Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:12:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082457.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_SRR3082457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082457.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:12:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,846,032
Mapped reads	2,608,939 / 91.67%
Unmapped reads	237,093 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,399 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	86,860 / 3.05%
Duplication rate	2.32%
Clipped reads	830,093 / 29.17%

2.2. ACGT Content

Number/percentage of A's	54,856,135 / 29.91%
Number/percentage of C's	34,232,844 / 18.67%
Number/percentage of T's	56,218,311 / 30.66%
Number/percentage of G's	38,076,725 / 20.76%
Number/percentage of N's	3,943 / 0%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.5363

2.4. Mapping Quality

Mean Mapping Quality	47.67

2.5. Mismatches and indels

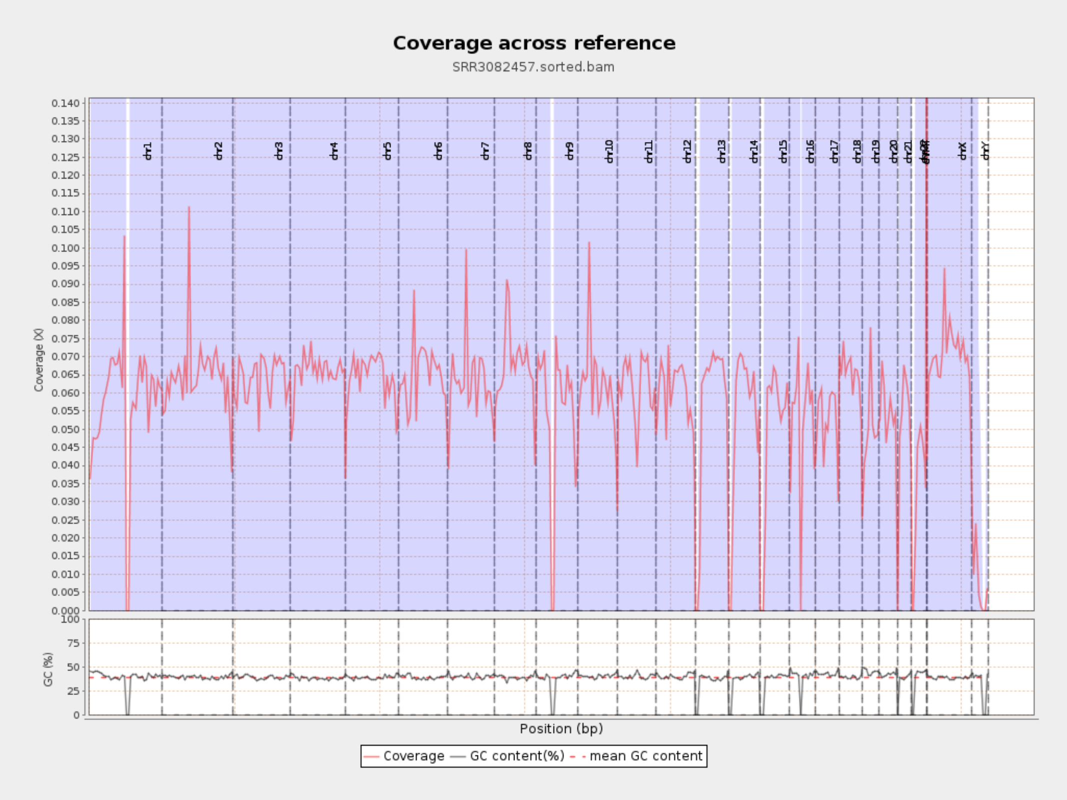
General error rate	0.86%
Mismatches	1,543,500
Insertions	15,382
Mapped reads with at least one insertion	0.59%
Deletions	41,681
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.47%

2.6. Chromosome stats

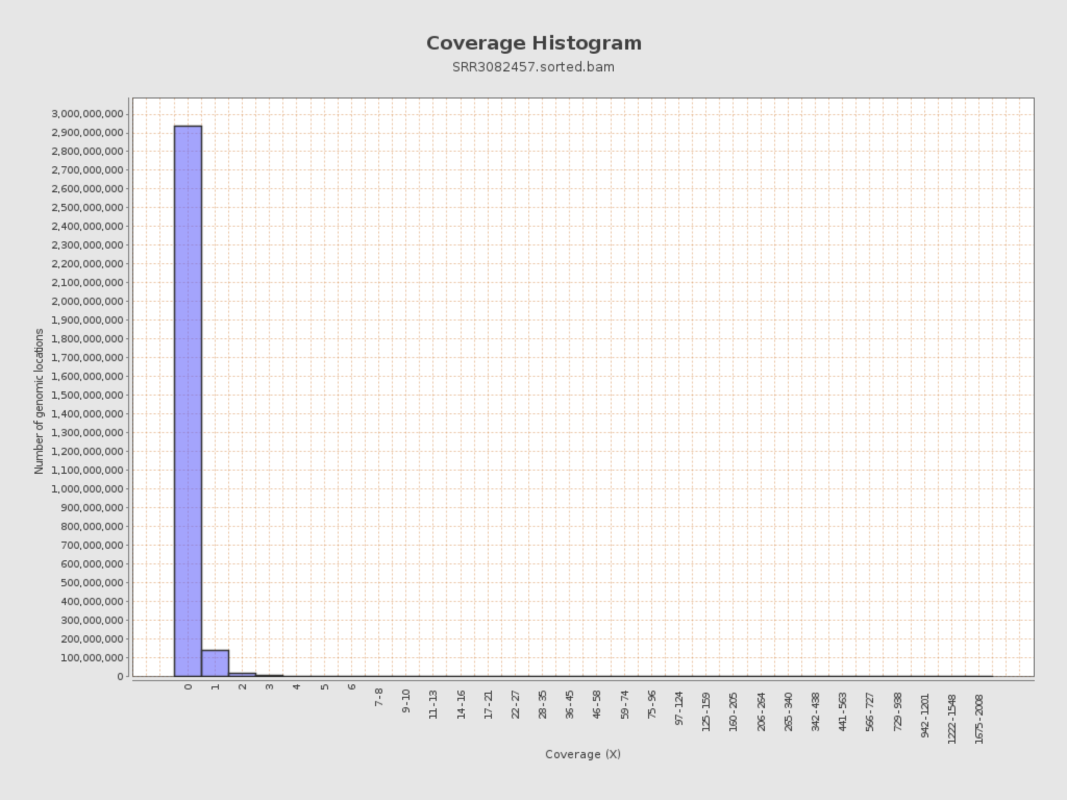
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14308215	0.0574	0.9506
chr2	243199373	15804302	0.065	0.5241
chr3	198022430	12675121	0.064	0.2844
chr4	191154276	12569174	0.0658	0.3013
chr5	180915260	11673517	0.0645	0.285
chr6	171115067	11132225	0.0651	0.358
chr7	159138663	10104410	0.0635	0.6258

chr8	146364022	9844007	0.0673	1.2293
chr9	141213431	7694225	0.0545	0.4413
chr10	135534747	8489934	0.0626	0.4829
chr11	135006516	8291930	0.0614	0.3961
chr12	133851895	8077930	0.0603	0.2791
chr13	115169878	6327145	0.0549	0.2591
chr14	107349540	5618552	0.0523	0.2809
chr15	102531392	4975795	0.0485	0.2445
chr16	90354753	4710805	0.0521	0.3059
chr17	81195210	4196676	0.0517	0.2926
chr18	78077248	5133572	0.0657	0.85
chr19	59128983	2971912	0.0503	0.7189
chr20	63025520	3428001	0.0544	0.2706
chr21	48129895	2429867	0.0505	0.271
chr22	51304566	1638006	0.0319	0.1953
chrMT	16571	4389	0.2649	0.5347
chrX	155270560	10909670	0.0703	0.3329
chrY	59373566	447740	0.0075	0.1766

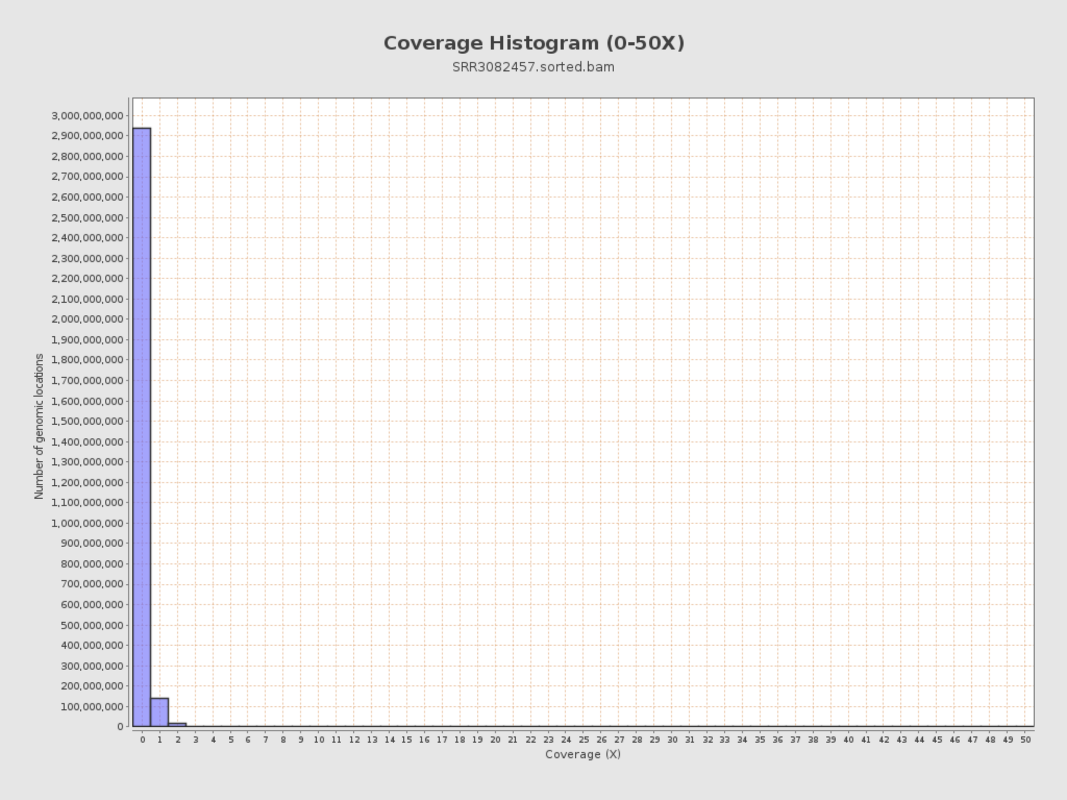
3. Results : Coverage across reference



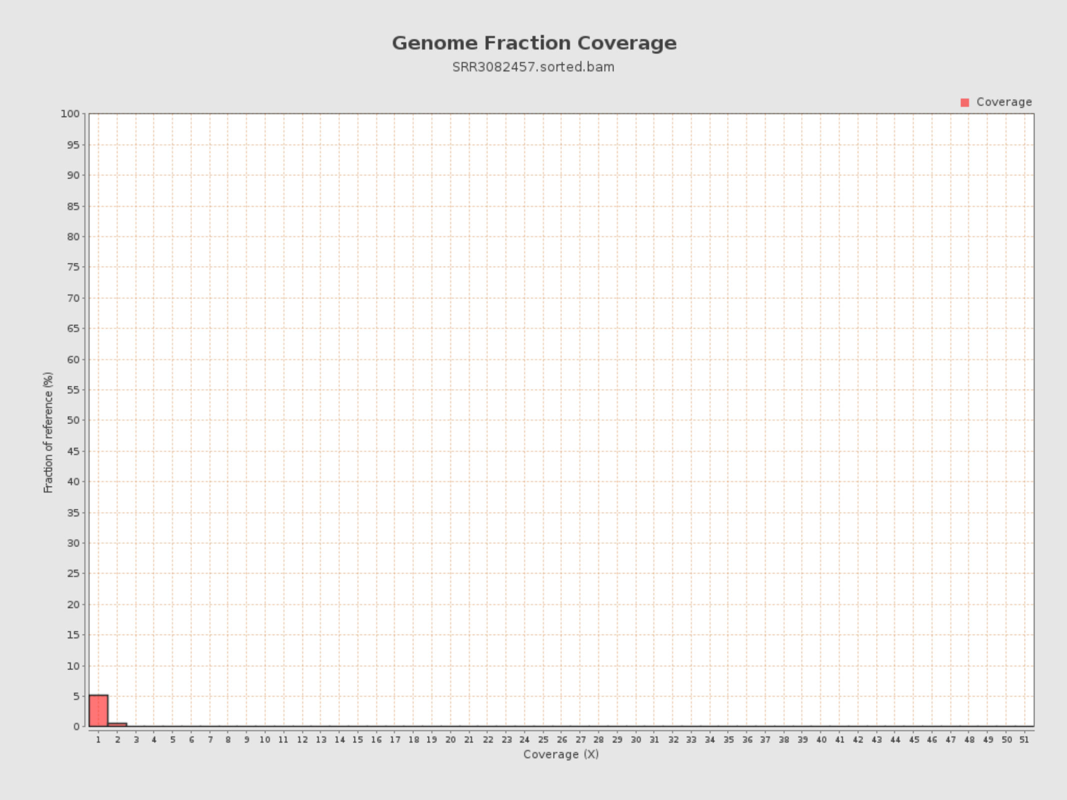
4. Results : Coverage Histogram



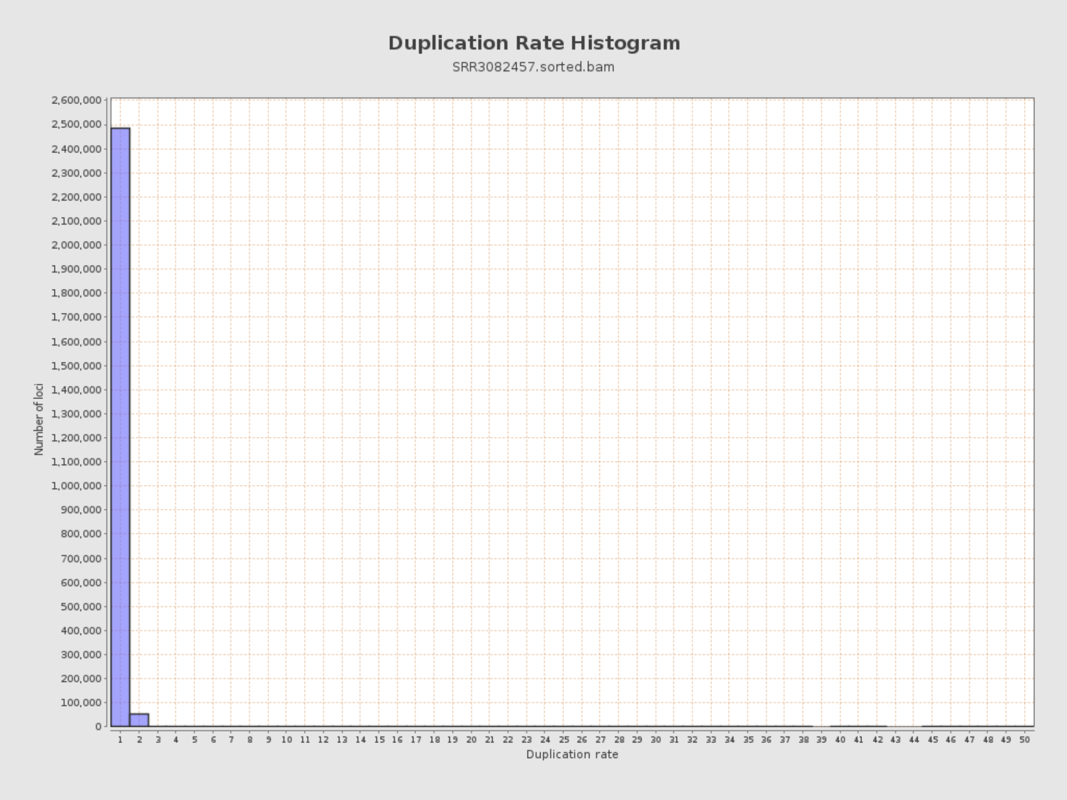
5. Results : Coverage Histogram (0-50X)



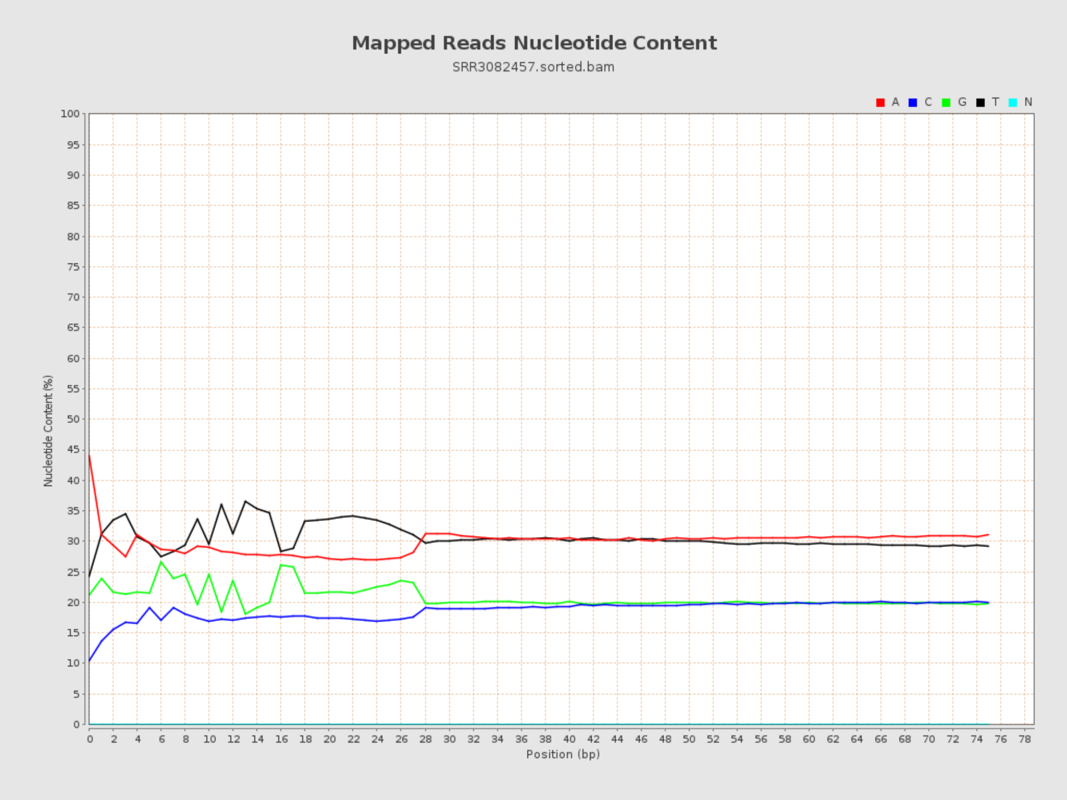
6. Results : Genome Fraction Coverage



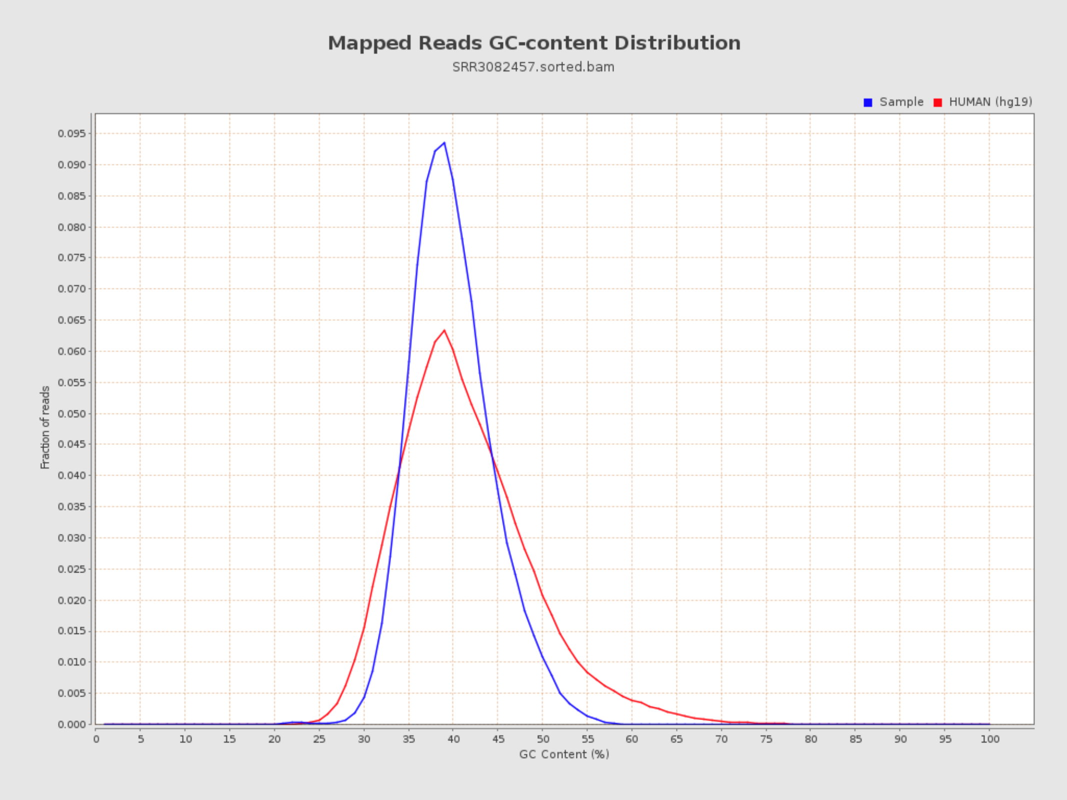
7. Results : Duplication Rate Histogram



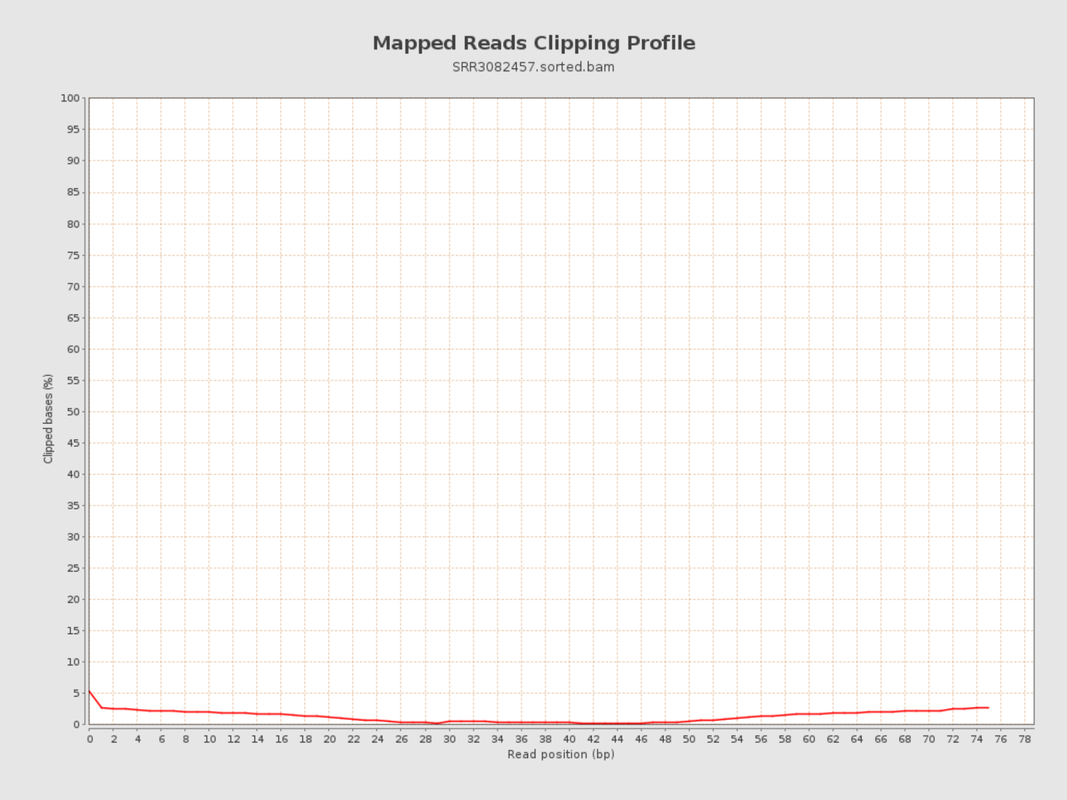
8. Results : Mapped Reads Nucleotide Content



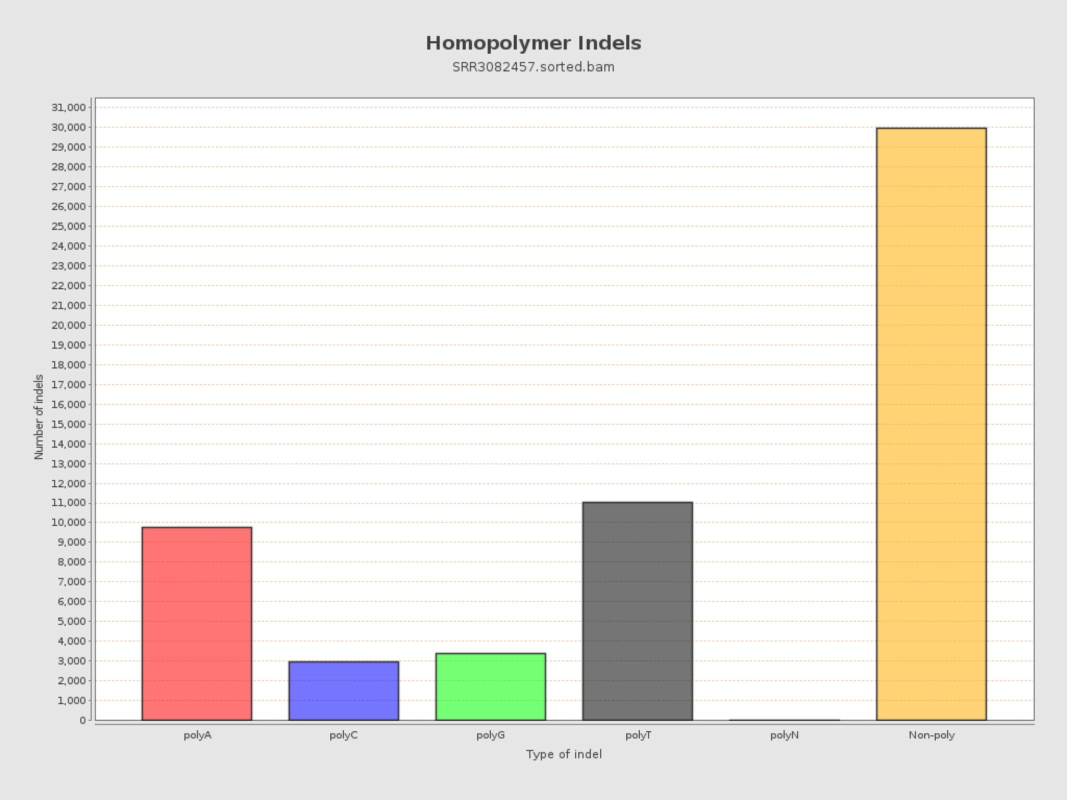
9. Results : Mapped Reads GC-content Distribution



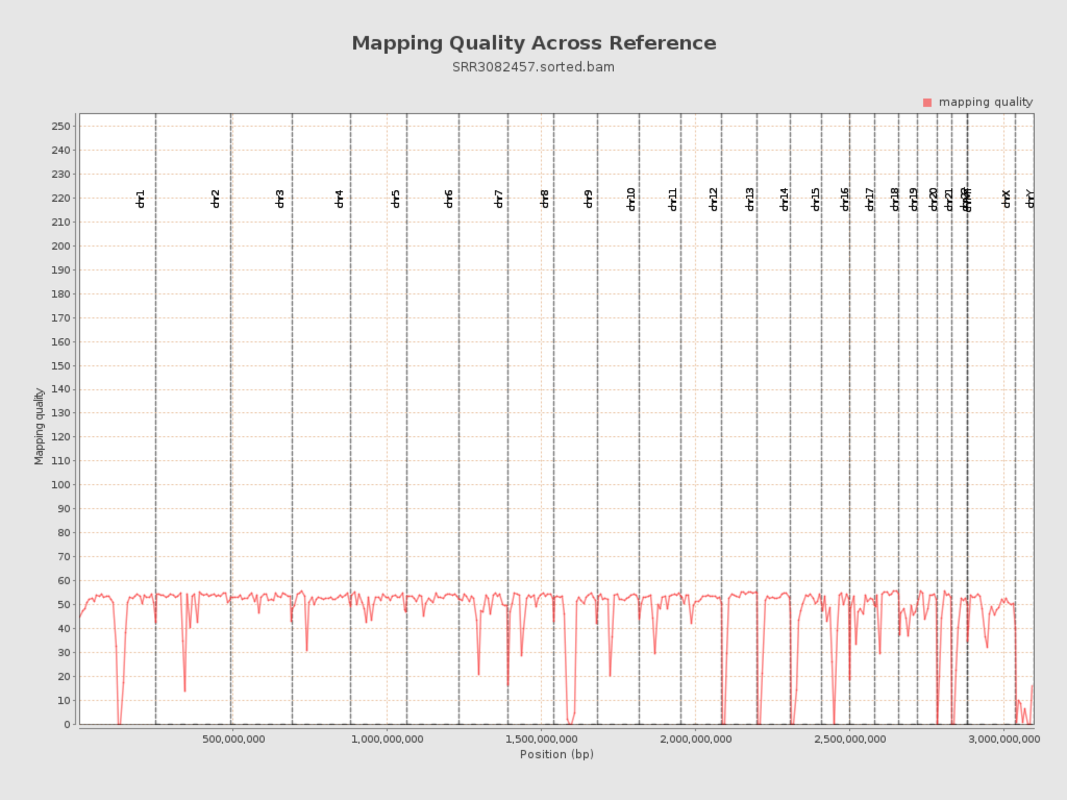
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram