Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:11:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124808.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_SRR3124808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:11:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	734,442
Mapped reads	732,423 / 99.73%
Unmapped reads	2,019 / 0.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	354,323 / 48.24%
Read min/max/mean length	30 / 151 / 182.58
Duplicated reads (estimated)	1,076,513 / 146.58%
Duplication rate	5.42%
Clipped reads	746,483 / 101.64%

2.2. ACGT Content

Number/percentage of A's	30,722,895 / 28.11%
Number/percentage of C's	18,837,782 / 17.23%
Number/percentage of T's	37,247,229 / 34.08%
Number/percentage of G's	22,498,905 / 20.58%
Number/percentage of N's	0 / 0%
GC Percentage	37.82%

2.3. Coverage

Mean	0.0353

Standard Deviation	105.5707

2.4. Mapping Quality

Mean Mapping Quality	49.62

2.5. Mismatches and indels

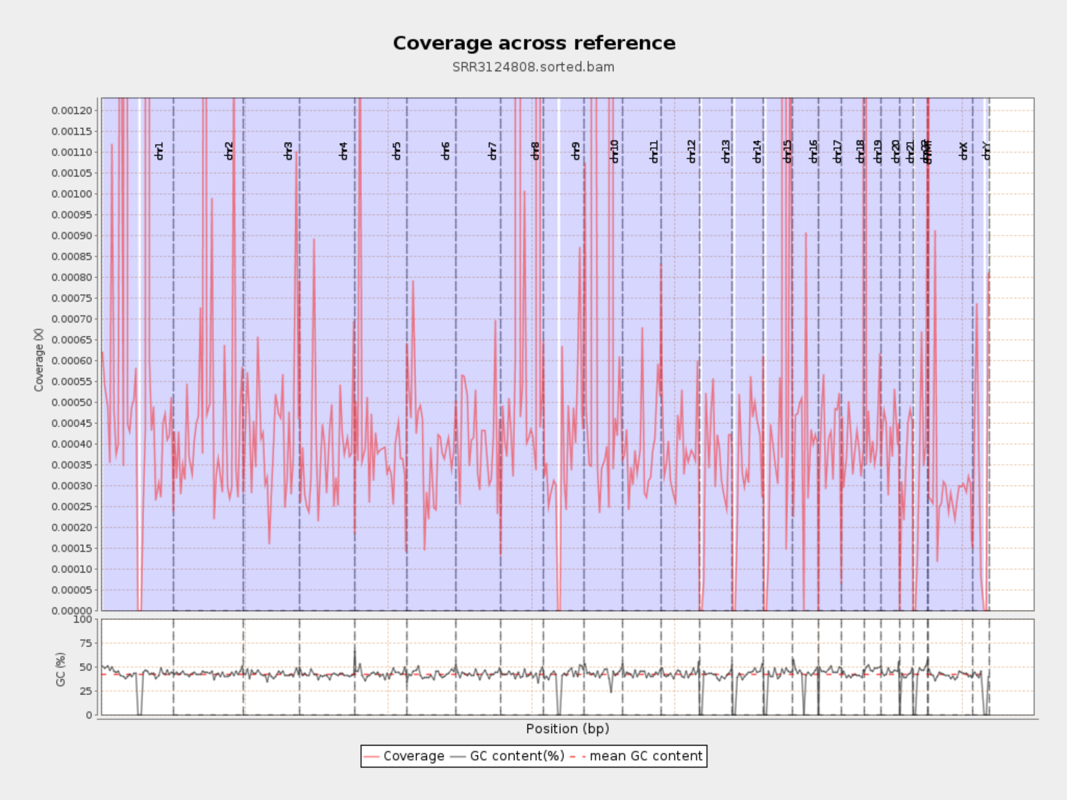
General error rate	0.77%
Mismatches	832,077
Insertions	7,556
Mapped reads with at least one insertion	1.03%
Deletions	31,688
Mapped reads with at least one deletion	4.28%
Homopolymer indels	51.51%

2.6. Chromosome stats

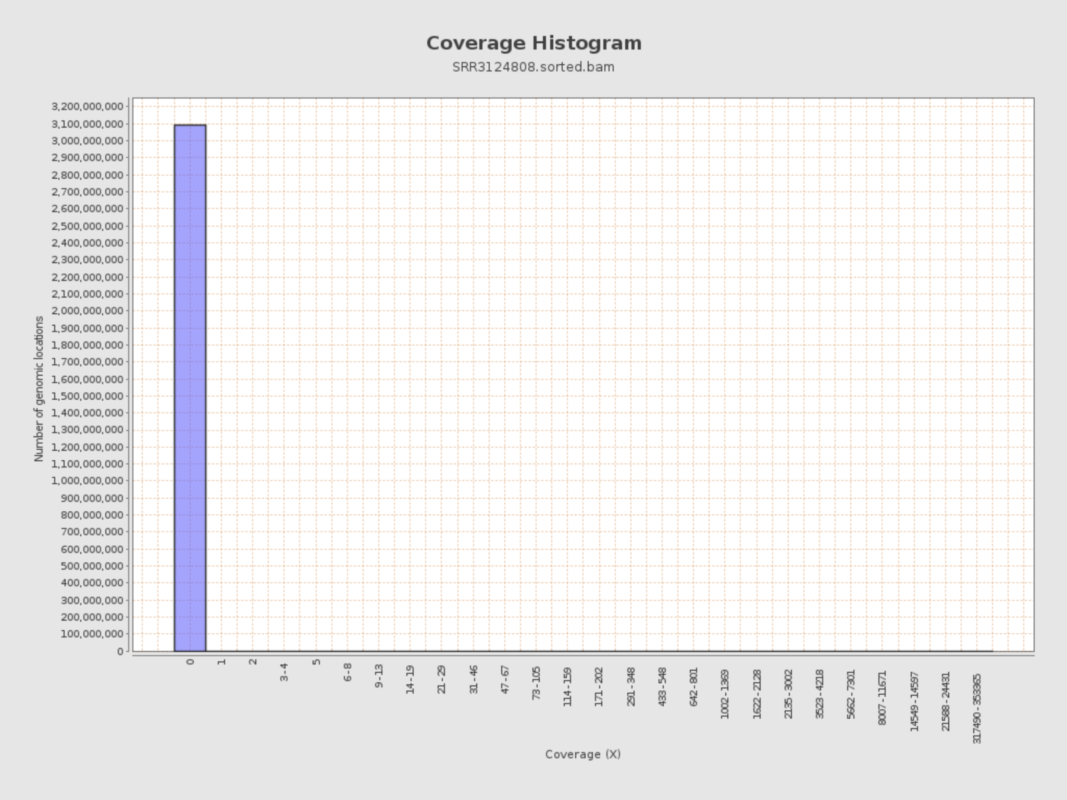
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2598915	0.0104	8.9651
chr2	243199373	138479	0.0006	0.1423
chr3	198022430	85457	0.0004	0.0259
chr4	191154276	74060	0.0004	0.0218
chr5	180915260	76191	0.0004	0.0269
chr6	171115067	69021	0.0004	0.0331
chr7	159138663	66125	0.0004	0.0227

chr8	146364022	1115592	0.0076	3.5909
chr9	141213431	52627	0.0004	0.0263
chr10	135534747	104408102	0.7703	504.38
chr11	135006516	52409	0.0004	0.0262
chr12	133851895	52266	0.0004	0.0199
chr13	115169878	37670	0.0003	0.0186
chr14	107349540	36654	0.0003	0.0211
chr15	102531392	181906	0.0018	0.8372
chr16	90354753	38138	0.0004	0.0211
chr17	81195210	33560	0.0004	0.0235
chr18	78077248	30226	0.0004	0.0206
chr19	59128983	65391	0.0011	0.3213
chr20	63025520	26658	0.0004	0.0206
chr21	48129895	16223	0.0003	0.0186
chr22	51304566	17514	0.0003	0.0268
chrMT	16571	296	0.0179	0.1325
chrX	155270560	46418	0.0003	0.0714
chrY	59373566	19771	0.0003	0.0214

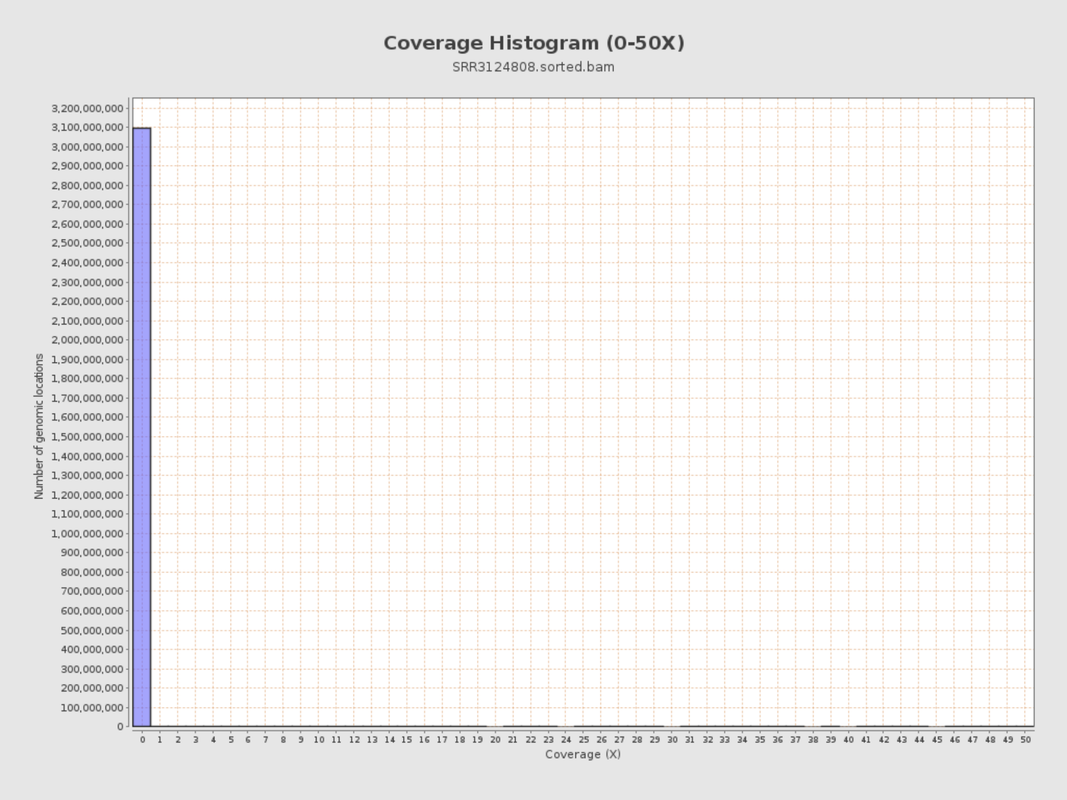
3. Results : Coverage across reference



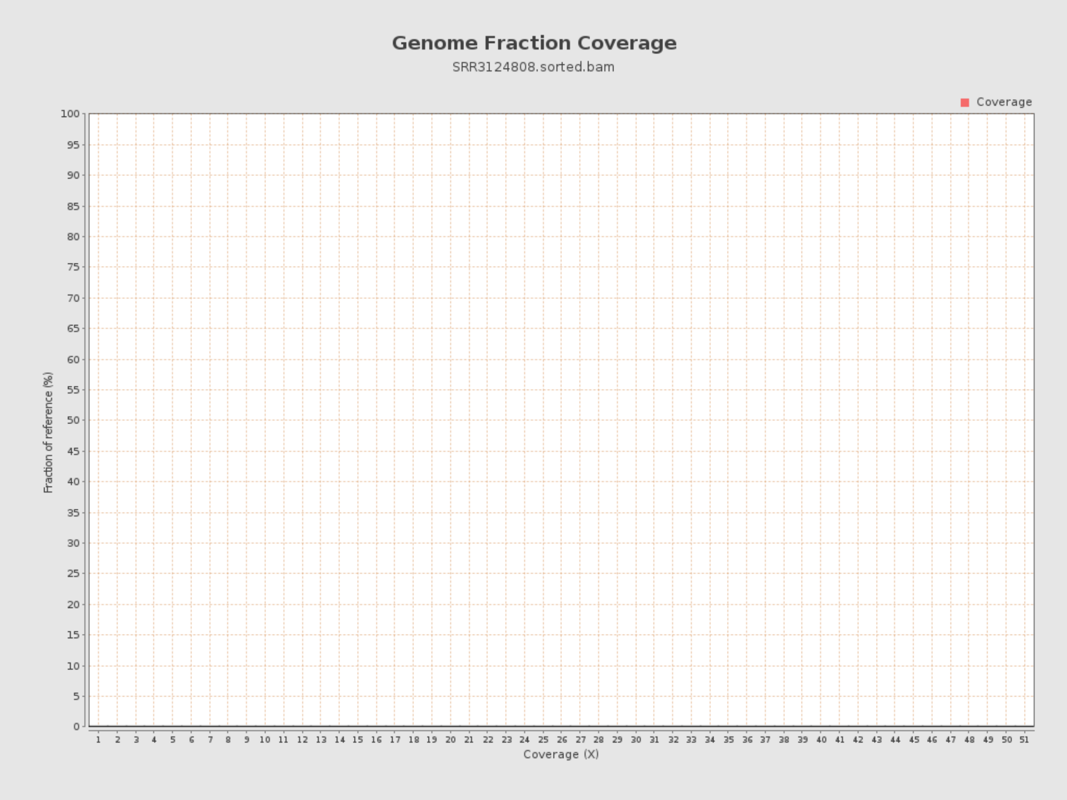
4. Results : Coverage Histogram



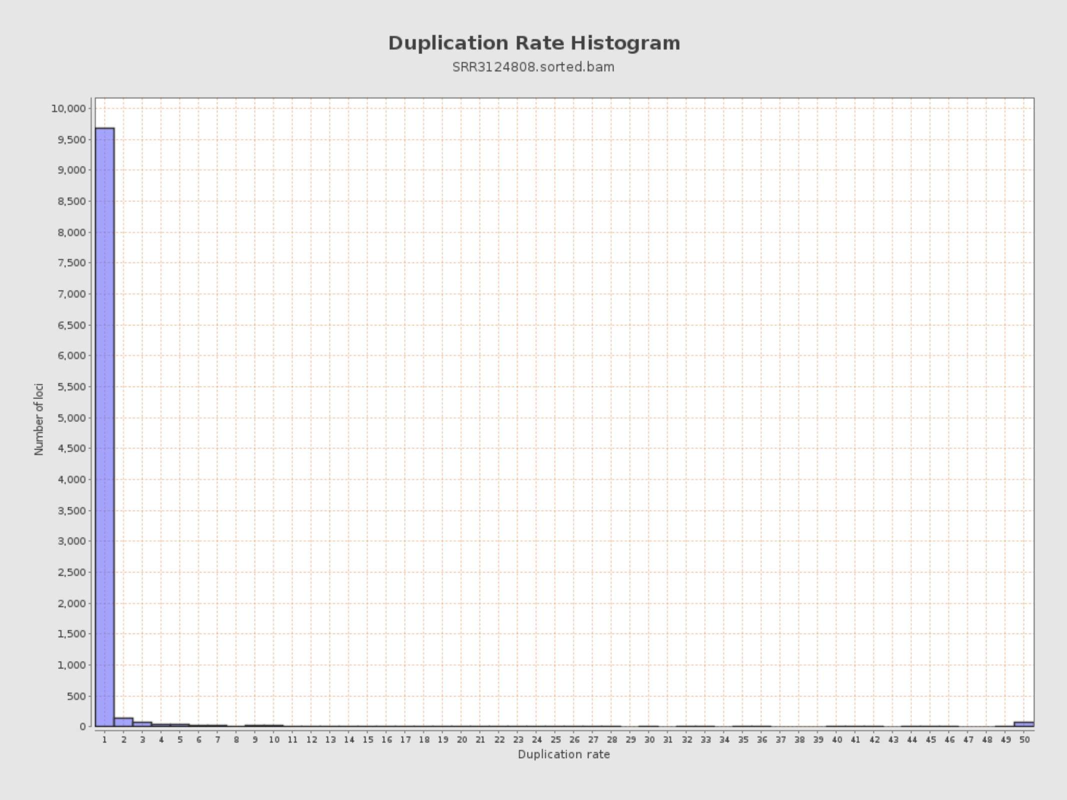
5. Results : Coverage Histogram (0-50X)



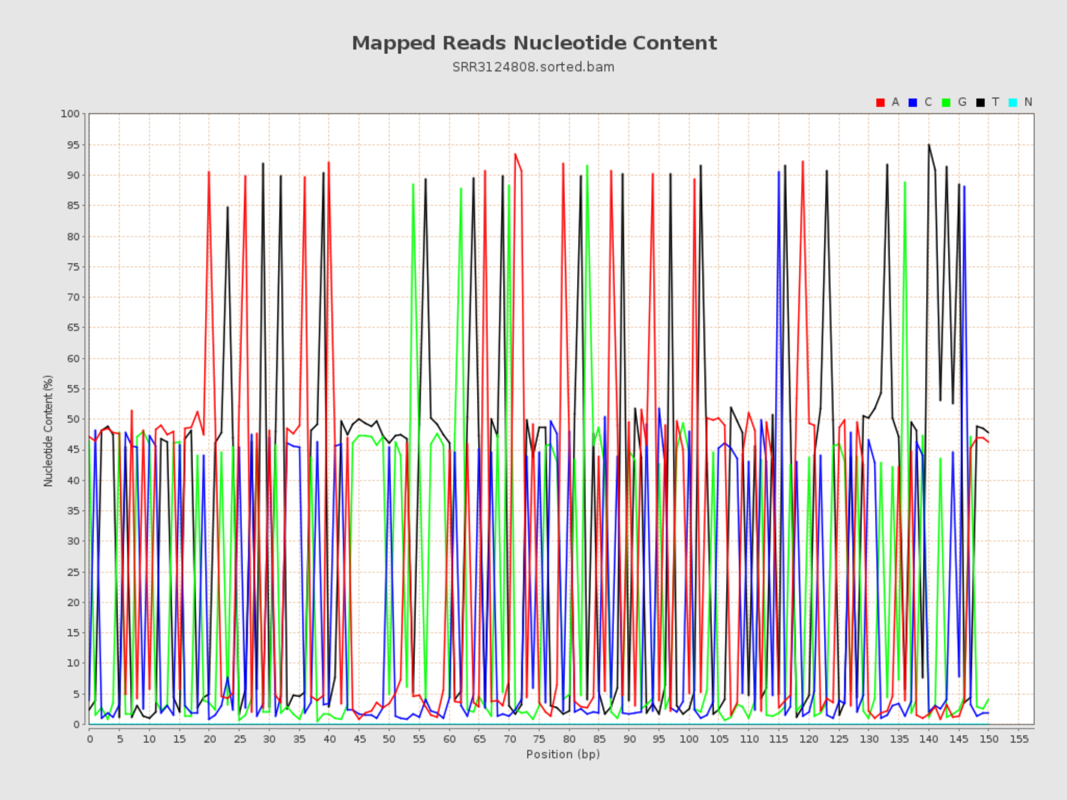
6. Results : Genome Fraction Coverage



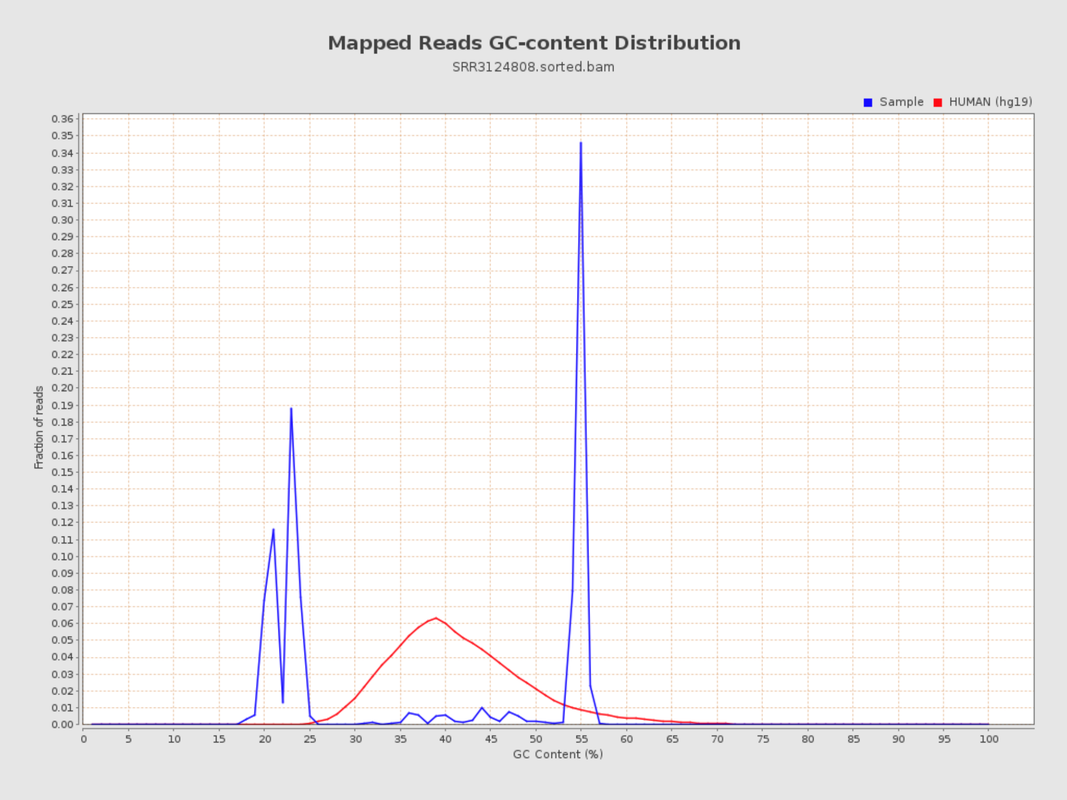
7. Results : Duplication Rate Histogram



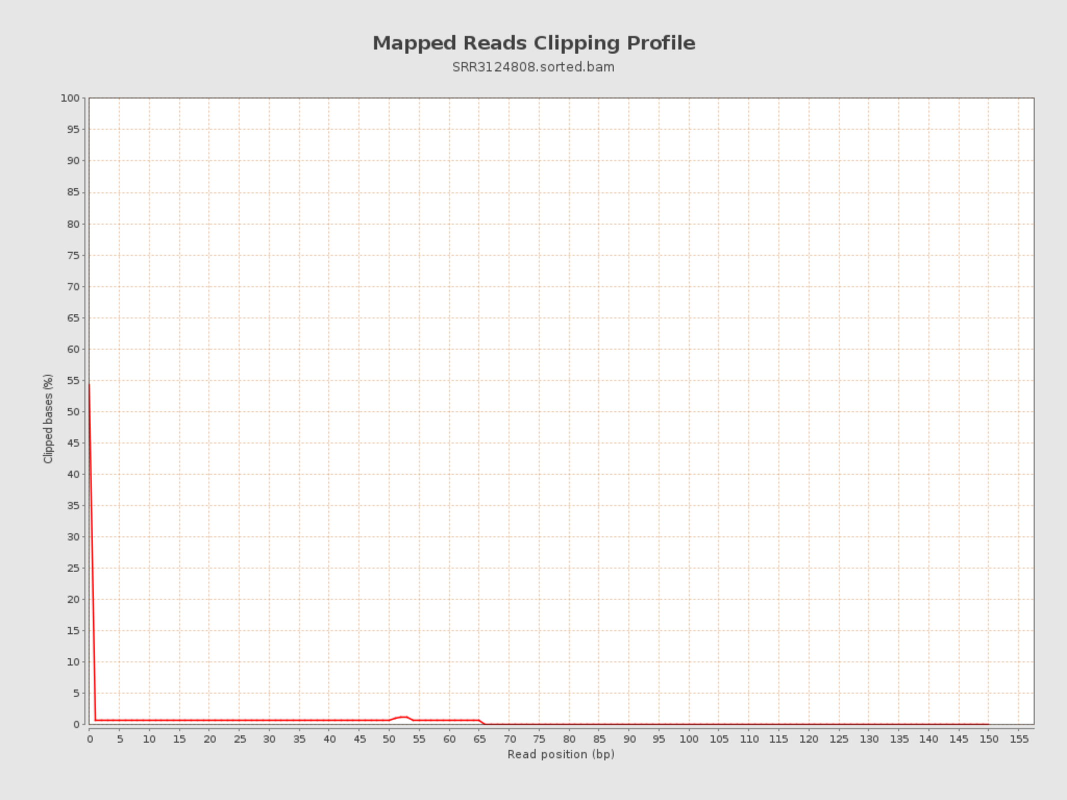
8. Results : Mapped Reads Nucleotide Content



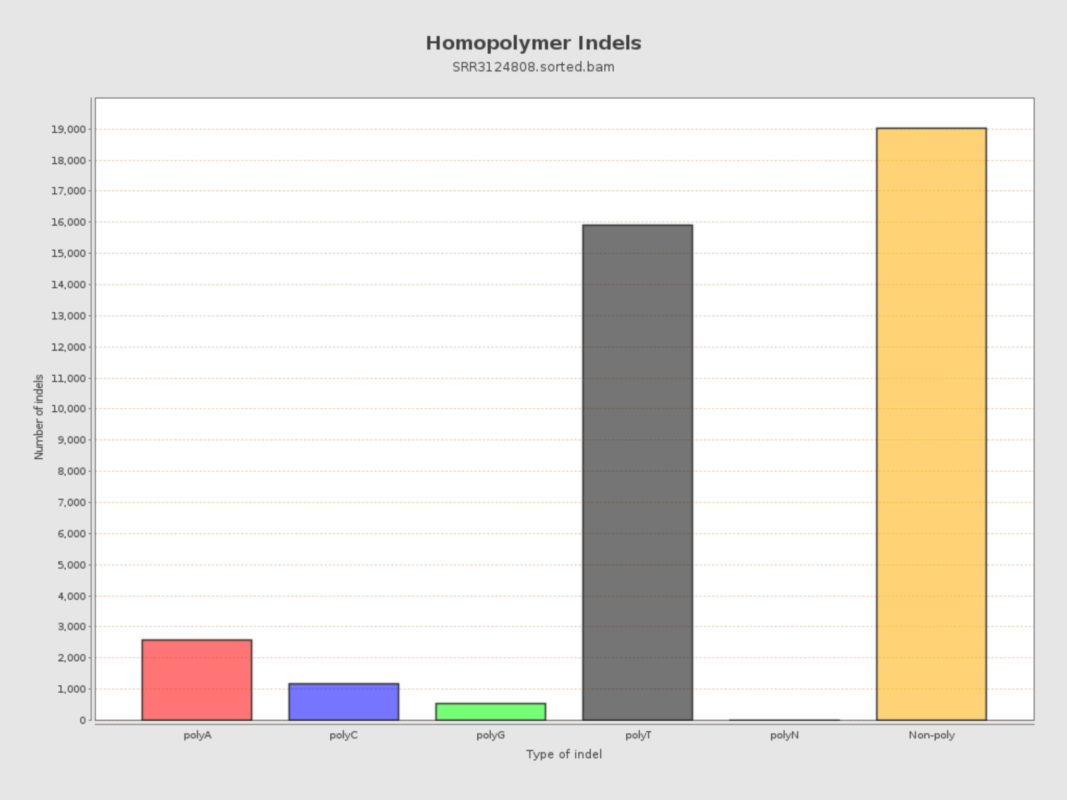
9. Results : Mapped Reads GC-content Distribution



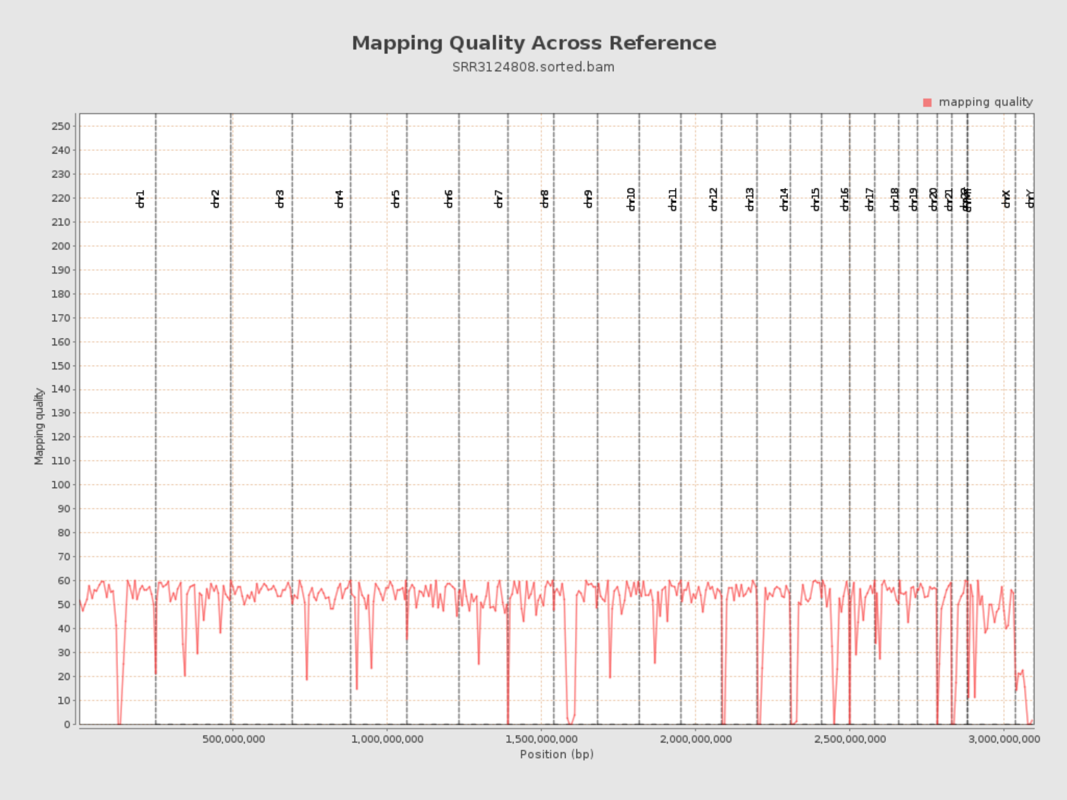
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram