Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:26:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084829.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_SRR3084829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:26:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,477,262
Mapped reads	1,363,924 / 92.33%
Unmapped reads	113,338 / 7.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,051 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	49,754 / 3.37%
Duplication rate	2.84%
Clipped reads	512,082 / 34.66%

2.2. ACGT Content

Number/percentage of A's	26,217,447 / 28.17%
Number/percentage of C's	17,122,651 / 18.4%
Number/percentage of T's	29,690,213 / 31.9%
Number/percentage of G's	20,019,851 / 21.51%
Number/percentage of N's	13,260 / 0.01%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2842

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

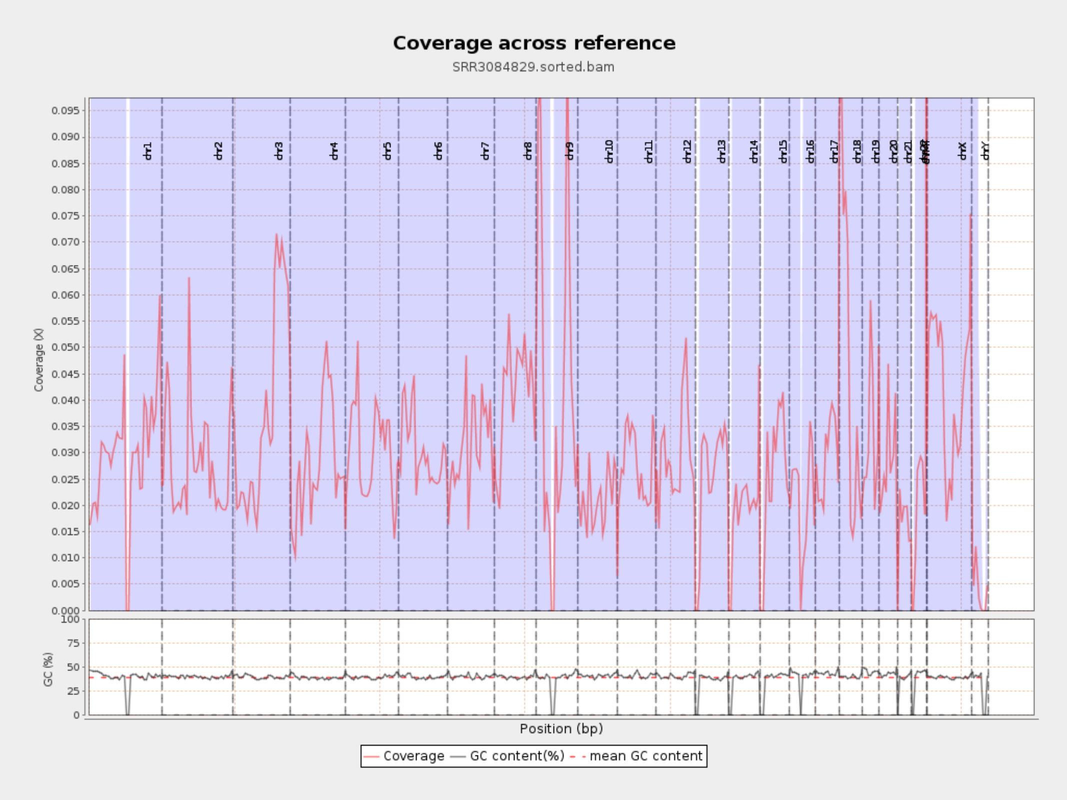
General error rate	0.83%
Mismatches	762,439
Insertions	7,827
Mapped reads with at least one insertion	0.57%
Deletions	22,838
Mapped reads with at least one deletion	1.66%
Homopolymer indels	48.68%

2.6. Chromosome stats

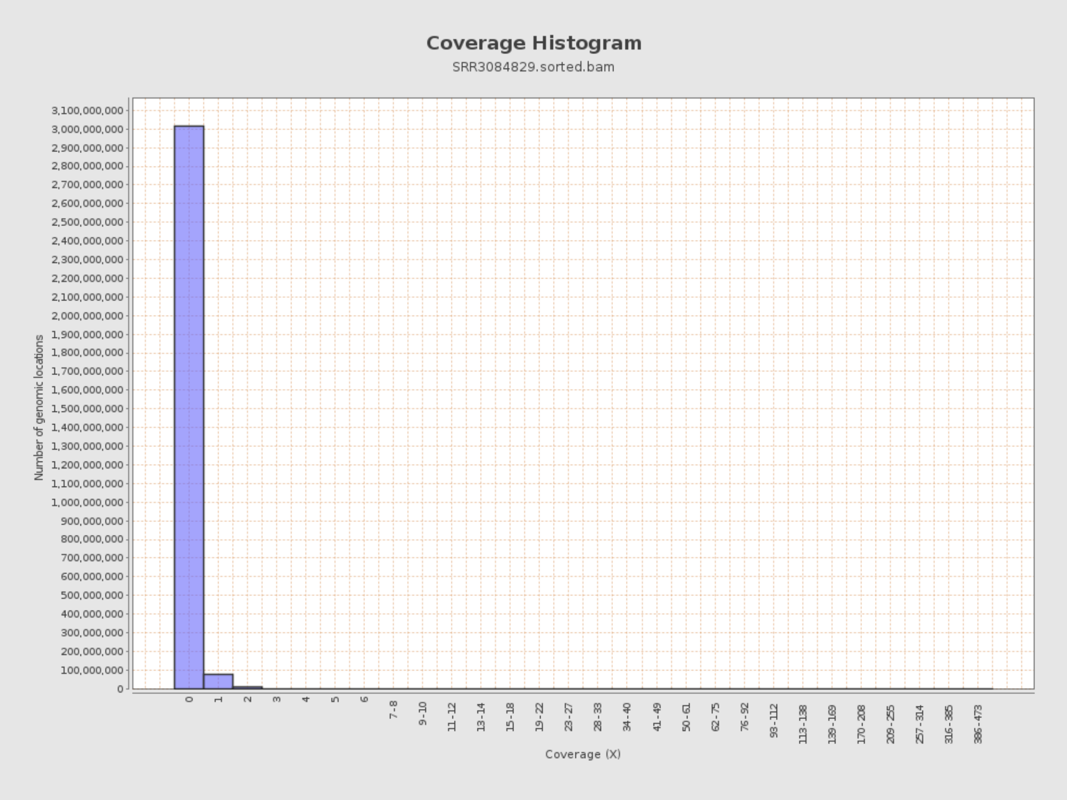
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7402852	0.0297	0.4456
chr2	243199373	6855639	0.0282	0.3804
chr3	198022430	7445449	0.0376	0.2135
chr4	191154276	5375032	0.0281	0.1866
chr5	180915260	5473351	0.0303	0.1968
chr6	171115067	5196319	0.0304	0.2007
chr7	159138663	4983045	0.0313	0.3273

chr8	146364022	5995489	0.041	0.3817
chr9	141213431	5964713	0.0422	0.3412
chr10	135534747	2845990	0.021	0.1995
chr11	135006516	3695047	0.0274	0.2553
chr12	133851895	4015680	0.03	0.1922
chr13	115169878	2894465	0.0251	0.1727
chr14	107349540	1963221	0.0183	0.1622
chr15	102531392	2616019	0.0255	0.1815
chr16	90354753	1921247	0.0213	0.18
chr17	81195210	2390206	0.0294	0.2043
chr18	78077248	3790349	0.0485	0.566
chr19	59128983	1983147	0.0335	0.3155
chr20	63025520	1817446	0.0288	0.1922
chr21	48129895	784368	0.0163	0.1525
chr22	51304566	902658	0.0176	0.1428
chrMT	16571	9423	0.5686	0.9077
chrX	155270560	6544412	0.0421	0.2438
chrY	59373566	236226	0.004	0.1256

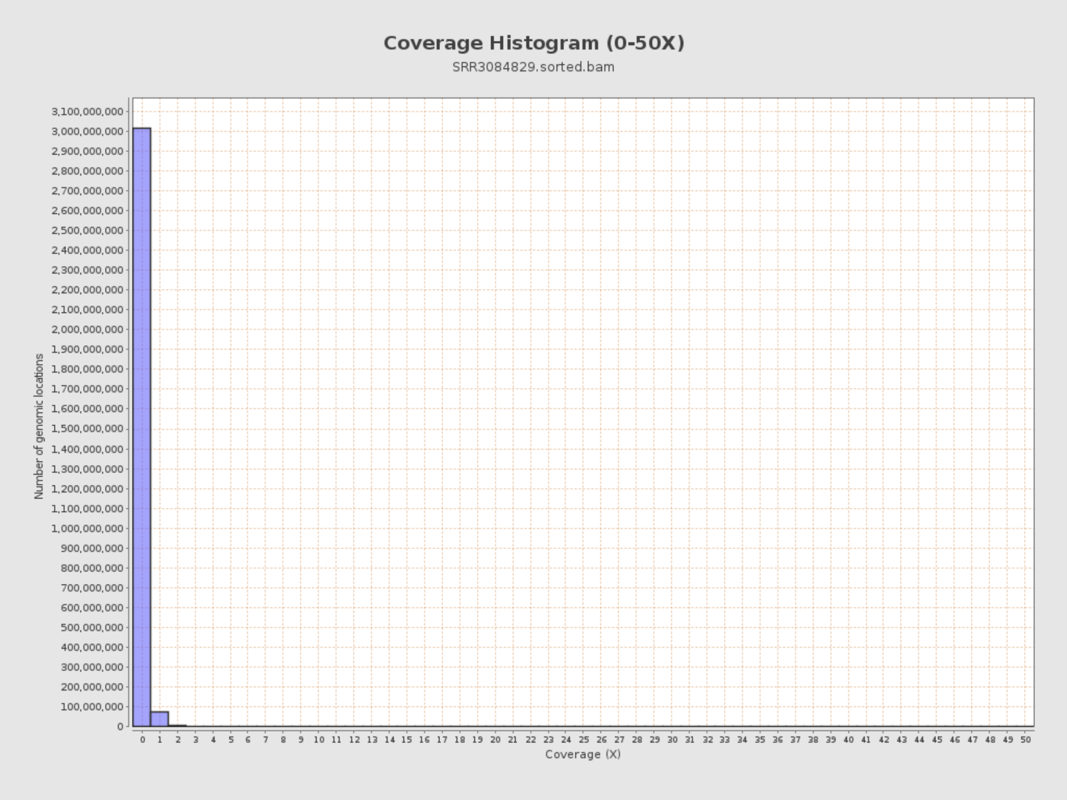
3. Results : Coverage across reference



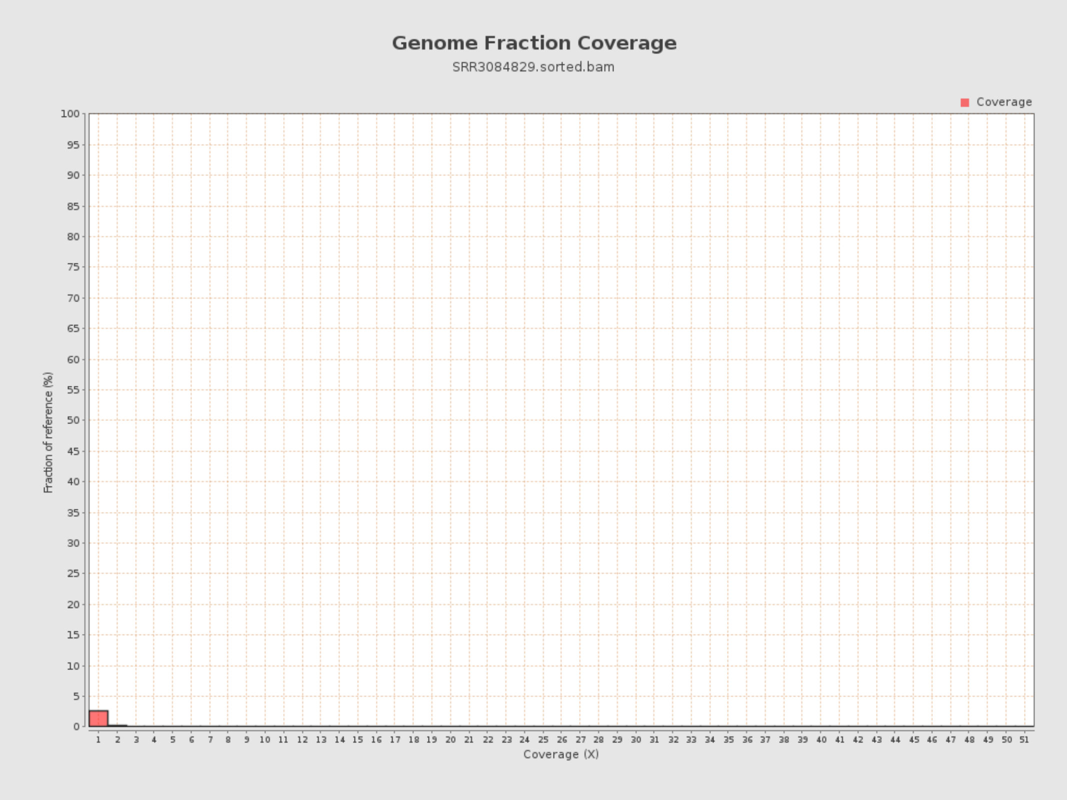
4. Results : Coverage Histogram



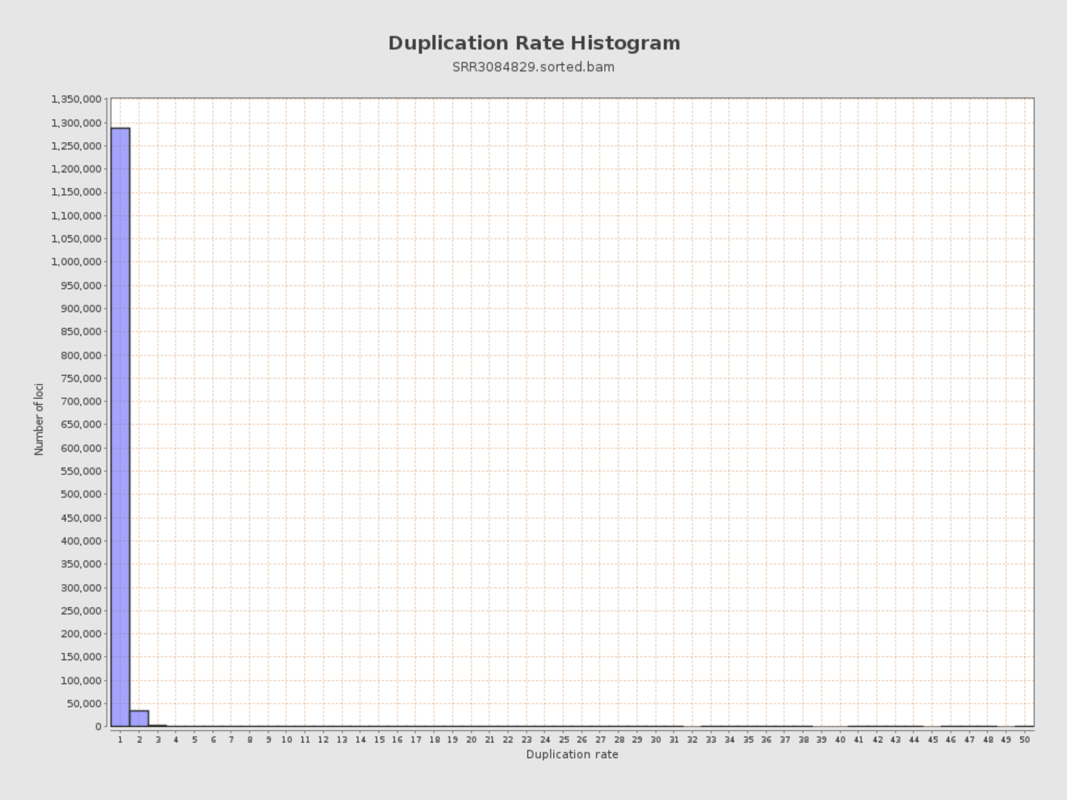
5. Results : Coverage Histogram (0-50X)



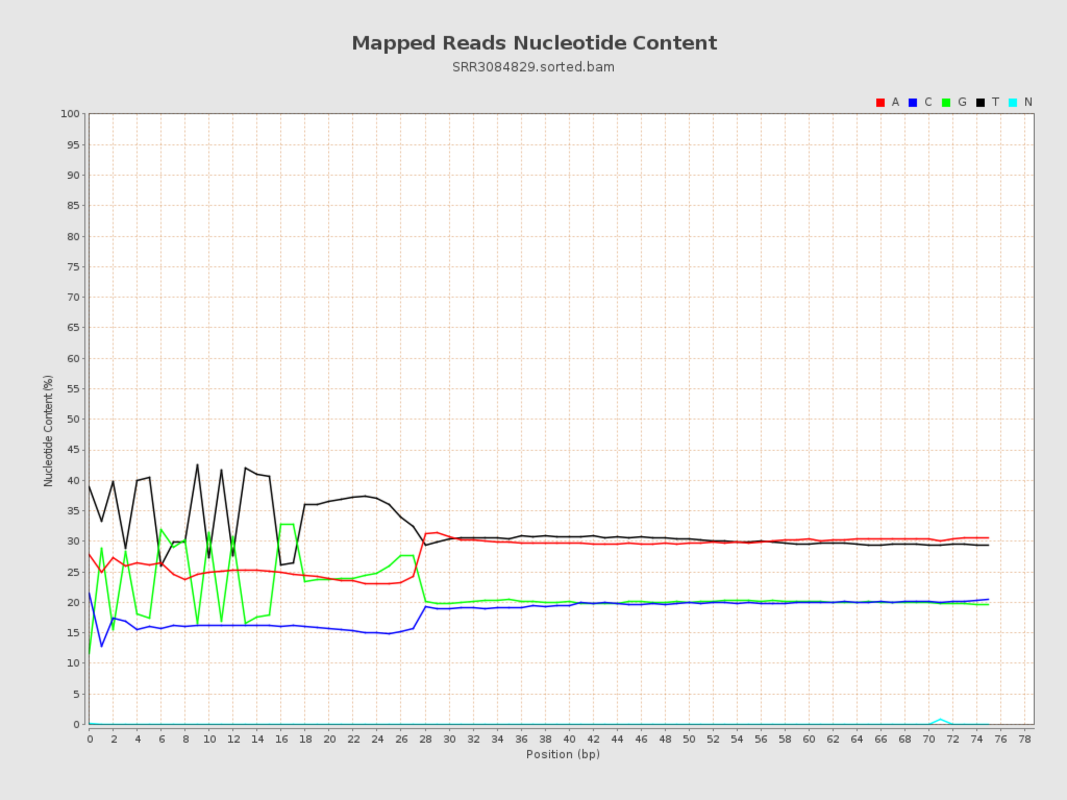
6. Results : Genome Fraction Coverage



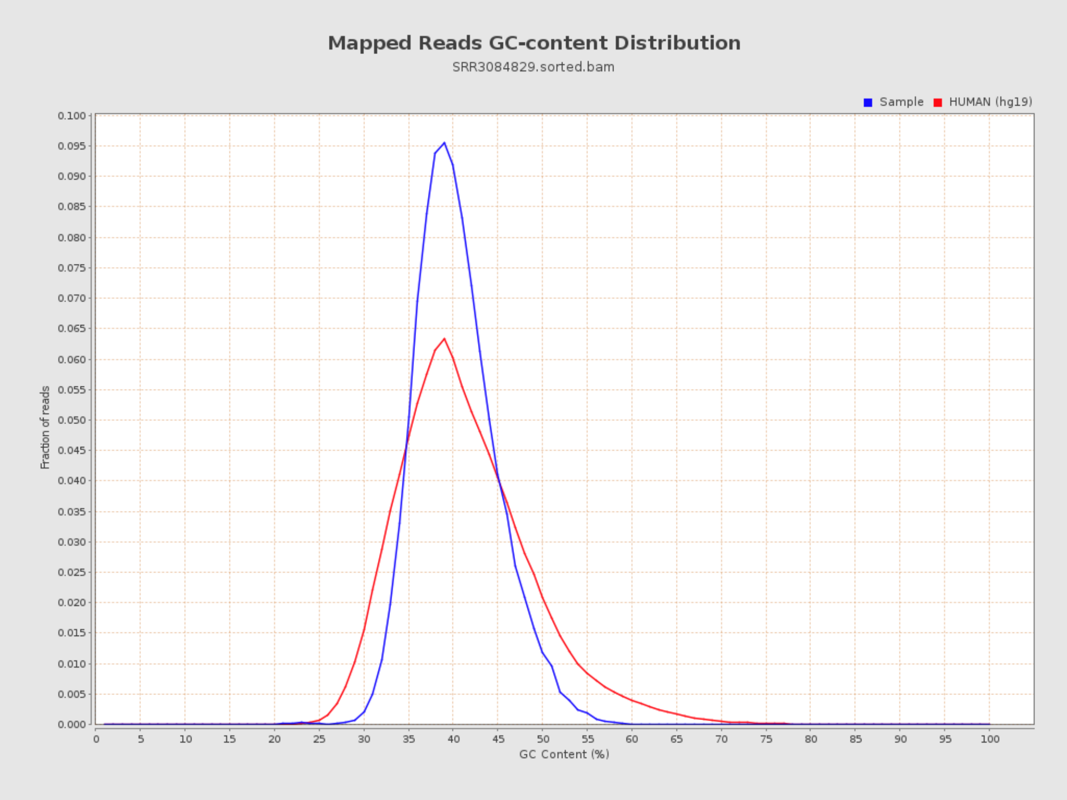
7. Results : Duplication Rate Histogram



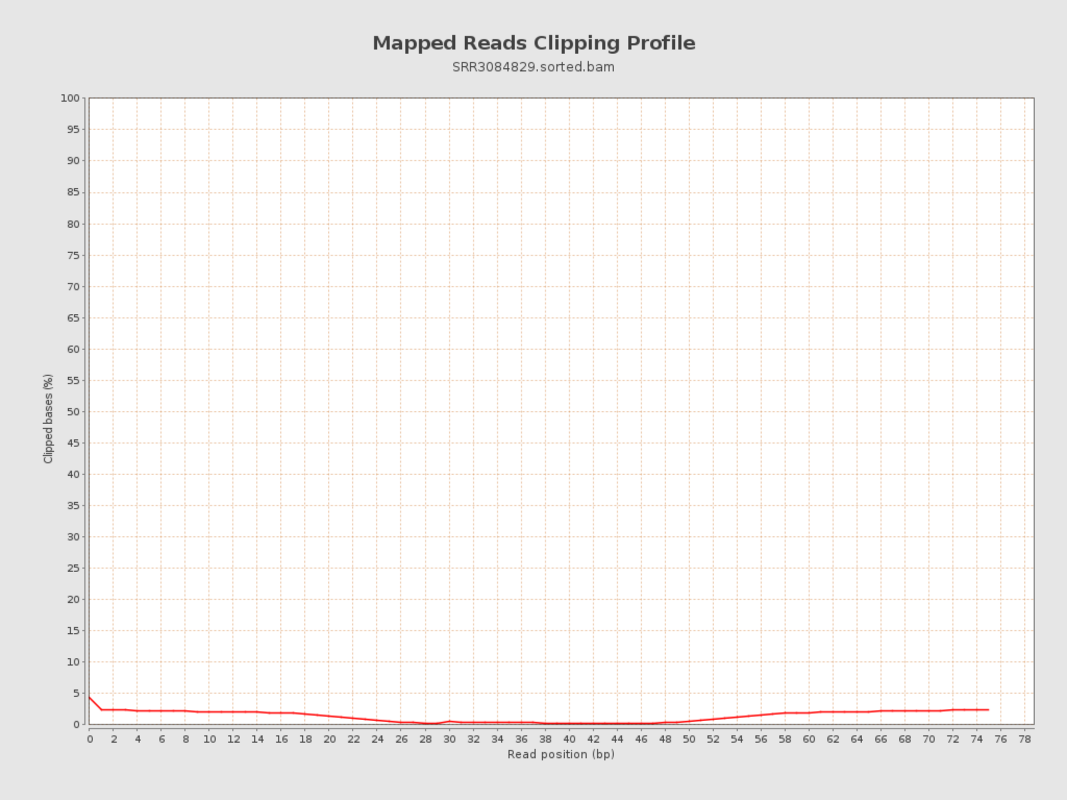
8. Results : Mapped Reads Nucleotide Content



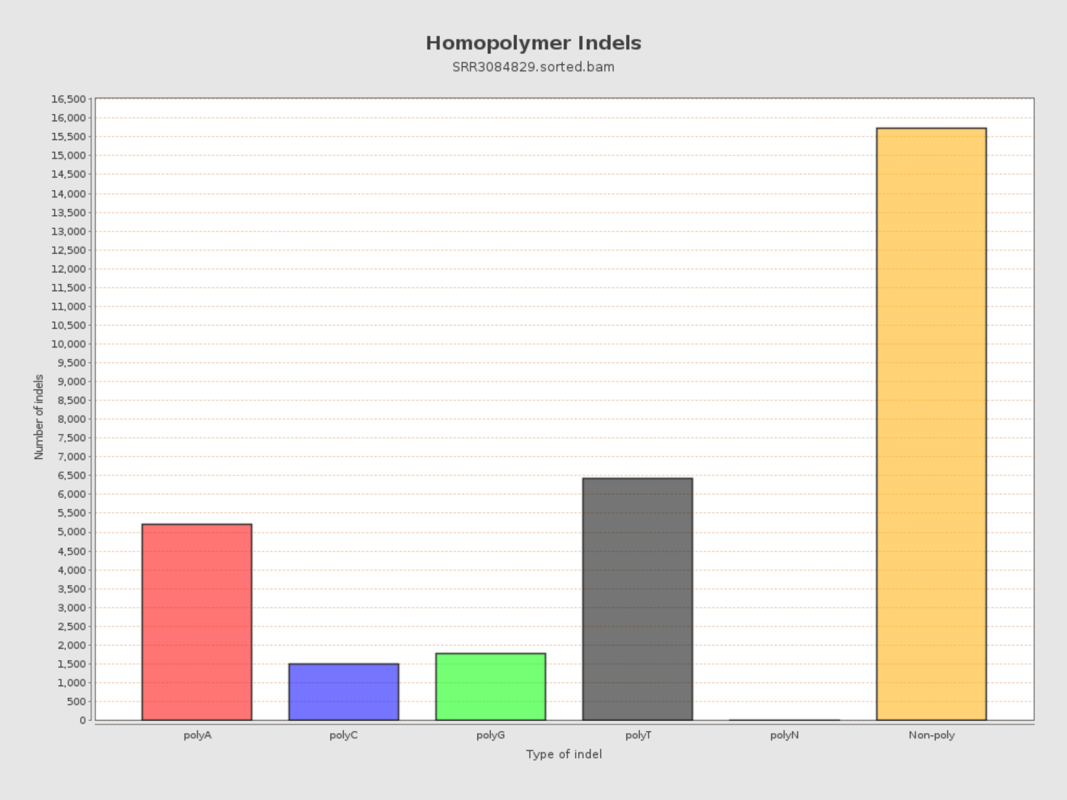
9. Results : Mapped Reads GC-content Distribution



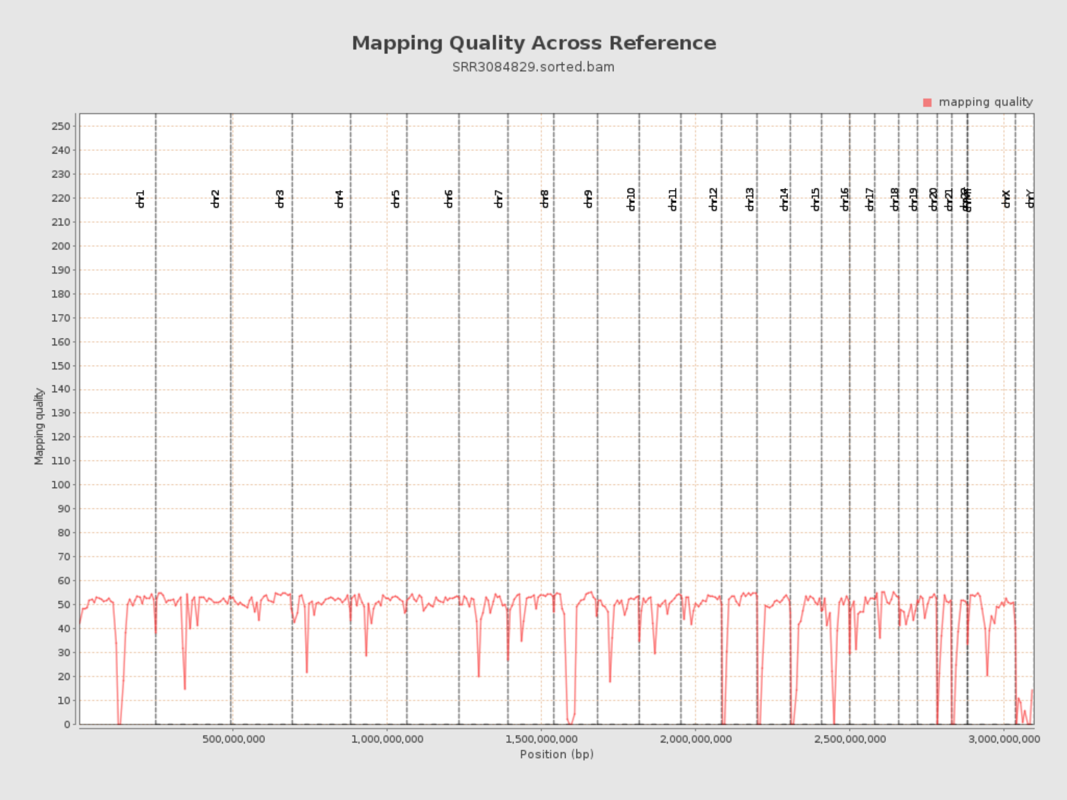
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram