Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:59:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084271.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_SRR3084271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:59:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,508,527
Mapped reads	1,213,716 / 80.46%
Unmapped reads	294,811 / 19.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,540 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	27,432 / 1.82%
Duplication rate	1.88%
Clipped reads	585,246 / 38.8%

2.2. ACGT Content

Number/percentage of A's	23,781,868 / 29.95%
Number/percentage of C's	14,615,724 / 18.4%
Number/percentage of T's	24,023,303 / 30.25%
Number/percentage of G's	16,990,464 / 21.4%
Number/percentage of N's	899 / 0%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2077

2.4. Mapping Quality

Mean Mapping Quality	46.93

2.5. Mismatches and indels

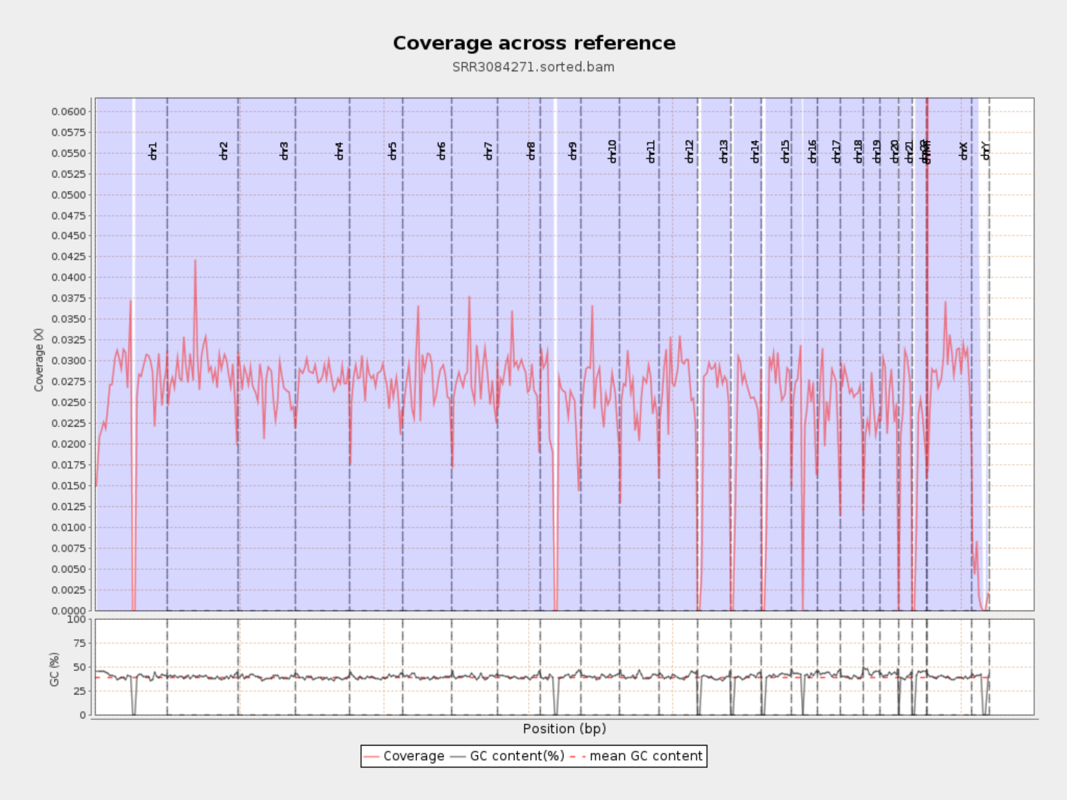
General error rate	0.87%
Mismatches	681,900
Insertions	5,784
Mapped reads with at least one insertion	0.47%
Deletions	16,574
Mapped reads with at least one deletion	1.35%
Homopolymer indels	47.41%

2.6. Chromosome stats

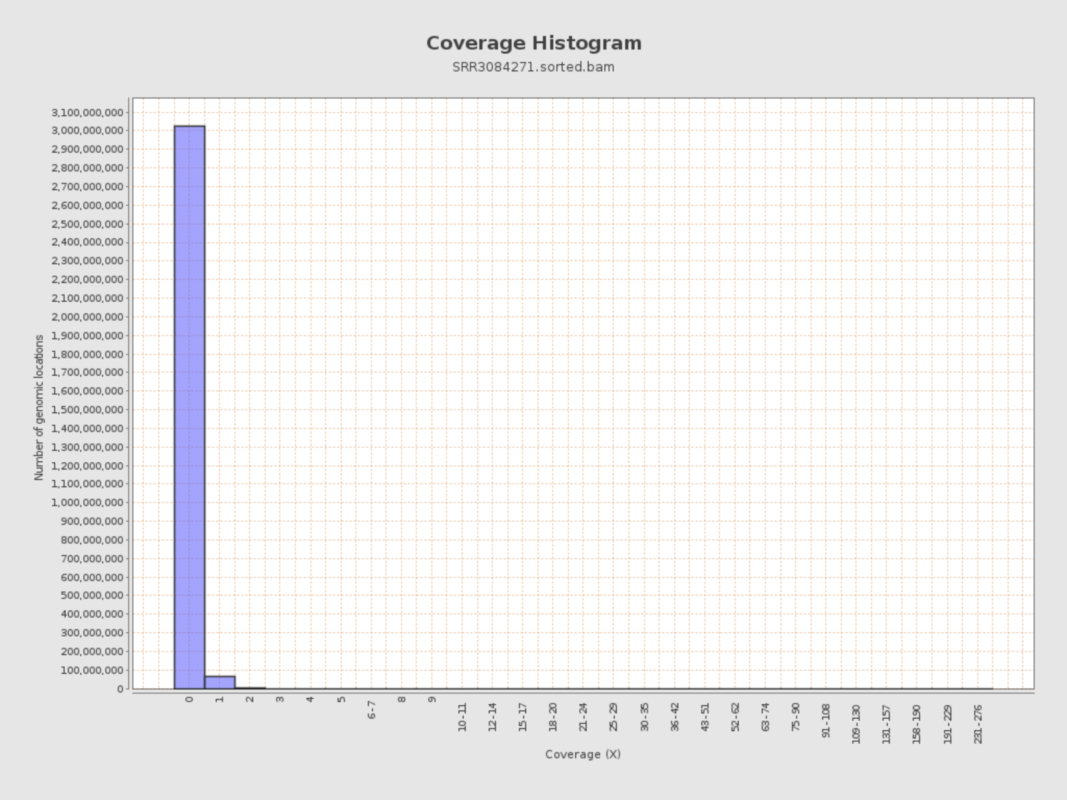
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6408781	0.0257	0.2922
chr2	243199373	7090290	0.0292	0.2365
chr3	198022430	5327722	0.0269	0.1757
chr4	191154276	5361592	0.028	0.1812
chr5	180915260	4942449	0.0273	0.1768
chr6	171115067	4740950	0.0277	0.2013
chr7	159138663	4398602	0.0276	0.234

chr8	146364022	4116453	0.0281	0.2354
chr9	141213431	3167943	0.0224	0.1888
chr10	135534747	3604779	0.0266	0.2124
chr11	135006516	3461173	0.0256	0.1858
chr12	133851895	3694064	0.0276	0.1779
chr13	115169878	2679188	0.0233	0.1626
chr14	107349540	2354691	0.0219	0.1636
chr15	102531392	2357248	0.023	0.1628
chr16	90354753	2055862	0.0228	0.1725
chr17	81195210	2007700	0.0247	0.1845
chr18	78077248	2078416	0.0266	0.35
chr19	59128983	1346098	0.0228	0.2234
chr20	63025520	1591075	0.0252	0.1731
chr21	48129895	1134654	0.0236	0.168
chr22	51304566	810418	0.0158	0.1335
chrMT	16571	9168	0.5533	0.8587
chrX	155270560	4532147	0.0292	0.1915
chrY	59373566	166696	0.0028	0.0661

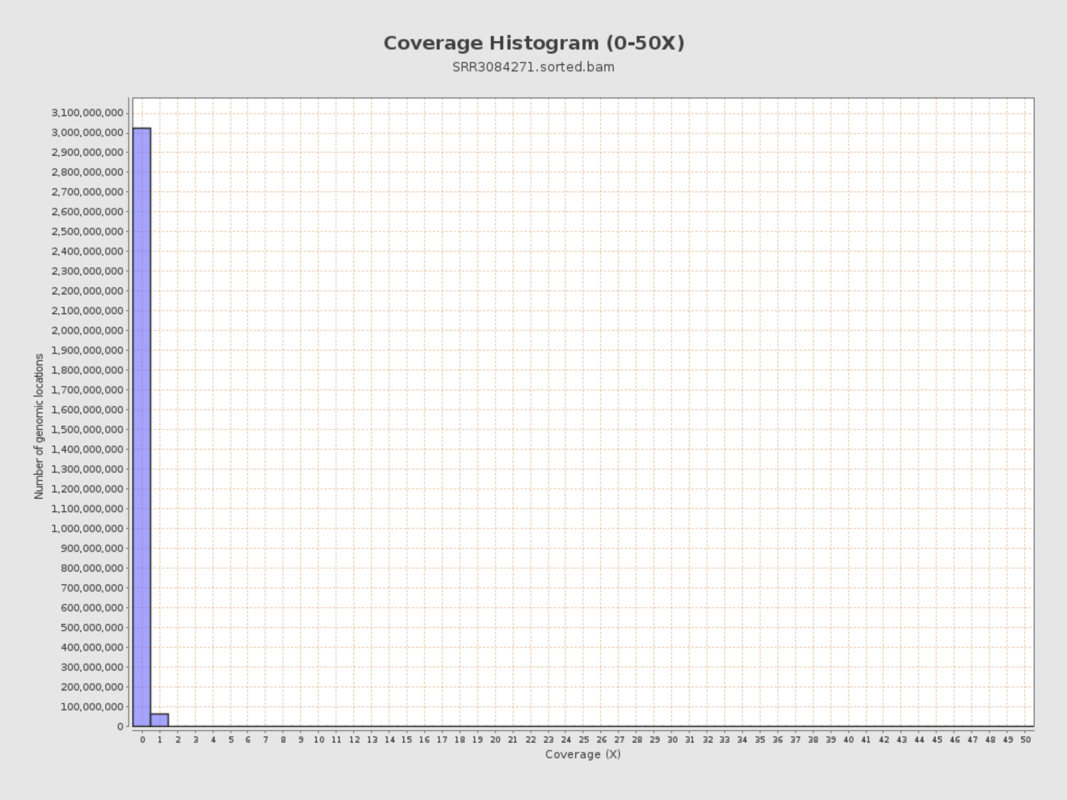
3. Results : Coverage across reference



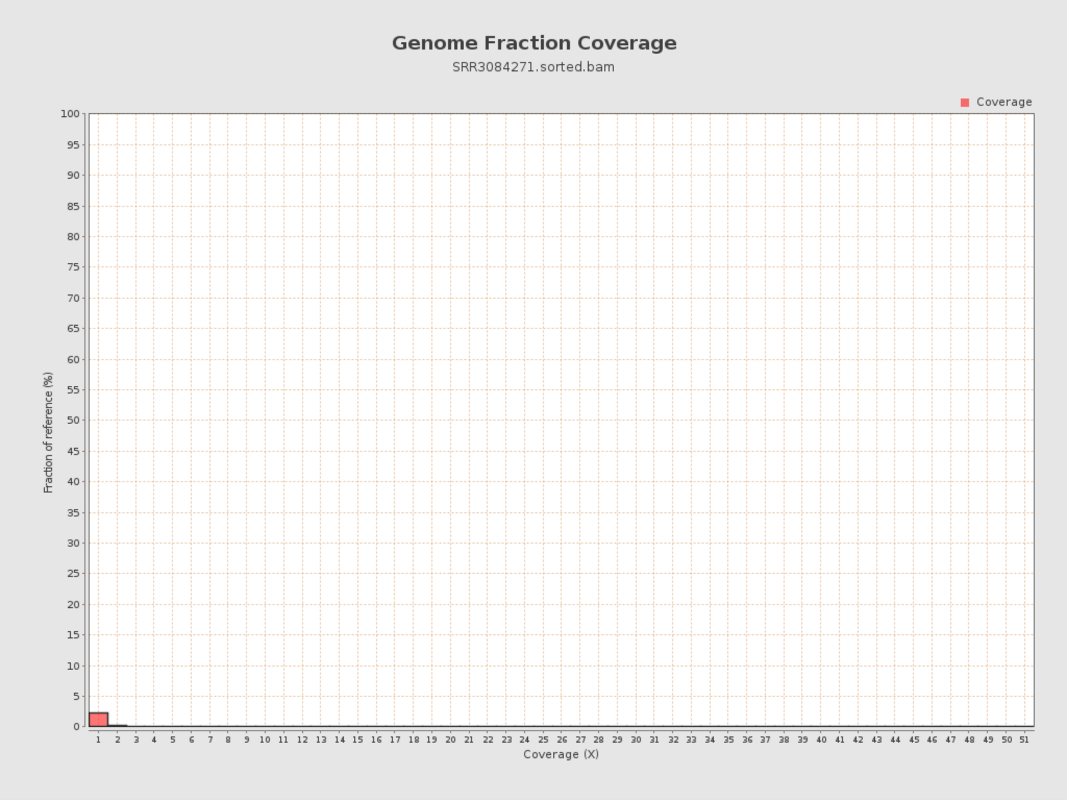
4. Results : Coverage Histogram



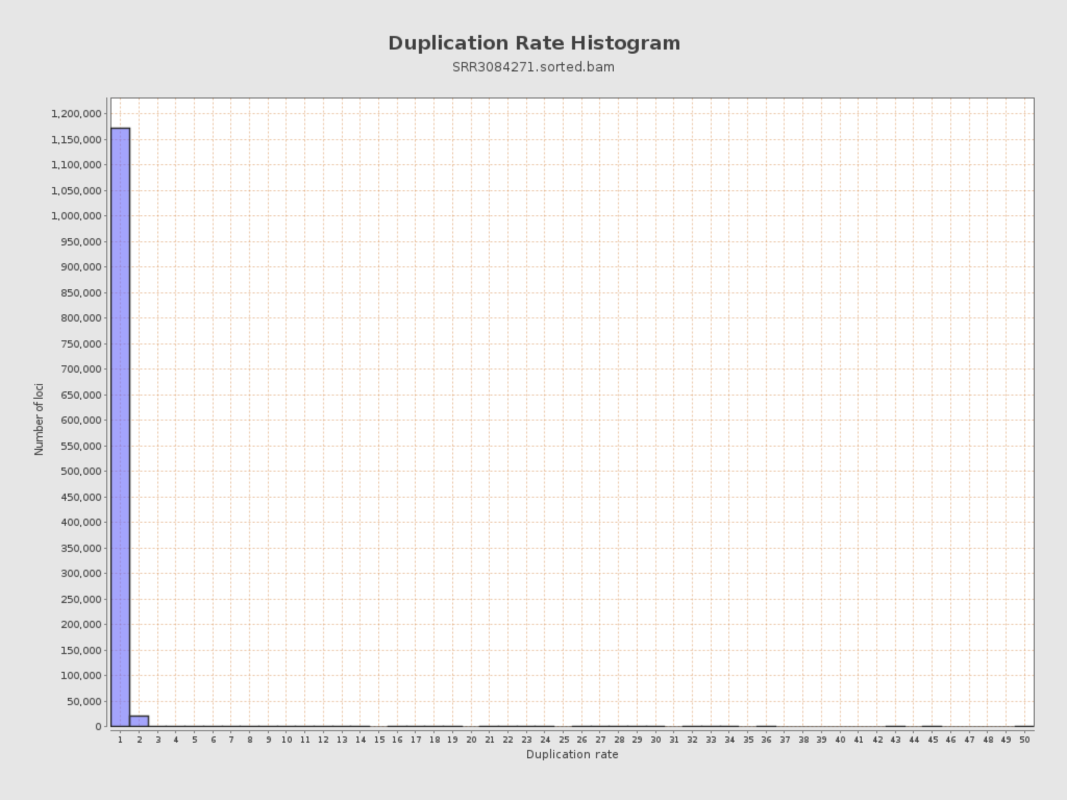
5. Results : Coverage Histogram (0-50X)



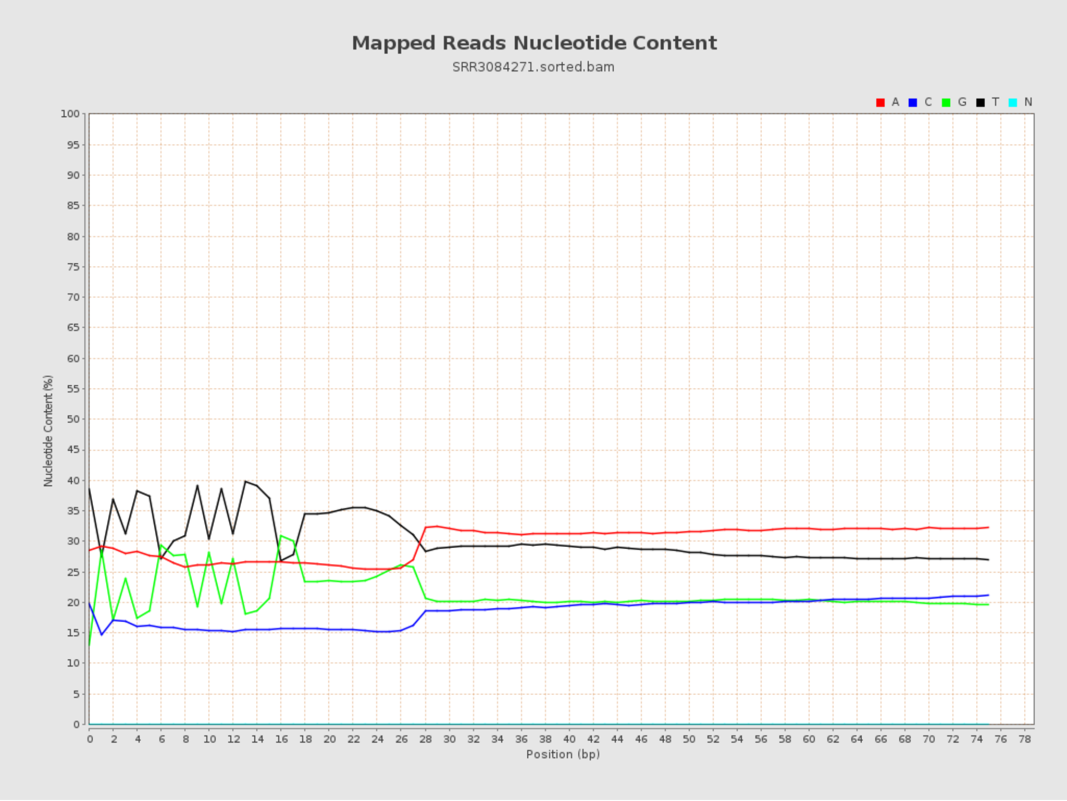
6. Results : Genome Fraction Coverage



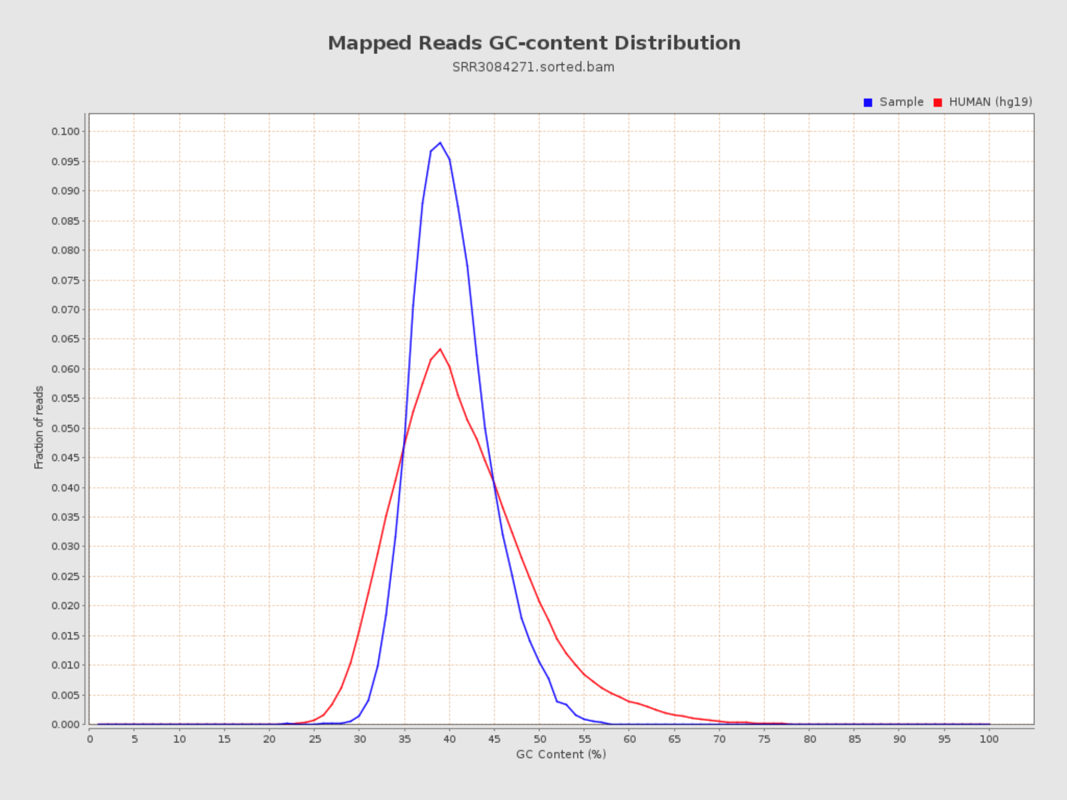
7. Results : Duplication Rate Histogram



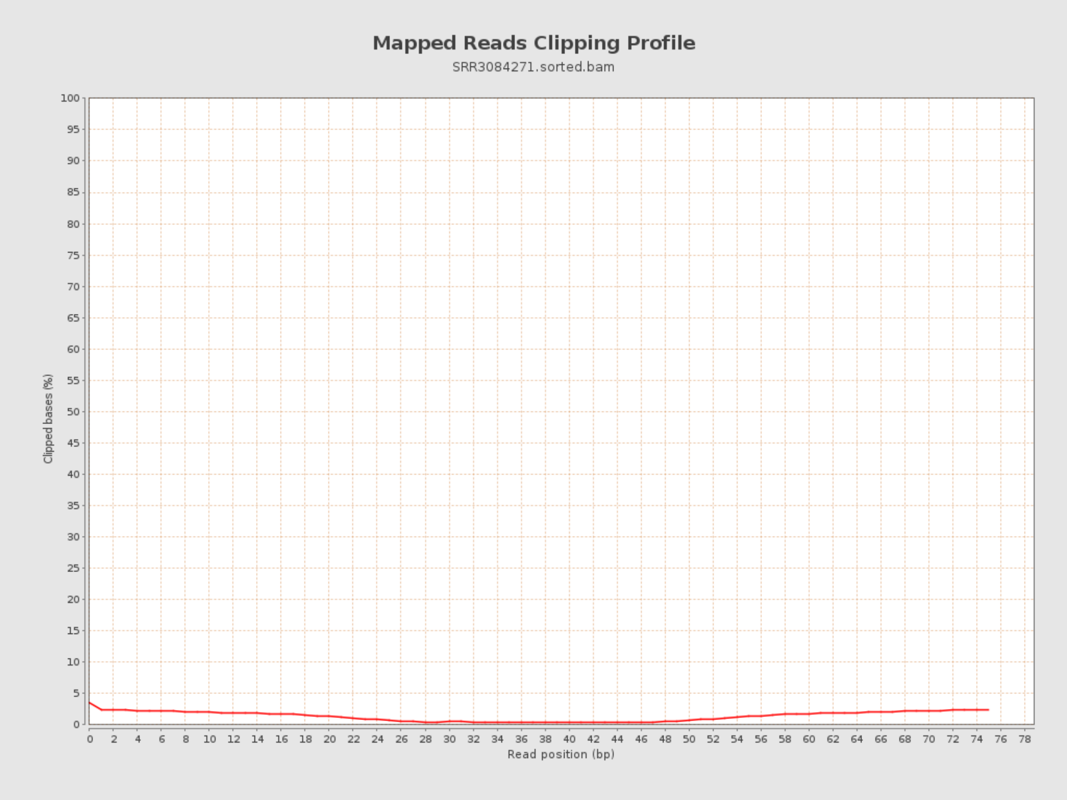
8. Results : Mapped Reads Nucleotide Content



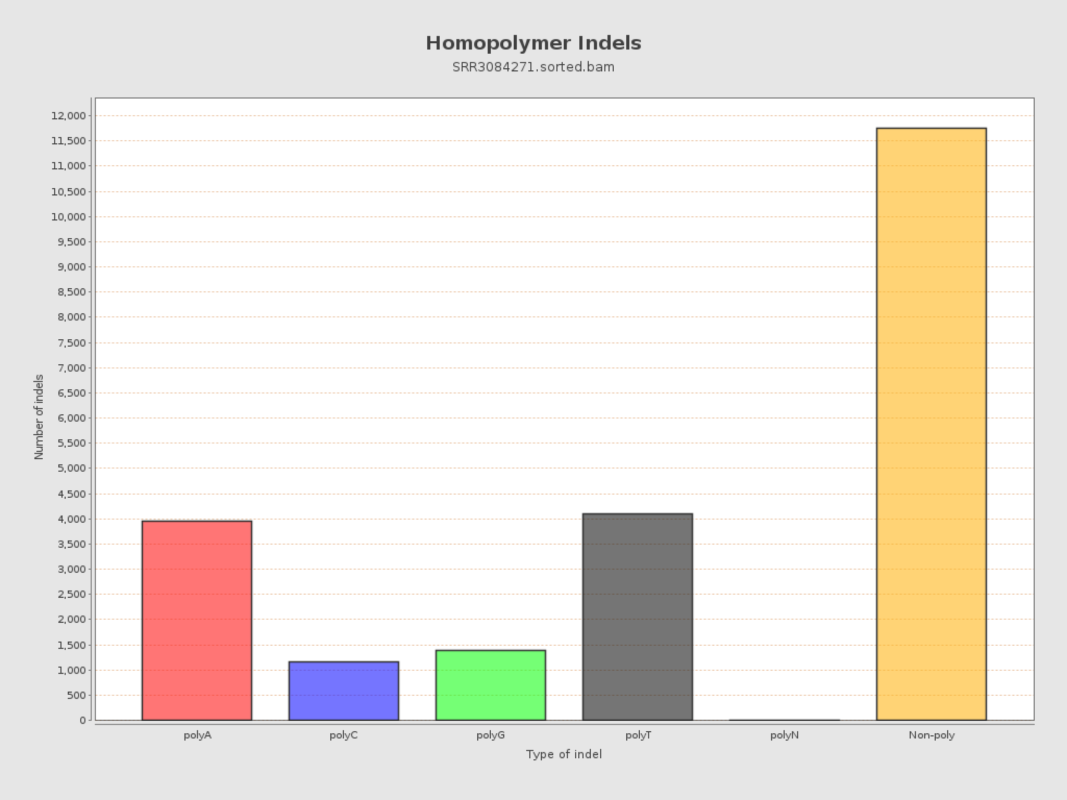
9. Results : Mapped Reads GC-content Distribution



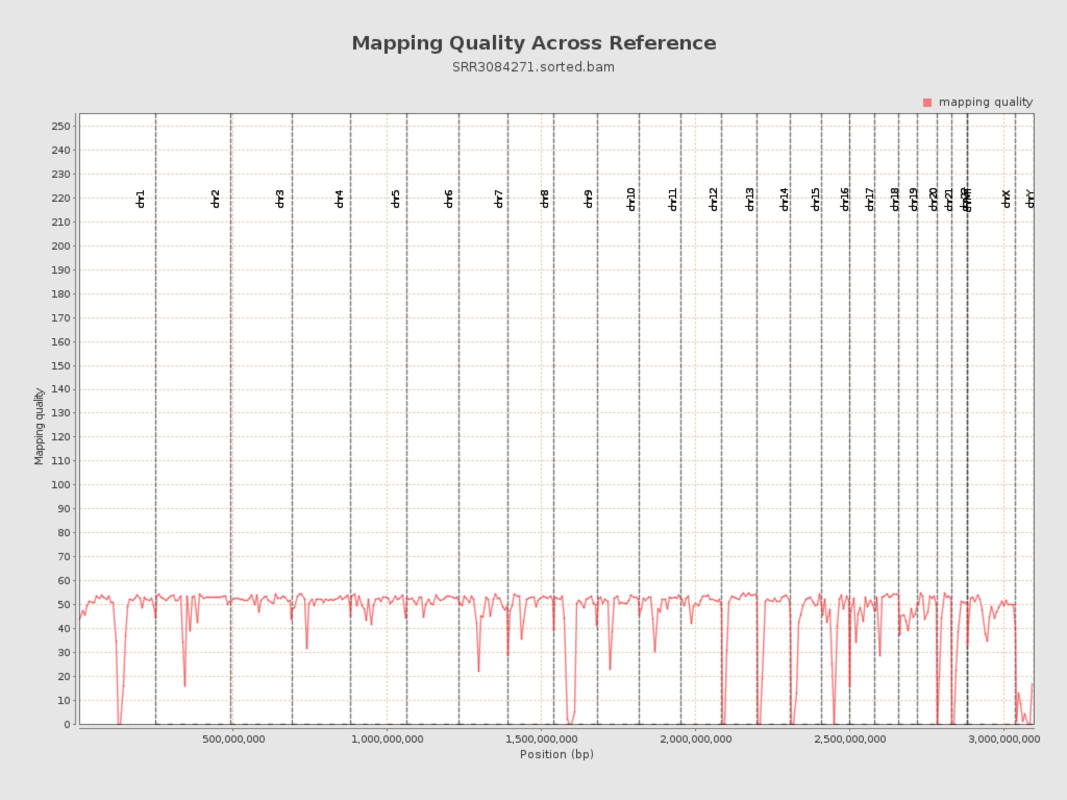
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram