Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:38:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751231.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_SRR8751231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:38:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,891,755
Mapped reads	4,517,789 / 92.36%
Unmapped reads	373,966 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	127,216 / 2.6%
Read min/max/mean length	30 / 101 / 102.08
Duplicated reads (estimated)	130,484 / 2.67%
Duplication rate	1.58%
Clipped reads	695,319 / 14.21%

2.2. ACGT Content

Number/percentage of A's	130,191,379 / 29.18%
Number/percentage of C's	92,829,561 / 20.8%
Number/percentage of T's	130,672,647 / 29.29%
Number/percentage of G's	92,500,327 / 20.73%
Number/percentage of N's	2,468 / 0%
GC Percentage	41.54%

2.3. Coverage

Mean	0.1442

Standard Deviation	1.2983

2.4. Mapping Quality

Mean Mapping Quality	51.28

2.5. Mismatches and indels

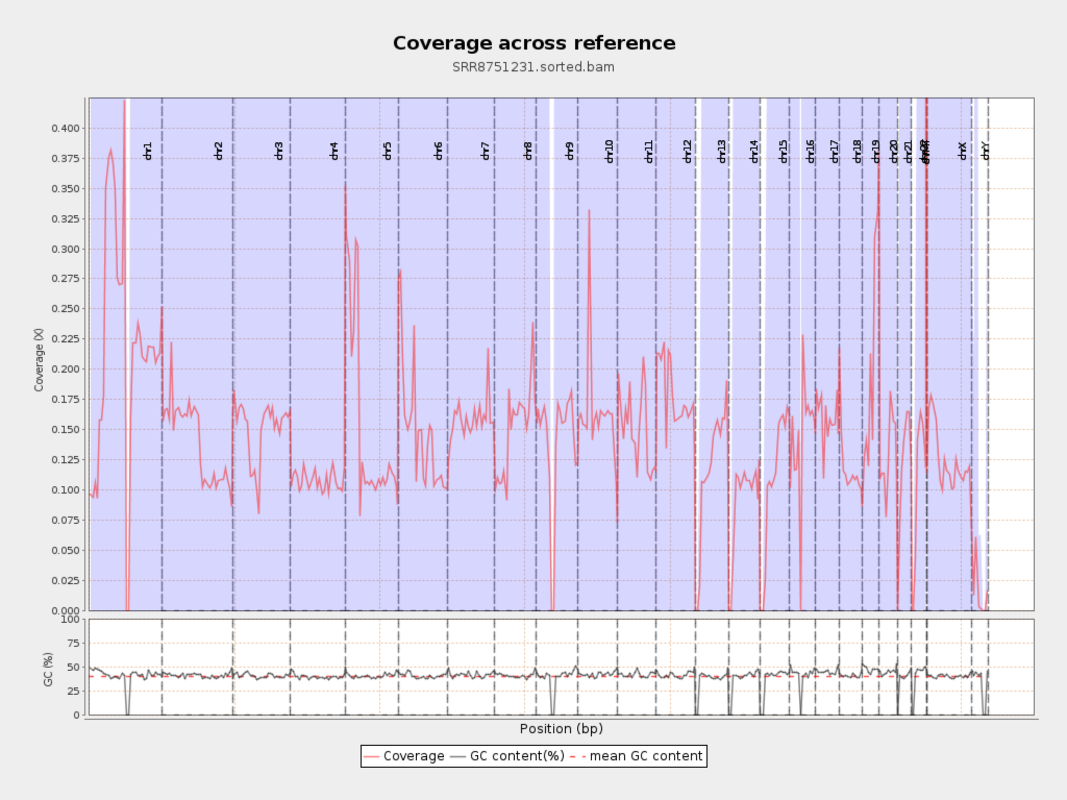
General error rate	0.39%
Mismatches	1,621,859
Insertions	75,551
Mapped reads with at least one insertion	1.65%
Deletions	59,680
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.4%

2.6. Chromosome stats

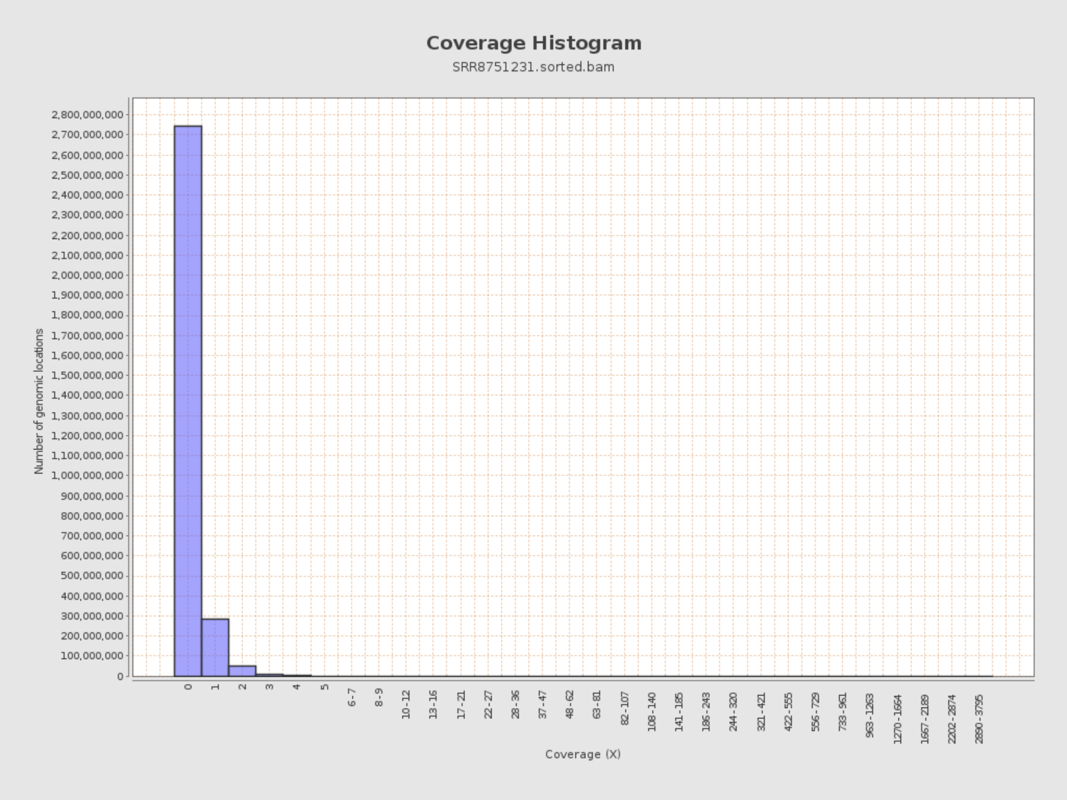
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54067969	0.2169	3.6145
chr2	243199373	33849444	0.1392	0.5514
chr3	198022430	29858701	0.1508	0.481
chr4	191154276	20573740	0.1076	0.4395
chr5	180915260	27270290	0.1507	0.4607
chr6	171115067	25499890	0.149	0.9496
chr7	159138663	25315914	0.1591	0.6999

chr8	146364022	22201833	0.1517	0.5133
chr9	141213431	19637256	0.1391	0.6484
chr10	135534747	22357743	0.165	1.7882
chr11	135006516	20307602	0.1504	0.7251
chr12	133851895	23998285	0.1793	0.4998
chr13	115169878	13335511	0.1158	0.3952
chr14	107349540	9600752	0.0894	0.364
chr15	102531392	10992593	0.1072	0.3799
chr16	90354753	12878498	0.1425	0.8396
chr17	81195210	12940987	0.1594	0.7593
chr18	78077248	9191909	0.1177	1.1636
chr19	59128983	11770987	0.1991	2.6317
chr20	63025520	8085662	0.1283	0.4301
chr21	48129895	5695387	0.1183	0.4452
chr22	51304566	5206239	0.1015	0.3745
chrMT	16571	1429636	86.2734	34.1395
chrX	155270560	19315204	0.1244	0.475
chrY	59373566	943278	0.0159	0.526

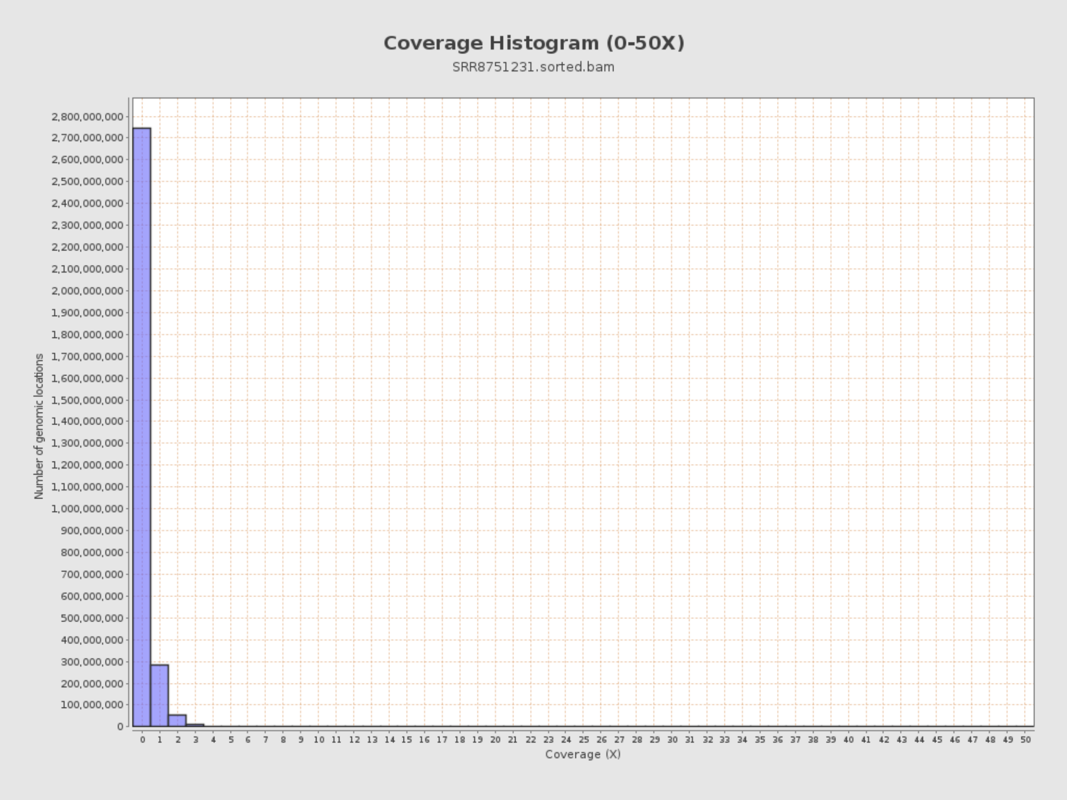
3. Results : Coverage across reference



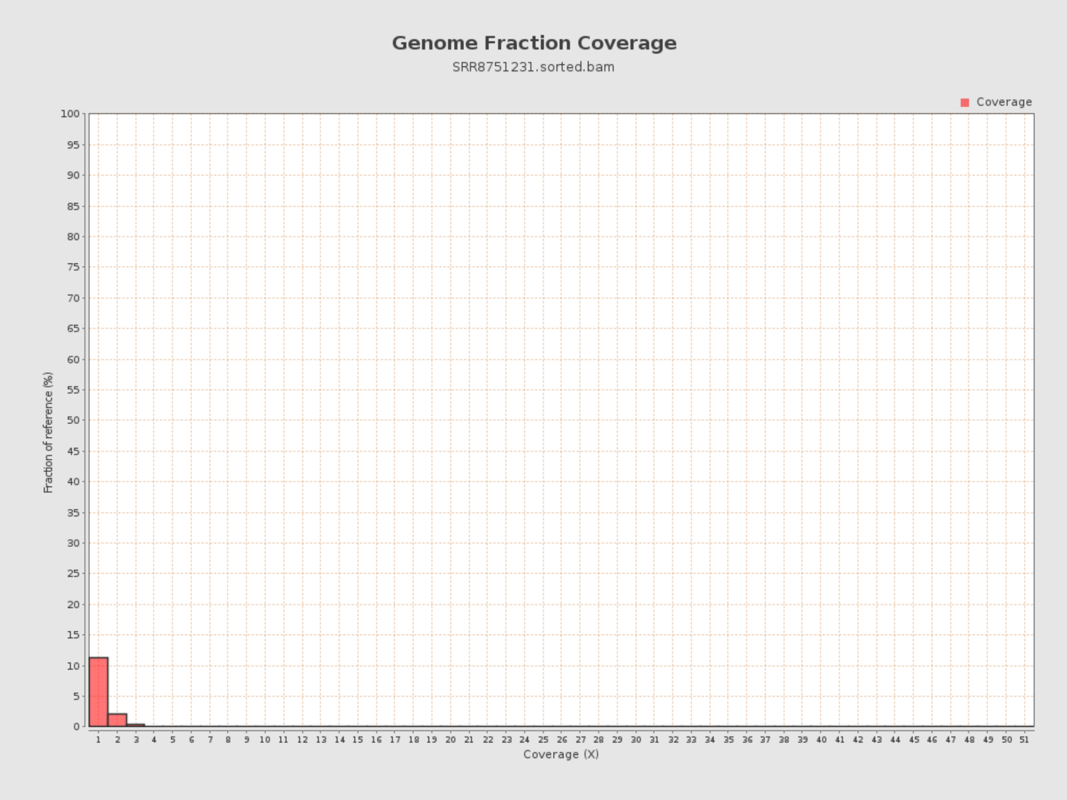
4. Results : Coverage Histogram



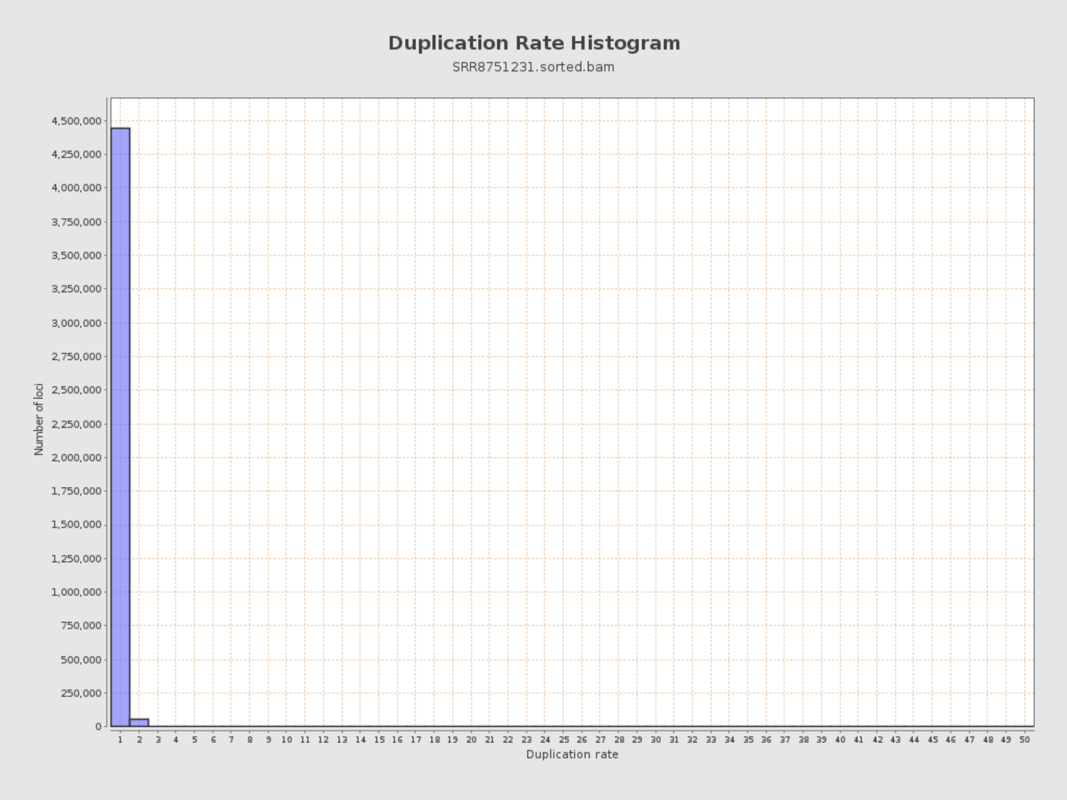
5. Results : Coverage Histogram (0-50X)



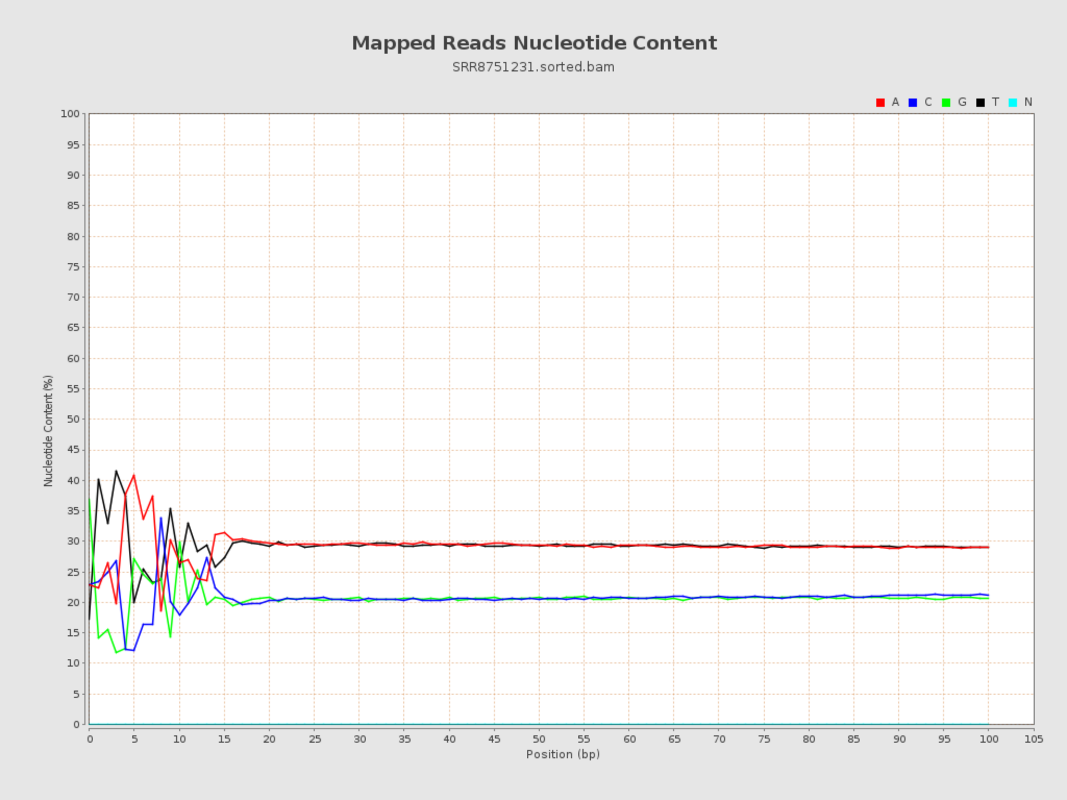
6. Results : Genome Fraction Coverage



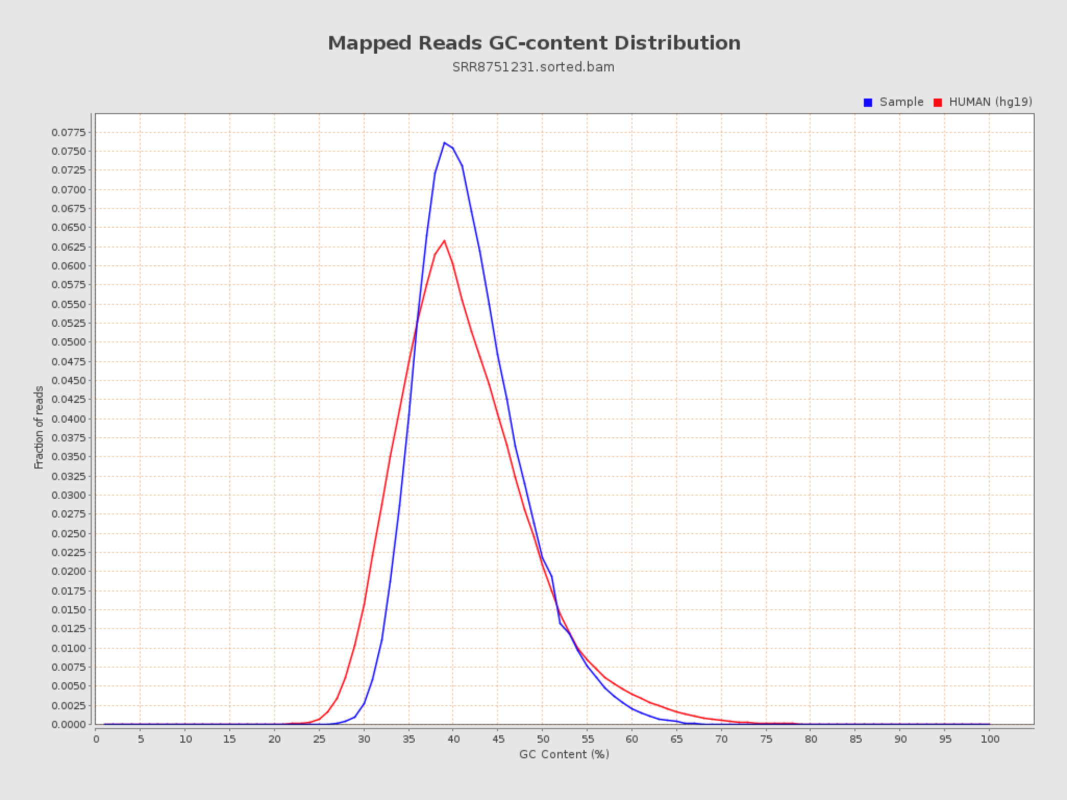
7. Results : Duplication Rate Histogram



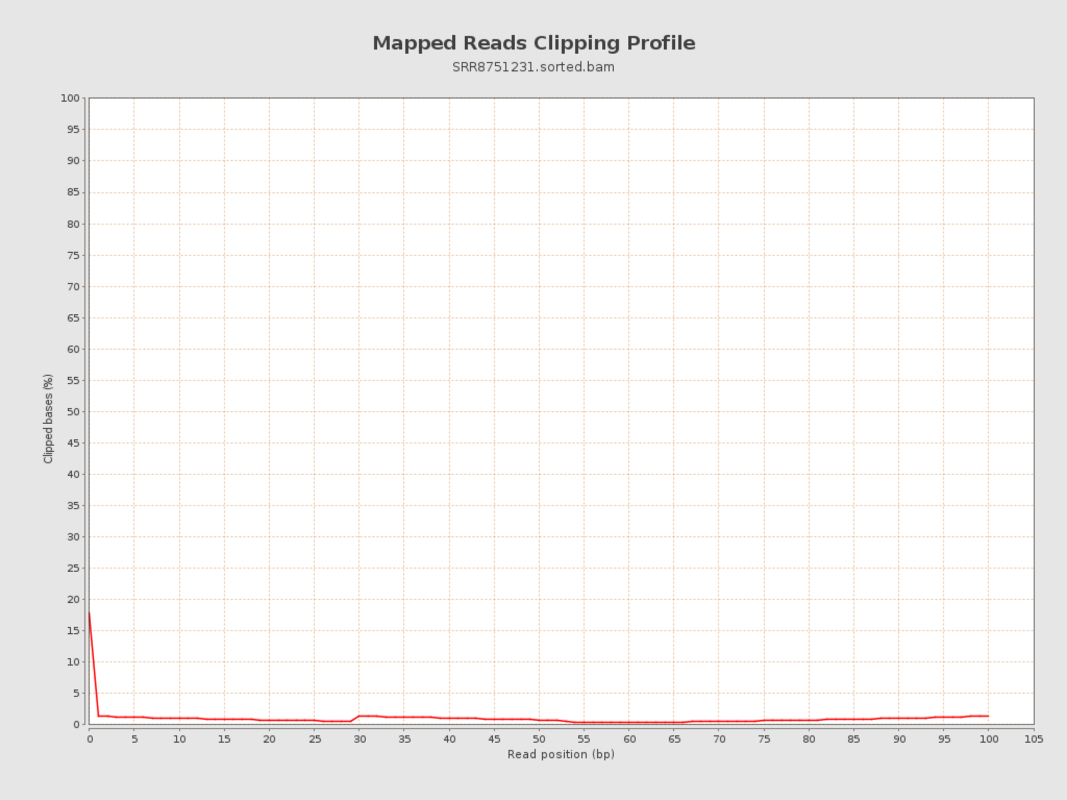
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



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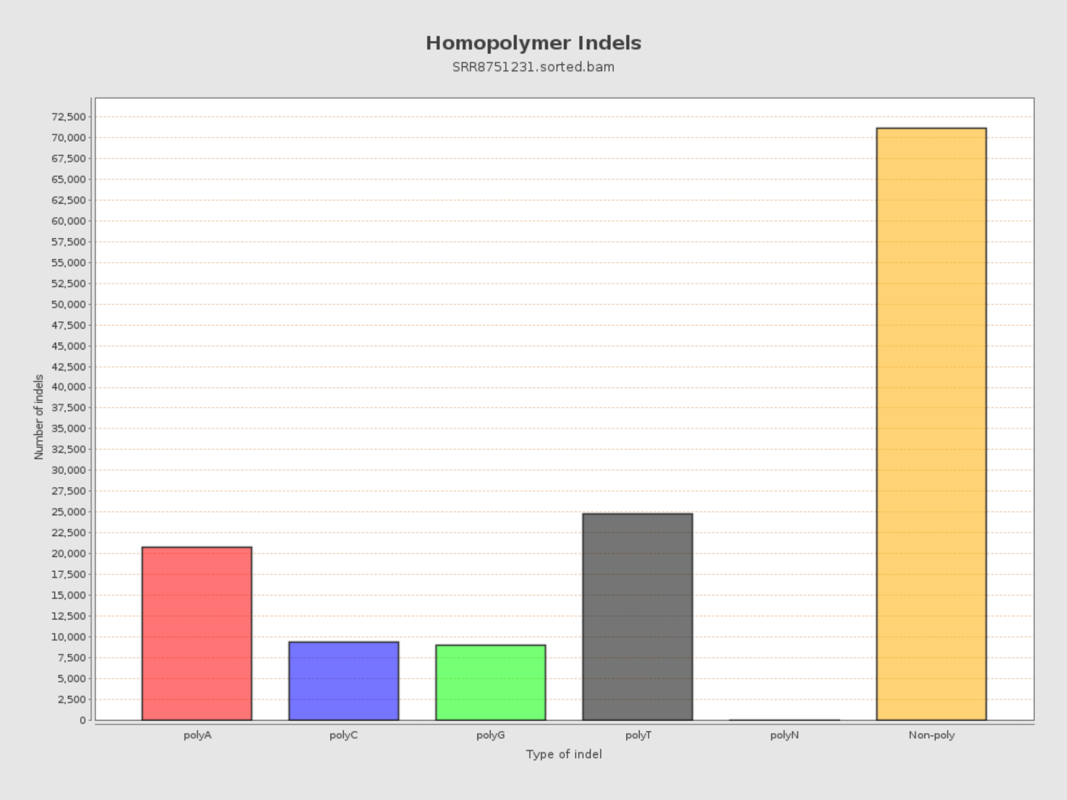
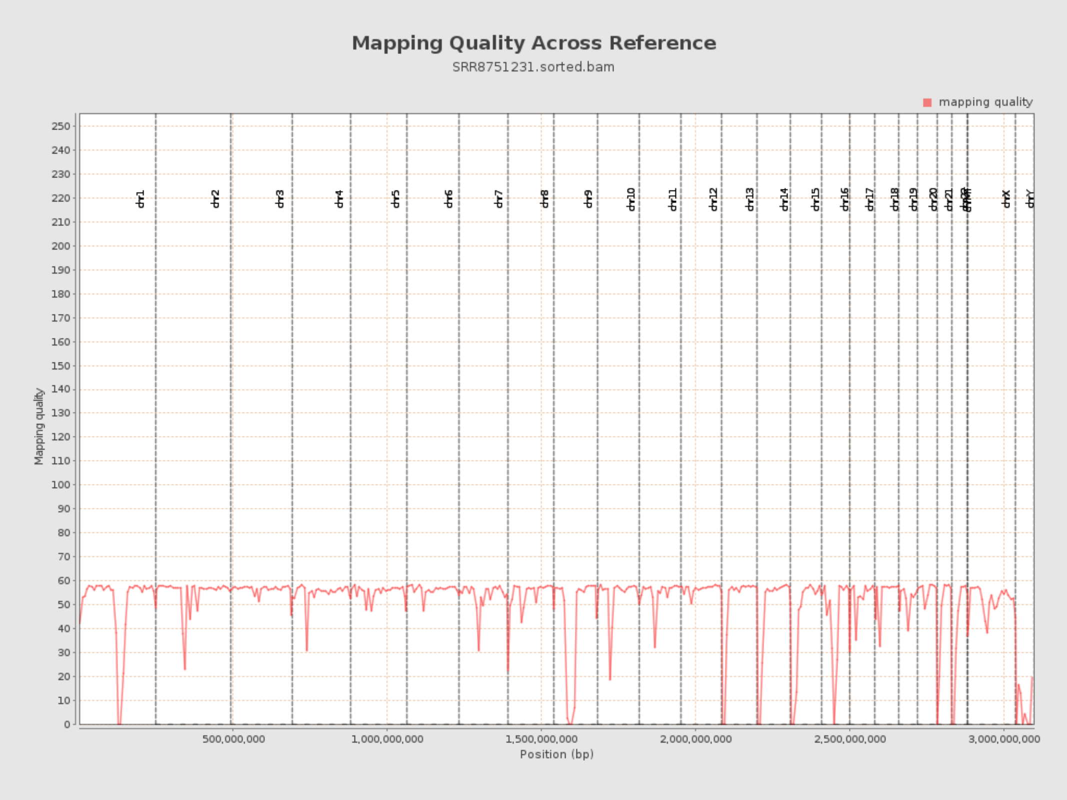
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram