Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:34:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082937.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_SRR3082937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082937.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:34:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,915,034
Mapped reads	1,755,715 / 91.68%
Unmapped reads	159,319 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,993 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	90,167 / 4.71%
Duplication rate	4.24%
Clipped reads	765,463 / 39.97%

2.2. ACGT Content

Number/percentage of A's	32,712,537 / 27.85%
Number/percentage of C's	21,298,723 / 18.13%
Number/percentage of T's	37,863,352 / 32.23%
Number/percentage of G's	25,583,575 / 21.78%
Number/percentage of N's	5,841 / 0%
GC Percentage	39.91%

2.3. Coverage

Mean	0.038

Standard Deviation	0.3124

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

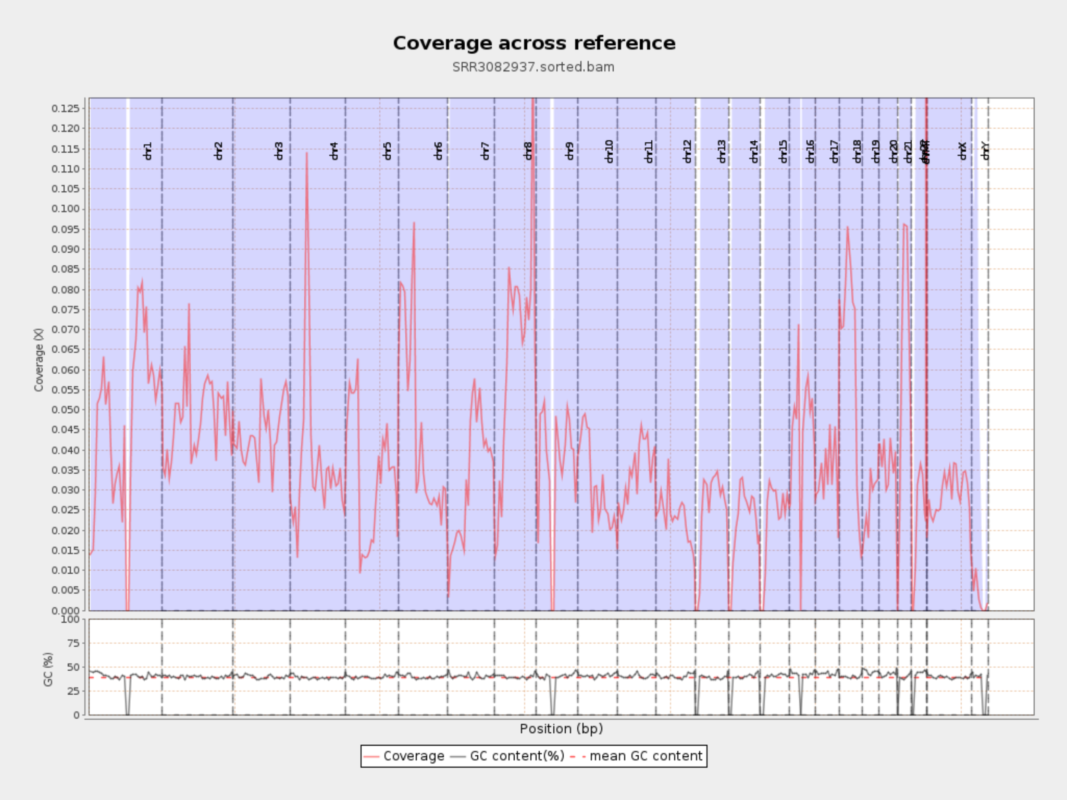
General error rate	0.73%
Mismatches	839,571
Insertions	10,103
Mapped reads with at least one insertion	0.57%
Deletions	27,527
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.3%

2.6. Chromosome stats

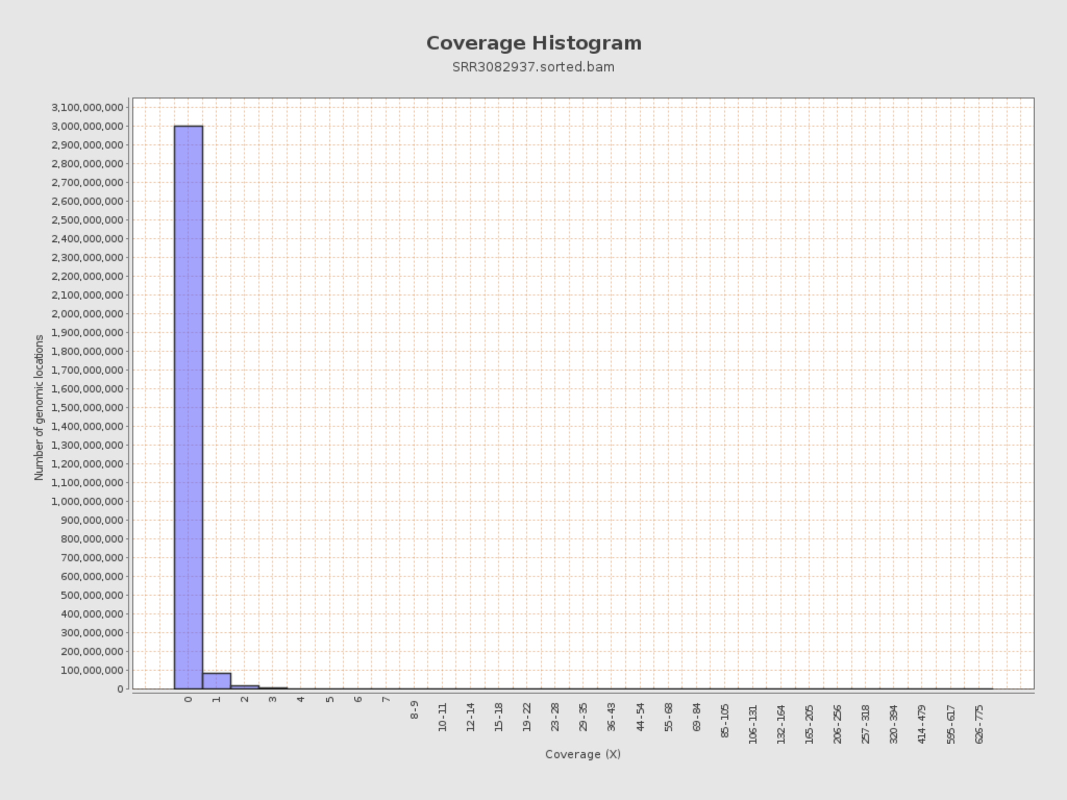
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11848875	0.0475	0.4226
chr2	243199373	11697322	0.0481	0.4859
chr3	198022430	8732819	0.0441	0.2451
chr4	191154276	7108140	0.0372	0.2351
chr5	180915260	6161776	0.0341	0.2174
chr6	171115067	7792680	0.0455	0.3158
chr7	159138663	5320508	0.0334	0.2465

chr8	146364022	9548043	0.0652	0.44
chr9	141213431	5089907	0.036	0.3271
chr10	135534747	4300452	0.0317	0.2515
chr11	135006516	4672776	0.0346	0.2635
chr12	133851895	3123214	0.0233	0.1857
chr13	115169878	2827712	0.0246	0.1845
chr14	107349540	2334570	0.0217	0.1998
chr15	102531392	2300330	0.0224	0.1812
chr16	90354753	4149589	0.0459	0.2679
chr17	81195210	2773928	0.0342	0.2444
chr18	78077248	5033312	0.0645	0.624
chr19	59128983	1600633	0.0271	0.2935
chr20	63025520	2281514	0.0362	0.2354
chr21	48129895	2926500	0.0608	0.3008
chr22	51304566	1098984	0.0214	0.1697
chrMT	16571	60497	3.6508	3.0301
chrX	155270560	4519053	0.0291	0.2197
chrY	59373566	206035	0.0035	0.0871

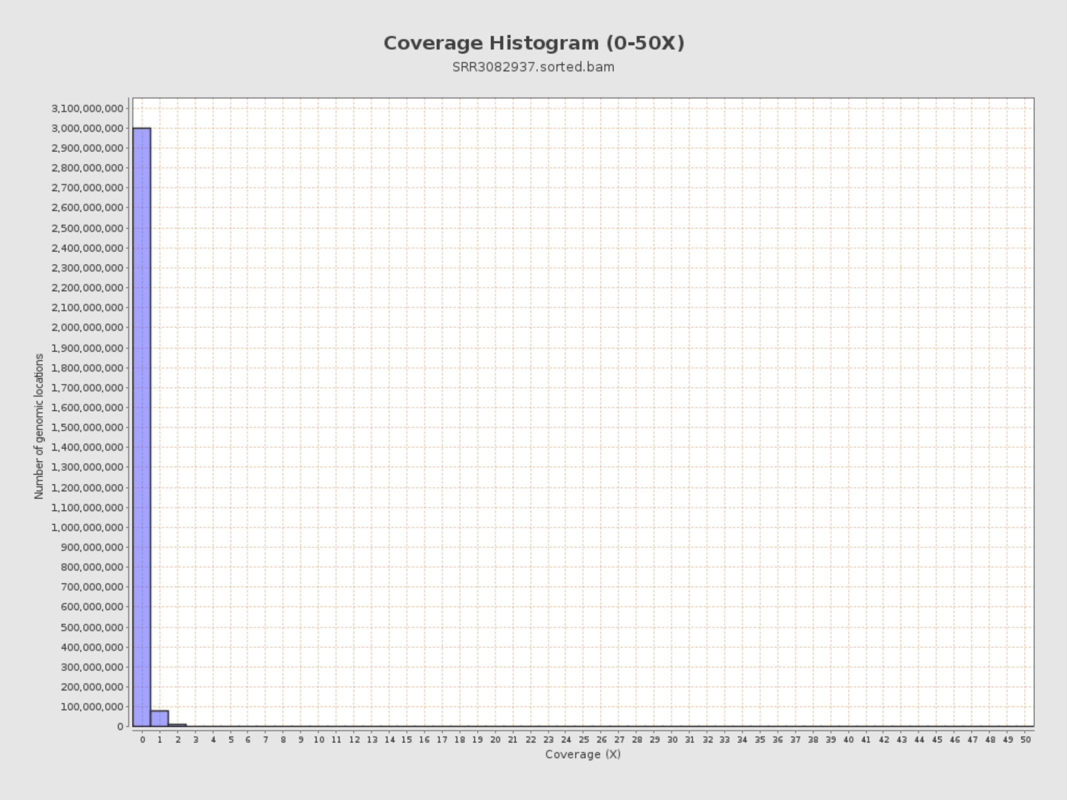
3. Results : Coverage across reference



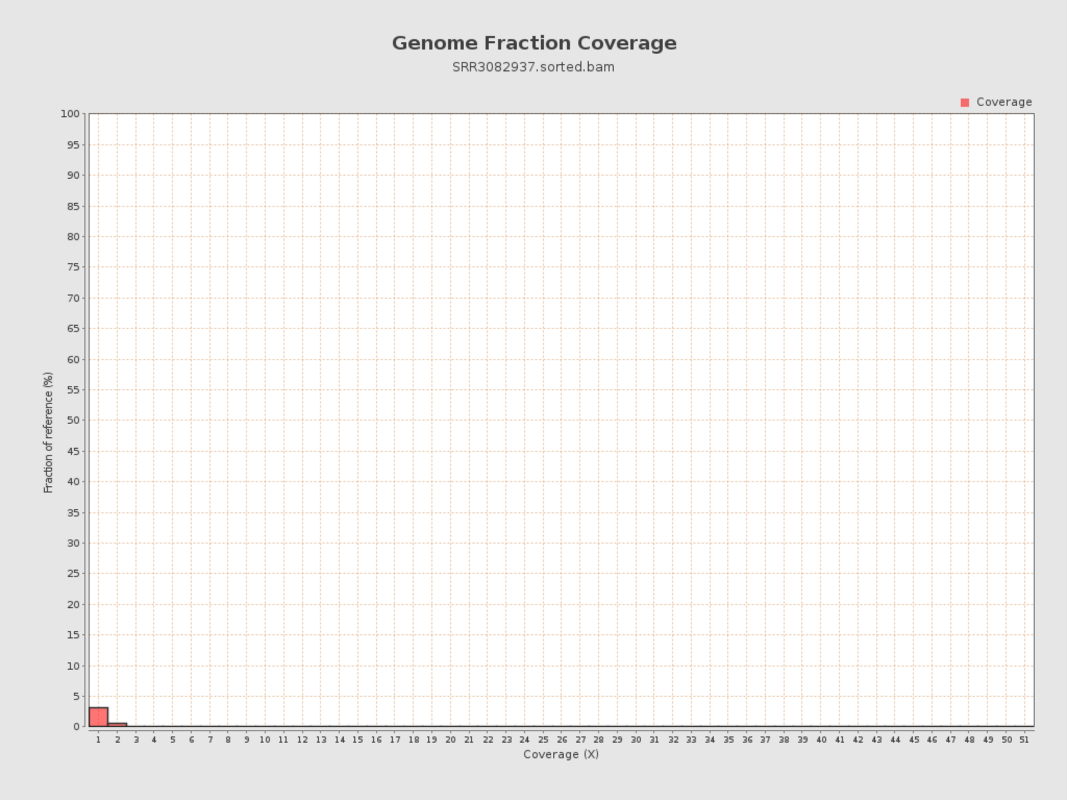
4. Results : Coverage Histogram



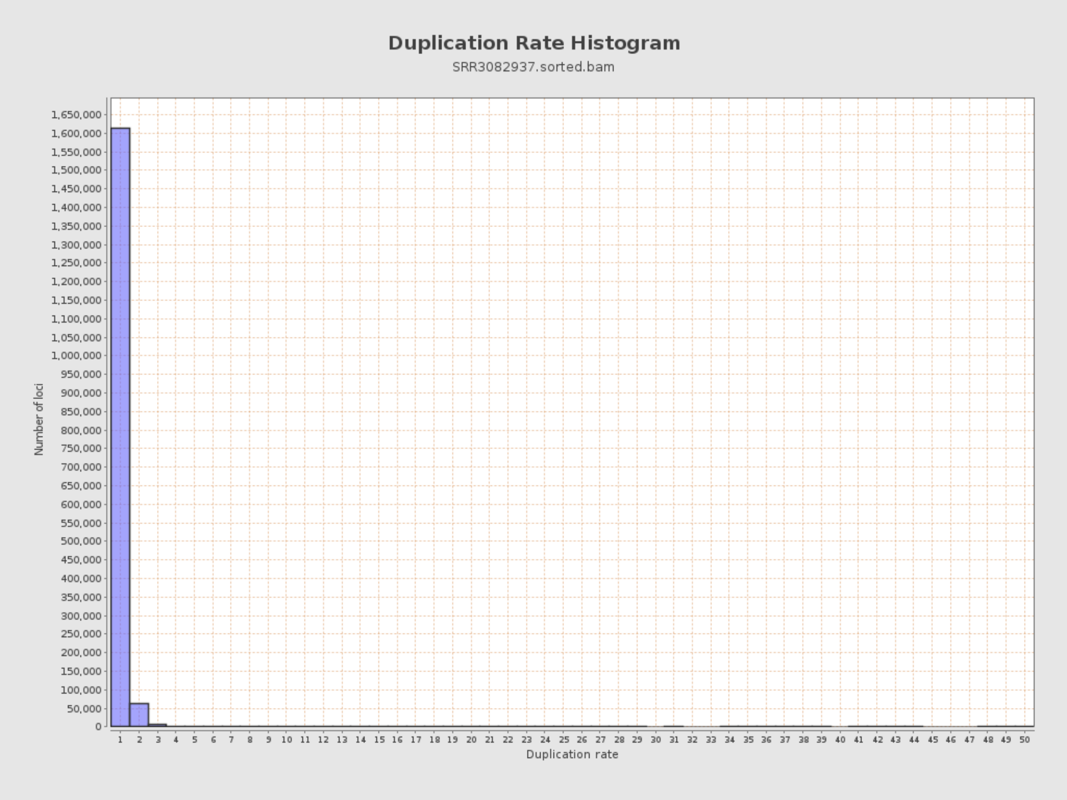
5. Results : Coverage Histogram (0-50X)



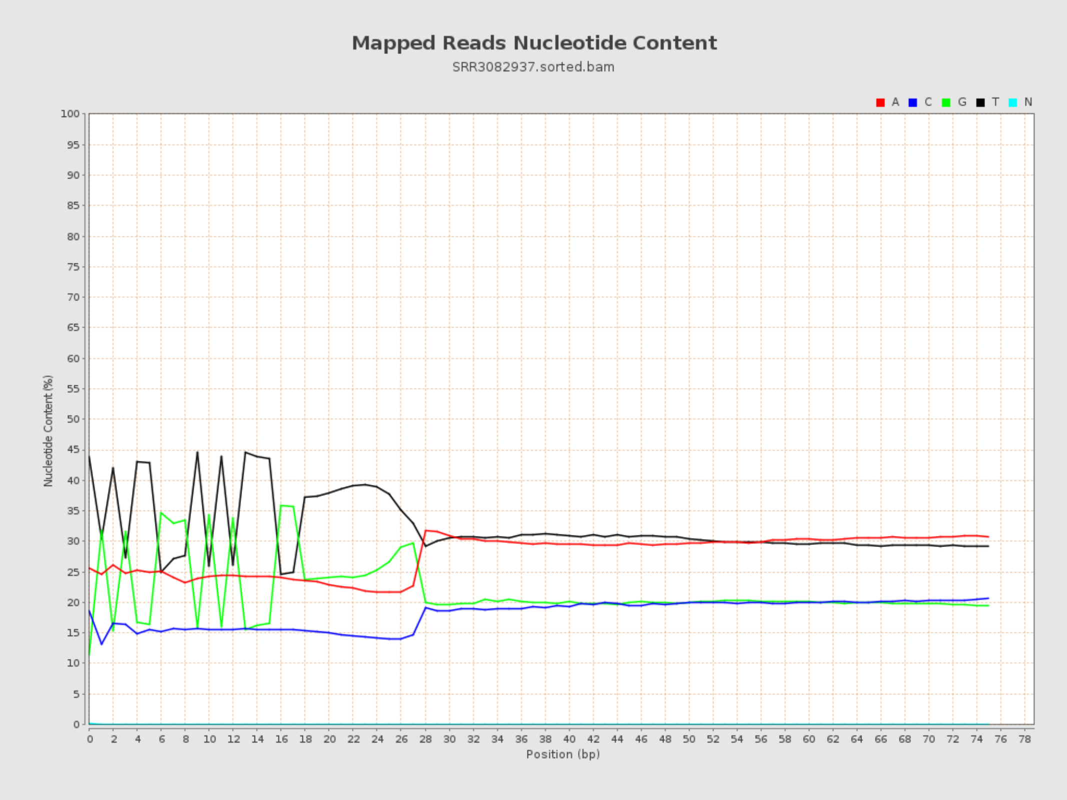
6. Results : Genome Fraction Coverage



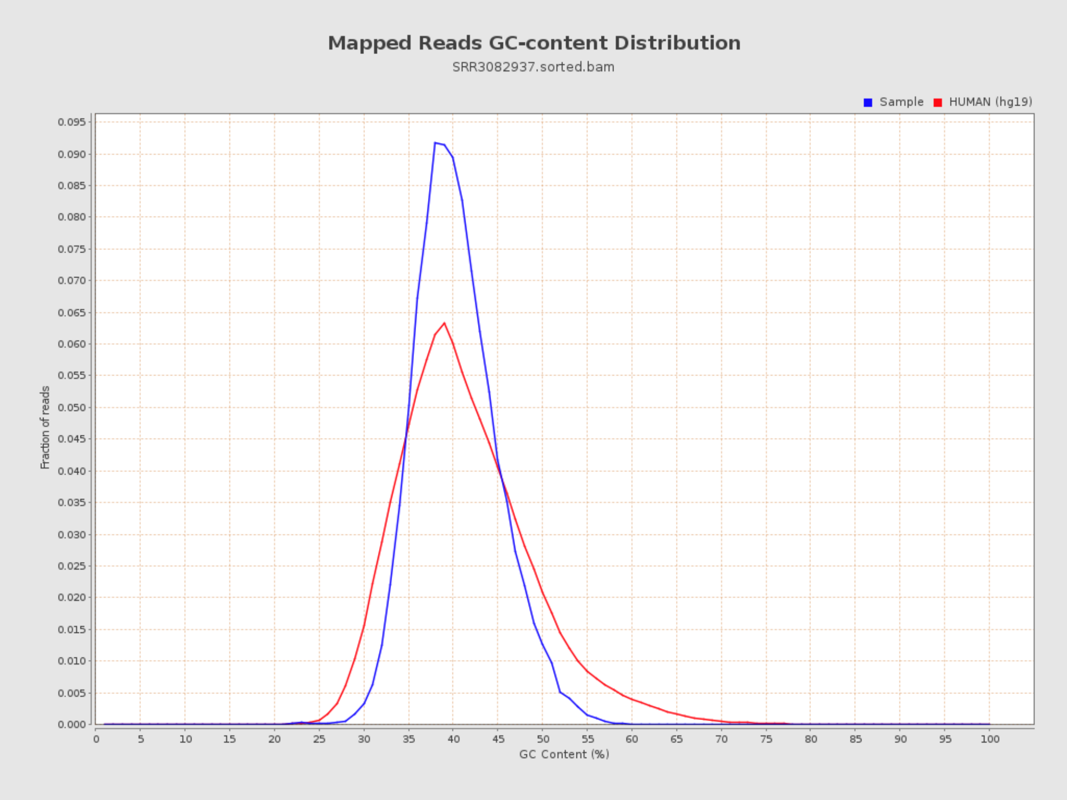
7. Results : Duplication Rate Histogram



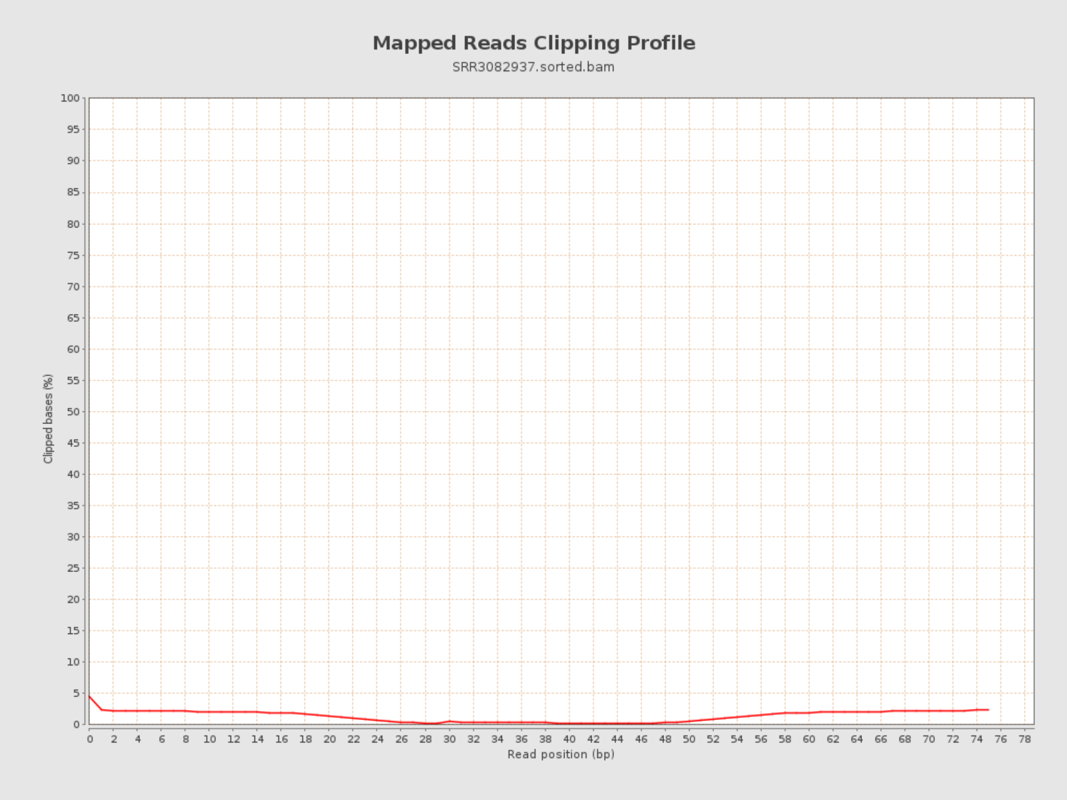
8. Results : Mapped Reads Nucleotide Content



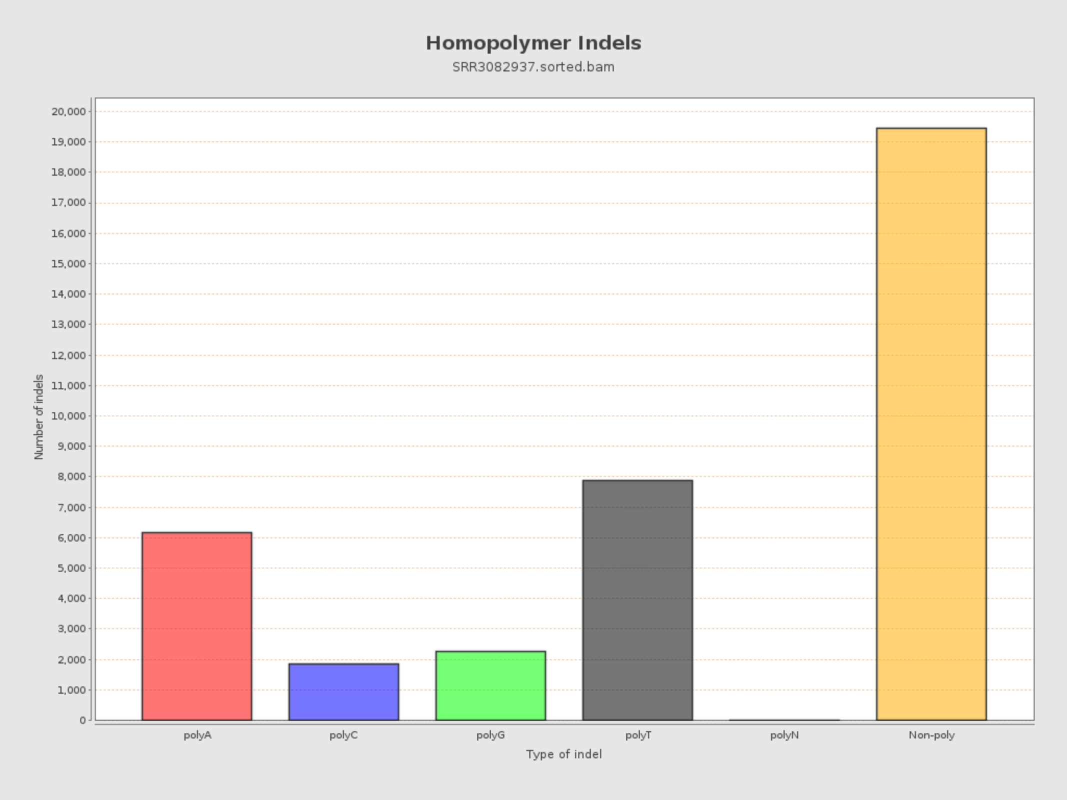
9. Results : Mapped Reads GC-content Distribution



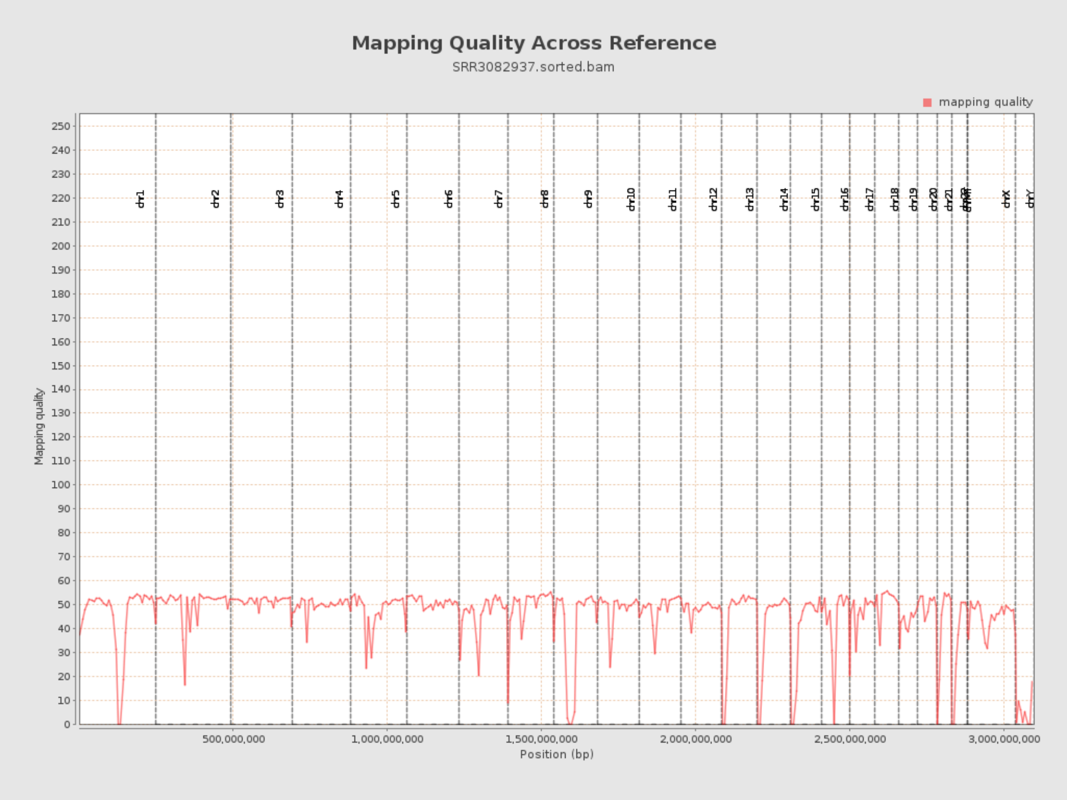
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram