Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:22:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084828.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_SRR3084828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:22:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,625,936
Mapped reads	1,494,222 / 91.9%
Unmapped reads	131,714 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,952 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	74,651 / 4.59%
Duplication rate	3.78%
Clipped reads	600,462 / 36.93%

2.2. ACGT Content

Number/percentage of A's	28,384,542 / 28.11%
Number/percentage of C's	18,433,510 / 18.25%
Number/percentage of T's	32,367,868 / 32.05%
Number/percentage of G's	21,778,326 / 21.57%
Number/percentage of N's	14,514 / 0.01%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3613

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

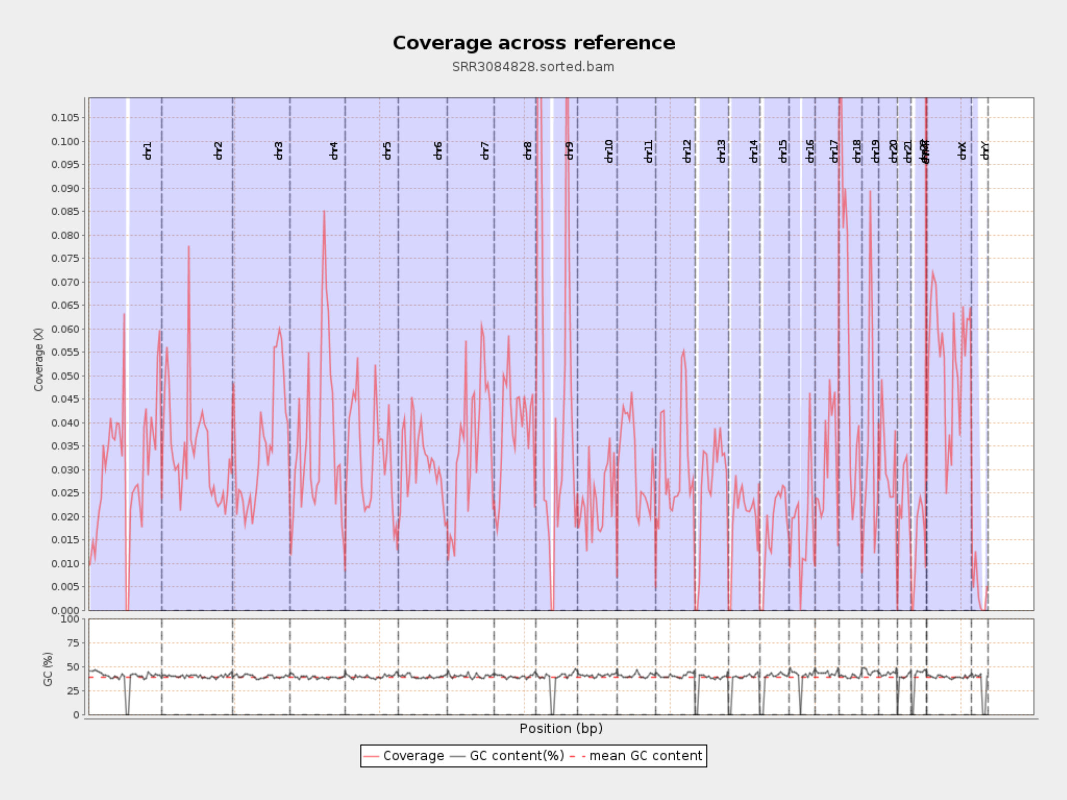
General error rate	0.84%
Mismatches	834,499
Insertions	8,592
Mapped reads with at least one insertion	0.57%
Deletions	24,315
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.8%

2.6. Chromosome stats

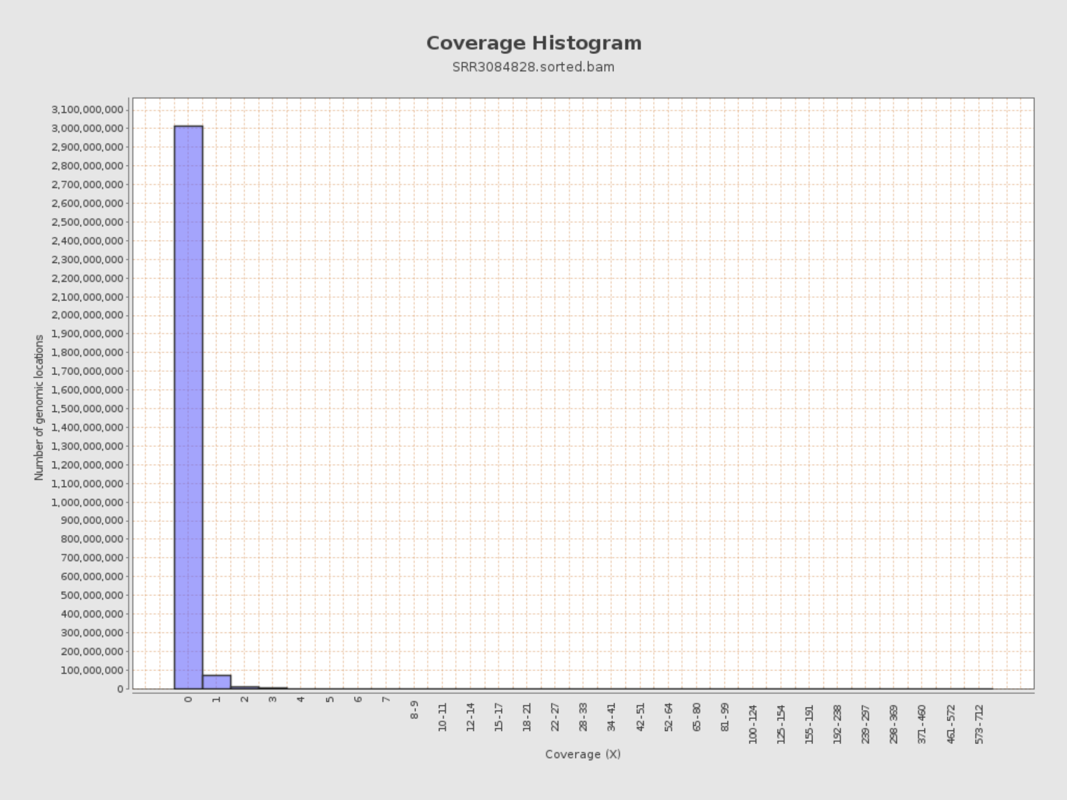
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7526714	0.0302	0.635
chr2	243199373	8307964	0.0342	0.4817
chr3	198022430	6997326	0.0353	0.2171
chr4	191154276	7001709	0.0366	0.2241
chr5	180915260	5984794	0.0331	0.2355
chr6	171115067	5313976	0.0311	0.2223
chr7	159138663	5728243	0.036	0.4055

chr8	146364022	5615025	0.0384	0.4627
chr9	141213431	7020271	0.0497	0.4267
chr10	135534747	3180272	0.0235	0.2433
chr11	135006516	4182709	0.031	0.3146
chr12	133851895	4189440	0.0313	0.2164
chr13	115169878	3022050	0.0262	0.1853
chr14	107349540	2066956	0.0193	0.1915
chr15	102531392	1769297	0.0173	0.1568
chr16	90354753	1674668	0.0185	0.1812
chr17	81195210	2528577	0.0311	0.2306
chr18	78077248	4457504	0.0571	0.8003
chr19	59128983	2172948	0.0367	0.4041
chr20	63025520	1988074	0.0315	0.2212
chr21	48129895	1046084	0.0217	0.1895
chr22	51304566	724610	0.0141	0.134
chrMT	16571	13663	0.8245	1.0768
chrX	155270560	8267951	0.0532	0.3051
chrY	59373566	237910	0.004	0.1279

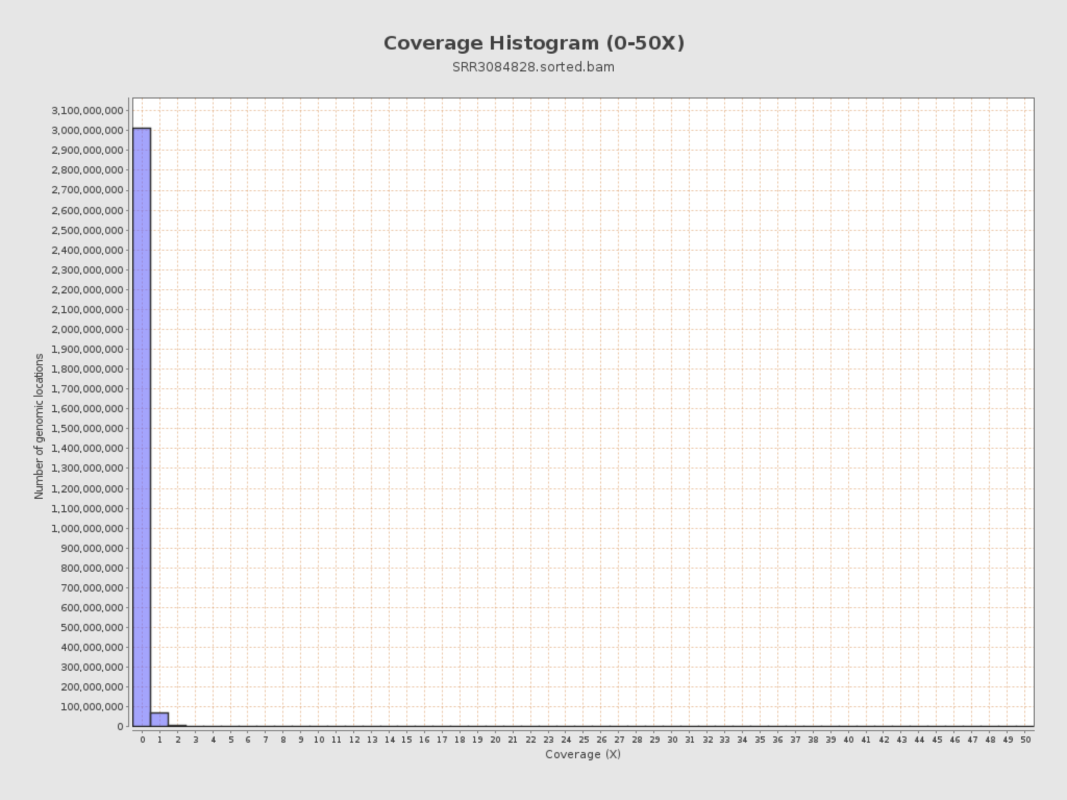
3. Results : Coverage across reference



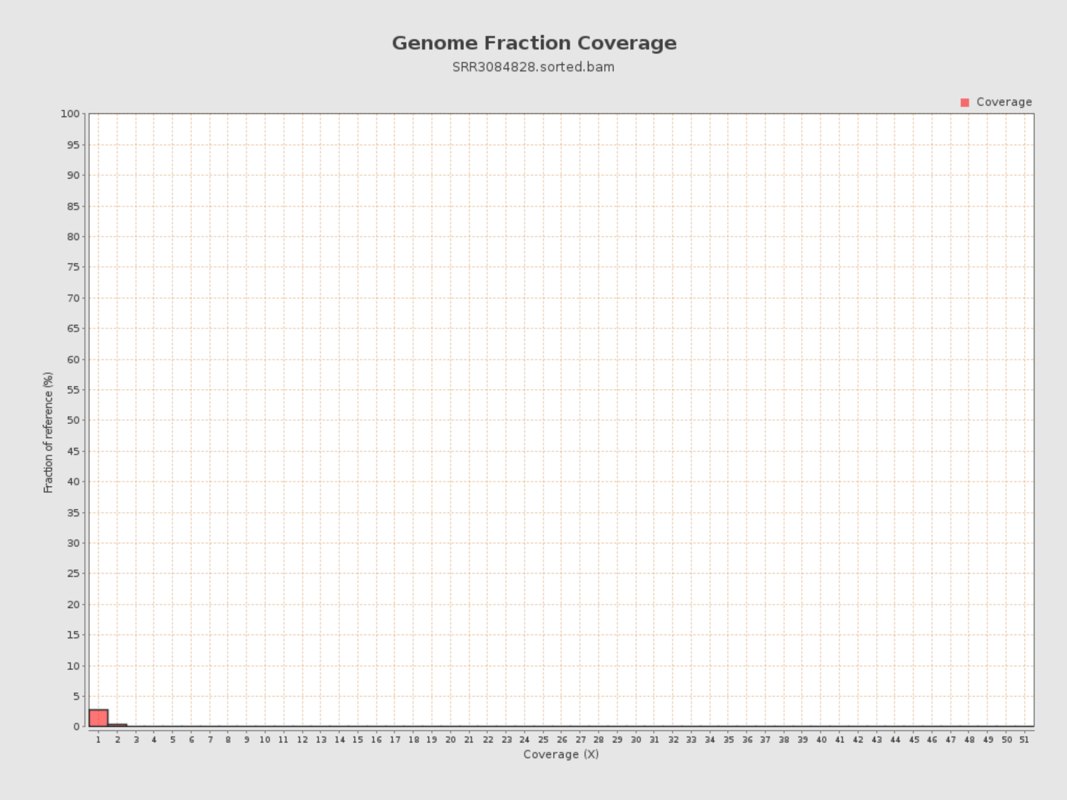
4. Results : Coverage Histogram



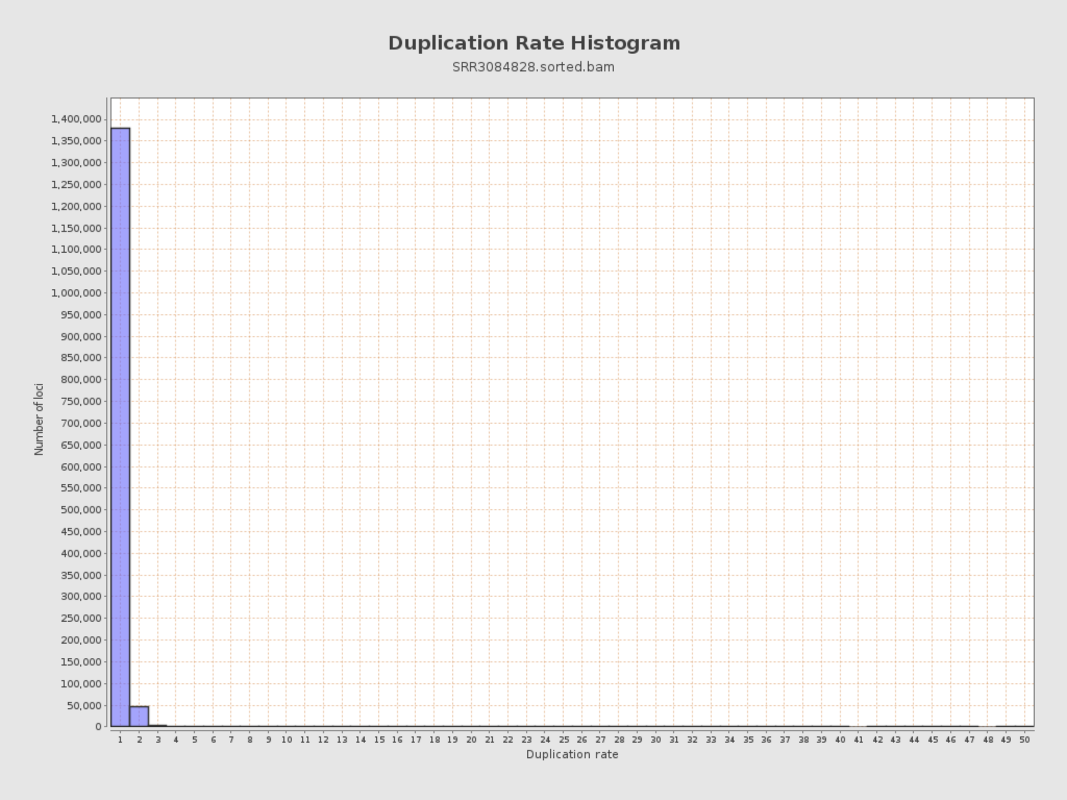
5. Results : Coverage Histogram (0-50X)



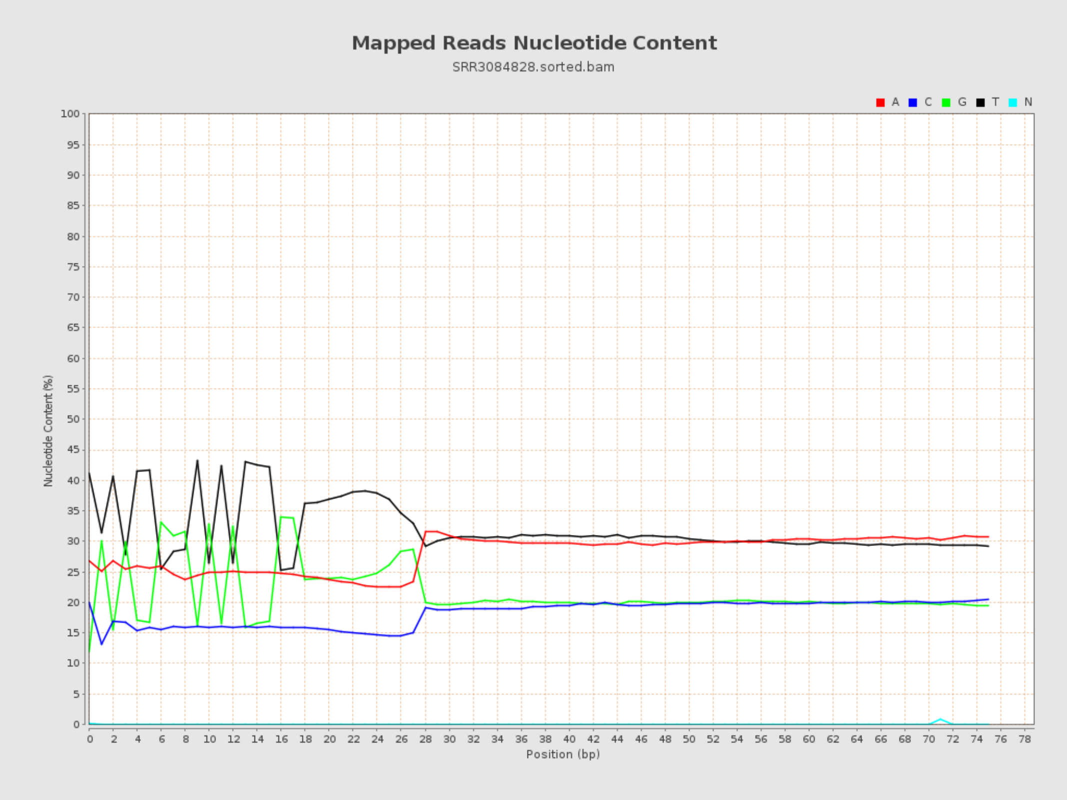
6. Results : Genome Fraction Coverage



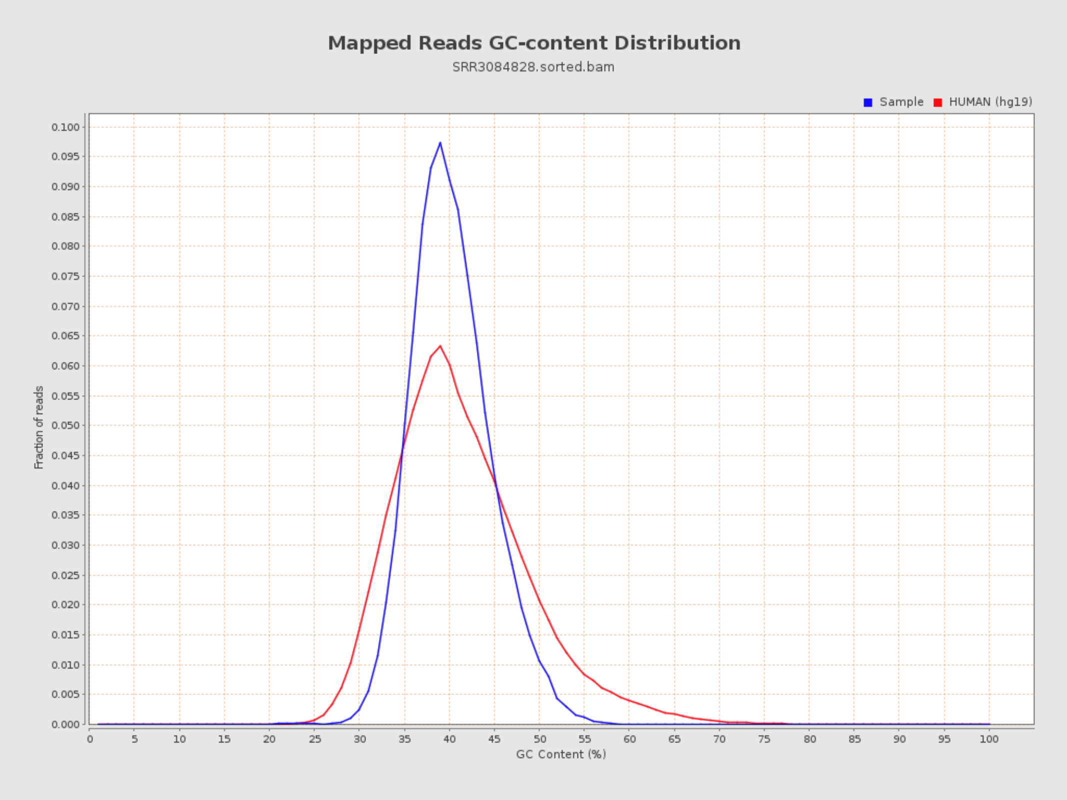
7. Results : Duplication Rate Histogram



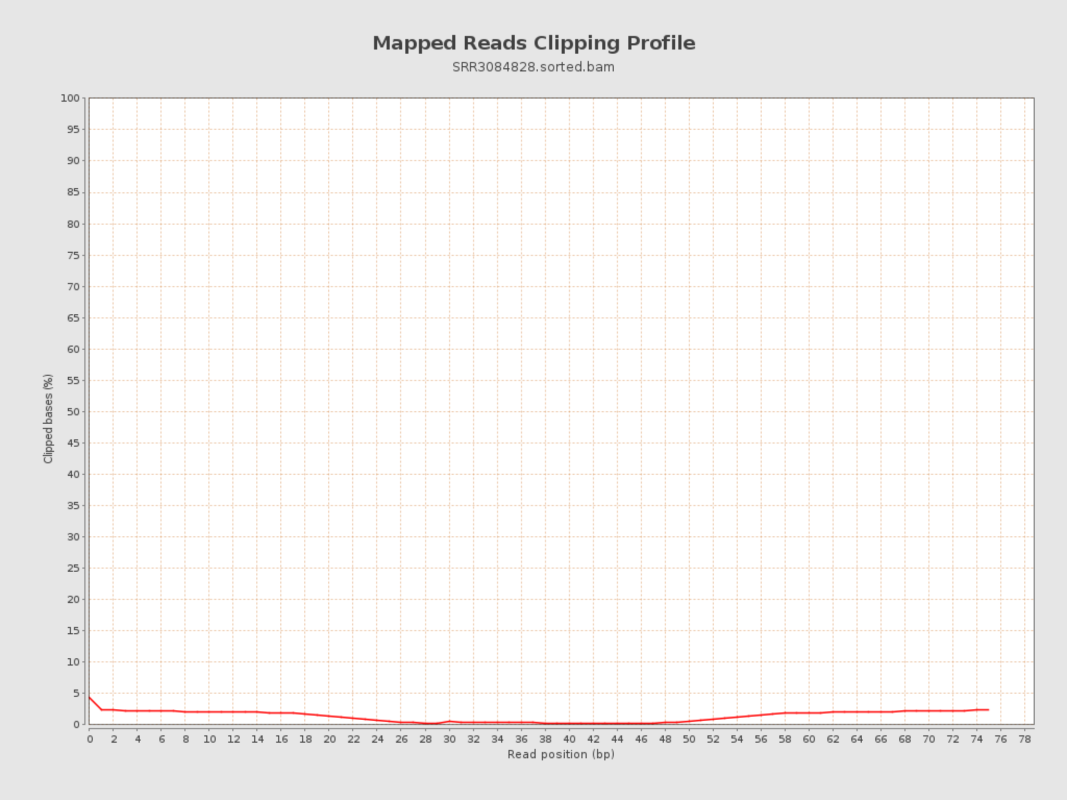
8. Results : Mapped Reads Nucleotide Content



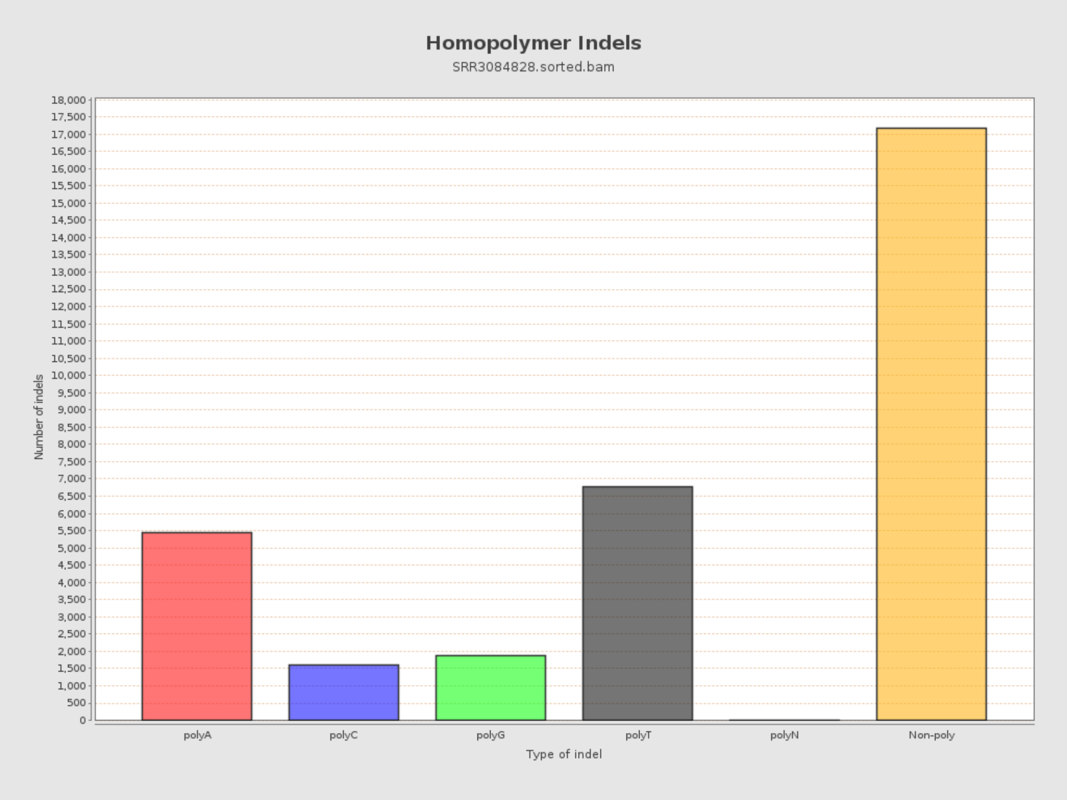
9. Results : Mapped Reads GC-content Distribution



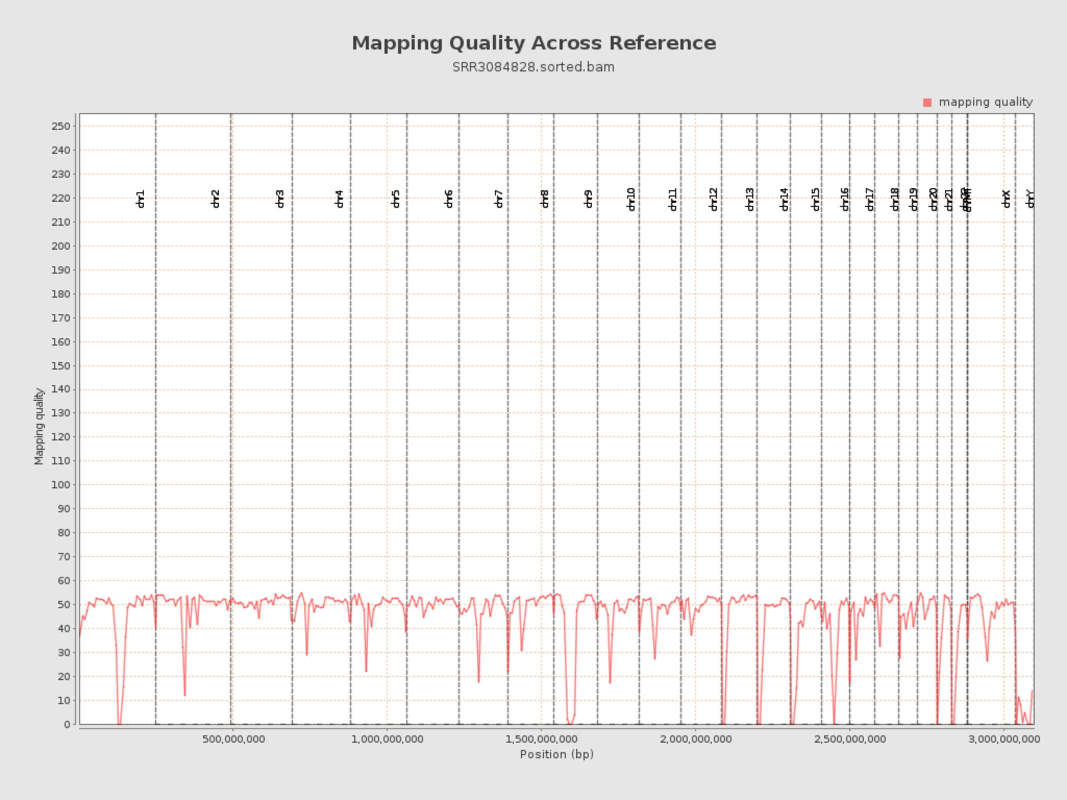
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram