Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:04:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084273.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_SRR3084273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084273.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:04:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,631,608
Mapped reads	1,264,102 / 77.48%
Unmapped reads	367,506 / 22.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,632 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	30,992 / 1.9%
Duplication rate	1.71%
Clipped reads	589,922 / 36.16%

2.2. ACGT Content

Number/percentage of A's	24,686,536 / 29.67%
Number/percentage of C's	15,702,592 / 18.87%
Number/percentage of T's	24,387,236 / 29.31%
Number/percentage of G's	18,434,480 / 22.15%
Number/percentage of N's	940 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2614

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

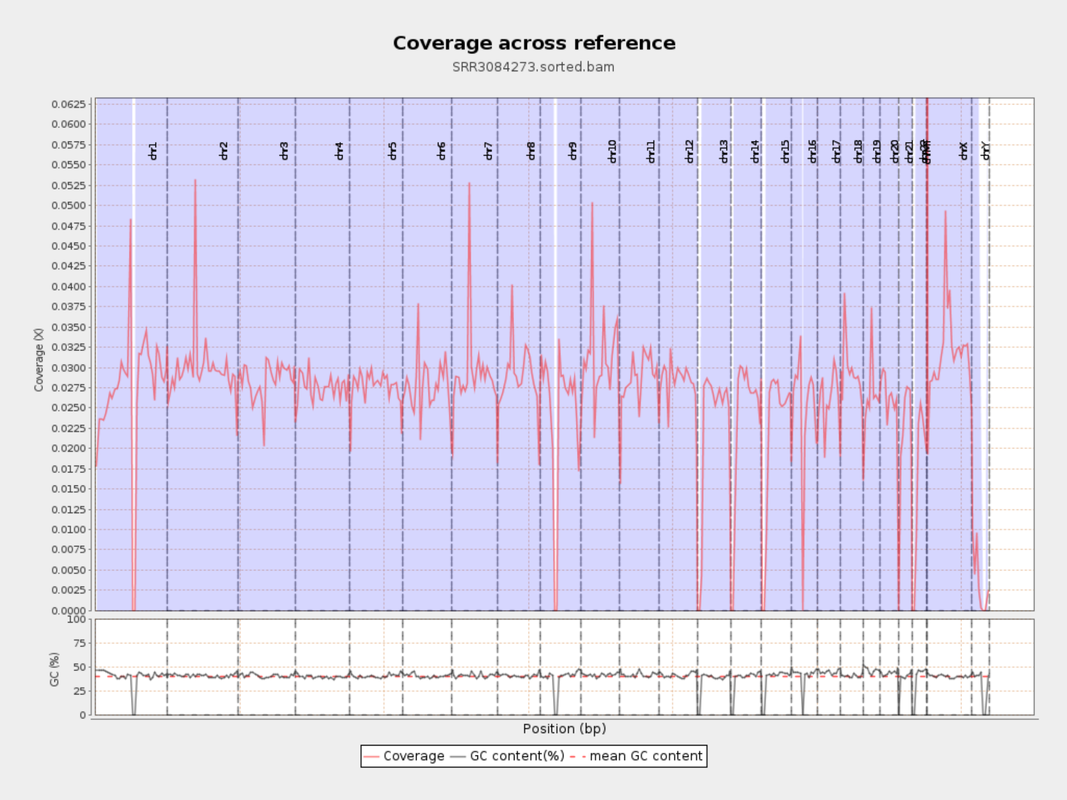
General error rate	0.83%
Mismatches	679,602
Insertions	6,148
Mapped reads with at least one insertion	0.48%
Deletions	15,377
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.62%

2.6. Chromosome stats

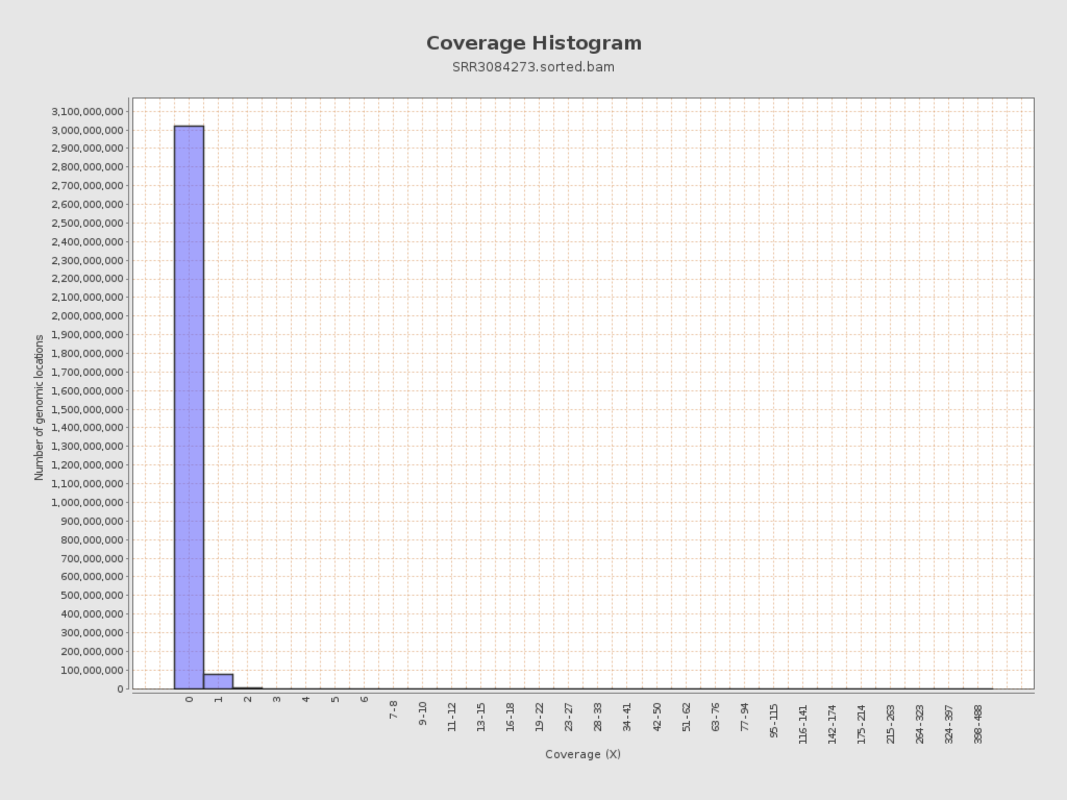
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6757529	0.0271	0.4518
chr2	243199373	7295971	0.03	0.3079
chr3	198022430	5627672	0.0284	0.1761
chr4	191154276	5254497	0.0275	0.1767
chr5	180915260	5047307	0.0279	0.1747
chr6	171115067	4739591	0.0277	0.2054
chr7	159138663	4681973	0.0294	0.3576

chr8	146364022	4240541	0.029	0.2458
chr9	141213431	3439347	0.0244	0.2378
chr10	135534747	4222370	0.0312	0.2865
chr11	135006516	3880966	0.0287	0.2306
chr12	133851895	3813562	0.0285	0.1776
chr13	115169878	2568833	0.0223	0.1548
chr14	107349540	2488813	0.0232	0.1746
chr15	102531392	2231827	0.0218	0.1609
chr16	90354753	2197868	0.0243	0.1851
chr17	81195210	2112668	0.026	0.1878
chr18	78077248	2305067	0.0295	0.5072
chr19	59128983	1579421	0.0267	0.3421
chr20	63025520	1651519	0.0262	0.1744
chr21	48129895	1040744	0.0216	0.1582
chr22	51304566	830916	0.0162	0.1317
chrMT	16571	42378	2.5574	2.1993
chrX	155270560	4983655	0.0321	0.2095
chrY	59373566	201449	0.0034	0.0778

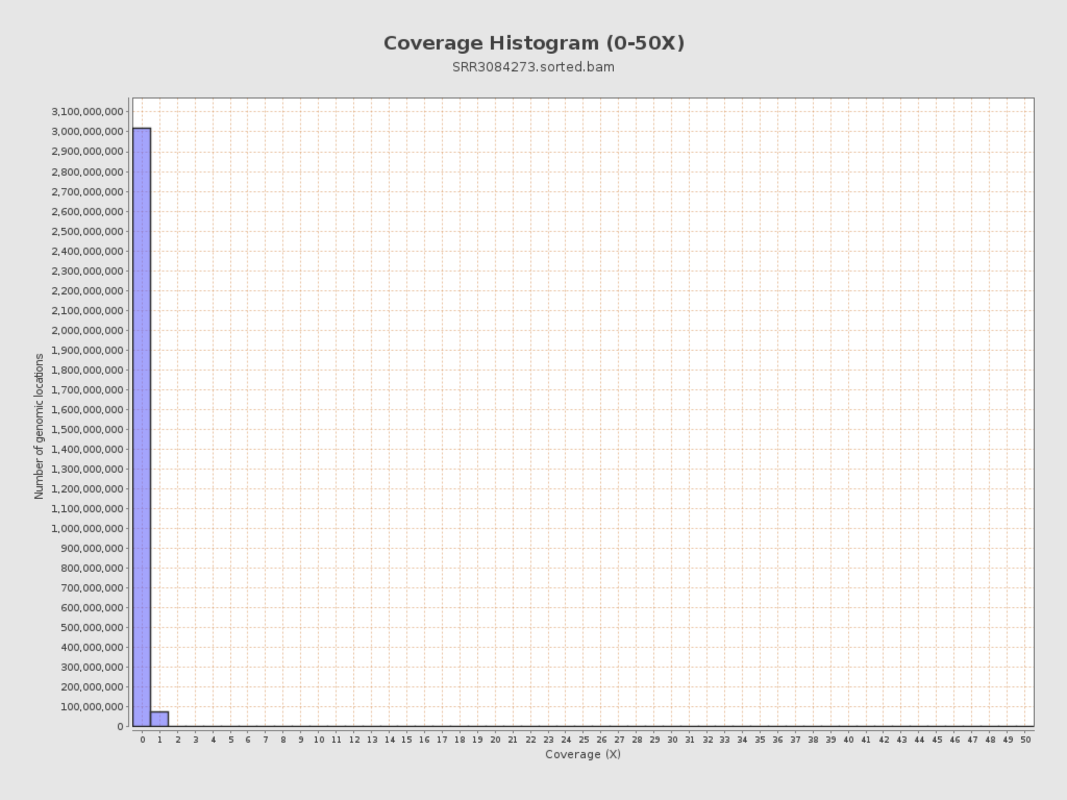
3. Results : Coverage across reference



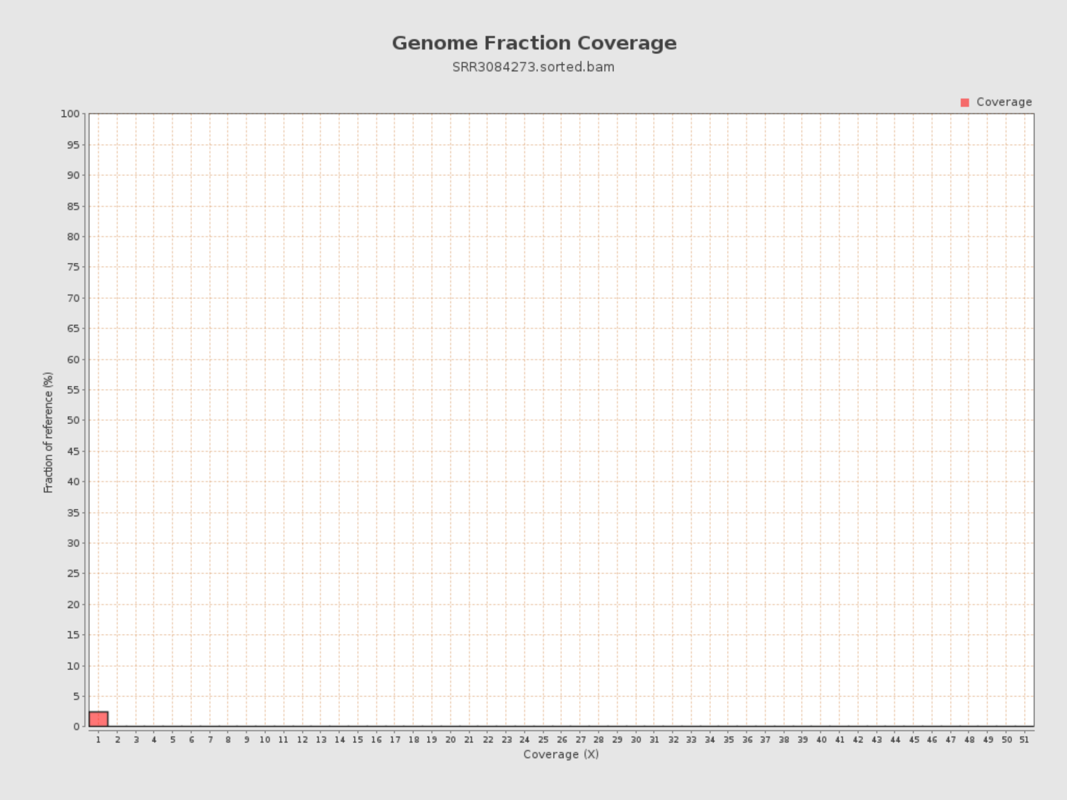
4. Results : Coverage Histogram



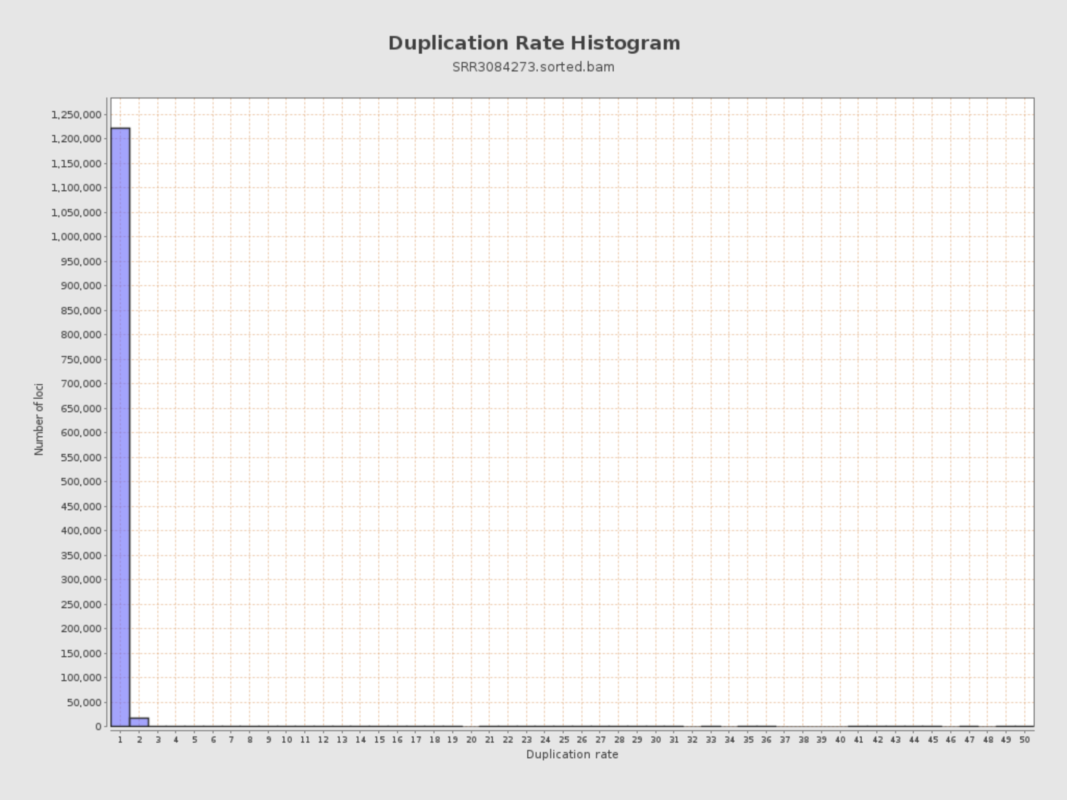
5. Results : Coverage Histogram (0-50X)



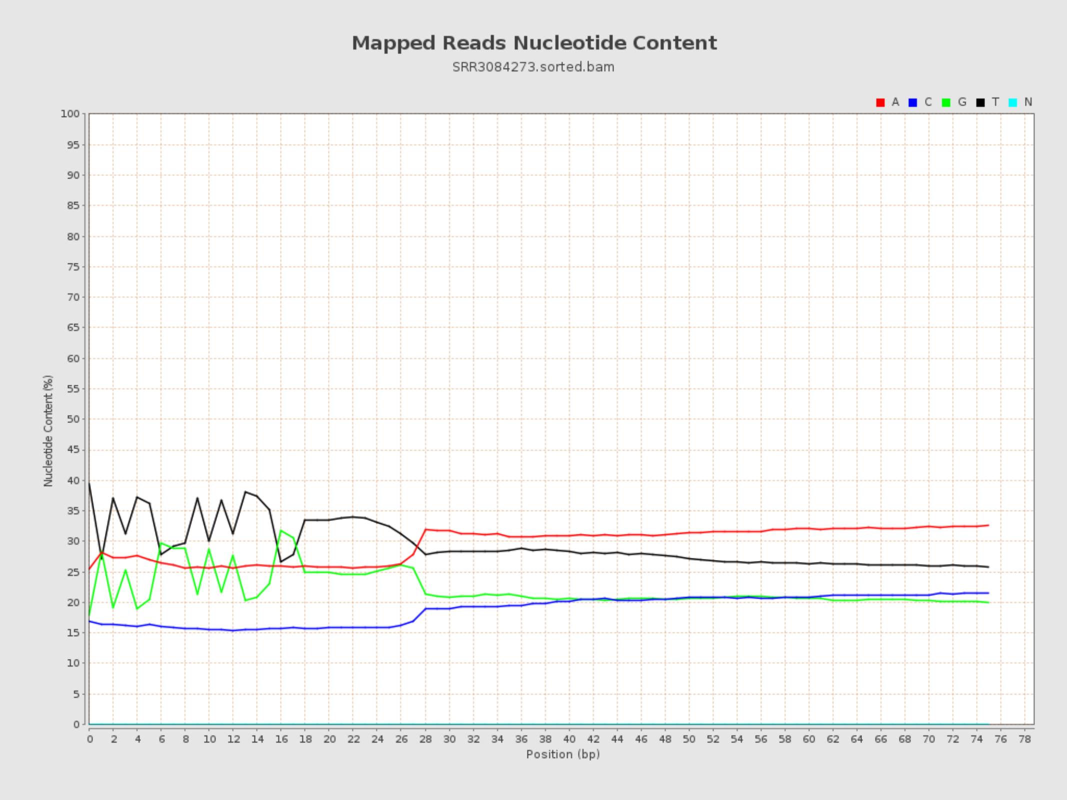
6. Results : Genome Fraction Coverage



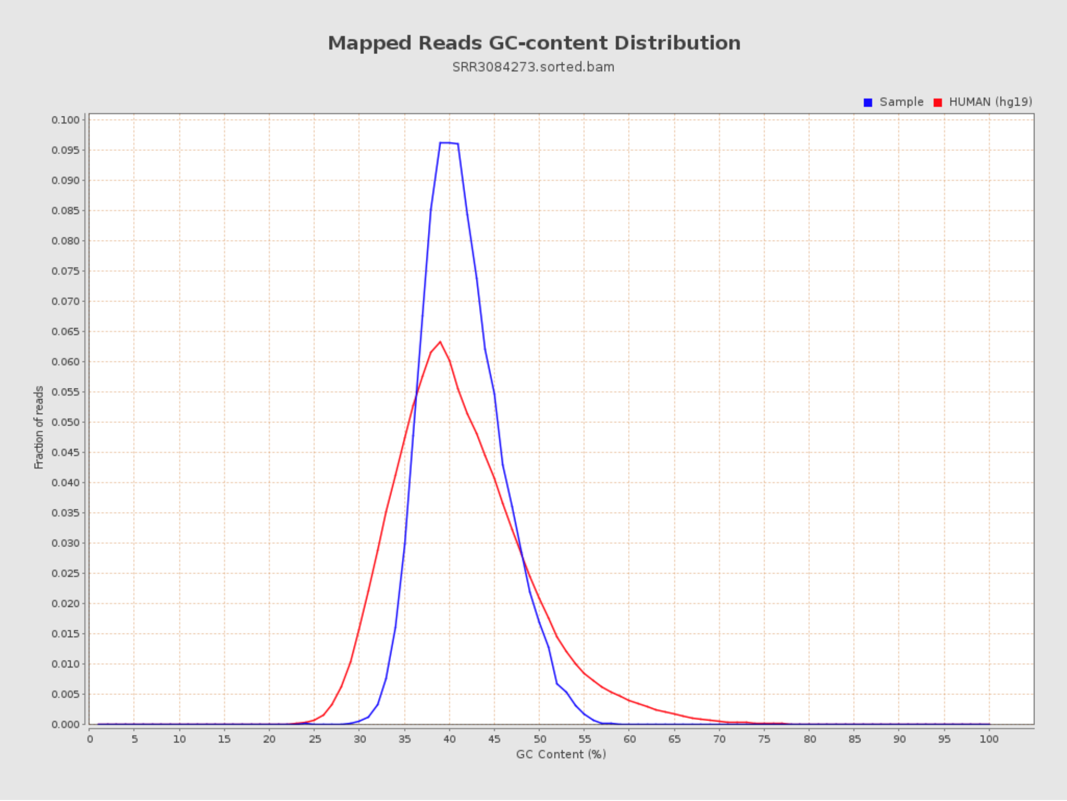
7. Results : Duplication Rate Histogram



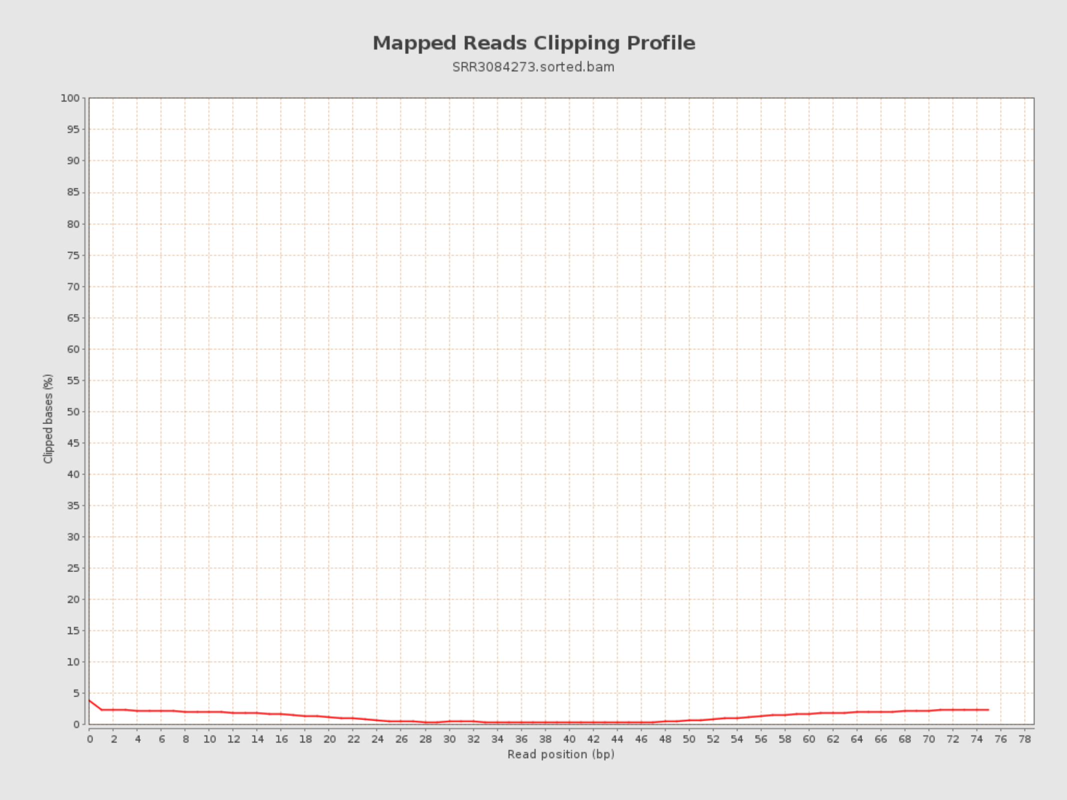
8. Results : Mapped Reads Nucleotide Content



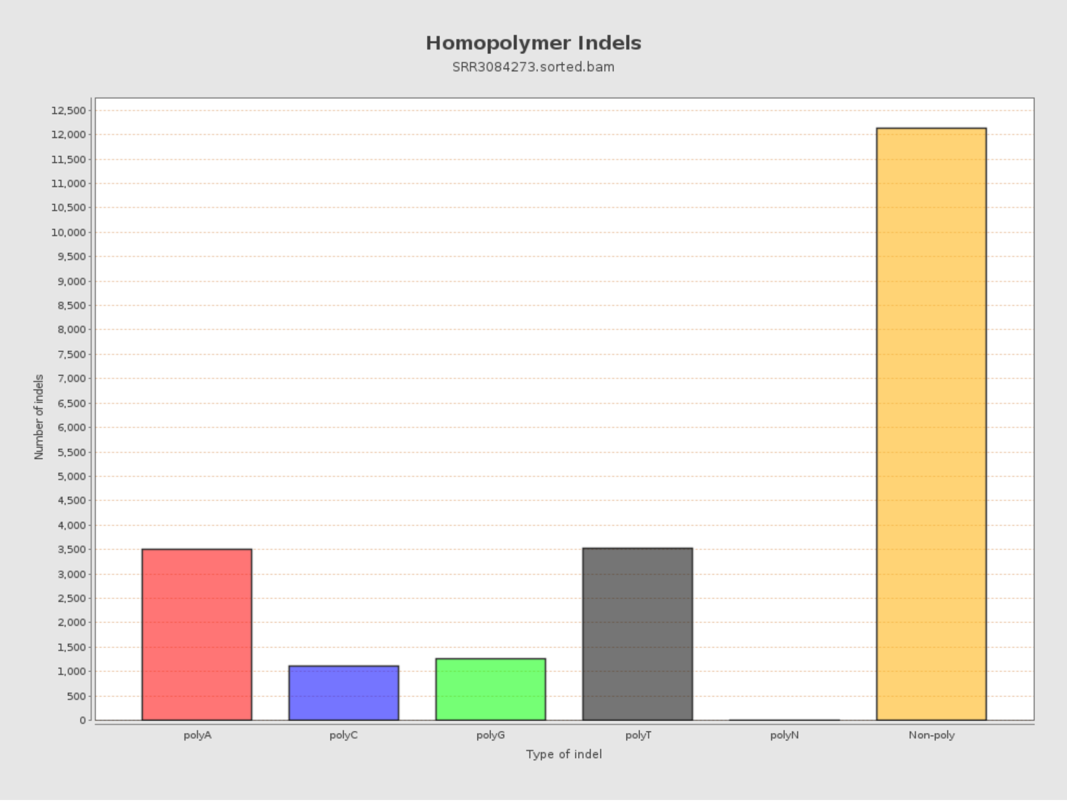
9. Results : Mapped Reads GC-content Distribution



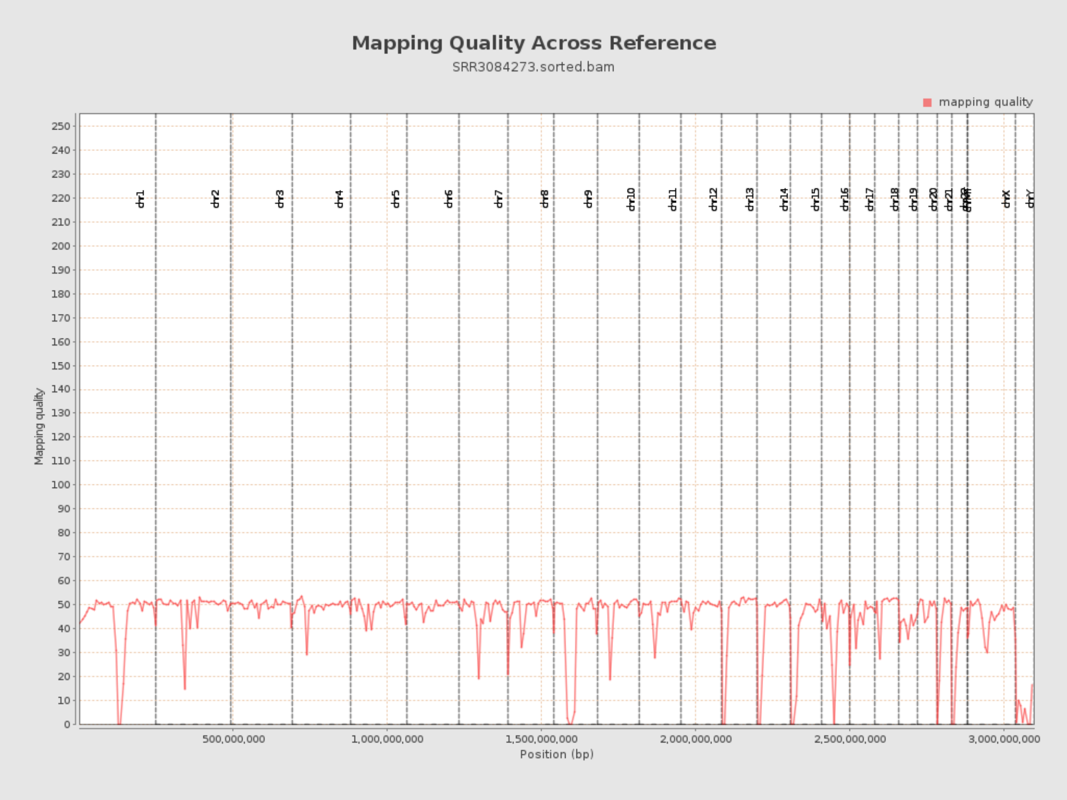
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram