Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:35:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549131.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_SRR1549131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:35:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,476,699
Mapped reads	11,815,430 / 87.67%
Unmapped reads	1,661,269 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	608,816 / 4.52%
Duplication rate	4.08%
Clipped reads	611,904 / 4.54%

2.2. ACGT Content

Number/percentage of A's	134,563,773 / 28.69%
Number/percentage of C's	98,994,351 / 21.11%
Number/percentage of T's	136,122,470 / 29.03%
Number/percentage of G's	99,161,511 / 21.15%
Number/percentage of N's	110,184 / 0.02%
GC Percentage	42.26%

2.3. Coverage

Mean	0.1515
Standard Deviation	0.8349

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Mismatches and indels

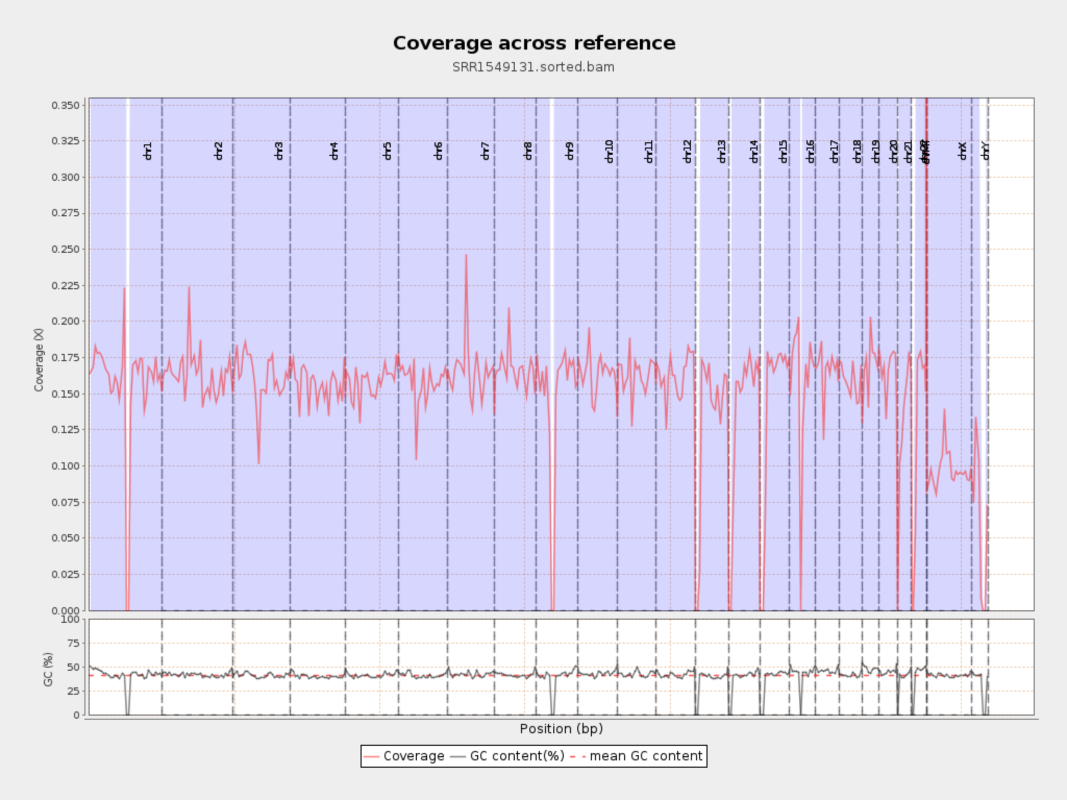
General error rate	0.33%
Mismatches	1,522,207
Insertions	11,781
Mapped reads with at least one insertion	0.1%
Deletions	35,774
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.87%

2.6. Chromosome stats

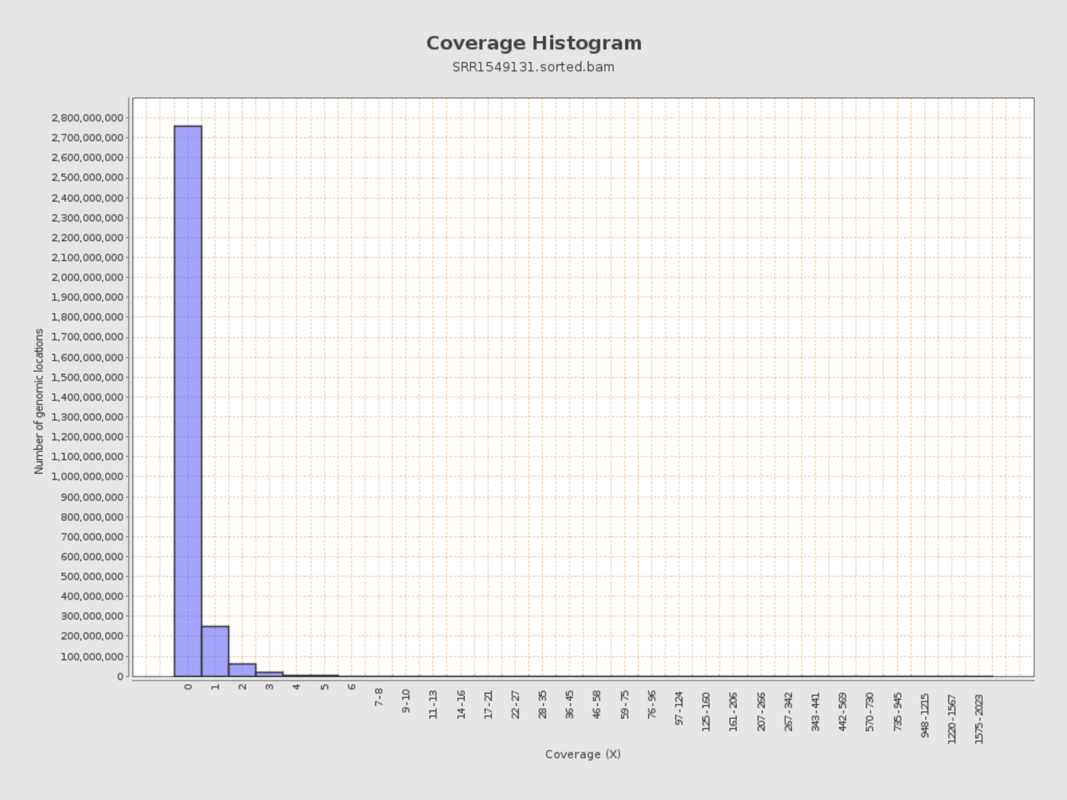
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38855228	0.1559	1.5549
chr2	243199373	39876691	0.164	0.8047
chr3	198022430	31915213	0.1612	0.5303
chr4	191154276	29808339	0.1559	0.5423
chr5	180915260	28605531	0.1581	0.5389
chr6	171115067	27019269	0.1579	0.6053
chr7	159138663	26510660	0.1666	1.2703
chr8	146364022	24419451	0.1668	0.7896

chr9	141213431	20377671	0.1443	0.7545
chr10	135534747	22299352	0.1645	0.784
chr11	135006516	21977259	0.1628	0.7204
chr12	133851895	21721161	0.1623	0.5586
chr13	115169878	14892173	0.1293	0.4647
chr14	107349540	14566426	0.1357	0.659
chr15	102531392	14408760	0.1405	0.4895
chr16	90354753	14278146	0.158	0.5863
chr17	81195210	13468050	0.1659	0.5927
chr18	78077248	12389625	0.1587	1.5183
chr19	59128983	10112448	0.171	1.3202
chr20	63025520	10456898	0.1659	0.5714
chr21	48129895	6229435	0.1294	0.5719
chr22	51304566	6059830	0.1181	0.5011
chrMT	16571	145843	8.8011	10.9964
chrX	155270560	15096048	0.0972	0.529
chrY	59373566	3507994	0.0591	0.4337

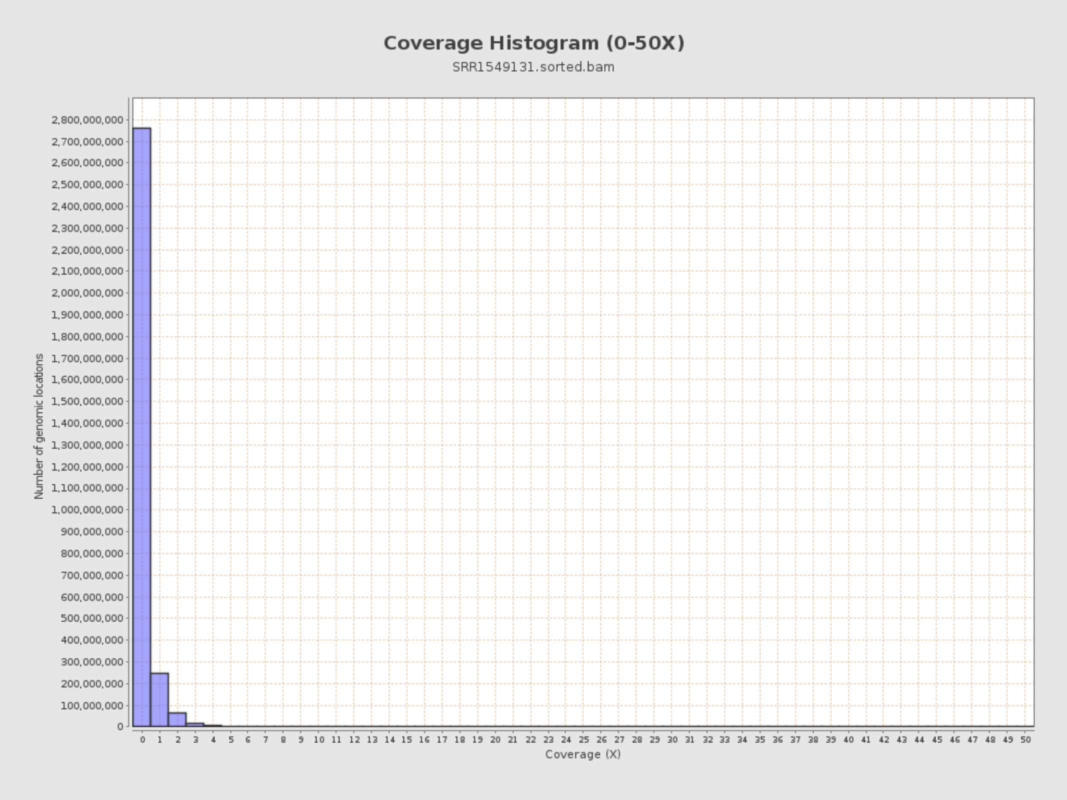
3. Results : Coverage across reference



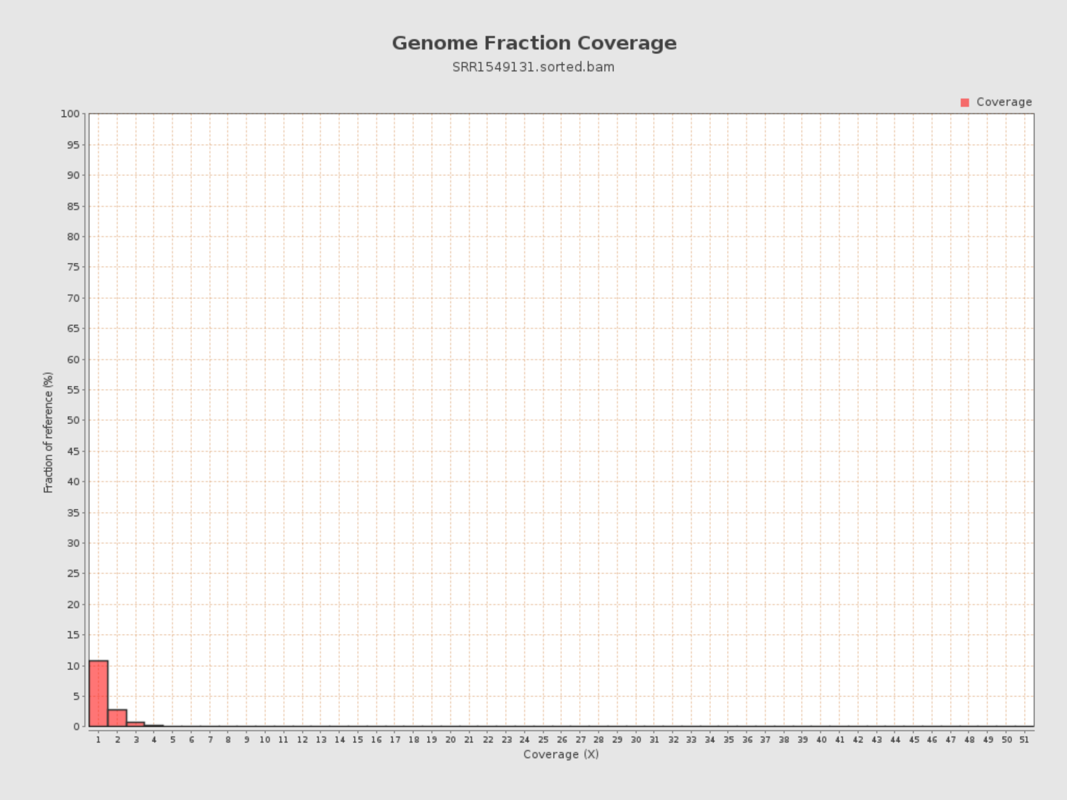
4. Results : Coverage Histogram



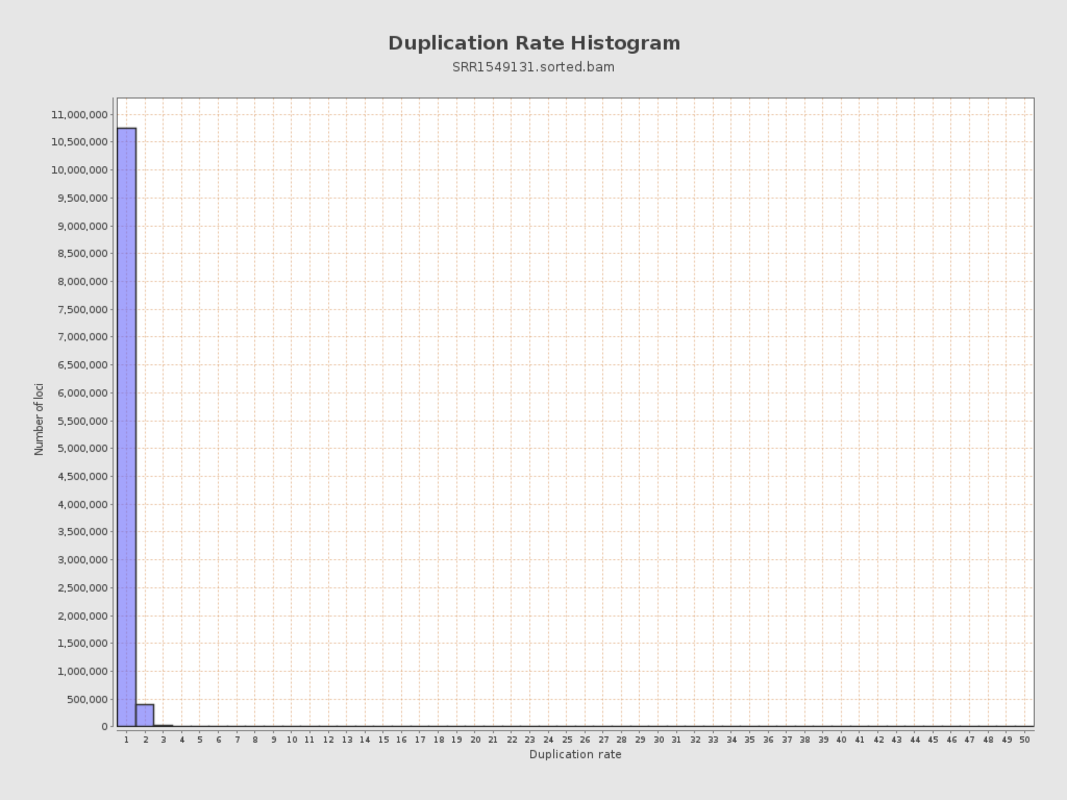
5. Results : Coverage Histogram (0-50X)



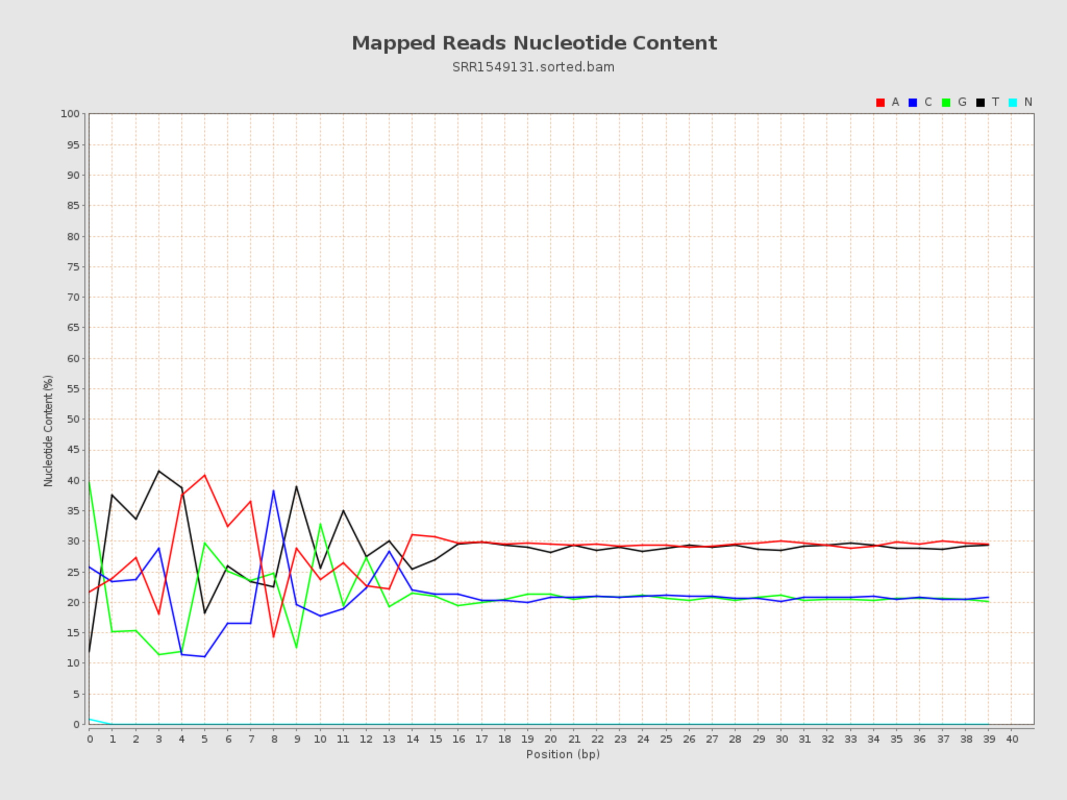
6. Results : Genome Fraction Coverage



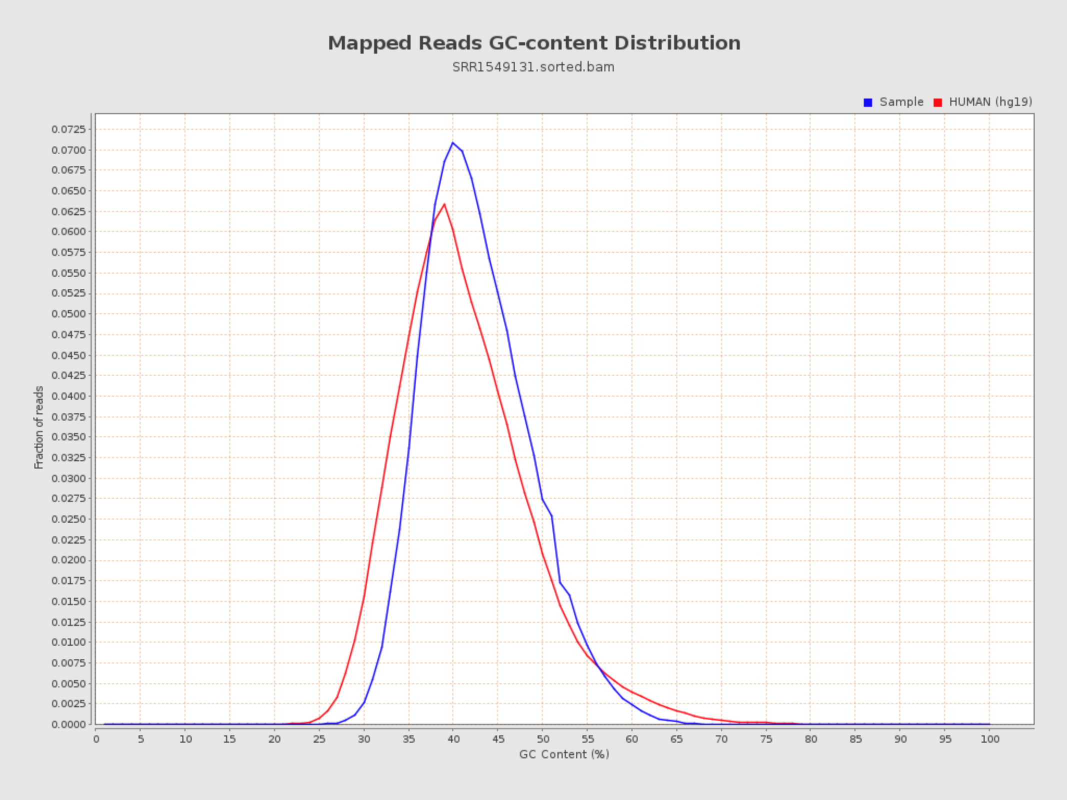
7. Results : Duplication Rate Histogram



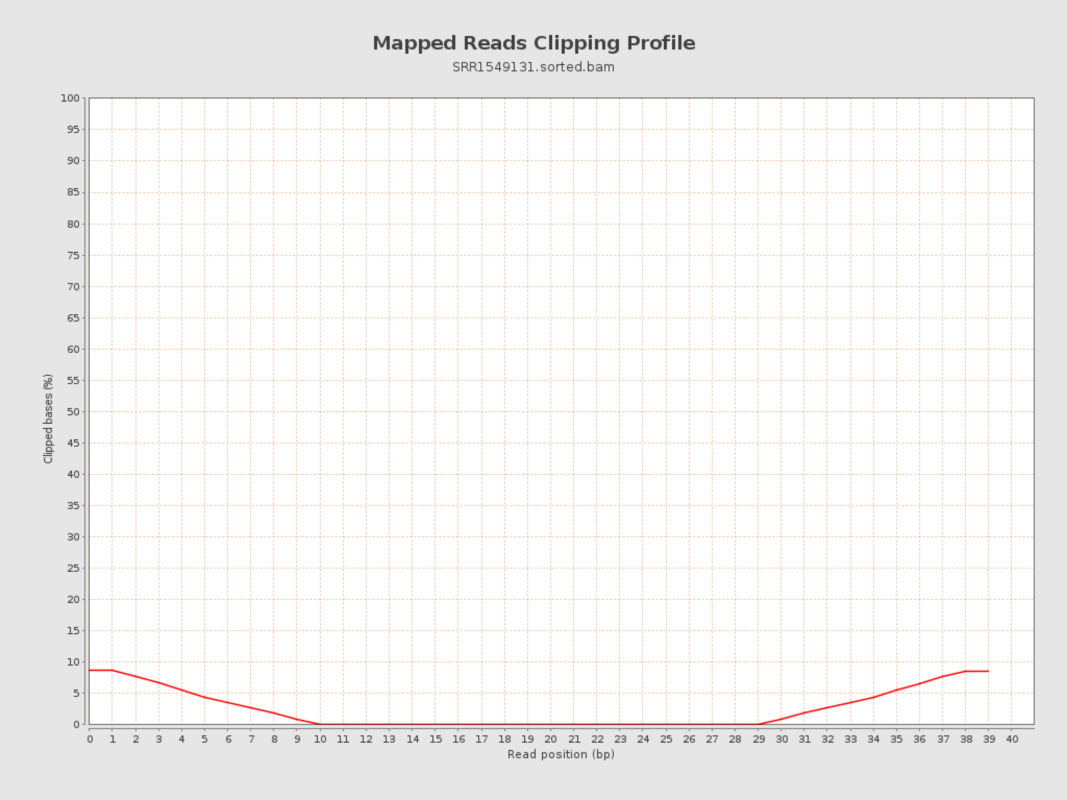
8. Results : Mapped Reads Nucleotide Content



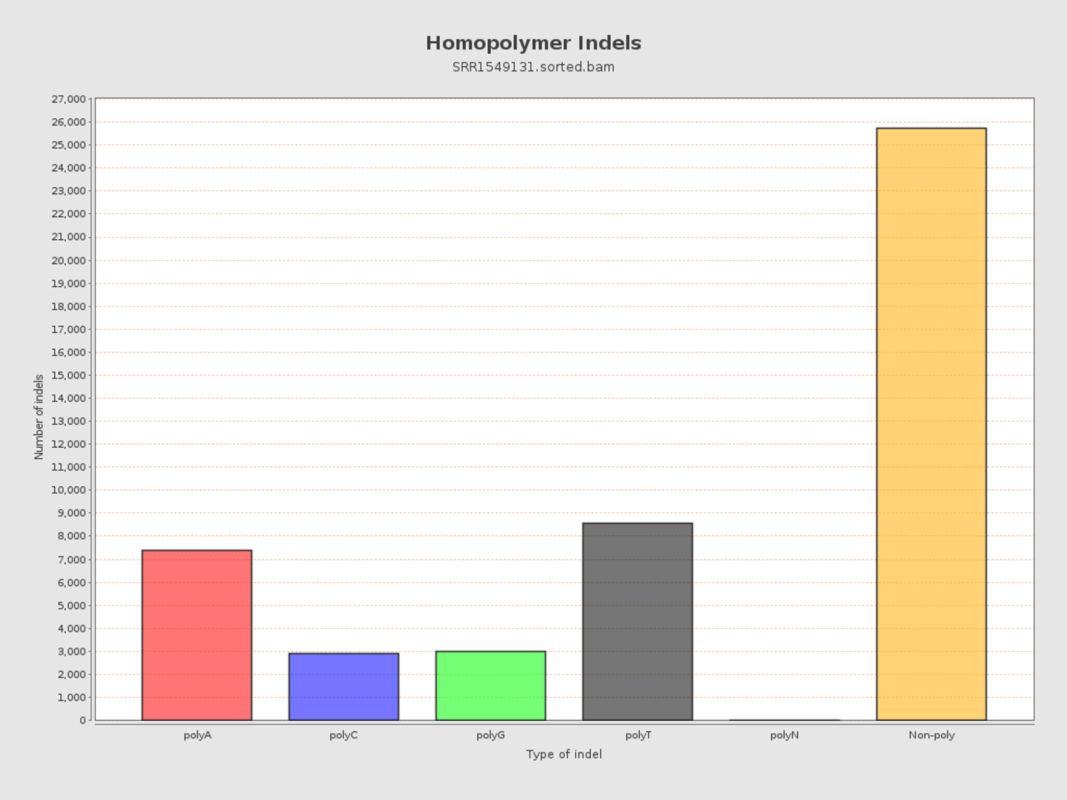
9. Results : Mapped Reads GC-content Distribution



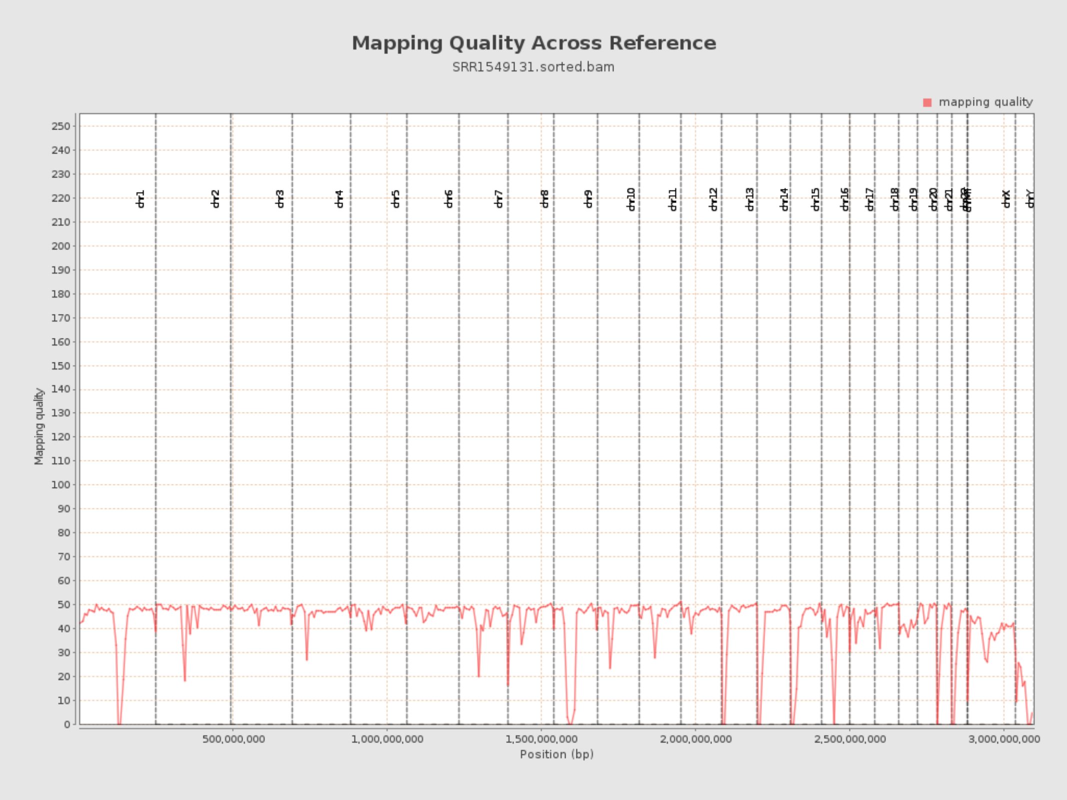
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram