Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:49:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080950.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_SRR3080950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:49:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,945,543
Mapped reads	2,434,856 / 82.66%
Unmapped reads	510,687 / 17.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,197 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	113,037 / 3.84%
Duplication rate	3.91%
Clipped reads	988,970 / 33.58%

2.2. ACGT Content

Number/percentage of A's	45,667,192 / 27.88%
Number/percentage of C's	29,291,321 / 17.88%
Number/percentage of T's	53,030,330 / 32.37%
Number/percentage of G's	35,492,953 / 21.67%
Number/percentage of N's	322,005 / 0.2%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.3765

2.4. Mapping Quality

Mean Mapping Quality	47.69

2.5. Mismatches and indels

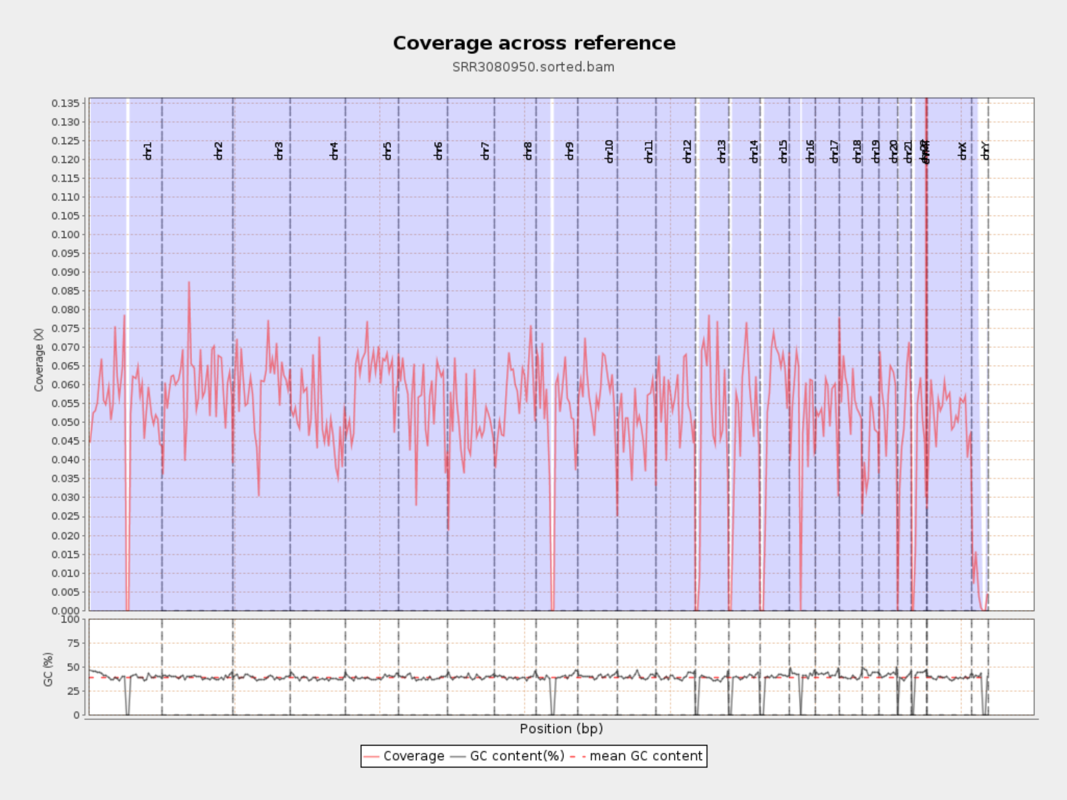
General error rate	0.98%
Mismatches	1,590,176
Insertions	12,079
Mapped reads with at least one insertion	0.49%
Deletions	33,226
Mapped reads with at least one deletion	1.35%
Homopolymer indels	49.68%

2.6. Chromosome stats

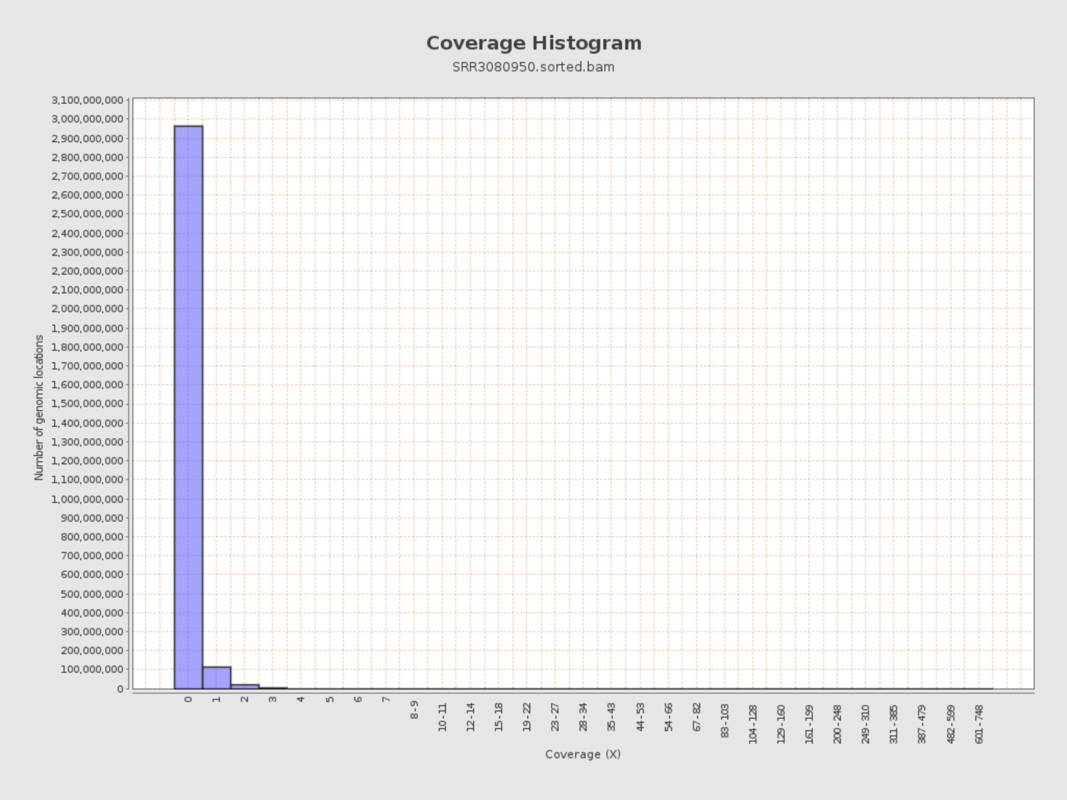
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13336788	0.0535	0.6519
chr2	243199373	14657918	0.0603	0.4018
chr3	198022430	11801693	0.0596	0.2853
chr4	191154276	9731034	0.0509	0.2704
chr5	180915260	11208302	0.062	0.2936
chr6	171115067	9584452	0.056	0.3086
chr7	159138663	7918005	0.0498	0.3852

chr8	146364022	8428066	0.0576	0.5406
chr9	141213431	7002536	0.0496	0.3868
chr10	135534747	7927720	0.0585	0.3285
chr11	135006516	6694986	0.0496	0.3072
chr12	133851895	7490877	0.056	0.2805
chr13	115169878	5657048	0.0491	0.2611
chr14	107349540	5091260	0.0474	0.2684
chr15	102531392	5358233	0.0523	0.2682
chr16	90354753	4548310	0.0503	0.2823
chr17	81195210	4264289	0.0525	0.2892
chr18	78077248	4536666	0.0581	0.6164
chr19	59128983	2572265	0.0435	0.4998
chr20	63025520	3598241	0.0571	0.289
chr21	48129895	2294541	0.0477	0.2665
chr22	51304566	1819606	0.0355	0.2199
chrMT	16571	27416	1.6545	1.7146
chrX	155270560	7988924	0.0515	0.2861
chrY	59373566	322187	0.0054	0.1164

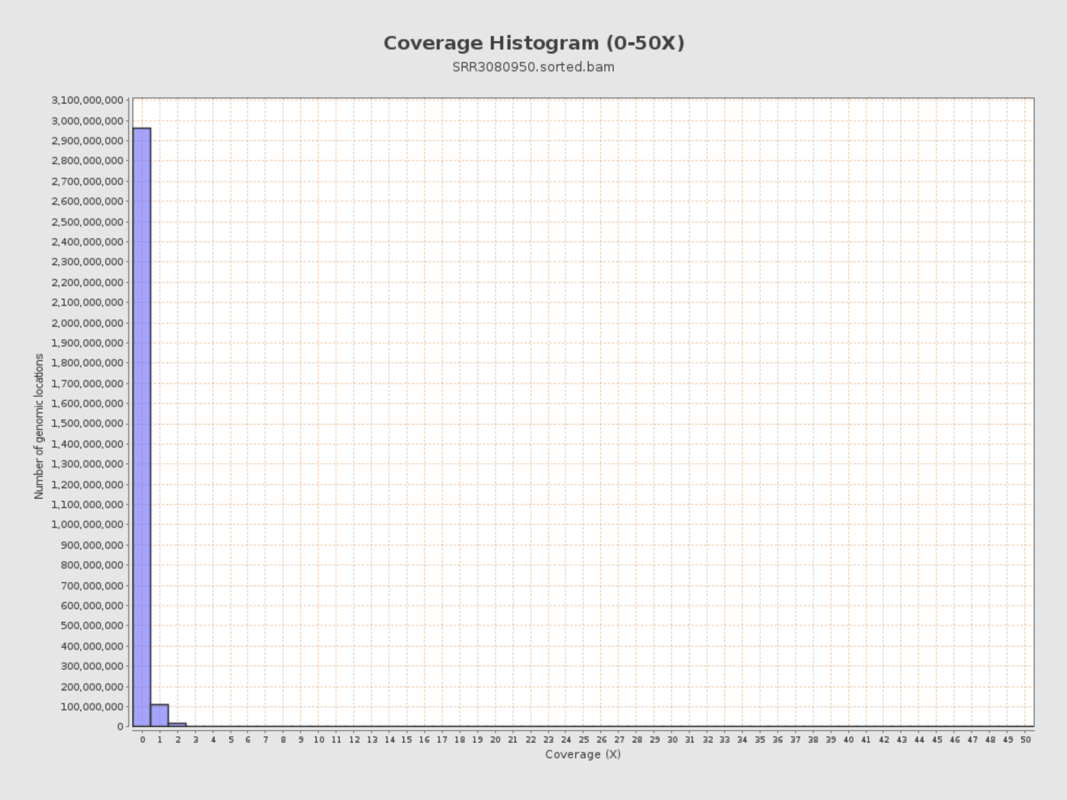
3. Results : Coverage across reference



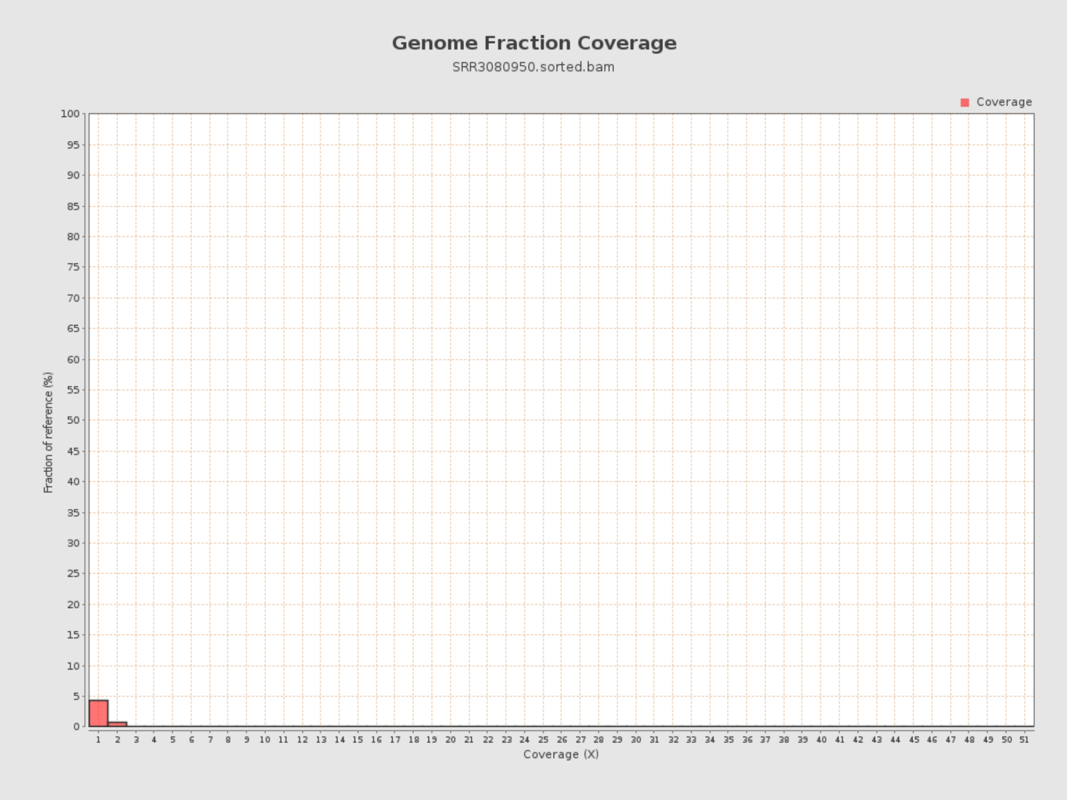
4. Results : Coverage Histogram



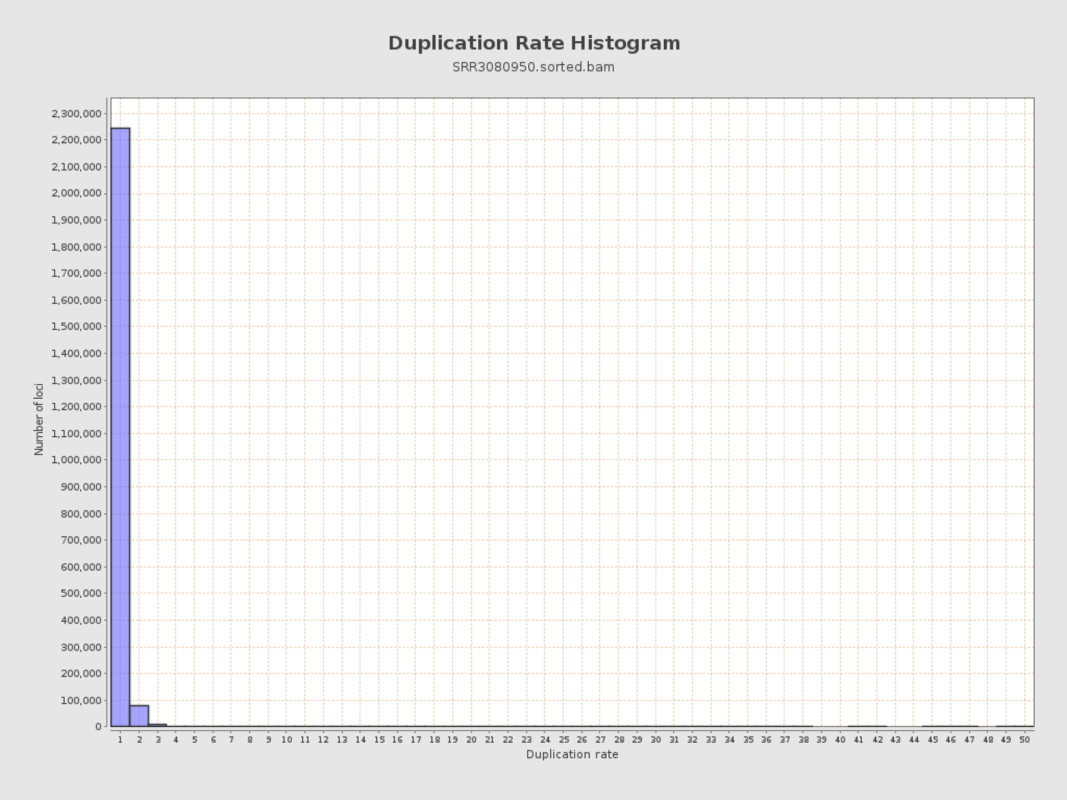
5. Results : Coverage Histogram (0-50X)



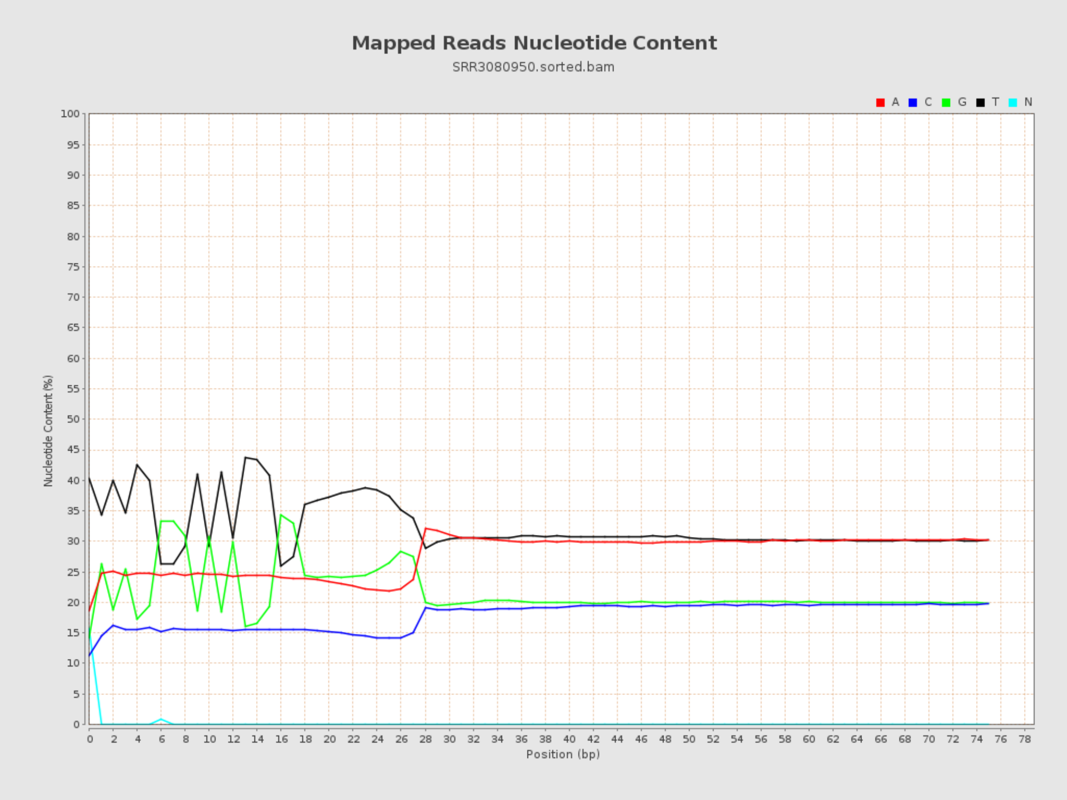
6. Results : Genome Fraction Coverage



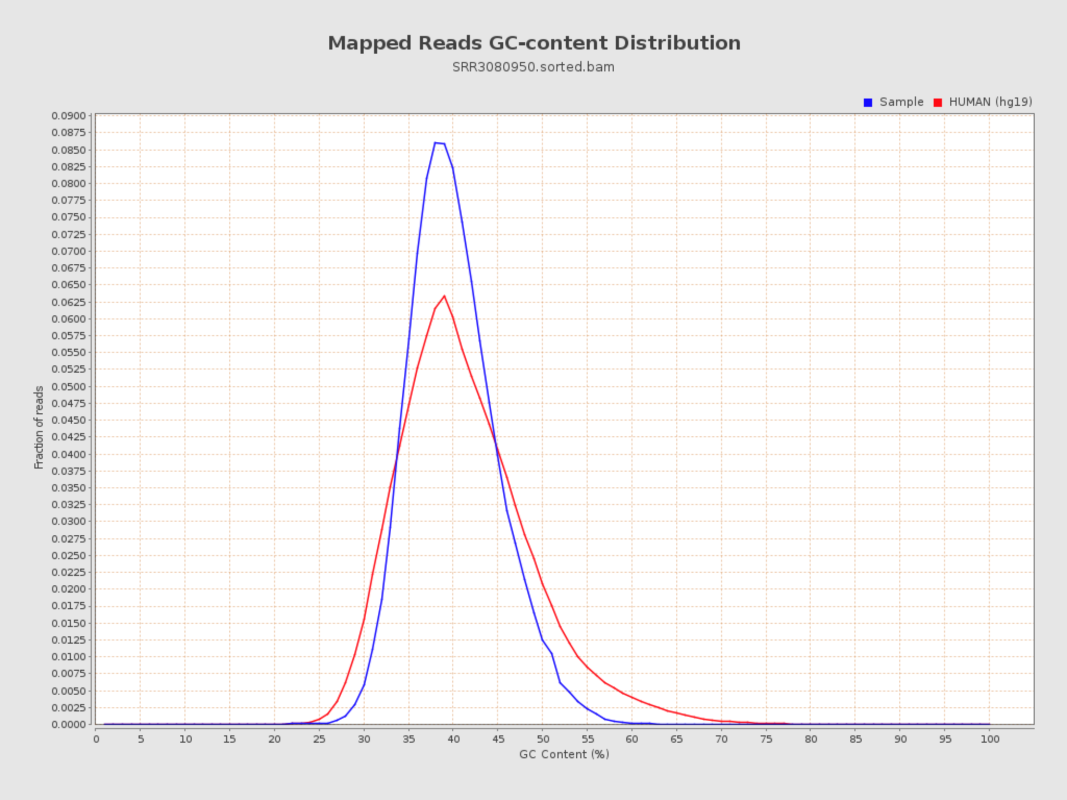
7. Results : Duplication Rate Histogram



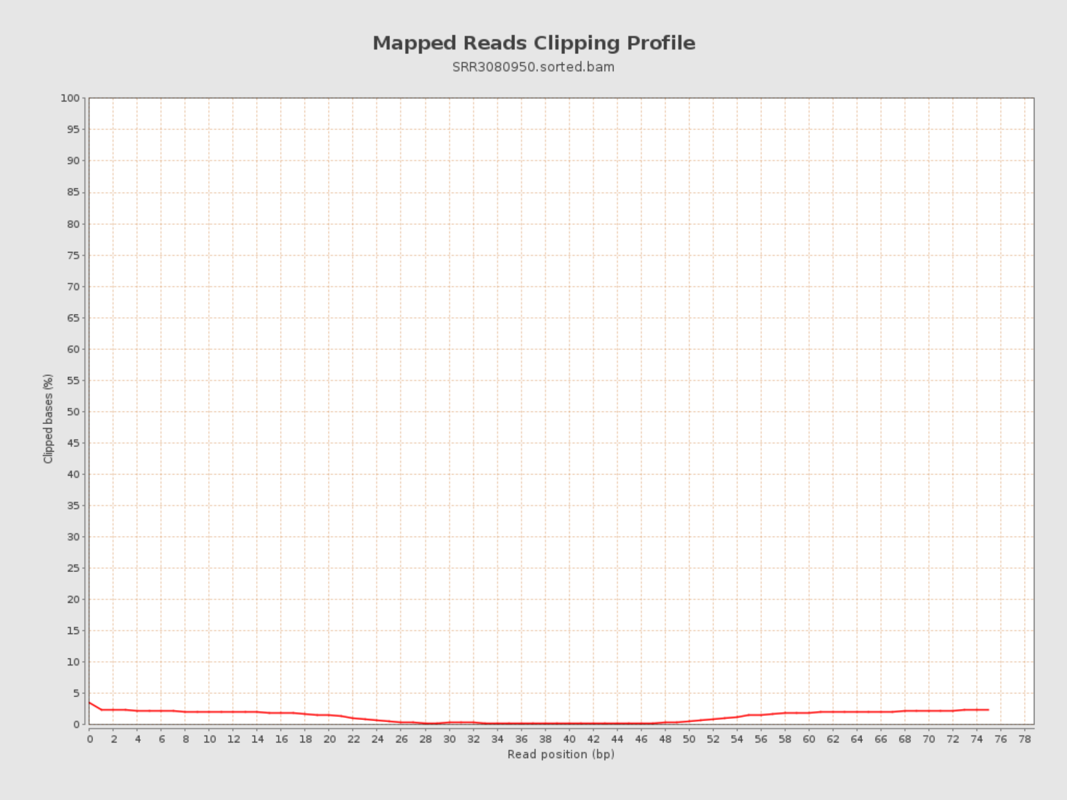
8. Results : Mapped Reads Nucleotide Content



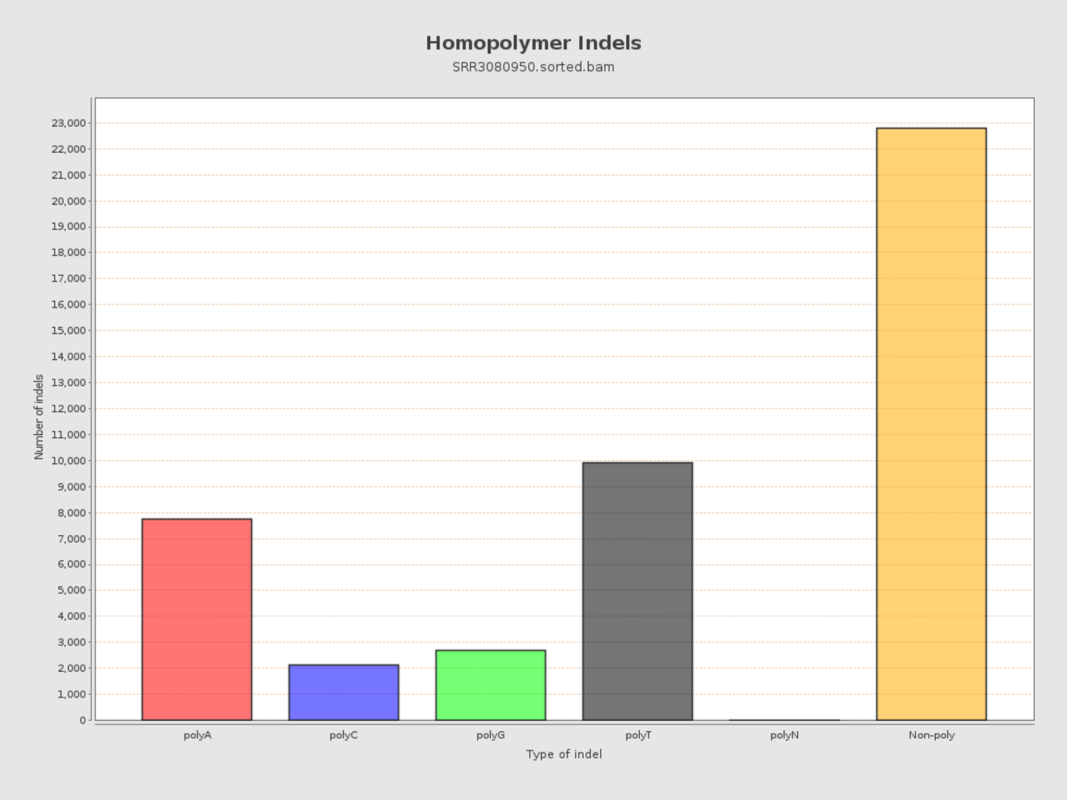
9. Results : Mapped Reads GC-content Distribution



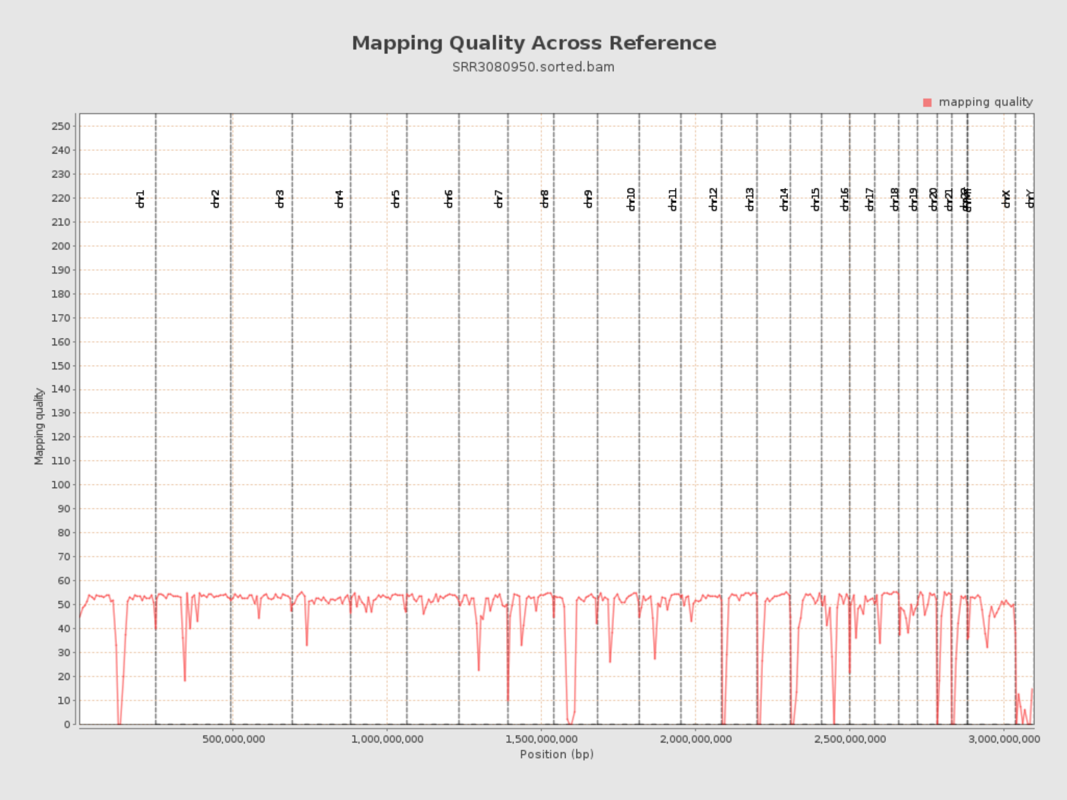
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram