Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751179.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_SRR8751179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:57:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,132,945
Mapped reads	4,115,437 / 99.58%
Unmapped reads	17,508 / 0.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,369 / 0.66%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	649,536 / 15.72%
Duplication rate	10.71%
Clipped reads	593,134 / 14.35%

2.2. ACGT Content

Number/percentage of A's	122,907,892 / 30.77%
Number/percentage of C's	77,217,989 / 19.33%
Number/percentage of T's	123,488,313 / 30.92%
Number/percentage of G's	75,768,743 / 18.97%
Number/percentage of N's	2,896 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	0.129

Standard Deviation	1.6802

2.4. Mapping Quality

Mean Mapping Quality	50.96

2.5. Mismatches and indels

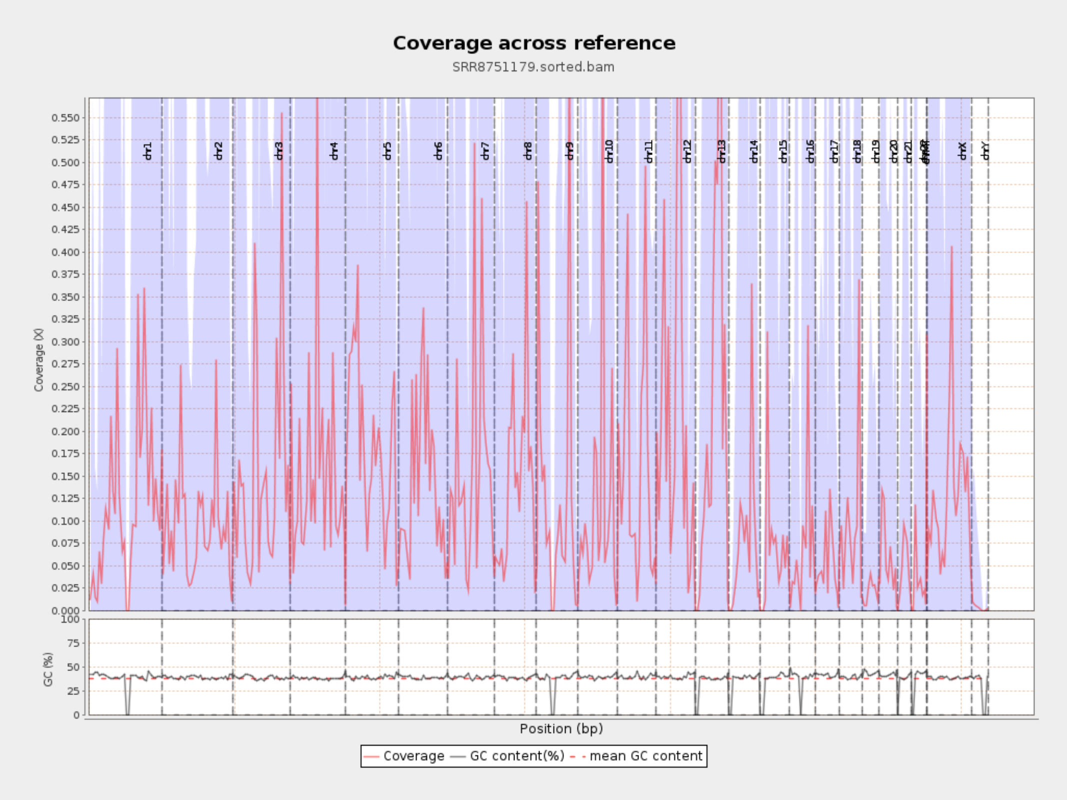
General error rate	0.23%
Mismatches	843,955
Insertions	35,998
Mapped reads with at least one insertion	0.87%
Deletions	43,226
Mapped reads with at least one deletion	1.04%
Homopolymer indels	48.13%

2.6. Chromosome stats

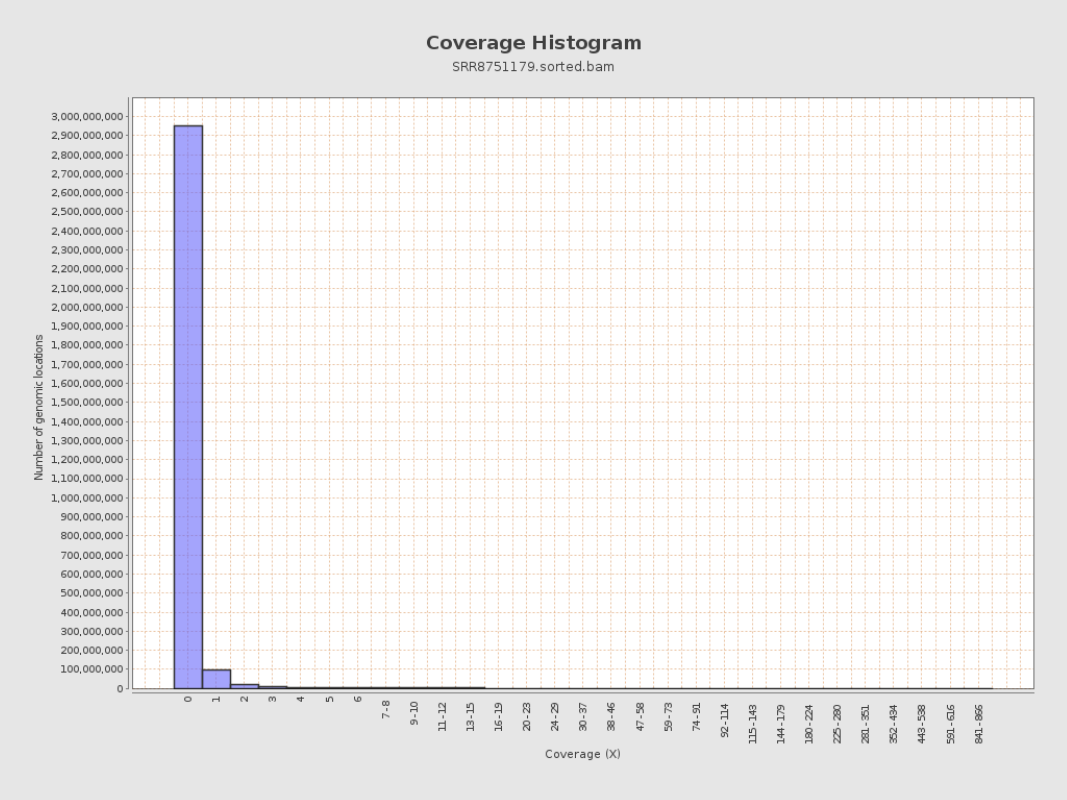
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30018894	0.1204	1.2145
chr2	243199373	23493656	0.0966	1.0237
chr3	198022430	30544982	0.1543	1.8458
chr4	191154276	29731601	0.1555	1.7714
chr5	180915260	33274154	0.1839	1.173
chr6	171115067	24343423	0.1423	1.6821
chr7	159138663	25543128	0.1605	1.729

chr8	146364022	21634452	0.1478	1.5404
chr9	141213431	19617314	0.1389	2.5211
chr10	135534747	17058420	0.1259	1.597
chr11	135006516	22330909	0.1654	1.7922
chr12	133851895	30927892	0.2311	3.3487
chr13	115169878	27054610	0.2349	3.05
chr14	107349540	8817554	0.0821	1.7151
chr15	102531392	7234469	0.0706	1.1546
chr16	90354753	6441369	0.0713	0.8373
chr17	81195210	4292766	0.0529	0.5419
chr18	78077248	7832784	0.1003	1.0092
chr19	59128983	1268678	0.0215	0.2022
chr20	63025520	3915968	0.0621	0.6337
chr21	48129895	2127389	0.0442	0.3746
chr22	51304566	1700003	0.0331	0.6375
chrMT	16571	5111	0.3084	0.5431
chrX	155270560	20059631	0.1292	1.5088
chrY	59373566	206502	0.0035	0.0831

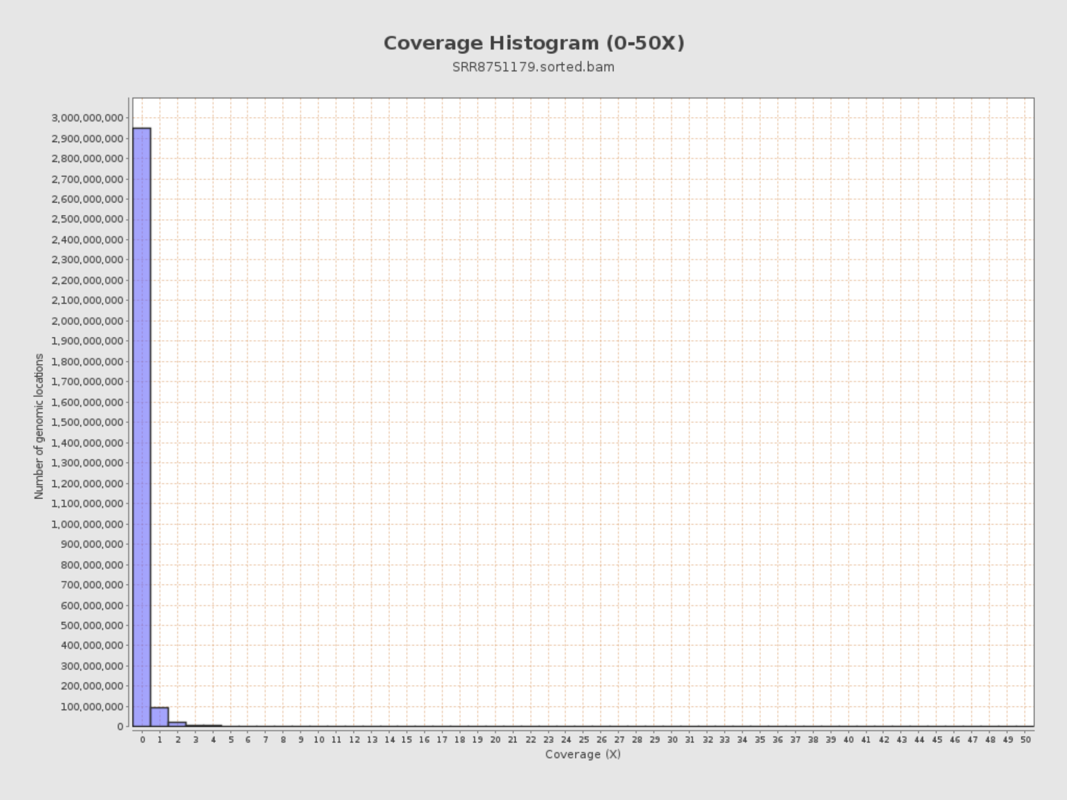
3. Results : Coverage across reference



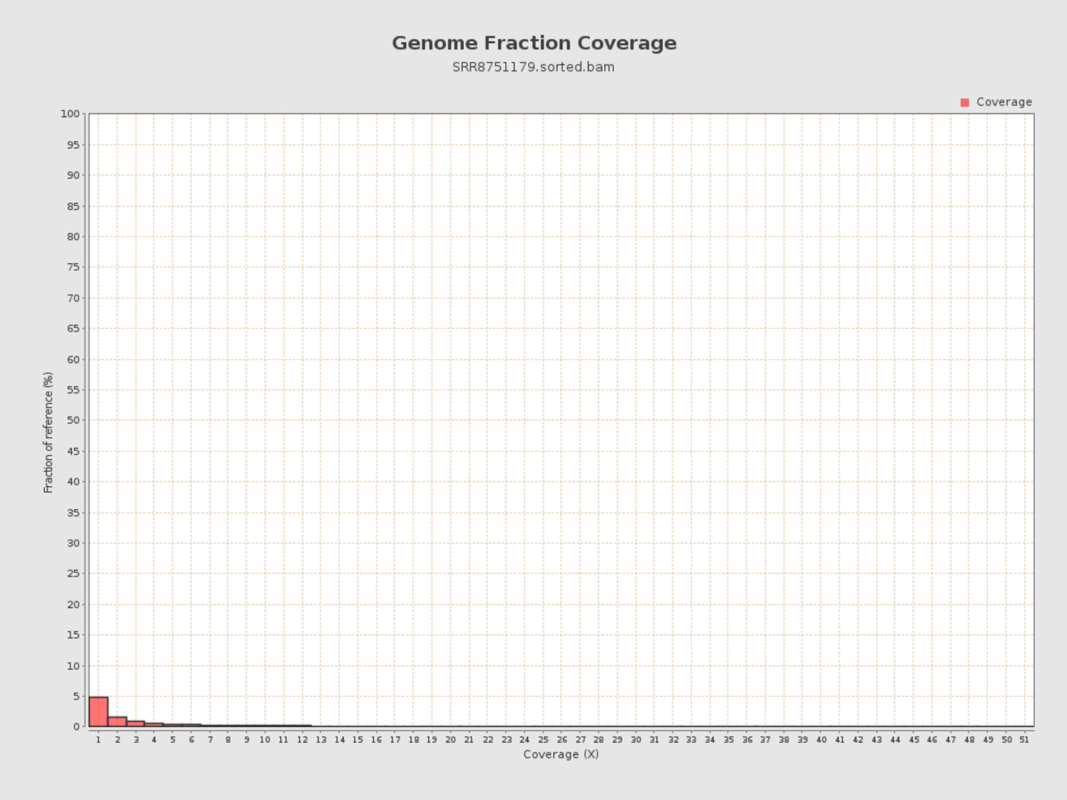
4. Results : Coverage Histogram



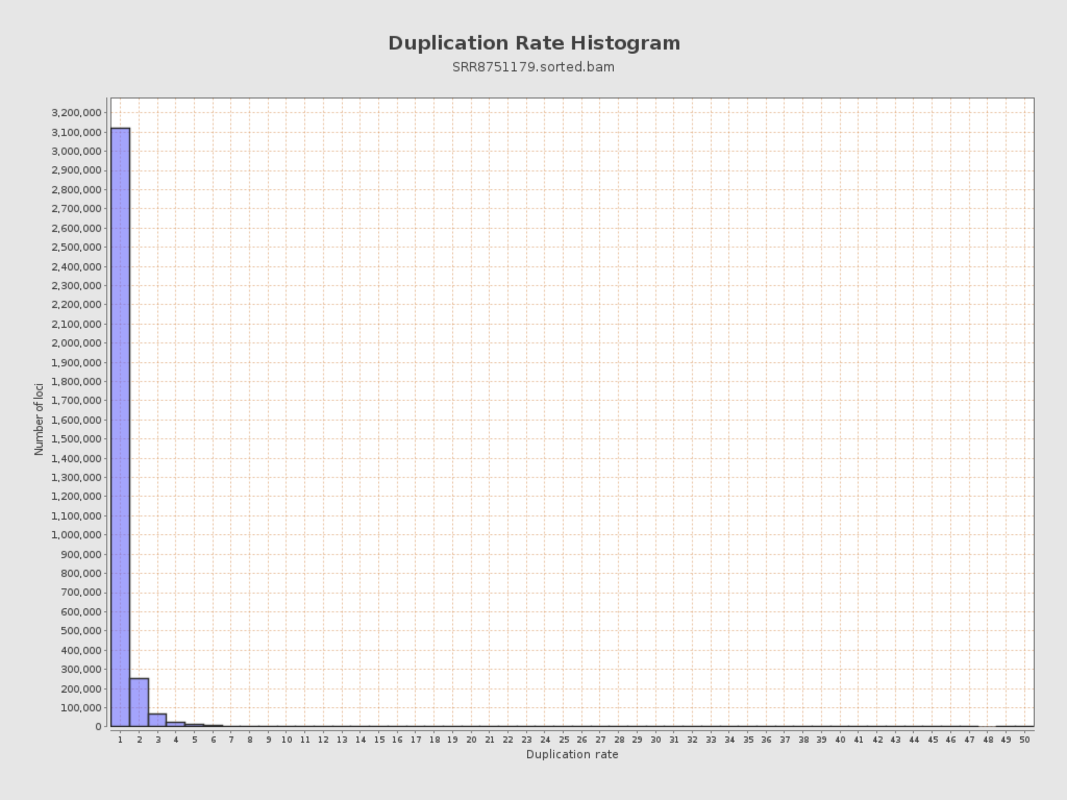
5. Results : Coverage Histogram (0-50X)



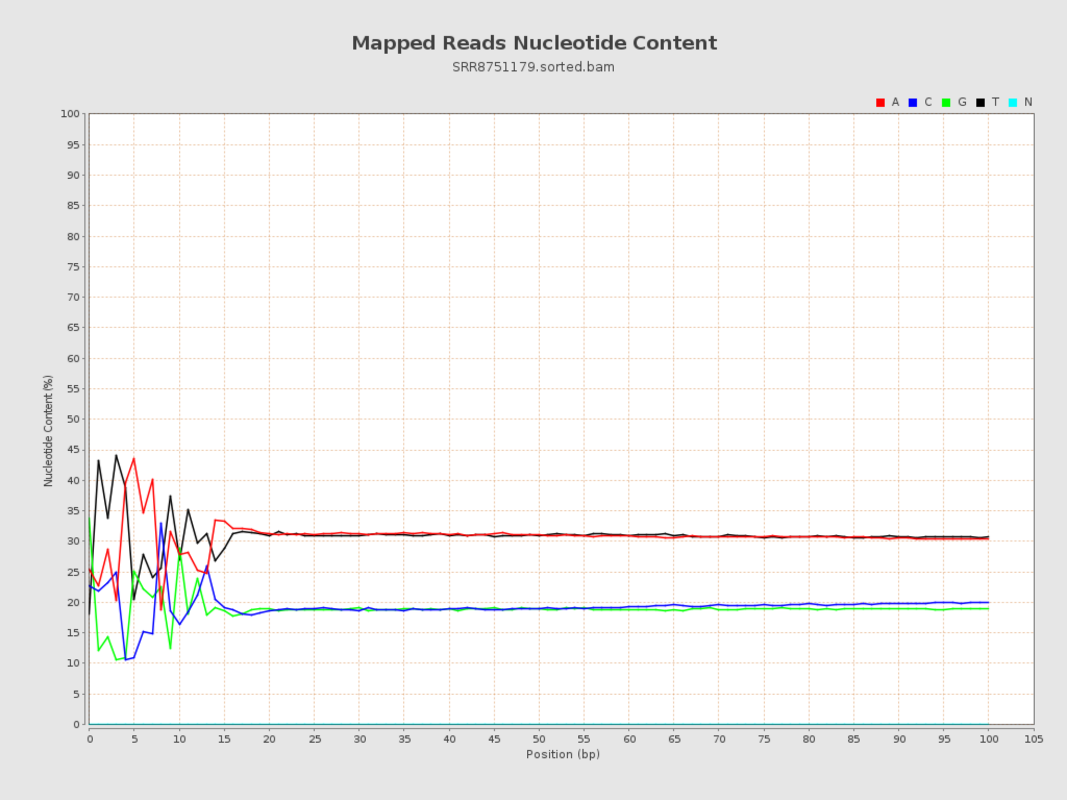
6. Results : Genome Fraction Coverage



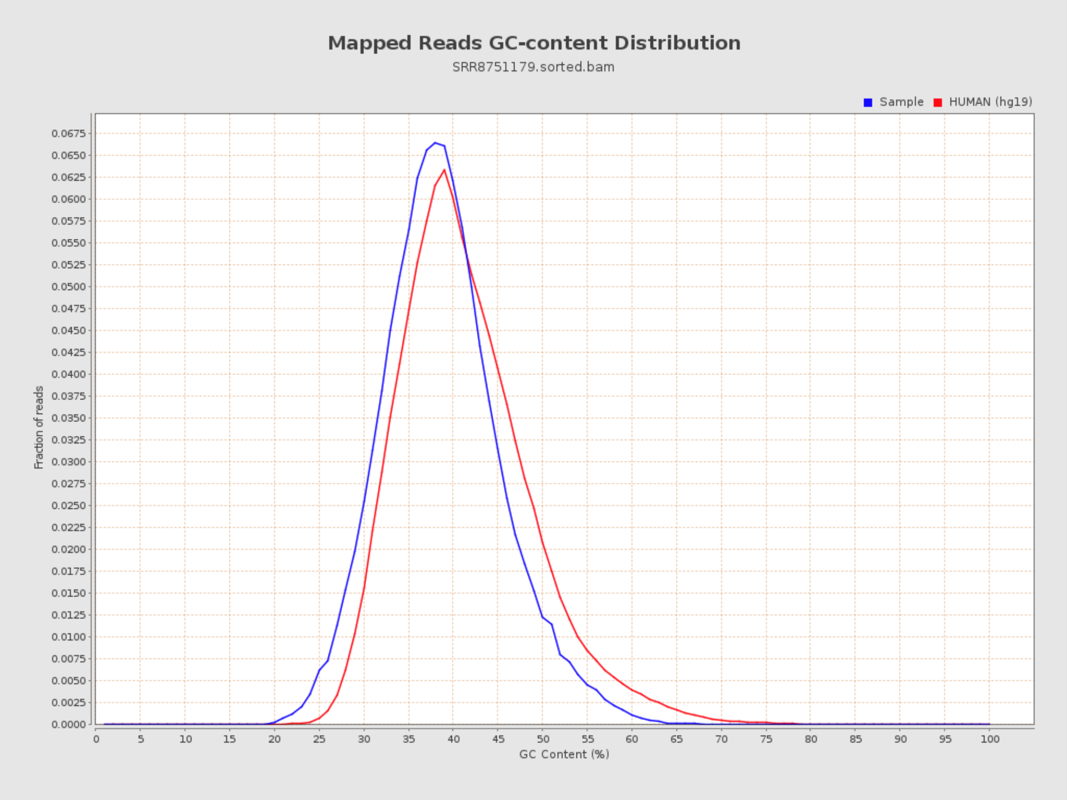
7. Results : Duplication Rate Histogram



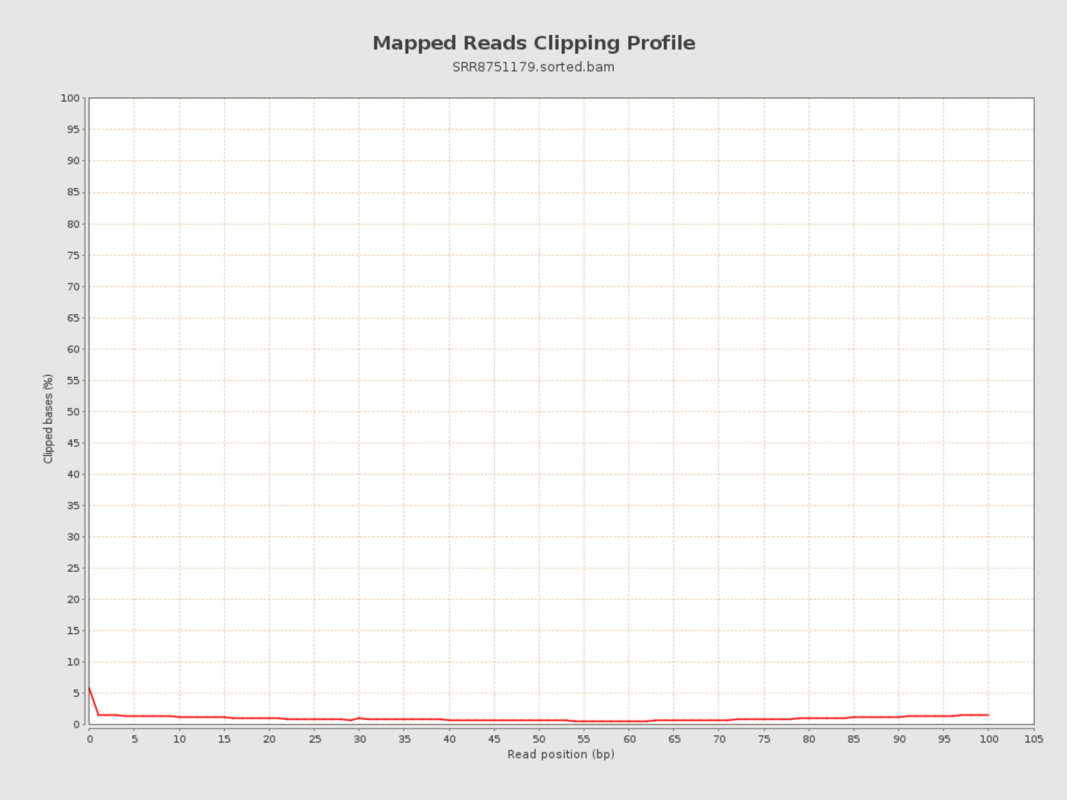
8. Results : Mapped Reads Nucleotide Content



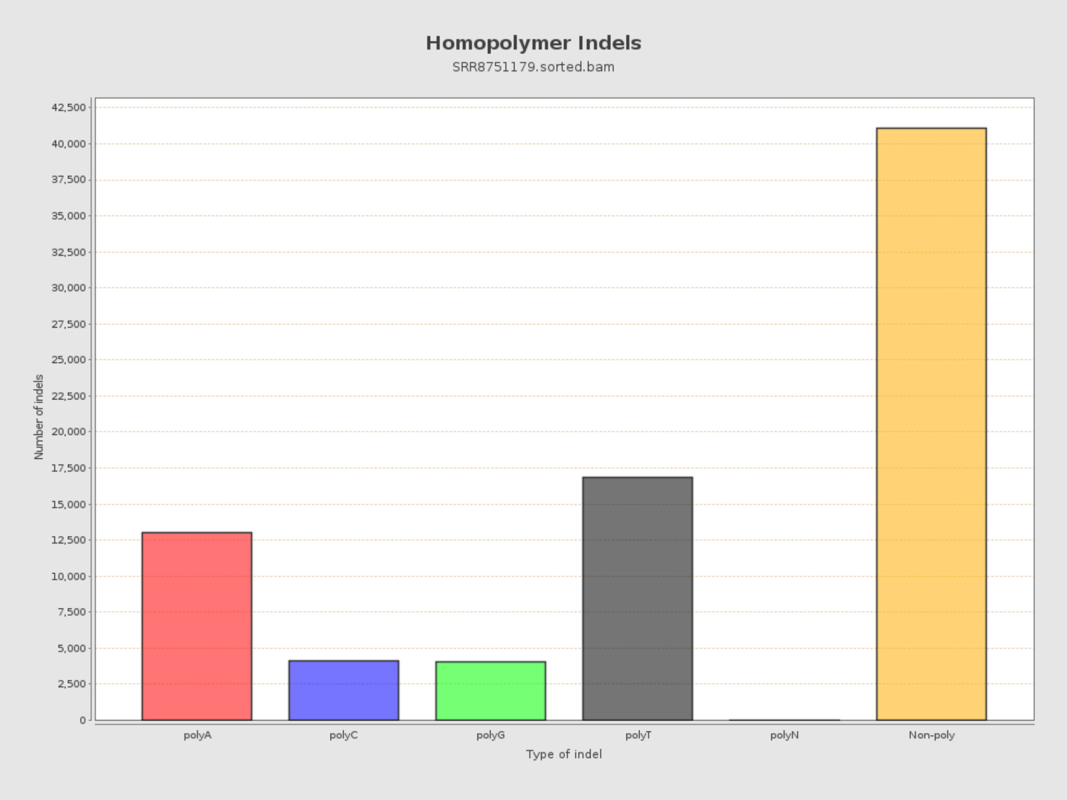
9. Results : Mapped Reads GC-content Distribution



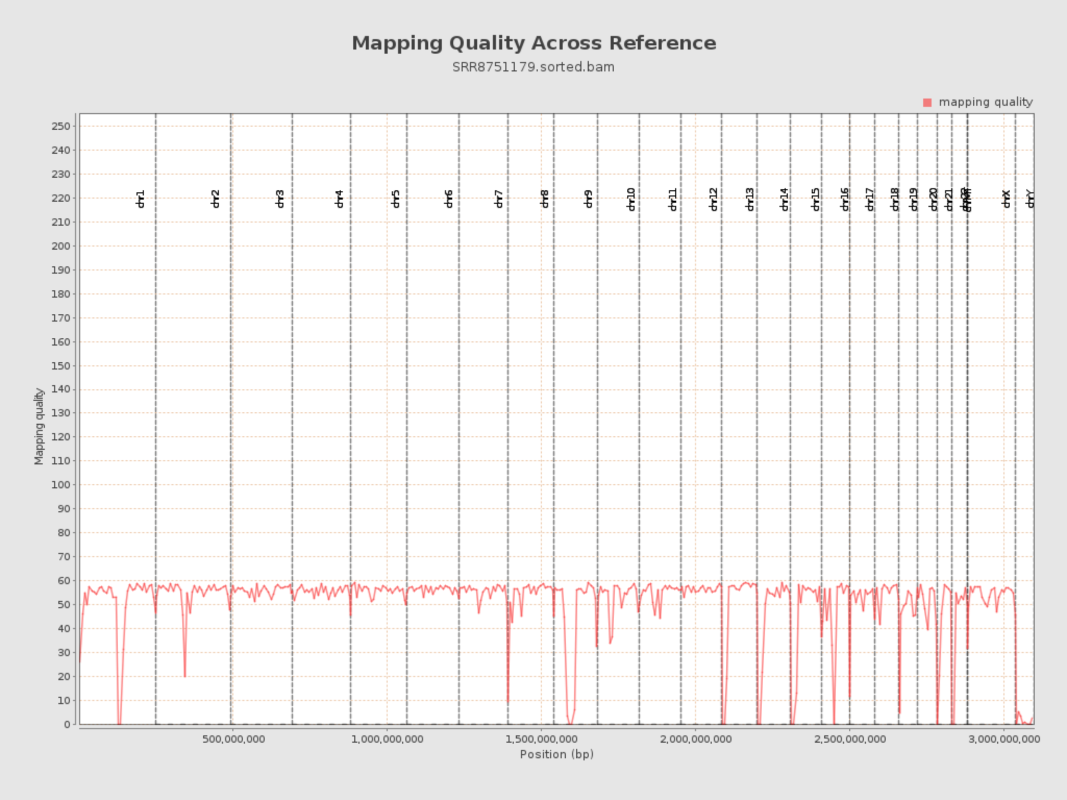
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram