Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:46:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081255.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_SRR3081255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:46:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,051,610
Mapped reads	4,402,115 / 87.14%
Unmapped reads	649,495 / 12.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,477 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	263,636 / 5.22%
Duplication rate	4.52%
Clipped reads	1,722,844 / 34.1%

2.2. ACGT Content

Number/percentage of A's	83,230,671 / 27.84%
Number/percentage of C's	54,571,467 / 18.25%
Number/percentage of T's	95,836,019 / 32.06%
Number/percentage of G's	65,252,526 / 21.83%
Number/percentage of N's	81,763 / 0.03%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0966

Standard Deviation	0.8039

2.4. Mapping Quality

Mean Mapping Quality	47.45

2.5. Mismatches and indels

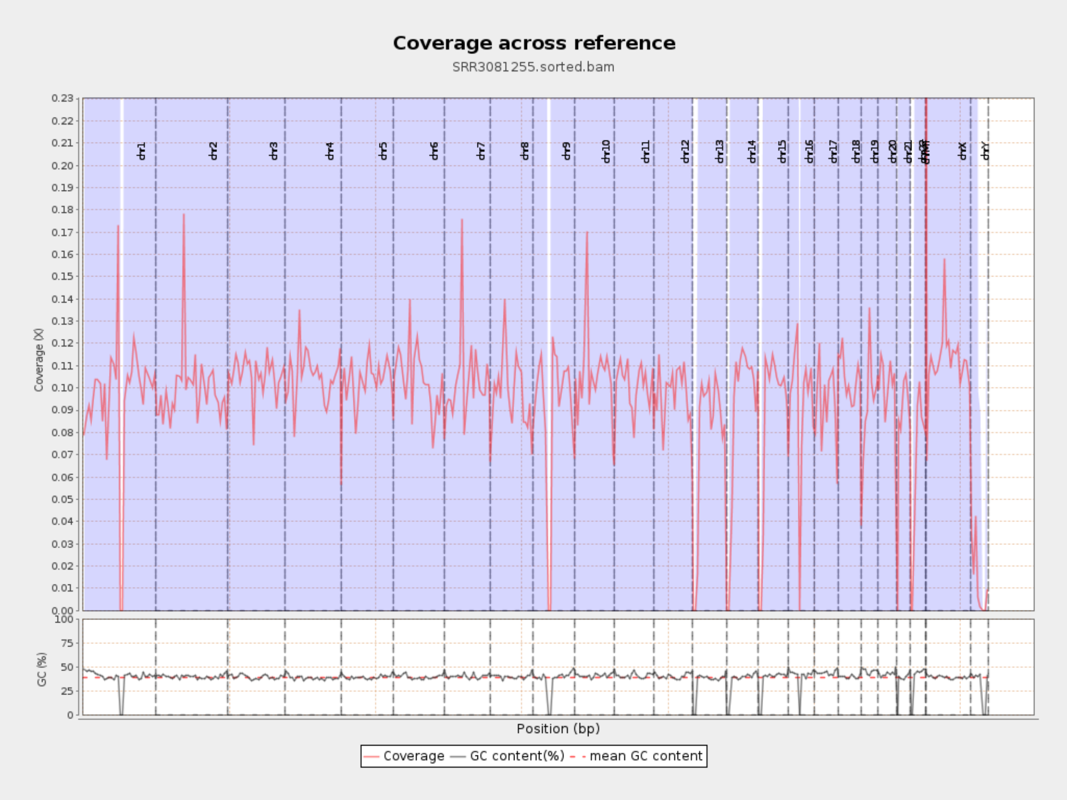
General error rate	0.87%
Mismatches	2,556,113
Insertions	26,039
Mapped reads with at least one insertion	0.59%
Deletions	73,173
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.84%

2.6. Chromosome stats

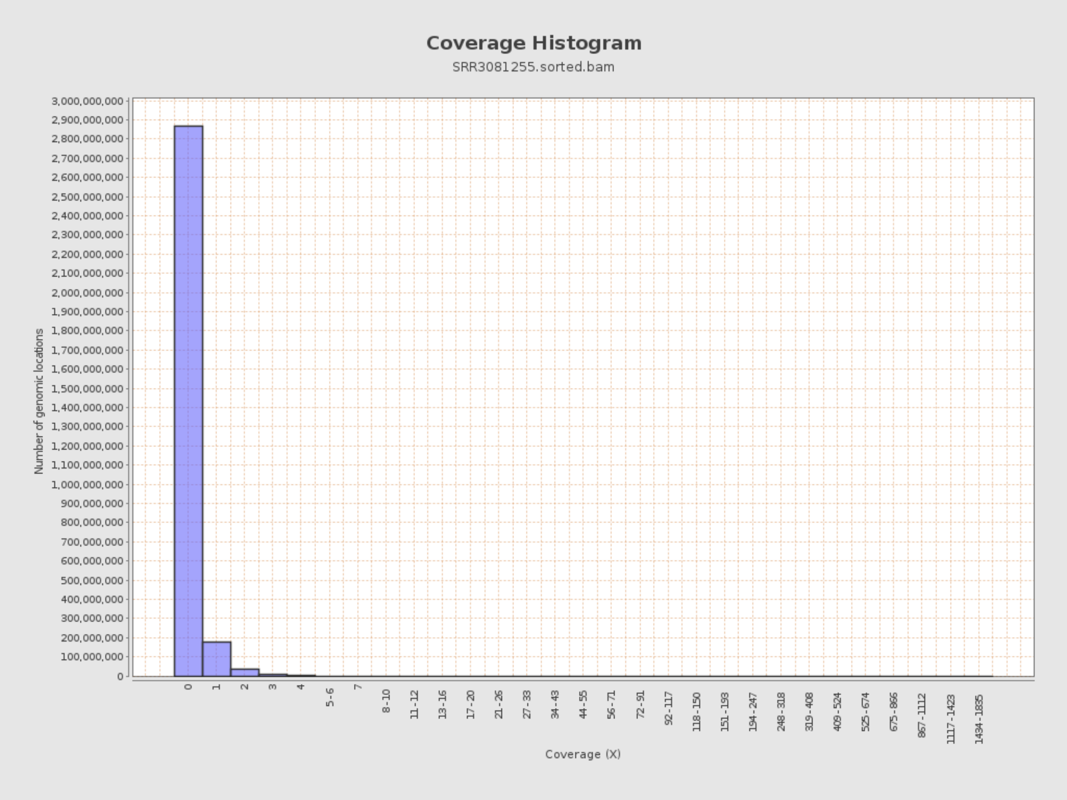
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23901035	0.0959	1.5863
chr2	243199373	24195672	0.0995	0.8001
chr3	198022430	20895757	0.1055	0.4051
chr4	191154276	20181474	0.1056	0.4676
chr5	180915260	18705431	0.1034	0.4047
chr6	171115067	17727206	0.1036	0.5349
chr7	159138663	16482233	0.1036	1.1356

chr8	146364022	14325858	0.0979	1.1941
chr9	141213431	12820969	0.0908	0.7522
chr10	135534747	14478674	0.1068	0.7795
chr11	135006516	13633776	0.101	0.6962
chr12	133851895	13078901	0.0977	0.4027
chr13	115169878	8845022	0.0768	0.3431
chr14	107349540	9561835	0.0891	0.4173
chr15	102531392	8731787	0.0852	0.3628
chr16	90354753	8266071	0.0915	0.4452
chr17	81195210	7698840	0.0948	0.5408
chr18	78077248	8153810	0.1044	1.4929
chr19	59128983	5563762	0.0941	1.0976
chr20	63025520	6376518	0.1012	0.4191
chr21	48129895	4051481	0.0842	0.4476
chr22	51304566	3264571	0.0636	0.3107
chrMT	16571	30546	1.8433	1.805
chrX	155270560	17358002	0.1118	0.4886
chrY	59373566	763906	0.0129	0.2993

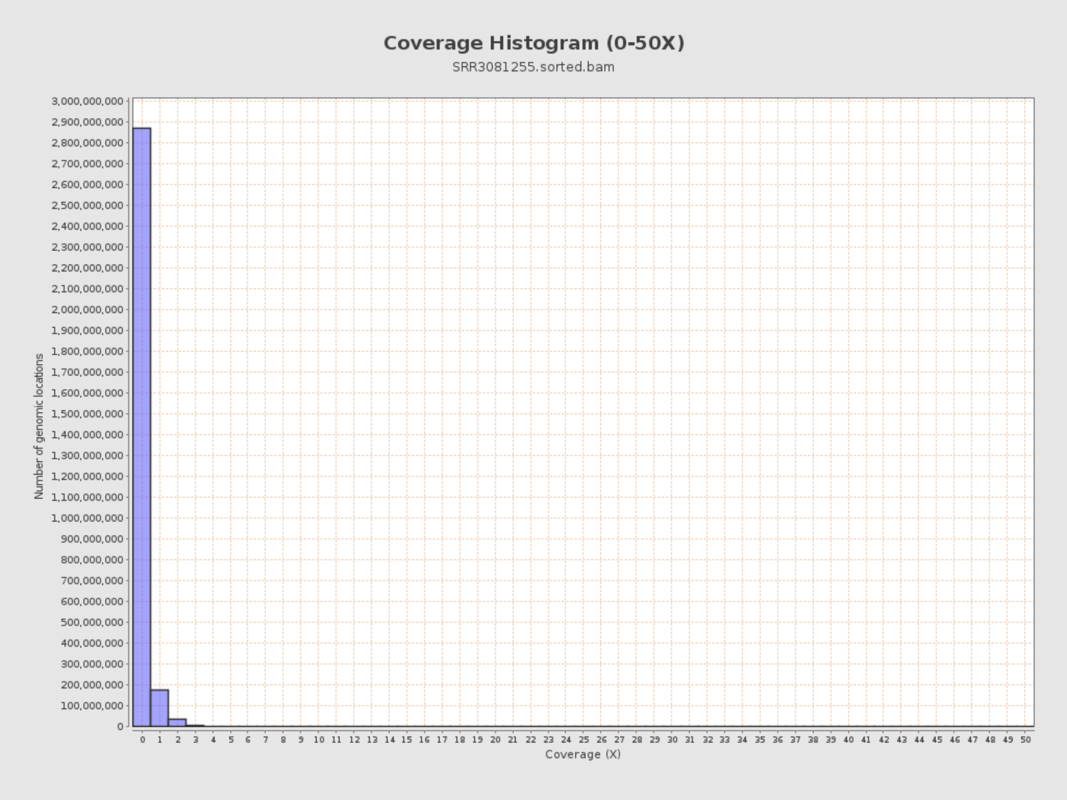
3. Results : Coverage across reference



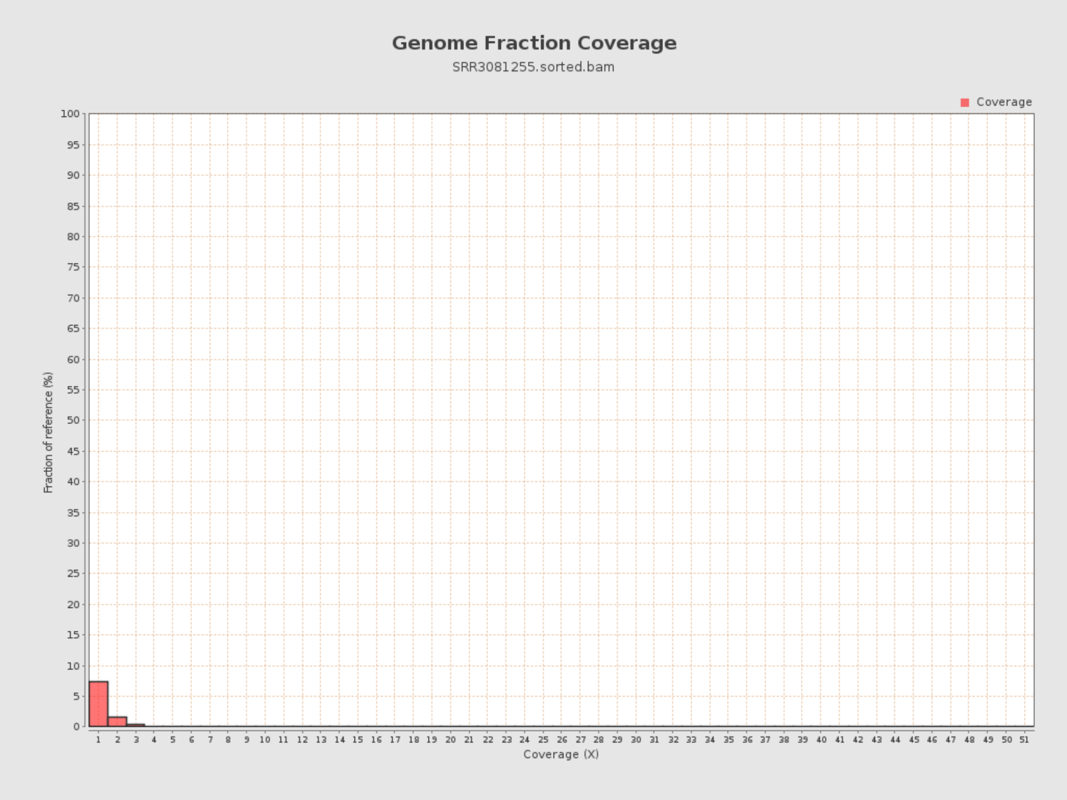
4. Results : Coverage Histogram



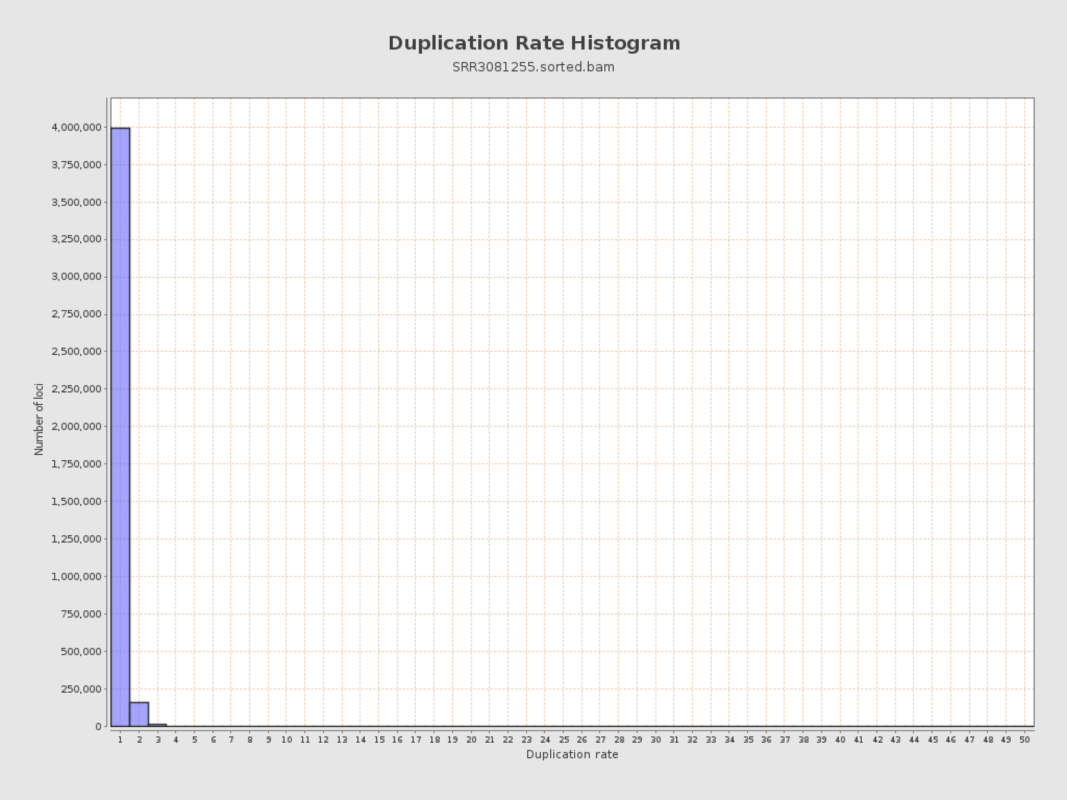
5. Results : Coverage Histogram (0-50X)



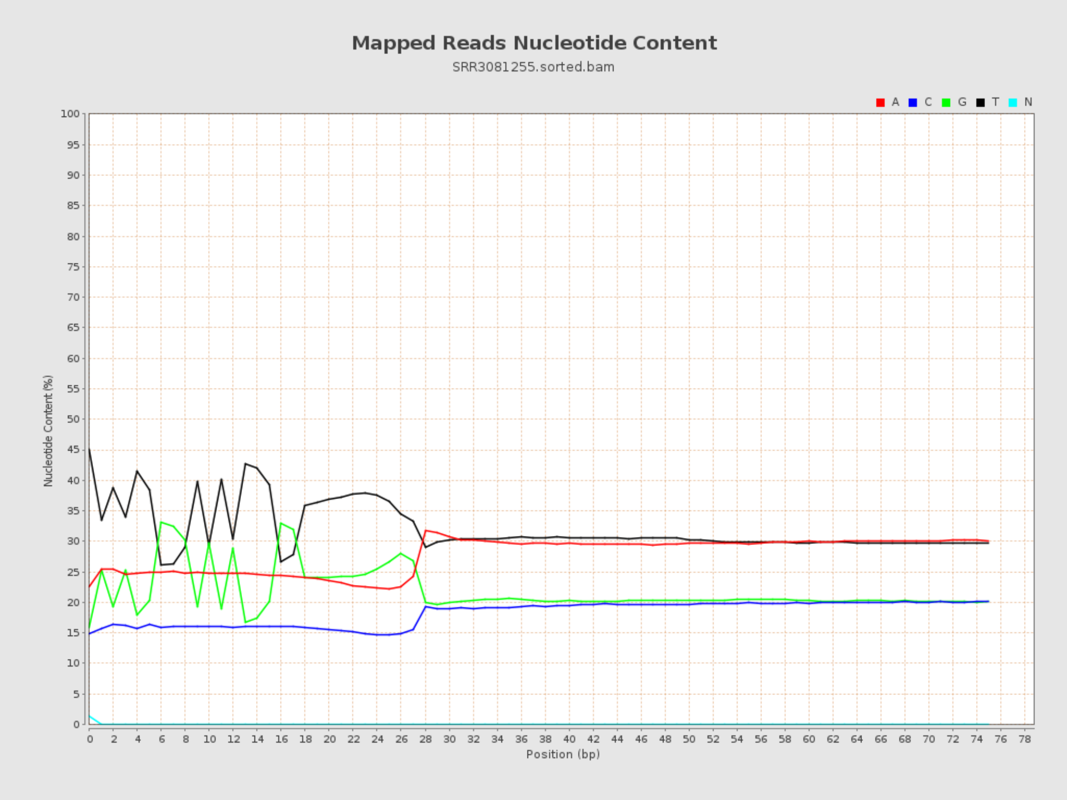
6. Results : Genome Fraction Coverage



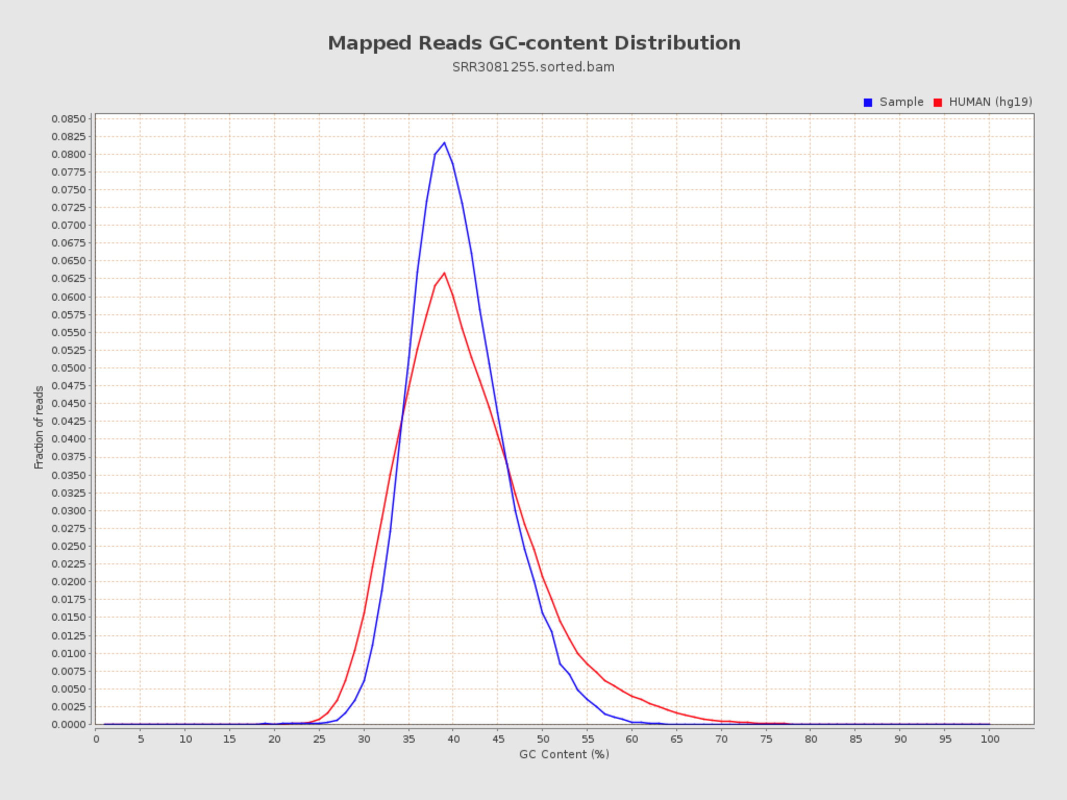
7. Results : Duplication Rate Histogram



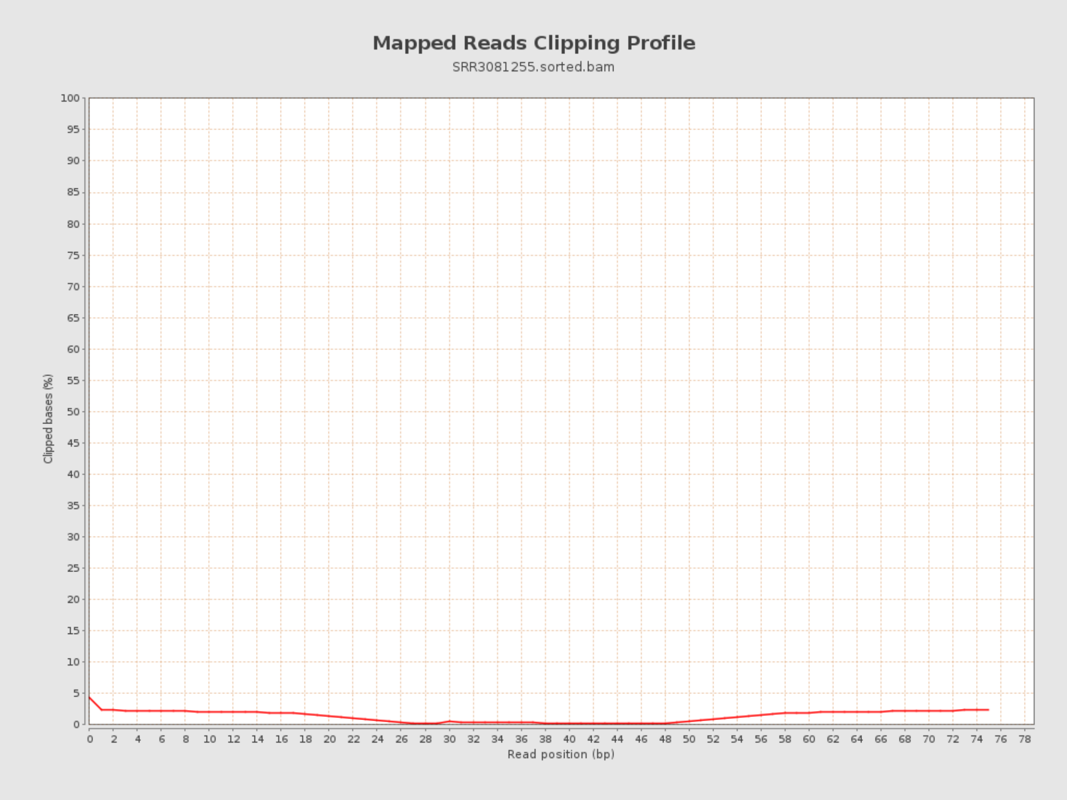
8. Results : Mapped Reads Nucleotide Content



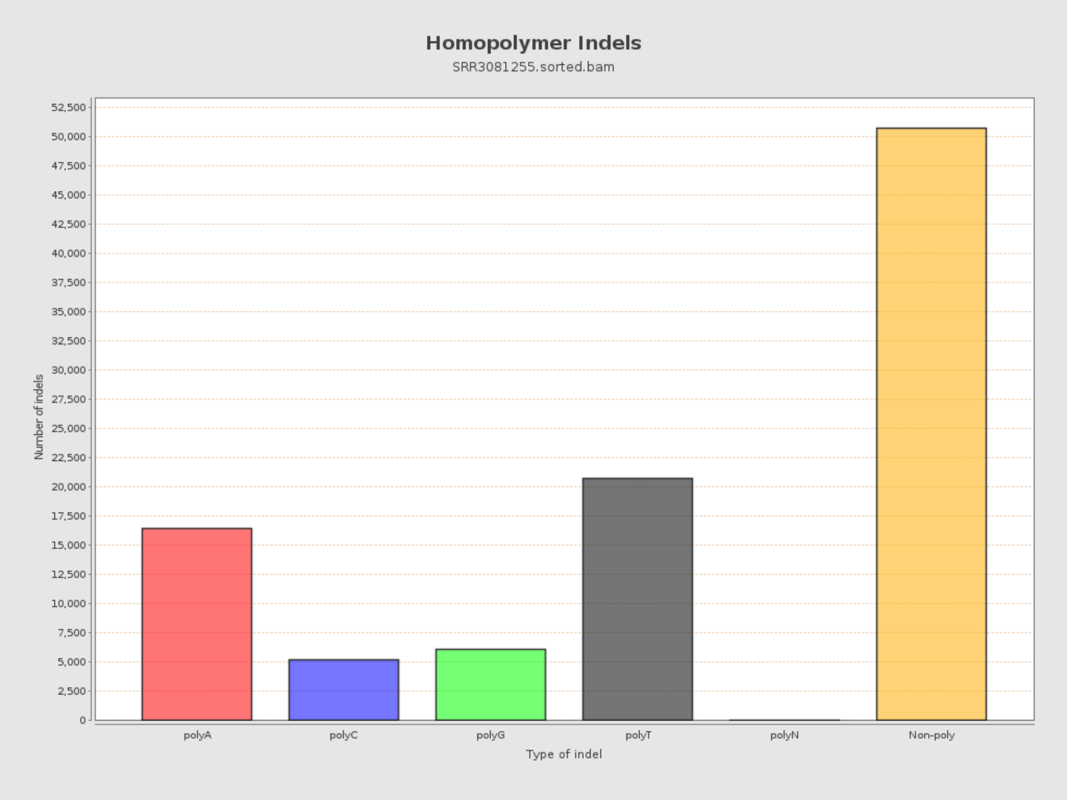
9. Results : Mapped Reads GC-content Distribution



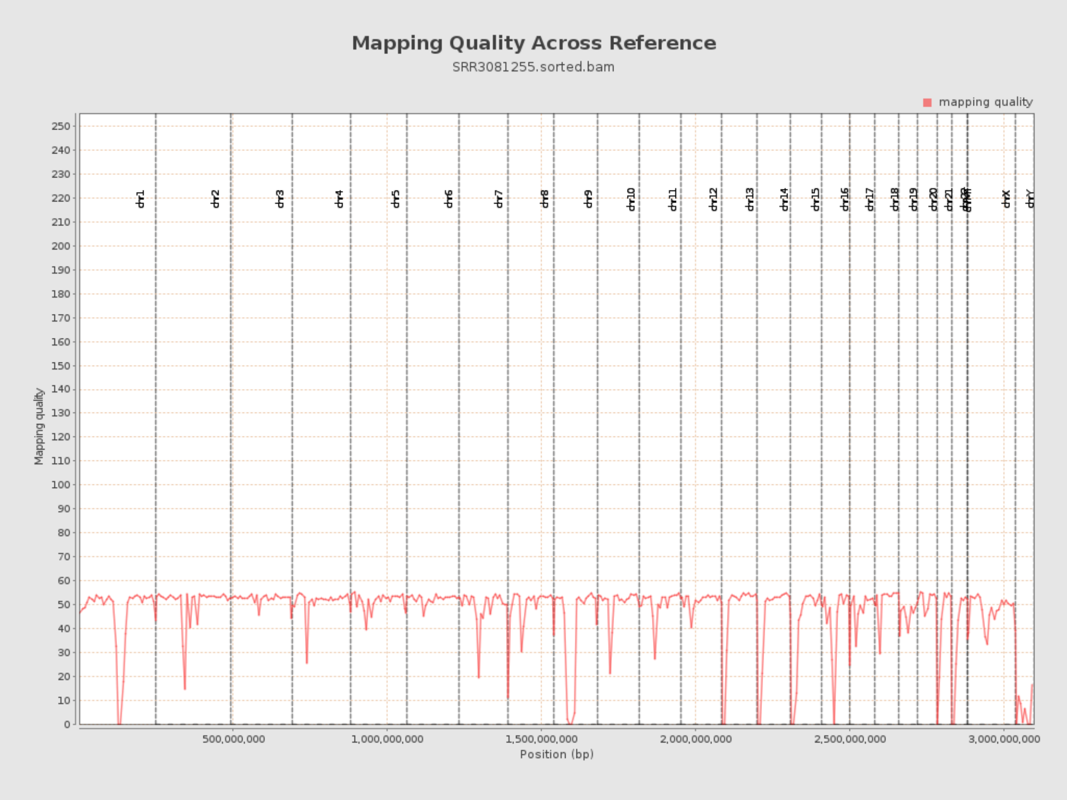
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram