Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 14:45:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751169.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_SRR8751169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 14:45:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,446,748
Mapped reads	4,233,450 / 95.2%
Unmapped reads	213,298 / 4.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	212,615 / 4.78%
Read min/max/mean length	30 / 101 / 102.97
Duplicated reads (estimated)	141,266 / 3.18%
Duplication rate	1.57%
Clipped reads	971,065 / 21.84%

2.2. ACGT Content

Number/percentage of A's	122,698,854 / 29.53%
Number/percentage of C's	84,841,793 / 20.42%
Number/percentage of T's	123,454,964 / 29.71%
Number/percentage of G's	84,565,247 / 20.35%
Number/percentage of N's	2,258 / 0%
GC Percentage	40.77%

2.3. Coverage

Mean	0.1343

Standard Deviation	1.4567

2.4. Mapping Quality

Mean Mapping Quality	50.99

2.5. Mismatches and indels

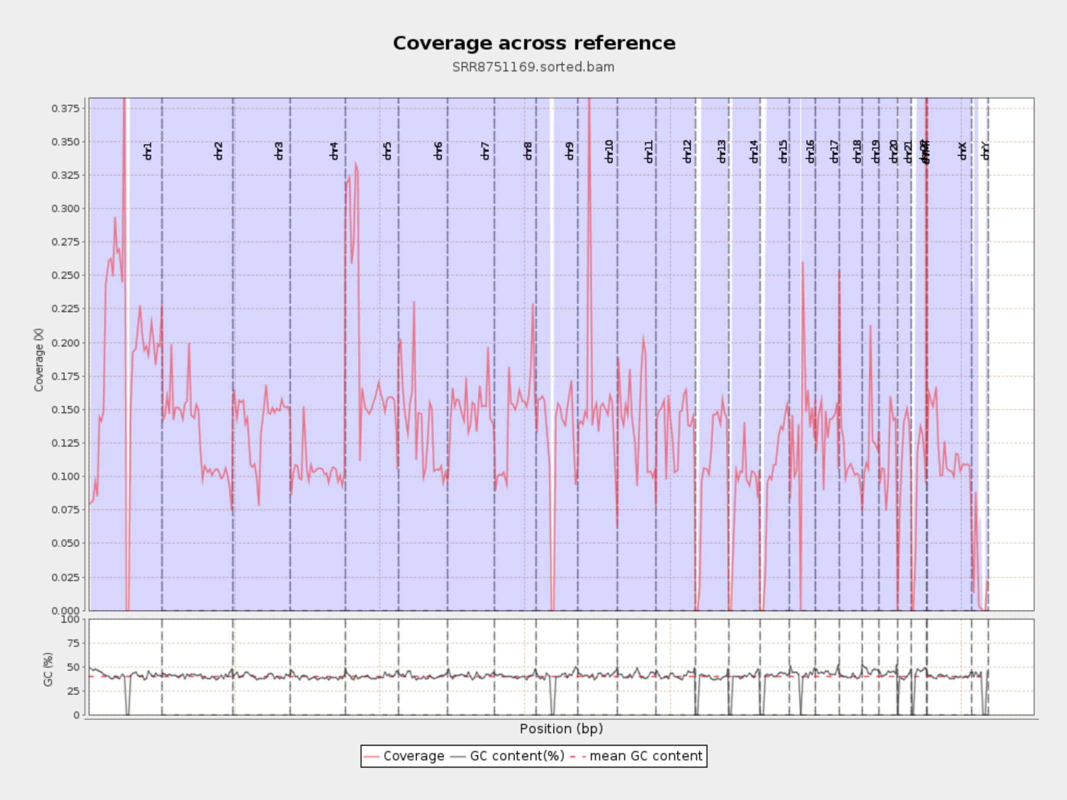
General error rate	0.54%
Mismatches	1,735,980
Insertions	377,940
Mapped reads with at least one insertion	8.49%
Deletions	66,028
Mapped reads with at least one deletion	1.53%
Homopolymer indels	54.04%

2.6. Chromosome stats

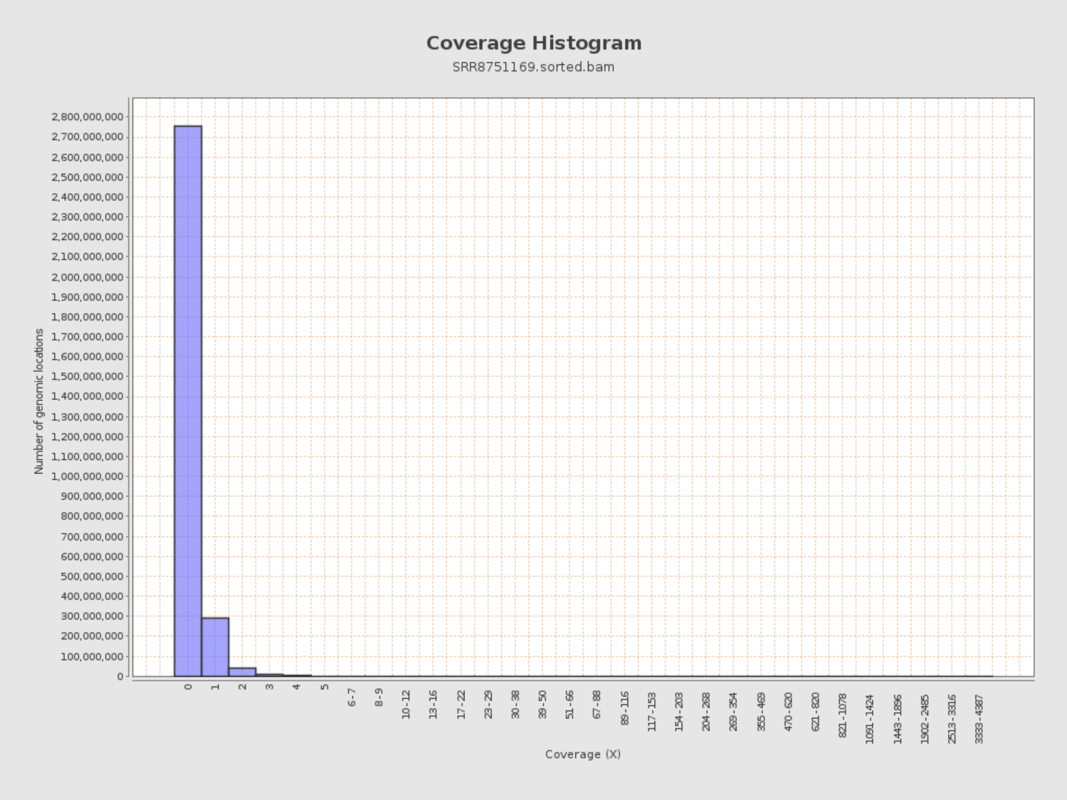
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47297680	0.1898	4.0614
chr2	243199373	31713262	0.1304	0.6509
chr3	198022430	27955224	0.1412	0.5163
chr4	191154276	19880692	0.104	0.5201
chr5	180915260	34711004	0.1919	0.502
chr6	171115067	23514418	0.1374	0.9323
chr7	159138663	24107240	0.1515	0.9247

chr8	146364022	21068039	0.1439	0.5833
chr9	141213431	18177374	0.1287	0.7502
chr10	135534747	21463461	0.1584	2.2809
chr11	135006516	19072697	0.1413	0.7522
chr12	133851895	18661264	0.1394	0.431
chr13	115169878	12350663	0.1072	0.3642
chr14	107349540	9190858	0.0856	0.4626
chr15	102531392	10008264	0.0976	0.3501
chr16	90354753	11914579	0.1319	1.0324
chr17	81195210	11049749	0.1361	0.6767
chr18	78077248	8972568	0.1149	1.6025
chr19	59128983	7480610	0.1265	2.8285
chr20	63025520	7248035	0.115	0.4057
chr21	48129895	5280898	0.1097	0.4677
chr22	51304566	4367922	0.0851	0.3298
chrMT	16571	554784	33.4792	13.3679
chrX	155270560	18484522	0.119	0.4677
chrY	59373566	1180638	0.0199	0.8295

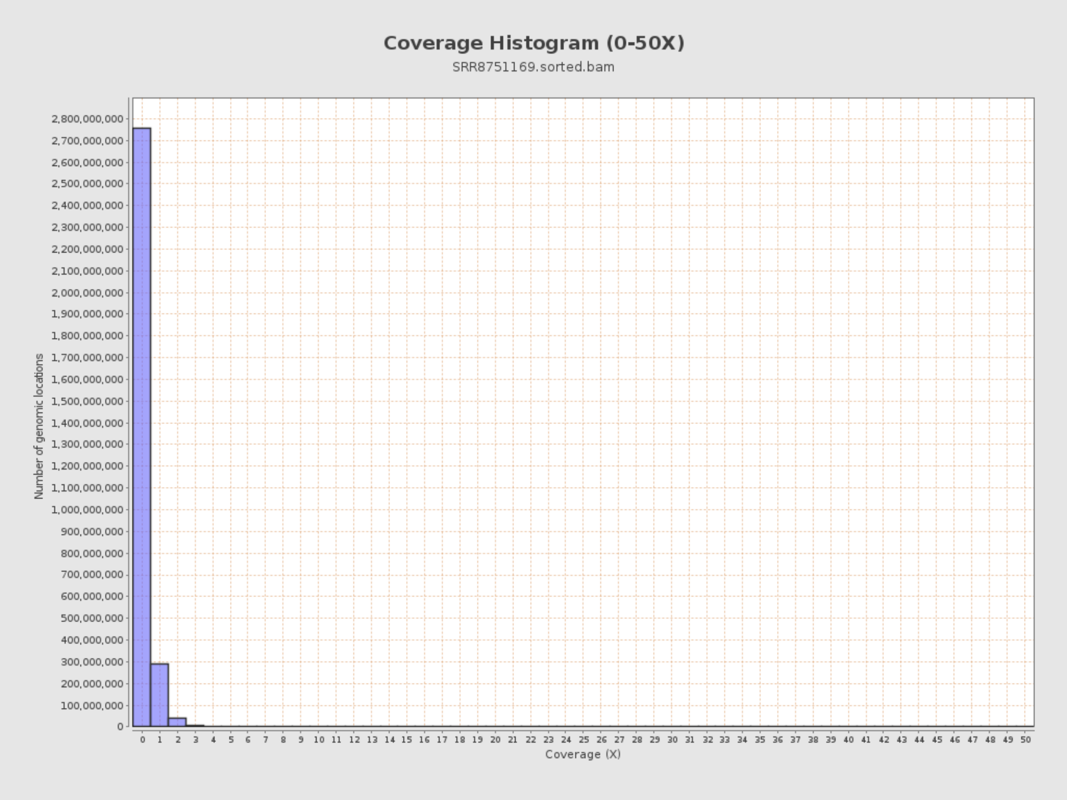
3. Results : Coverage across reference



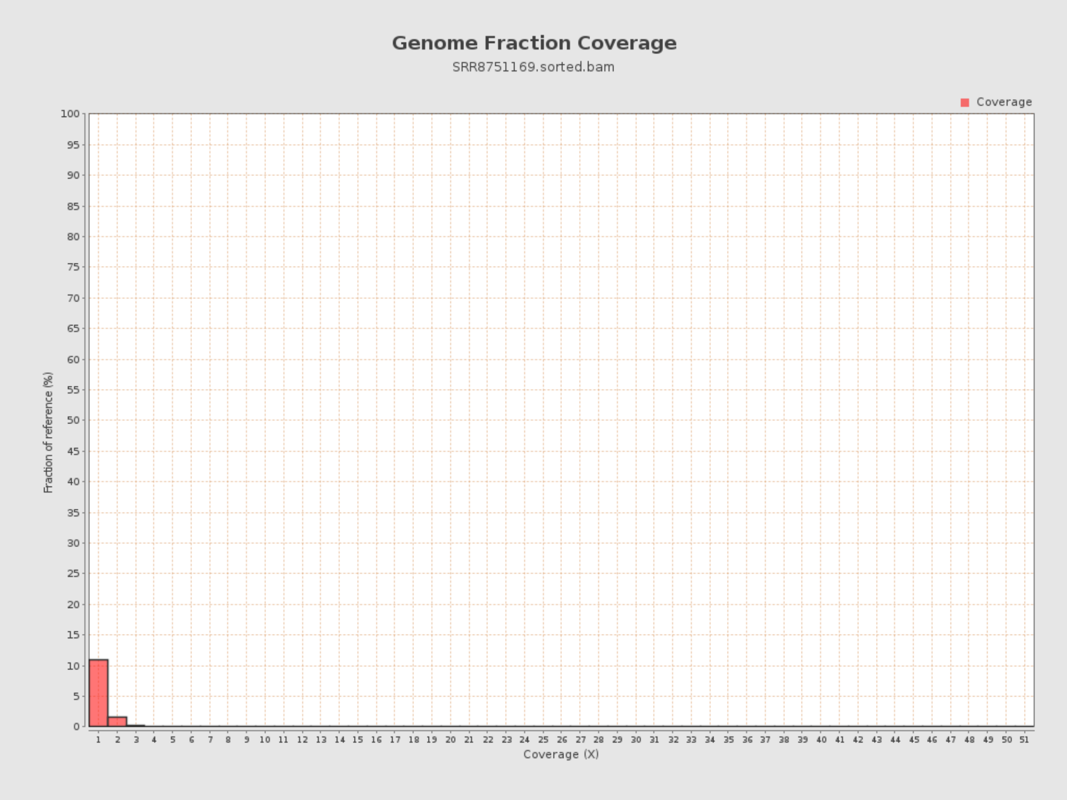
4. Results : Coverage Histogram



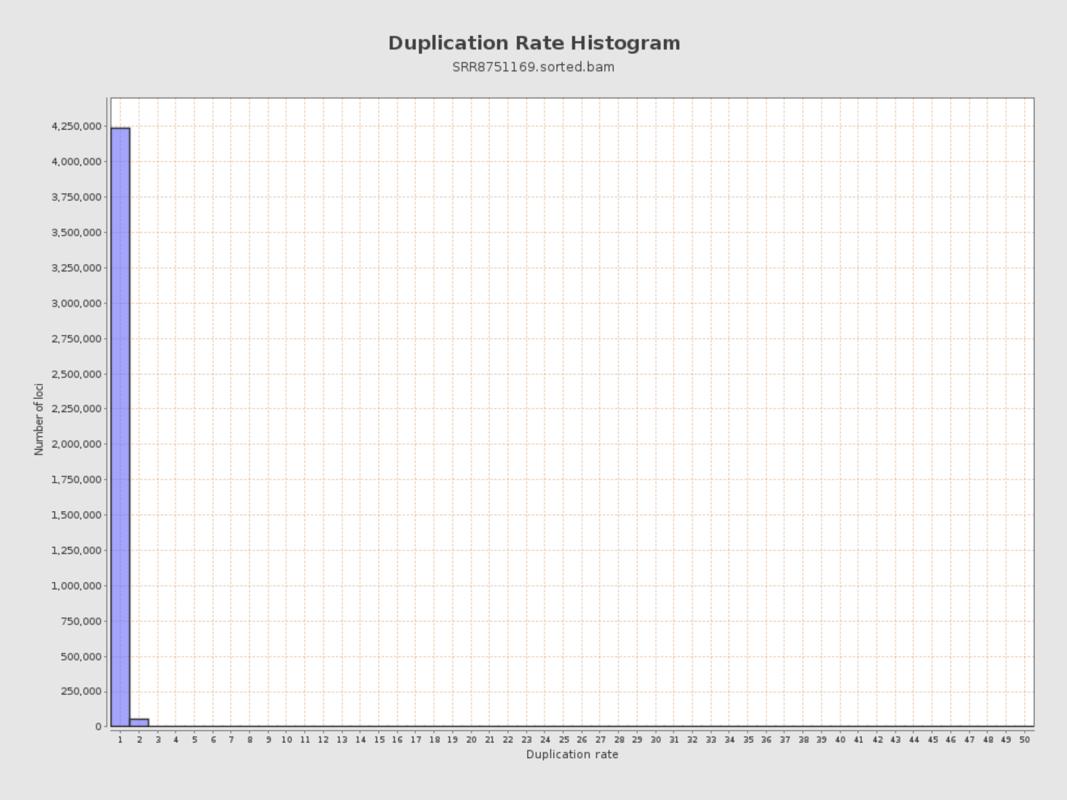
5. Results : Coverage Histogram (0-50X)



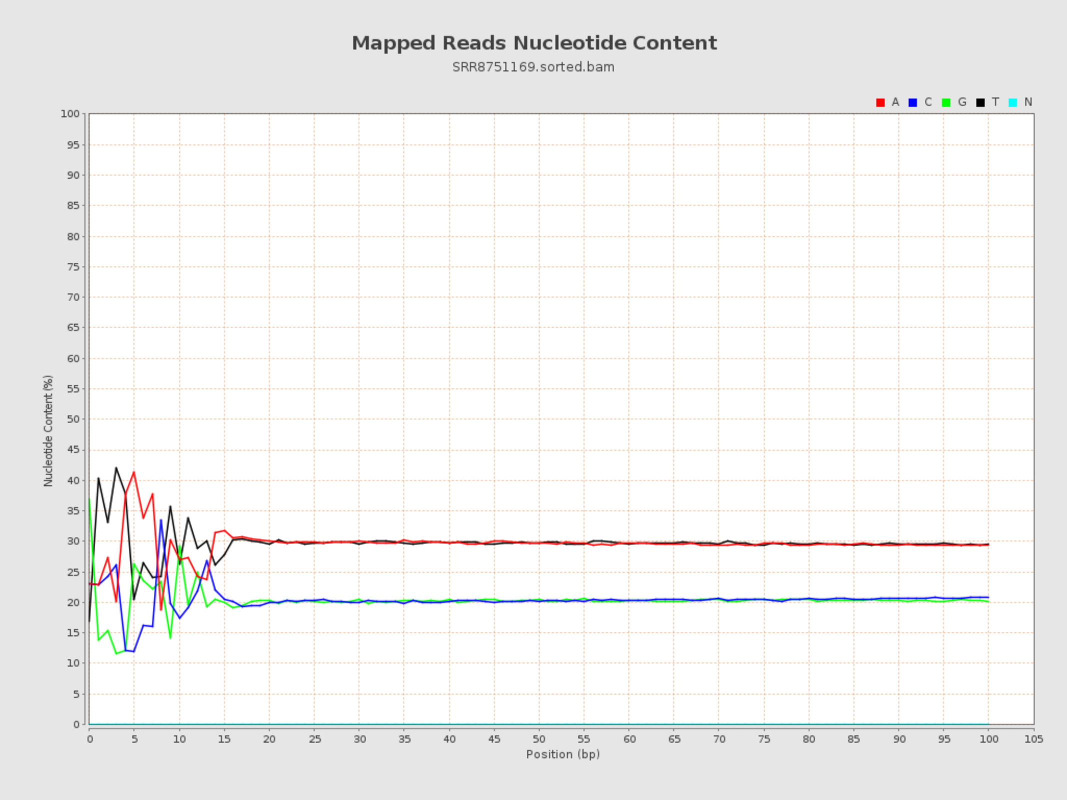
6. Results : Genome Fraction Coverage



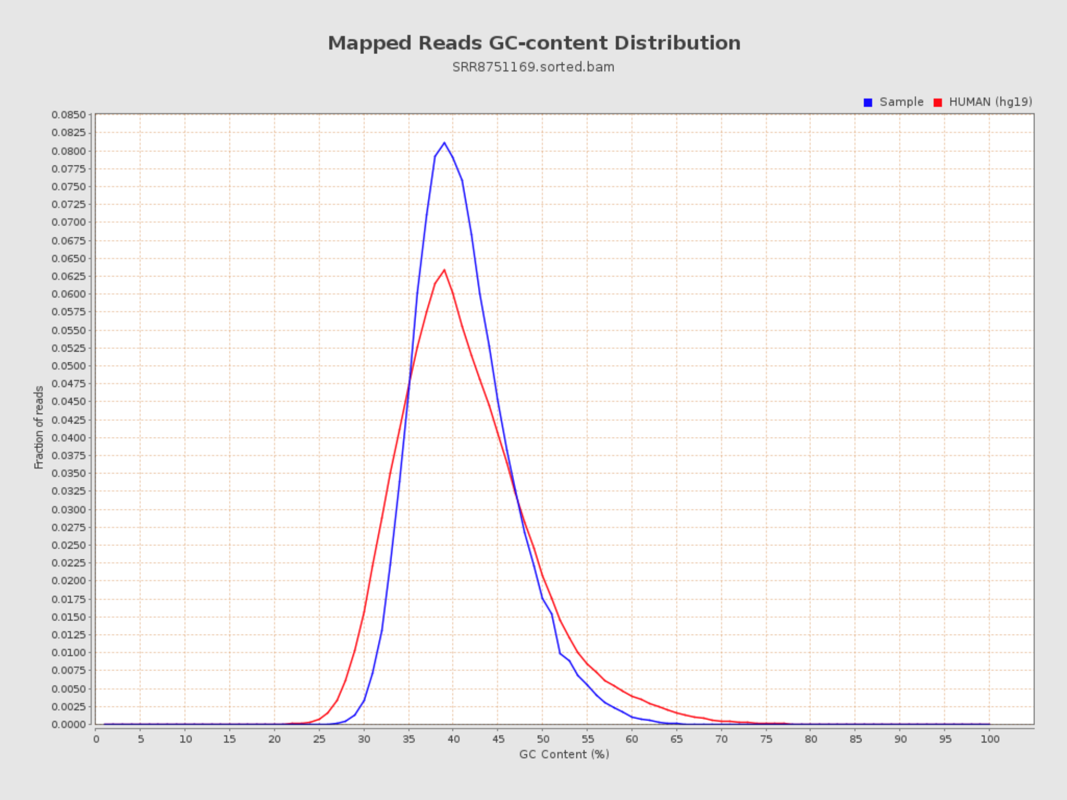
7. Results : Duplication Rate Histogram



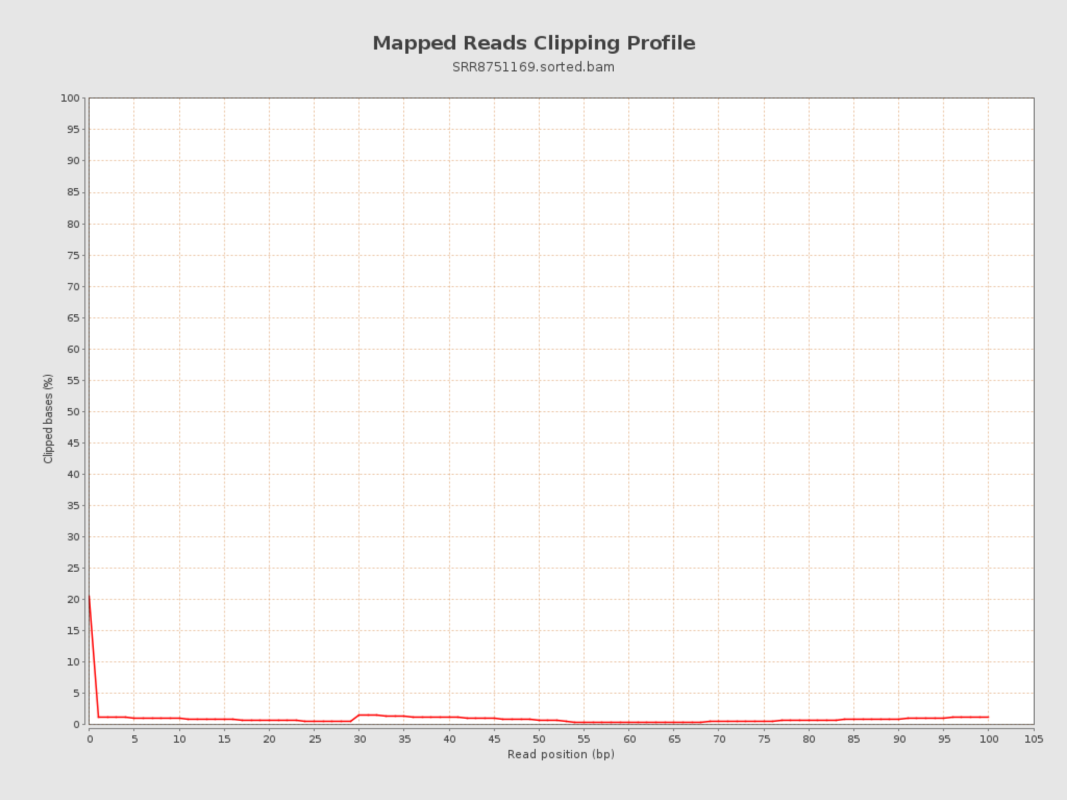
8. Results : Mapped Reads Nucleotide Content



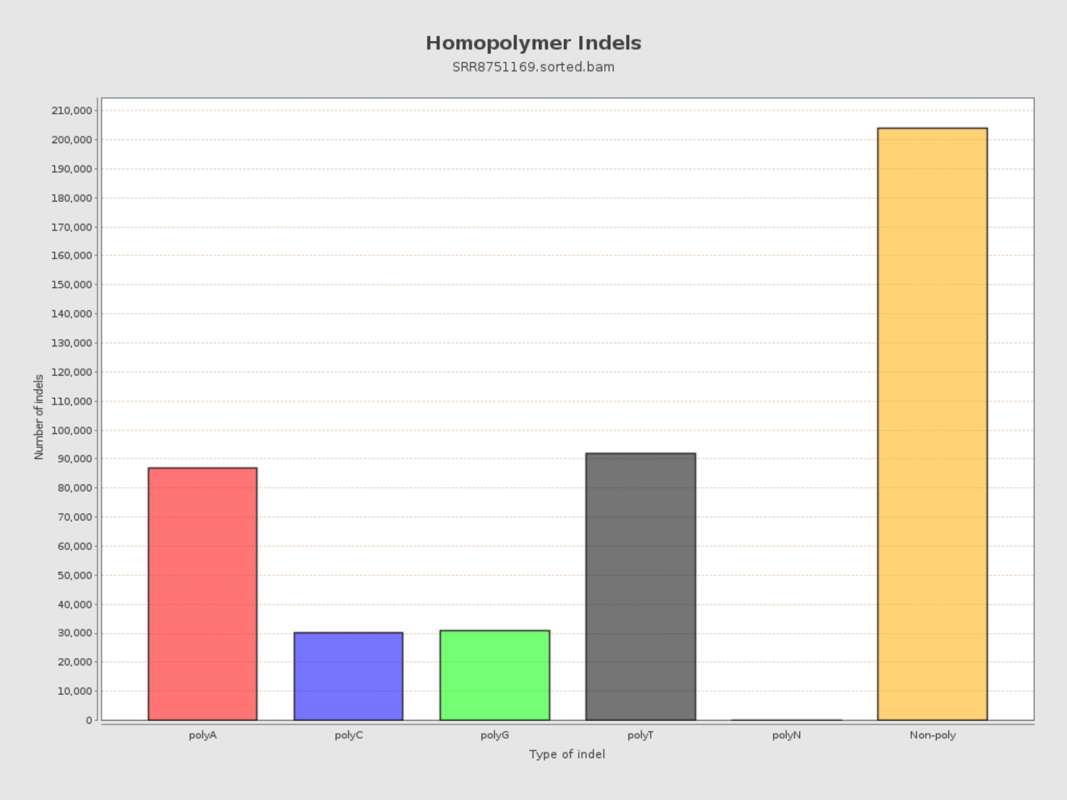
9. Results : Mapped Reads GC-content Distribution



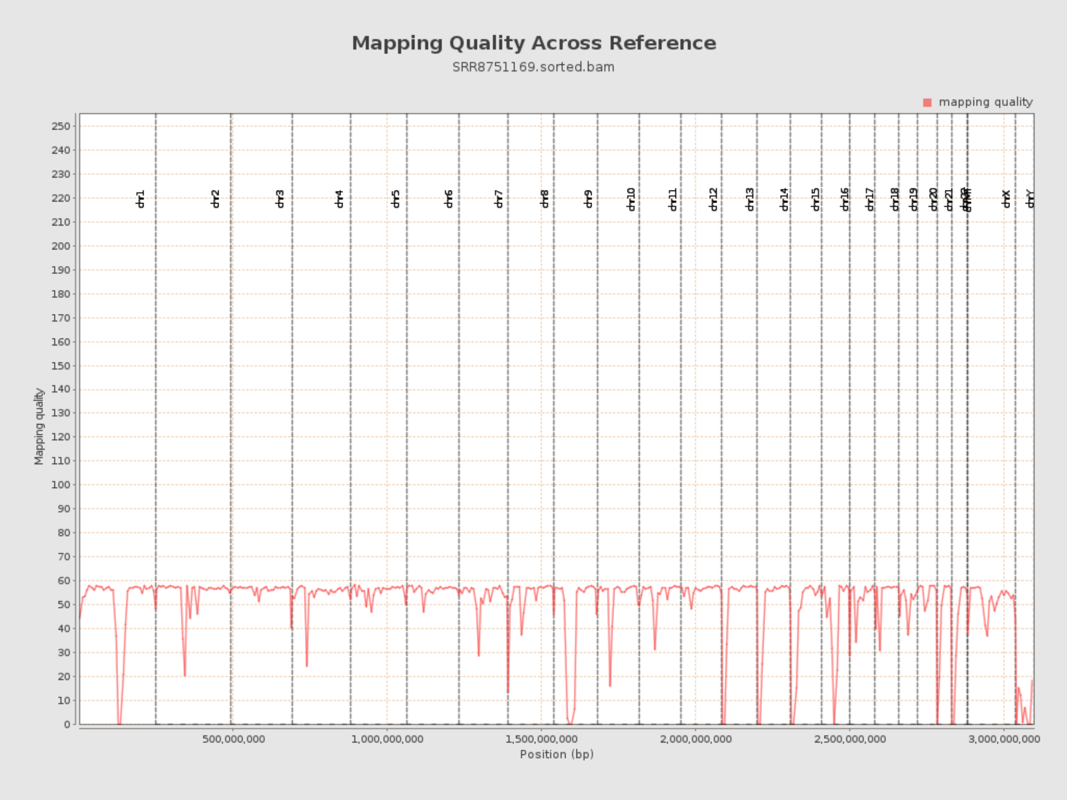
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram