Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:51:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081133.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_SRR3081133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:51:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,924,848
Mapped reads	1,703,893 / 88.52%
Unmapped reads	220,955 / 11.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,062 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	63,486 / 3.3%
Duplication rate	2.87%
Clipped reads	808,381 / 42%

2.2. ACGT Content

Number/percentage of A's	31,215,868 / 27.67%
Number/percentage of C's	20,958,147 / 18.57%
Number/percentage of T's	35,136,642 / 31.14%
Number/percentage of G's	25,491,153 / 22.59%
Number/percentage of N's	33,170 / 0.03%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.3249

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

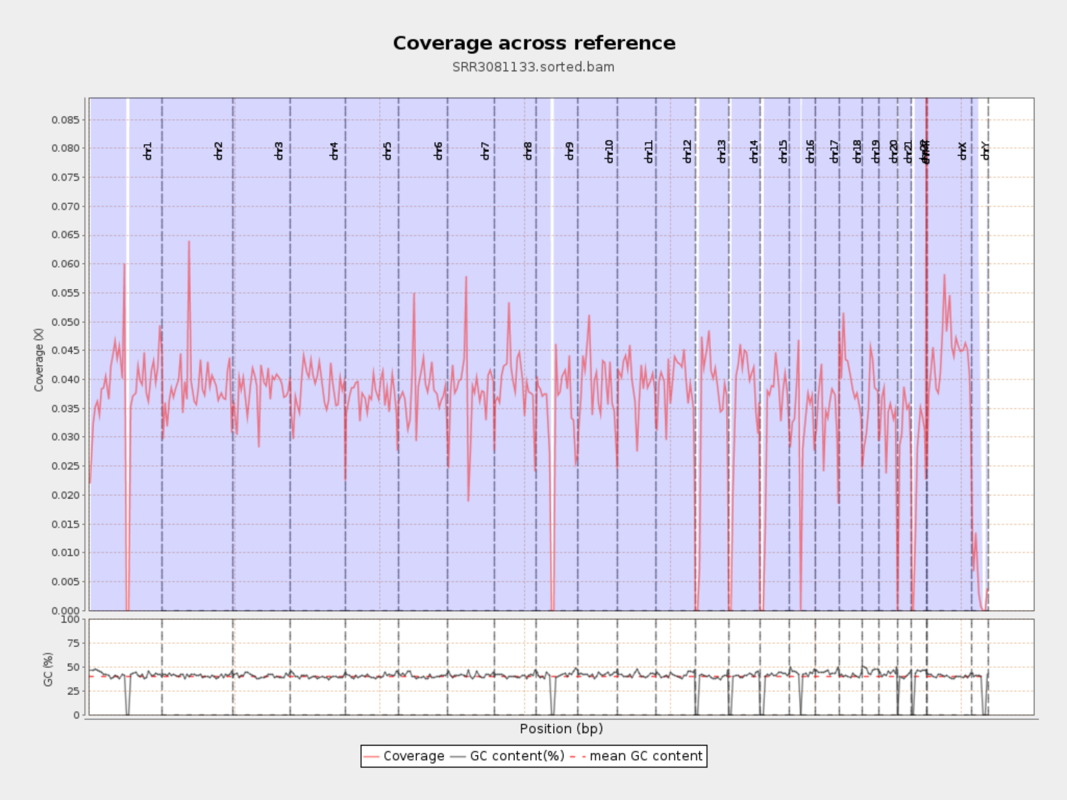
General error rate	0.85%
Mismatches	946,693
Insertions	8,971
Mapped reads with at least one insertion	0.52%
Deletions	24,830
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.19%

2.6. Chromosome stats

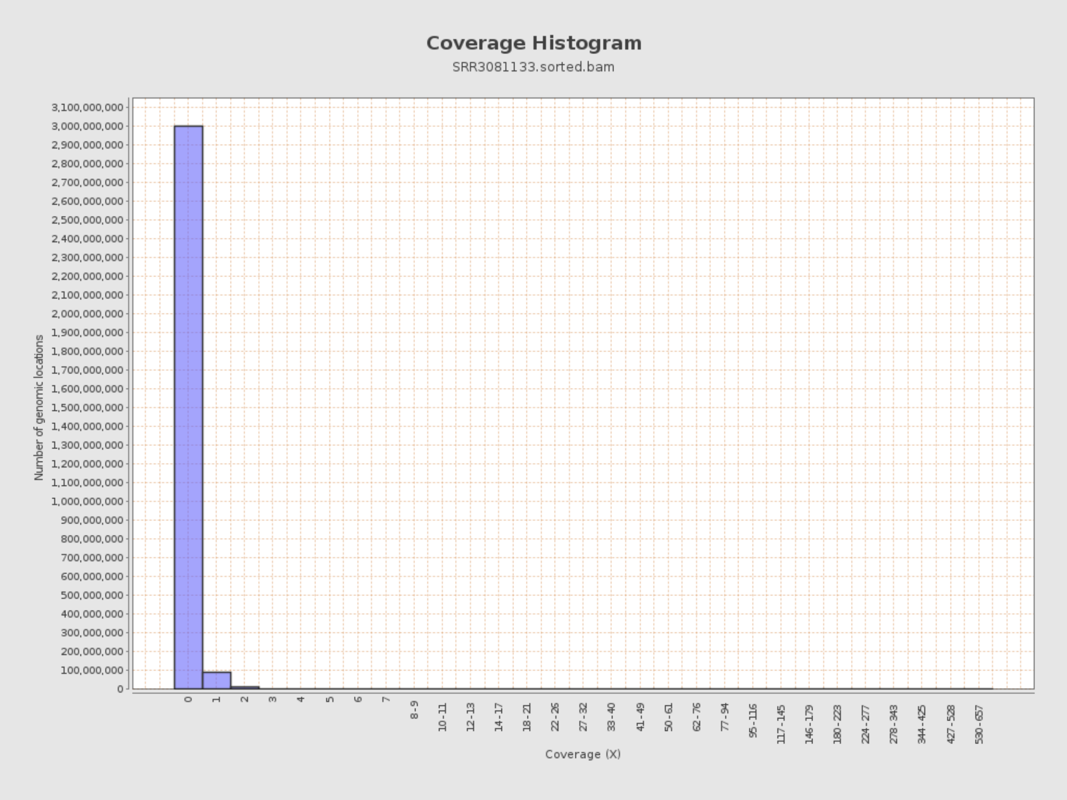
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9381610	0.0376	0.5096
chr2	243199373	9468978	0.0389	0.4237
chr3	198022430	7571863	0.0382	0.2146
chr4	191154276	7355255	0.0385	0.2254
chr5	180915260	6746211	0.0373	0.2132
chr6	171115067	6548179	0.0383	0.2794
chr7	159138663	6049555	0.038	0.4852

chr8	146364022	5766428	0.0394	0.3804
chr9	141213431	4665962	0.033	0.3121
chr10	135534747	5305682	0.0391	0.2717
chr11	135006516	5335314	0.0395	0.3017
chr12	133851895	5214713	0.039	0.221
chr13	115169878	3911350	0.034	0.2026
chr14	107349540	3677562	0.0343	0.226
chr15	102531392	3188462	0.0311	0.2012
chr16	90354753	2873669	0.0318	0.2189
chr17	81195210	2731037	0.0336	0.226
chr18	78077248	3177046	0.0407	0.6017
chr19	59128983	2140012	0.0362	0.3743
chr20	63025520	2069275	0.0328	0.2079
chr21	48129895	1434994	0.0298	0.205
chr22	51304566	1134979	0.0221	0.1627
chrMT	16571	2747	0.1658	0.4821
chrX	155270560	6852169	0.0441	0.2602
chrY	59373566	272089	0.0046	0.1038

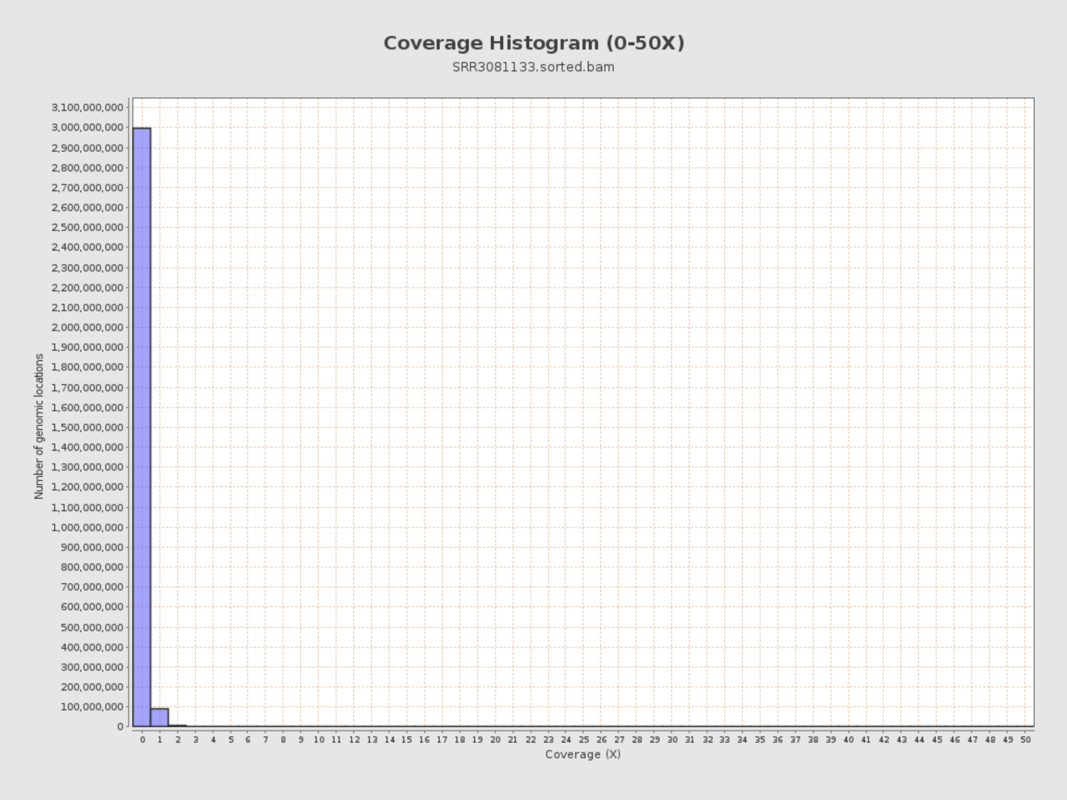
3. Results : Coverage across reference



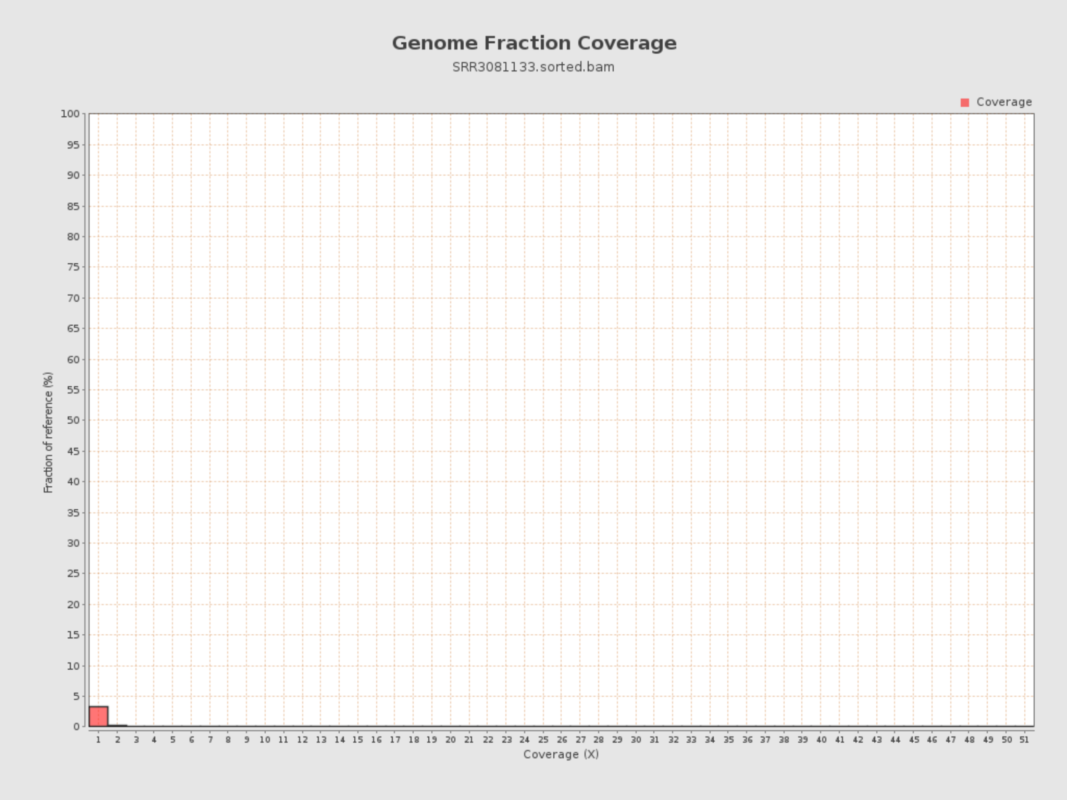
4. Results : Coverage Histogram



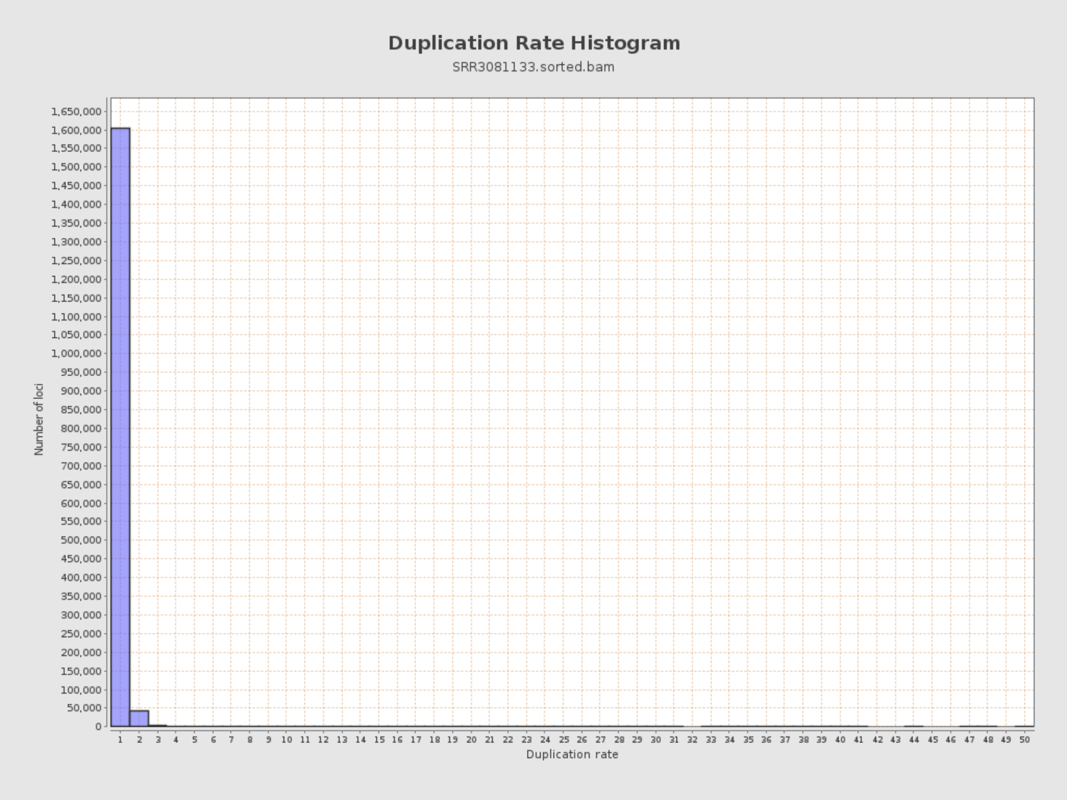
5. Results : Coverage Histogram (0-50X)



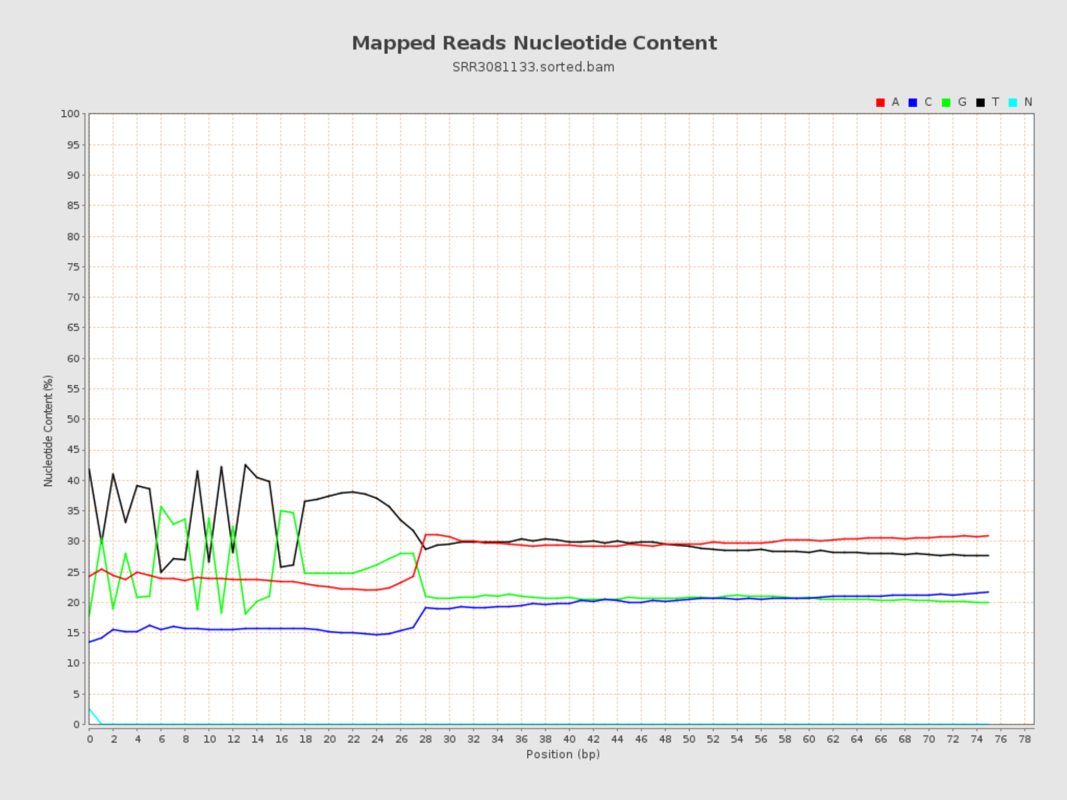
6. Results : Genome Fraction Coverage



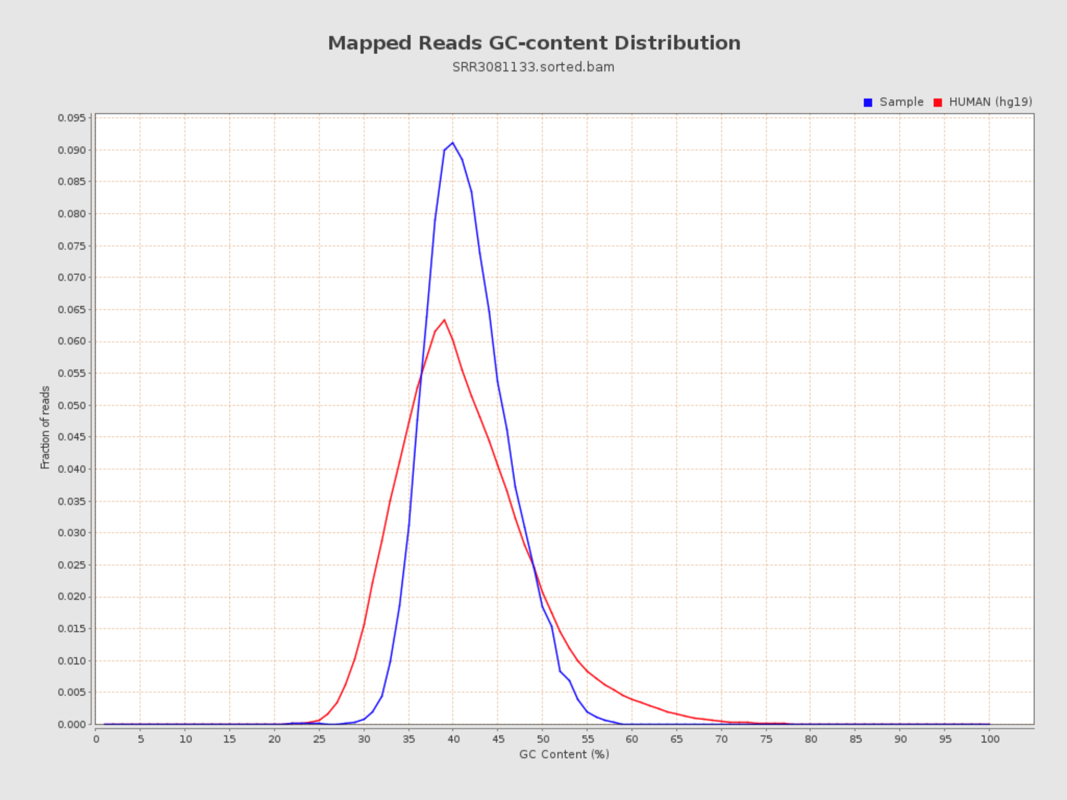
7. Results : Duplication Rate Histogram



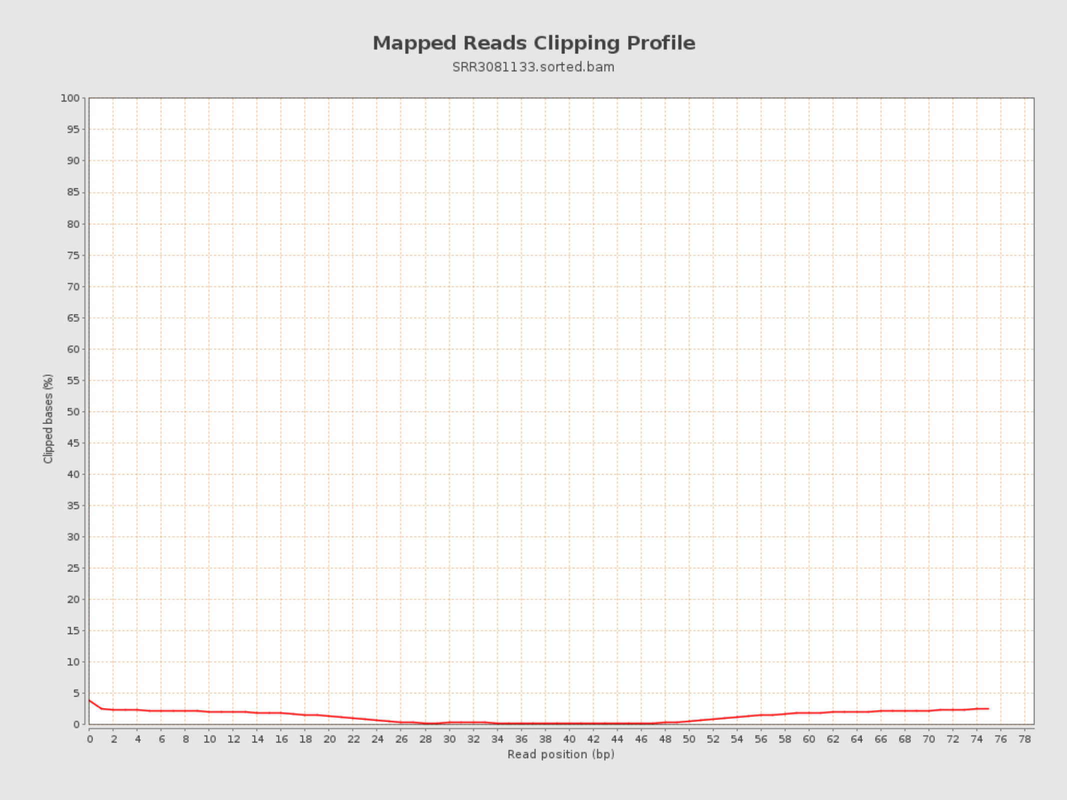
8. Results : Mapped Reads Nucleotide Content



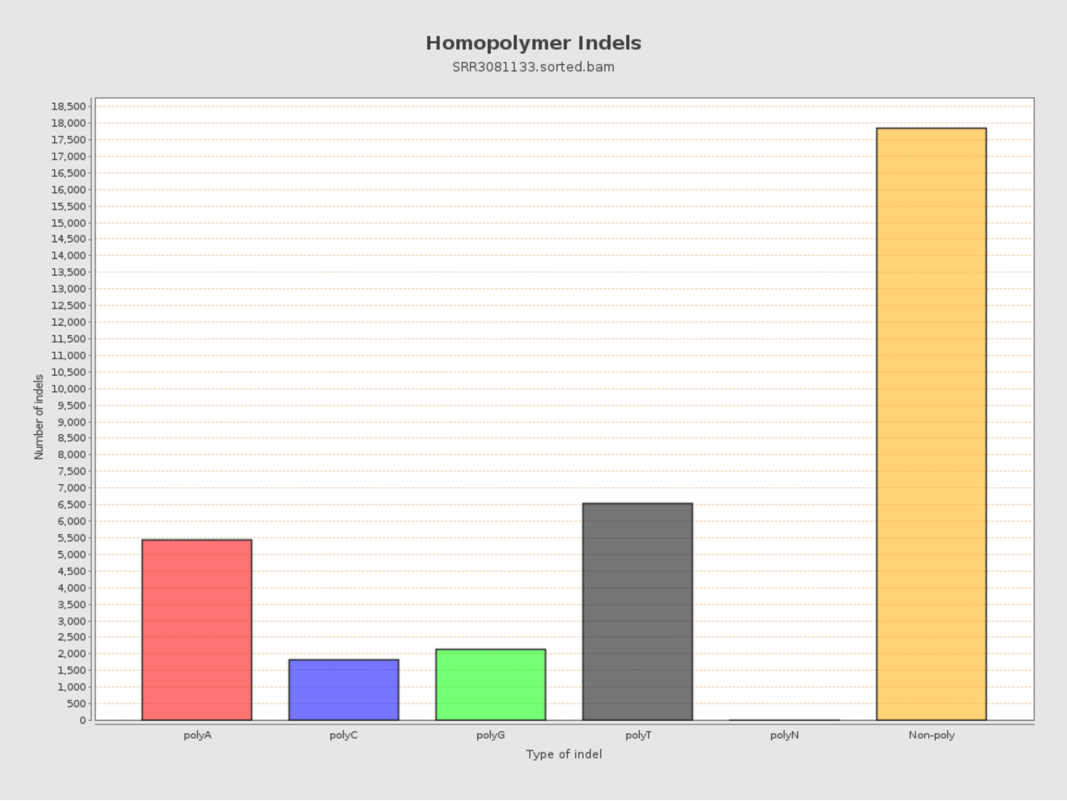
9. Results : Mapped Reads GC-content Distribution



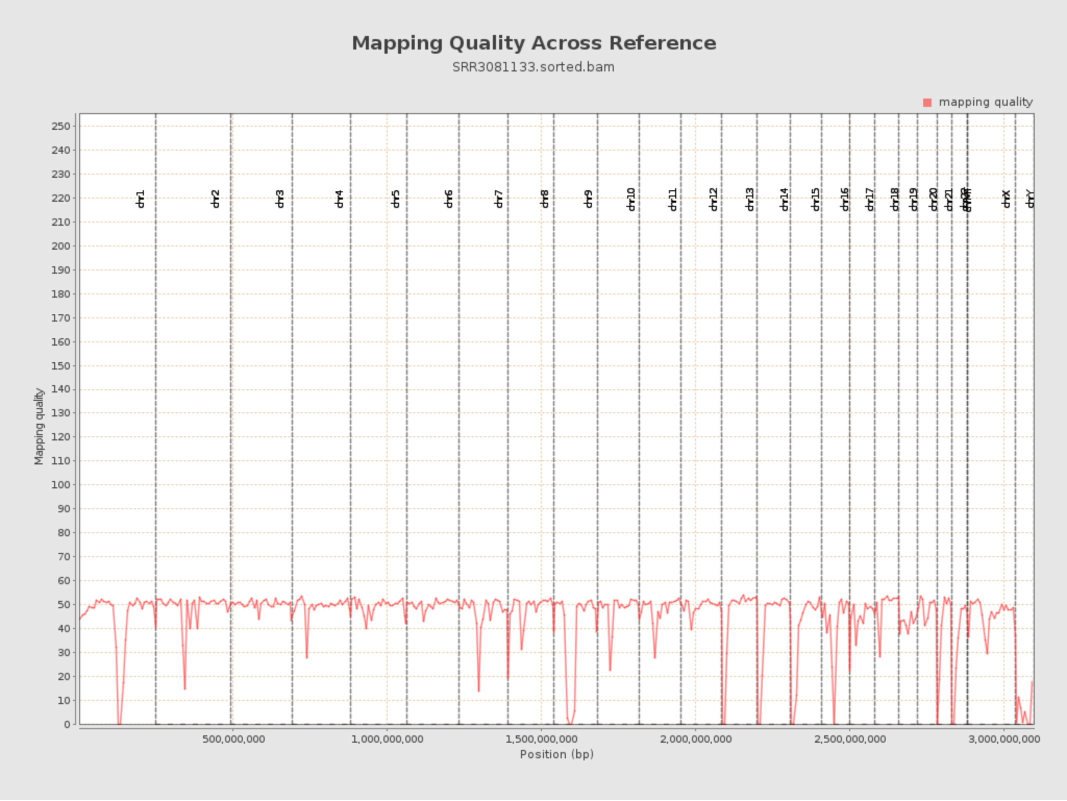
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram