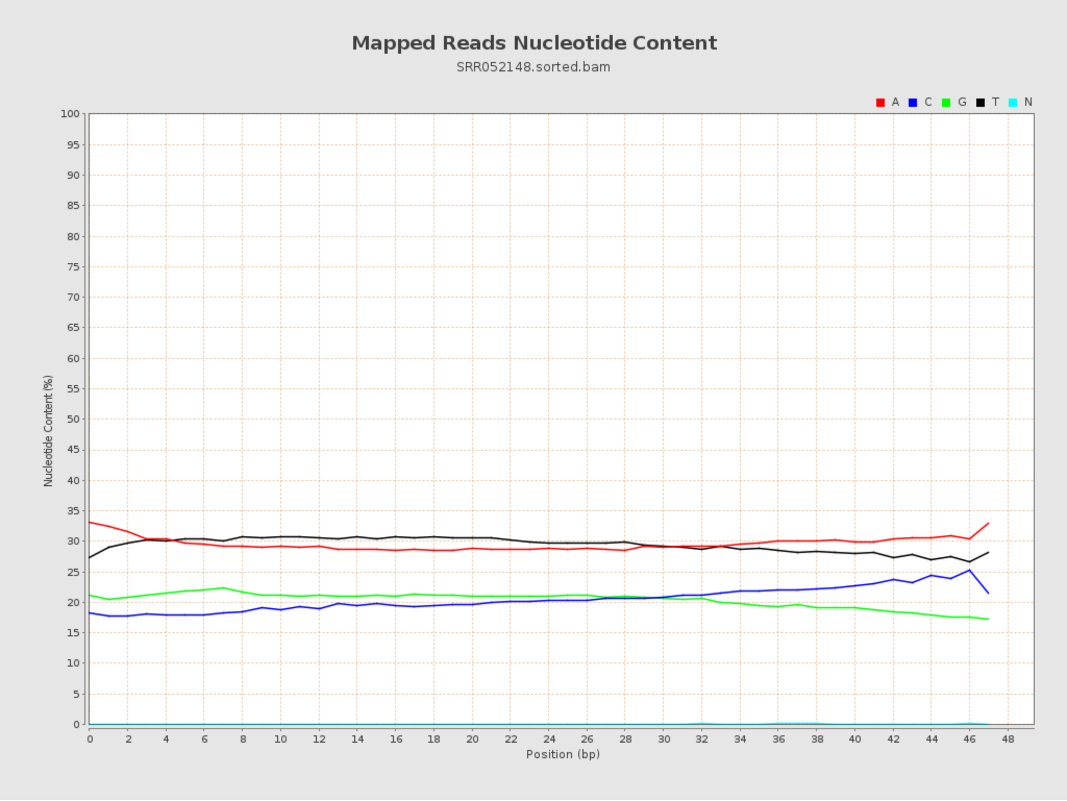
6. Results : Genome Fraction Coverage



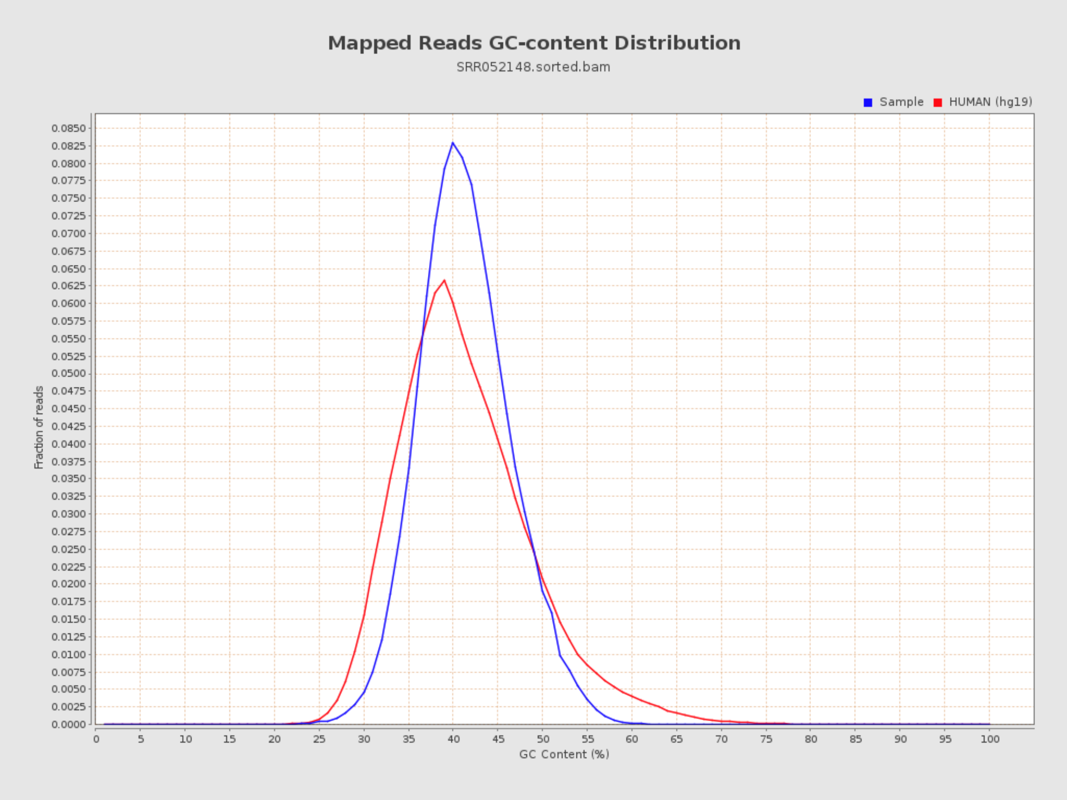
7. Results : Duplication Rate Histogram



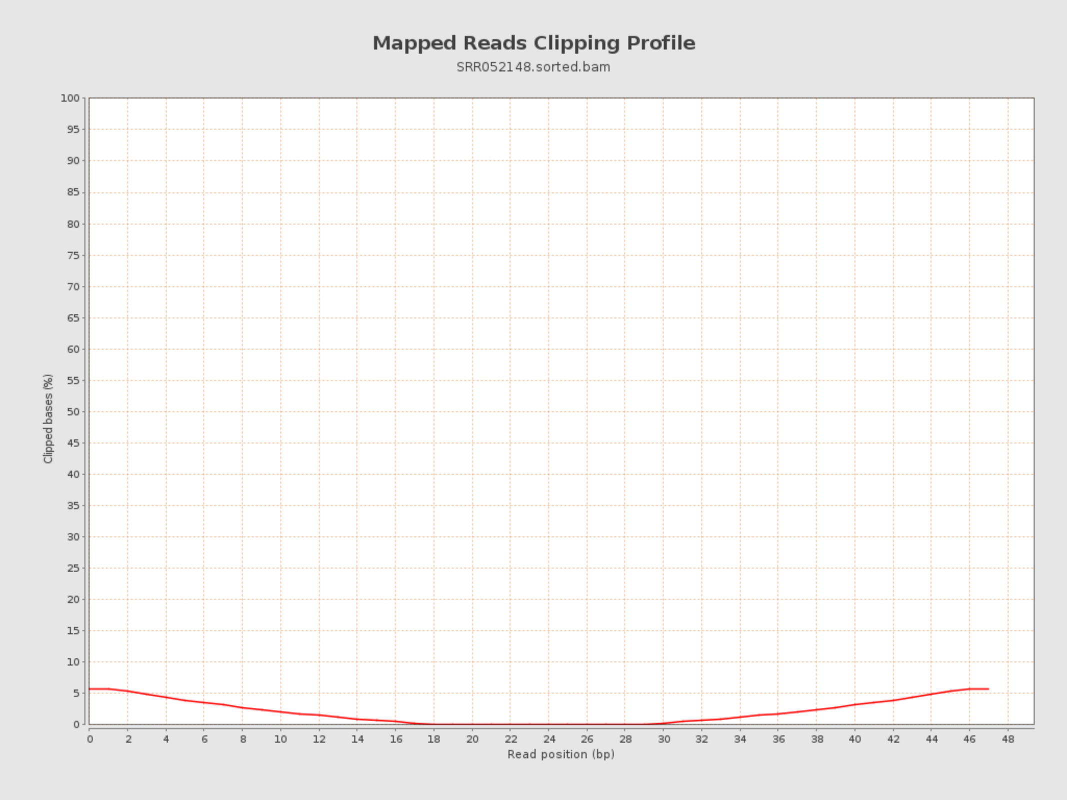
8. Results : Mapped Reads Nucleotide Content



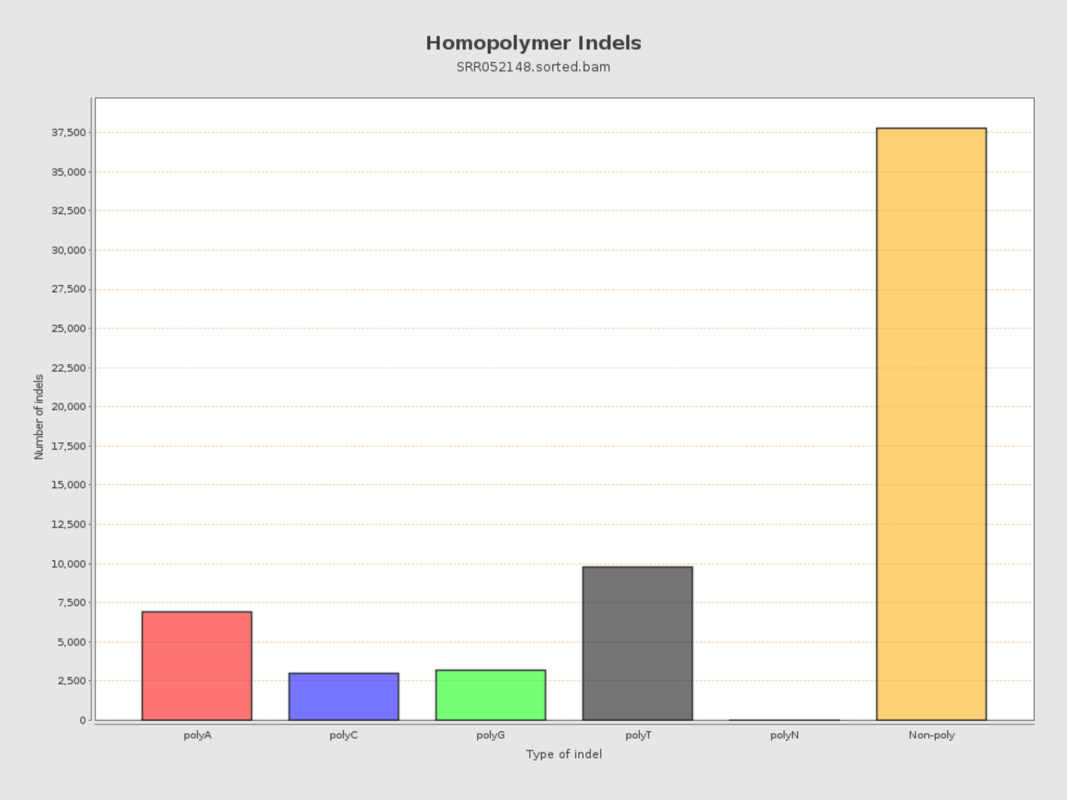
9. Results : Mapped Reads GC-content Distribution



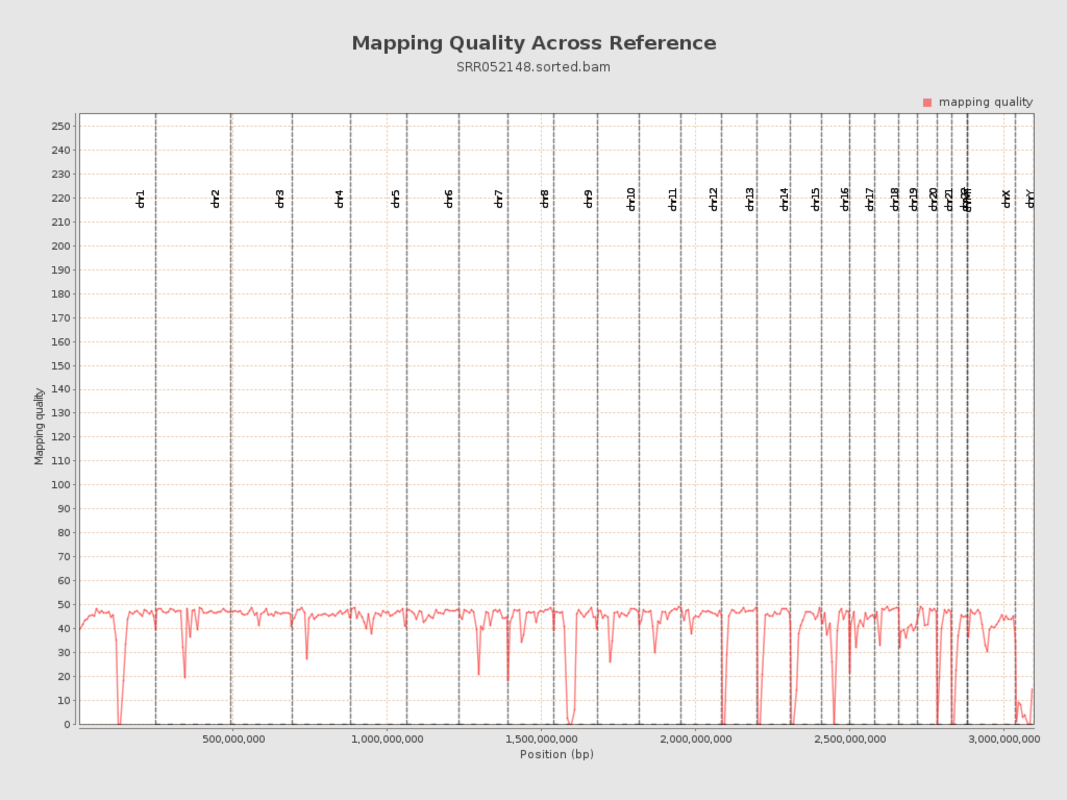
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram