Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:44:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236082.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_SRR6236082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:44:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,261,549
Mapped reads	1,052,608 / 83.44%
Unmapped reads	208,941 / 16.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,703 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	47,374 / 3.76%
Duplication rate	3.67%
Clipped reads	536,129 / 42.5%

2.2. ACGT Content

Number/percentage of A's	18,269,118 / 26.67%
Number/percentage of C's	12,252,705 / 17.89%
Number/percentage of T's	22,135,395 / 32.32%
Number/percentage of G's	15,798,667 / 23.07%
Number/percentage of N's	33,287 / 0.05%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2299

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

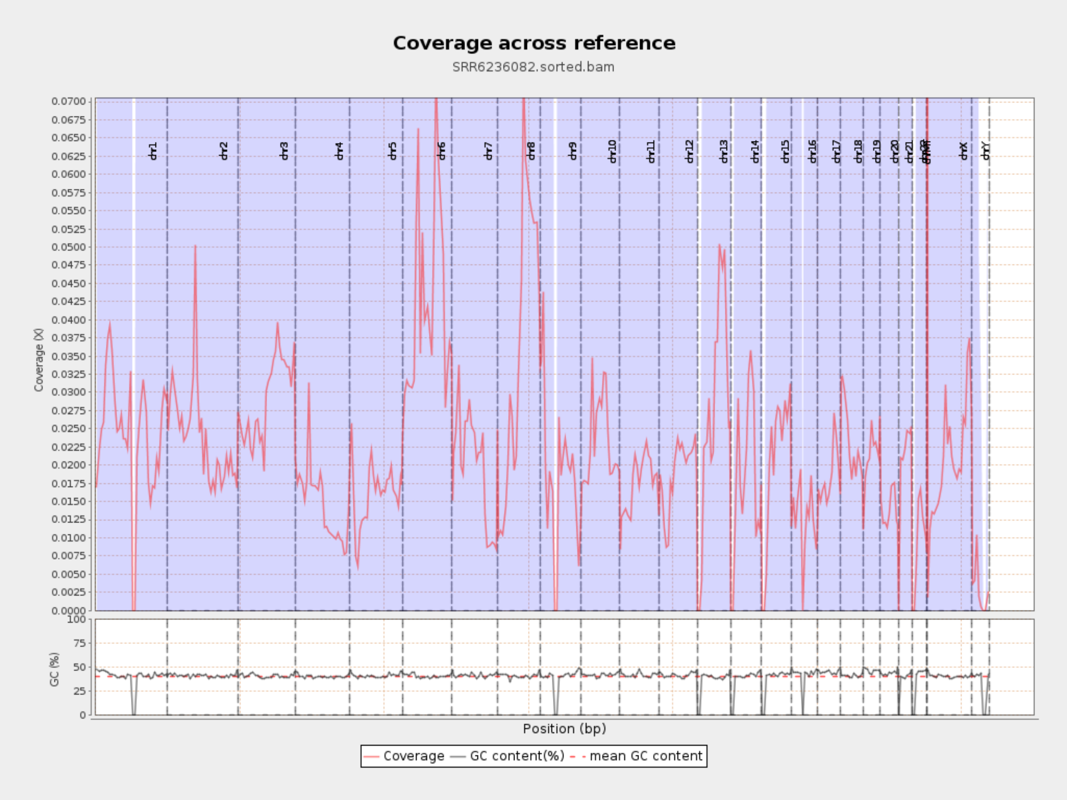
General error rate	0.85%
Mismatches	569,624
Insertions	4,933
Mapped reads with at least one insertion	0.46%
Deletions	19,622
Mapped reads with at least one deletion	1.84%
Homopolymer indels	46.66%

2.6. Chromosome stats

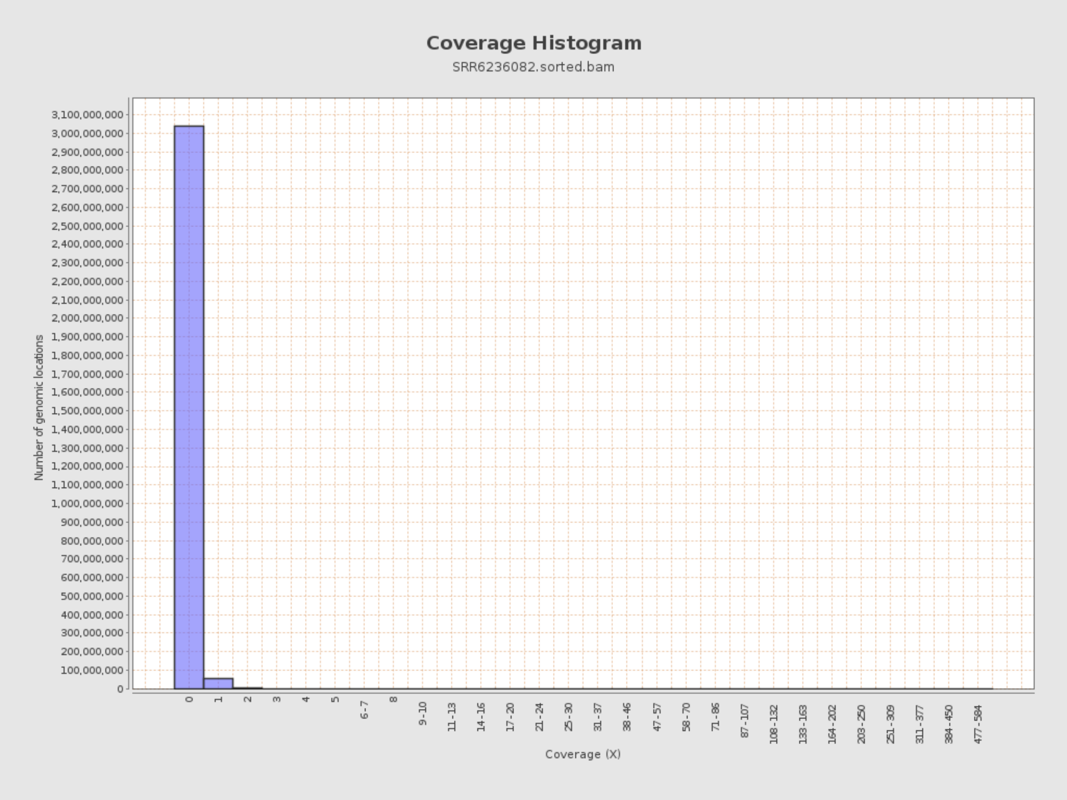
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6026269	0.0242	0.3141
chr2	243199373	5838024	0.024	0.2801
chr3	198022430	5766884	0.0291	0.1898
chr4	191154276	2796693	0.0146	0.1595
chr5	180915260	2914310	0.0161	0.1418
chr6	171115067	7290744	0.0426	0.3132
chr7	159138663	3135433	0.0197	0.1966

chr8	146364022	5367137	0.0367	0.421
chr9	141213431	2619899	0.0186	0.2187
chr10	135534747	3176420	0.0234	0.2181
chr11	135006516	2385266	0.0177	0.1956
chr12	133851895	2516694	0.0188	0.1576
chr13	115169878	3179198	0.0276	0.1865
chr14	107349540	1900079	0.0177	0.1507
chr15	102531392	2093098	0.0204	0.1674
chr16	90354753	1123056	0.0124	0.1335
chr17	81195210	1511961	0.0186	0.1624
chr18	78077248	1828275	0.0234	0.3455
chr19	59128983	1268646	0.0215	0.2215
chr20	63025520	866614	0.0138	0.1334
chr21	48129895	999944	0.0208	0.1699
chr22	51304566	492313	0.0096	0.1072
chrMT	16571	26807	1.6177	1.7581
chrX	155270560	3229409	0.0208	0.1718
chrY	59373566	169705	0.0029	0.0875

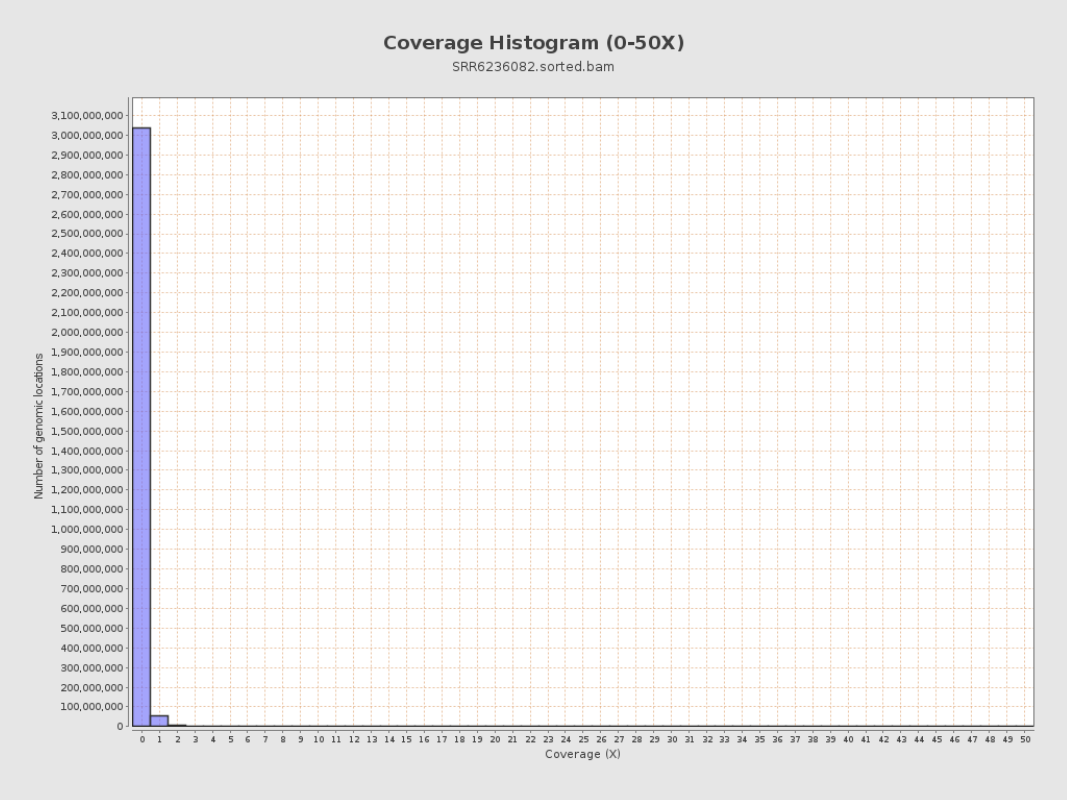
3. Results : Coverage across reference



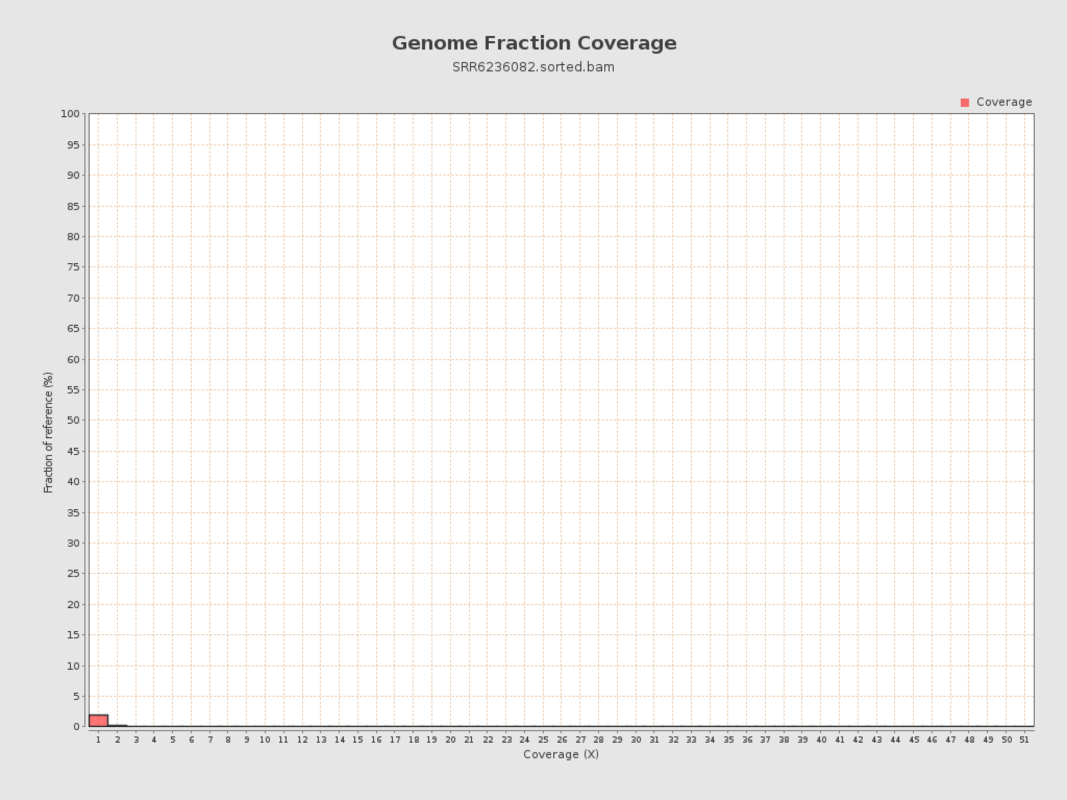
4. Results : Coverage Histogram



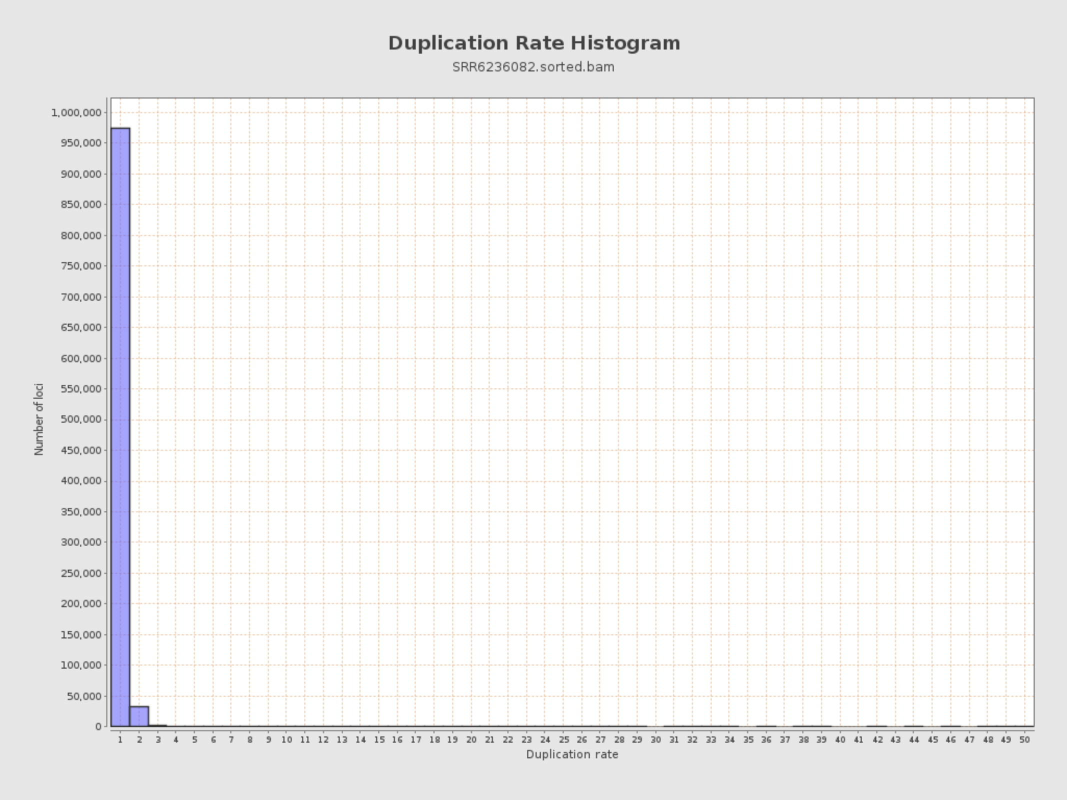
5. Results : Coverage Histogram (0-50X)



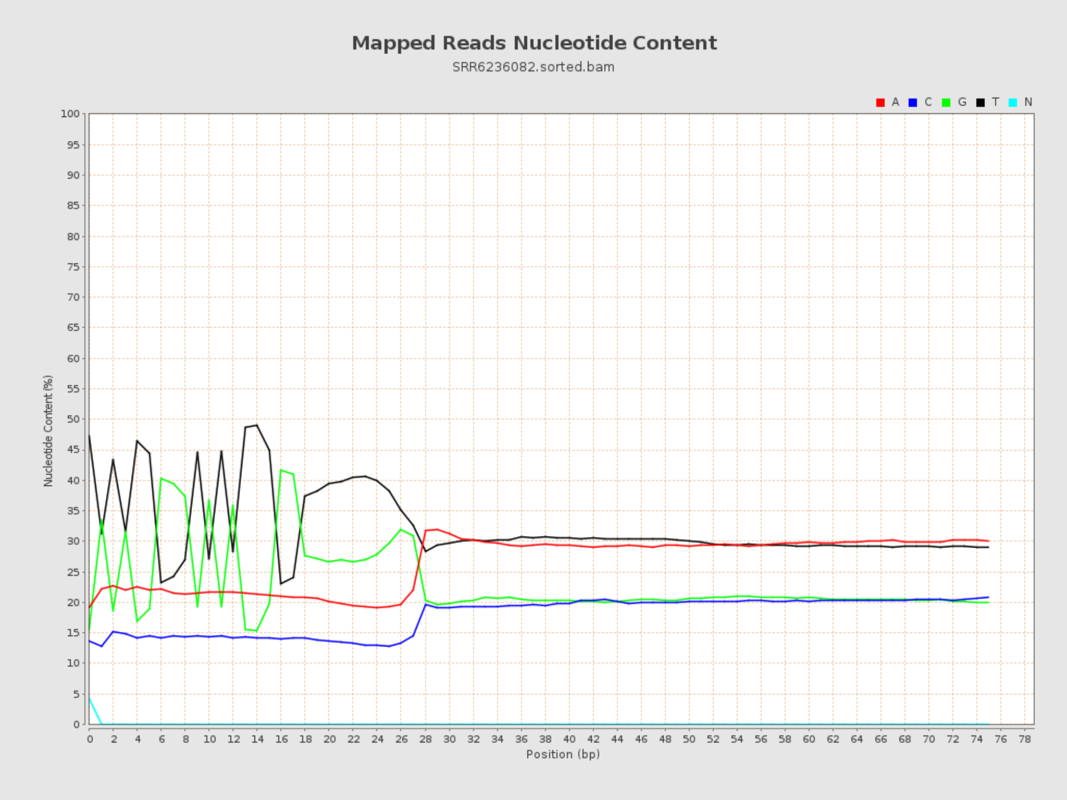
6. Results : Genome Fraction Coverage



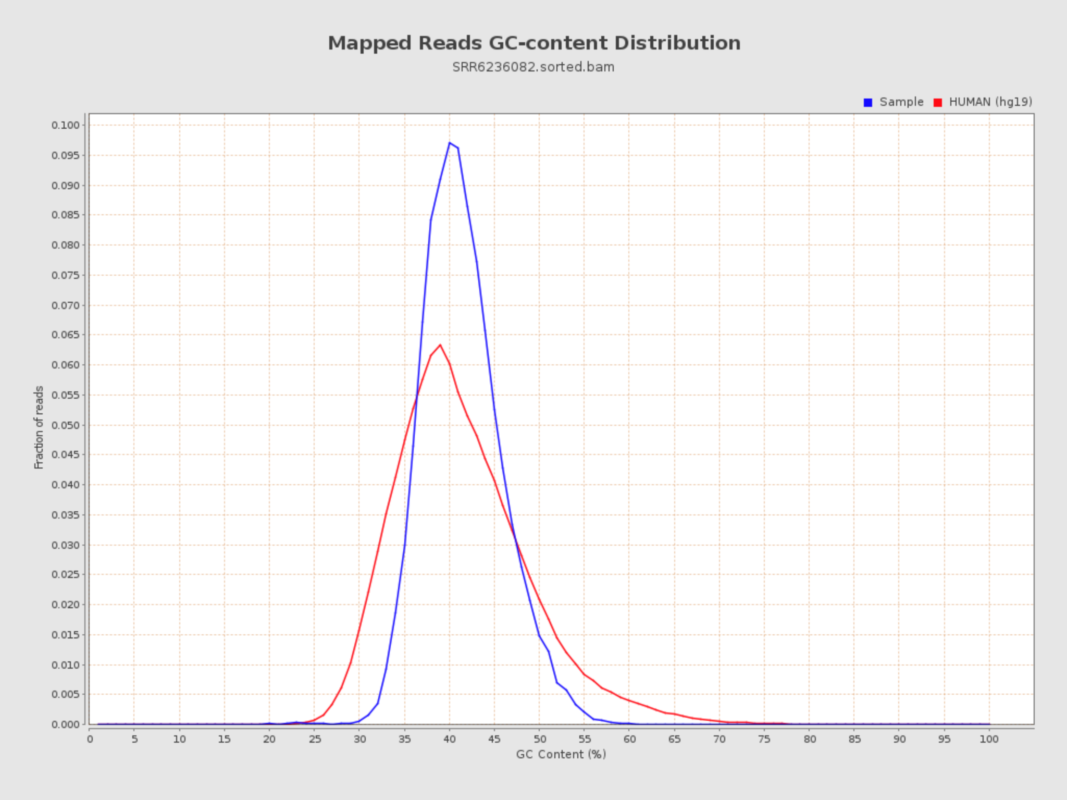
7. Results : Duplication Rate Histogram



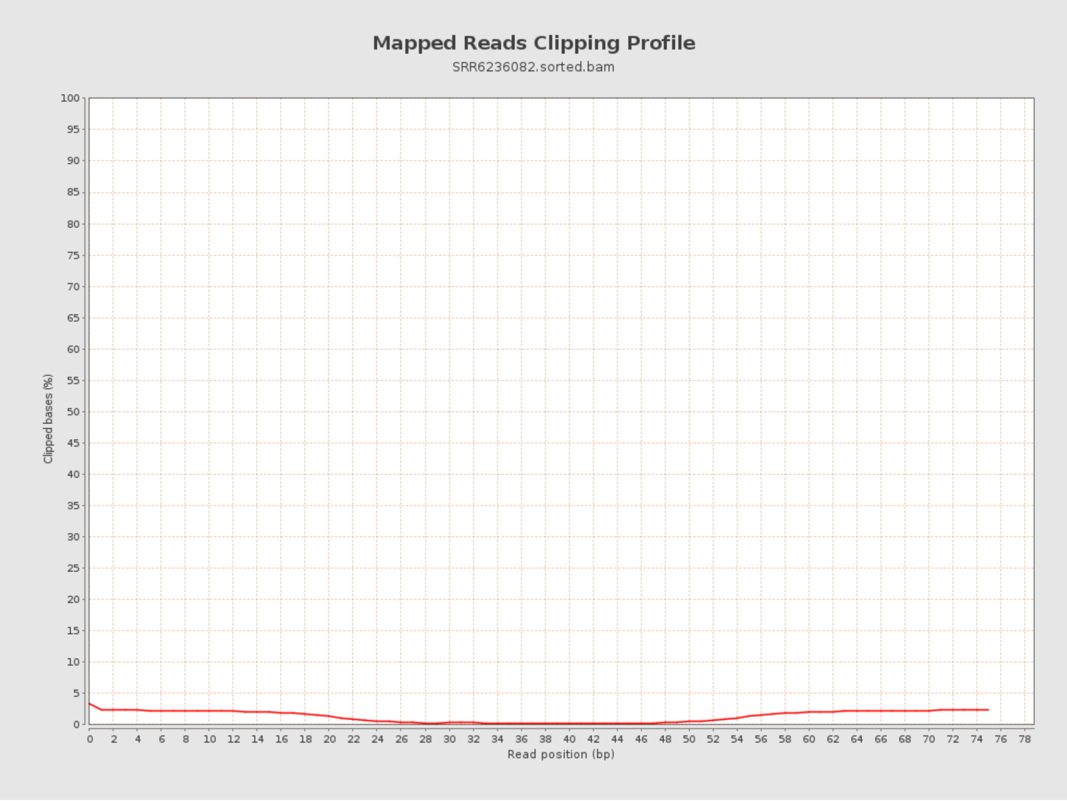
8. Results : Mapped Reads Nucleotide Content



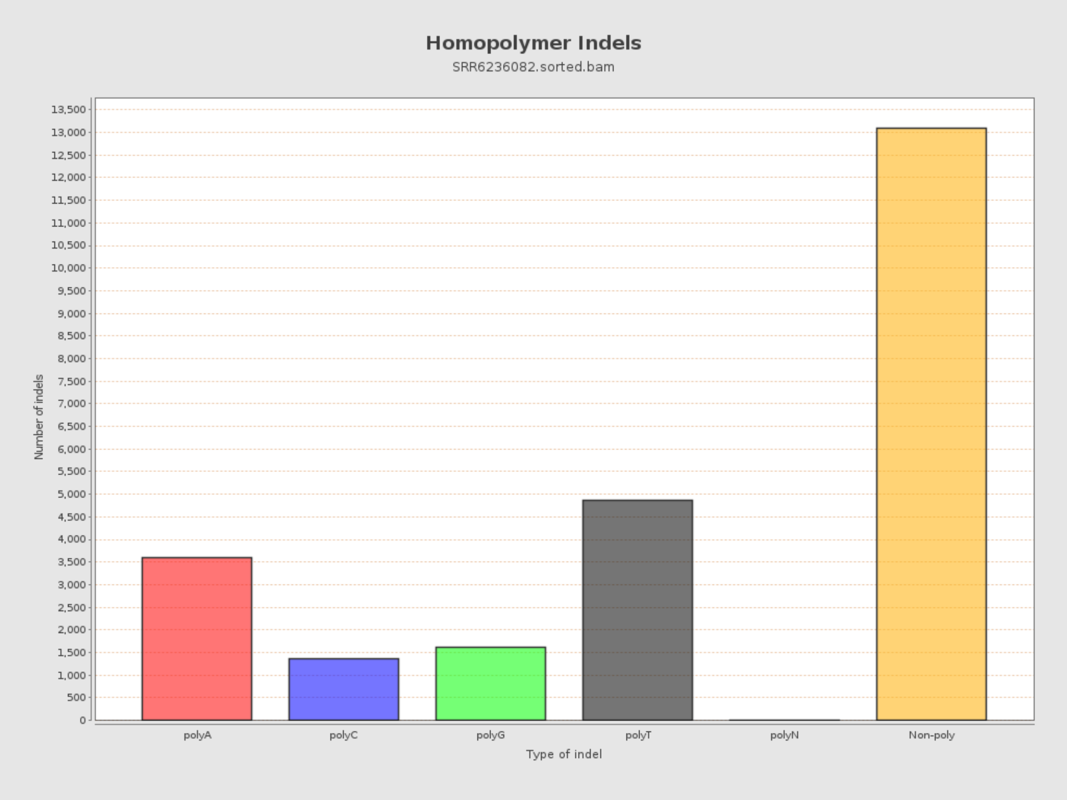
9. Results : Mapped Reads GC-content Distribution



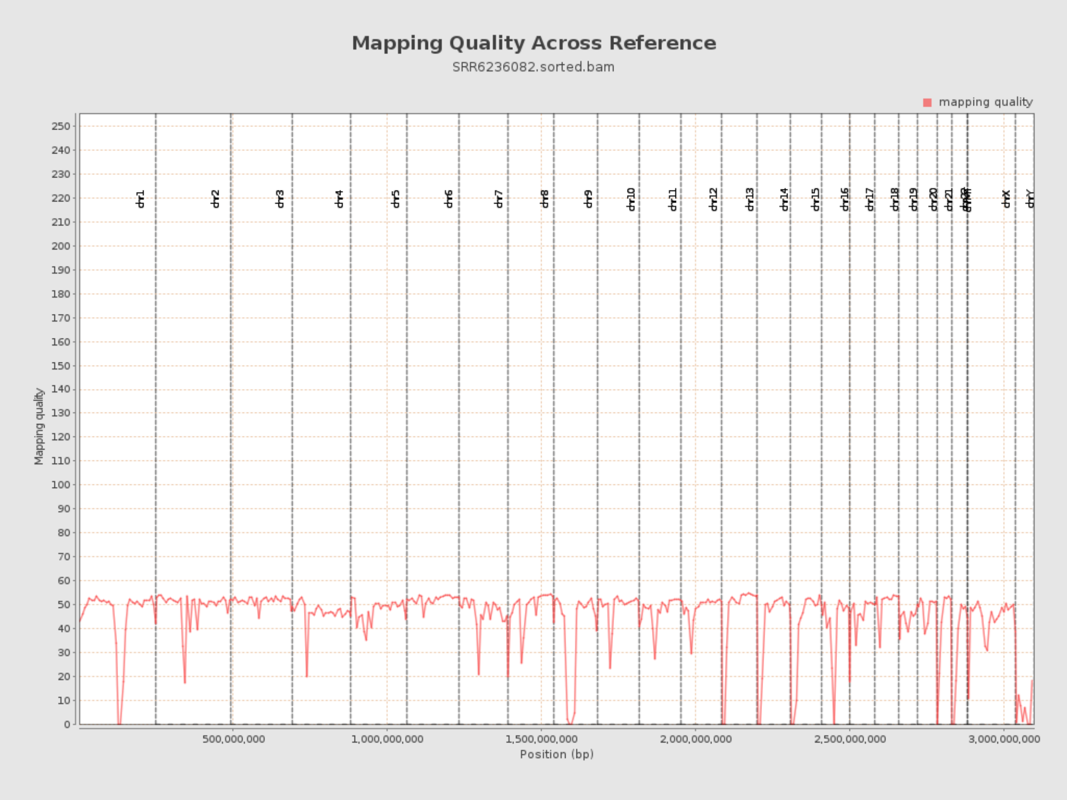
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram