Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:35:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124787.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_SRR3124787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:35:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	720,499
Mapped reads	719,535 / 99.87%
Unmapped reads	964 / 0.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	341,498 / 47.4%
Read min/max/mean length	30 / 151 / 182.2
Duplicated reads (estimated)	1,045,830 / 145.15%
Duplication rate	2.71%
Clipped reads	714,021 / 99.1%

2.2. ACGT Content

Number/percentage of A's	29,783,129 / 27.76%
Number/percentage of C's	18,418,785 / 17.17%
Number/percentage of T's	36,547,676 / 34.07%
Number/percentage of G's	22,530,172 / 21%
Number/percentage of N's	0 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	0.0347

Standard Deviation	107.8328

2.4. Mapping Quality

Mean Mapping Quality	50.32

2.5. Mismatches and indels

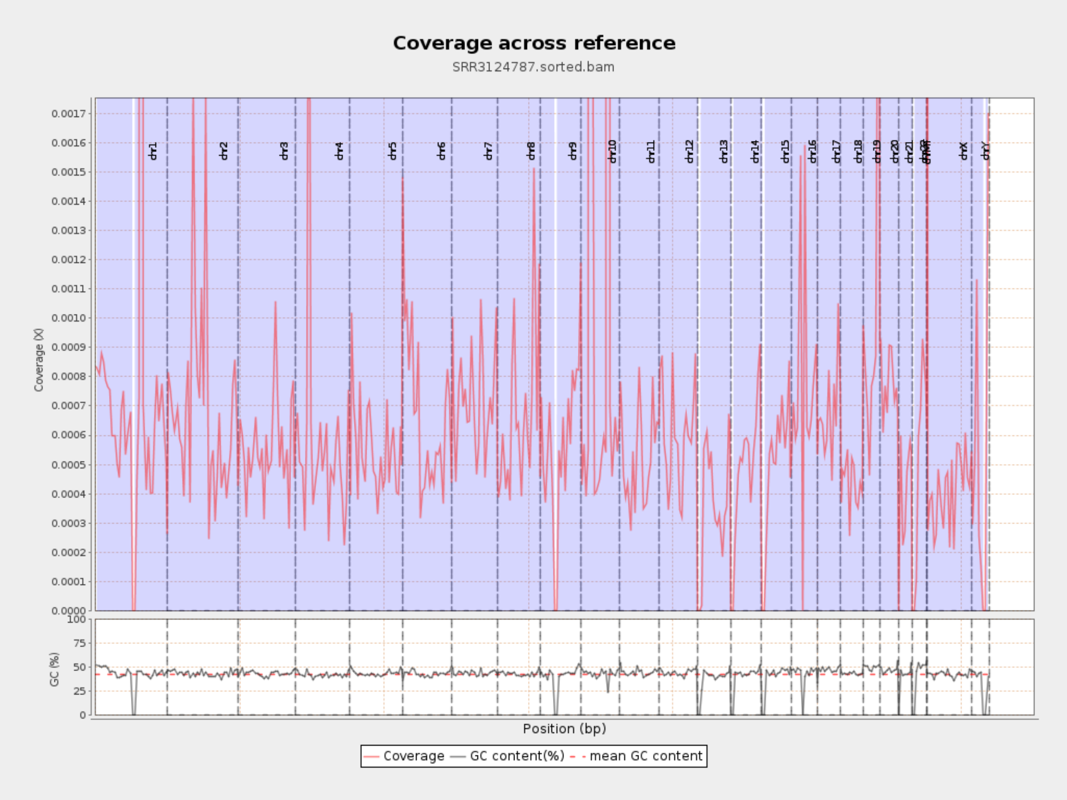
General error rate	0.73%
Mismatches	776,585
Insertions	5,808
Mapped reads with at least one insertion	0.8%
Deletions	29,192
Mapped reads with at least one deletion	4.02%
Homopolymer indels	54.19%

2.6. Chromosome stats

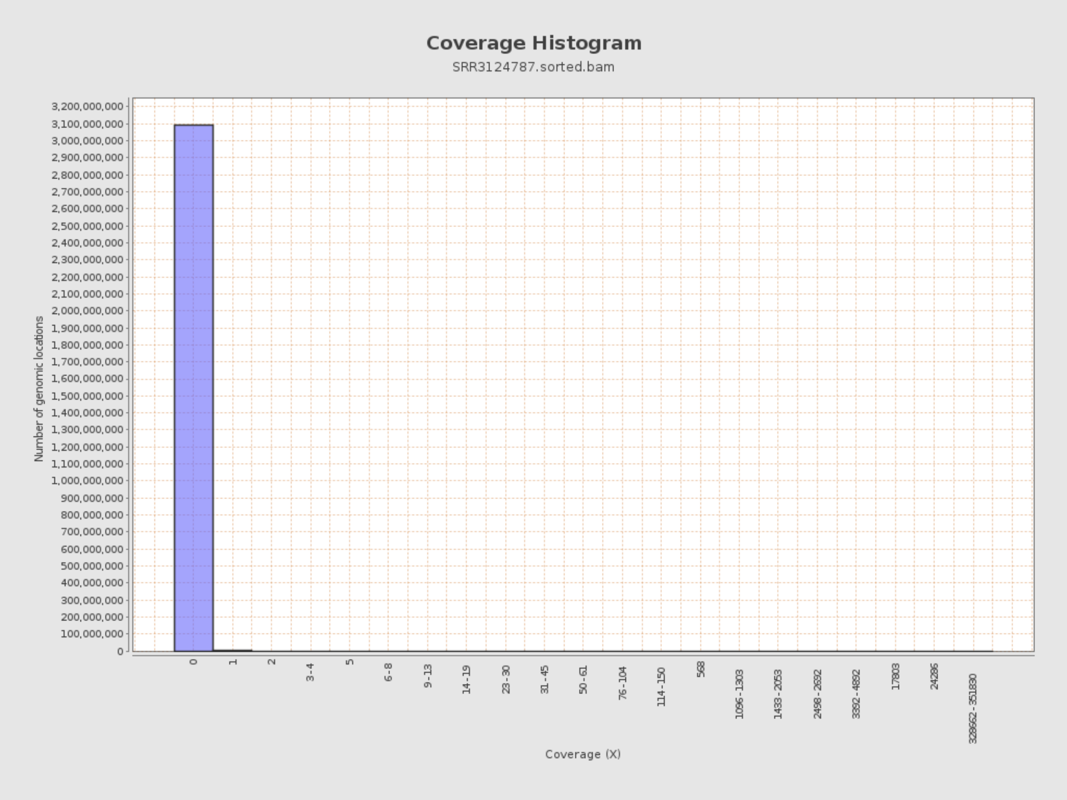
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1262526	0.0051	4.1863
chr2	243199373	169246	0.0007	0.0498
chr3	198022430	112084	0.0006	0.024
chr4	191154276	114207	0.0006	0.0374
chr5	180915260	101315	0.0006	0.0239
chr6	171115067	114028	0.0007	0.0553
chr7	159138663	115568	0.0007	0.0277

chr8	146364022	97724	0.0007	0.0342
chr9	141213431	77387	0.0005	0.0243
chr10	135534747	104433196	0.7705	515.3209
chr11	135006516	71454	0.0005	0.0315
chr12	133851895	80791	0.0006	0.0248
chr13	115169878	40403	0.0004	0.0188
chr14	107349540	52638	0.0005	0.0223
chr15	102531392	50877	0.0005	0.023
chr16	90354753	69446	0.0008	0.0425
chr17	81195210	55411	0.0007	0.0274
chr18	78077248	33695	0.0004	0.0212
chr19	59128983	62424	0.0011	0.1632
chr20	63025520	48726	0.0008	0.0284
chr21	48129895	19330	0.0004	0.0204
chr22	51304566	25192	0.0005	0.0321
chrMT	16571	9058	0.5466	0.7775
chrX	155270560	63176	0.0004	0.0204
chrY	59373566	30516	0.0005	0.032

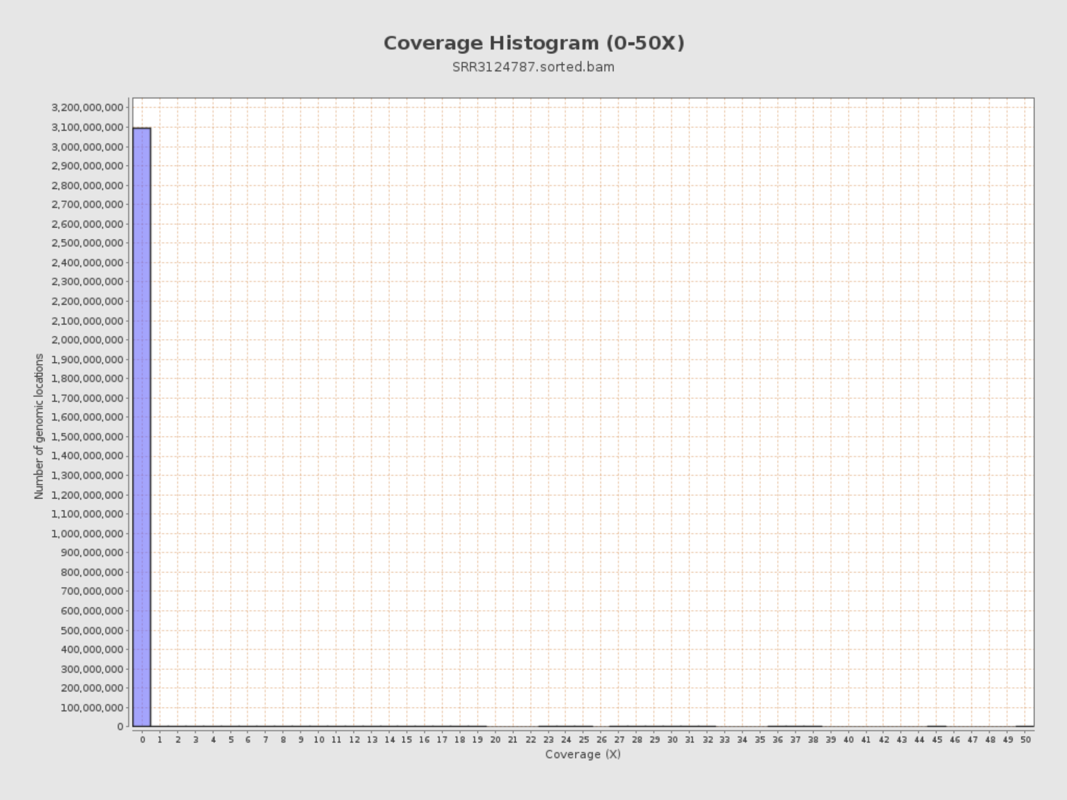
3. Results : Coverage across reference



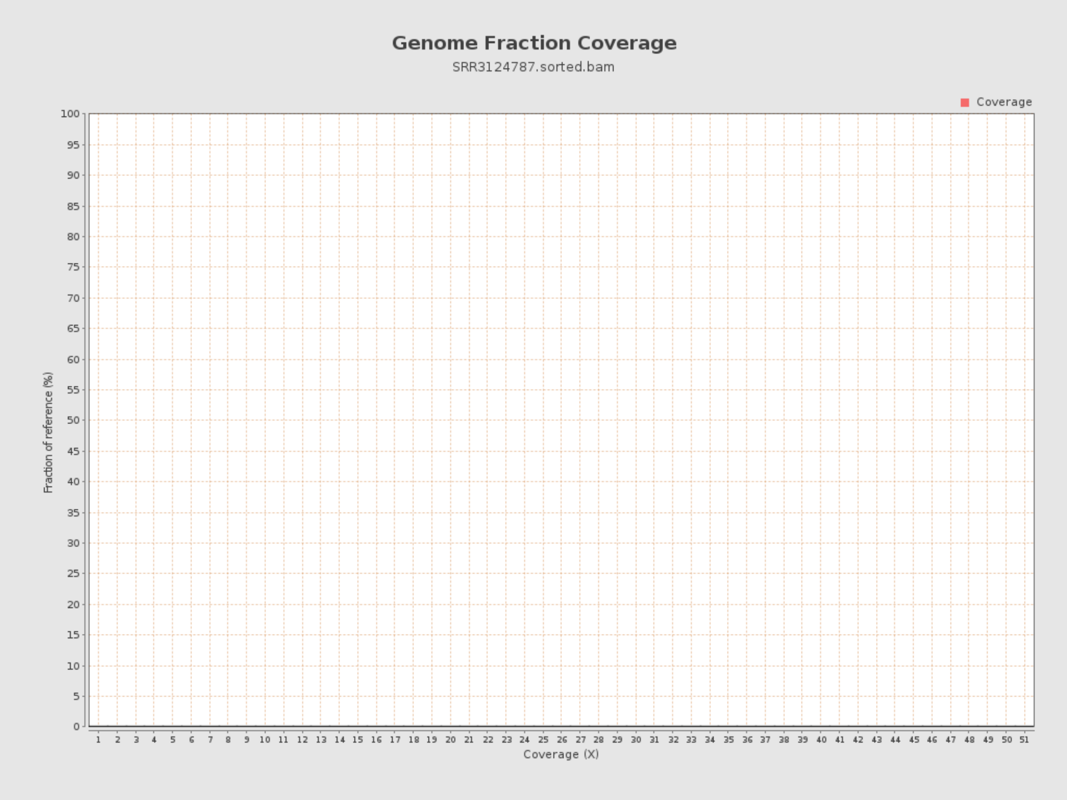
4. Results : Coverage Histogram



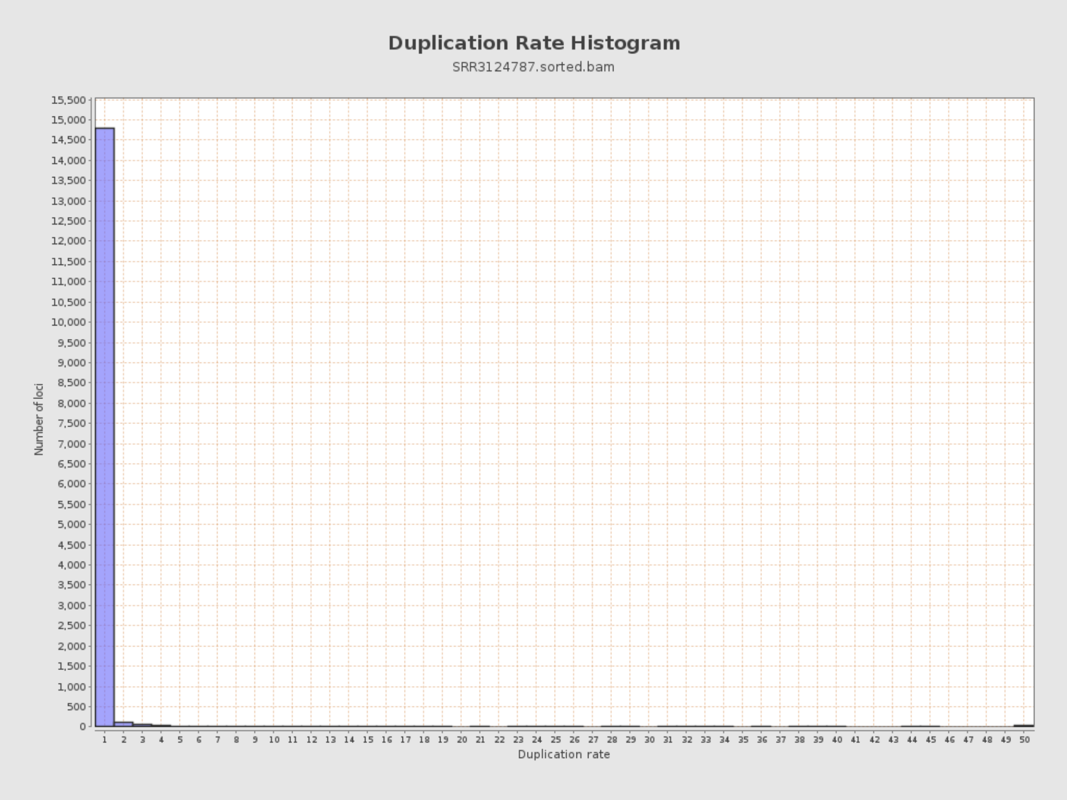
5. Results : Coverage Histogram (0-50X)



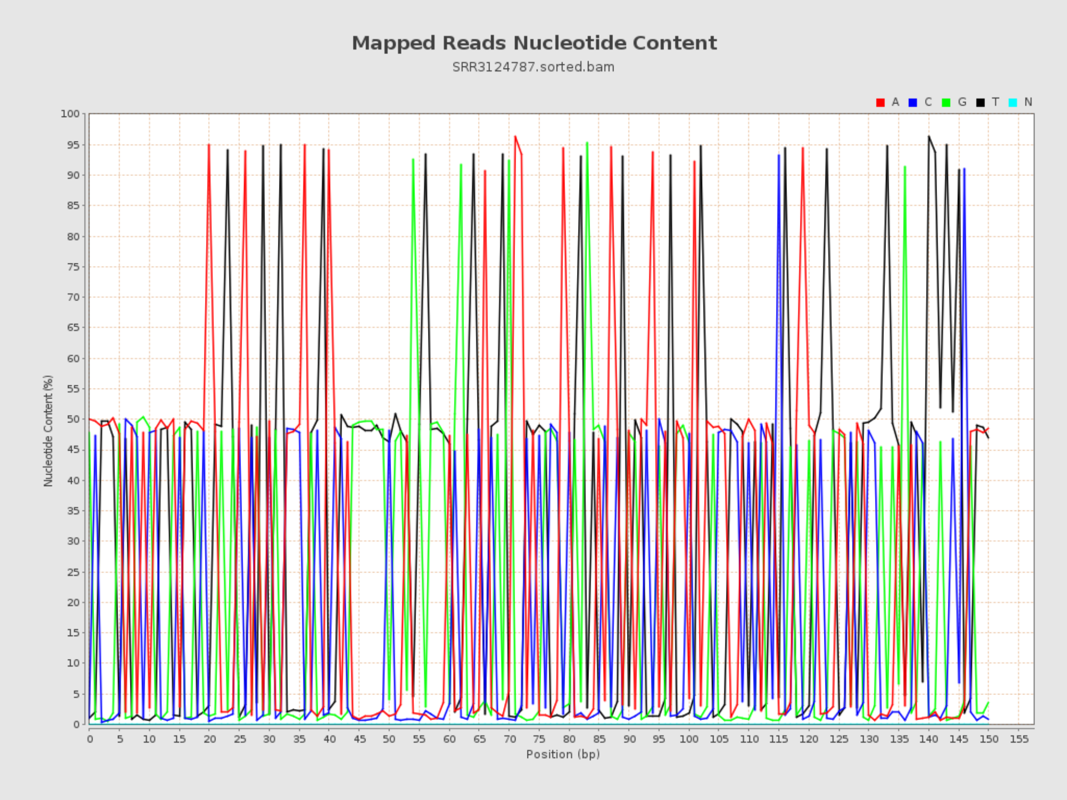
6. Results : Genome Fraction Coverage



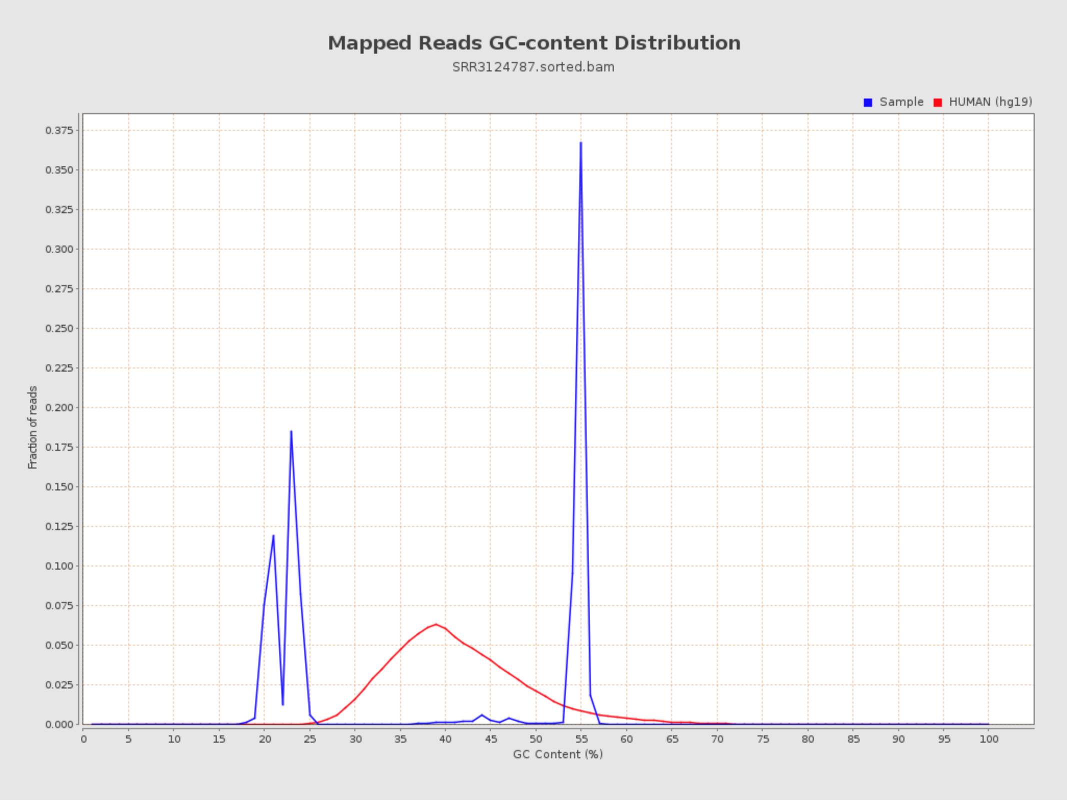
7. Results : Duplication Rate Histogram



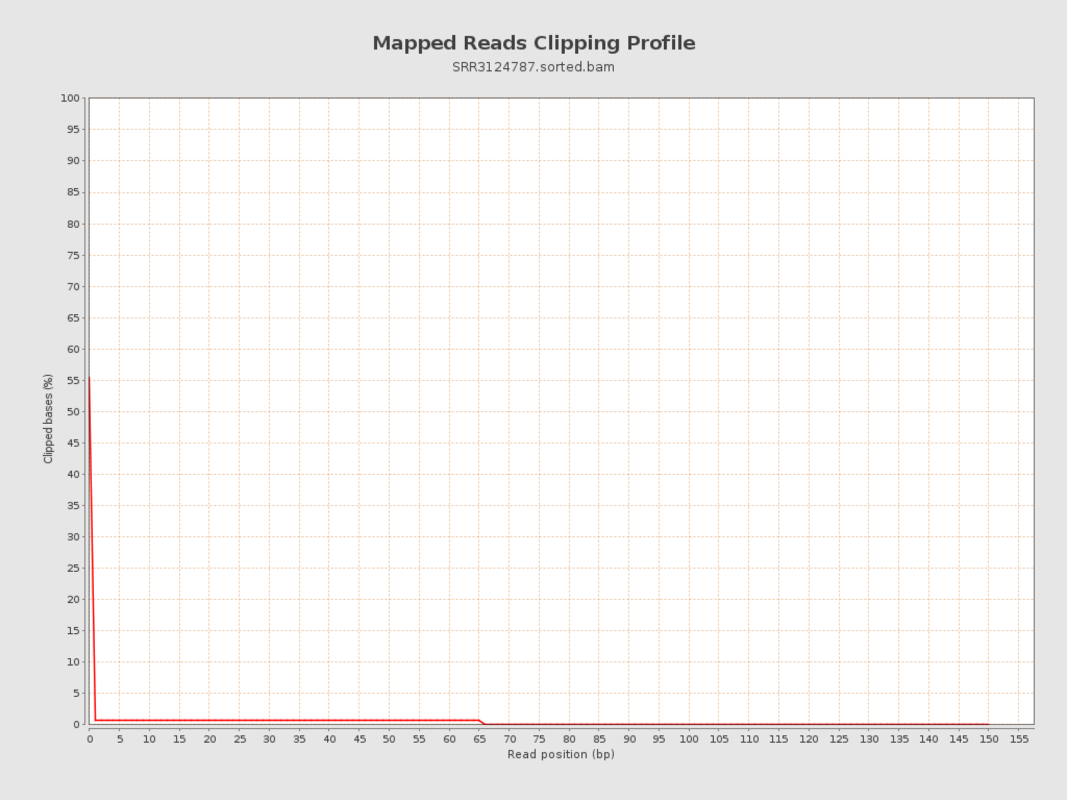
8. Results : Mapped Reads Nucleotide Content



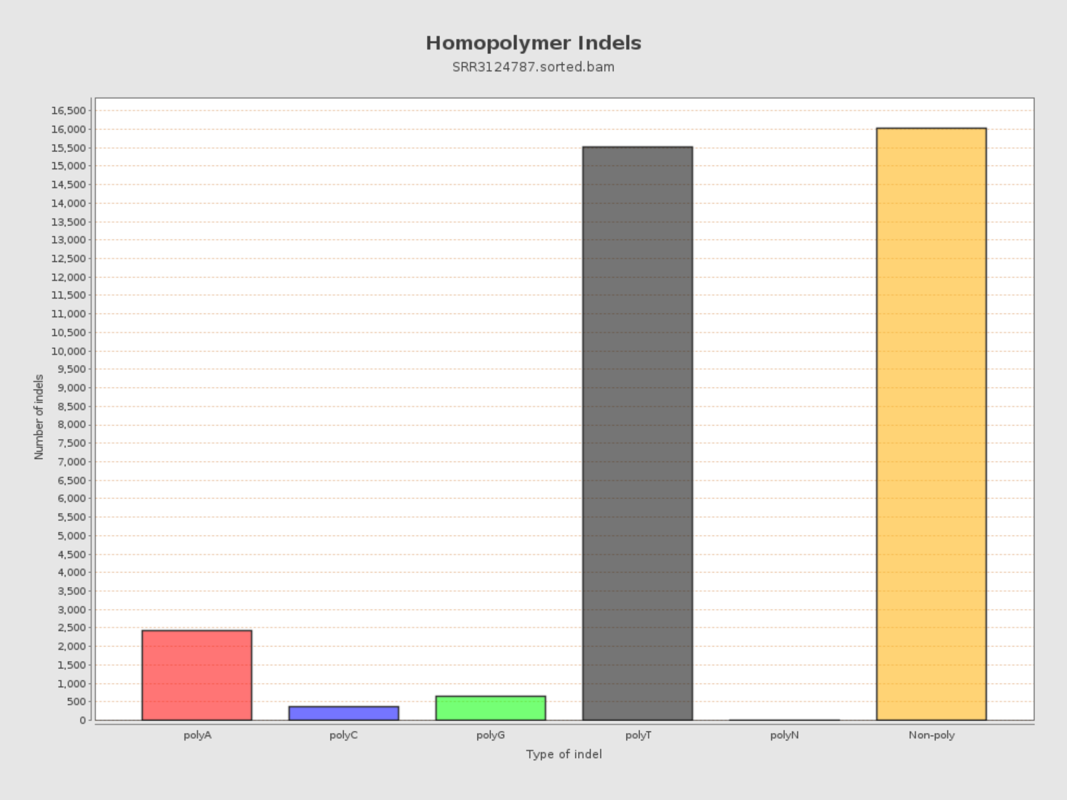
9. Results : Mapped Reads GC-content Distribution



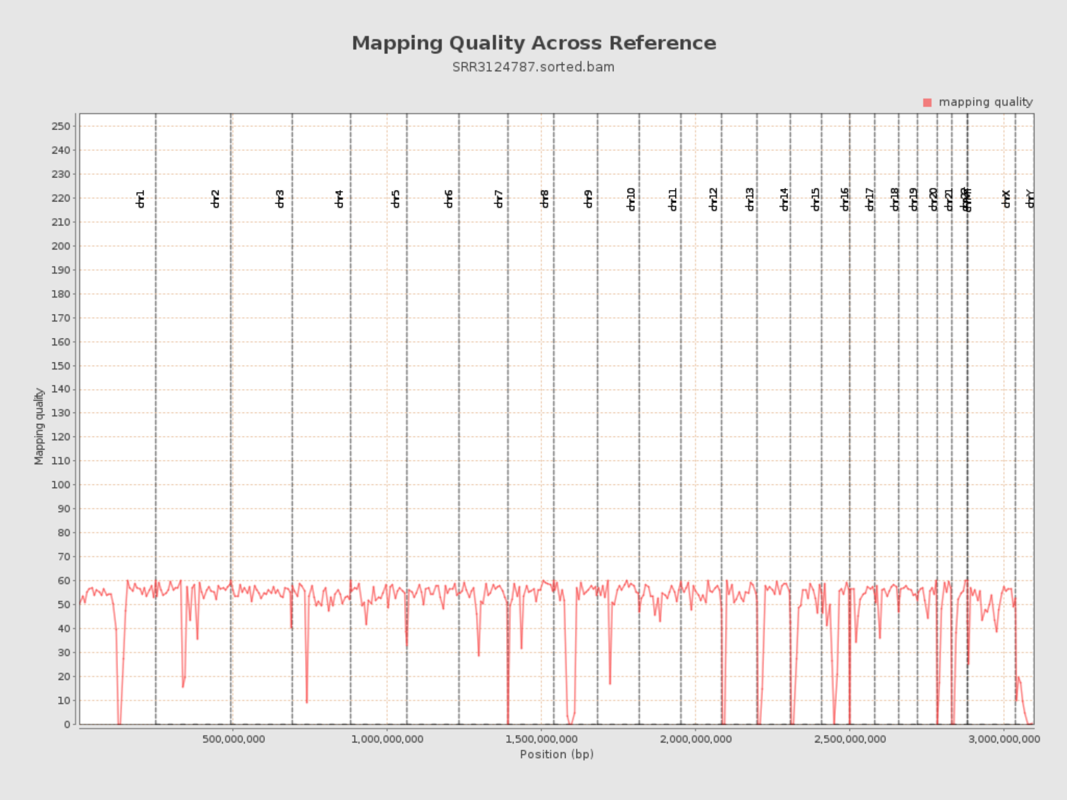
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram