Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:35:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084850.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_SRR3084850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:35:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,831,495
Mapped reads	2,516,653 / 88.88%
Unmapped reads	314,842 / 11.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,277 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	143,550 / 5.07%
Duplication rate	4.79%
Clipped reads	858,763 / 30.33%

2.2. ACGT Content

Number/percentage of A's	50,695,541 / 29.11%
Number/percentage of C's	31,755,714 / 18.23%
Number/percentage of T's	56,153,262 / 32.24%
Number/percentage of G's	35,520,041 / 20.4%
Number/percentage of N's	27,485 / 0.02%
GC Percentage	38.63%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.461

2.4. Mapping Quality

Mean Mapping Quality	48.2

2.5. Mismatches and indels

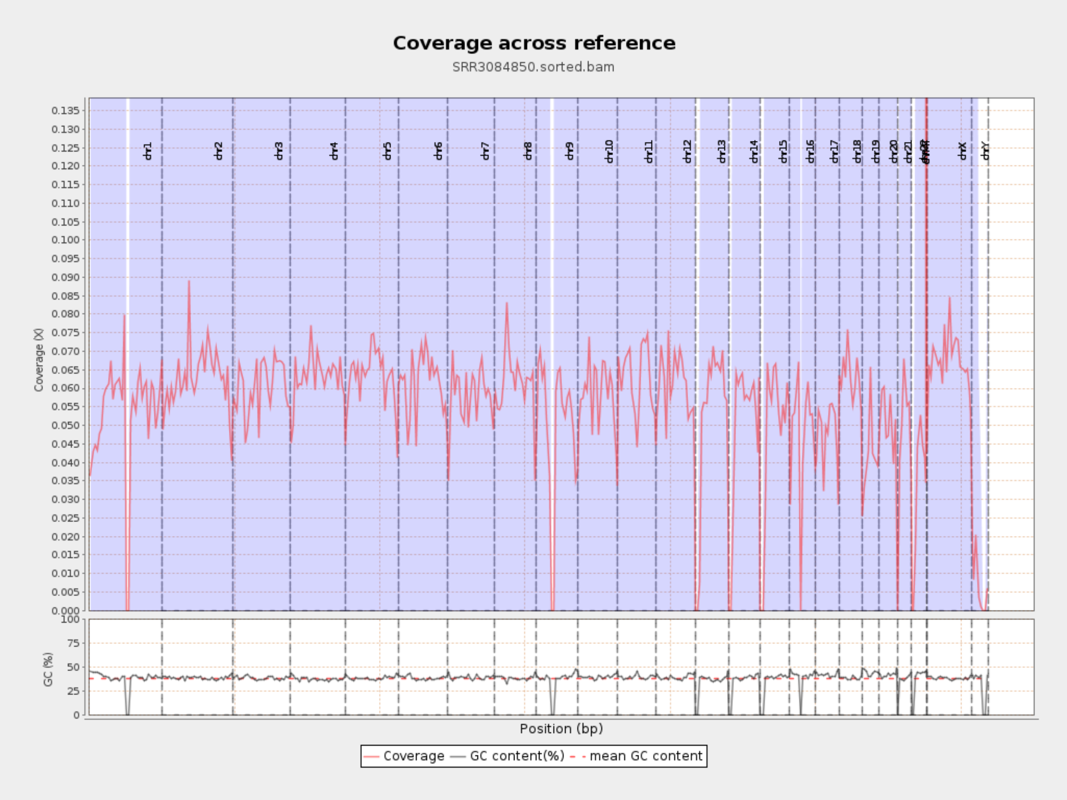
General error rate	0.84%
Mismatches	1,433,505
Insertions	14,060
Mapped reads with at least one insertion	0.55%
Deletions	37,939
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.63%

2.6. Chromosome stats

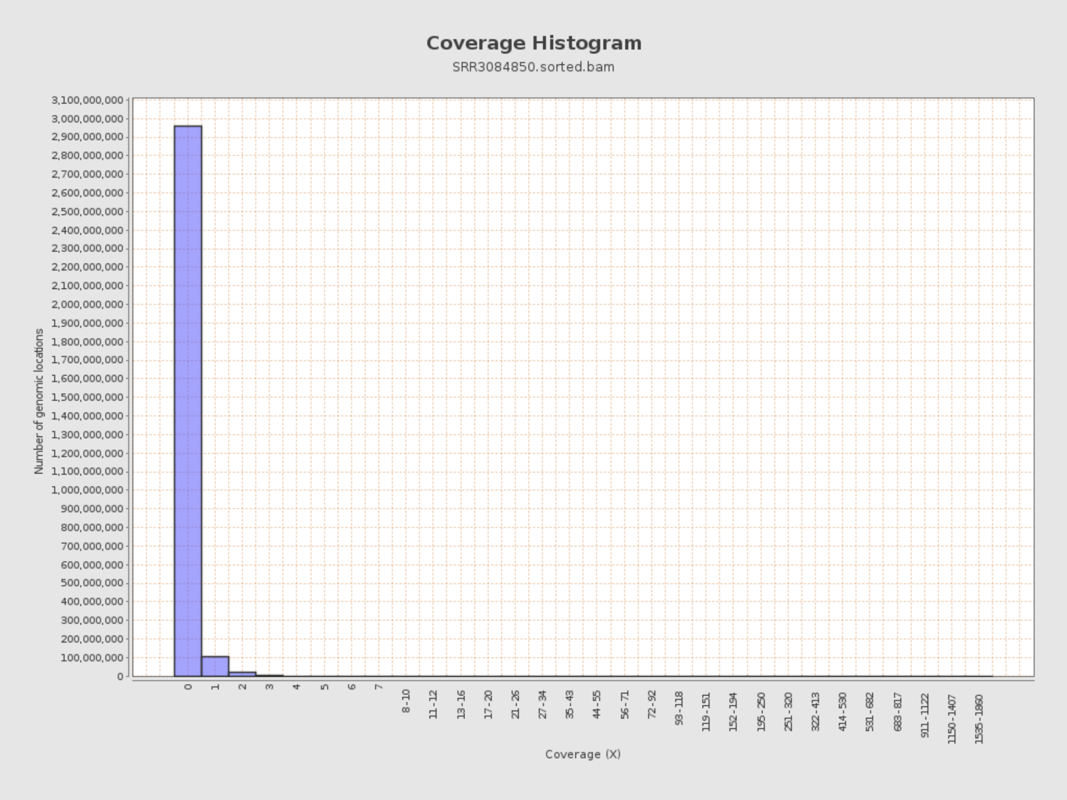
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13185286	0.0529	0.6882
chr2	243199373	15307956	0.0629	0.4194
chr3	198022430	11986553	0.0605	0.3014
chr4	191154276	12100847	0.0633	0.3175
chr5	180915260	11474269	0.0634	0.3096
chr6	171115067	10541062	0.0616	0.3071
chr7	159138663	9295235	0.0584	0.3455

chr8	146364022	9002808	0.0615	1.1825
chr9	141213431	7096841	0.0503	0.4019
chr10	135534747	7977047	0.0589	0.3748
chr11	135006516	8422836	0.0624	0.3916
chr12	133851895	8175659	0.0611	0.3056
chr13	115169878	5935392	0.0515	0.2769
chr14	107349540	5219453	0.0486	0.2858
chr15	102531392	4888905	0.0477	0.2646
chr16	90354753	4335366	0.048	0.2881
chr17	81195210	3822617	0.0471	0.2936
chr18	78077248	4950093	0.0634	0.7381
chr19	59128983	2506220	0.0424	0.4767
chr20	63025520	3182484	0.0505	0.2842
chr21	48129895	2273062	0.0472	0.2804
chr22	51304566	1609744	0.0314	0.2109
chrMT	16571	117328	7.0803	4.6267
chrX	155270560	10423715	0.0671	0.3424
chrY	59373566	388769	0.0065	0.1588

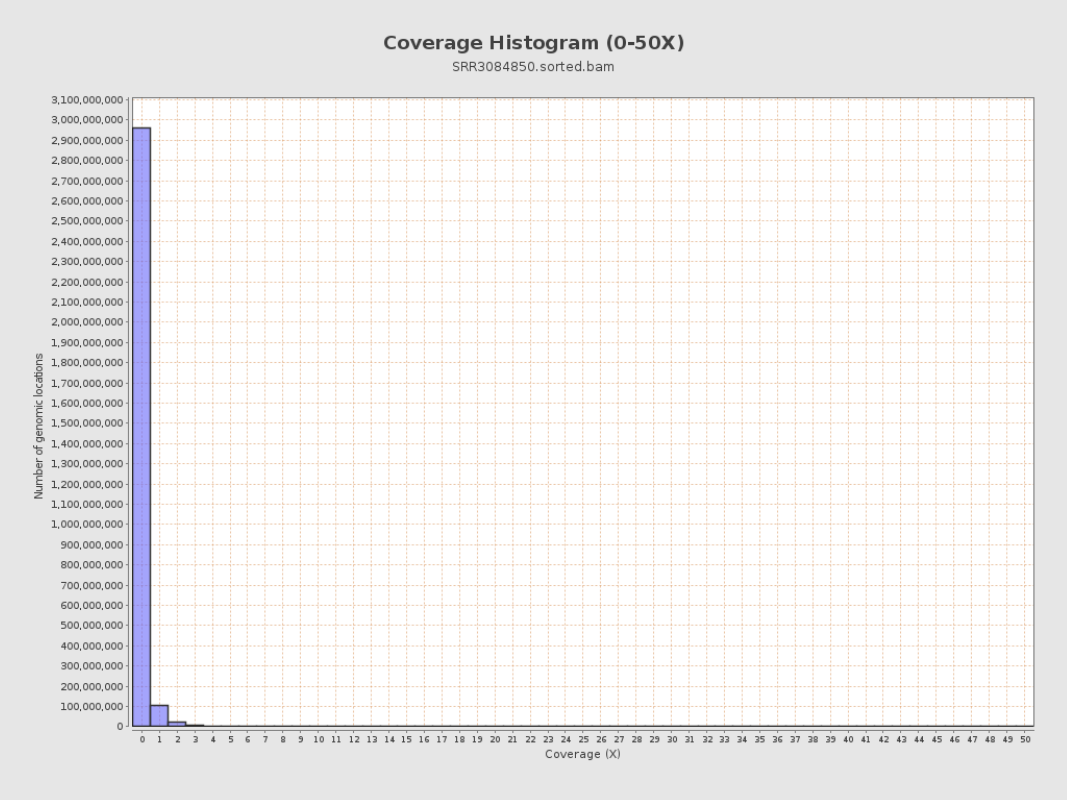
3. Results : Coverage across reference



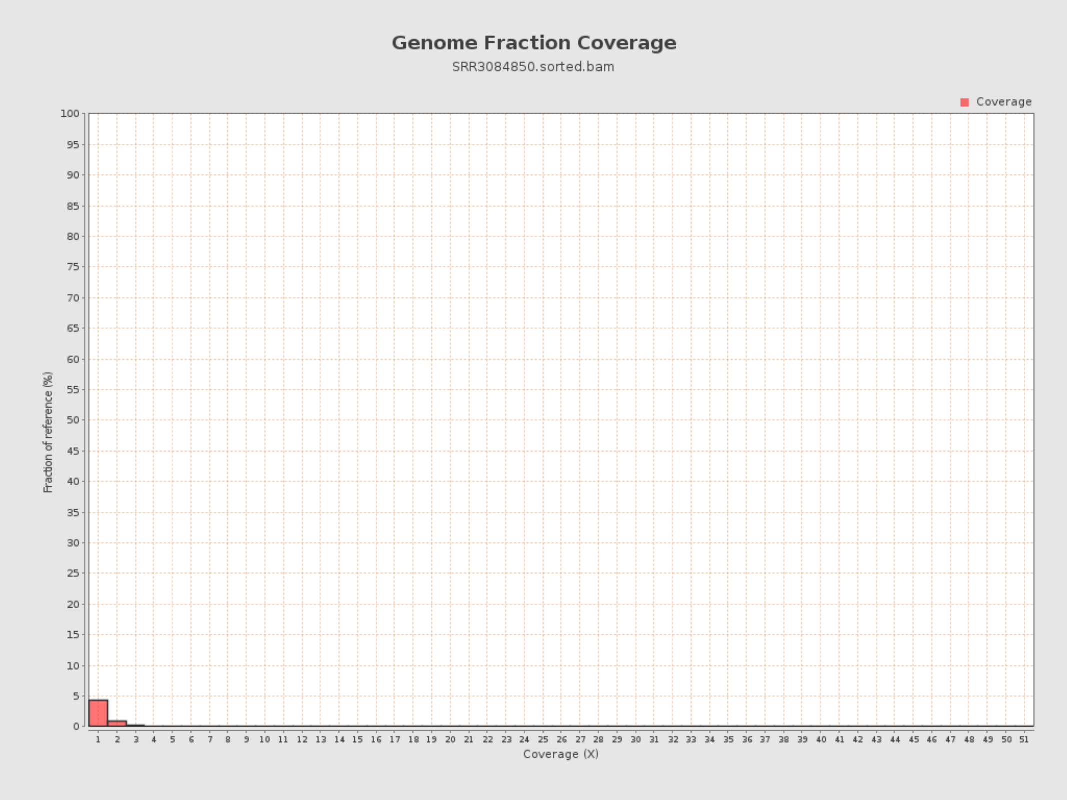
4. Results : Coverage Histogram



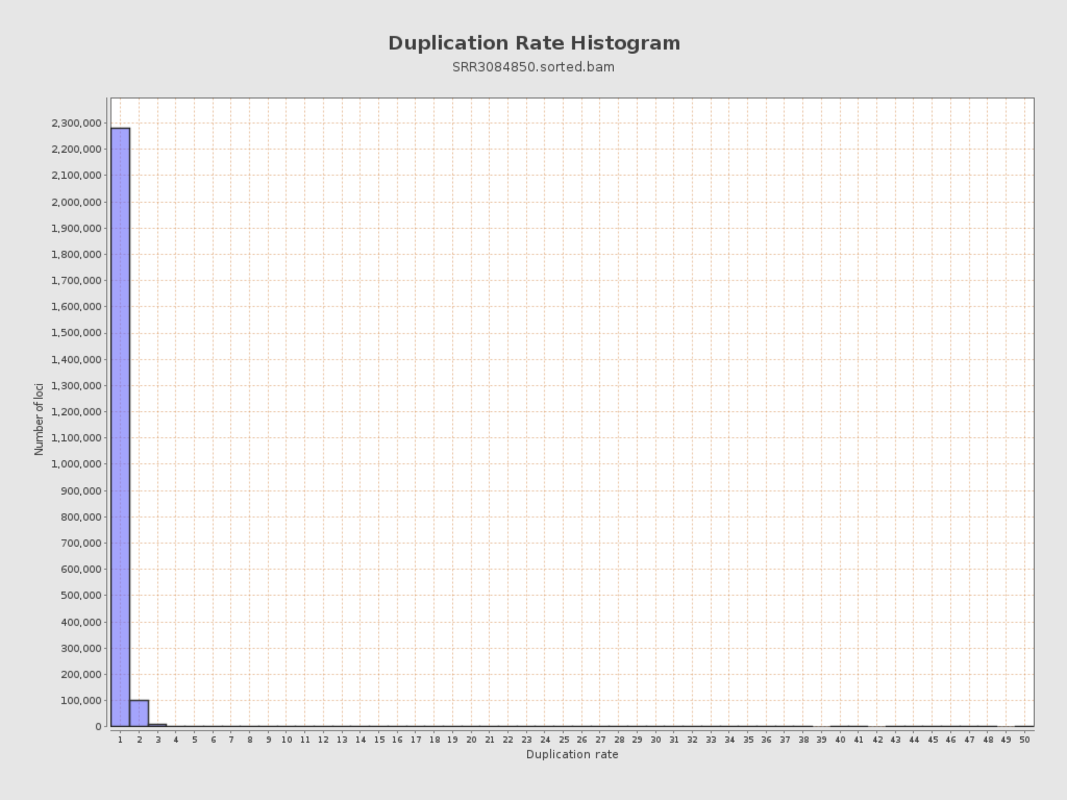
5. Results : Coverage Histogram (0-50X)



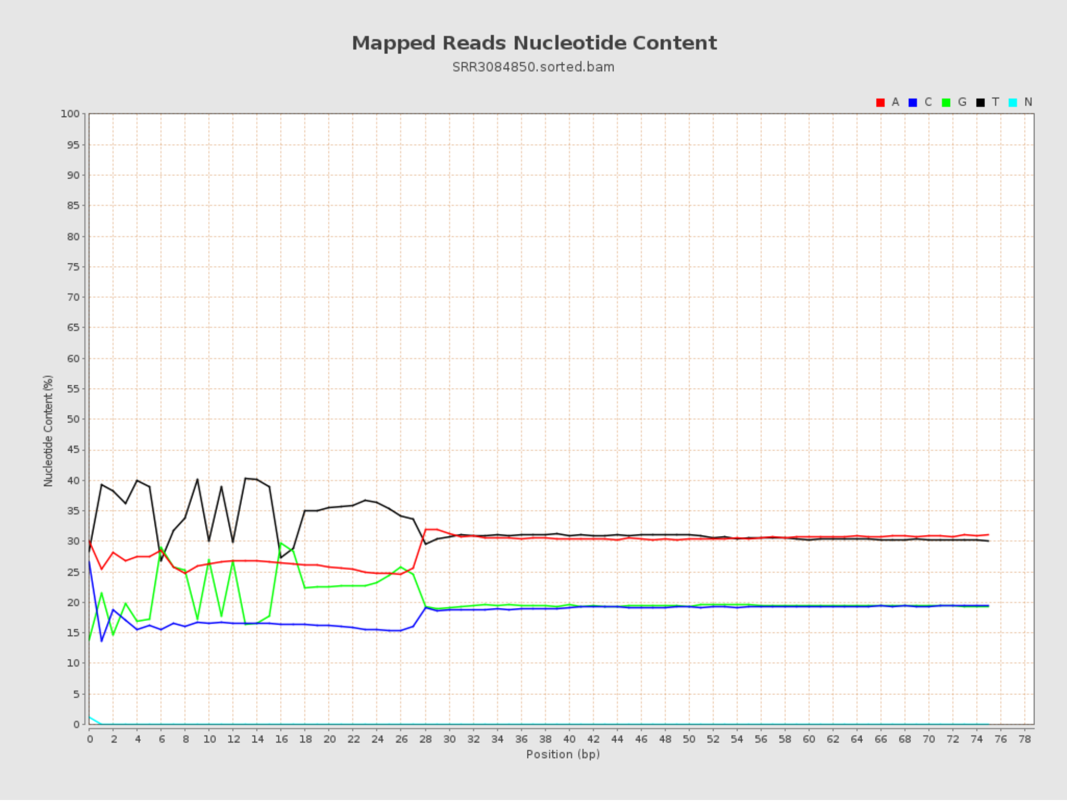
6. Results : Genome Fraction Coverage



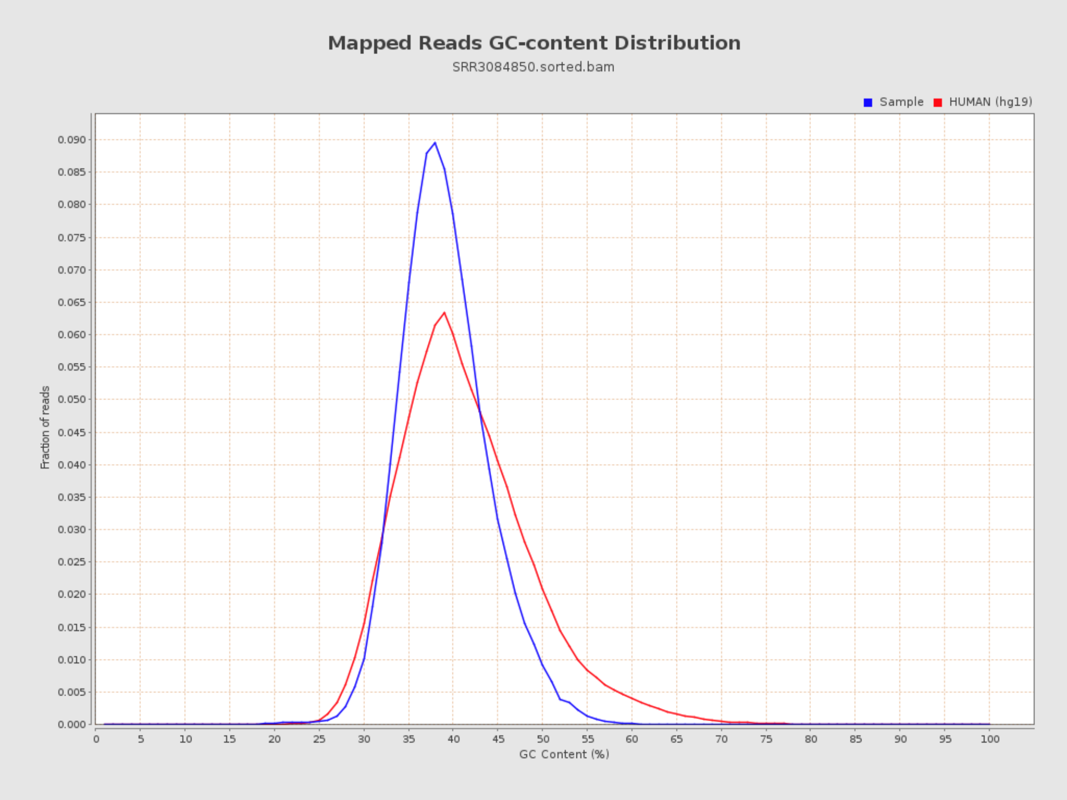
7. Results : Duplication Rate Histogram



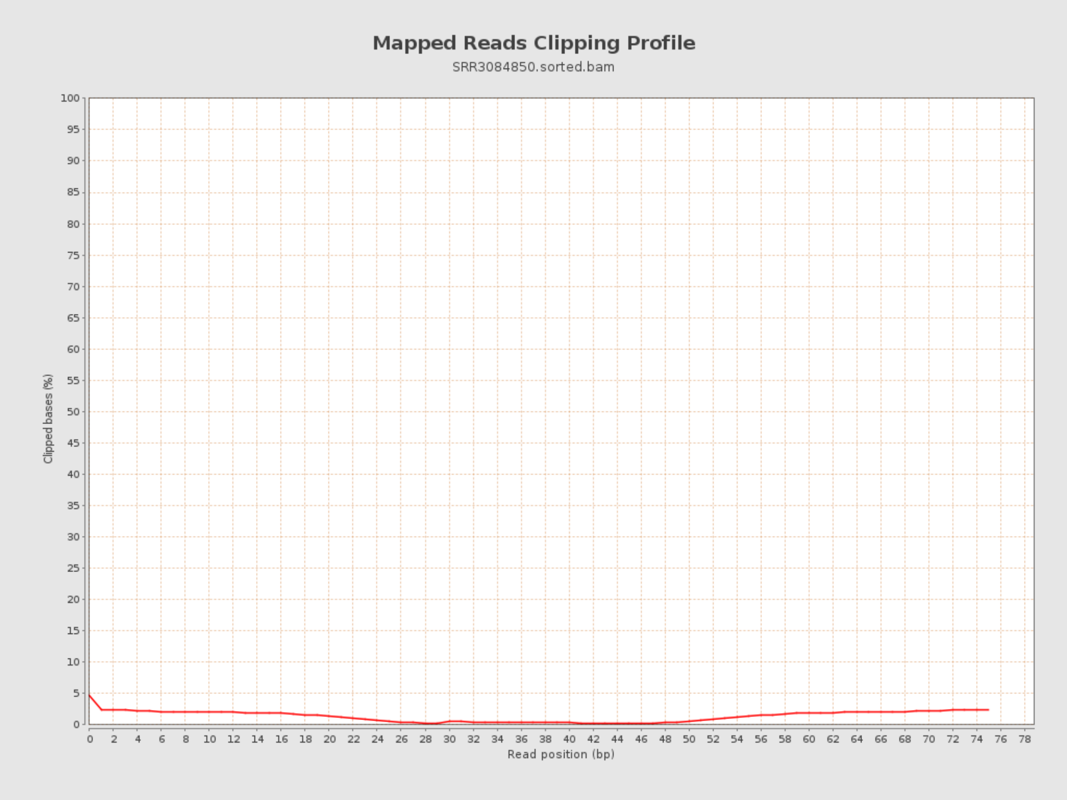
8. Results : Mapped Reads Nucleotide Content



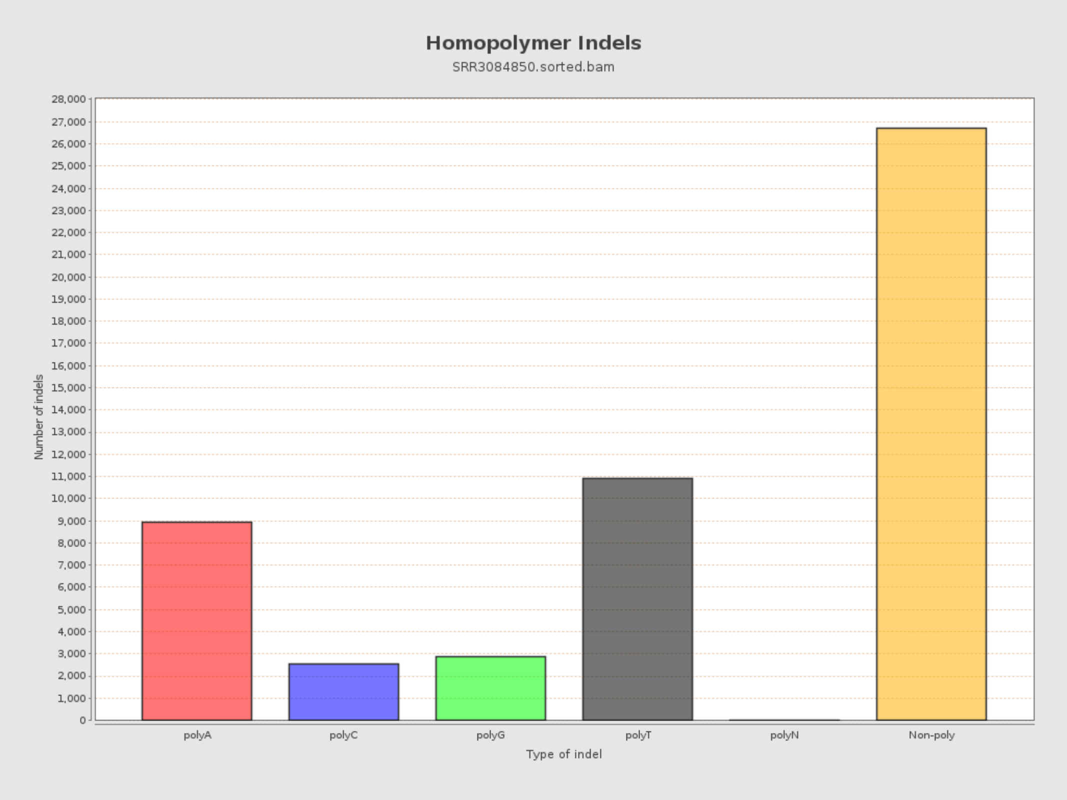
9. Results : Mapped Reads GC-content Distribution



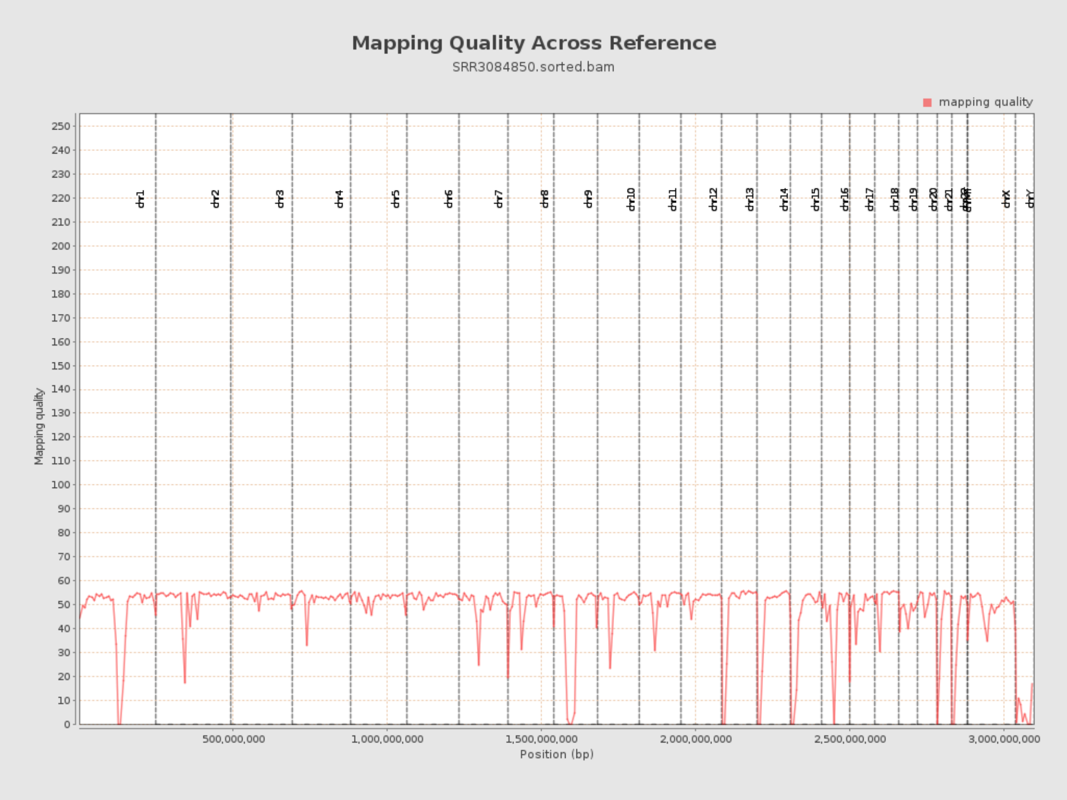
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram