Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:48:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084337.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_SRR3084337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,443,714
Mapped reads	2,184,837 / 89.41%
Unmapped reads	258,877 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,390 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	68,236 / 2.79%
Duplication rate	2.57%
Clipped reads	1,122,388 / 45.93%

2.2. ACGT Content

Number/percentage of A's	39,412,890 / 27.5%
Number/percentage of C's	27,856,254 / 19.44%
Number/percentage of T's	43,299,936 / 30.21%
Number/percentage of G's	32,593,109 / 22.74%
Number/percentage of N's	166,616 / 0.12%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.3148

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

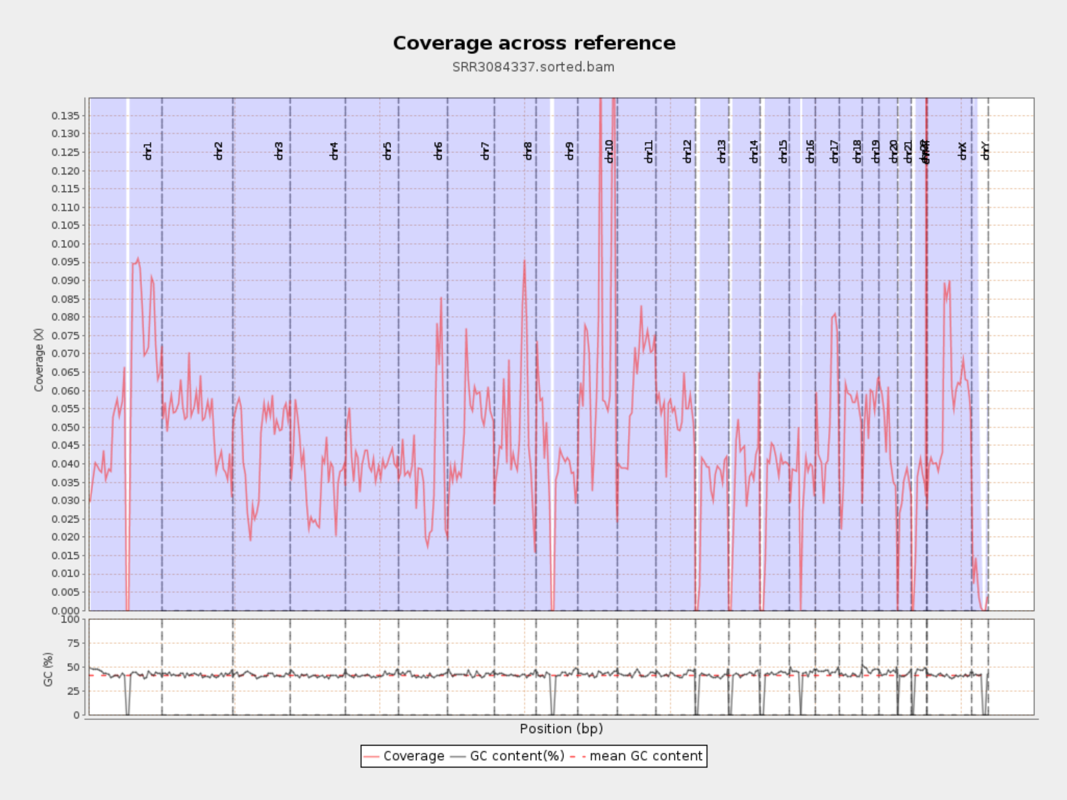
General error rate	1.03%
Mismatches	1,456,333
Insertions	11,304
Mapped reads with at least one insertion	0.51%
Deletions	31,111
Mapped reads with at least one deletion	1.41%
Homopolymer indels	45.57%

2.6. Chromosome stats

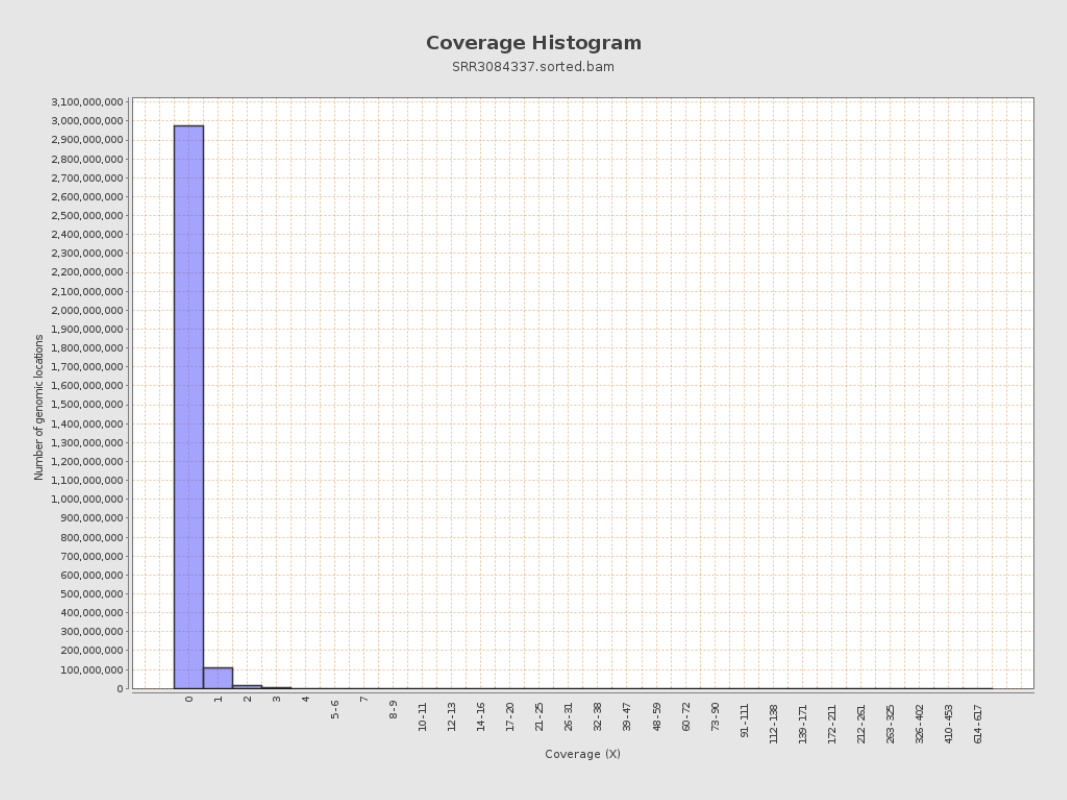
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14249702	0.0572	0.4614
chr2	243199373	12539731	0.0516	0.3945
chr3	198022430	9072895	0.0458	0.2432
chr4	191154276	6931494	0.0363	0.2212
chr5	180915260	7393767	0.0409	0.2273
chr6	171115067	6775262	0.0396	0.2552
chr7	159138663	8078427	0.0508	0.4704

chr8	146364022	7146591	0.0488	0.2944
chr9	141213431	5446740	0.0386	0.2653
chr10	135534747	10049119	0.0741	0.4158
chr11	135006516	8082161	0.0599	0.3282
chr12	133851895	7221517	0.054	0.2635
chr13	115169878	3633675	0.0316	0.2003
chr14	107349540	3742806	0.0349	0.2162
chr15	102531392	3423934	0.0334	0.2152
chr16	90354753	3116789	0.0345	0.2297
chr17	81195210	4402794	0.0542	0.2781
chr18	78077248	3972019	0.0509	0.418
chr19	59128983	3268098	0.0553	0.3789
chr20	63025520	2954990	0.0469	0.2468
chr21	48129895	1431867	0.0298	0.202
chr22	51304566	1322897	0.0258	0.1785
chrMT	16571	6533	0.3942	0.7093
chrX	155270560	8803348	0.0567	0.2895
chrY	59373566	311835	0.0053	0.1049

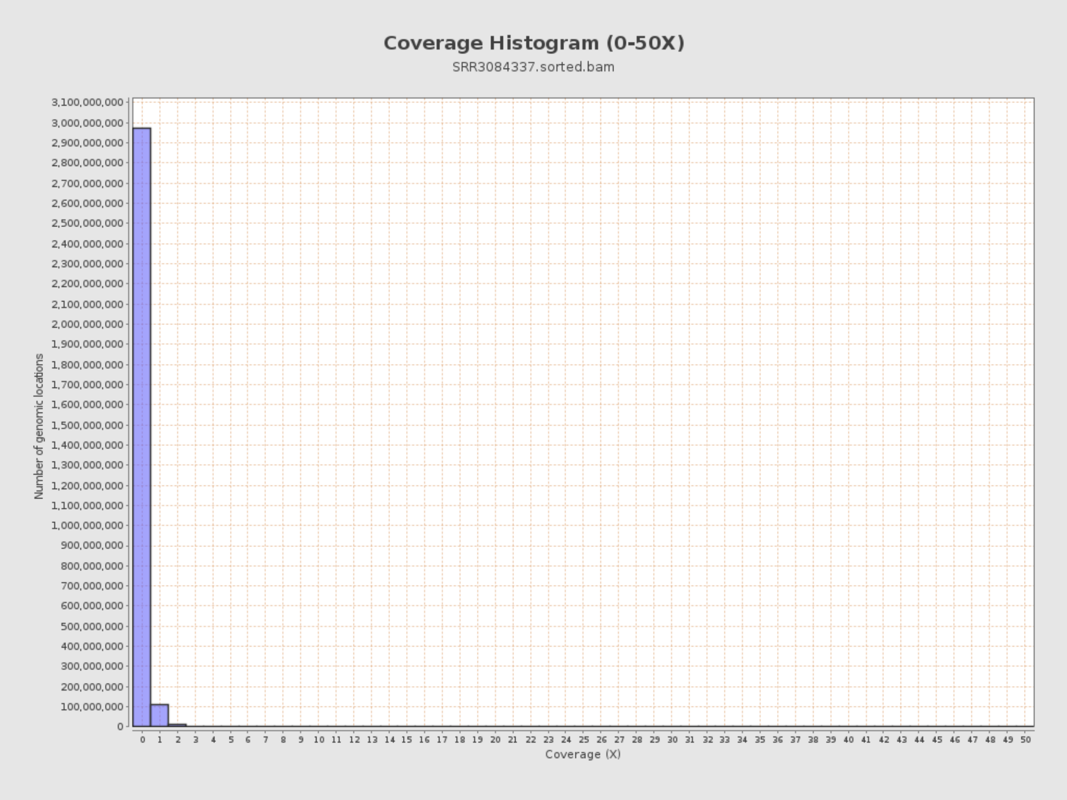
3. Results : Coverage across reference



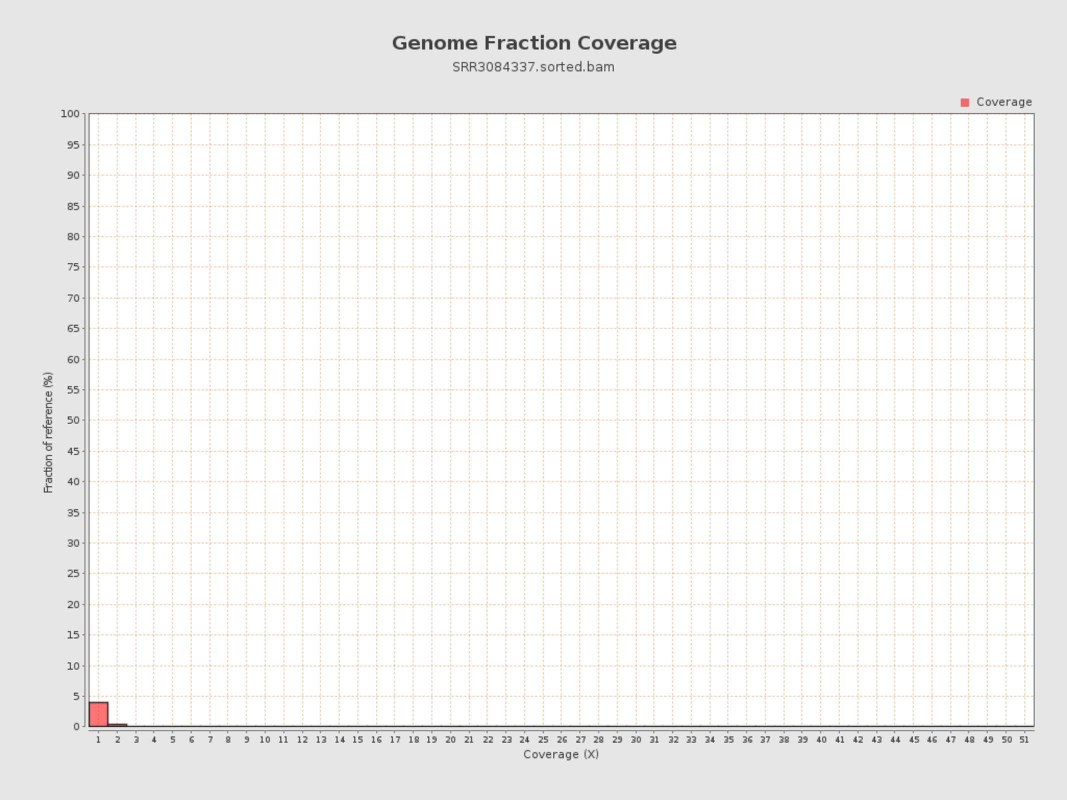
4. Results : Coverage Histogram



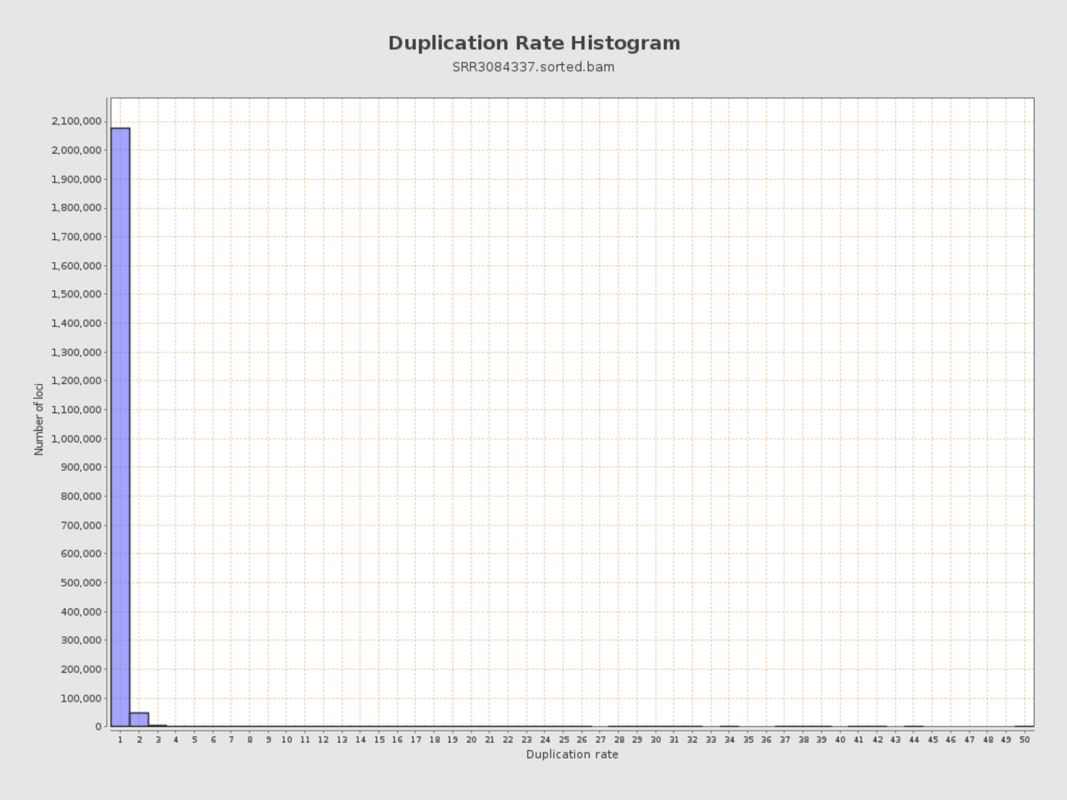
5. Results : Coverage Histogram (0-50X)



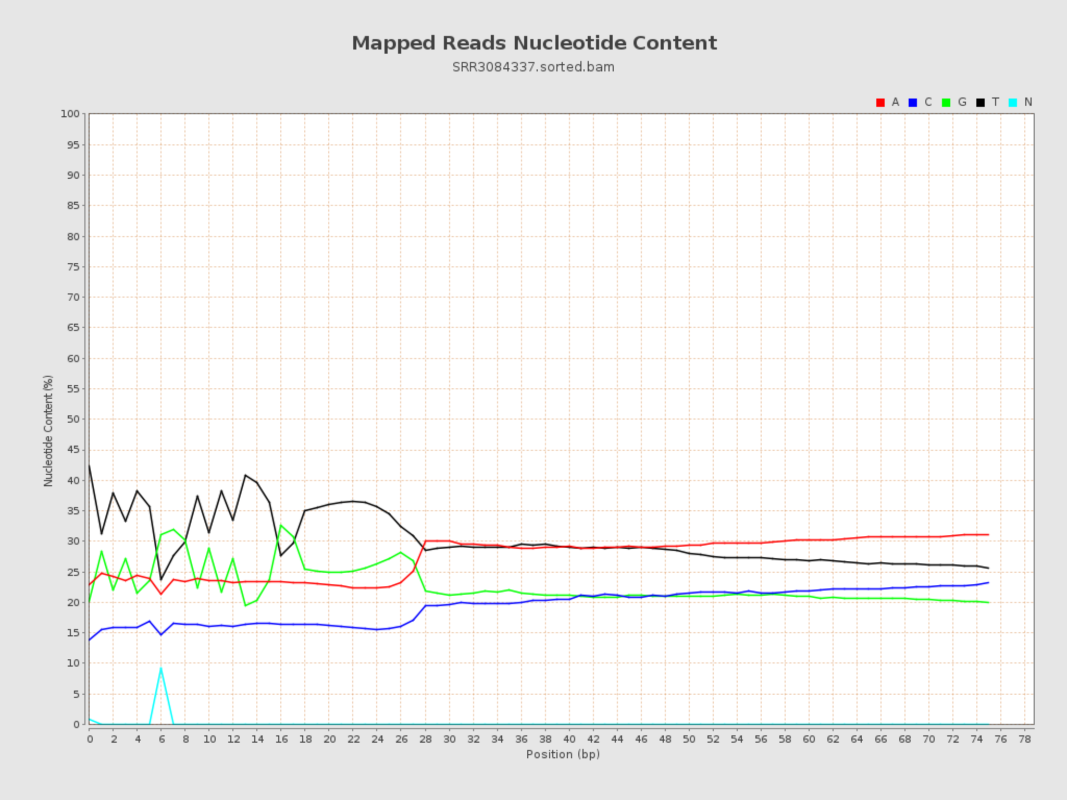
6. Results : Genome Fraction Coverage



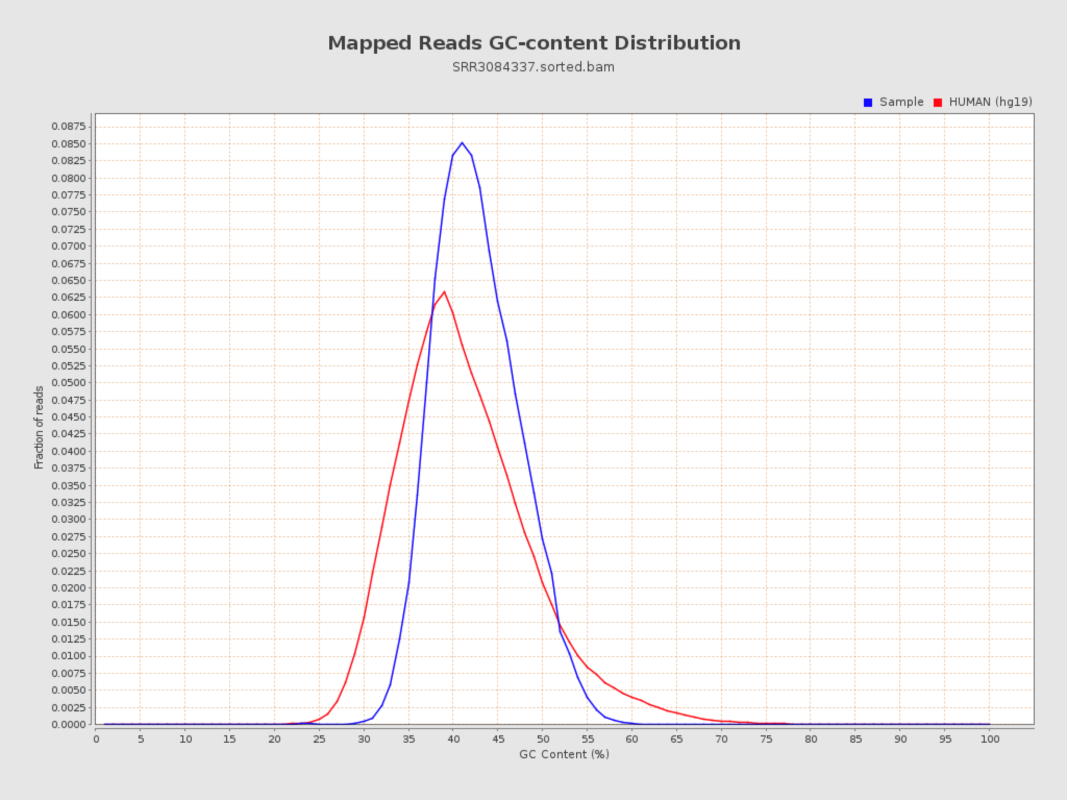
7. Results : Duplication Rate Histogram



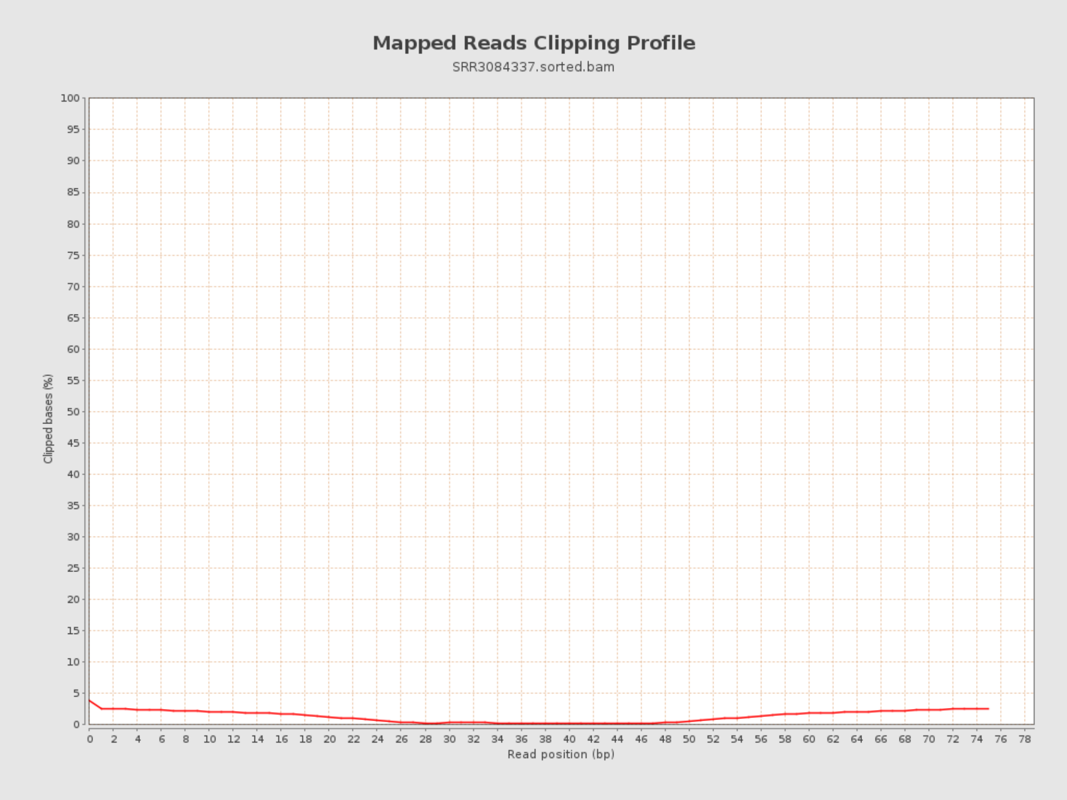
8. Results : Mapped Reads Nucleotide Content



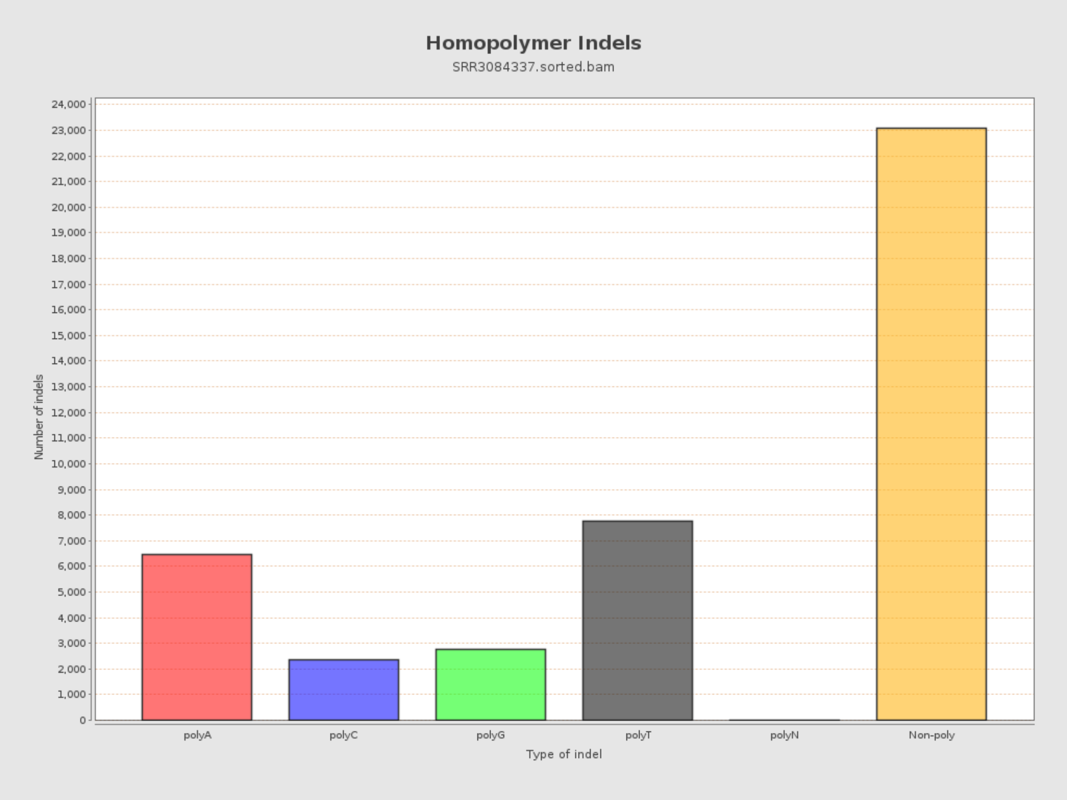
9. Results : Mapped Reads GC-content Distribution



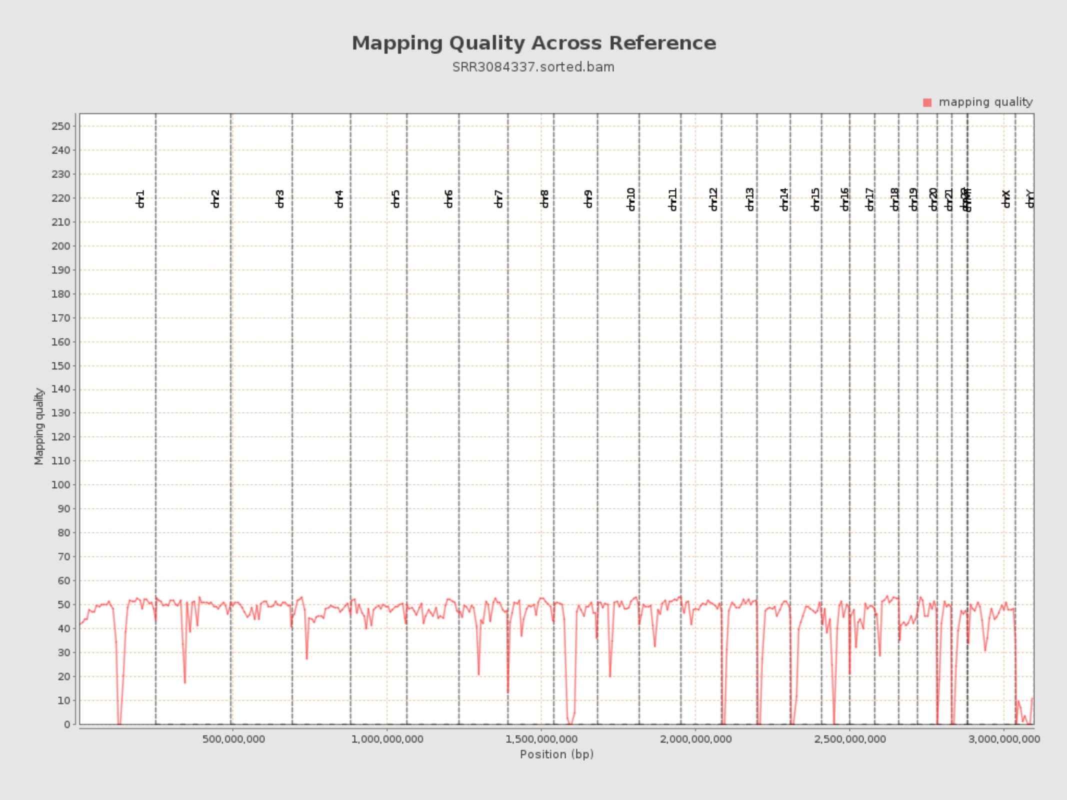
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram