Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:10:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081235.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_SRR3081235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:10:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,873,736
Mapped reads	1,664,341 / 88.82%
Unmapped reads	209,395 / 11.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,136 / 1.18%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	66,122 / 3.53%
Duplication rate	3.39%
Clipped reads	812,102 / 43.34%

2.2. ACGT Content

Number/percentage of A's	31,386,242 / 28.49%
Number/percentage of C's	21,052,020 / 19.11%
Number/percentage of T's	33,929,556 / 30.8%
Number/percentage of G's	23,793,927 / 21.6%
Number/percentage of N's	4,705 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.2708

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

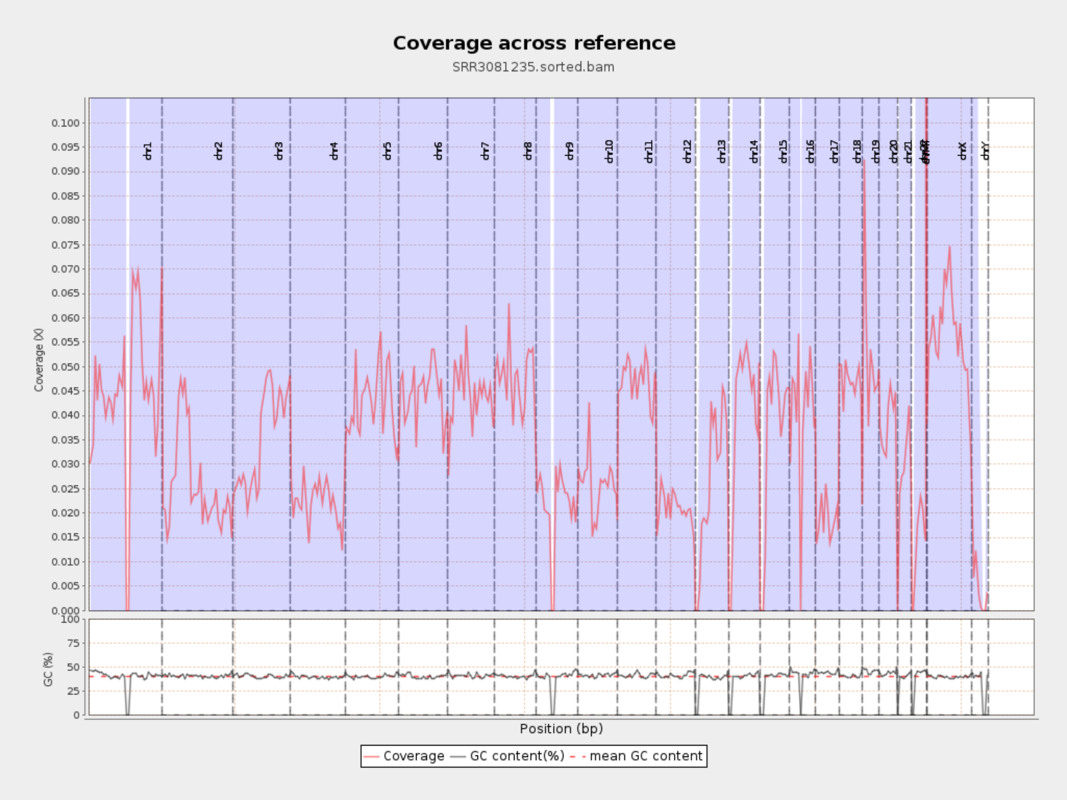
General error rate	0.85%
Mismatches	921,172
Insertions	8,281
Mapped reads with at least one insertion	0.49%
Deletions	25,435
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.41%

2.6. Chromosome stats

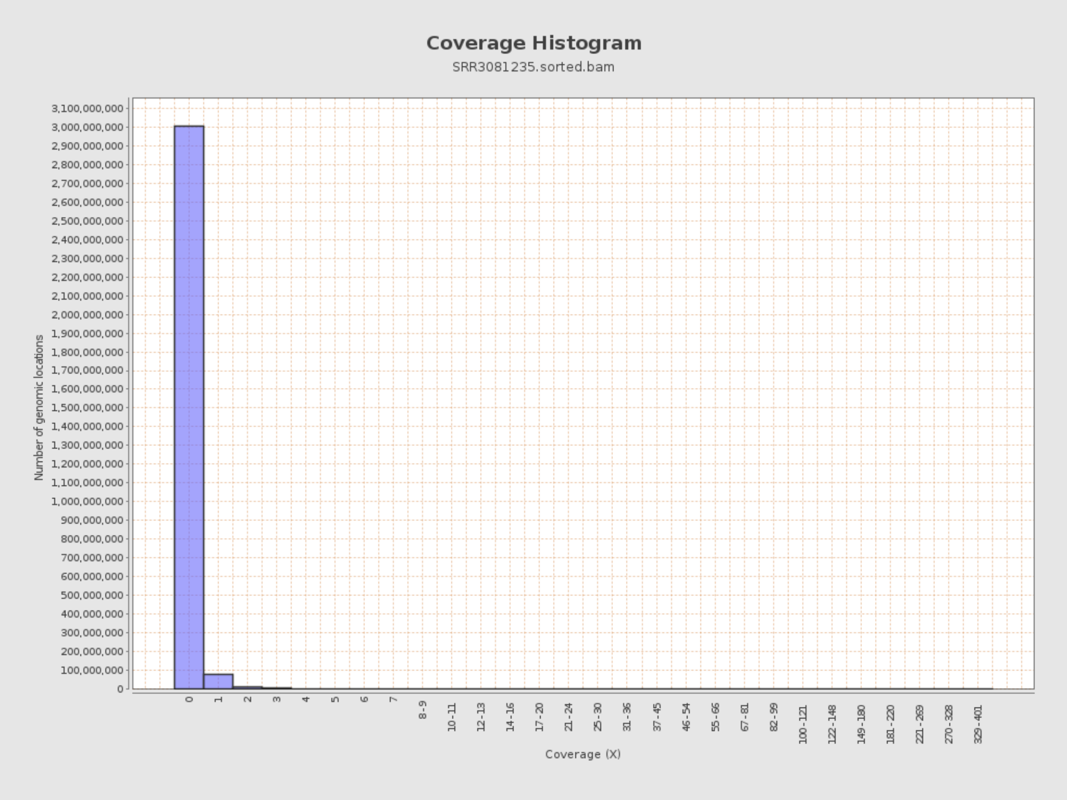
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11080659	0.0445	0.4222
chr2	243199373	6318950	0.026	0.2847
chr3	198022430	6954643	0.0351	0.2193
chr4	191154276	4252556	0.0222	0.179
chr5	180915260	7740432	0.0428	0.241
chr6	171115067	7583163	0.0443	0.2603
chr7	159138663	7085421	0.0445	0.3326

chr8	146364022	7027024	0.048	0.3164
chr9	141213431	2994419	0.0212	0.2011
chr10	135534747	3510080	0.0259	0.2569
chr11	135006516	6311788	0.0468	0.3304
chr12	133851895	2784630	0.0208	0.1687
chr13	115169878	3104427	0.027	0.1916
chr14	107349540	4248186	0.0396	0.2347
chr15	102531392	3702592	0.0361	0.2255
chr16	90354753	3686229	0.0408	0.2397
chr17	81195210	1509550	0.0186	0.1758
chr18	78077248	3692633	0.0473	0.3278
chr19	59128983	3135617	0.053	0.3636
chr20	63025520	2383389	0.0378	0.2277
chr21	48129895	1351693	0.0281	0.1996
chr22	51304566	694332	0.0135	0.1329
chrMT	16571	18963	1.1443	1.3936
chrX	155270560	8738844	0.0563	0.2923
chrY	59373566	298290	0.005	0.0981

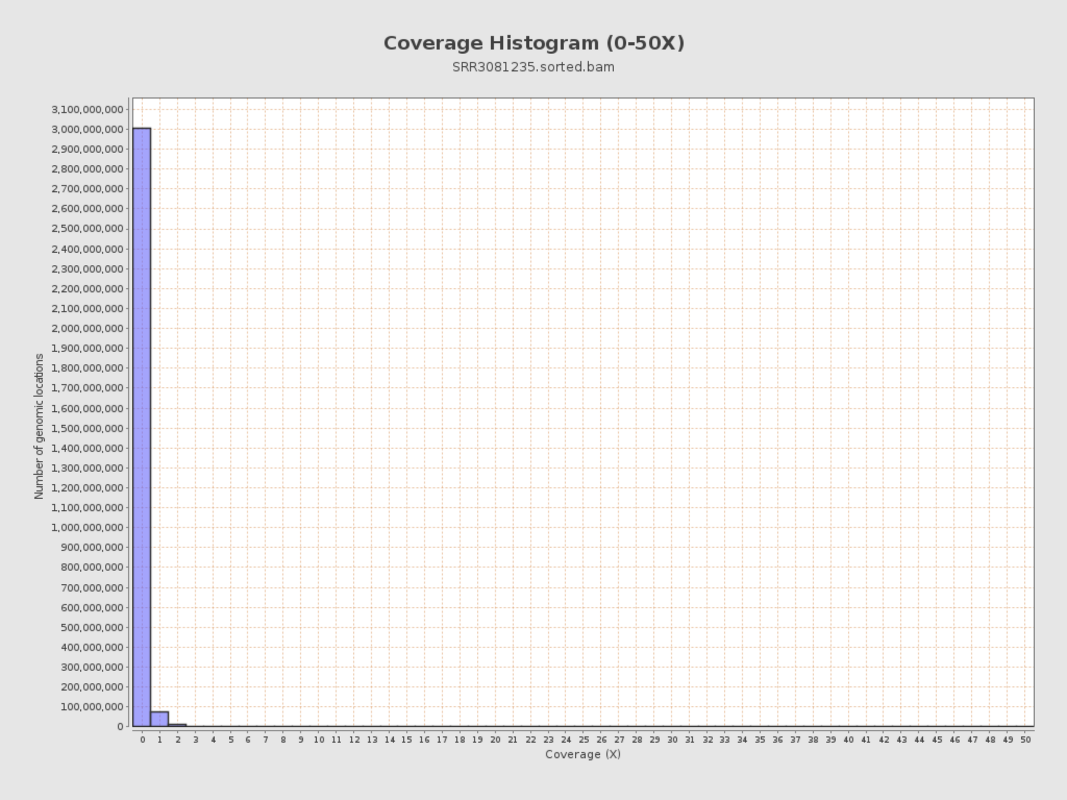
3. Results : Coverage across reference



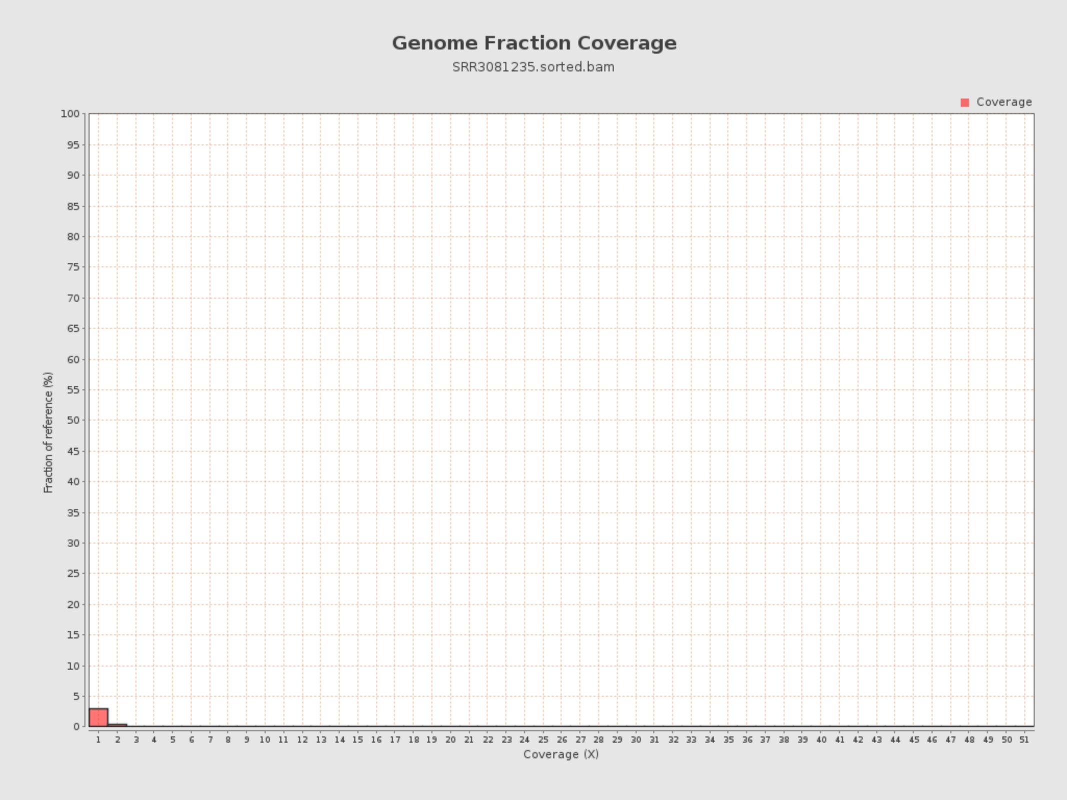
4. Results : Coverage Histogram



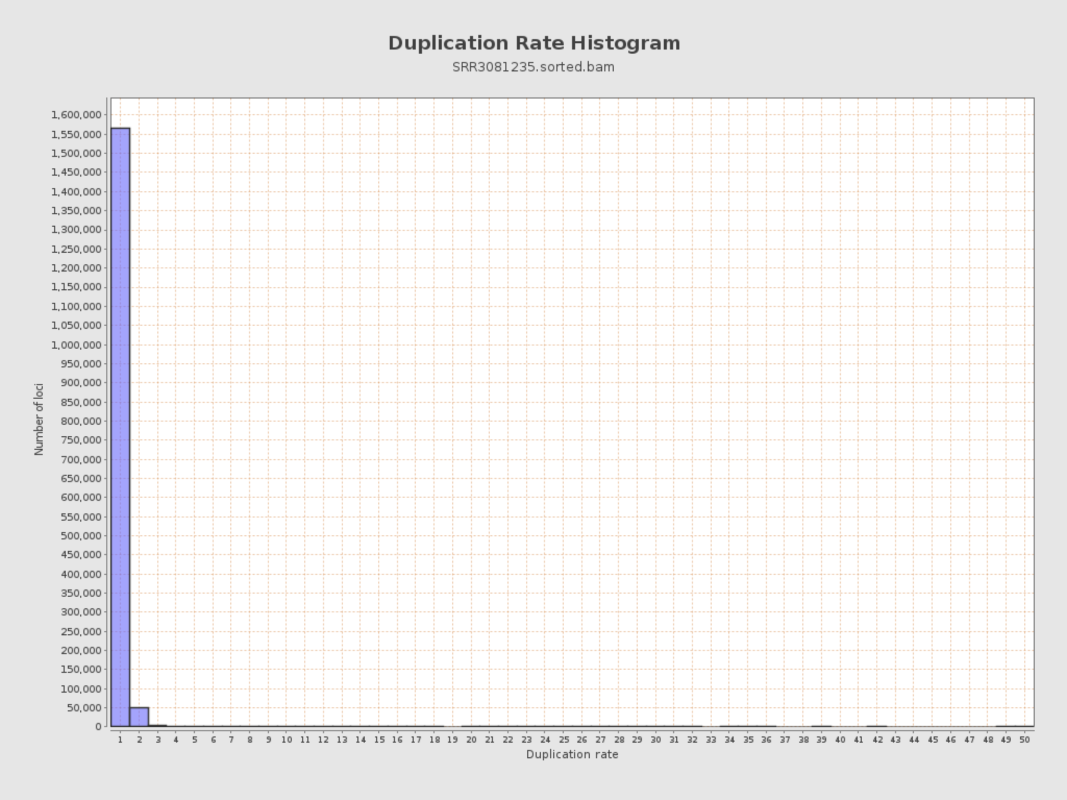
5. Results : Coverage Histogram (0-50X)



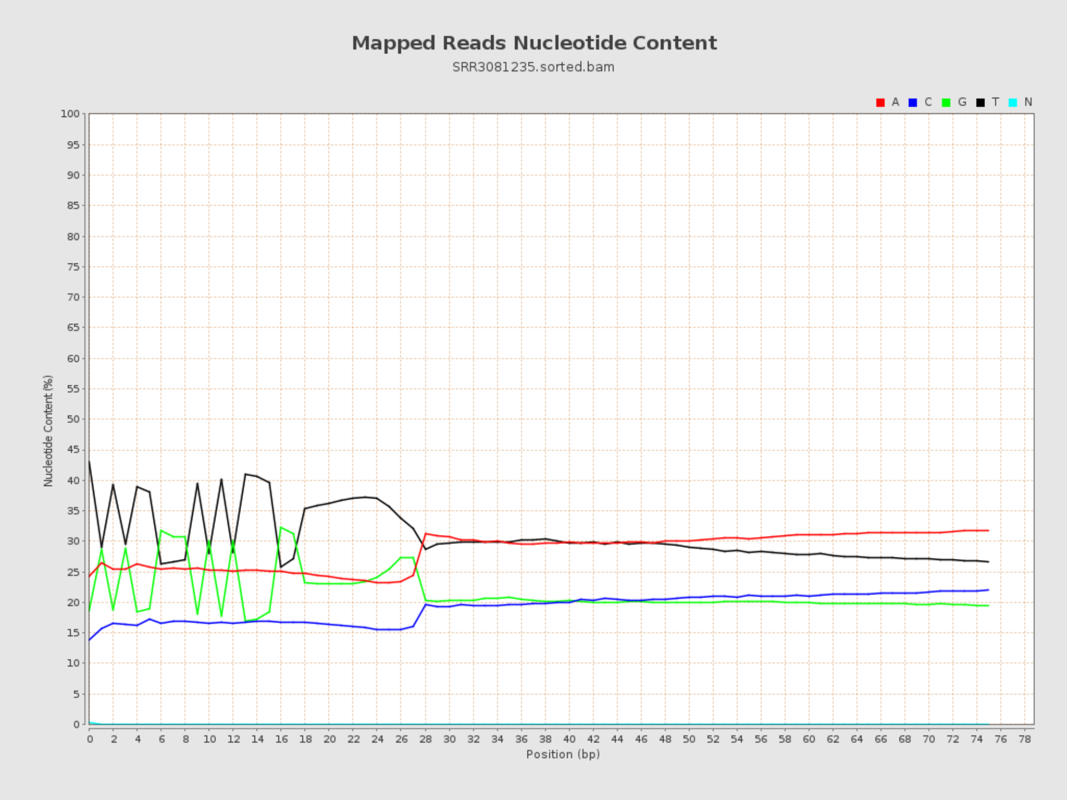
6. Results : Genome Fraction Coverage



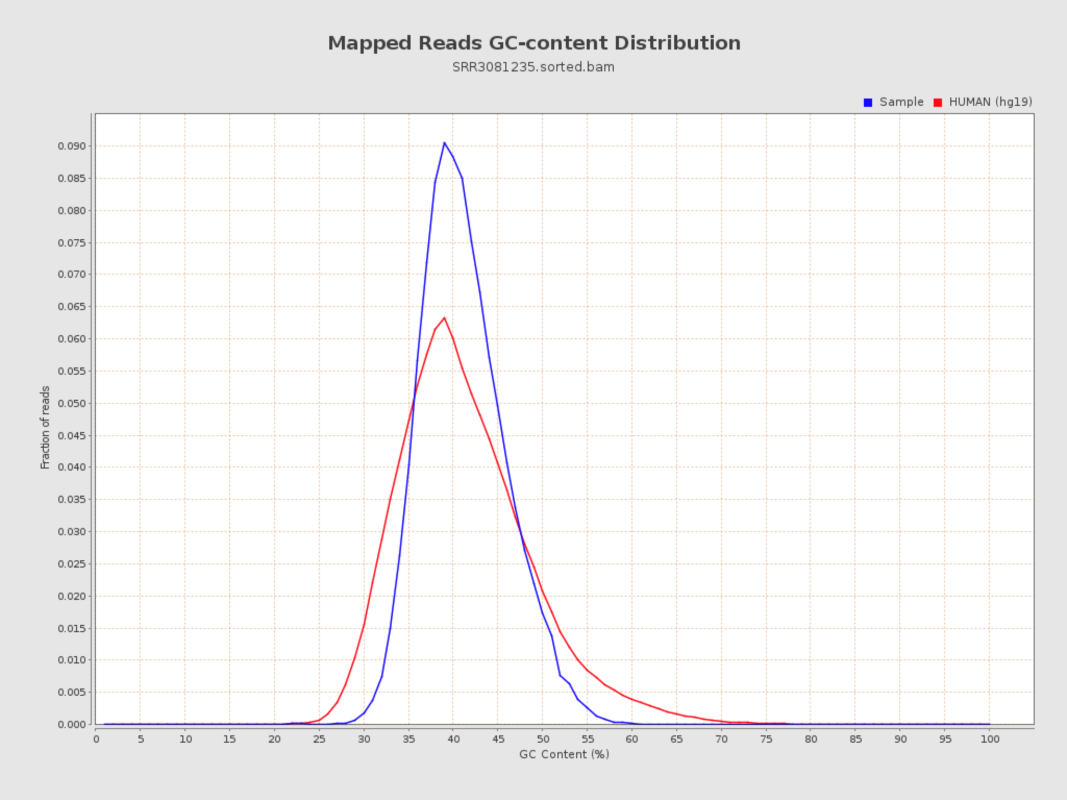
7. Results : Duplication Rate Histogram



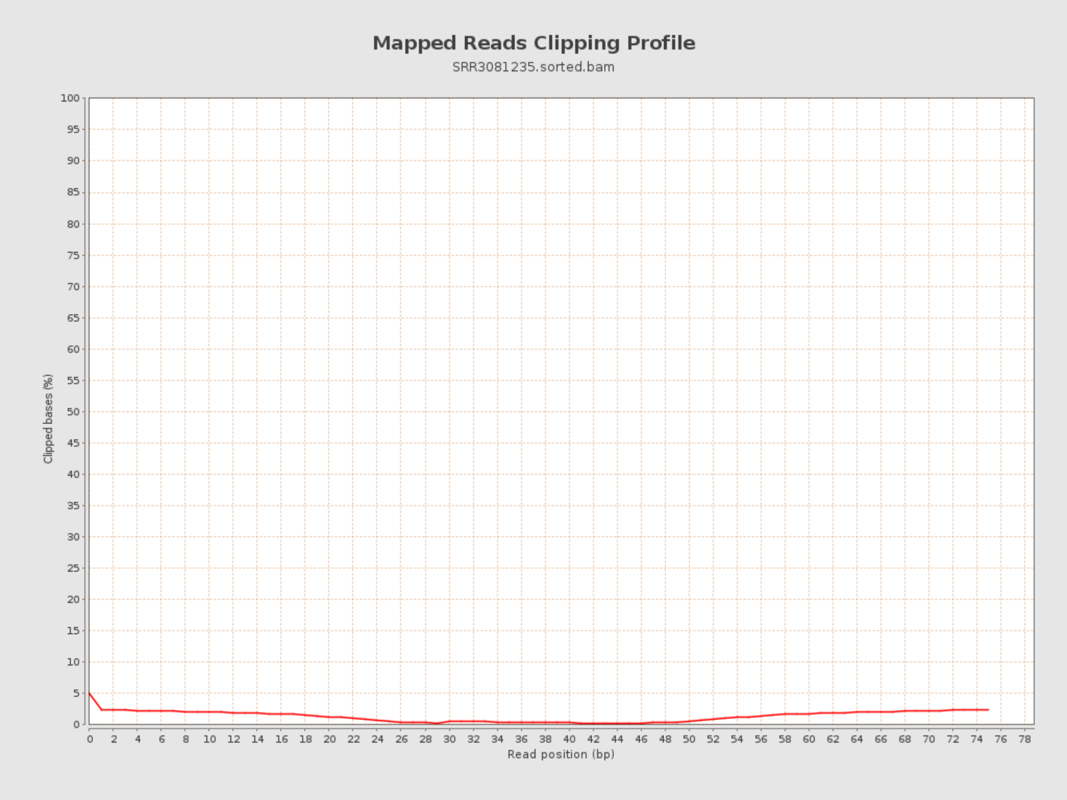
8. Results : Mapped Reads Nucleotide Content



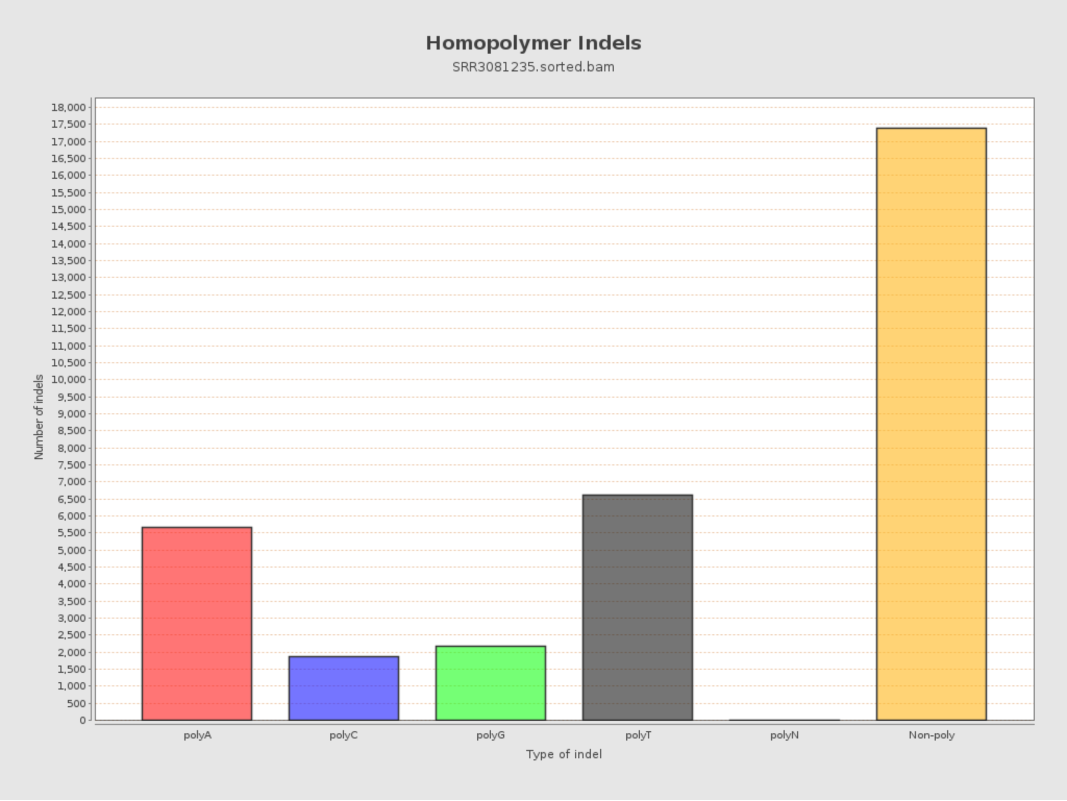
9. Results : Mapped Reads GC-content Distribution



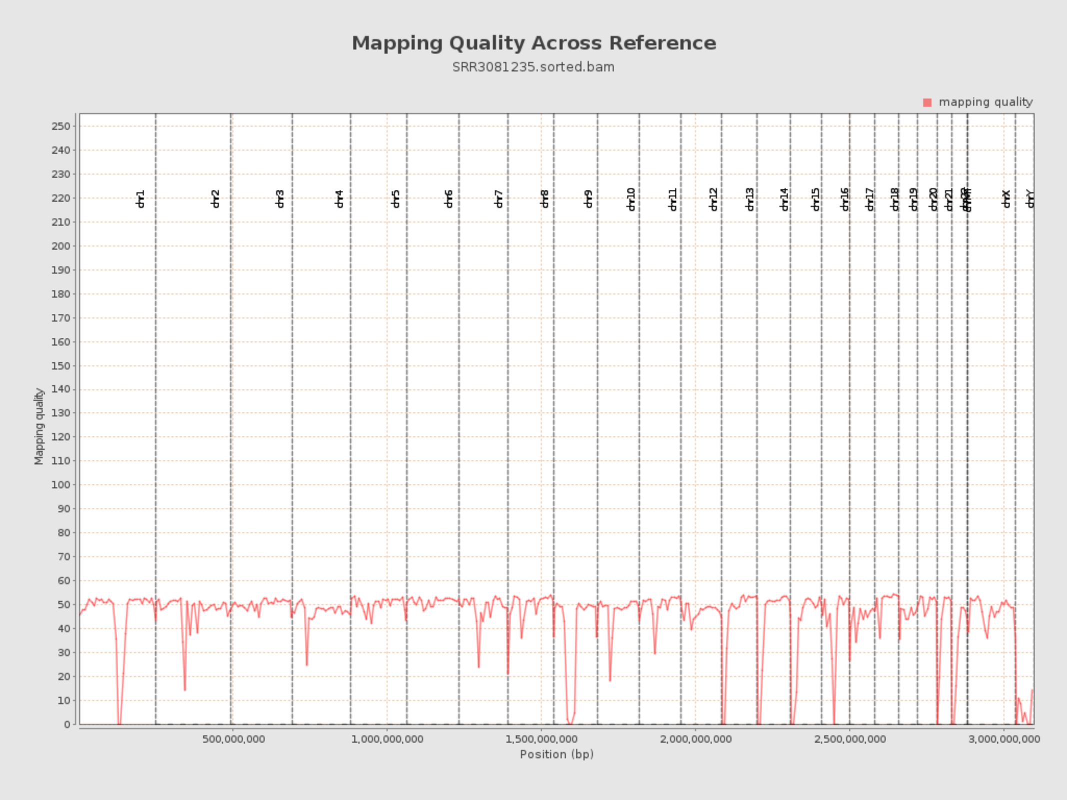
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram