Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:52:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082918.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_SRR3082918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,983,166
Mapped reads	1,766,643 / 89.08%
Unmapped reads	216,523 / 10.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,017 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	87,914 / 4.43%
Duplication rate	4.04%
Clipped reads	820,061 / 41.35%

2.2. ACGT Content

Number/percentage of A's	31,137,544 / 26.64%
Number/percentage of C's	21,913,747 / 18.75%
Number/percentage of T's	36,701,907 / 31.41%
Number/percentage of G's	27,102,325 / 23.19%
Number/percentage of N's	5,526 / 0%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3281

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

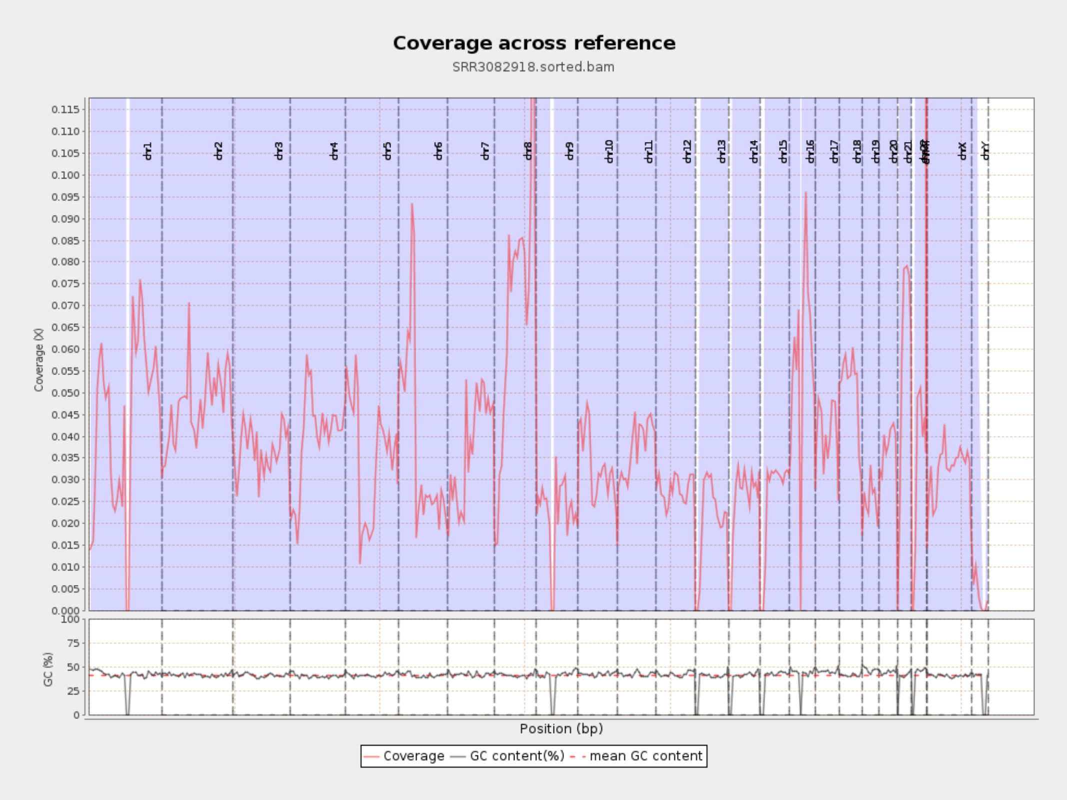
General error rate	0.77%
Mismatches	887,260
Insertions	9,606
Mapped reads with at least one insertion	0.54%
Deletions	27,810
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.39%

2.6. Chromosome stats

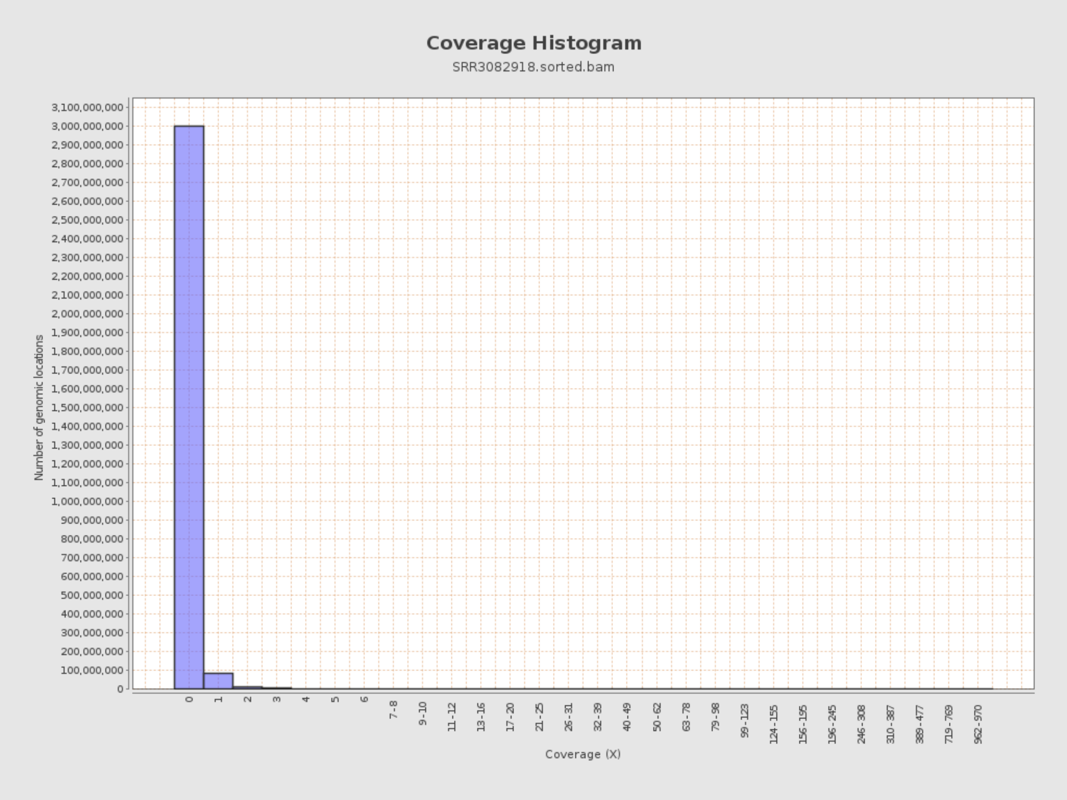
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10959442	0.044	0.467
chr2	243199373	11516310	0.0474	0.5396
chr3	198022430	7348661	0.0371	0.2215
chr4	191154276	7568185	0.0396	0.2376
chr5	180915260	6426732	0.0355	0.2184
chr6	171115067	6580088	0.0385	0.2772
chr7	159138663	6038159	0.0379	0.3879

chr8	146364022	10446408	0.0714	0.3756
chr9	141213431	3143694	0.0223	0.2901
chr10	135534747	4567709	0.0337	0.2549
chr11	135006516	4980620	0.0369	0.2973
chr12	133851895	3702989	0.0277	0.1947
chr13	115169878	2351028	0.0204	0.1675
chr14	107349540	2635534	0.0246	0.1946
chr15	102531392	2586788	0.0252	0.1963
chr16	90354753	5214156	0.0577	0.2933
chr17	81195210	3276149	0.0403	0.2564
chr18	78077248	4046241	0.0518	0.6458
chr19	59128983	1497999	0.0253	0.3474
chr20	63025520	2366012	0.0375	0.2382
chr21	48129895	2741482	0.057	0.2821
chr22	51304566	1610609	0.0314	0.2047
chrMT	16571	51606	3.1142	2.5941
chrX	155270560	5029099	0.0324	0.237
chrY	59373566	221161	0.0037	0.0836

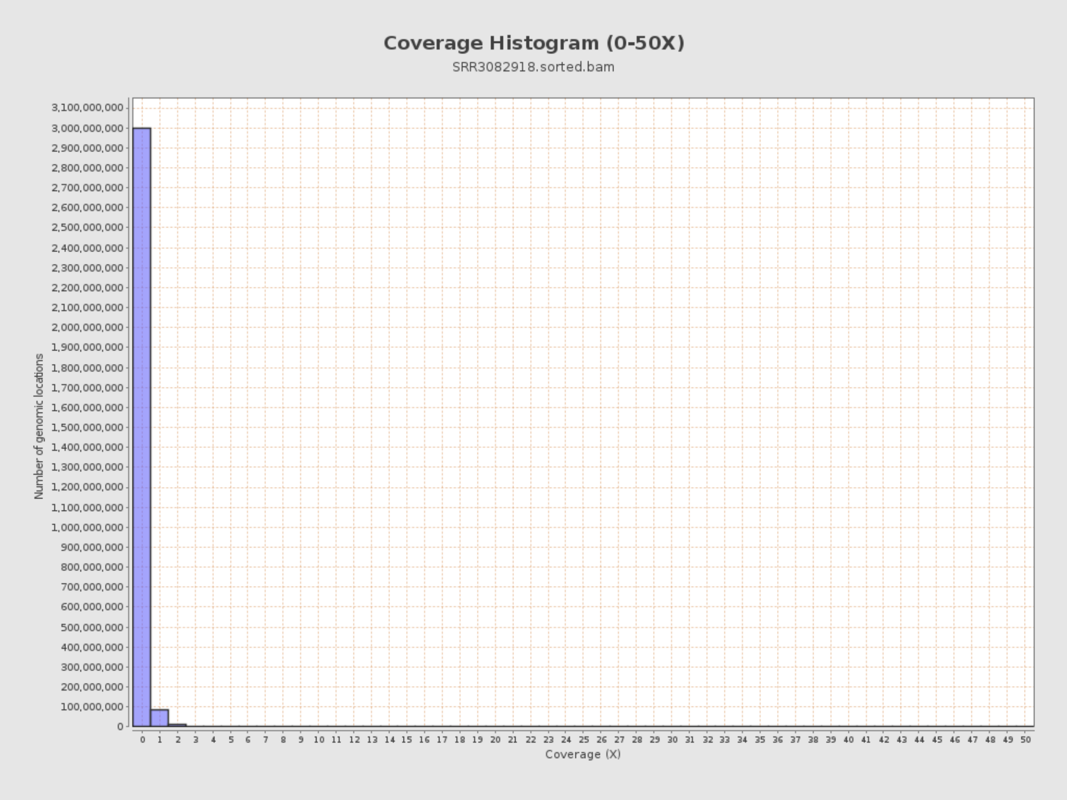
3. Results : Coverage across reference



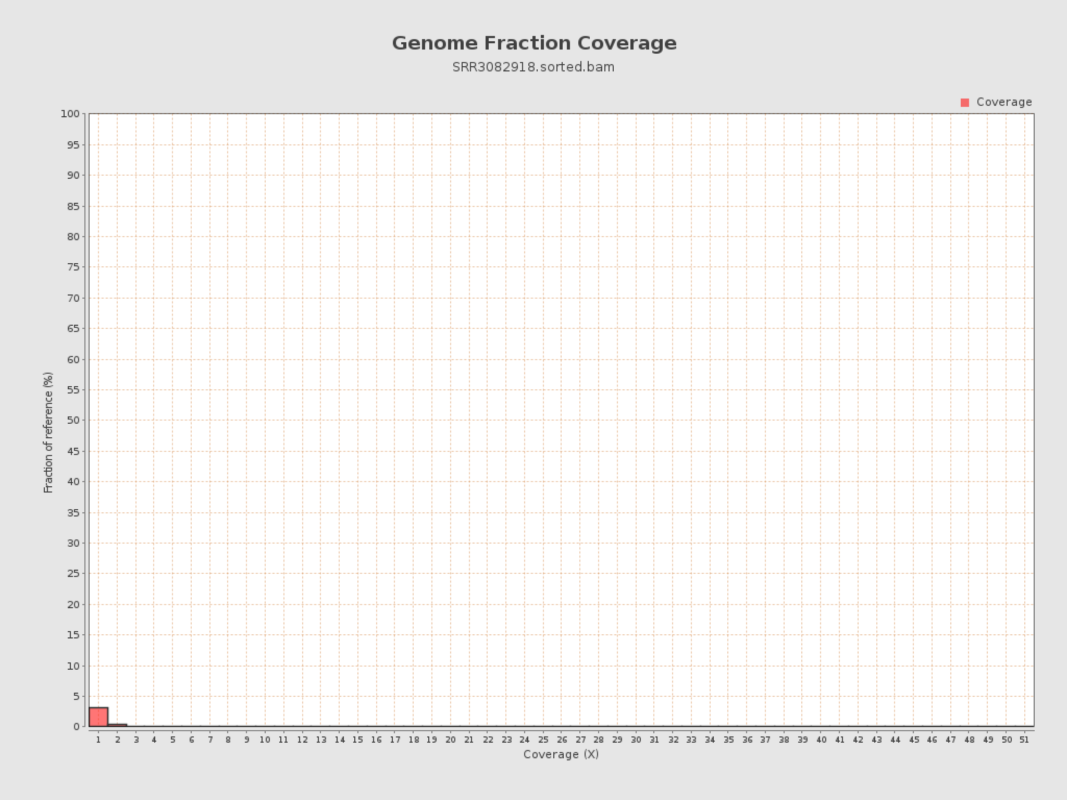
4. Results : Coverage Histogram



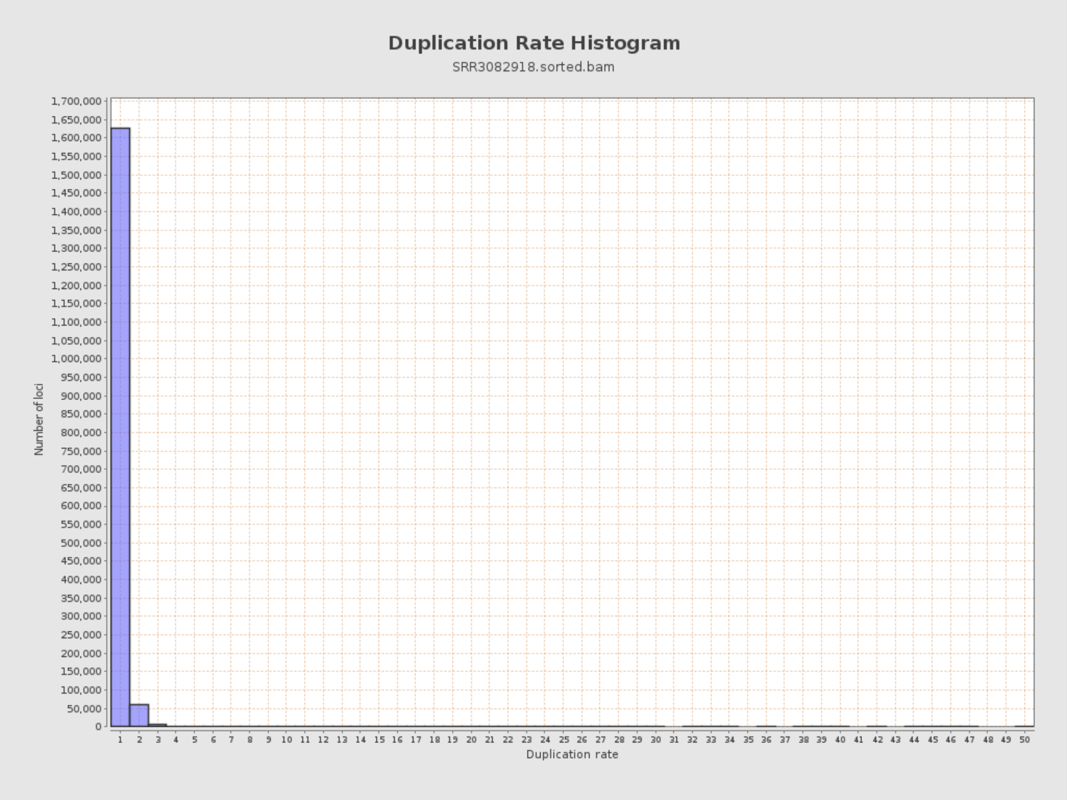
5. Results : Coverage Histogram (0-50X)



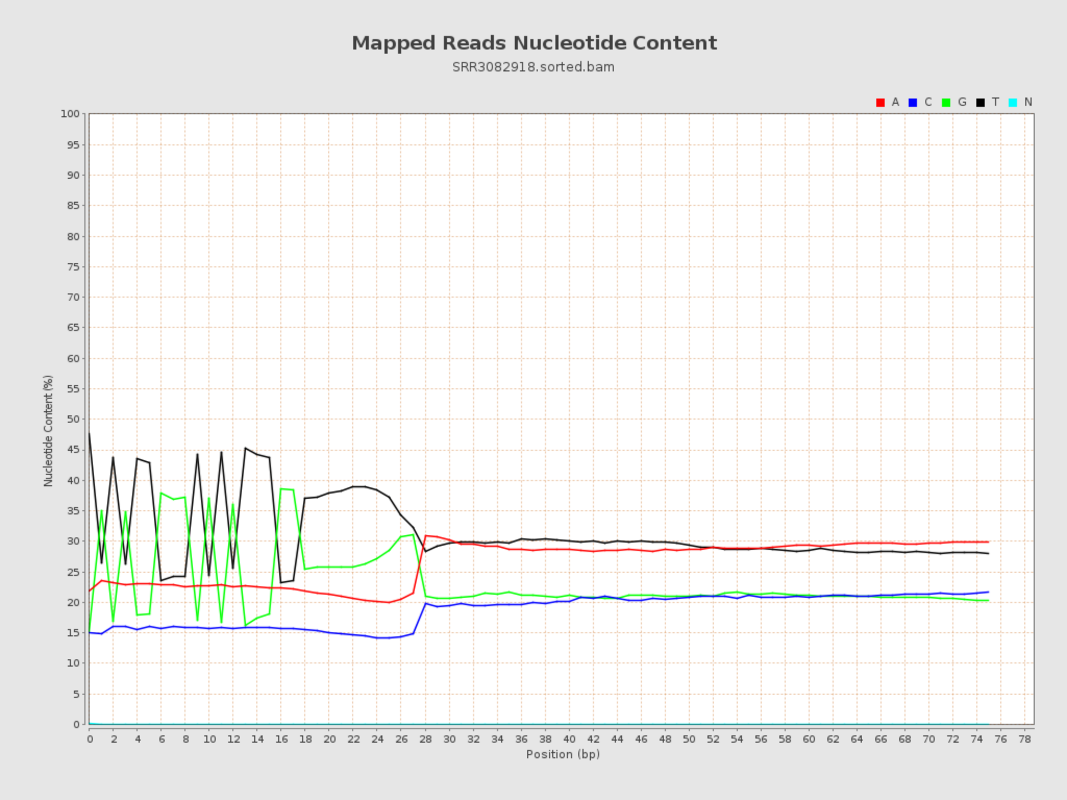
6. Results : Genome Fraction Coverage



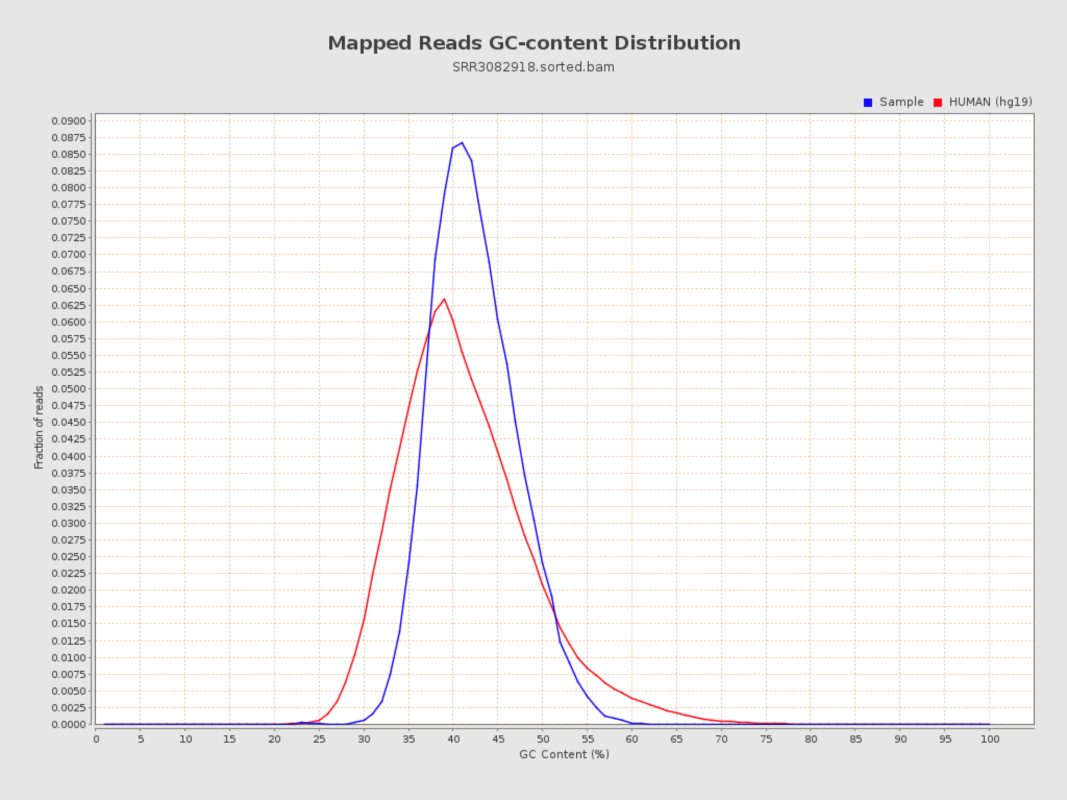
7. Results : Duplication Rate Histogram



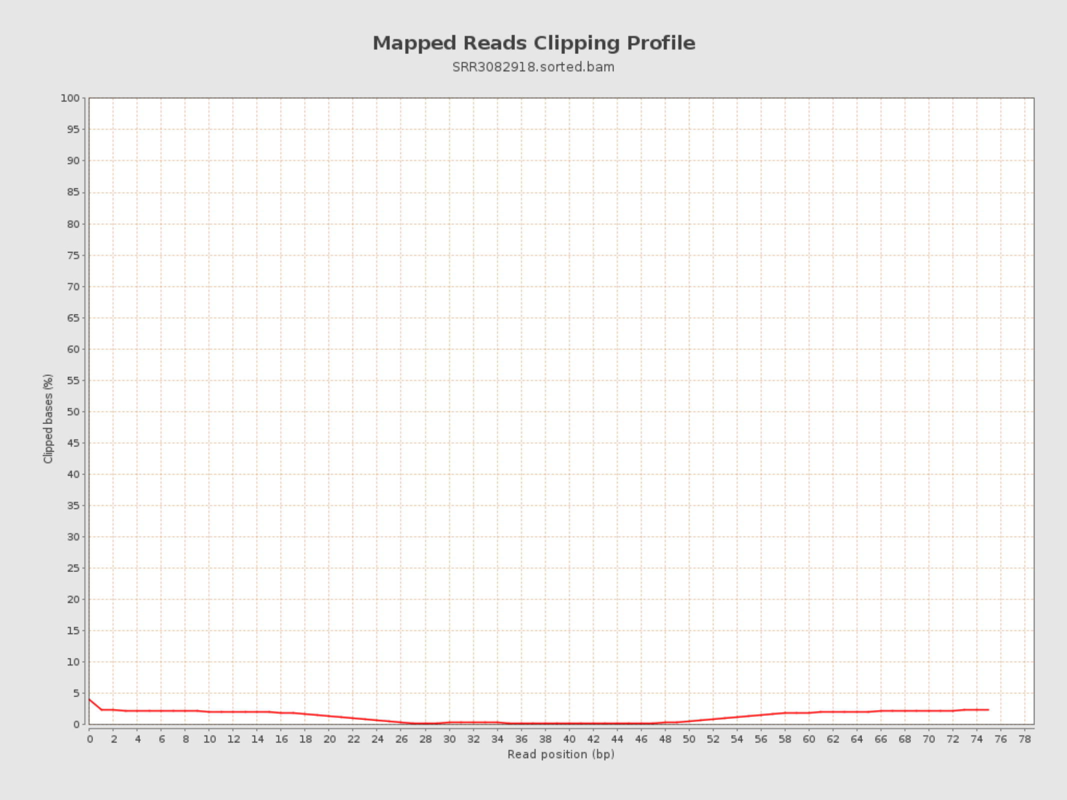
8. Results : Mapped Reads Nucleotide Content



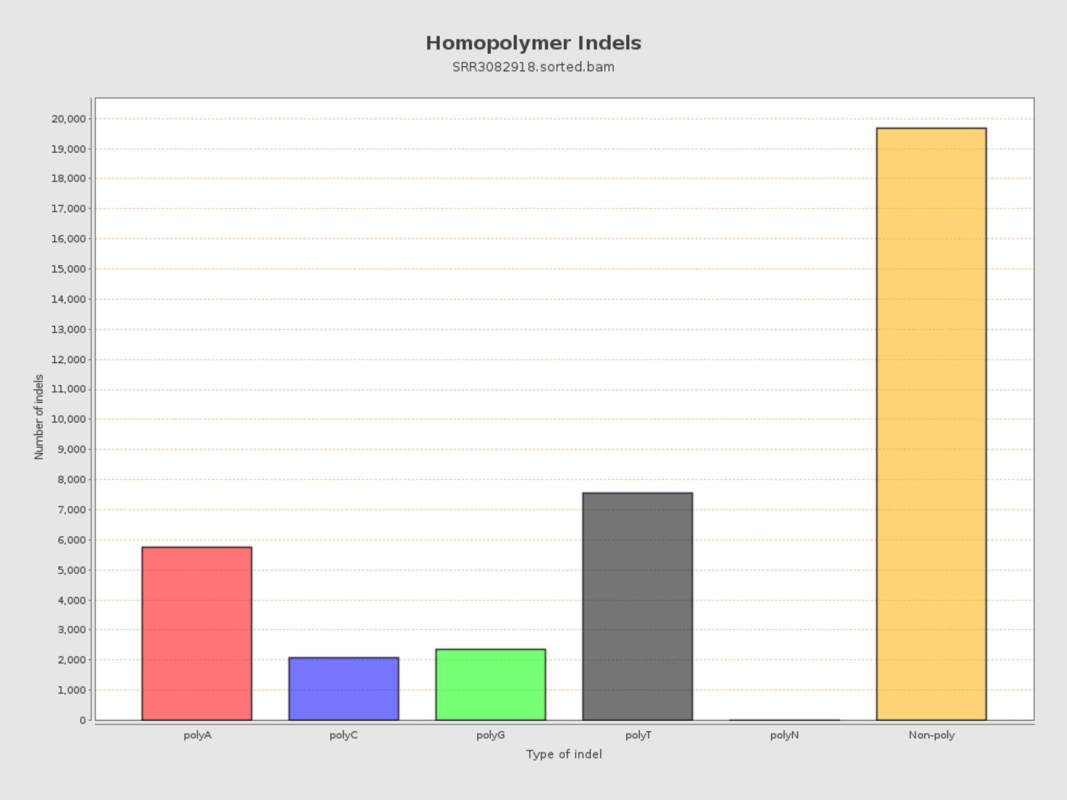
9. Results : Mapped Reads GC-content Distribution



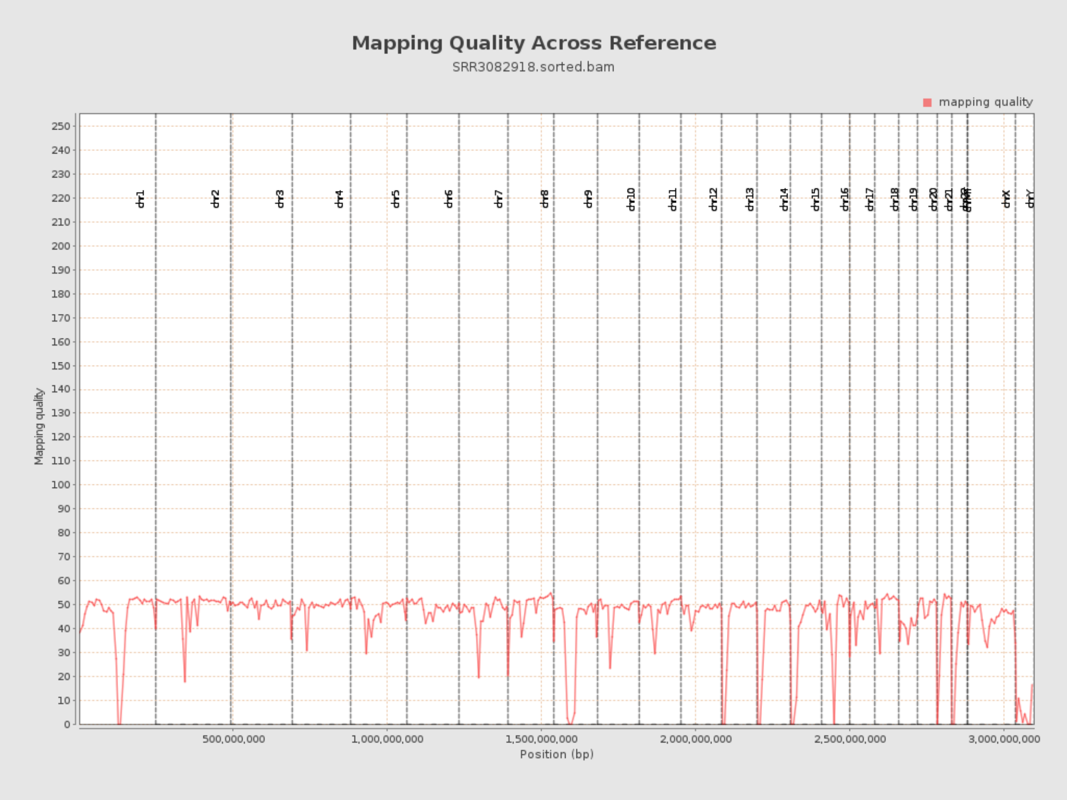
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram