Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:06:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818846.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_SRR1818846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:06:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,728,711
Mapped reads	1,668,665 / 96.53%
Unmapped reads	60,046 / 3.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,973 / 1.62%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	382,305 / 22.12%
Duplication rate	19.8%
Clipped reads	1,684,895 / 97.47%

2.2. ACGT Content

Number/percentage of A's	44,125,027 / 28.59%
Number/percentage of C's	33,192,992 / 21.51%
Number/percentage of T's	45,234,135 / 29.31%
Number/percentage of G's	31,763,140 / 20.58%
Number/percentage of N's	2,194 / 0%
GC Percentage	42.09%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.5744

2.4. Mapping Quality

Mean Mapping Quality	49.42

2.5. Mismatches and indels

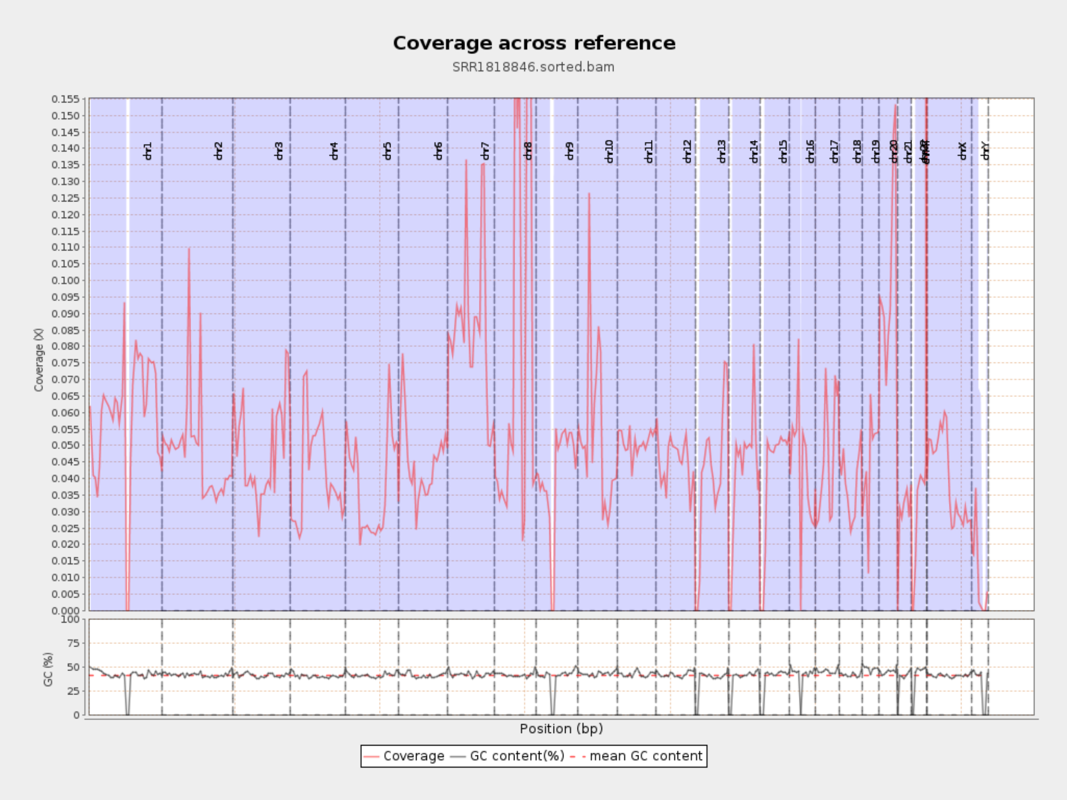
General error rate	0.65%
Mismatches	950,173
Insertions	21,846
Mapped reads with at least one insertion	1.26%
Deletions	50,147
Mapped reads with at least one deletion	2.93%
Homopolymer indels	40.83%

2.6. Chromosome stats

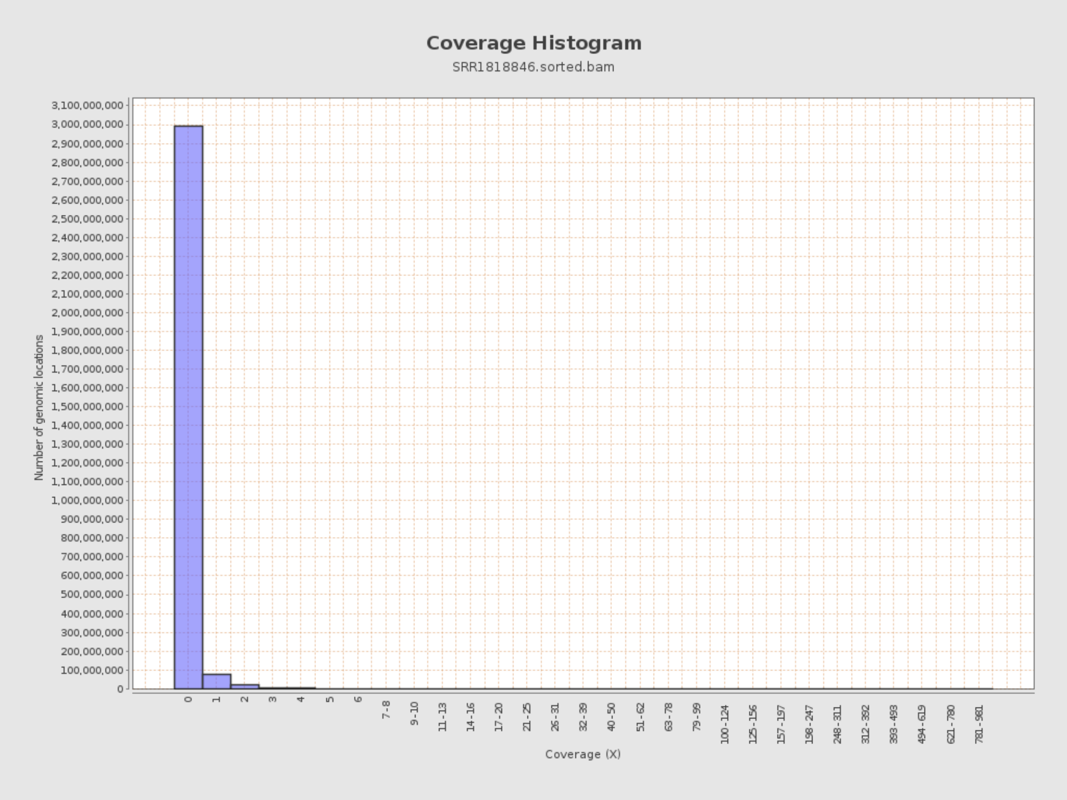
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14575871	0.0585	0.826
chr2	243199373	11716046	0.0482	0.8189
chr3	198022430	9636851	0.0487	0.3006
chr4	191154276	7873147	0.0412	0.3666
chr5	180915260	6832900	0.0378	0.276
chr6	171115067	7678432	0.0449	0.314
chr7	159138663	13832408	0.0869	1.2097

chr8	146364022	13387910	0.0915	0.5141
chr9	141213431	5755106	0.0408	0.4897
chr10	135534747	7206803	0.0532	0.7892
chr11	135006516	6864093	0.0508	0.3614
chr12	133851895	6085175	0.0455	0.2915
chr13	115169878	4756342	0.0413	0.2701
chr14	107349540	4517130	0.0421	0.2998
chr15	102531392	4187137	0.0408	0.2705
chr16	90354753	3811205	0.0422	0.5845
chr17	81195210	3811207	0.0469	0.3765
chr18	78077248	2999481	0.0384	0.5665
chr19	59128983	2638230	0.0446	0.6993
chr20	63025520	6367644	0.101	0.461
chr21	48129895	1401964	0.0291	0.2821
chr22	51304566	1398025	0.0272	0.2468
chrMT	16571	261024	15.7519	10.1502
chrX	155270560	6239580	0.0402	0.3186
chrY	59373566	581361	0.0098	0.7168

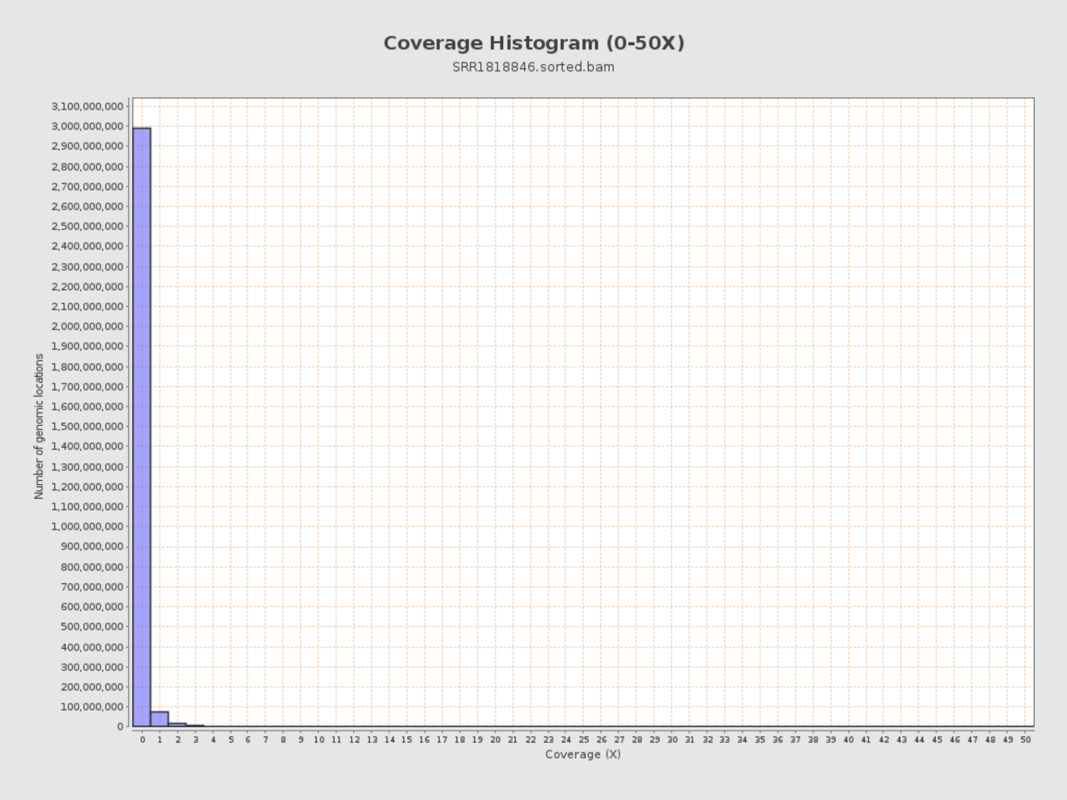
3. Results : Coverage across reference



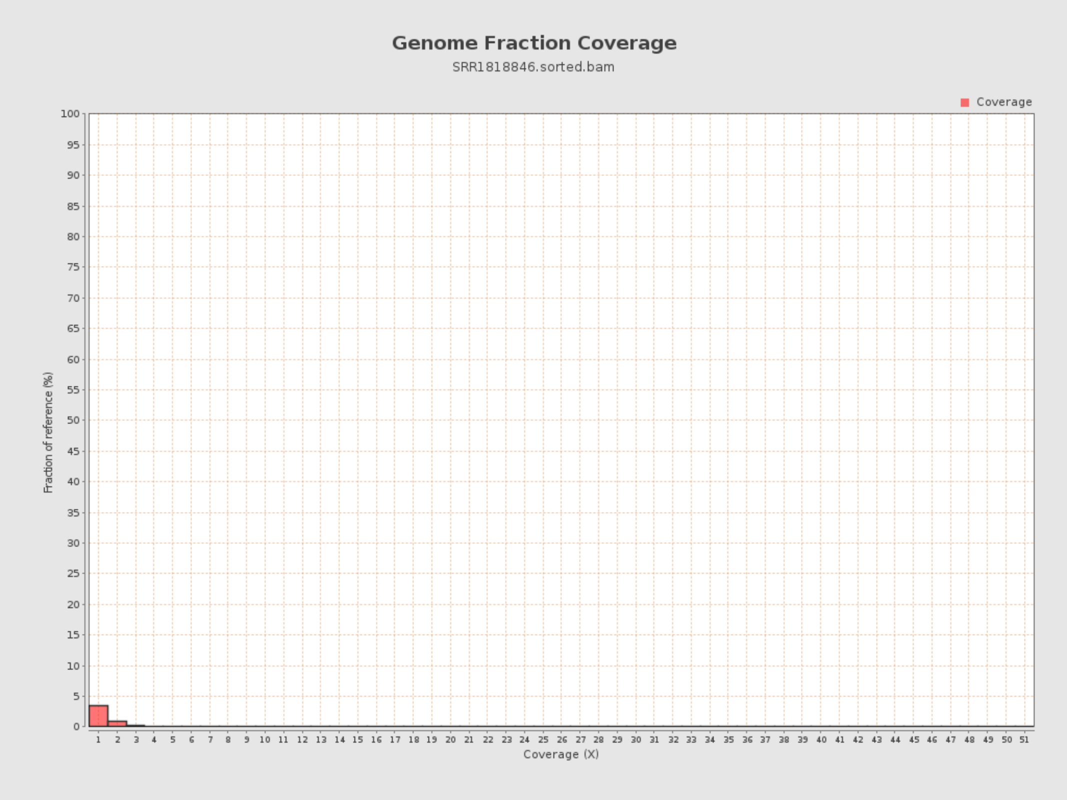
4. Results : Coverage Histogram



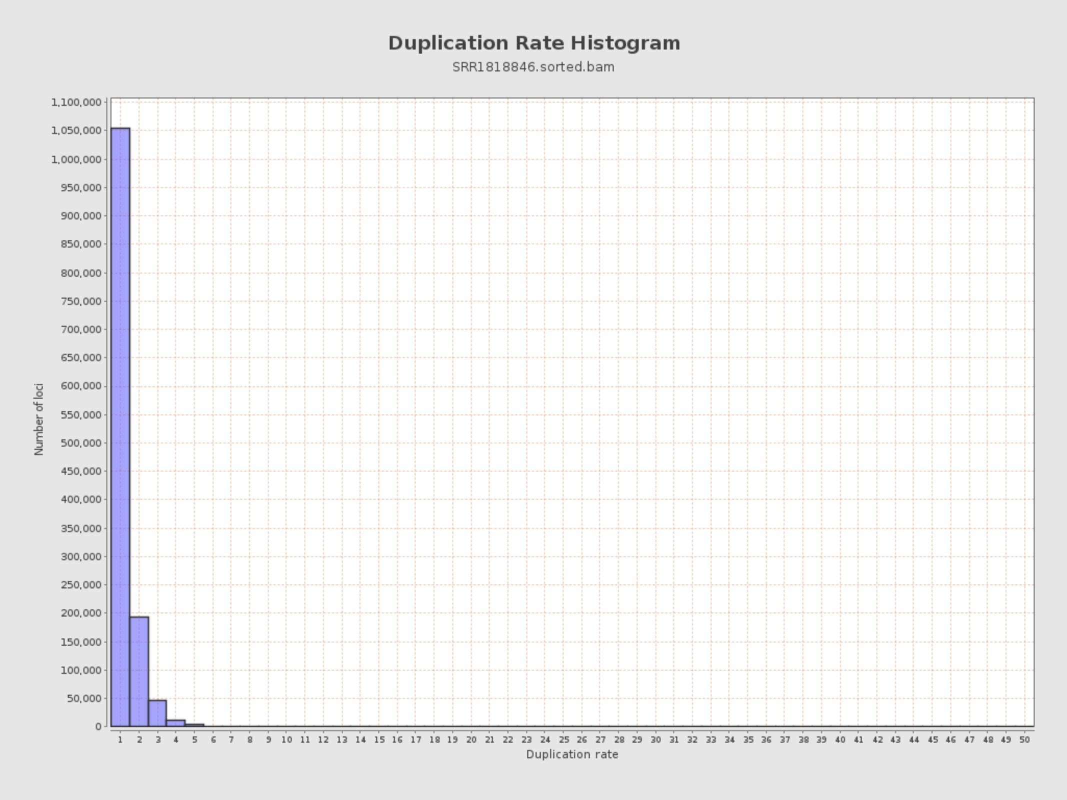
5. Results : Coverage Histogram (0-50X)



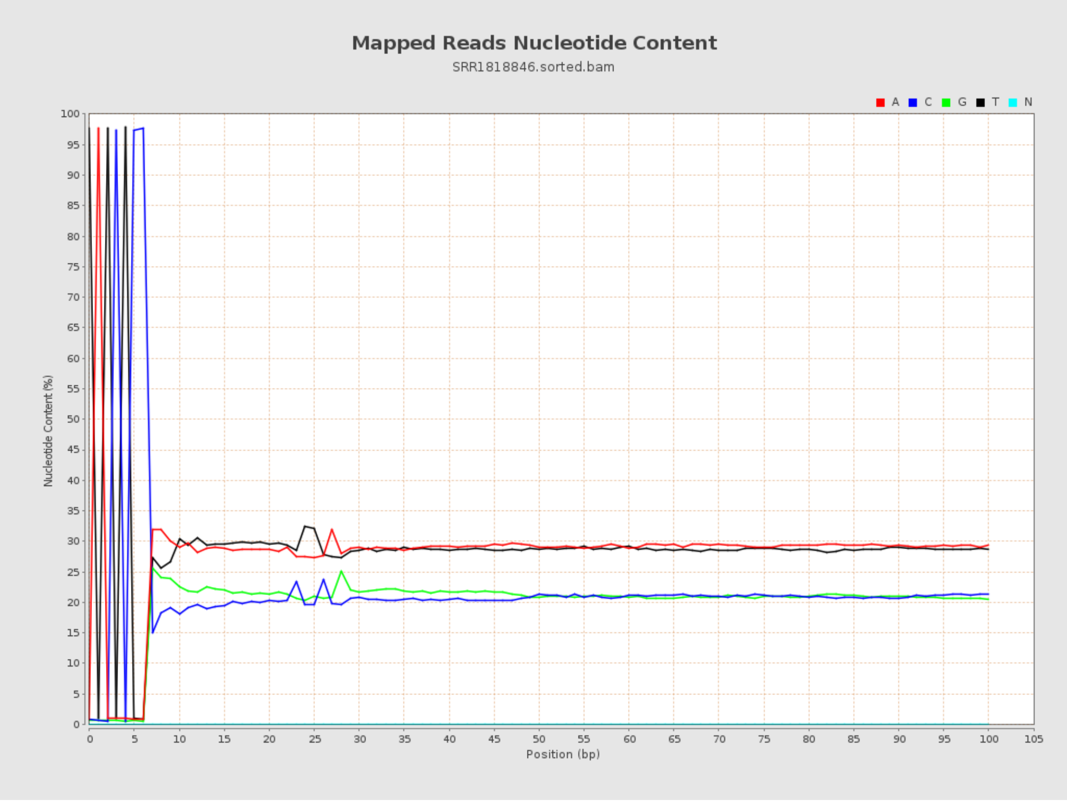
6. Results : Genome Fraction Coverage



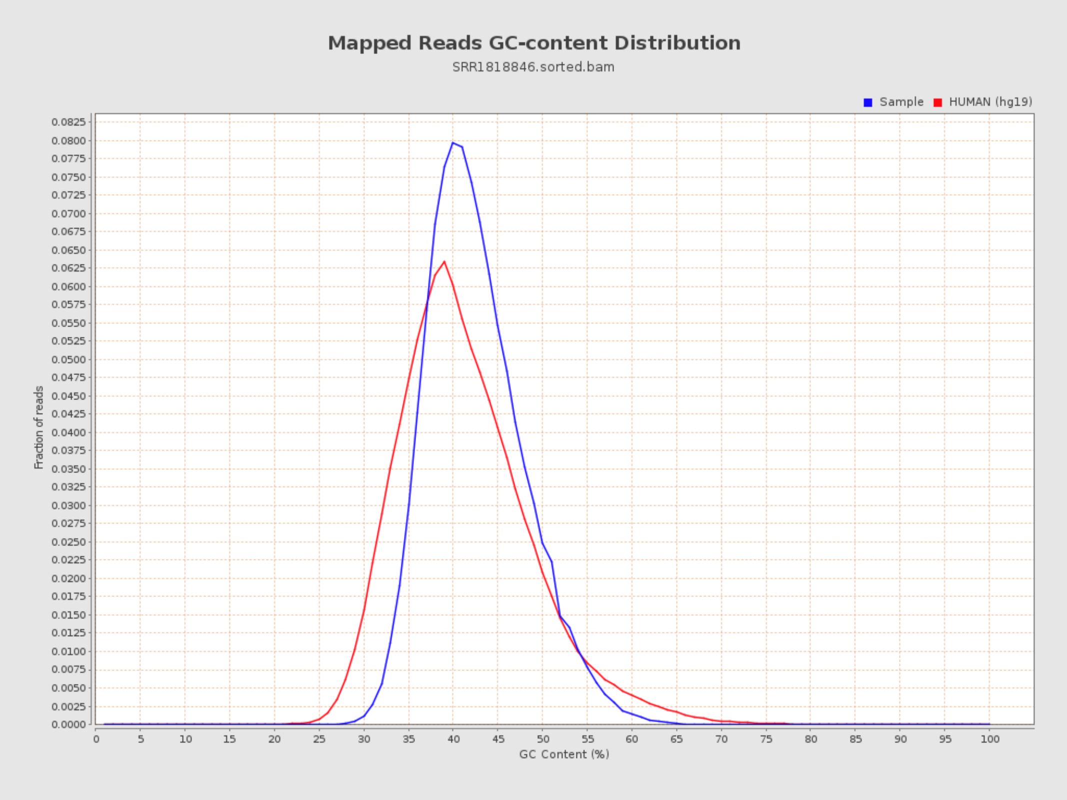
7. Results : Duplication Rate Histogram



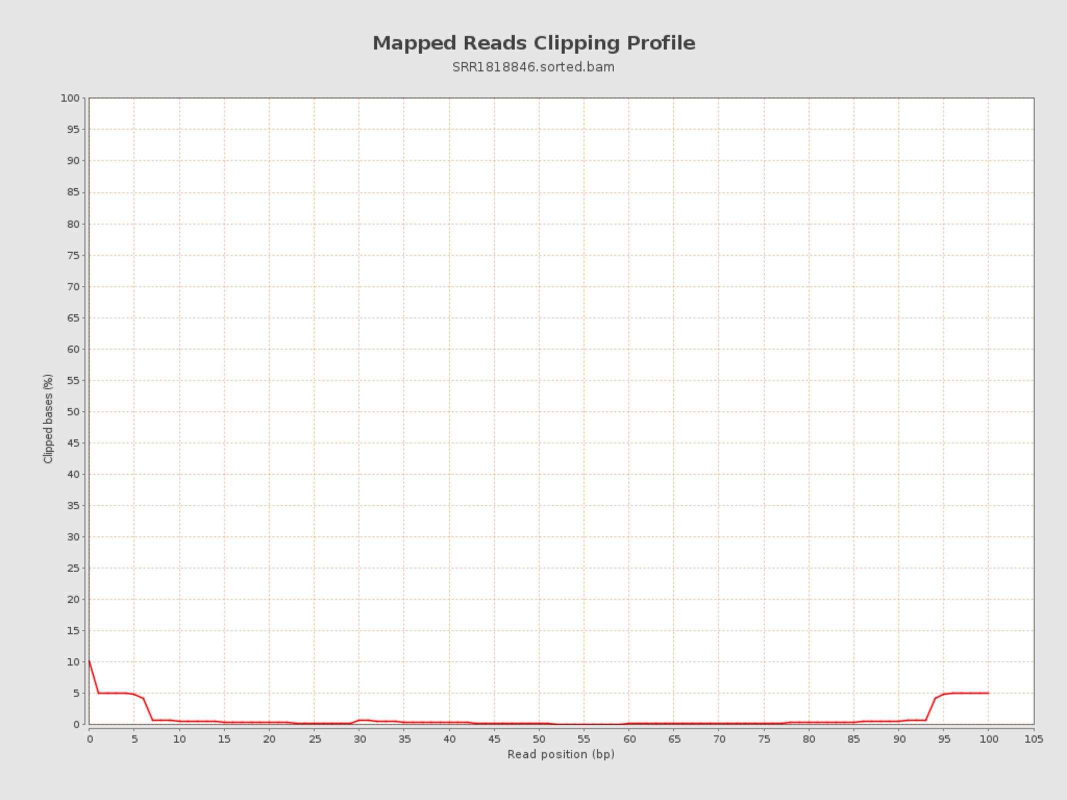
8. Results : Mapped Reads Nucleotide Content



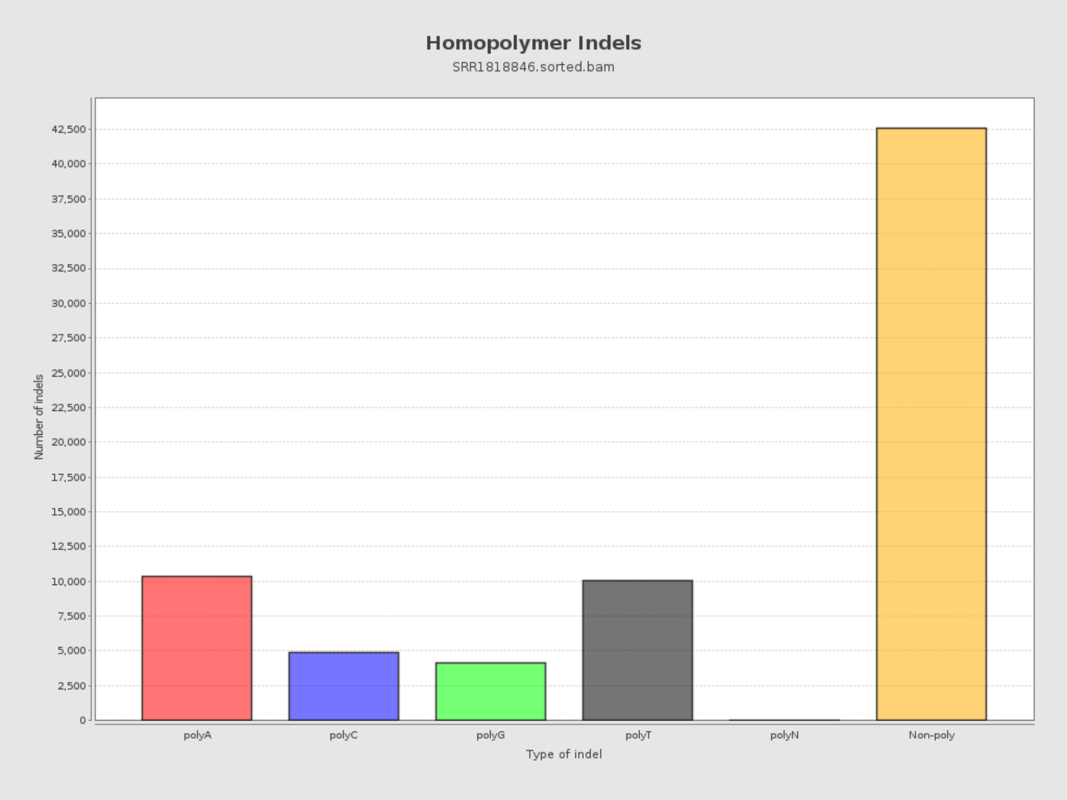
9. Results : Mapped Reads GC-content Distribution



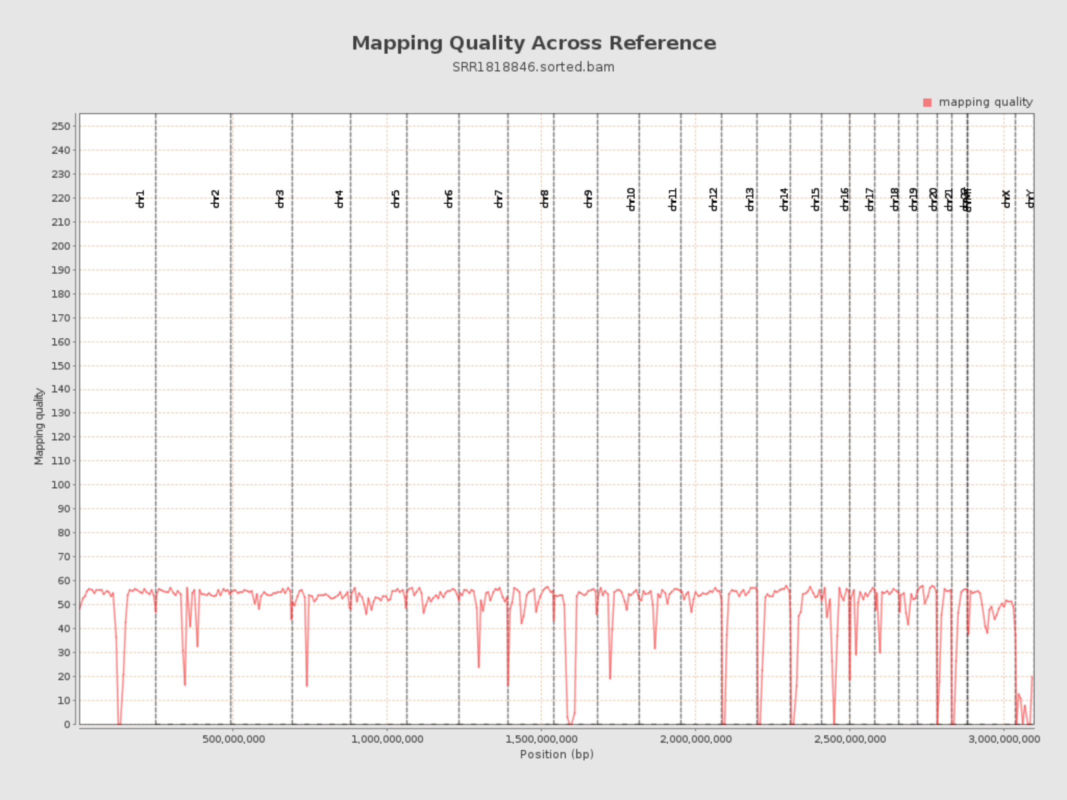
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram