Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:58:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082329.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_SRR3082329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:58:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,269
Mapped reads	1,823,402 / 89.11%
Unmapped reads	222,867 / 10.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,814 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	61,137 / 2.99%
Duplication rate	2.41%
Clipped reads	774,091 / 37.83%

2.2. ACGT Content

Number/percentage of A's	35,625,269 / 28.84%
Number/percentage of C's	23,258,330 / 18.83%
Number/percentage of T's	37,990,312 / 30.75%
Number/percentage of G's	26,665,051 / 21.58%
Number/percentage of N's	2,567 / 0%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.3793

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

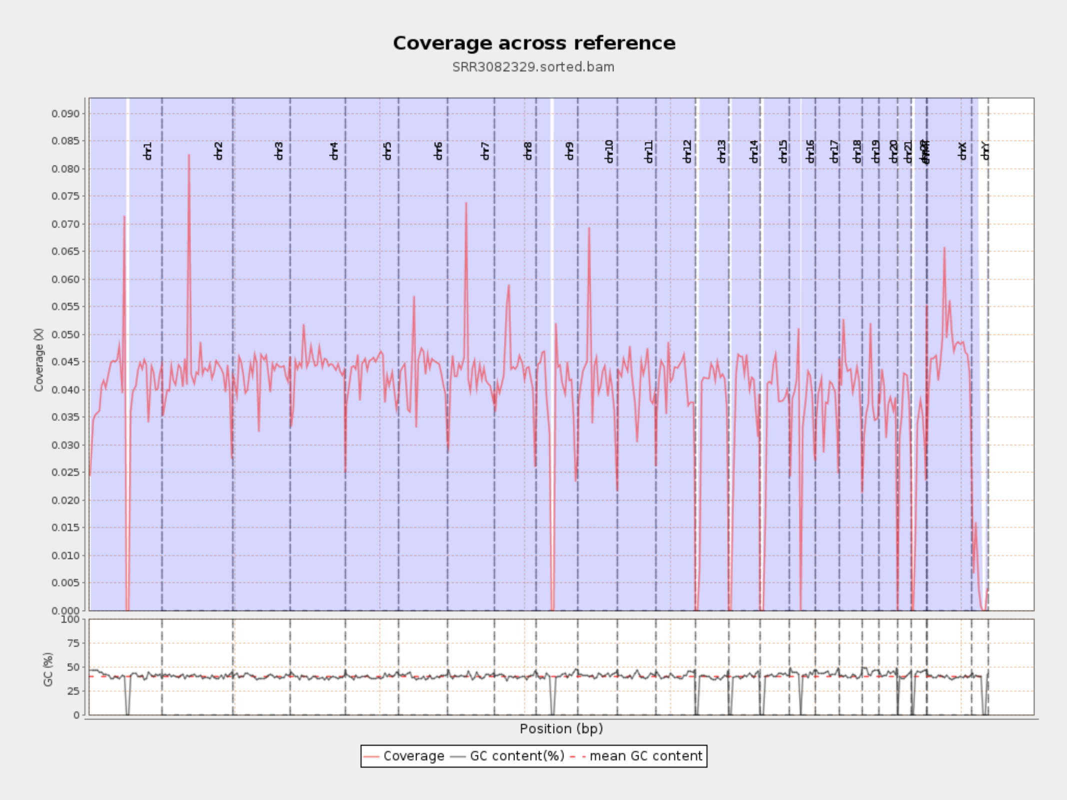
General error rate	0.88%
Mismatches	1,065,777
Insertions	10,477
Mapped reads with at least one insertion	0.57%
Deletions	27,806
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.73%

2.6. Chromosome stats

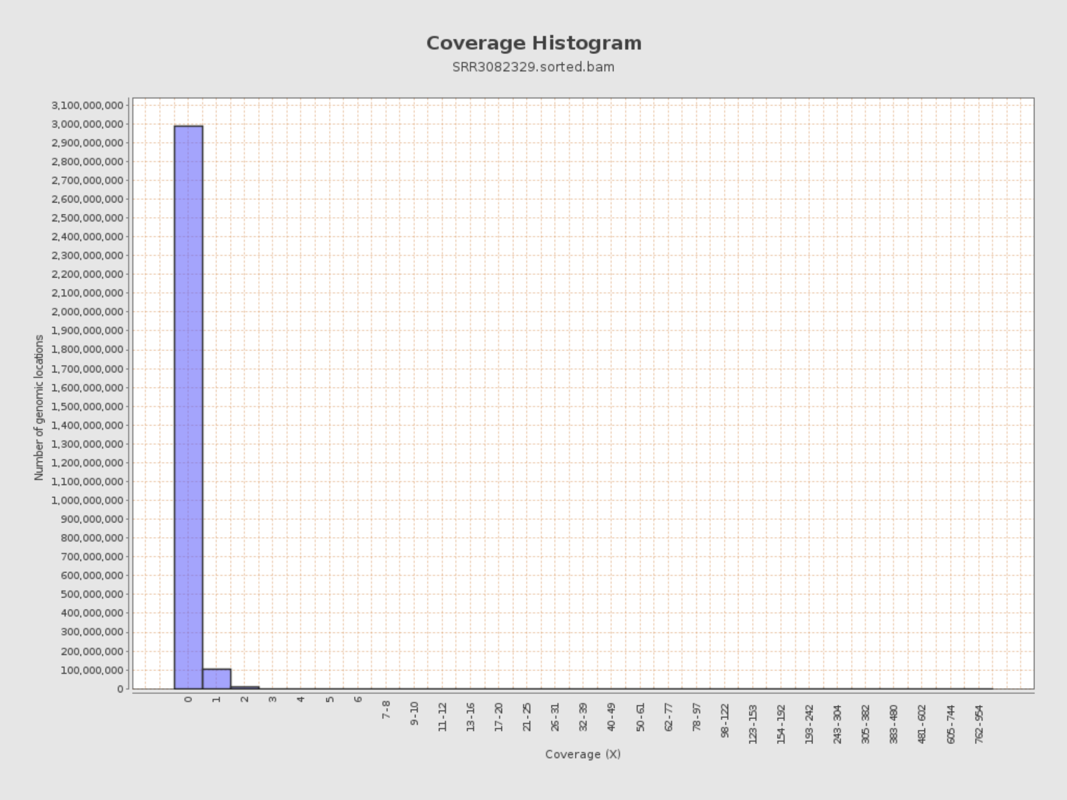
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9783561	0.0393	0.6679
chr2	243199373	10576764	0.0435	0.4516
chr3	198022430	8515106	0.043	0.2267
chr4	191154276	8466834	0.0443	0.2394
chr5	180915260	7762011	0.0429	0.2256
chr6	171115067	7396407	0.0432	0.2682
chr7	159138663	6961615	0.0437	0.5148

chr8	146364022	6326033	0.0432	0.6198
chr9	141213431	5190885	0.0368	0.3375
chr10	135534747	5750281	0.0424	0.3552
chr11	135006516	5566920	0.0412	0.3205
chr12	133851895	5586272	0.0417	0.2265
chr13	115169878	4031466	0.035	0.2018
chr14	107349540	3769504	0.0351	0.2212
chr15	102531392	3383653	0.033	0.2015
chr16	90354753	3193714	0.0353	0.2424
chr17	81195210	2988061	0.0368	0.2274
chr18	78077248	3366719	0.0431	0.627
chr19	59128983	2183424	0.0369	0.5329
chr20	63025520	2340157	0.0371	0.2167
chr21	48129895	1600930	0.0333	0.2136
chr22	51304566	1204458	0.0235	0.1645
chrMT	16571	919	0.0555	0.2413
chrX	155270560	7322756	0.0472	0.266
chrY	59373566	318288	0.0054	0.1222

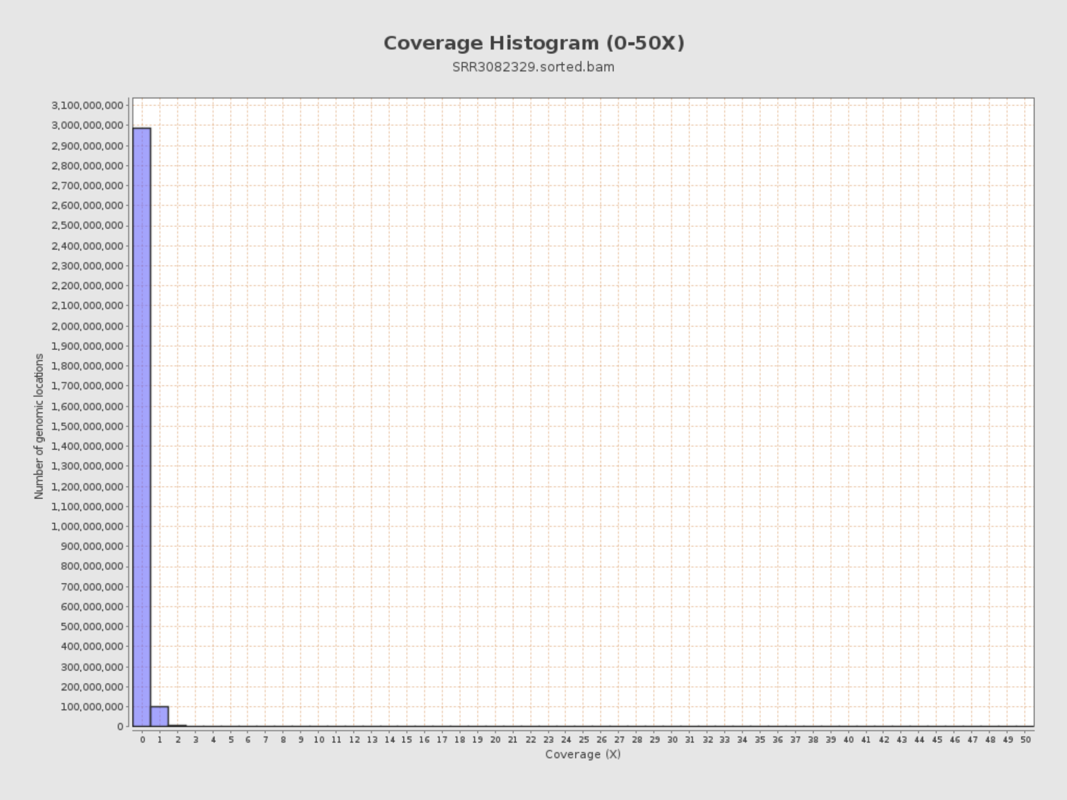
3. Results : Coverage across reference



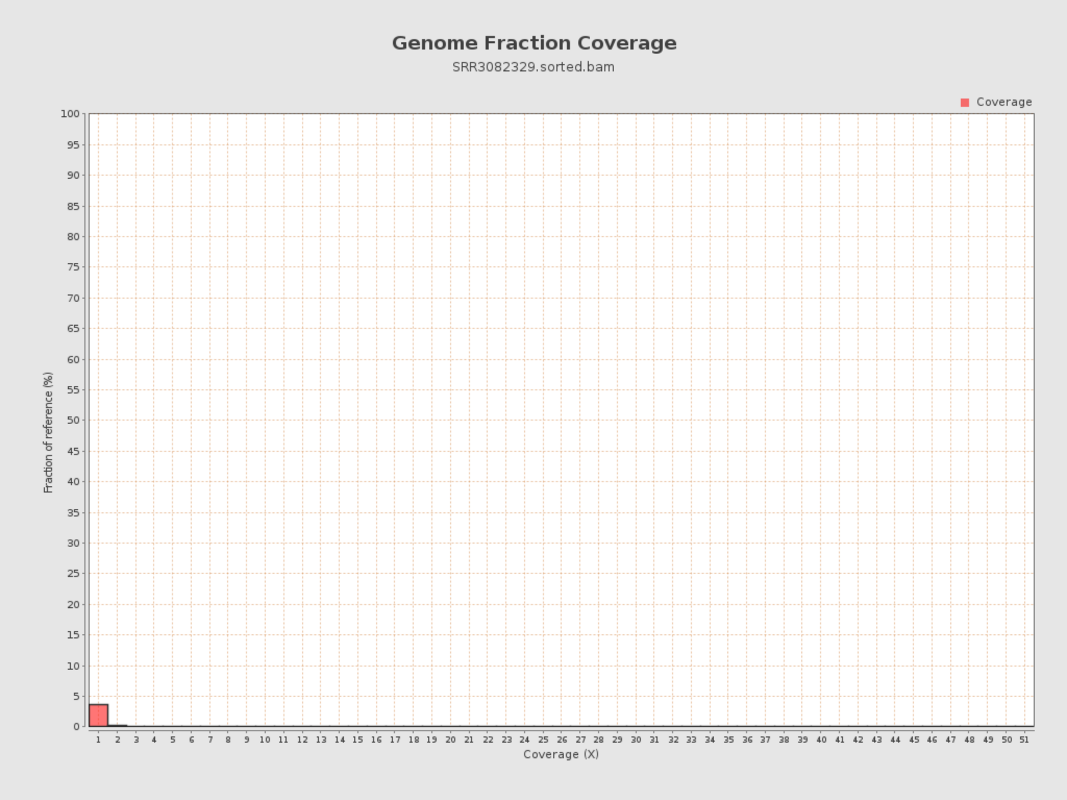
4. Results : Coverage Histogram



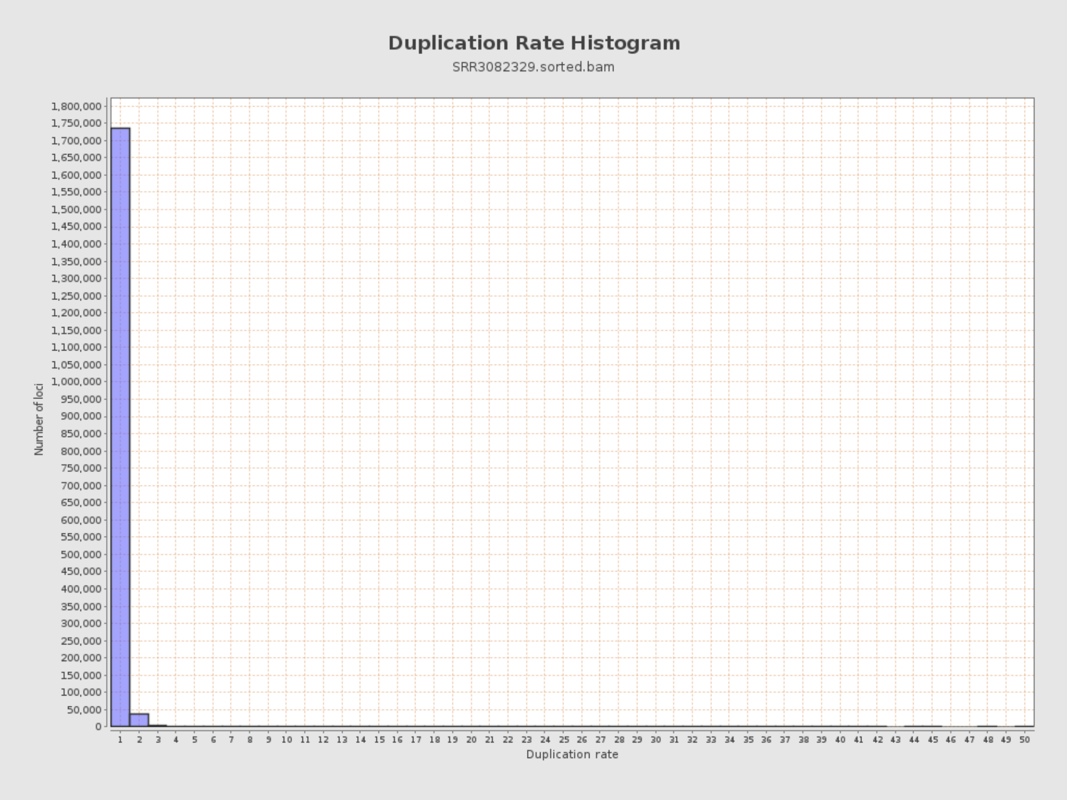
5. Results : Coverage Histogram (0-50X)



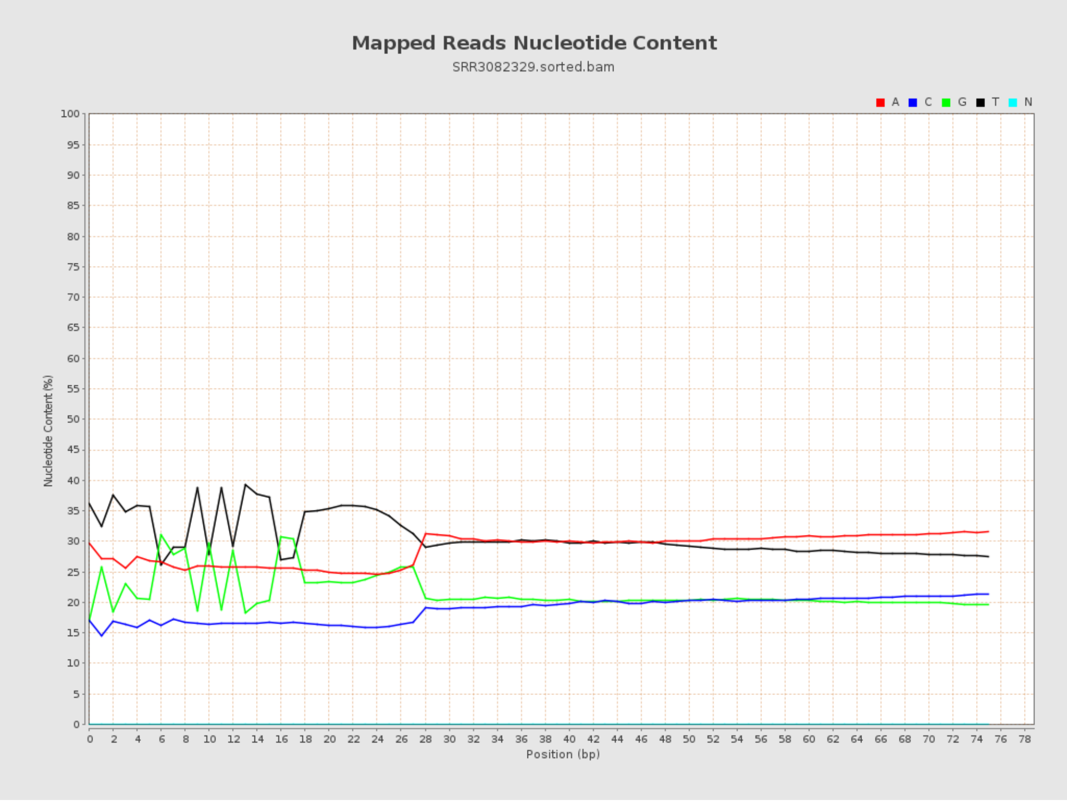
6. Results : Genome Fraction Coverage



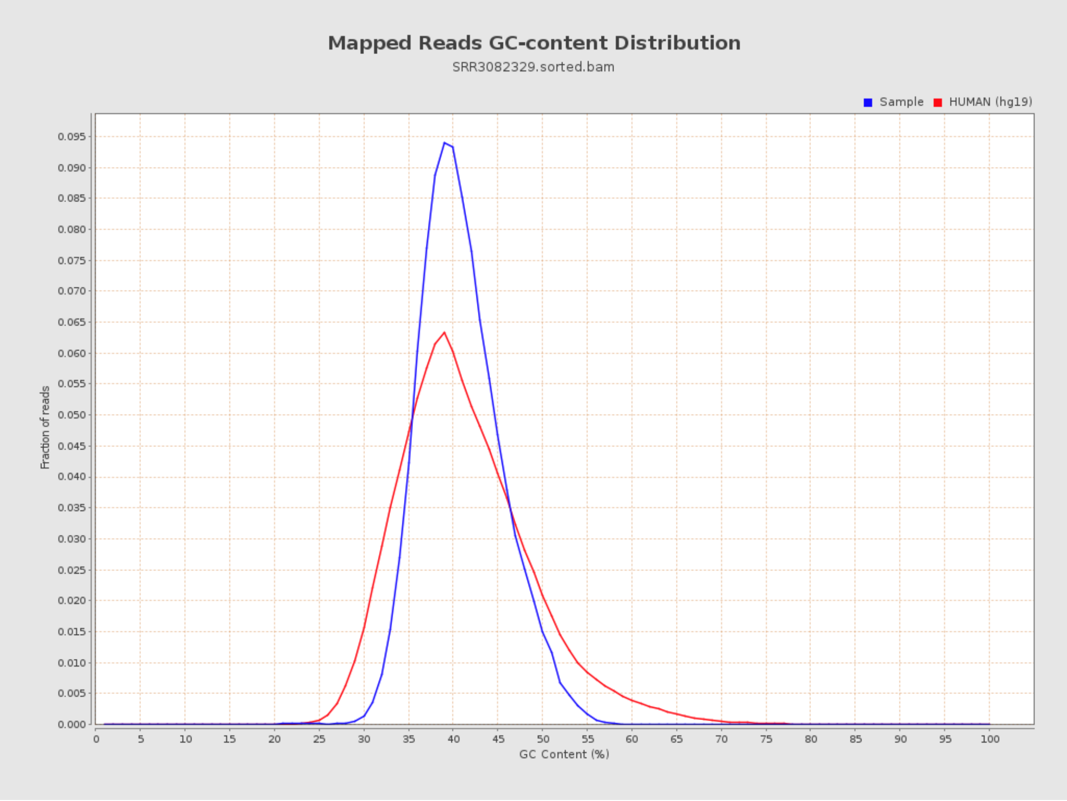
7. Results : Duplication Rate Histogram



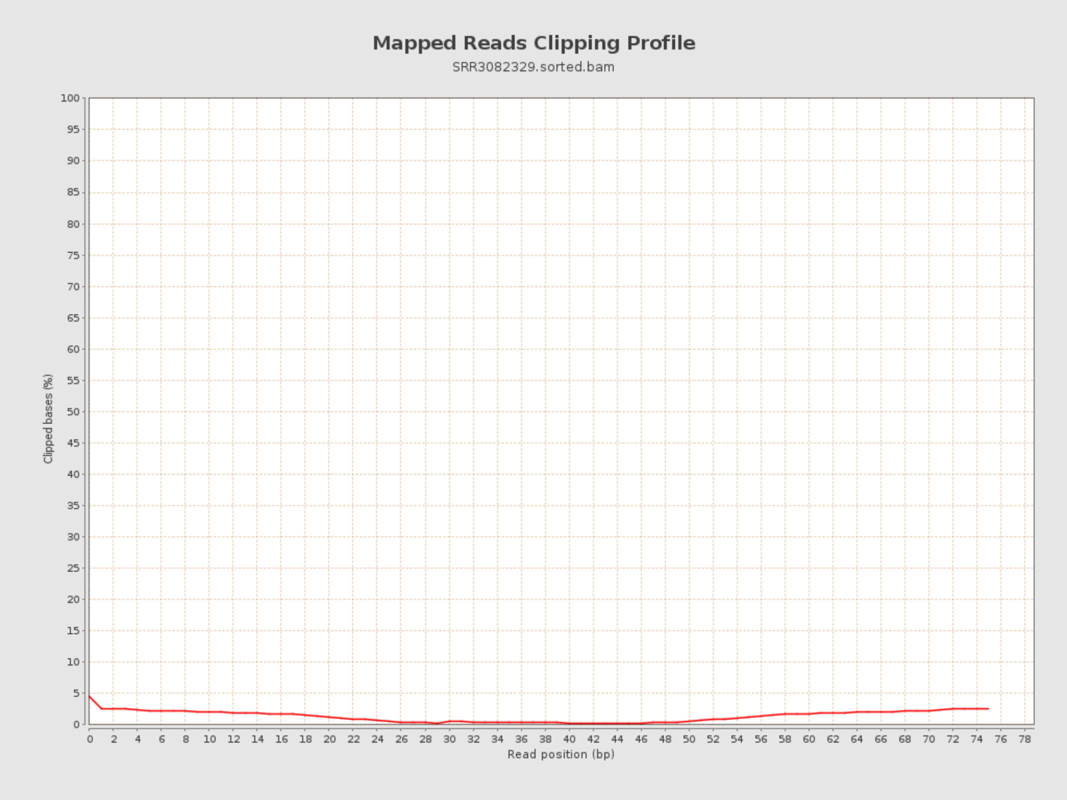
8. Results : Mapped Reads Nucleotide Content



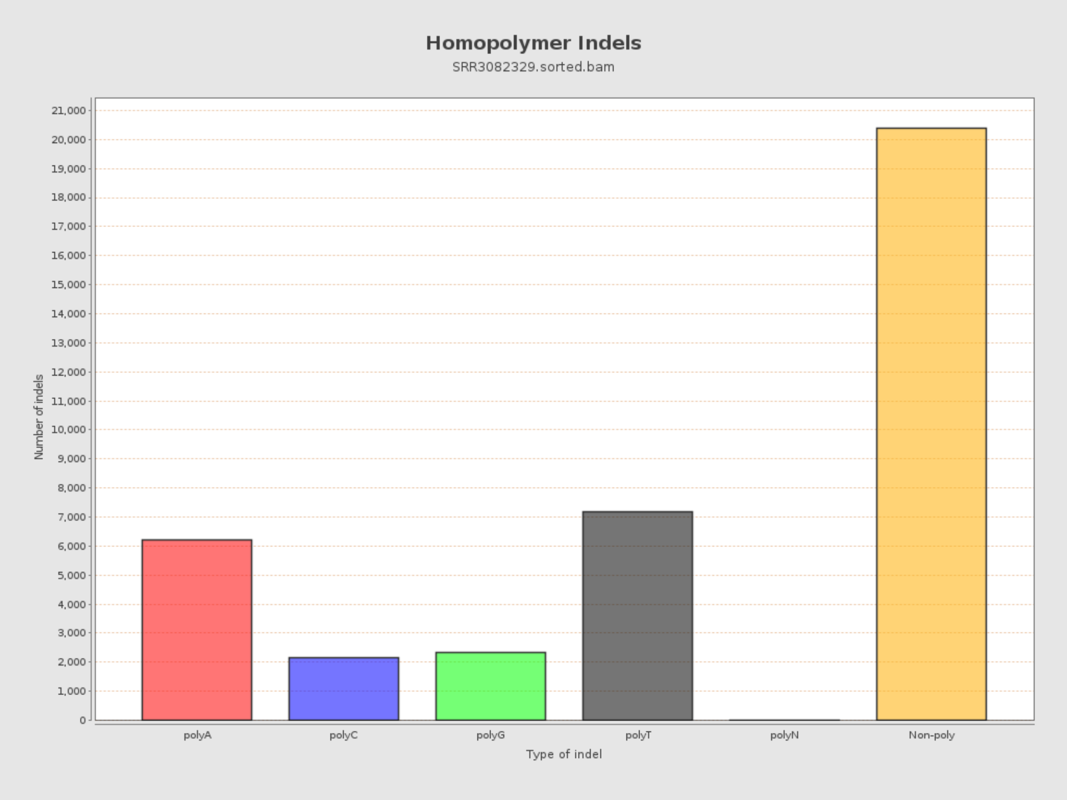
9. Results : Mapped Reads GC-content Distribution



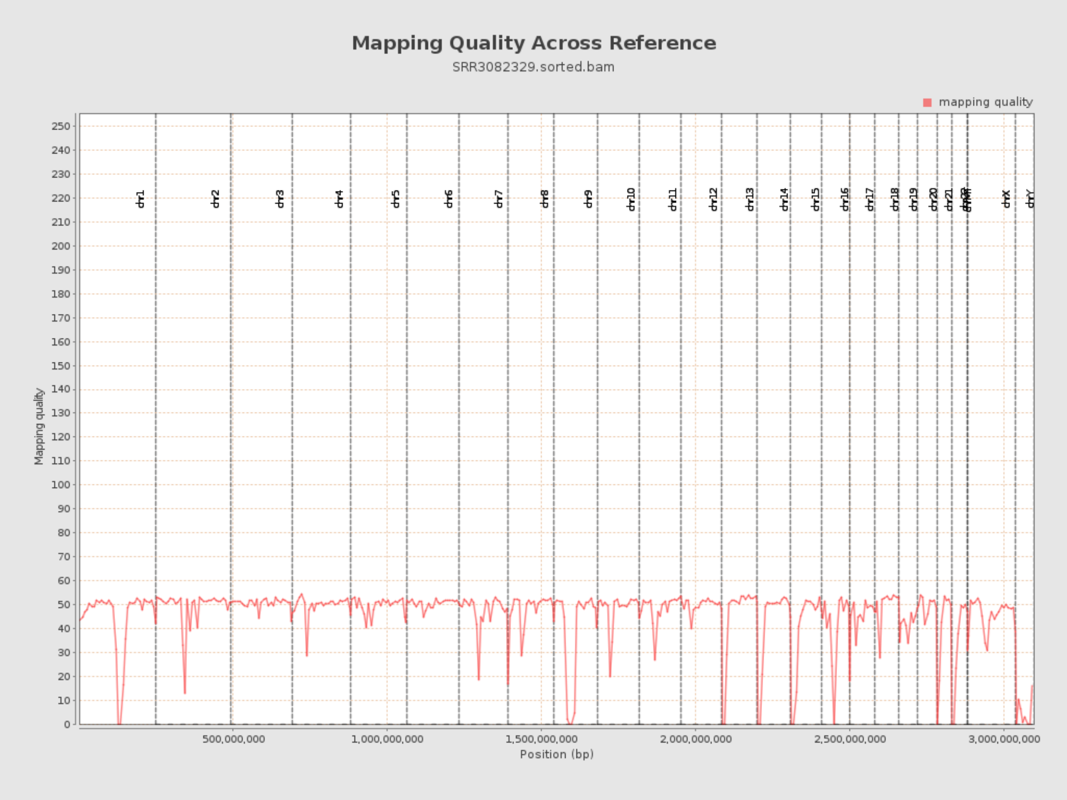
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram