Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:44:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084853.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_SRR3084853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:44:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,560,997
Mapped reads	2,102,856 / 82.11%
Unmapped reads	458,141 / 17.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,143 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	129,261 / 5.05%
Duplication rate	5.39%
Clipped reads	933,419 / 36.45%

2.2. ACGT Content

Number/percentage of A's	38,369,663 / 27.28%
Number/percentage of C's	26,655,497 / 18.95%
Number/percentage of T's	43,914,041 / 31.23%
Number/percentage of G's	31,673,743 / 22.52%
Number/percentage of N's	20,967 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0454

Standard Deviation	0.3097

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

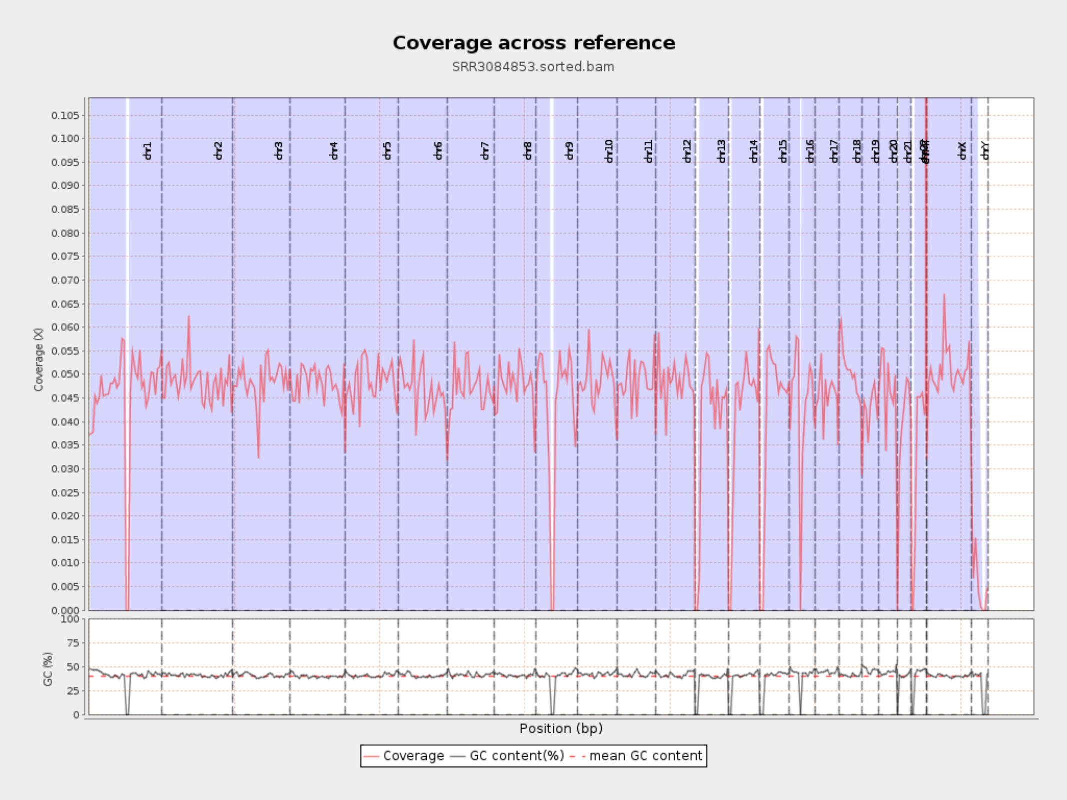
General error rate	0.85%
Mismatches	1,182,932
Insertions	10,219
Mapped reads with at least one insertion	0.48%
Deletions	28,009
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.7%

2.6. Chromosome stats

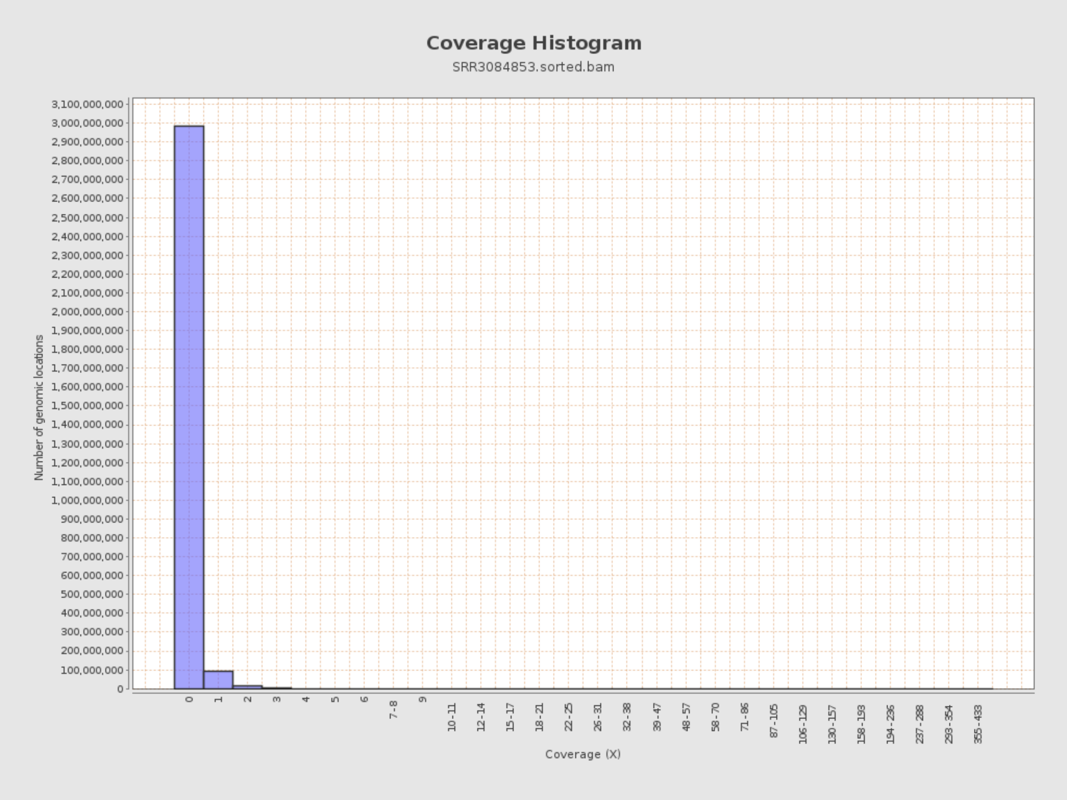
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11241839	0.0451	0.3946
chr2	243199373	11799064	0.0485	0.3491
chr3	198022430	9593152	0.0484	0.2621
chr4	191154276	9220131	0.0482	0.2688
chr5	180915260	8746787	0.0483	0.2638
chr6	171115067	8020685	0.0469	0.274
chr7	159138663	7518733	0.0472	0.3214

chr8	146364022	6963263	0.0476	0.3744
chr9	141213431	6028759	0.0427	0.3211
chr10	135534747	6615456	0.0488	0.332
chr11	135006516	6595681	0.0489	0.2974
chr12	133851895	6506284	0.0486	0.2678
chr13	115169878	4447394	0.0386	0.2355
chr14	107349540	4292688	0.04	0.25
chr15	102531392	4225244	0.0412	0.2434
chr16	90354753	3917131	0.0434	0.2593
chr17	81195210	3676256	0.0453	0.2764
chr18	78077248	3985021	0.051	0.5364
chr19	59128983	2507523	0.0424	0.3221
chr20	63025520	2986784	0.0474	0.2667
chr21	48129895	1817587	0.0378	0.2415
chr22	51304566	1582348	0.0308	0.2084
chrMT	16571	244312	14.7433	7.9129
chrX	155270560	7827258	0.0504	0.2848
chrY	59373566	323633	0.0055	0.1128

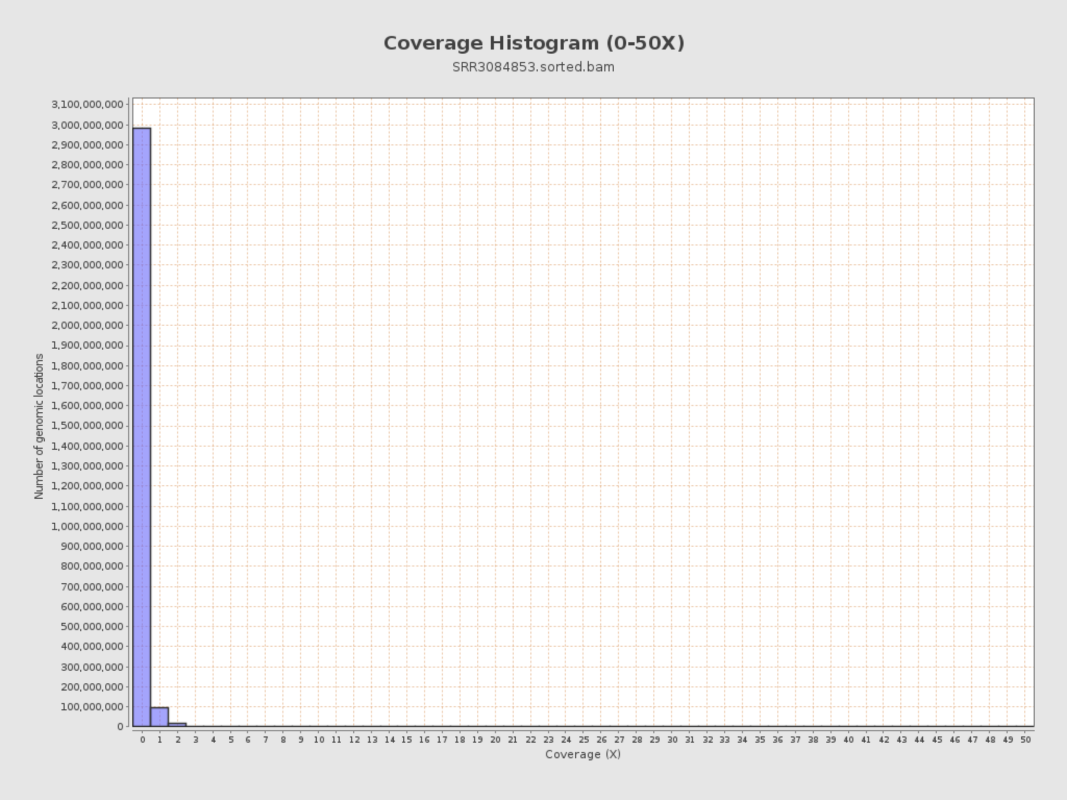
3. Results : Coverage across reference



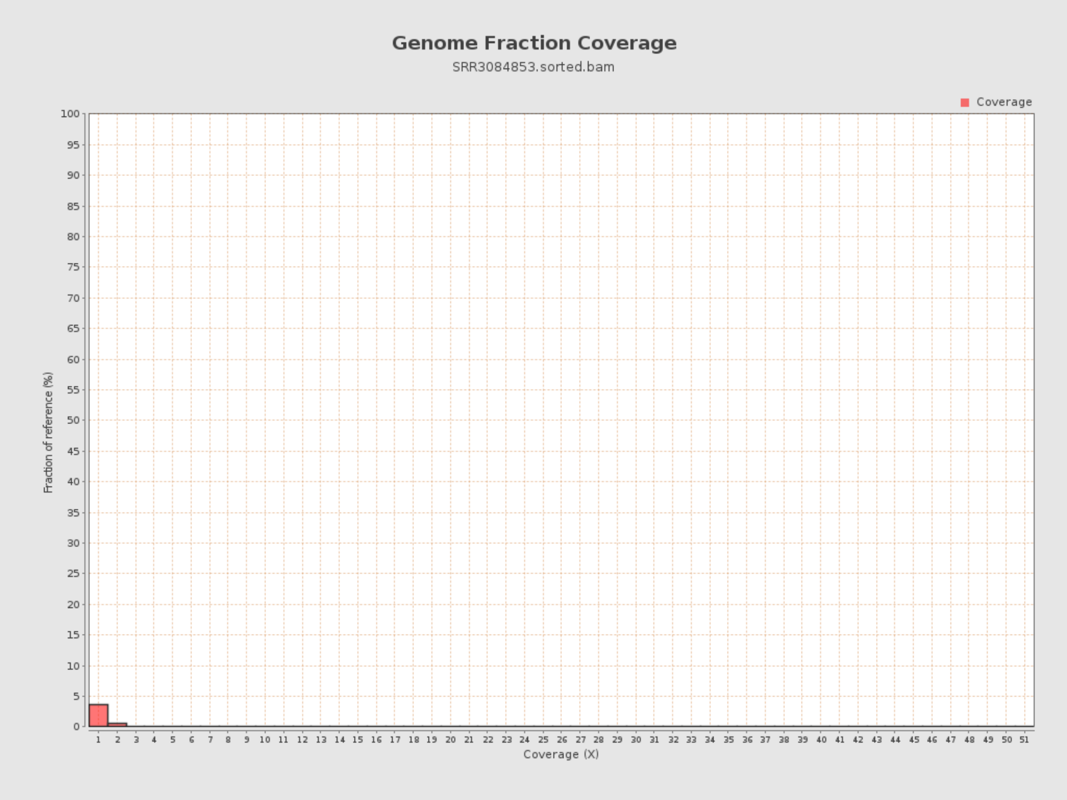
4. Results : Coverage Histogram



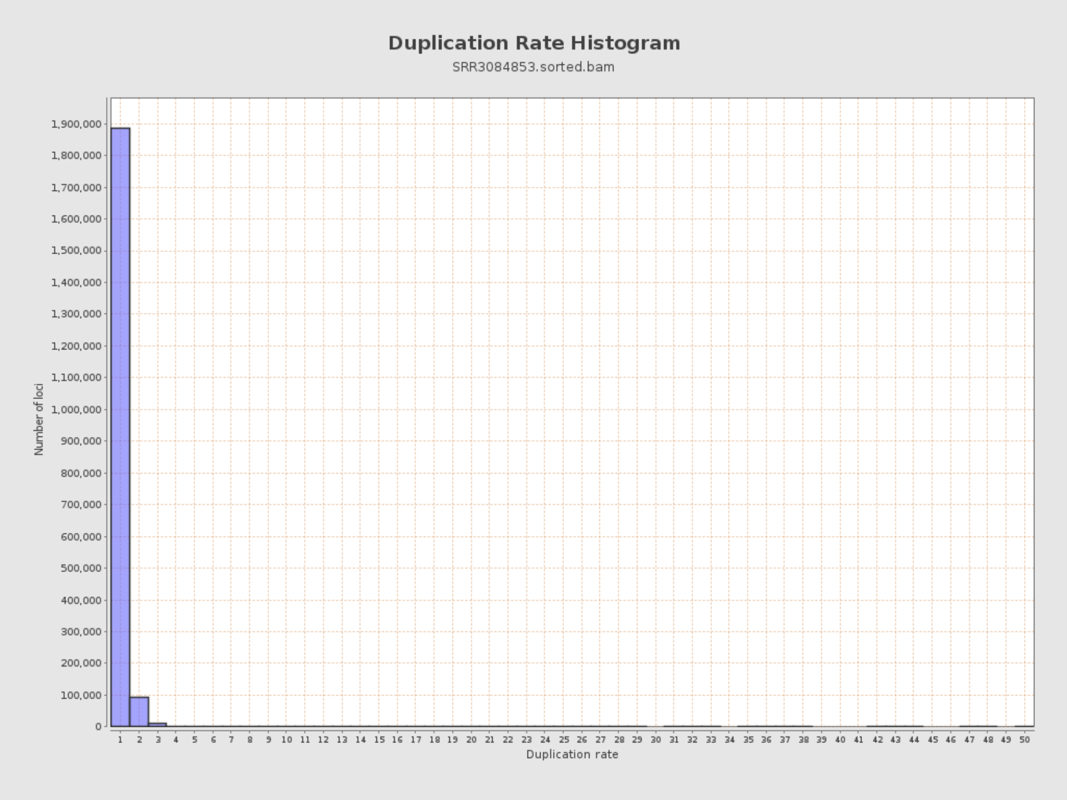
5. Results : Coverage Histogram (0-50X)



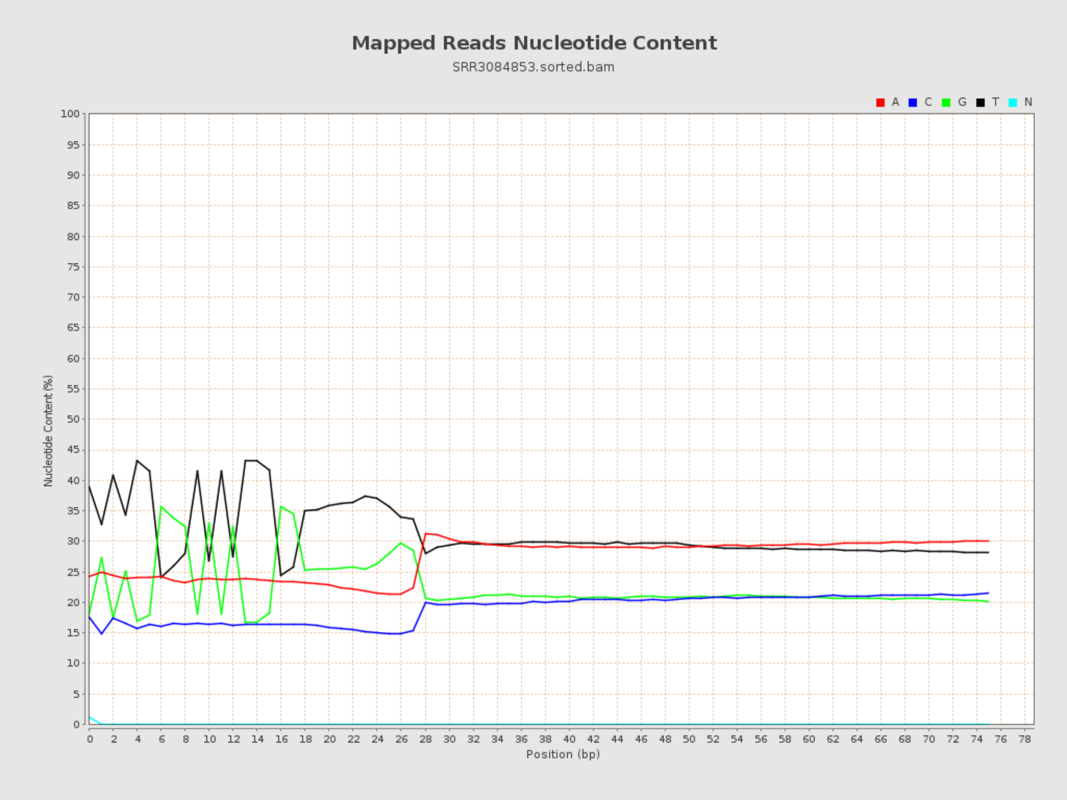
6. Results : Genome Fraction Coverage



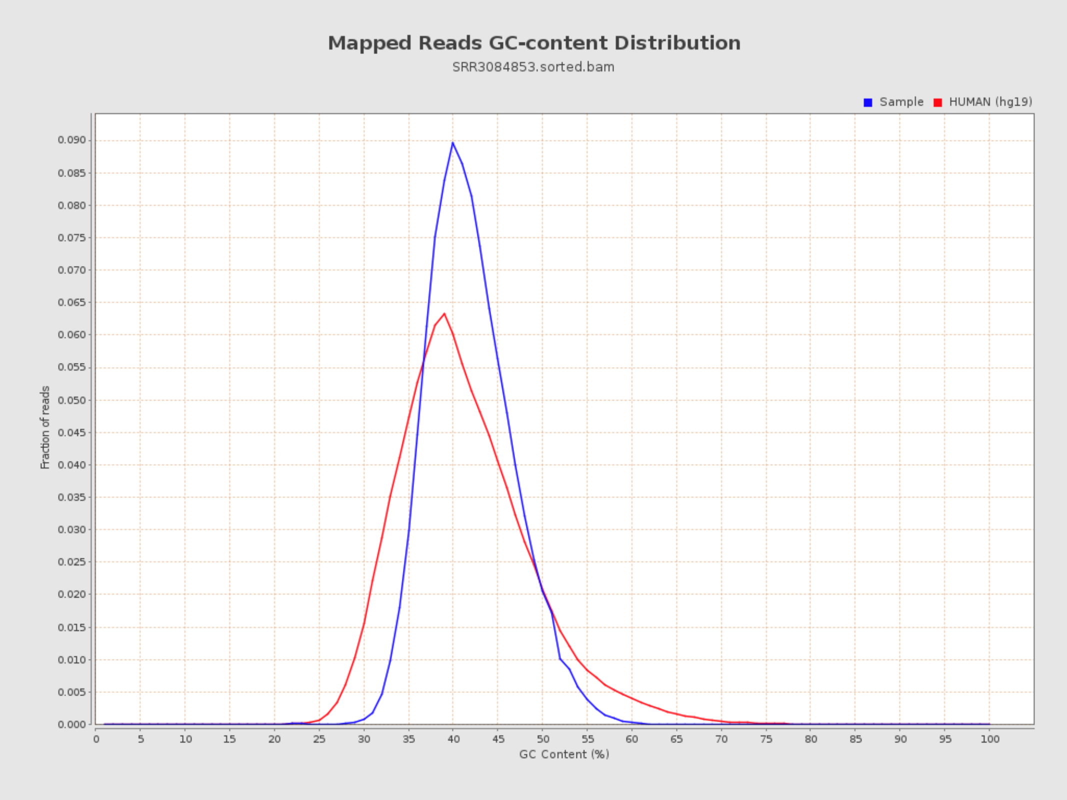
7. Results : Duplication Rate Histogram



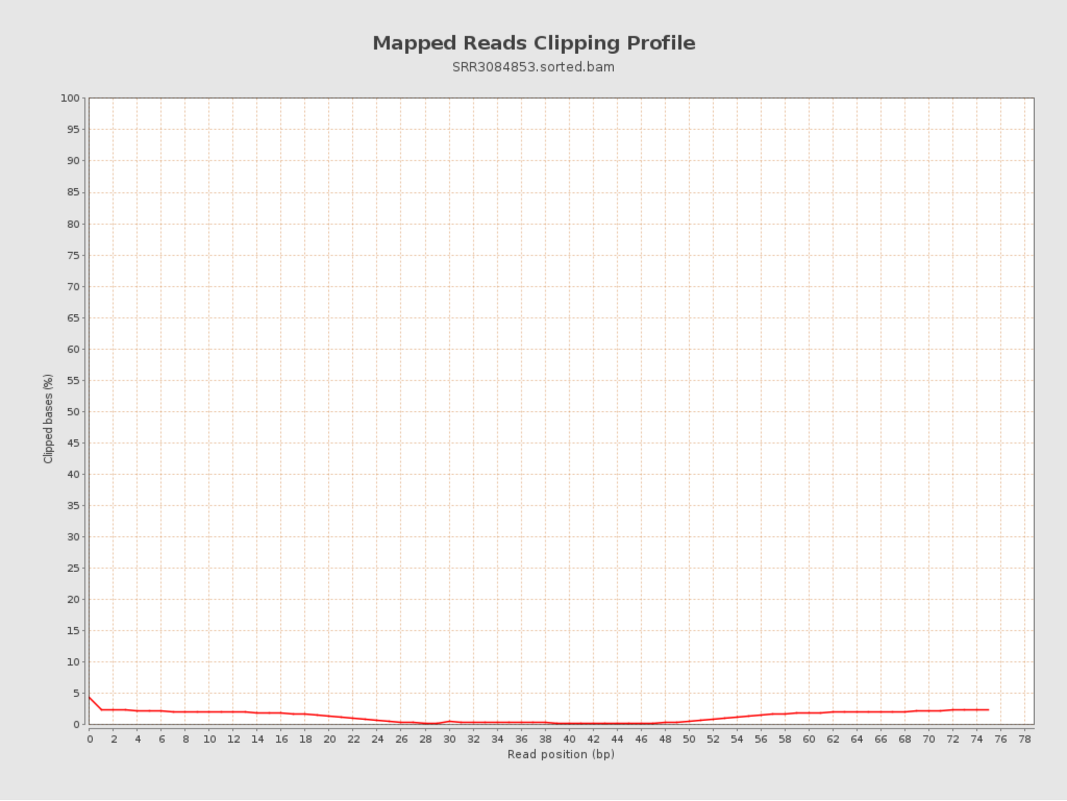
8. Results : Mapped Reads Nucleotide Content



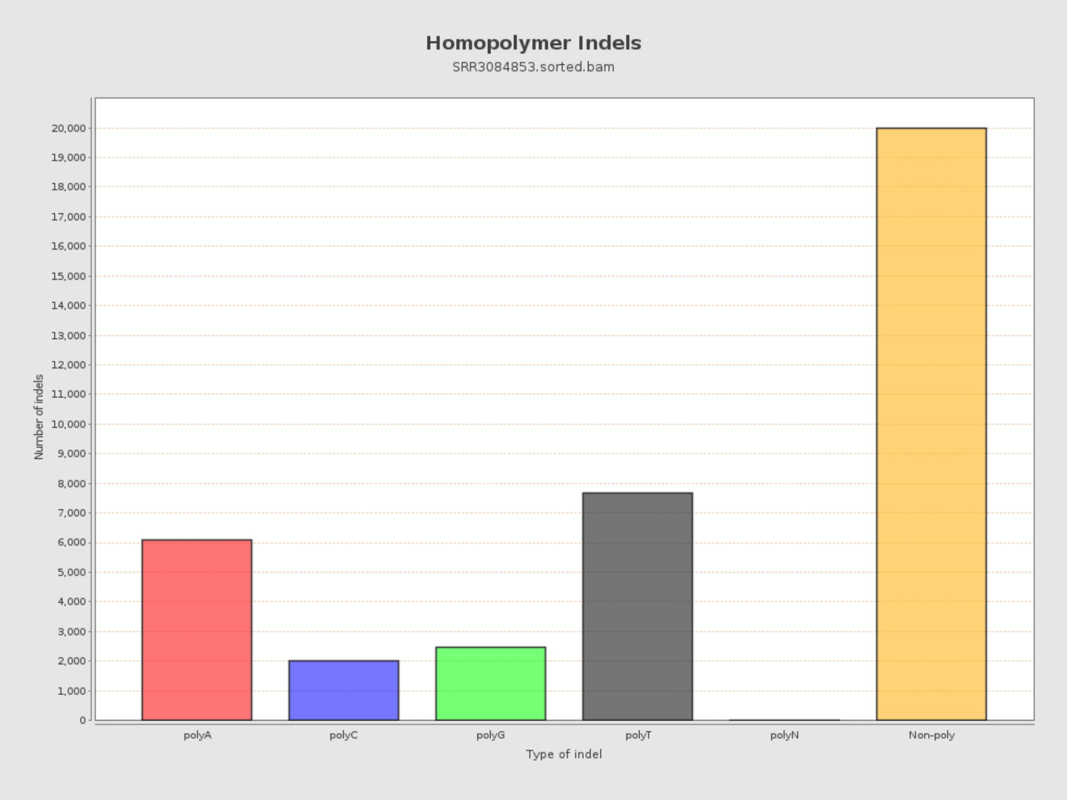
9. Results : Mapped Reads GC-content Distribution



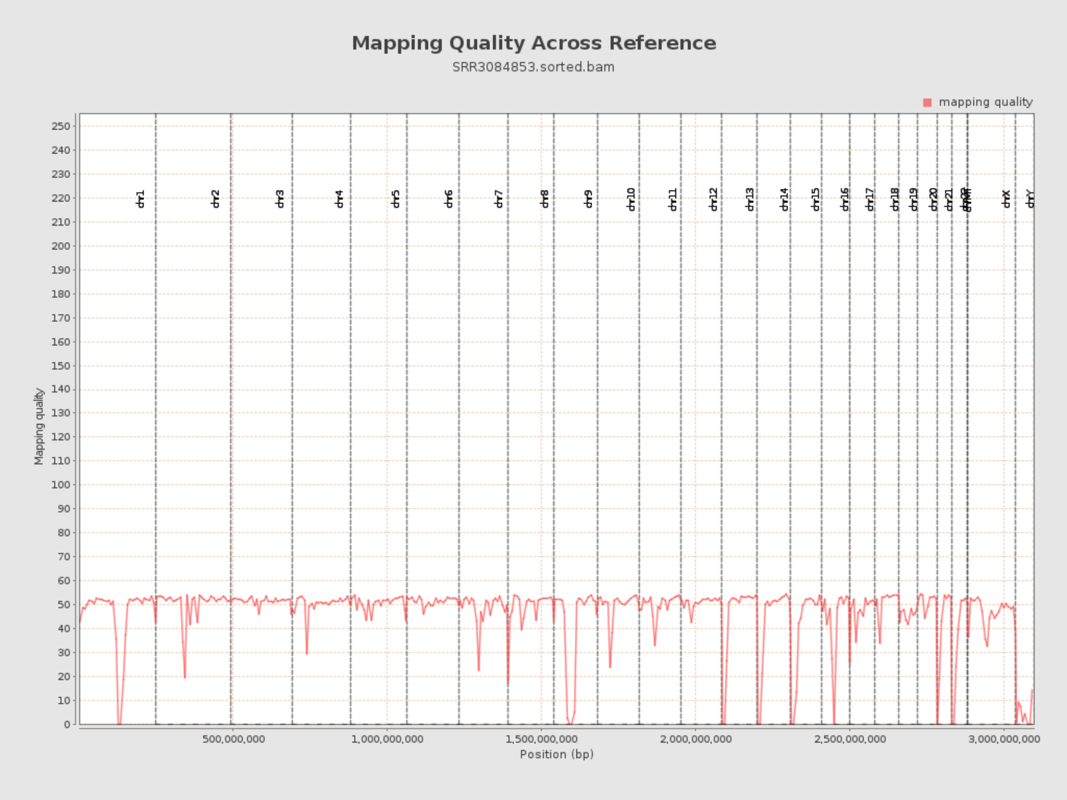
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram