Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:51:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751178.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_SRR8751178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:51:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,862,328
Mapped reads	3,310,338 / 68.08%
Unmapped reads	1,551,990 / 31.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	192,309 / 3.96%
Read min/max/mean length	30 / 101 / 102.63
Duplicated reads (estimated)	127,124 / 2.61%
Duplication rate	1.86%
Clipped reads	796,698 / 16.39%

2.2. ACGT Content

Number/percentage of A's	97,575,216 / 29.95%
Number/percentage of C's	65,263,273 / 20.03%
Number/percentage of T's	97,999,922 / 30.08%
Number/percentage of G's	64,931,280 / 19.93%
Number/percentage of N's	2,337 / 0%
GC Percentage	39.96%

2.3. Coverage

Mean	0.1053

Standard Deviation	1.4389

2.4. Mapping Quality

Mean Mapping Quality	51.03

2.5. Mismatches and indels

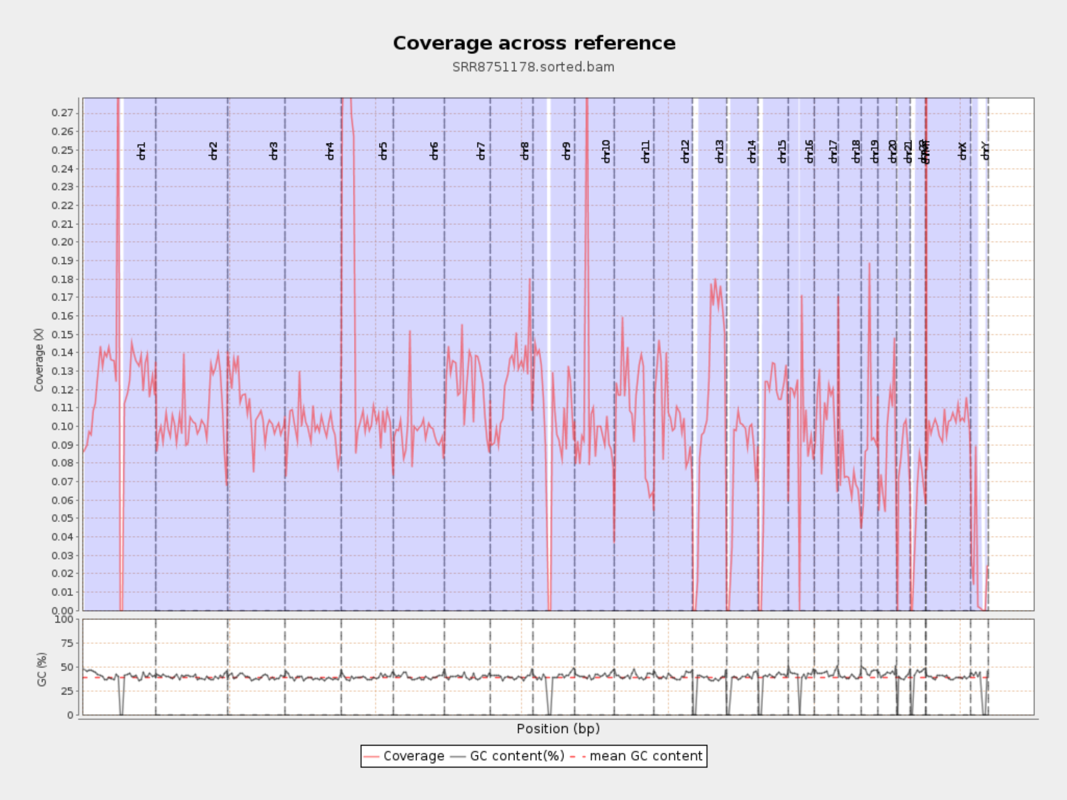
General error rate	0.48%
Mismatches	1,331,698
Insertions	172,997
Mapped reads with at least one insertion	5.05%
Deletions	49,428
Mapped reads with at least one deletion	1.46%
Homopolymer indels	51.6%

2.6. Chromosome stats

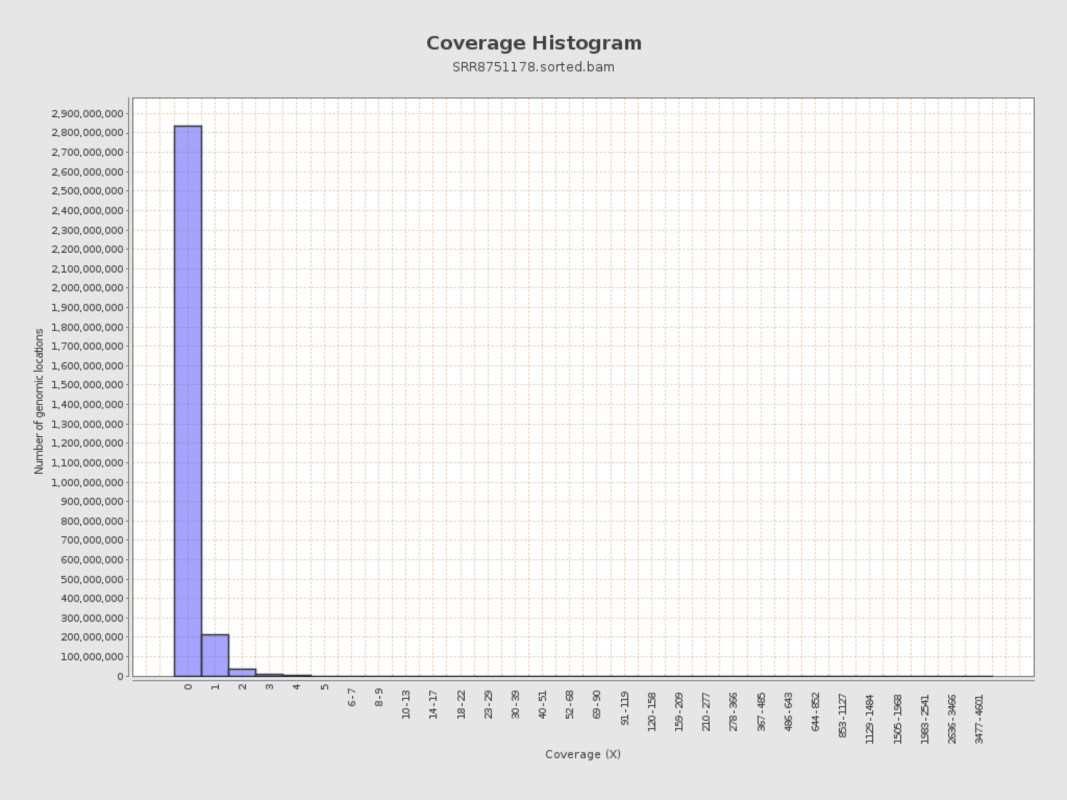
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30669456	0.123	4.1935
chr2	243199373	25471902	0.1047	0.5597
chr3	198022430	21577235	0.109	0.4566
chr4	191154276	19016815	0.0995	0.4431
chr5	180915260	26537198	0.1467	0.4789
chr6	171115067	16755799	0.0979	0.6536
chr7	159138663	19557658	0.1229	0.8358

chr8	146364022	18054410	0.1234	1.0031
chr9	141213431	14299246	0.1013	0.6832
chr10	135534747	14279097	0.1054	1.9313
chr11	135006516	14634655	0.1084	0.5576
chr12	133851895	14285353	0.1067	0.3937
chr13	115169878	13328480	0.1157	0.3958
chr14	107349540	8517373	0.0793	0.3598
chr15	102531392	10295398	0.1004	0.368
chr16	90354753	8945774	0.099	0.7365
chr17	81195210	8604983	0.106	0.5872
chr18	78077248	5933923	0.076	1.5349
chr19	59128983	5756516	0.0974	2.773
chr20	63025520	5741718	0.0911	0.3653
chr21	48129895	3764761	0.0782	0.3794
chr22	51304566	2650219	0.0517	0.2654
chrMT	16571	337454	20.3641	12.5836
chrX	155270560	15706747	0.1012	0.4218
chrY	59373566	1158912	0.0195	0.8739

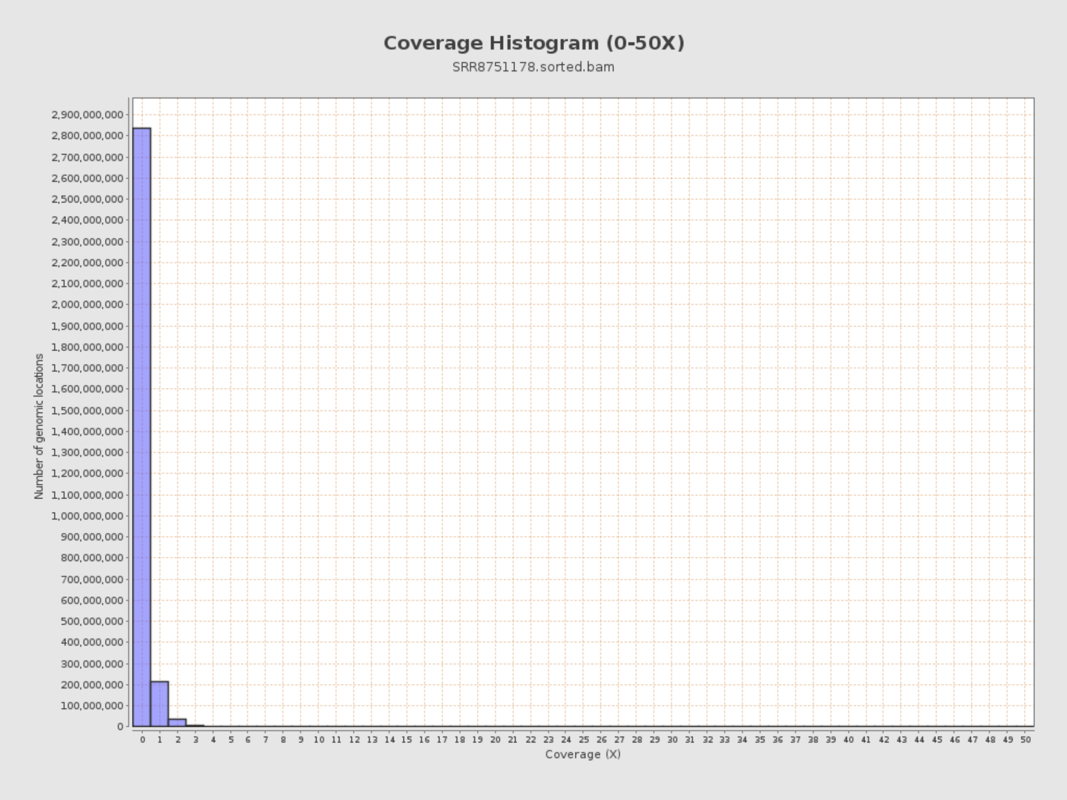
3. Results : Coverage across reference



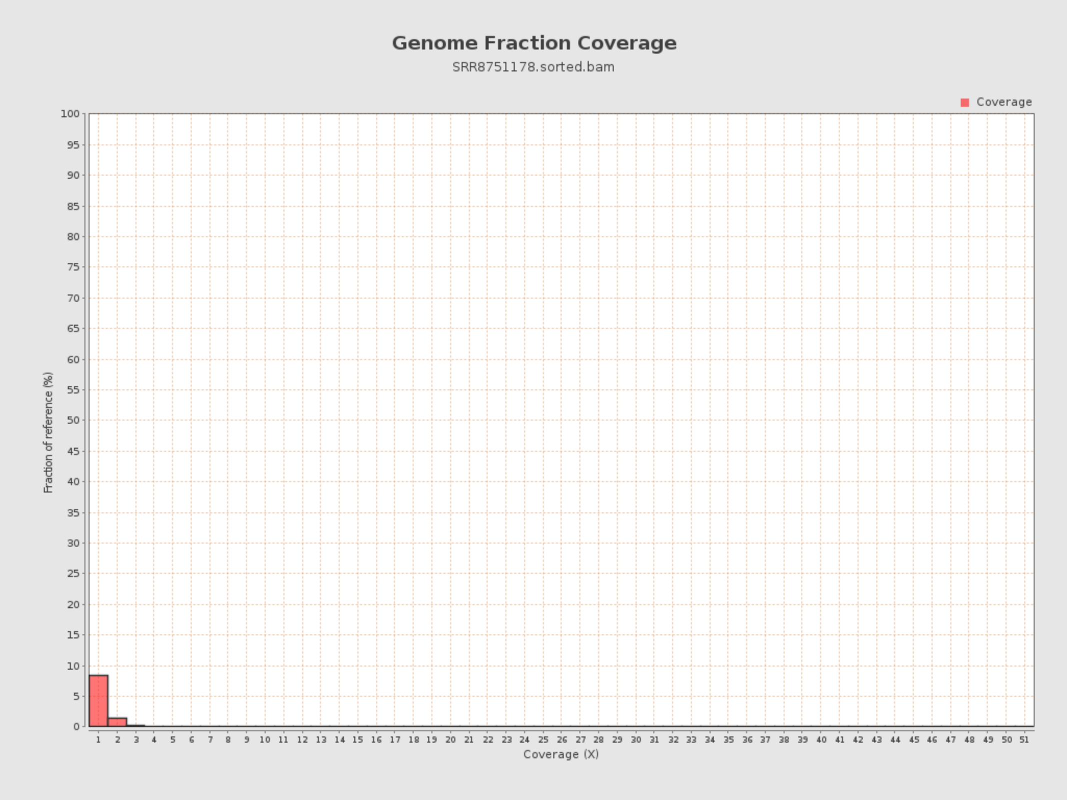
4. Results : Coverage Histogram



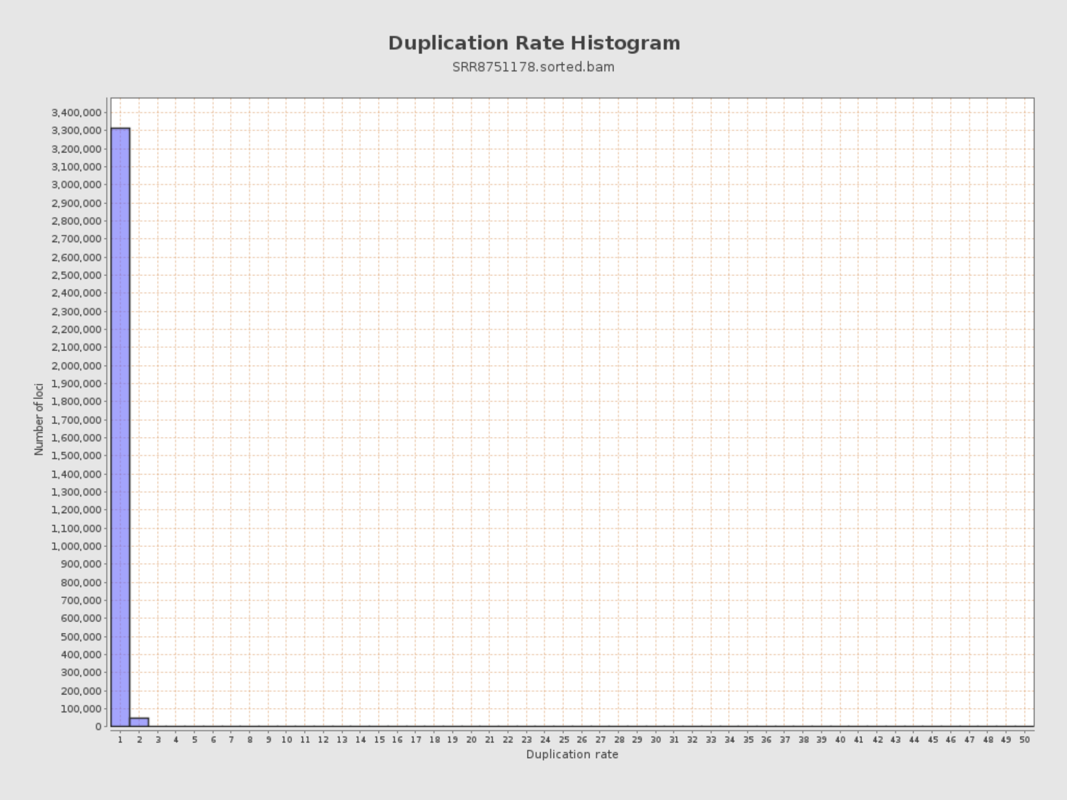
5. Results : Coverage Histogram (0-50X)



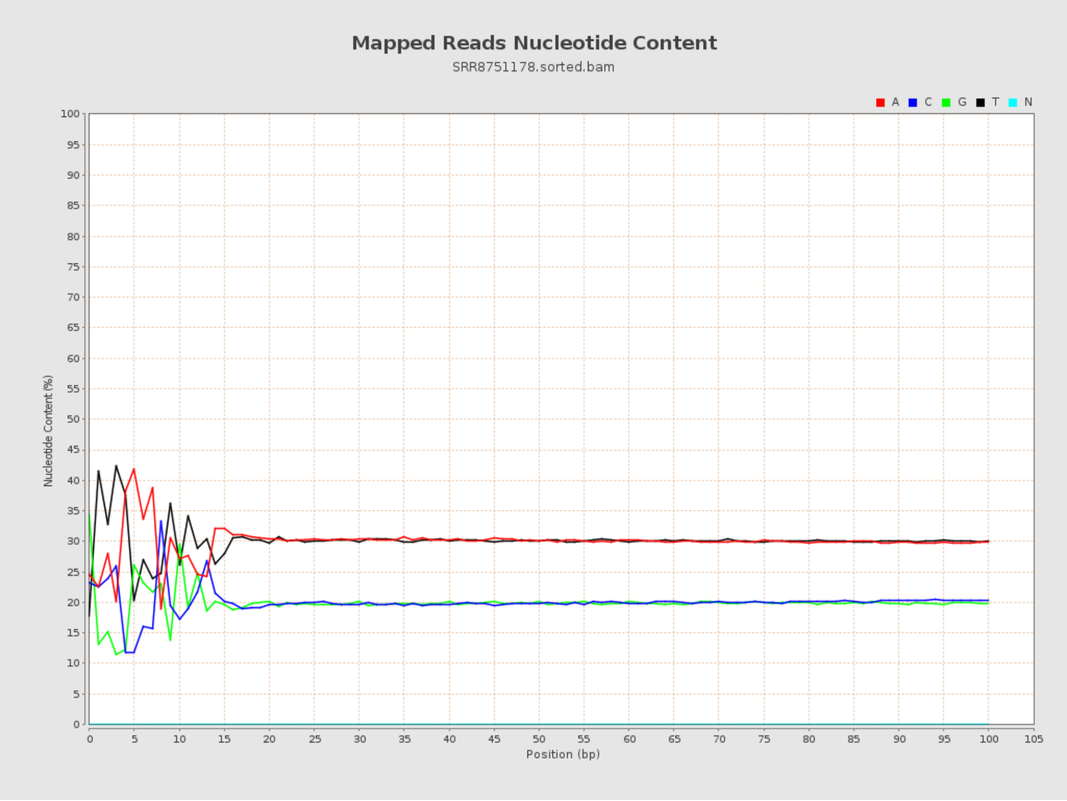
6. Results : Genome Fraction Coverage



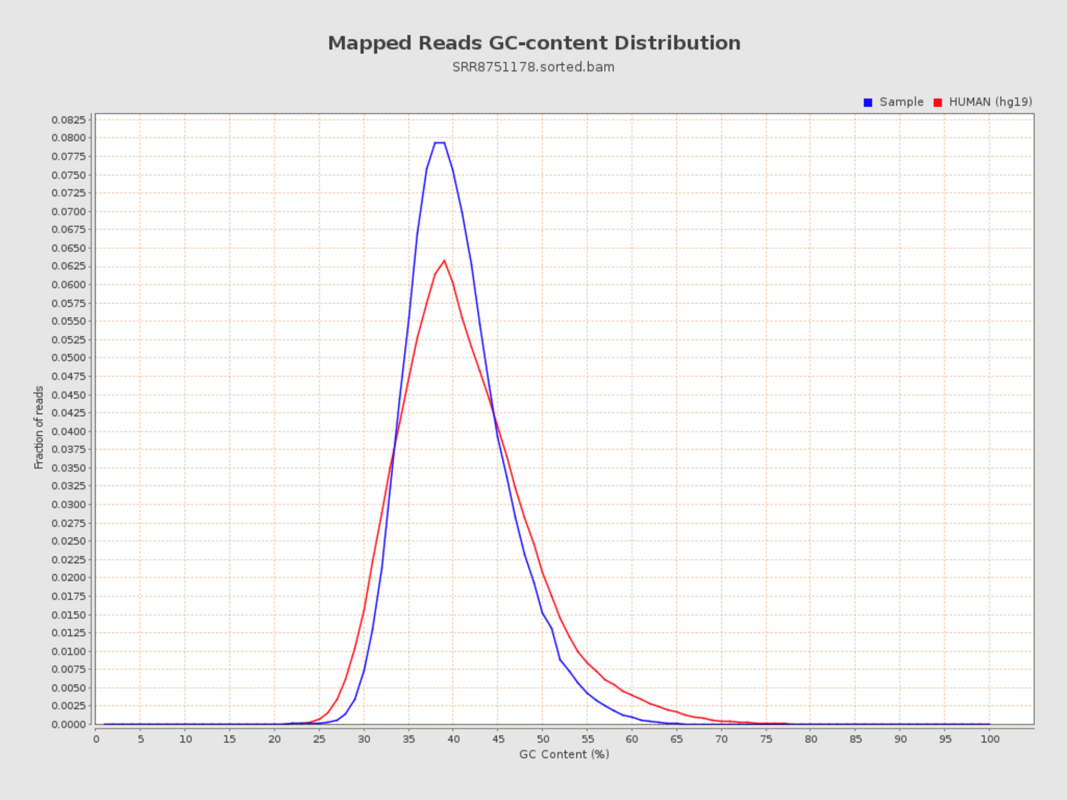
7. Results : Duplication Rate Histogram



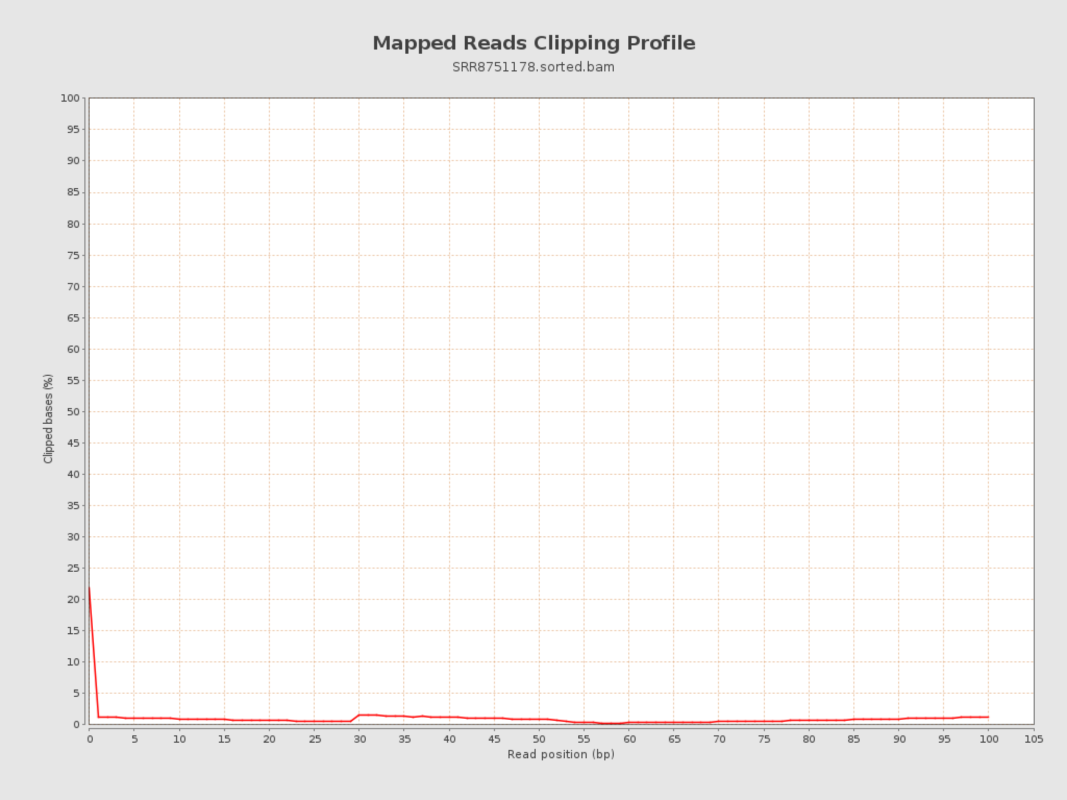
8. Results : Mapped Reads Nucleotide Content



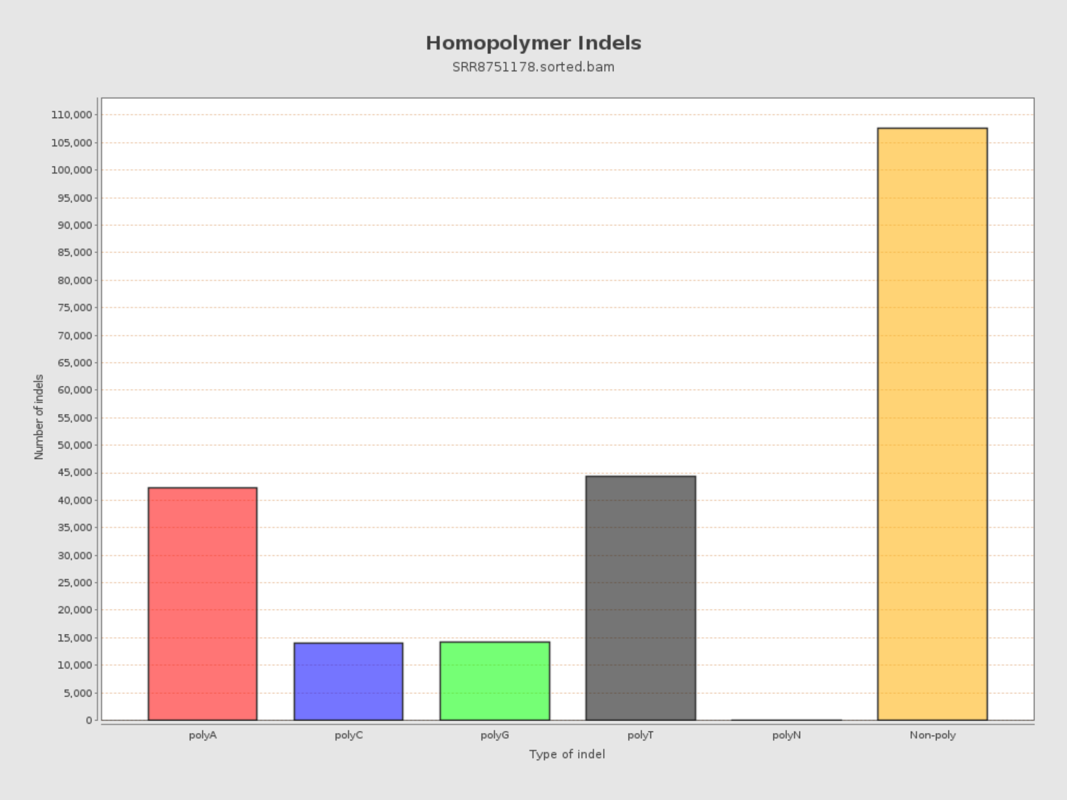
9. Results : Mapped Reads GC-content Distribution



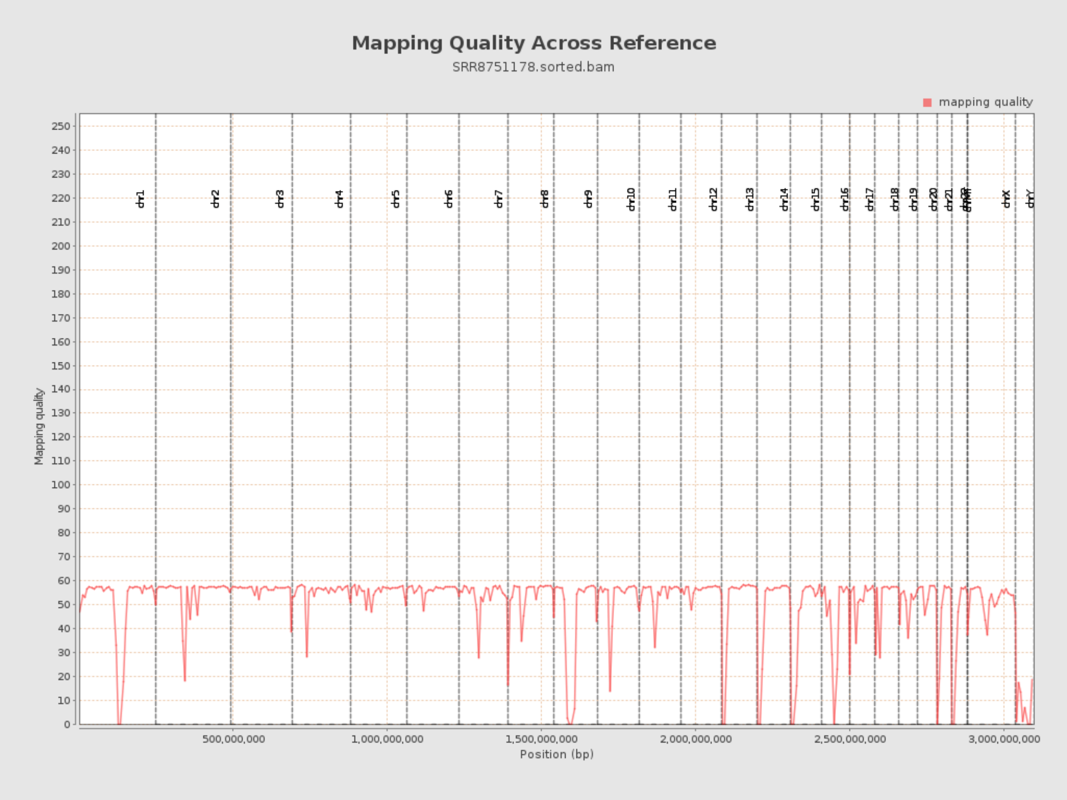
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram