Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:52:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714152.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_ERR9714152 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:52:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	720,660
Mapped reads	695,953 / 96.57%
Unmapped reads	24,707 / 3.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,963 / 1.8%
Read min/max/mean length	30 / 151 / 144.83
Duplicated reads (estimated)	673,009 / 93.39%
Duplication rate	35.34%
Clipped reads	655,098 / 90.9%

2.2. ACGT Content

Number/percentage of A's	26,303,335 / 29.23%
Number/percentage of C's	18,127,358 / 20.14%
Number/percentage of T's	25,955,822 / 28.84%
Number/percentage of G's	19,612,357 / 21.79%
Number/percentage of N's	690 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0297

Standard Deviation	34.2643

2.4. Mapping Quality

Mean Mapping Quality	37.18

2.5. Mismatches and indels

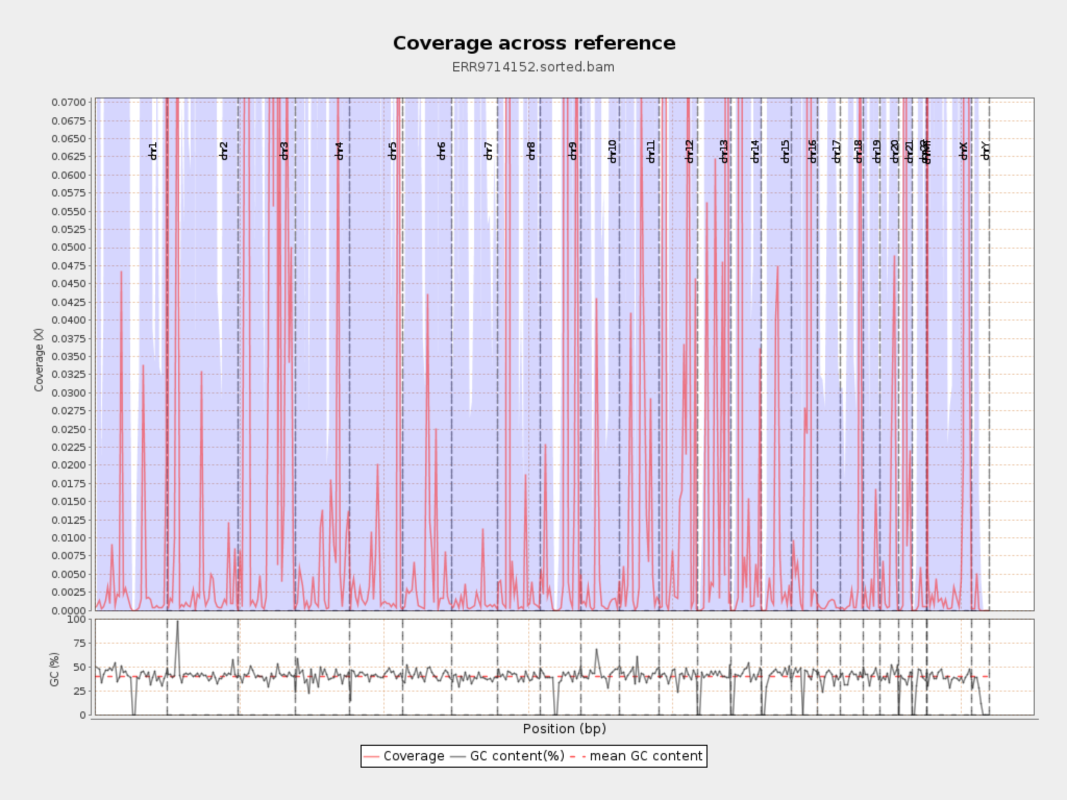
General error rate	3.88%
Mismatches	3,377,398
Insertions	53,298
Mapped reads with at least one insertion	7.46%
Deletions	373,458
Mapped reads with at least one deletion	51.07%
Homopolymer indels	32.26%

2.6. Chromosome stats

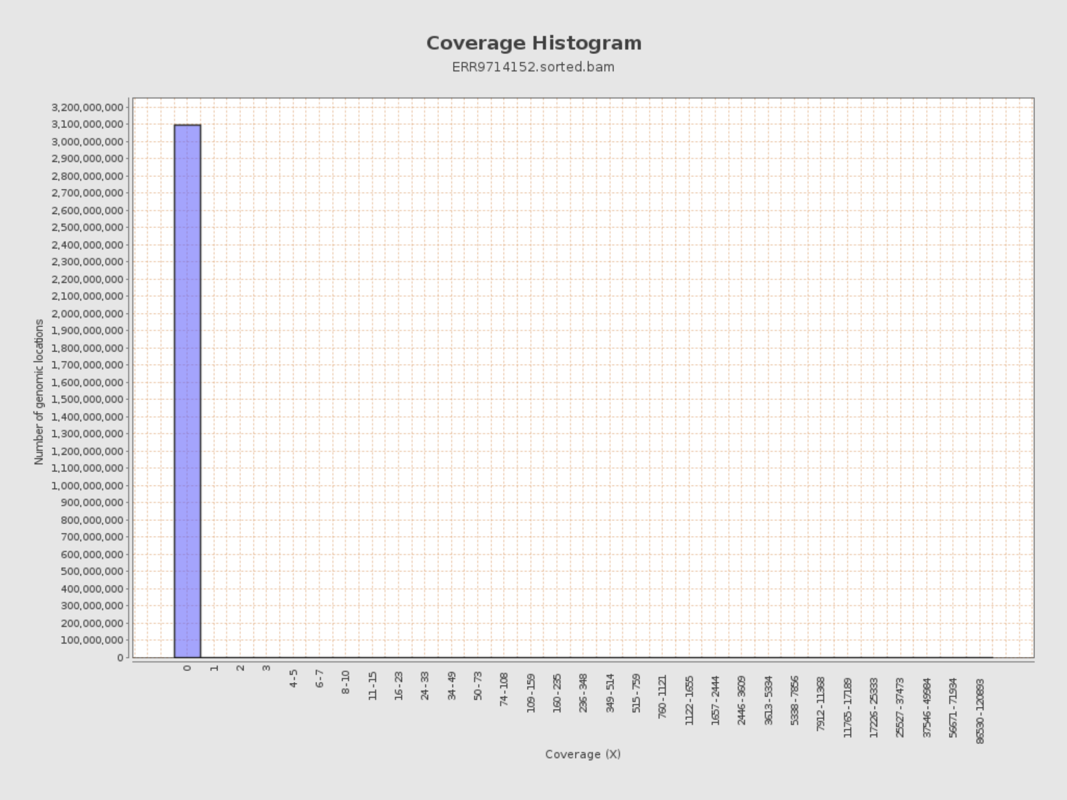
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2378699	0.0095	6.3538
chr2	243199373	1505338	0.0062	3.0145
chr3	198022430	23505851	0.1187	68.5954
chr4	191154276	1480518	0.0077	3.1179
chr5	180915260	1574480	0.0087	5.5785
chr6	171115067	973138	0.0057	1.9376
chr7	159138663	232790	0.0015	0.368

chr8	146364022	8145376	0.0557	37.0203
chr9	141213431	3564839	0.0252	14.5617
chr10	135534747	491727	0.0036	2.2559
chr11	135006516	1775495	0.0132	3.9635
chr12	133851895	10360692	0.0774	44.6656
chr13	115169878	3453073	0.03	12.6864
chr14	107349540	6446710	0.0601	43.9413
chr15	102531392	857360	0.0084	1.9284
chr16	90354753	17457763	0.1932	145.8623
chr17	81195210	57098	0.0007	0.1168
chr18	78077248	827024	0.0106	6.4028
chr19	59128983	201065	0.0034	1.2466
chr20	63025520	667751	0.0106	2.1187
chr21	48129895	1674920	0.0348	13.8841
chr22	51304566	61634	0.0012	0.4422
chrMT	16571	49126	2.9646	24.383
chrX	155270560	4179987	0.0269	11.4771
chrY	59373566	44592	0.0008	0.3465

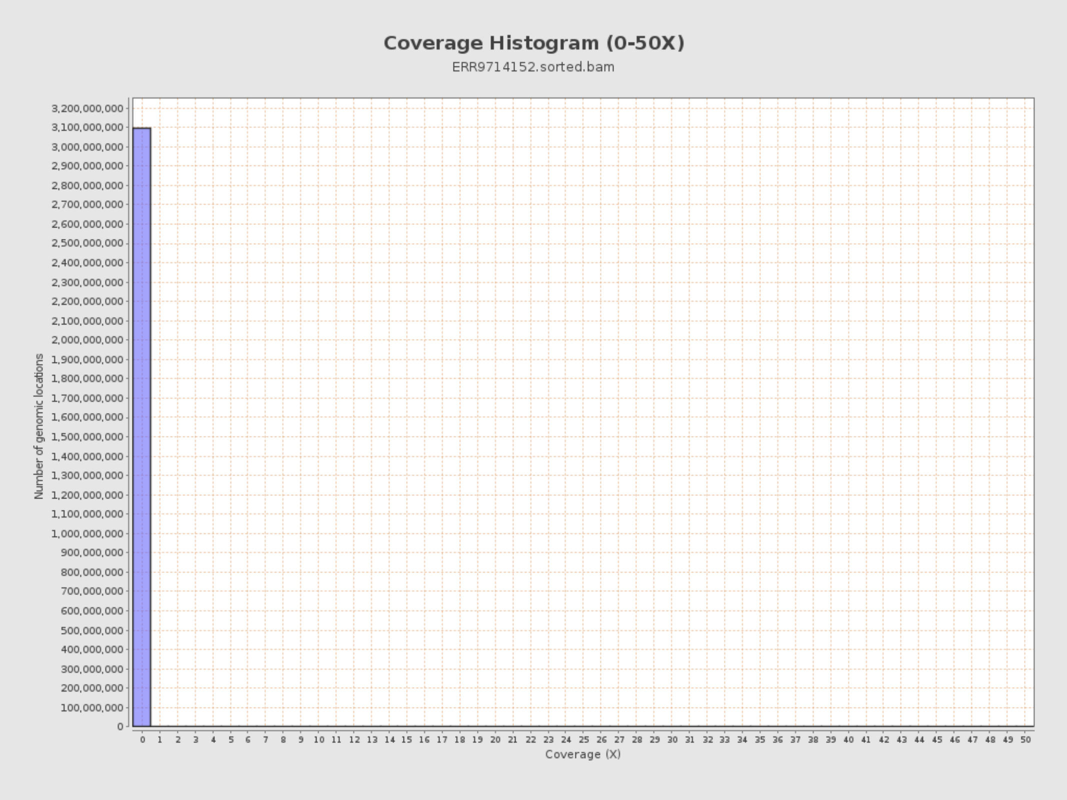
3. Results : Coverage across reference



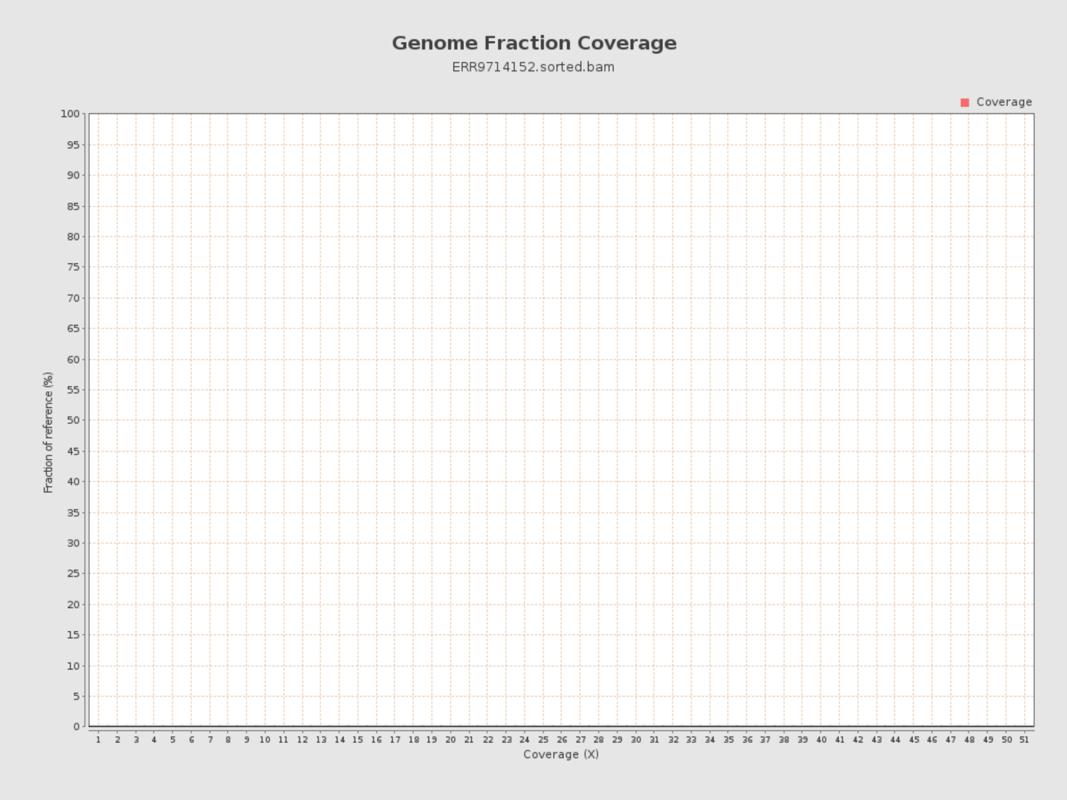
4. Results : Coverage Histogram



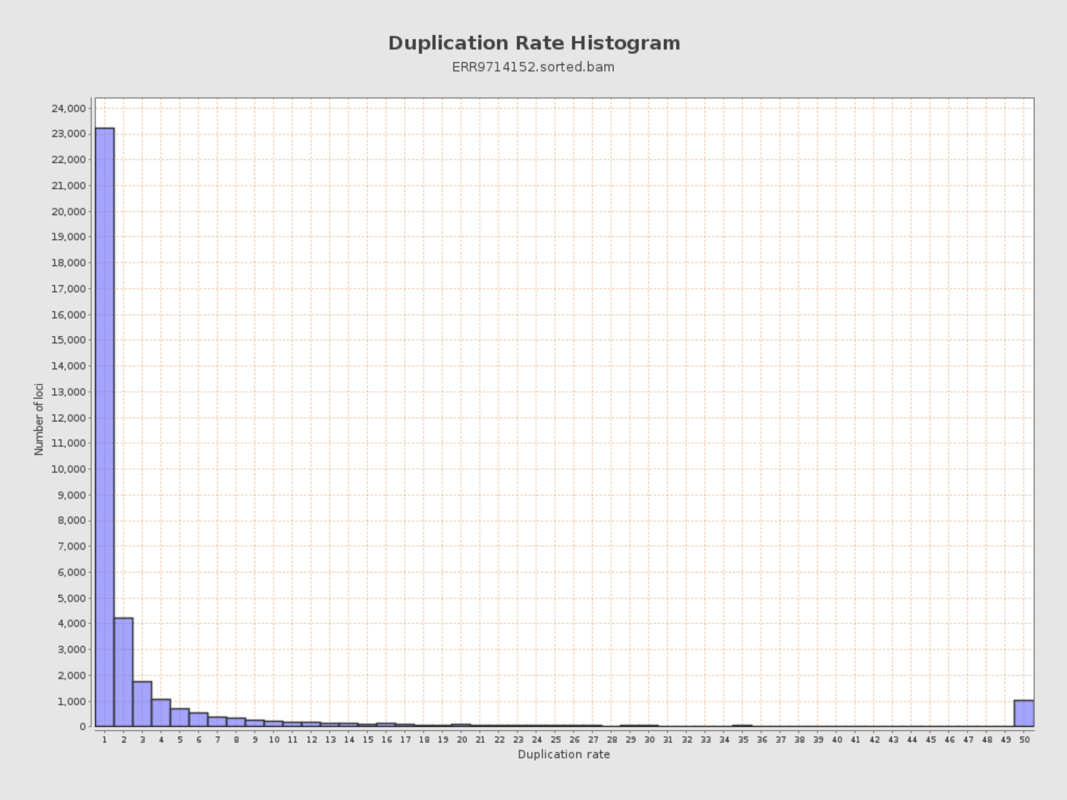
5. Results : Coverage Histogram (0-50X)



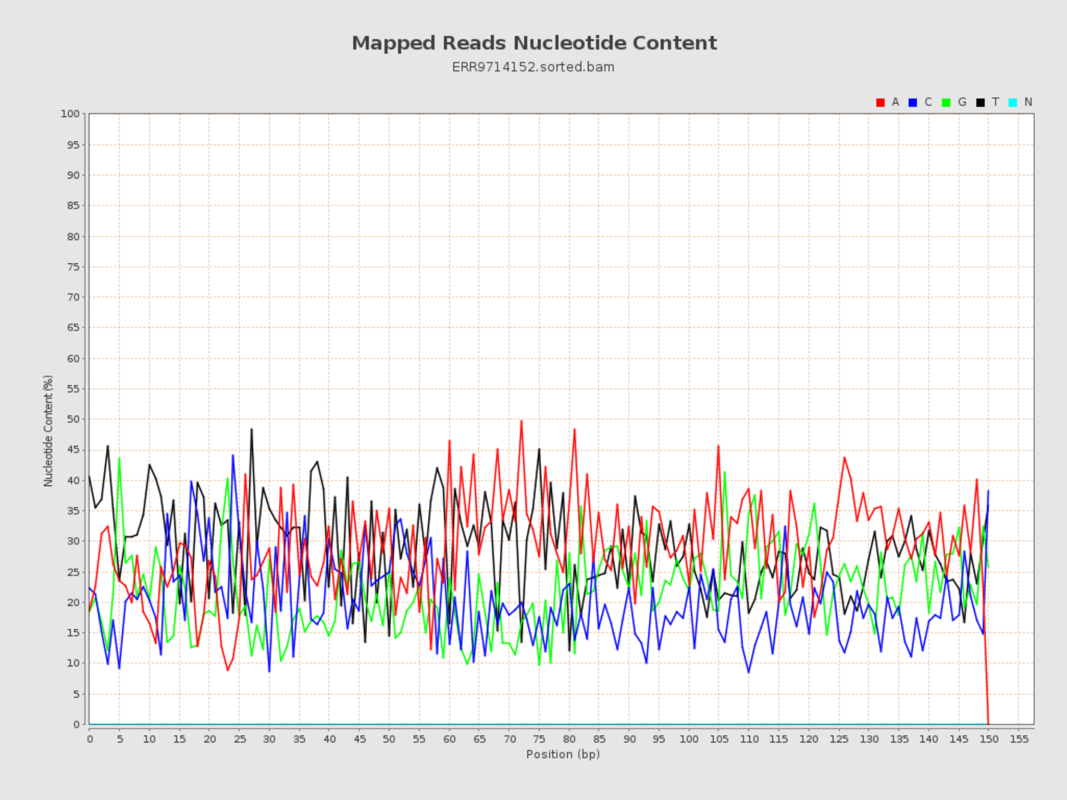
6. Results : Genome Fraction Coverage



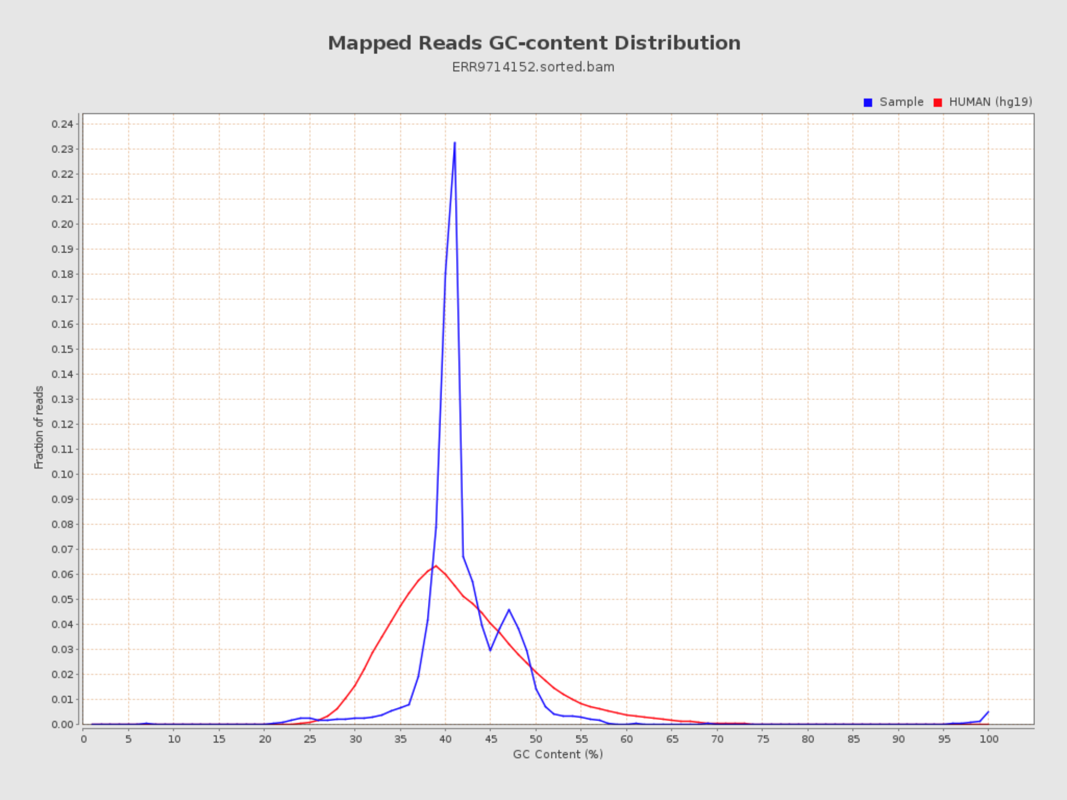
7. Results : Duplication Rate Histogram



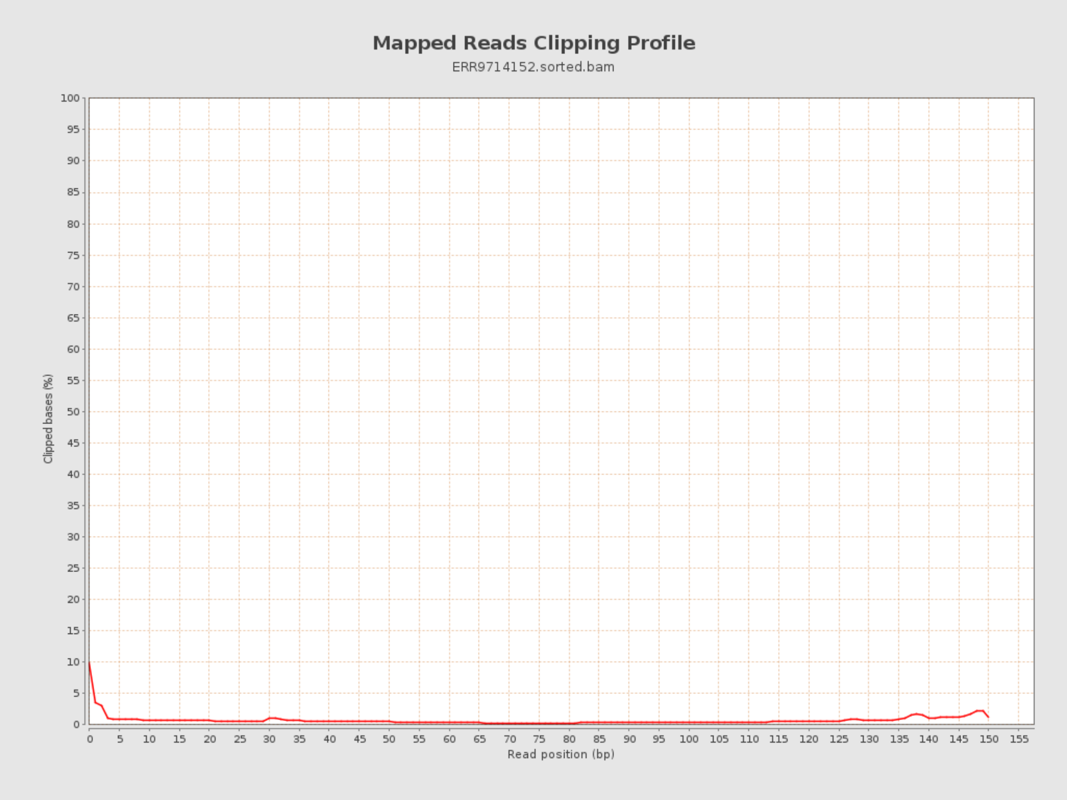
8. Results : Mapped Reads Nucleotide Content



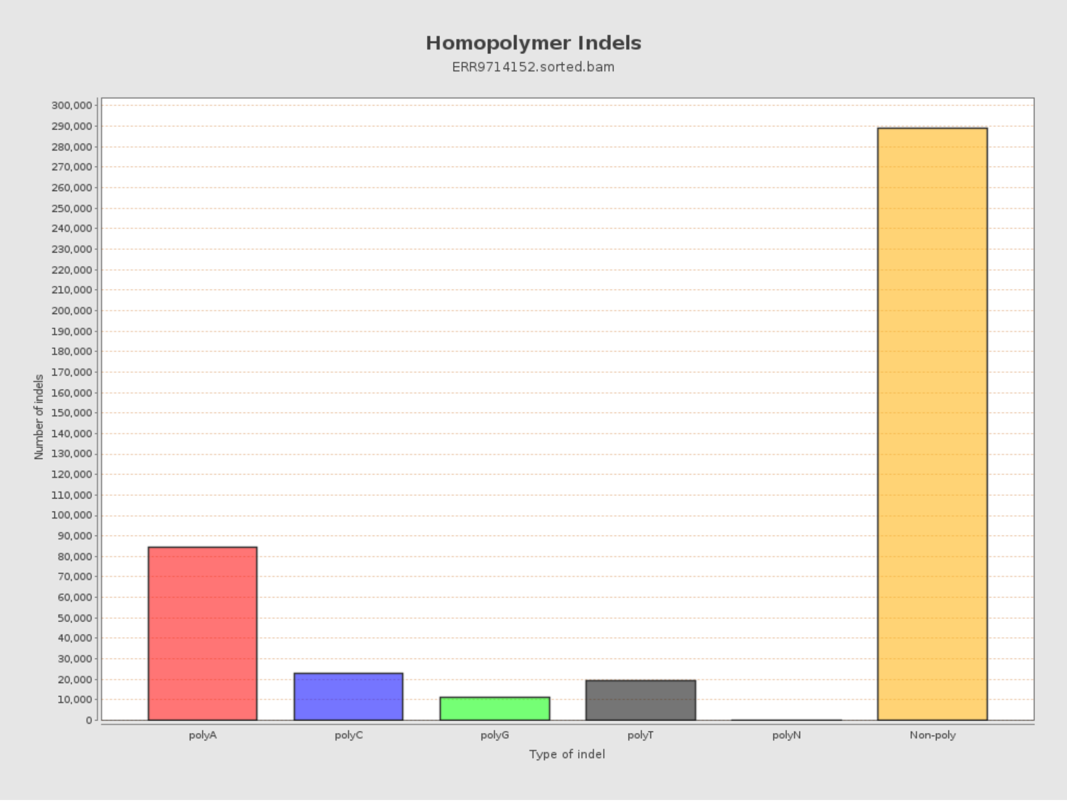
9. Results : Mapped Reads GC-content Distribution



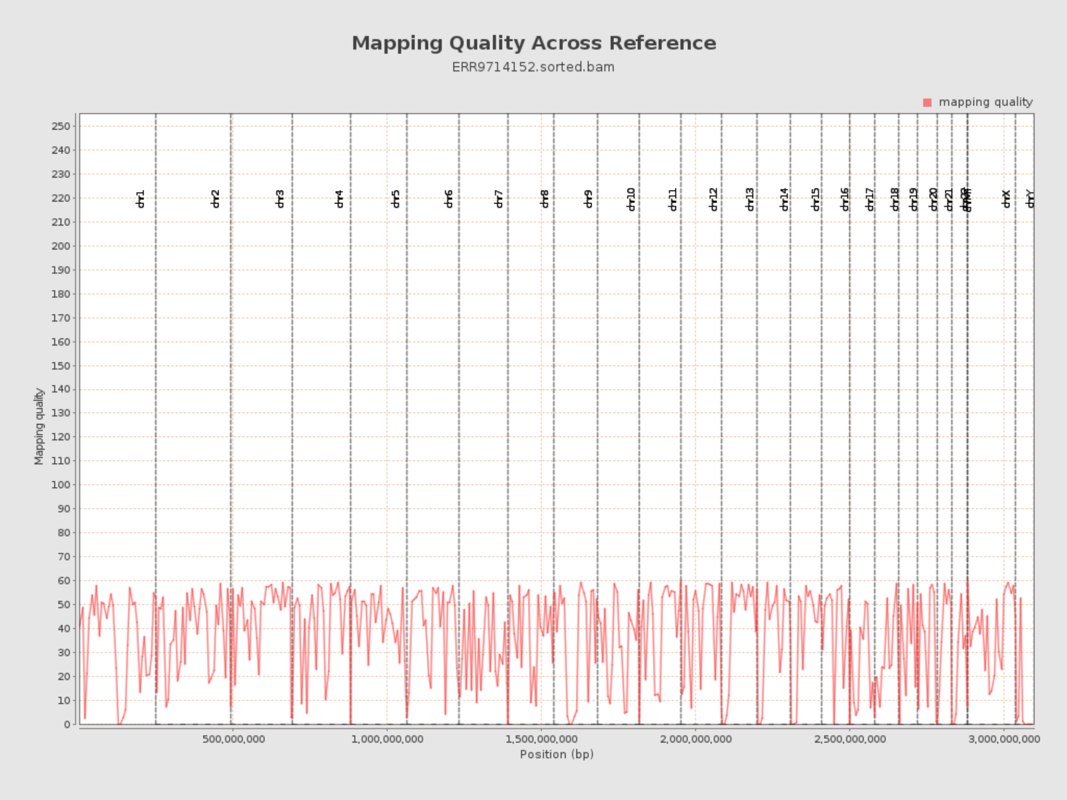
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram