Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:57:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081113.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_SRR3081113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:56:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,450,556
Mapped reads	2,254,754 / 92.01%
Unmapped reads	195,802 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,789 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	96,867 / 3.95%
Duplication rate	3.38%
Clipped reads	949,132 / 38.73%

2.2. ACGT Content

Number/percentage of A's	41,866,650 / 27.51%
Number/percentage of C's	29,904,356 / 19.65%
Number/percentage of T's	46,162,172 / 30.33%
Number/percentage of G's	34,247,846 / 22.5%
Number/percentage of N's	1,648 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.3932

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

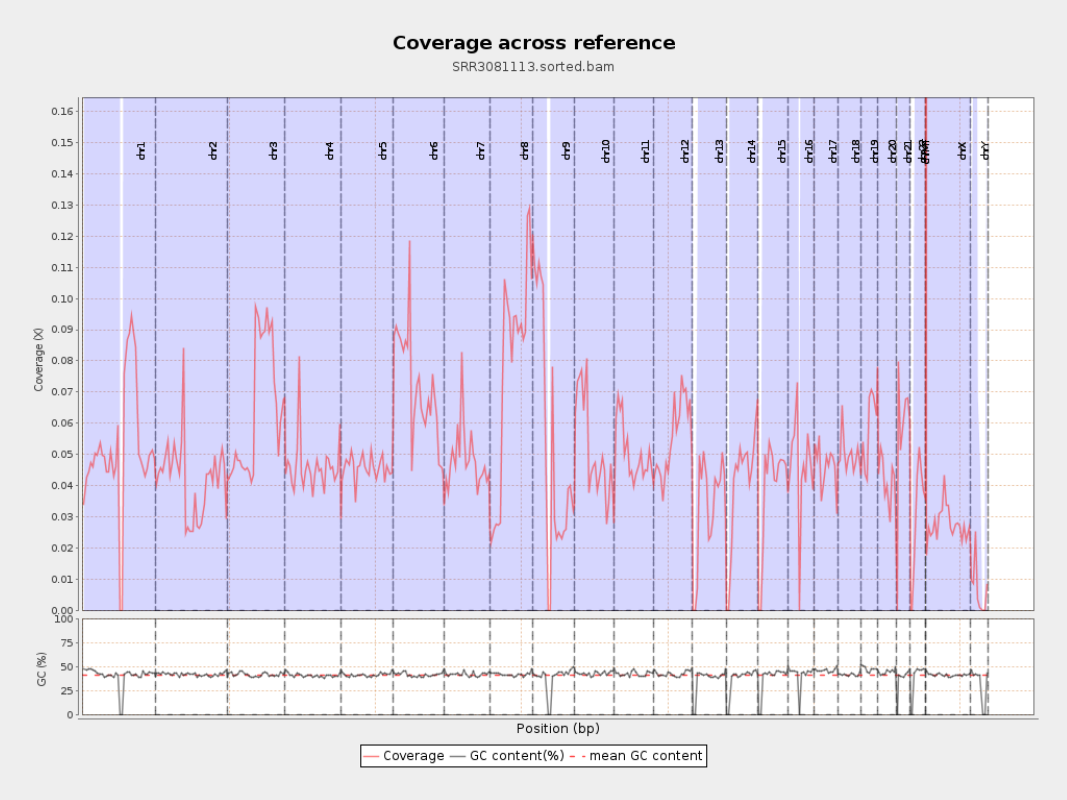
General error rate	0.89%
Mismatches	1,331,594
Insertions	11,571
Mapped reads with at least one insertion	0.51%
Deletions	32,470
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.7%

2.6. Chromosome stats

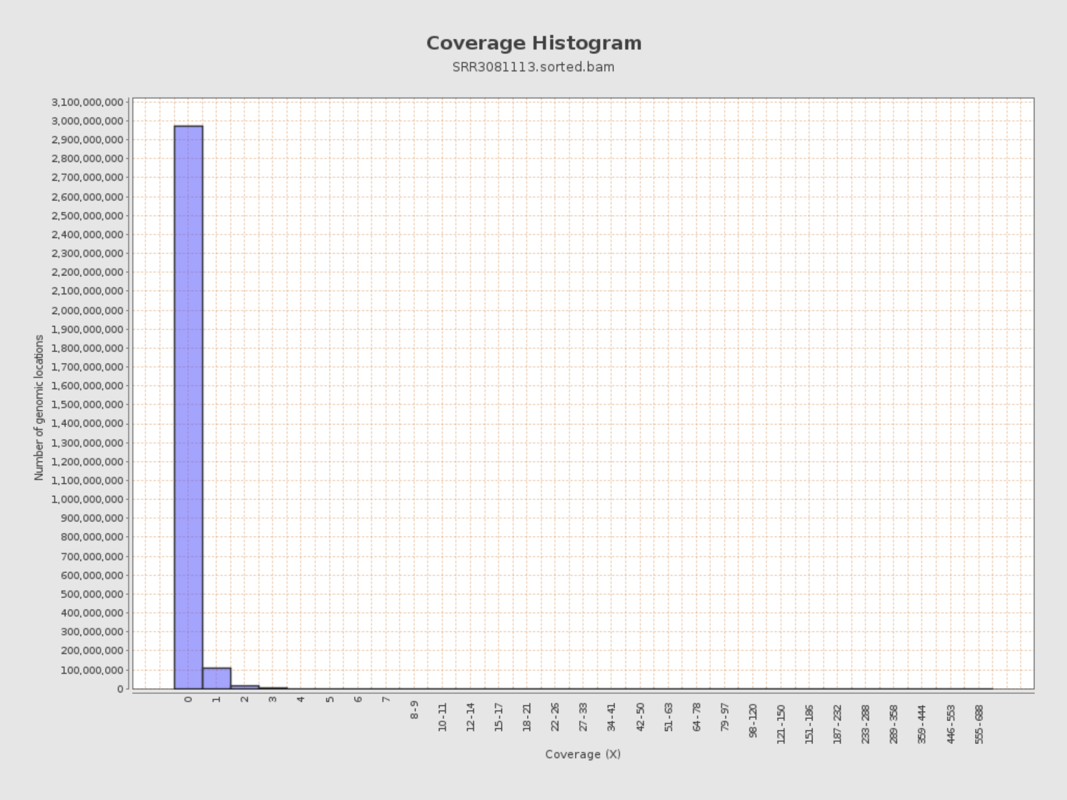
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12894304	0.0517	0.5259
chr2	243199373	10267904	0.0422	0.4414
chr3	198022430	12604156	0.0637	0.296
chr4	191154276	8864899	0.0464	0.2862
chr5	180915260	8284019	0.0458	0.2496
chr6	171115067	12294895	0.0719	0.4417
chr7	159138663	7711333	0.0485	0.546

chr8	146364022	11422467	0.078	0.4491
chr9	141213431	7425396	0.0526	0.4862
chr10	135534747	7052613	0.052	0.374
chr11	135006516	6784374	0.0503	0.342
chr12	133851895	7454720	0.0557	0.2884
chr13	115169878	3821126	0.0332	0.2116
chr14	107349540	4332602	0.0404	0.3052
chr15	102531392	3920105	0.0382	0.2299
chr16	90354753	4063099	0.045	0.2985
chr17	81195210	3808538	0.0469	0.2679
chr18	78077248	3910037	0.0501	0.8624
chr19	59128983	3462249	0.0586	0.433
chr20	63025520	2646250	0.042	0.2575
chr21	48129895	2839460	0.059	0.3604
chr22	51304566	1565709	0.0305	0.2029
chrMT	16571	116576	7.0349	4.8988
chrX	155270560	4282309	0.0276	0.2339
chrY	59373566	411442	0.0069	0.1788

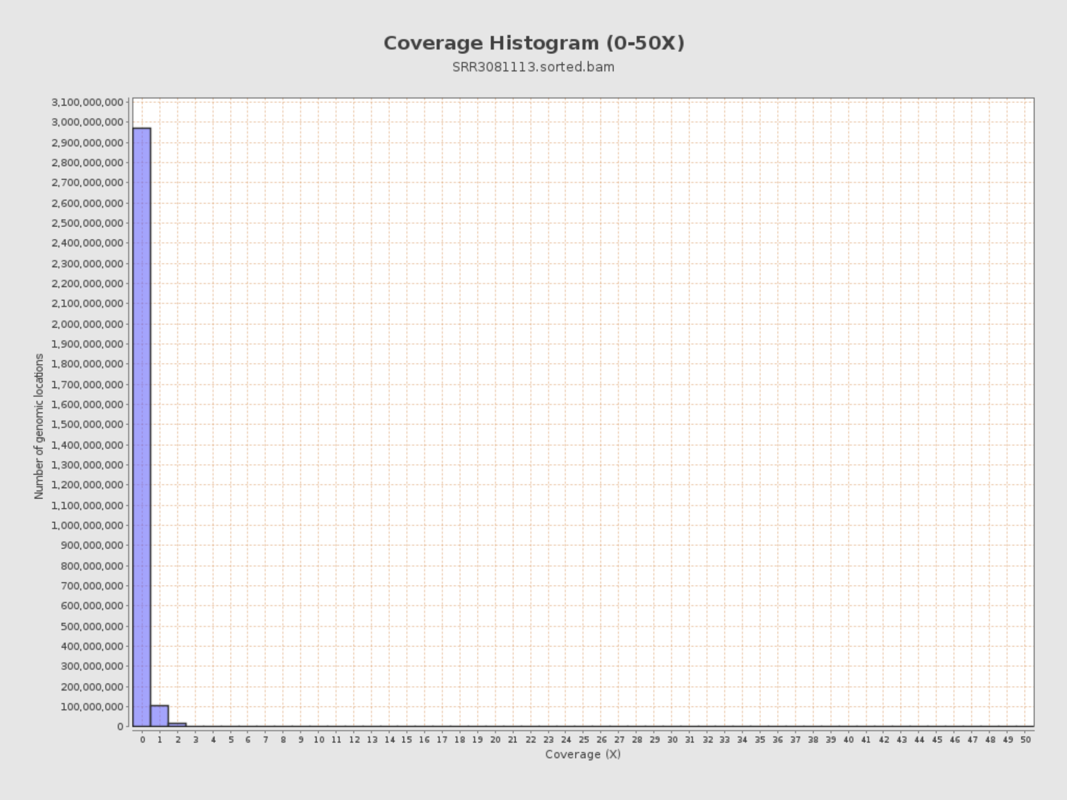
3. Results : Coverage across reference



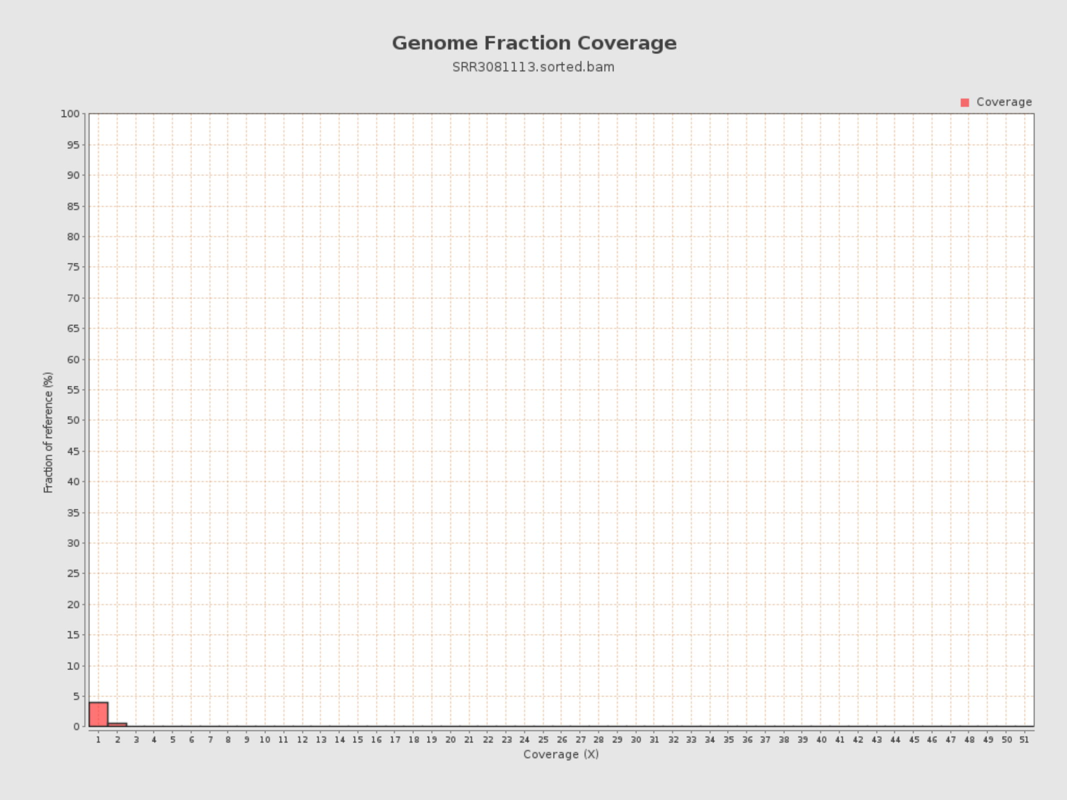
4. Results : Coverage Histogram



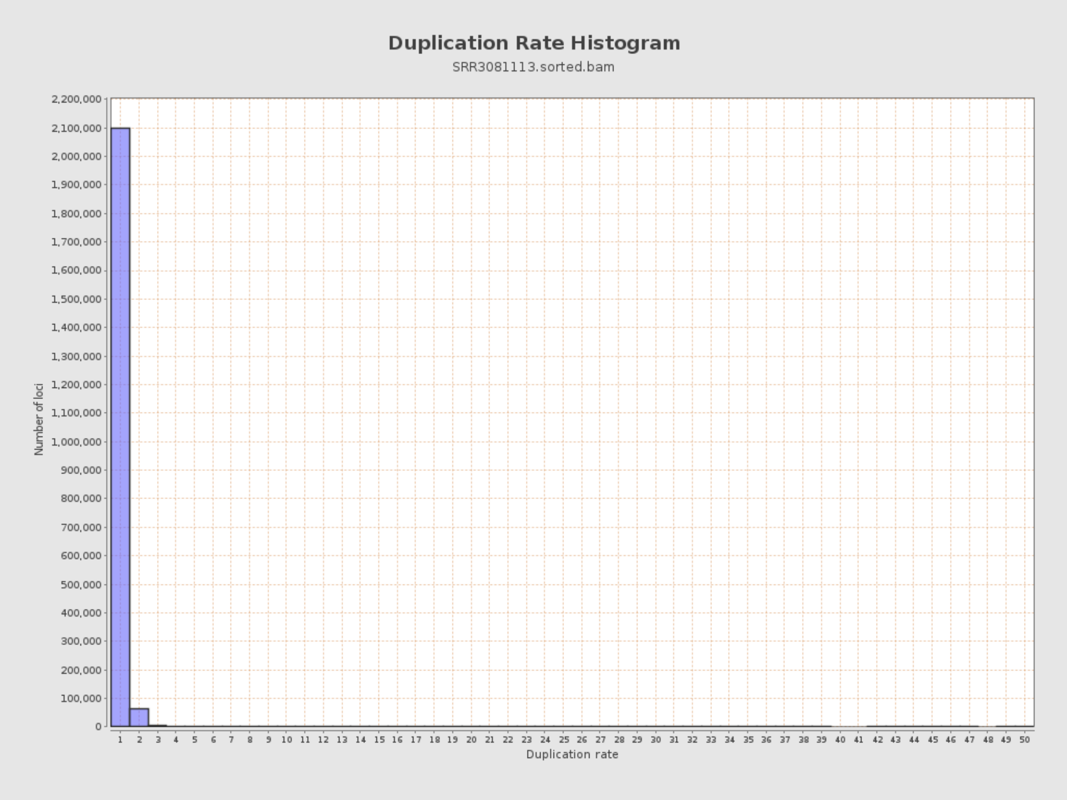
5. Results : Coverage Histogram (0-50X)



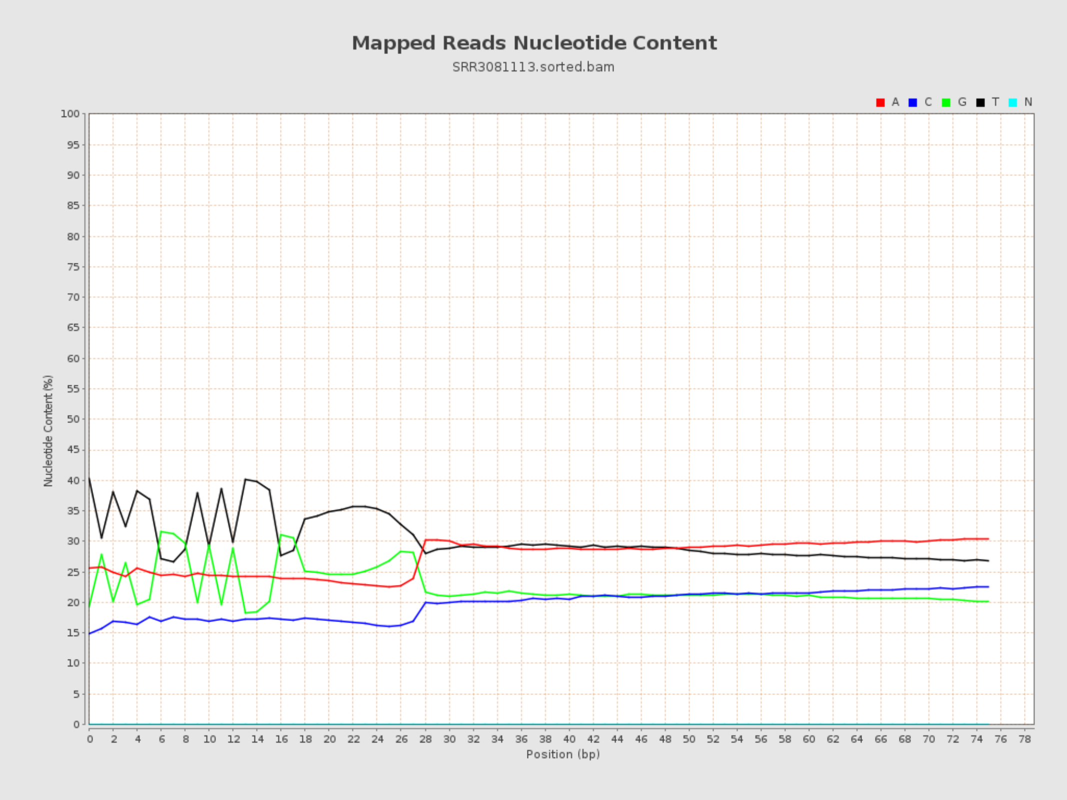
6. Results : Genome Fraction Coverage



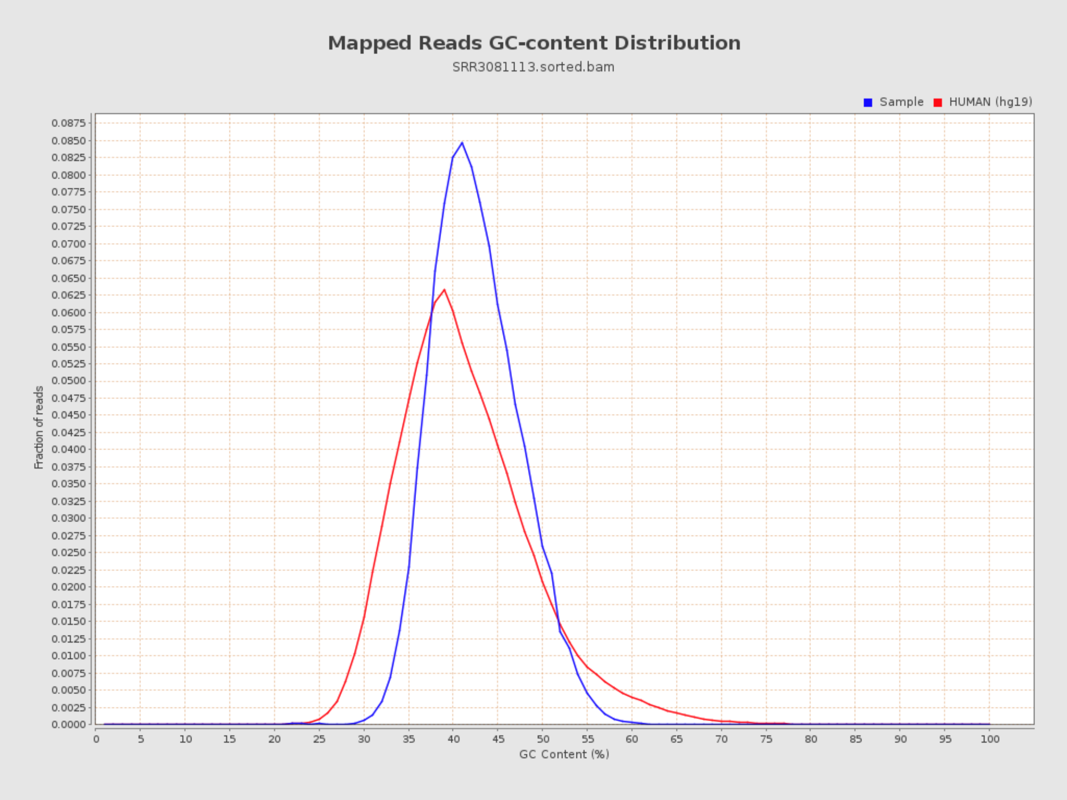
7. Results : Duplication Rate Histogram



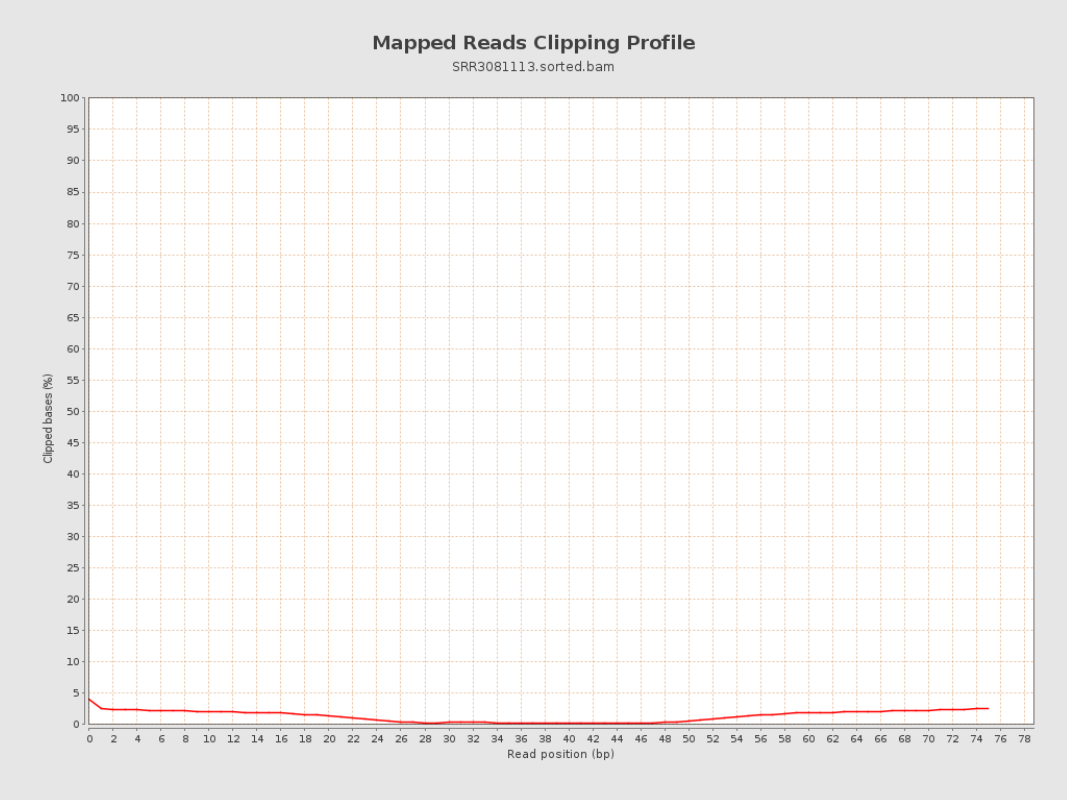
8. Results : Mapped Reads Nucleotide Content



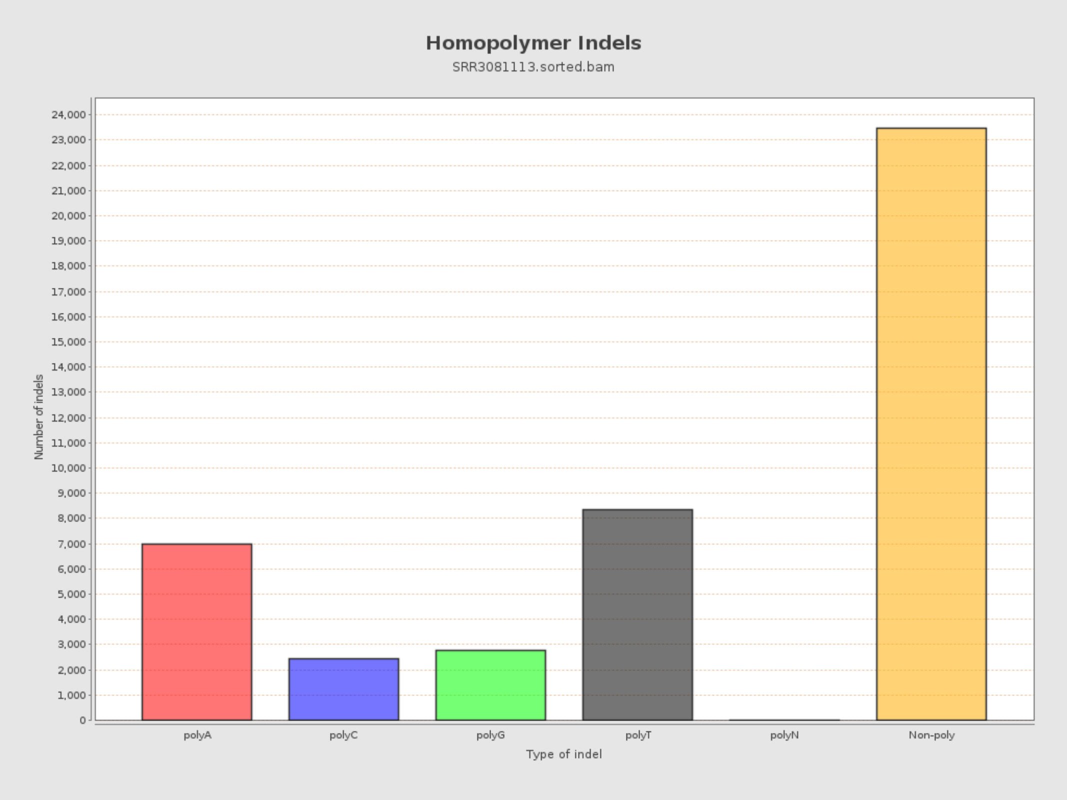
9. Results : Mapped Reads GC-content Distribution



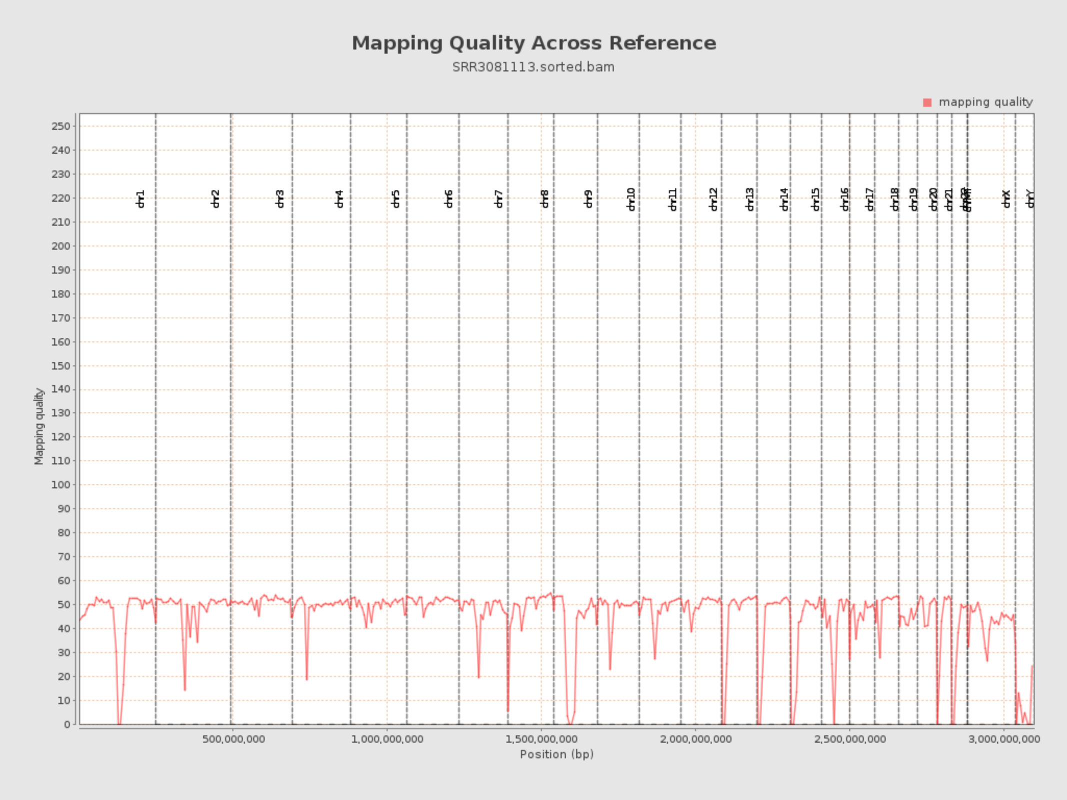
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram