Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:59:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714268.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_ERR9714268 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:59:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	351,782
Mapped reads	102,441 / 29.12%
Unmapped reads	249,341 / 70.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,763 / 1.07%
Read min/max/mean length	30 / 151 / 84.16
Duplicated reads (estimated)	88,723 / 25.22%
Duplication rate	40.08%
Clipped reads	89,611 / 25.47%

2.2. ACGT Content

Number/percentage of A's	2,784,336 / 23.26%
Number/percentage of C's	2,097,021 / 17.52%
Number/percentage of T's	2,605,935 / 21.77%
Number/percentage of G's	4,481,988 / 37.45%
Number/percentage of N's	219 / 0%
GC Percentage	54.96%

2.3. Coverage

Mean	0.0039

Standard Deviation	2.972

2.4. Mapping Quality

Mean Mapping Quality	47.87

2.5. Mismatches and indels

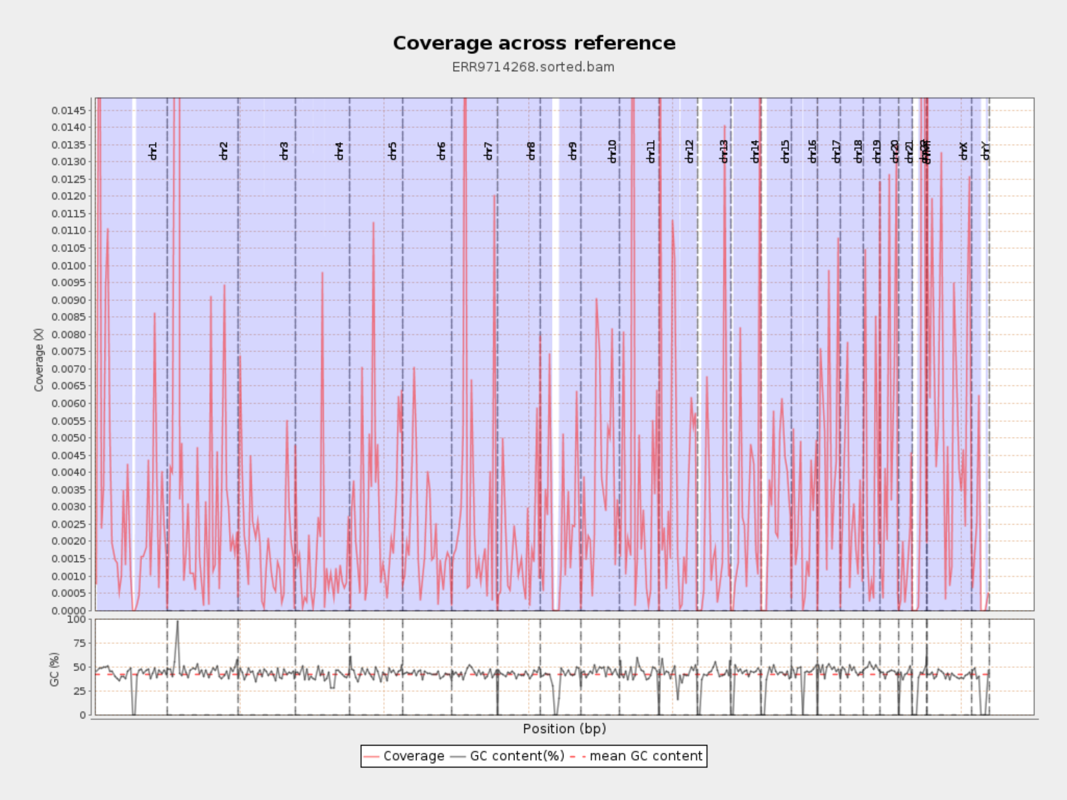
General error rate	4.11%
Mismatches	445,241
Insertions	13,380
Mapped reads with at least one insertion	11.91%
Deletions	34,848
Mapped reads with at least one deletion	32.19%
Homopolymer indels	31.3%

2.6. Chromosome stats

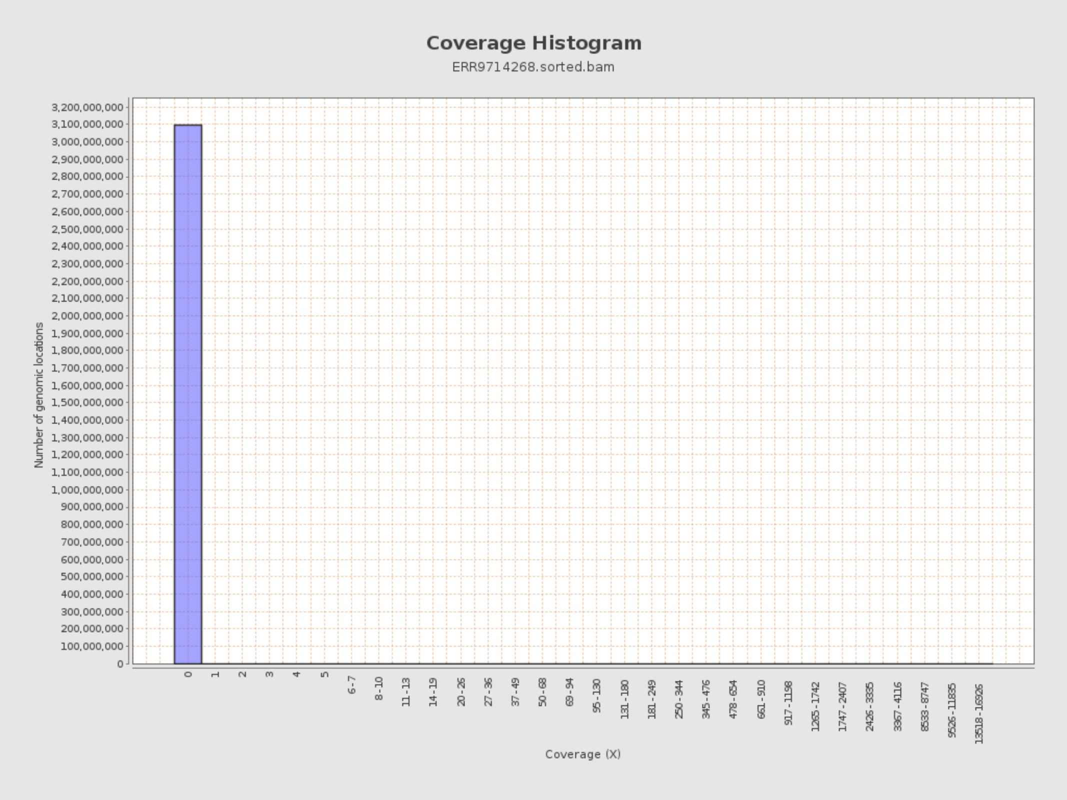
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	829109	0.0033	0.7679
chr2	243199373	3102057	0.0128	10.2795
chr3	198022430	396499	0.002	0.4242
chr4	191154276	285787	0.0015	0.3581
chr5	180915260	558994	0.0031	0.6449
chr6	171115067	352622	0.0021	0.3129
chr7	159138663	546591	0.0034	1.1921

chr8	146364022	247041	0.0017	0.2927
chr9	141213431	334333	0.0024	0.4274
chr10	135534747	496262	0.0037	0.5889
chr11	135006516	554918	0.0041	1.0881
chr12	133851895	565551	0.0042	0.9648
chr13	115169878	293434	0.0025	0.6603
chr14	107349540	372490	0.0035	0.8023
chr15	102531392	317291	0.0031	0.4617
chr16	90354753	221789	0.0025	0.3972
chr17	81195210	401053	0.0049	0.8321
chr18	78077248	222111	0.0028	0.6142
chr19	59128983	222635	0.0038	0.7265
chr20	63025520	343125	0.0054	1.1222
chr21	48129895	68534	0.0014	0.2413
chr22	51304566	341289	0.0067	2.3539
chrMT	16571	81166	4.8981	37.2202
chrX	155270560	935228	0.006	0.6844
chrY	59373566	87949	0.0015	0.5007

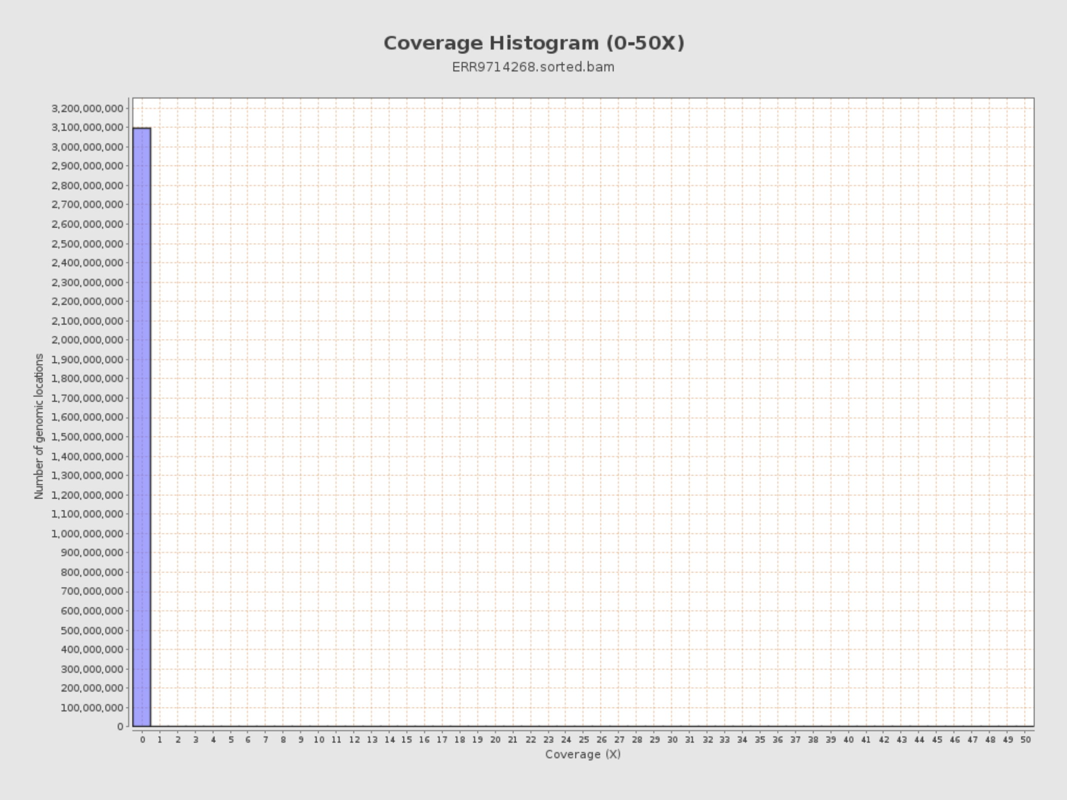
3. Results : Coverage across reference



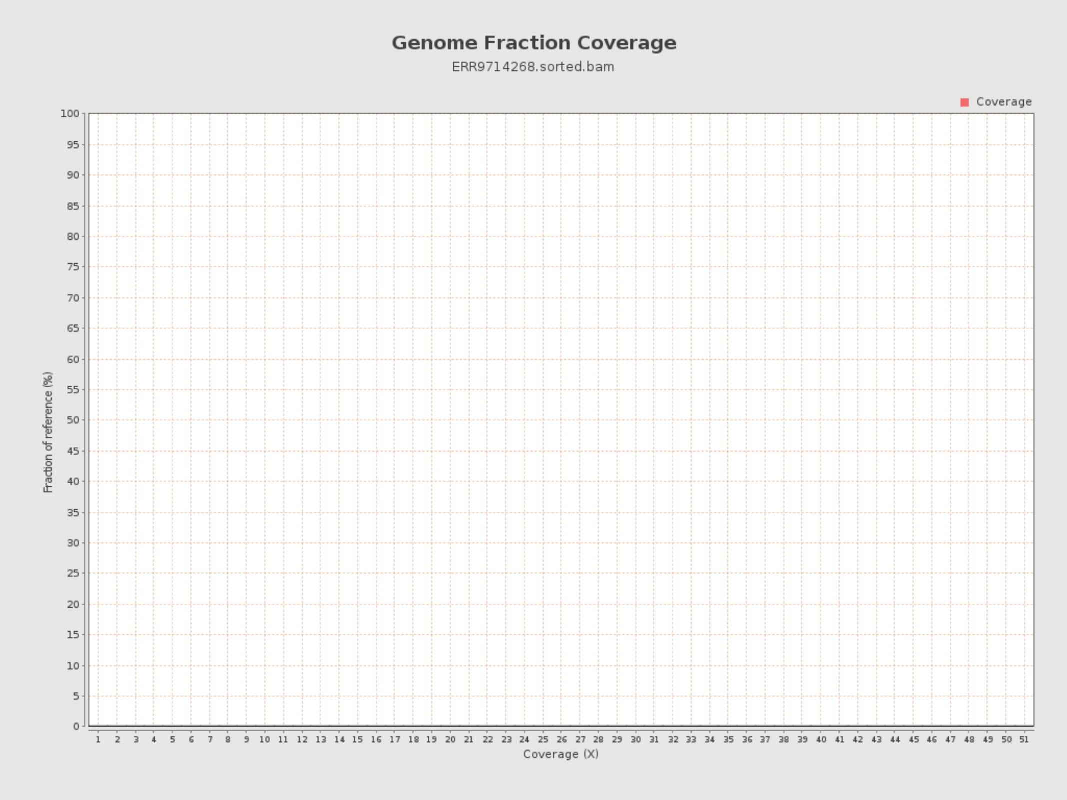
4. Results : Coverage Histogram



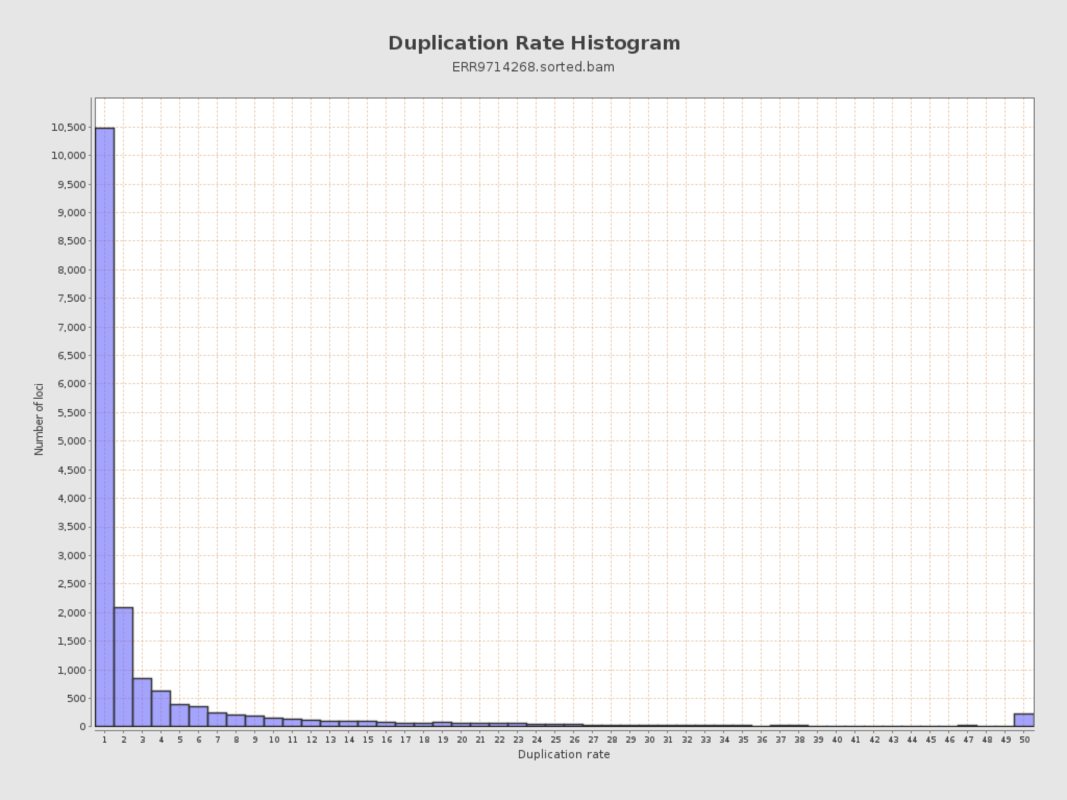
5. Results : Coverage Histogram (0-50X)



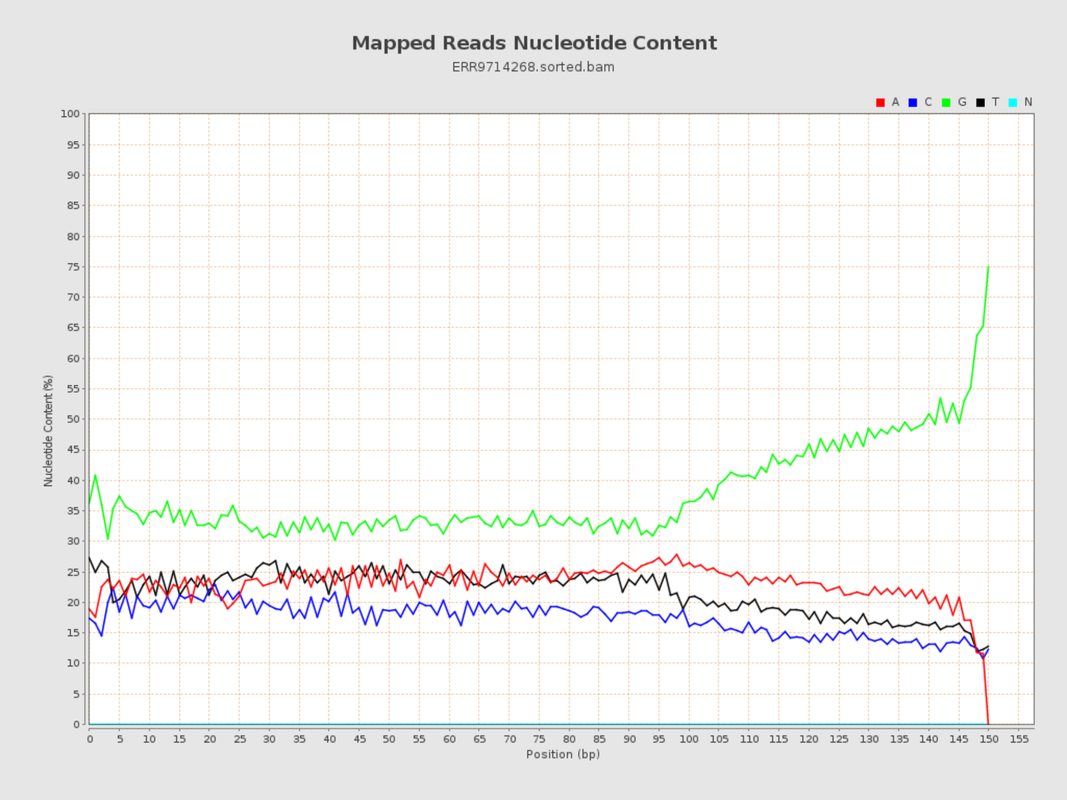
6. Results : Genome Fraction Coverage



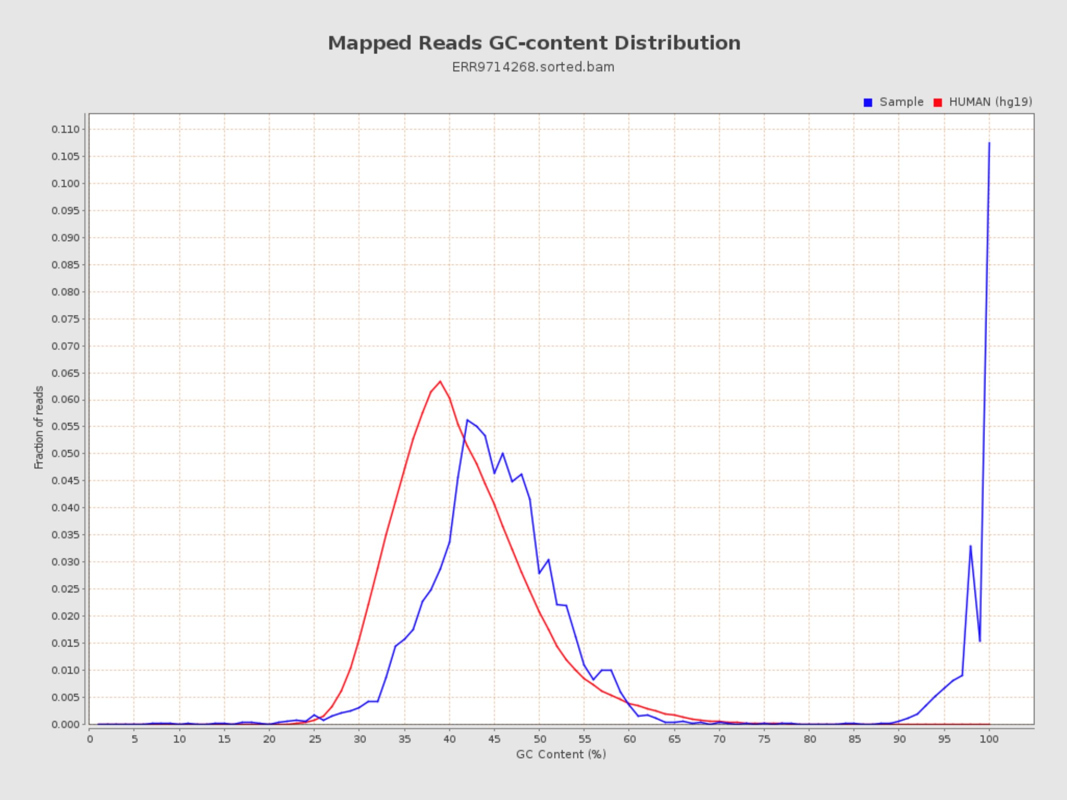
7. Results : Duplication Rate Histogram



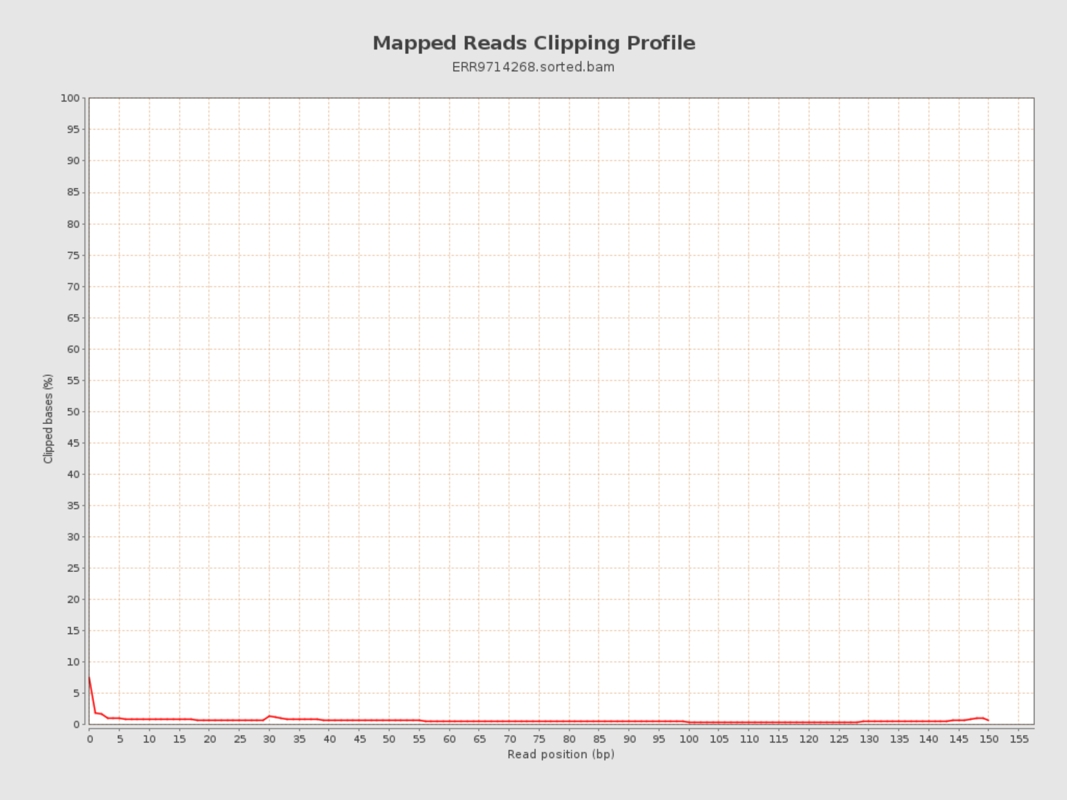
8. Results : Mapped Reads Nucleotide Content



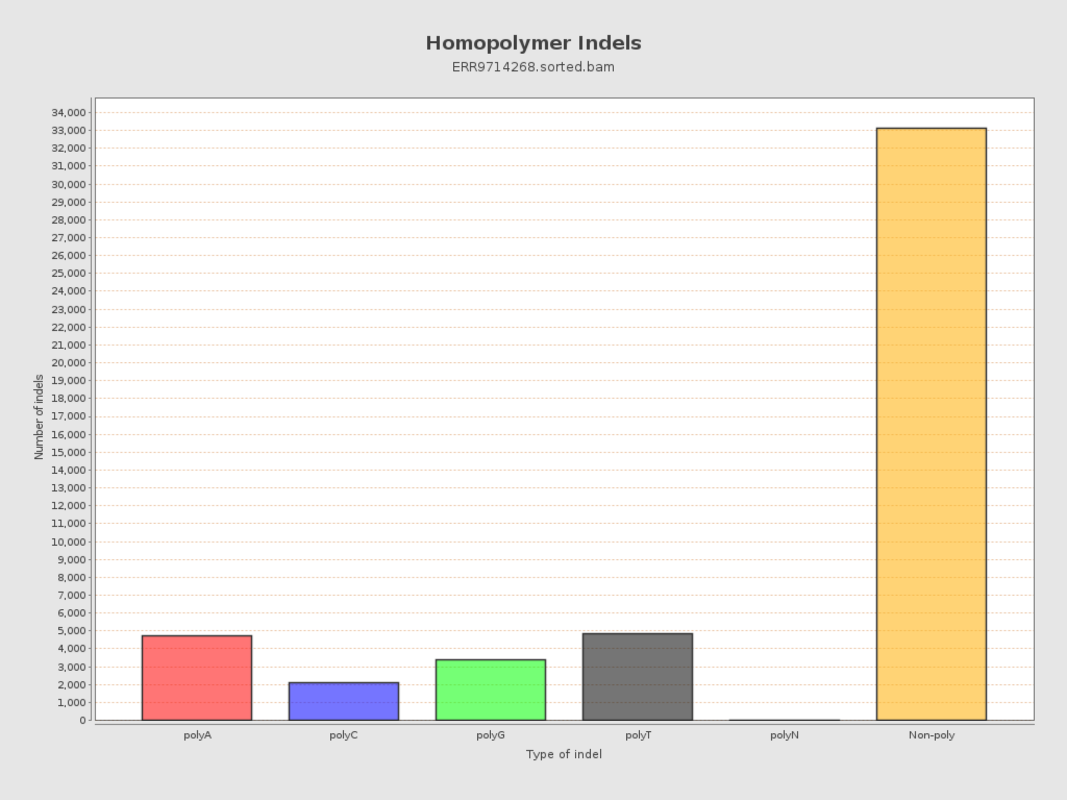
9. Results : Mapped Reads GC-content Distribution



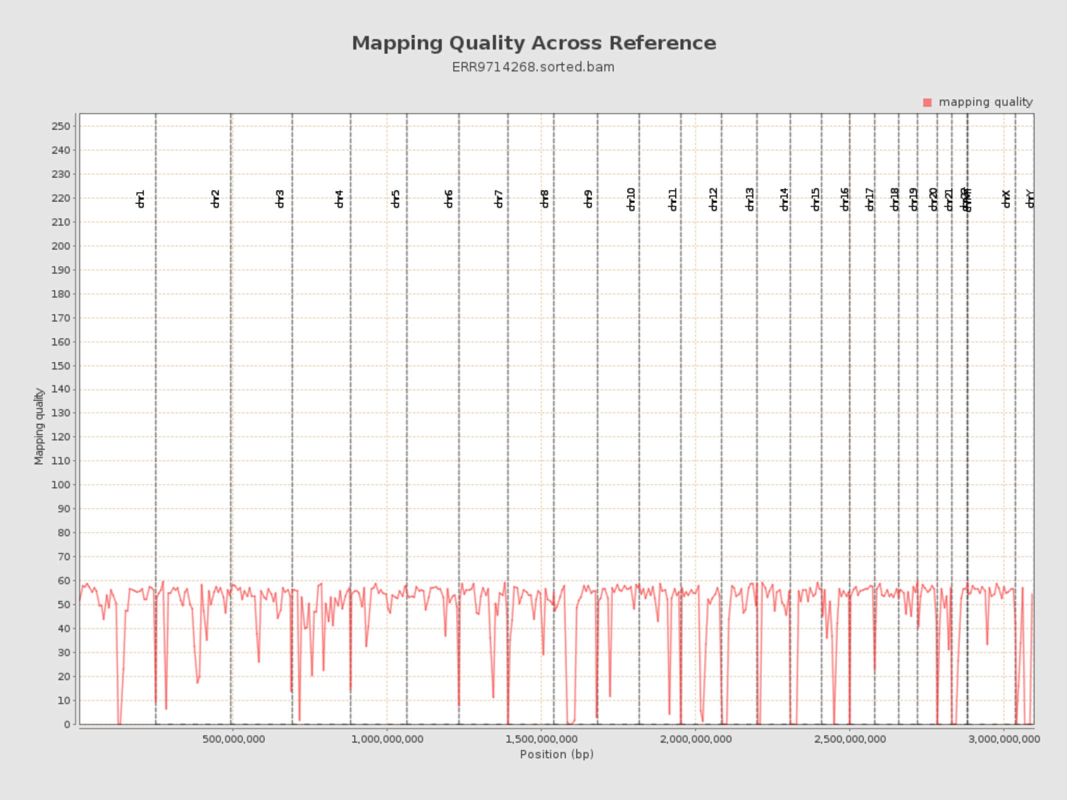
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram