Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:08:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751227.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_SRR8751227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:08:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,684,265
Mapped reads	4,188,570 / 89.42%
Unmapped reads	495,695 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	164,014 / 3.5%
Read min/max/mean length	30 / 101 / 102.45
Duplicated reads (estimated)	141,252 / 3.02%
Duplication rate	1.73%
Clipped reads	853,719 / 18.23%

2.2. ACGT Content

Number/percentage of A's	119,888,616 / 29.14%
Number/percentage of C's	85,840,316 / 20.86%
Number/percentage of T's	120,530,368 / 29.29%
Number/percentage of G's	85,185,415 / 20.7%
Number/percentage of N's	2,222 / 0%
GC Percentage	41.57%

2.3. Coverage

Mean	0.133

Standard Deviation	1.3677

2.4. Mapping Quality

Mean Mapping Quality	51.2

2.5. Mismatches and indels

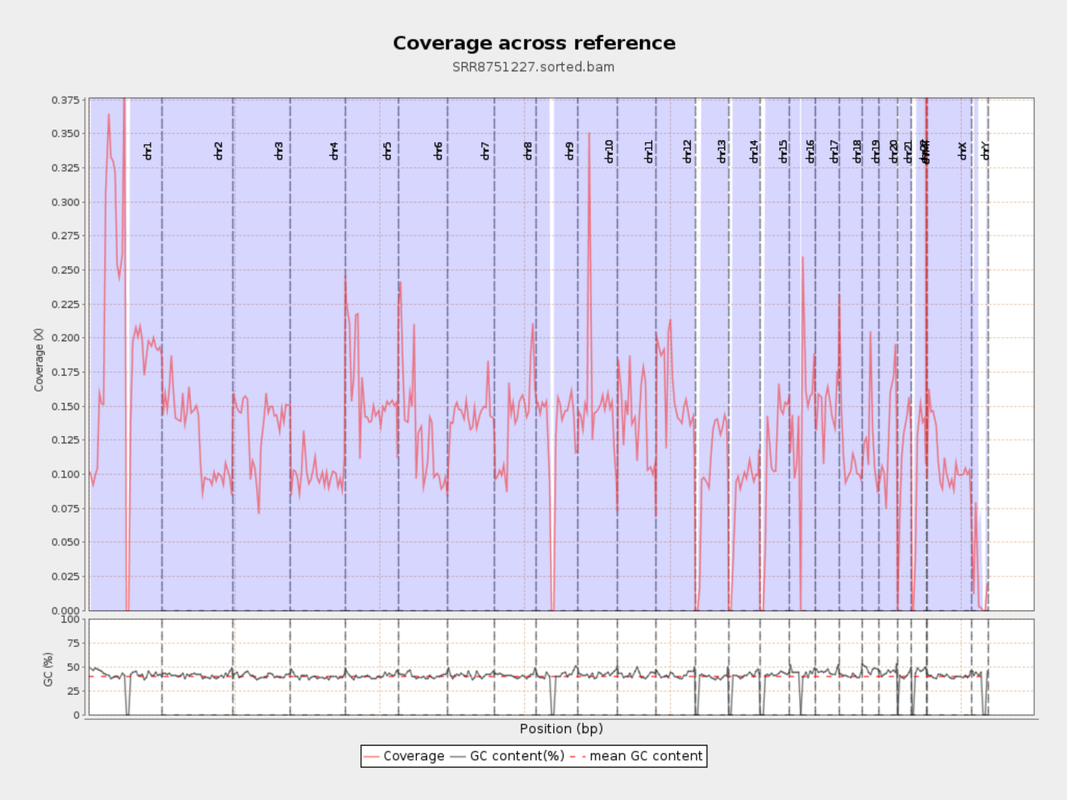
General error rate	0.43%
Mismatches	1,598,161
Insertions	111,955
Mapped reads with at least one insertion	2.61%
Deletions	57,258
Mapped reads with at least one deletion	1.34%
Homopolymer indels	48.59%

2.6. Chromosome stats

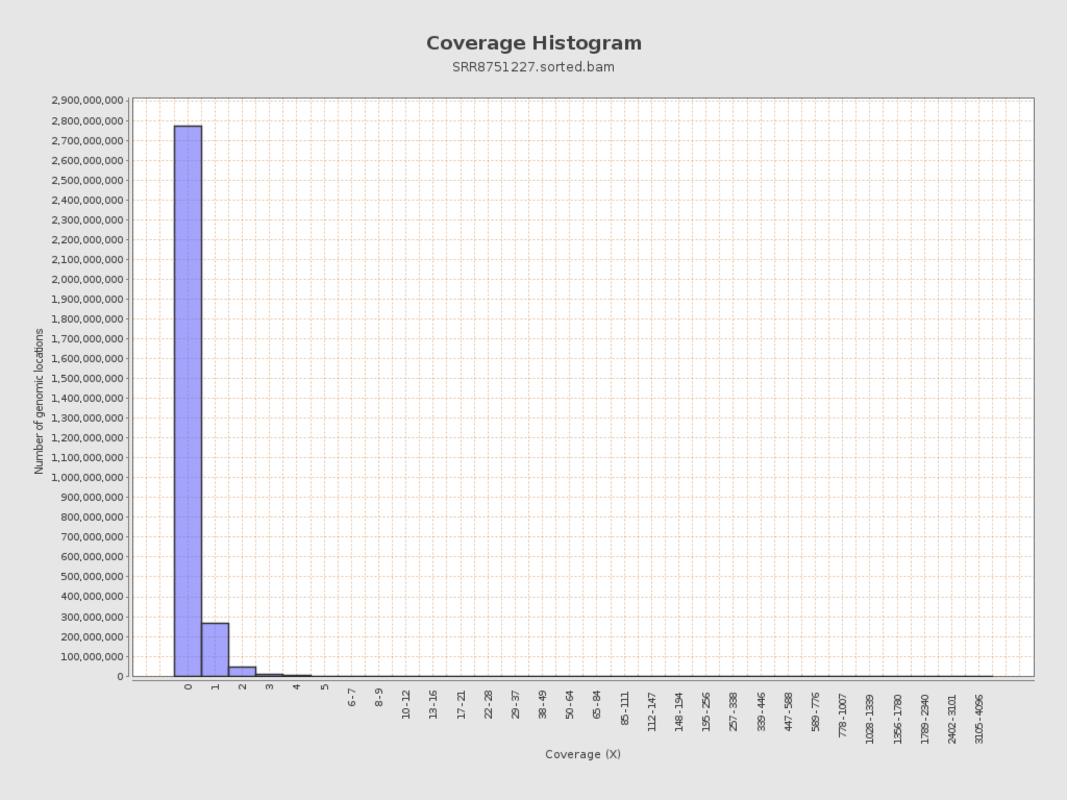
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49601575	0.199	3.8205
chr2	243199373	30760369	0.1265	0.591
chr3	198022430	27076832	0.1367	0.4905
chr4	191154276	18953355	0.0992	0.4842
chr5	180915260	28851562	0.1595	0.4818
chr6	171115067	22700796	0.1327	0.825
chr7	159138663	23030368	0.1447	0.7647

chr8	146364022	20377044	0.1392	0.5356
chr9	141213431	18024737	0.1276	0.6446
chr10	135534747	21007309	0.155	1.9307
chr11	135006516	18895983	0.14	0.7543
chr12	133851895	21735003	0.1624	0.4927
chr13	115169878	11577853	0.1005	0.3702
chr14	107349540	8750560	0.0815	0.3564
chr15	102531392	11163345	0.1089	0.3846
chr16	90354753	12722889	0.1408	1.0284
chr17	81195210	12117587	0.1492	0.6611
chr18	78077248	8890961	0.1139	1.317
chr19	59128983	7356556	0.1244	2.6848
chr20	63025520	8166626	0.1296	0.4395
chr21	48129895	5383942	0.1119	0.448
chr22	51304566	4831922	0.0942	0.3624
chrMT	16571	1587160	95.7794	38.0556
chrX	155270560	16941575	0.1091	0.4633
chrY	59373566	1068181	0.018	0.7203

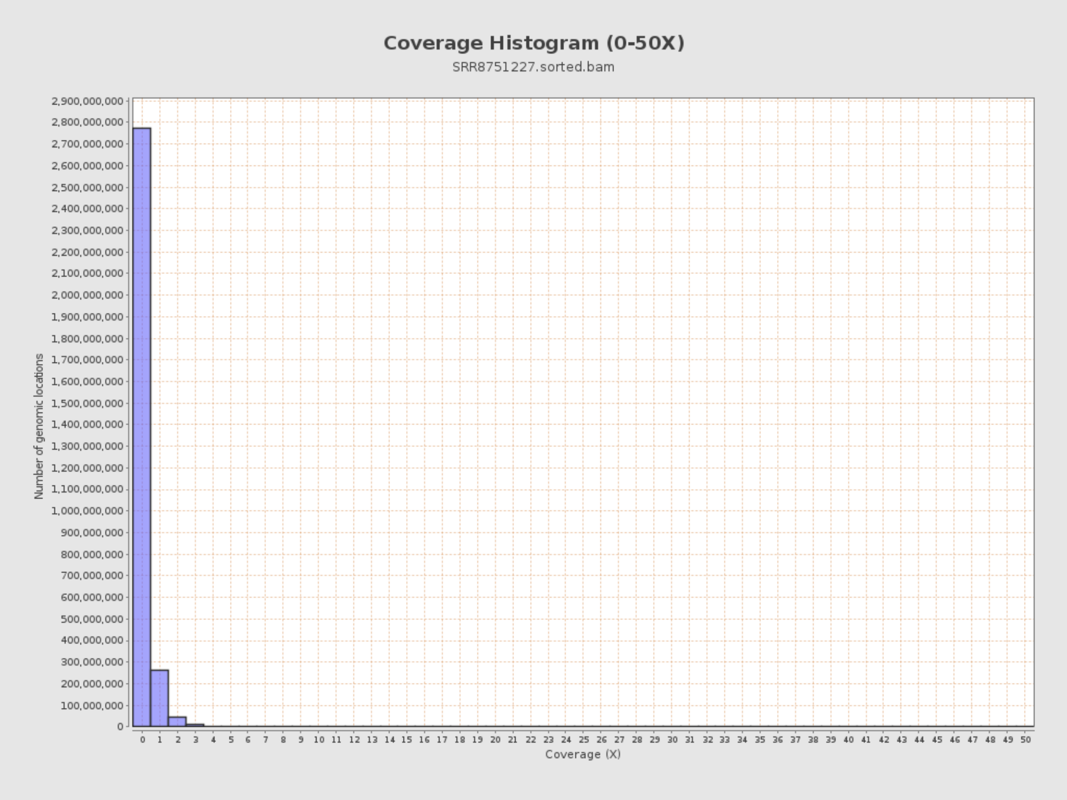
3. Results : Coverage across reference



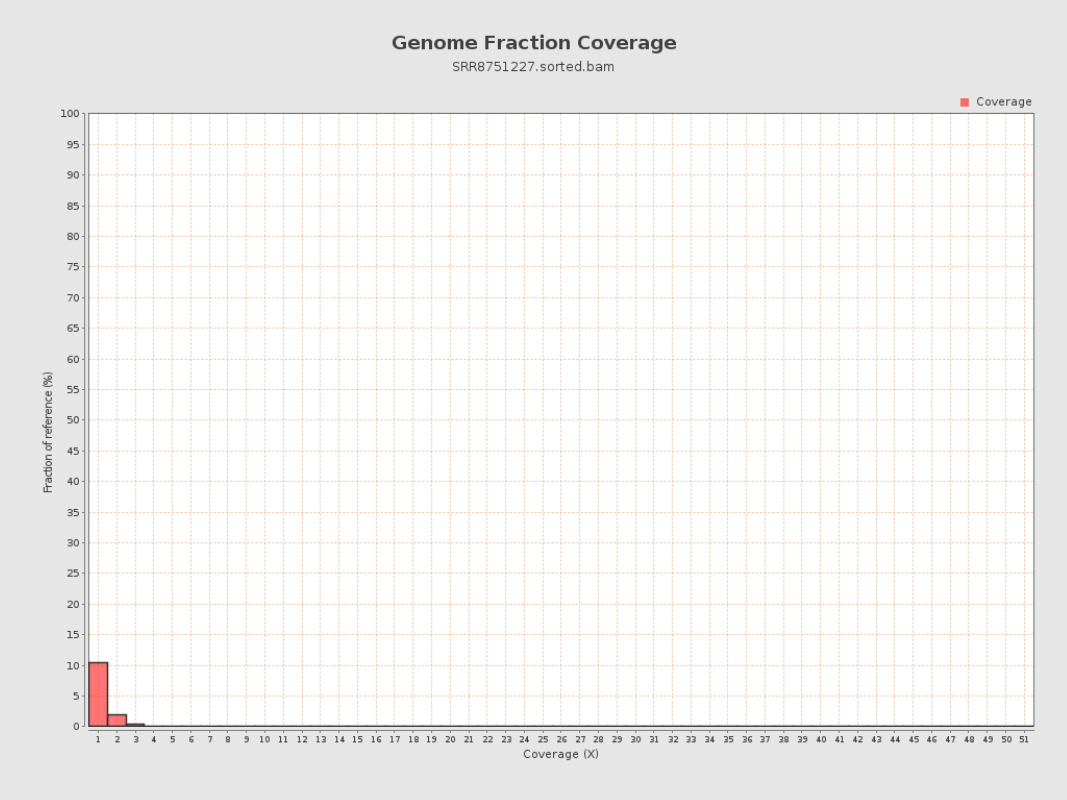
4. Results : Coverage Histogram



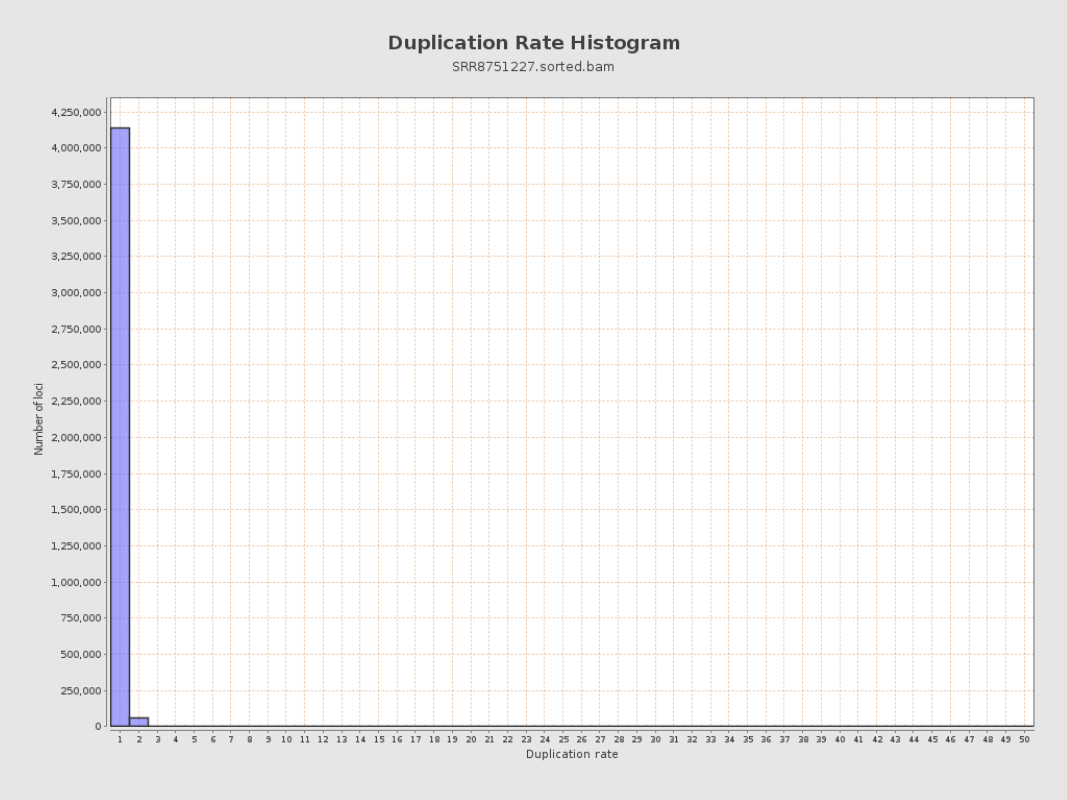
5. Results : Coverage Histogram (0-50X)



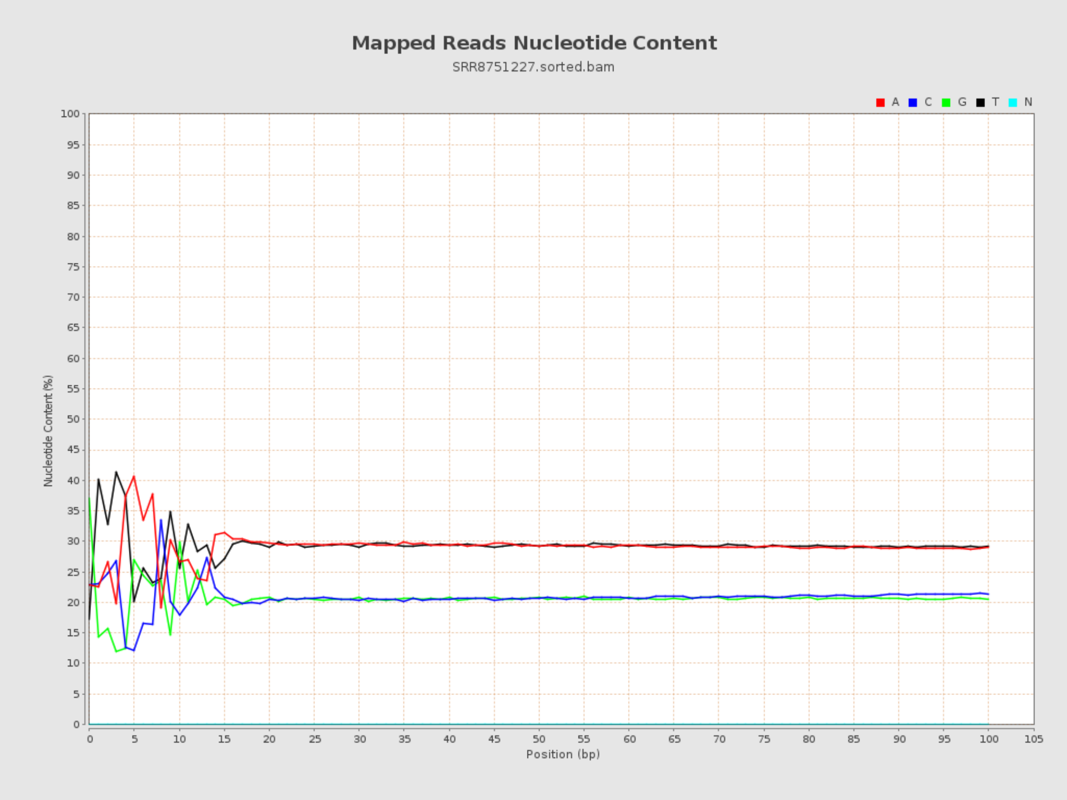
6. Results : Genome Fraction Coverage



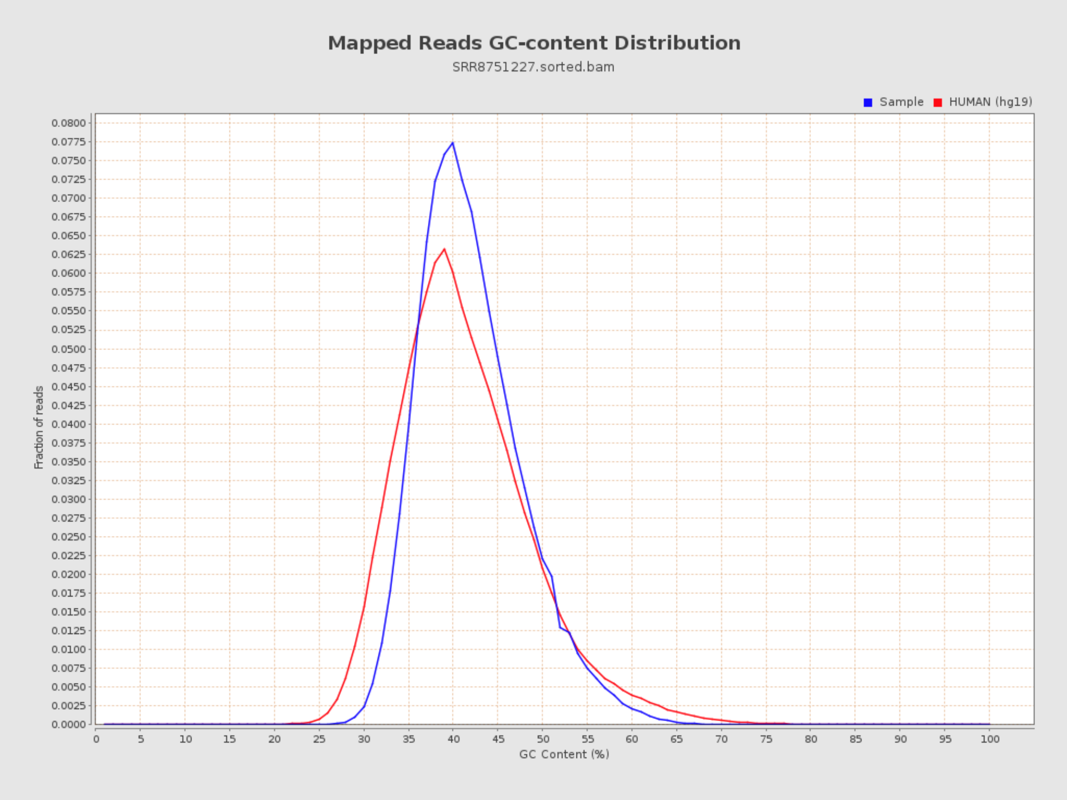
7. Results : Duplication Rate Histogram



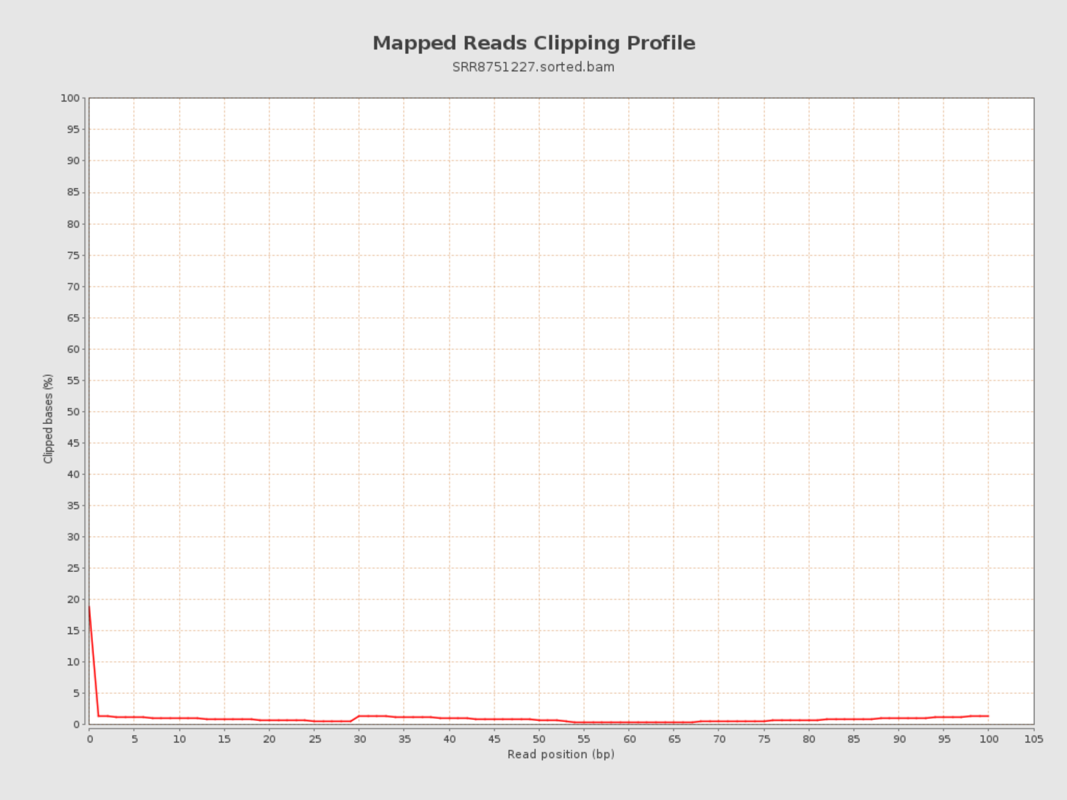
8. Results : Mapped Reads Nucleotide Content



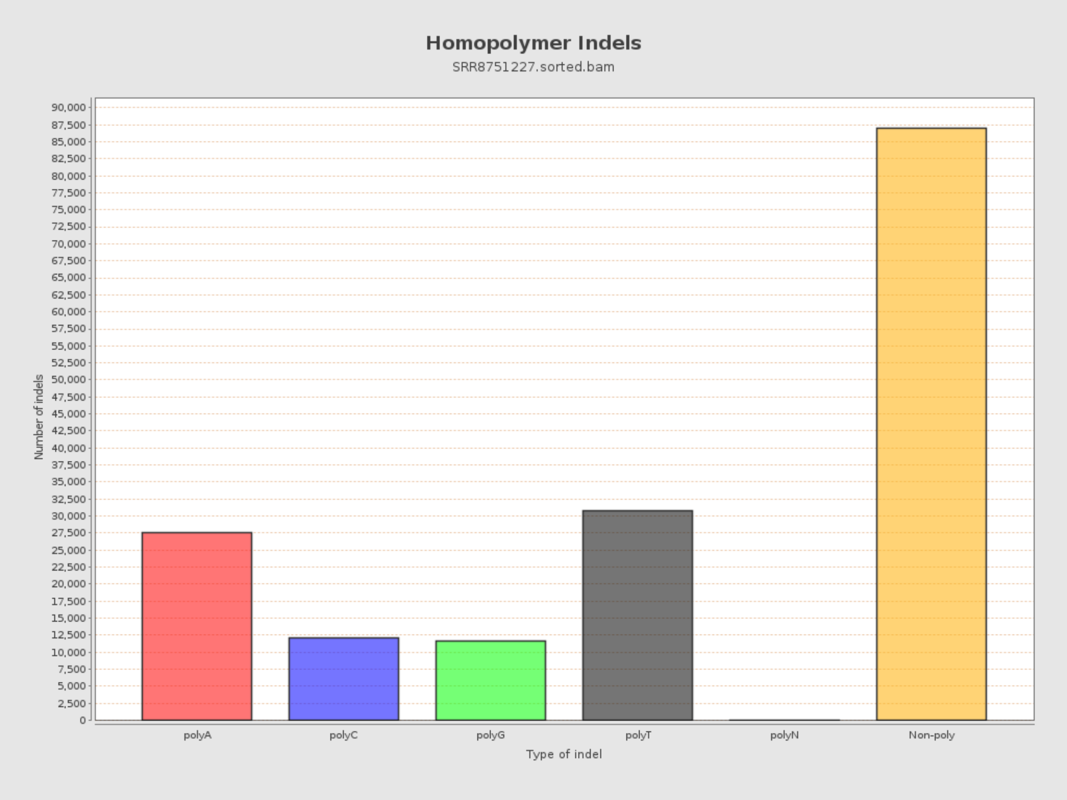
9. Results : Mapped Reads GC-content Distribution



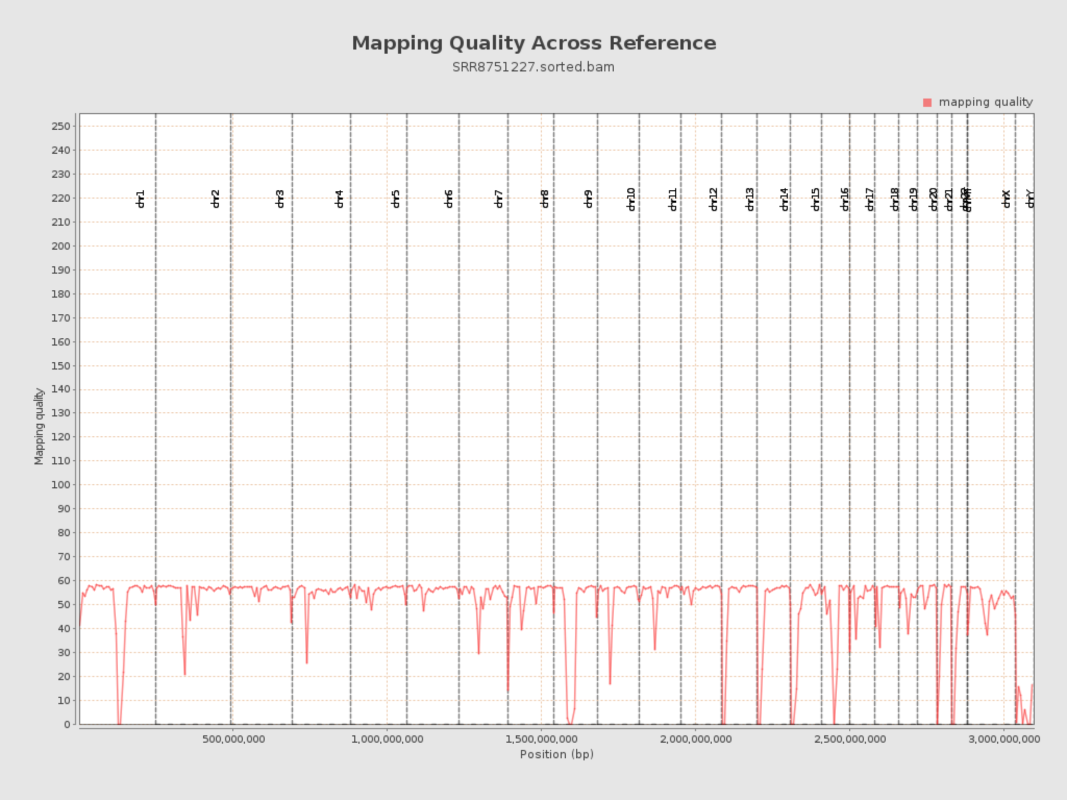
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram