Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:02:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751180.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_SRR8751180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:02:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,758,699
Mapped reads	4,731,686 / 99.43%
Unmapped reads	27,013 / 0.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,992 / 0.74%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	1,178,422 / 24.76%
Duplication rate	14.18%
Clipped reads	744,867 / 15.65%

2.2. ACGT Content

Number/percentage of A's	140,914,659 / 30.77%
Number/percentage of C's	88,598,874 / 19.34%
Number/percentage of T's	141,607,914 / 30.92%
Number/percentage of G's	86,888,642 / 18.97%
Number/percentage of N's	3,424 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	0.148

Standard Deviation	3.1565

2.4. Mapping Quality

Mean Mapping Quality	50.47

2.5. Mismatches and indels

General error rate	0.25%
Mismatches	1,032,656
Insertions	47,970
Mapped reads with at least one insertion	0.97%
Deletions	49,526
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.29%

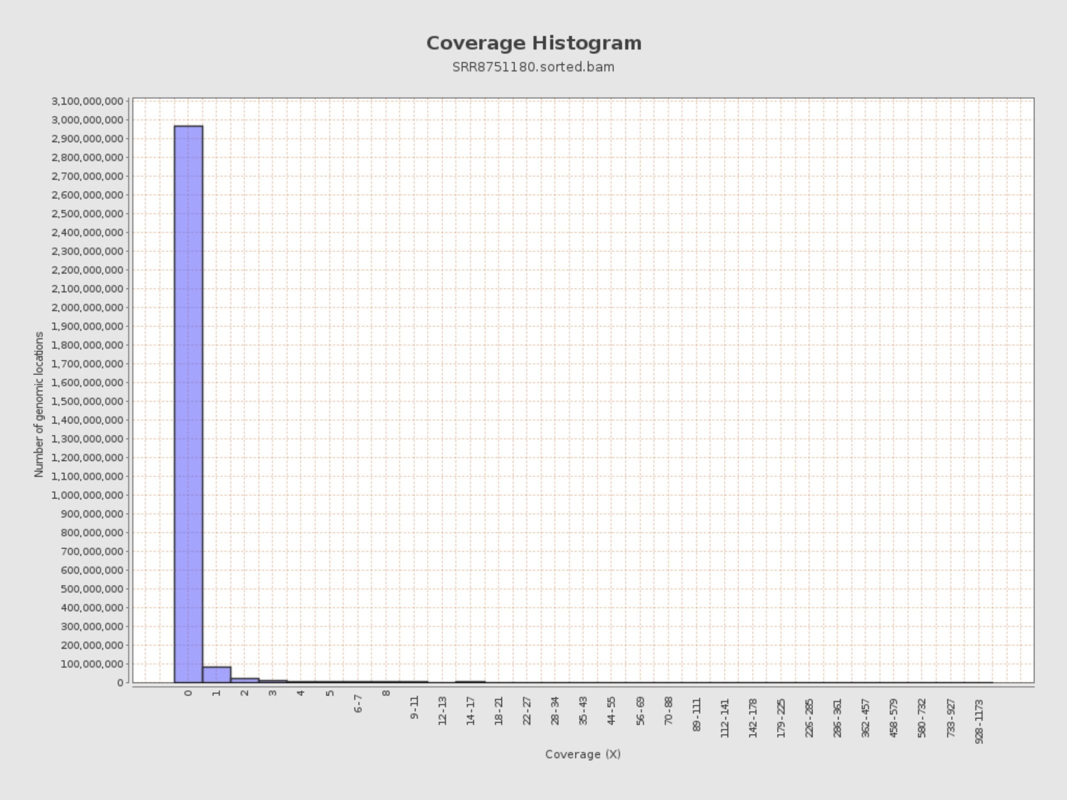
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48232956	0.1935	2.4526
chr2	243199373	38023593	0.1563	2.3756
chr3	198022430	31354609	0.1583	2.8482
chr4	191154276	28777161	0.1505	3.0431
chr5	180915260	44143950	0.244	2.5393
chr6	171115067	29719632	0.1737	5.4148
chr7	159138663	22705311	0.1427	1.4621

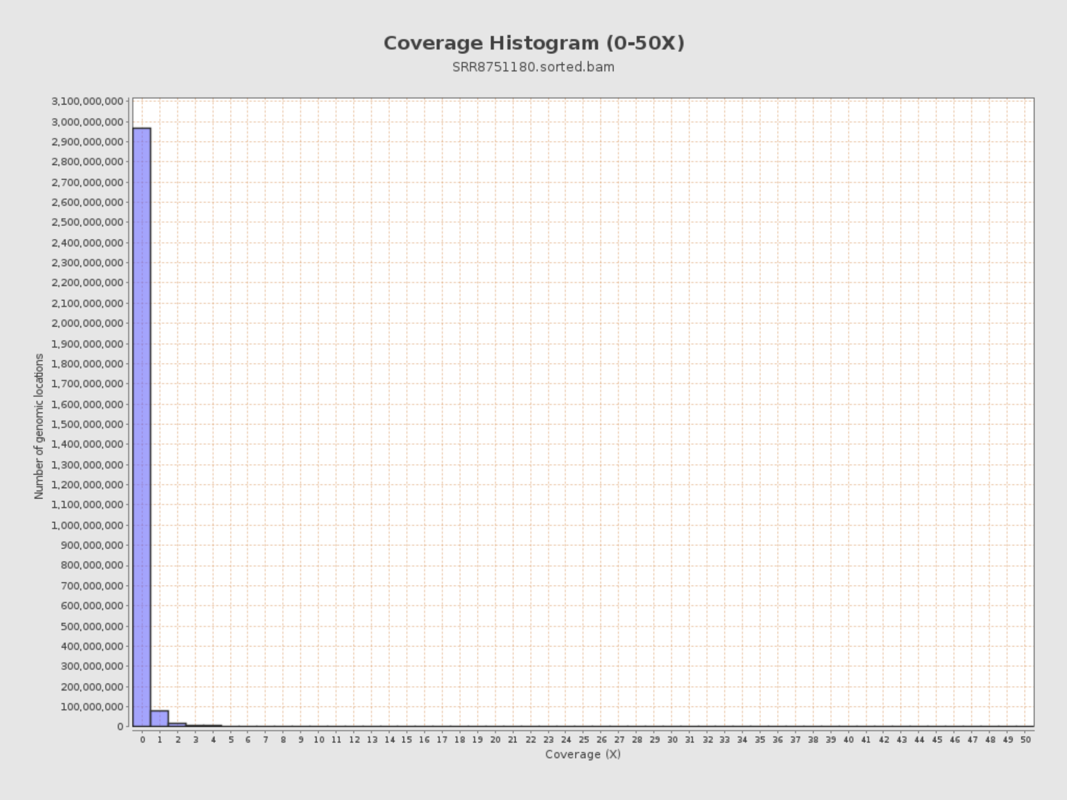
chr8	146364022	20648935	0.1411	1.491
chr9	141213431	26011639	0.1842	4.3543
chr10	135534747	24109022	0.1779	5.018
chr11	135006516	28471523	0.2109	4.2188
chr12	133851895	33032571	0.2468	7.4831
chr13	115169878	11140277	0.0967	1.4636
chr14	107349540	8414590	0.0784	1.0174
chr15	102531392	11157395	0.1088	1.7341
chr16	90354753	6306461	0.0698	1.2618
chr17	81195210	3929024	0.0484	0.6612
chr18	78077248	8639434	0.1107	1.226
chr19	59128983	2325630	0.0393	1.1479
chr20	63025520	3445652	0.0547	0.7394
chr21	48129895	7296120	0.1516	2.5332
chr22	51304566	3082601	0.0601	1.8607
chrMT	16571	15475	0.9339	1.0628
chrX	155270560	16859645	0.1086	1.091
chrY	59373566	275643	0.0046	0.1786

3. Results : Coverage across reference

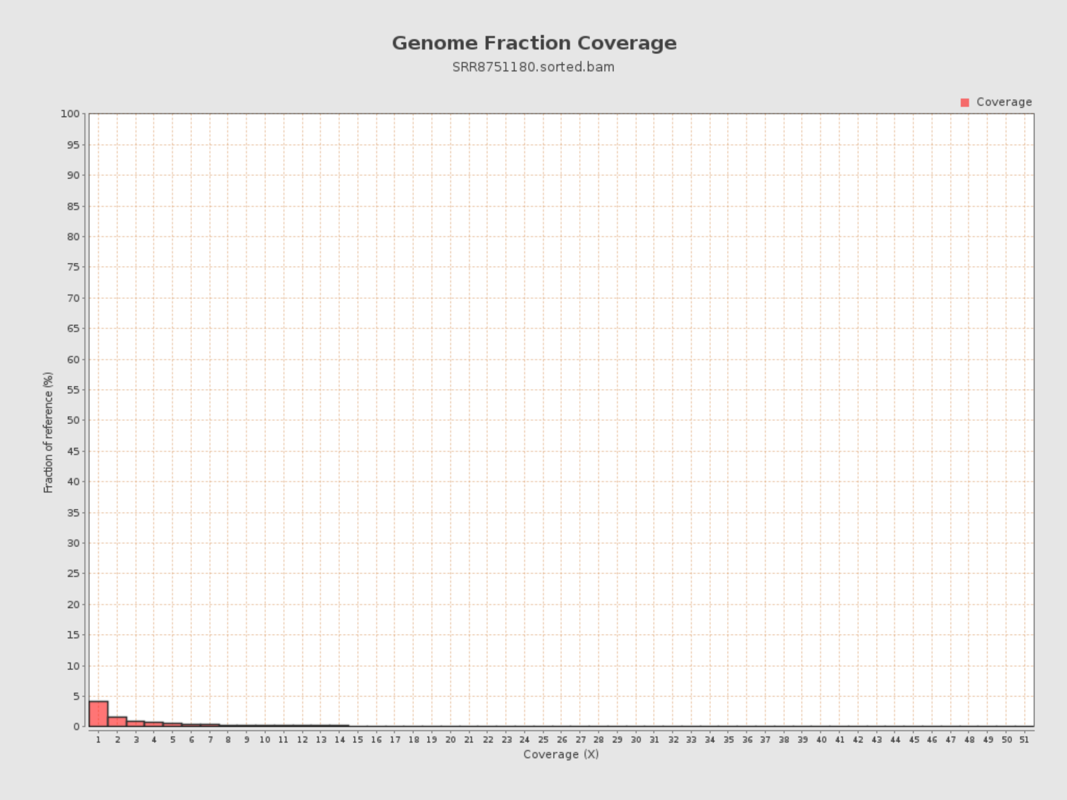
4. Results : Coverage Histogram



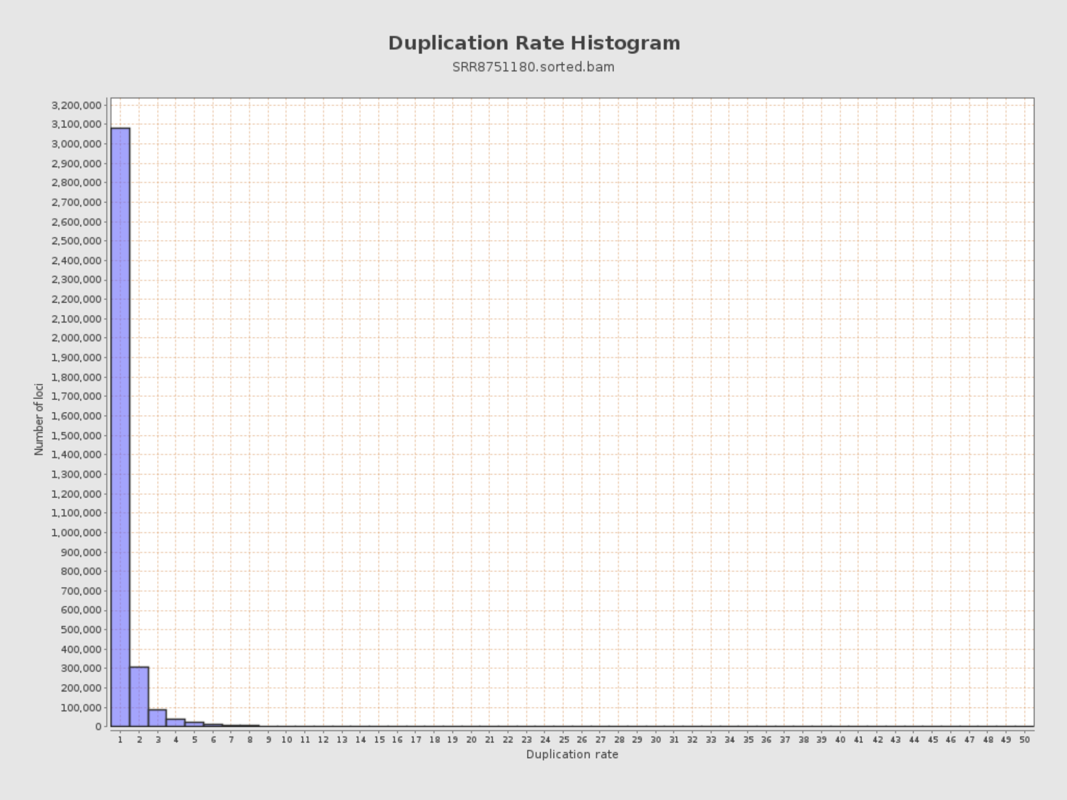
5. Results : Coverage Histogram (0-50X)



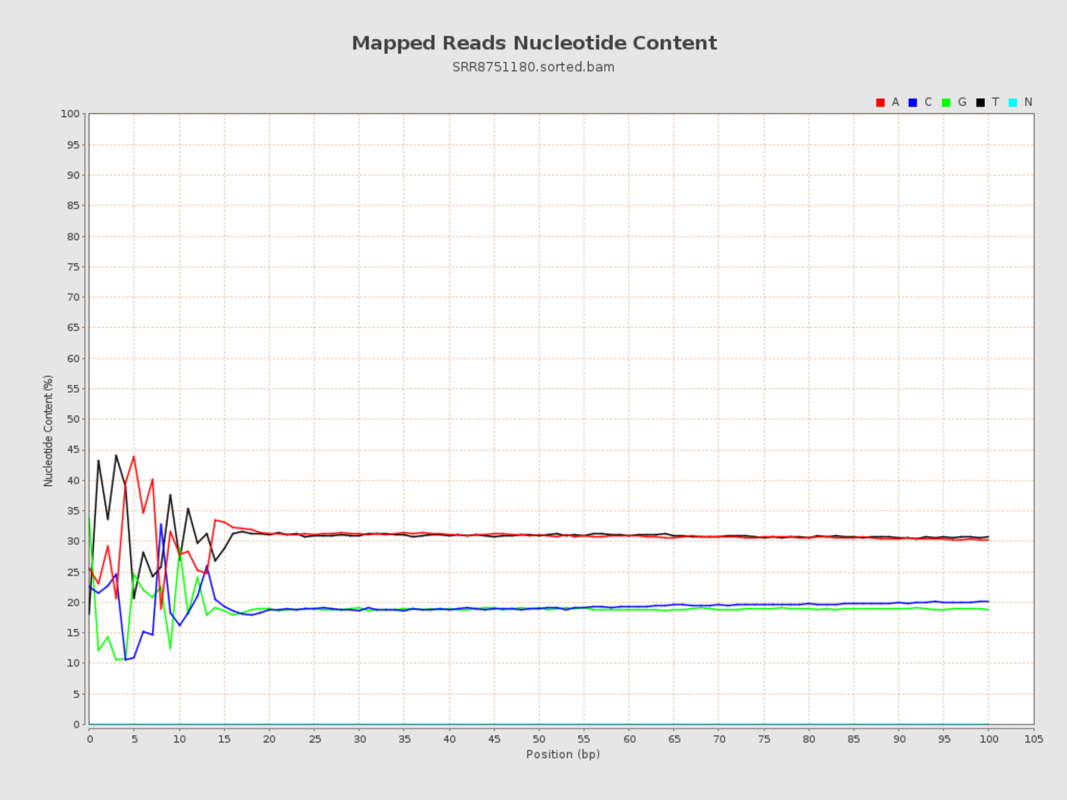
6. Results : Genome Fraction Coverage



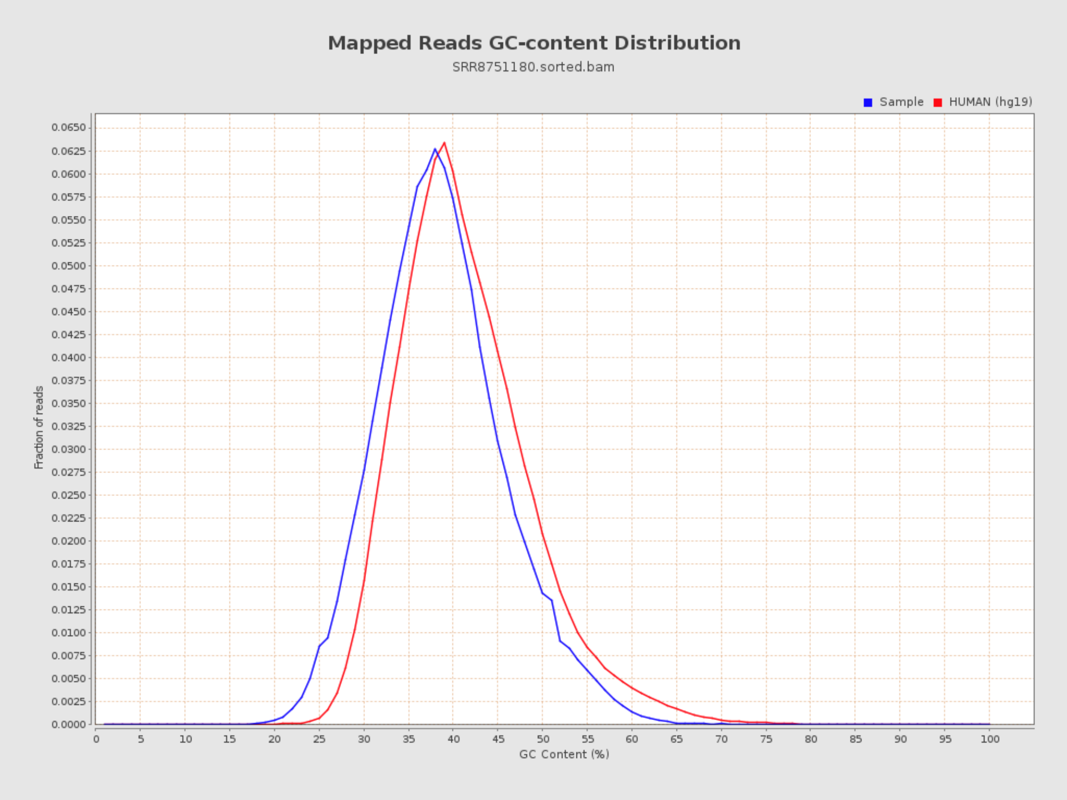
7. Results : Duplication Rate Histogram



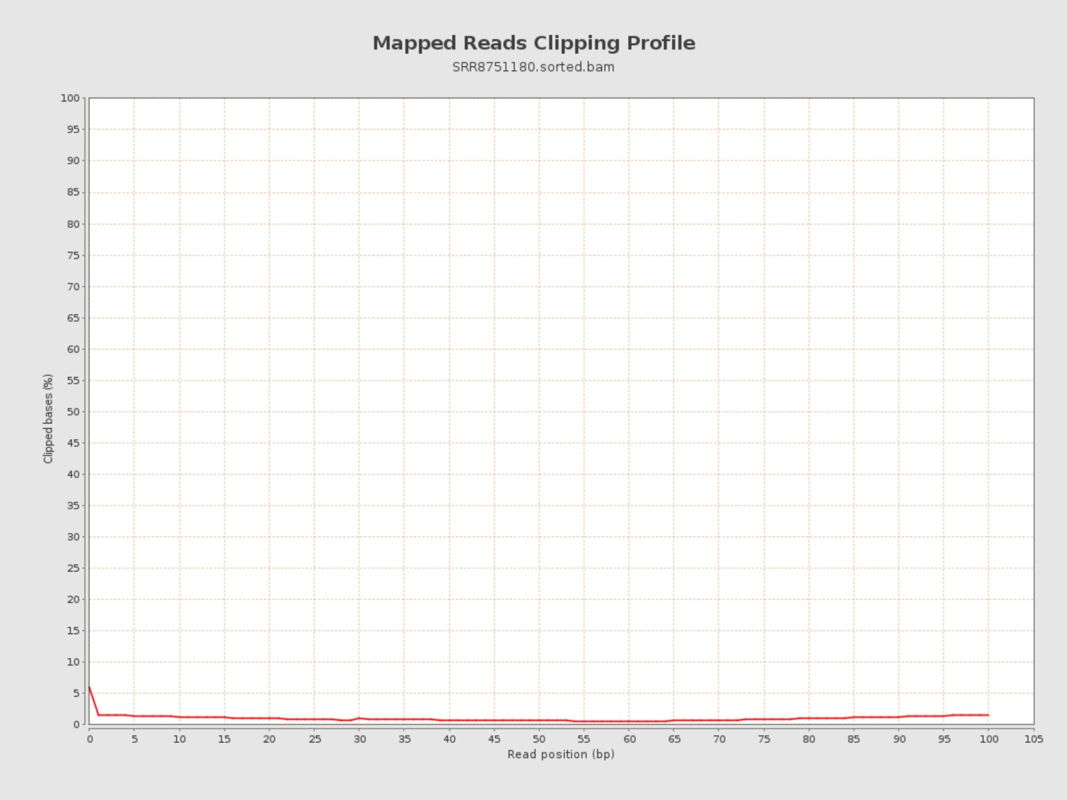
8. Results : Mapped Reads Nucleotide Content



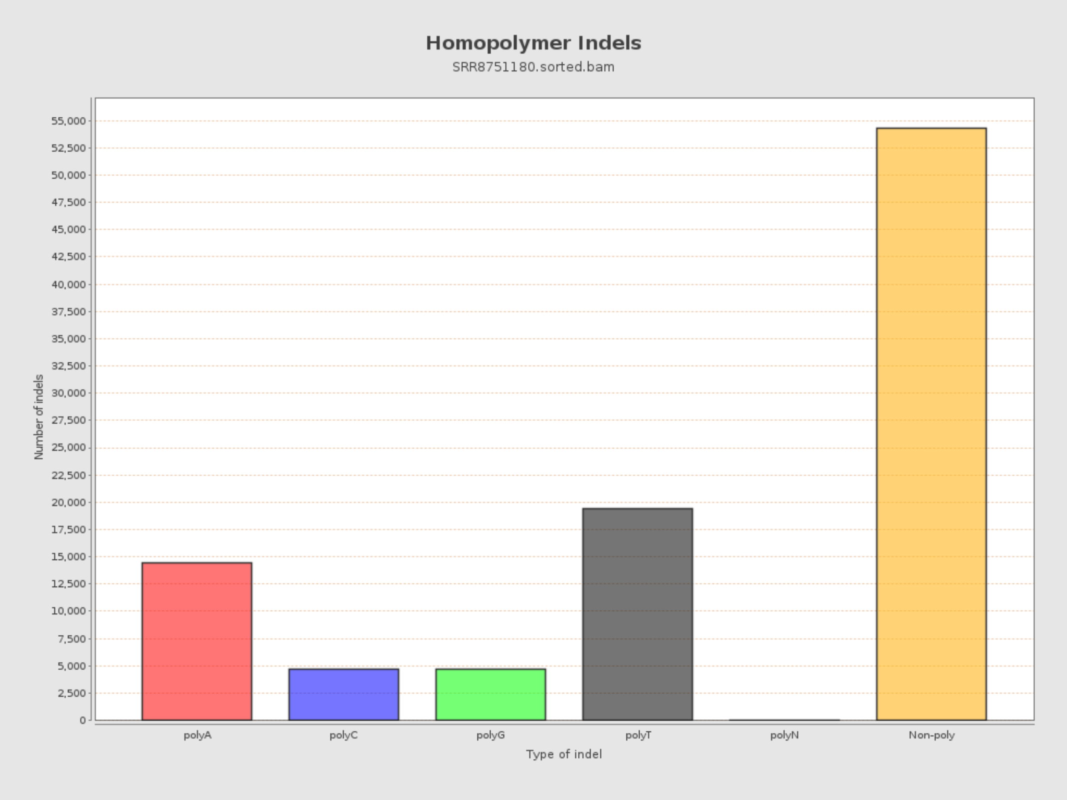
9. Results : Mapped Reads GC-content Distribution



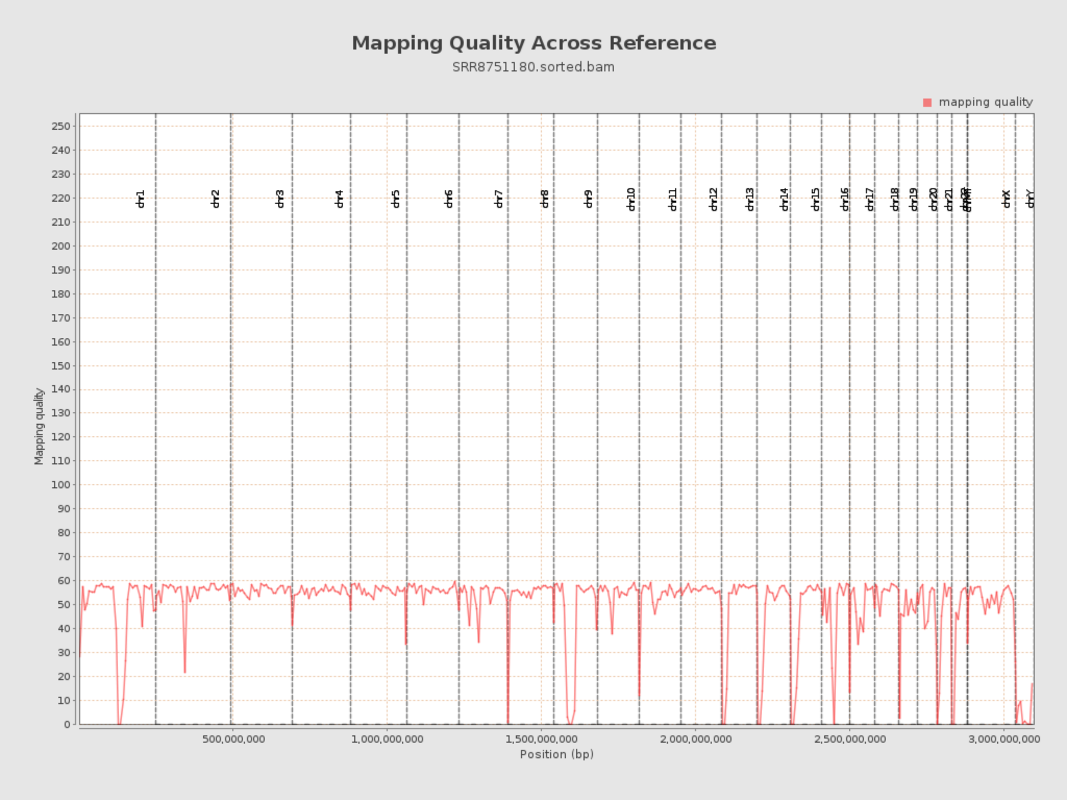
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram