Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:22:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714249.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_ERR9714249 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:22:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	361,044
Mapped reads	56,463 / 15.64%
Unmapped reads	304,581 / 84.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	933 / 0.26%
Read min/max/mean length	30 / 151 / 61.67
Duplicated reads (estimated)	55,302 / 15.32%
Duplication rate	32.28%
Clipped reads	28,740 / 7.96%

2.2. ACGT Content

Number/percentage of A's	118,572 / 2.01%
Number/percentage of C's	46,563 / 0.79%
Number/percentage of T's	60,021 / 1.02%
Number/percentage of G's	5,661,476 / 96.17%
Number/percentage of N's	144 / 0%
GC Percentage	96.96%

2.3. Coverage

Mean	0.0019

Standard Deviation	7.2576

2.4. Mapping Quality

Mean Mapping Quality	11.21

2.5. Mismatches and indels

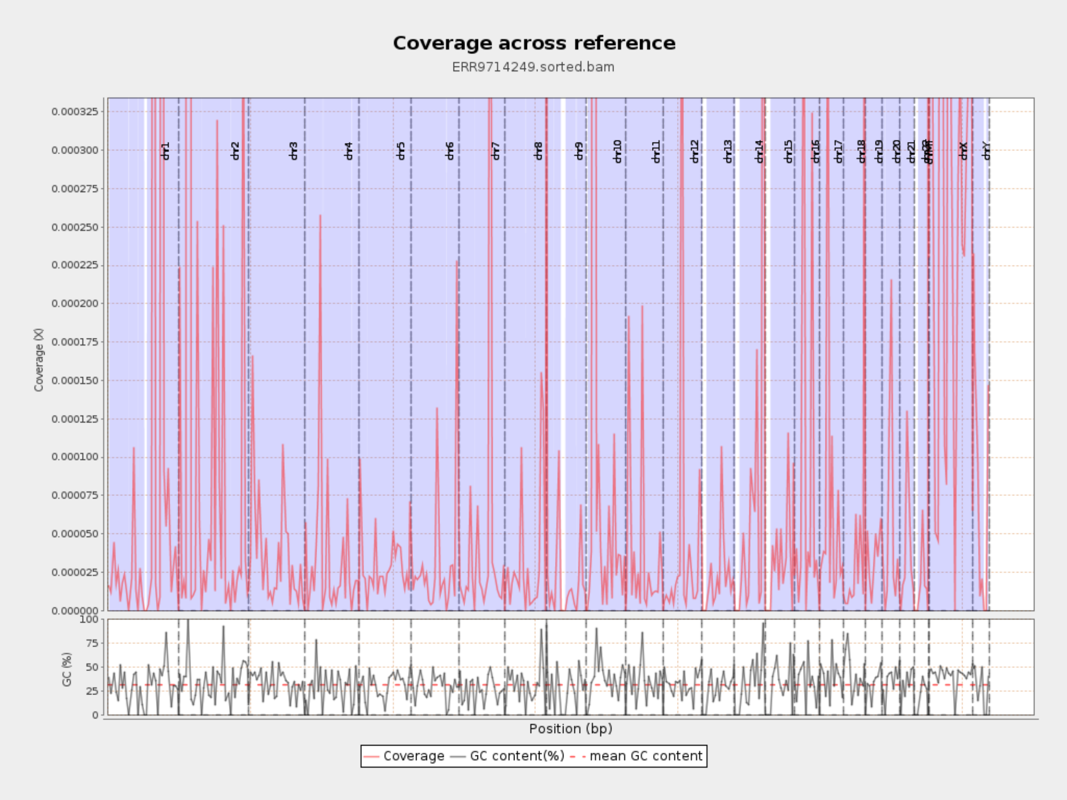
General error rate	3.3%
Mismatches	147,710
Insertions	6,825
Mapped reads with at least one insertion	8.24%
Deletions	2,838
Mapped reads with at least one deletion	4.79%
Homopolymer indels	63.05%

2.6. Chromosome stats

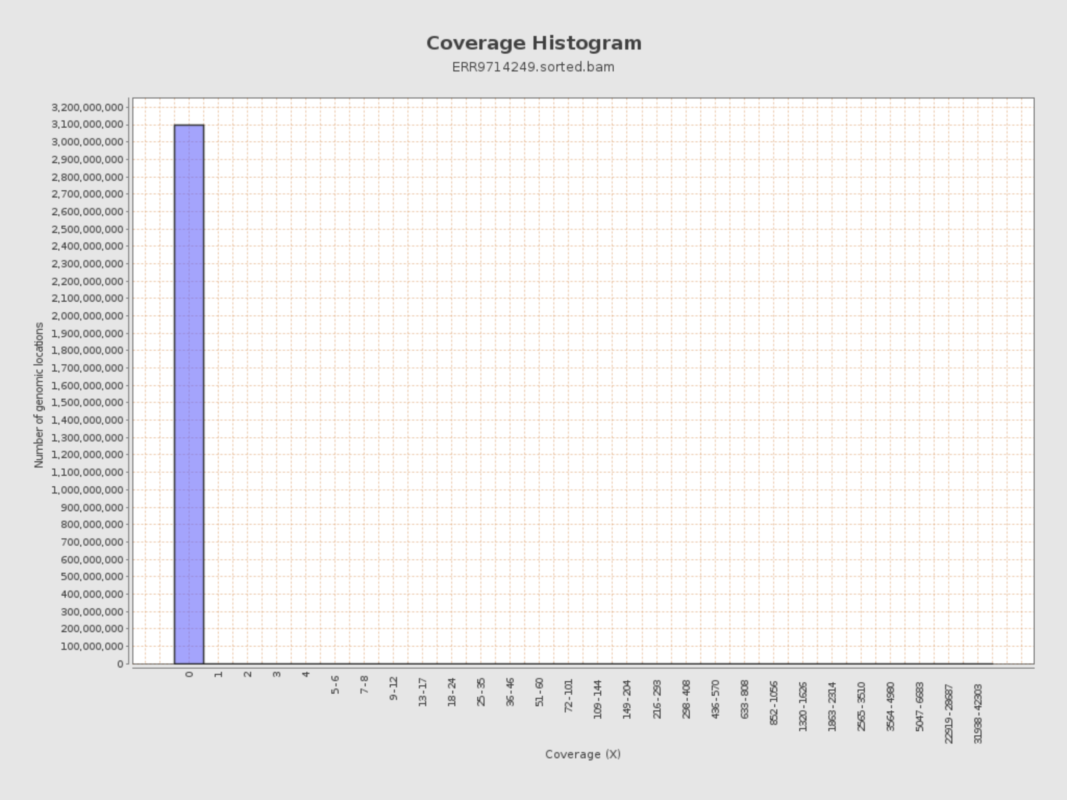
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28979	0.0001	0.1714
chr2	243199373	5691084	0.0234	25.8922
chr3	198022430	7290	0	0.0131
chr4	191154276	6593	0	0.0146
chr5	180915260	5233	0	0.0078
chr6	171115067	5631	0	0.0124
chr7	159138663	8752	0.0001	0.0724

chr8	146364022	4793	0	0.0164
chr9	141213431	3222	0	0.0109
chr10	135534747	19012	0.0001	0.2226
chr11	135006516	5006	0	0.0209
chr12	133851895	6665	0	0.038
chr13	115169878	2573	0	0.0094
chr14	107349540	9062	0.0001	0.0857
chr15	102531392	3347	0	0.0123
chr16	90354753	7872	0.0001	0.032
chr17	81195210	6475	0.0001	0.0651
chr18	78077248	4005	0.0001	0.0496
chr19	59128983	2031	0	0.0078
chr20	63025520	3453	0.0001	0.0144
chr21	48129895	2166	0	0.0136
chr22	51304566	878	0	0.0049
chrMT	16571	9066	0.5471	2.6306
chrX	155270560	50508	0.0003	0.0504
chrY	59373566	4626	0.0001	0.0214

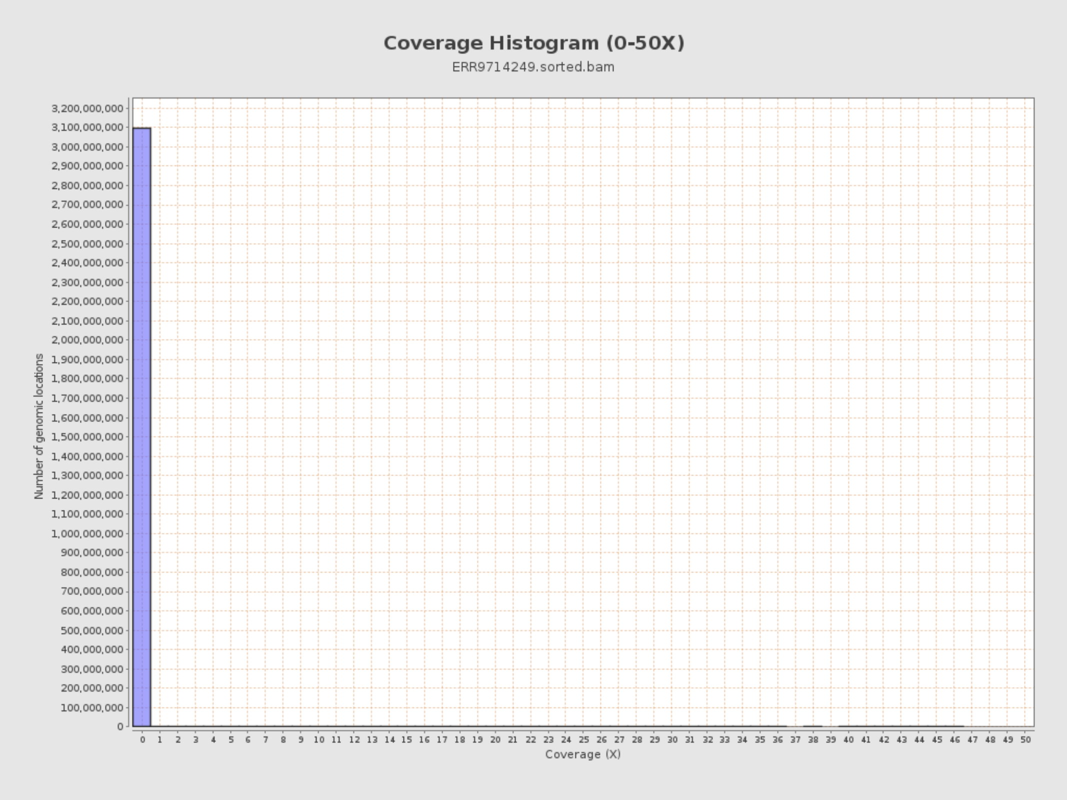
3. Results : Coverage across reference



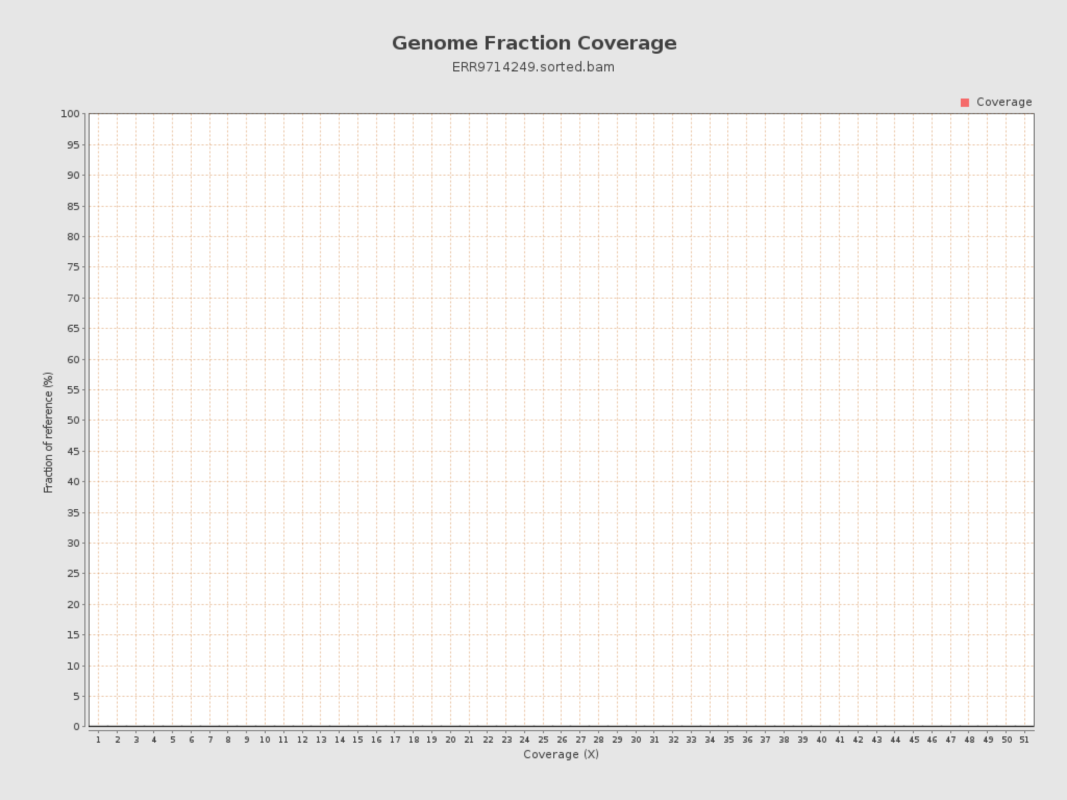
4. Results : Coverage Histogram



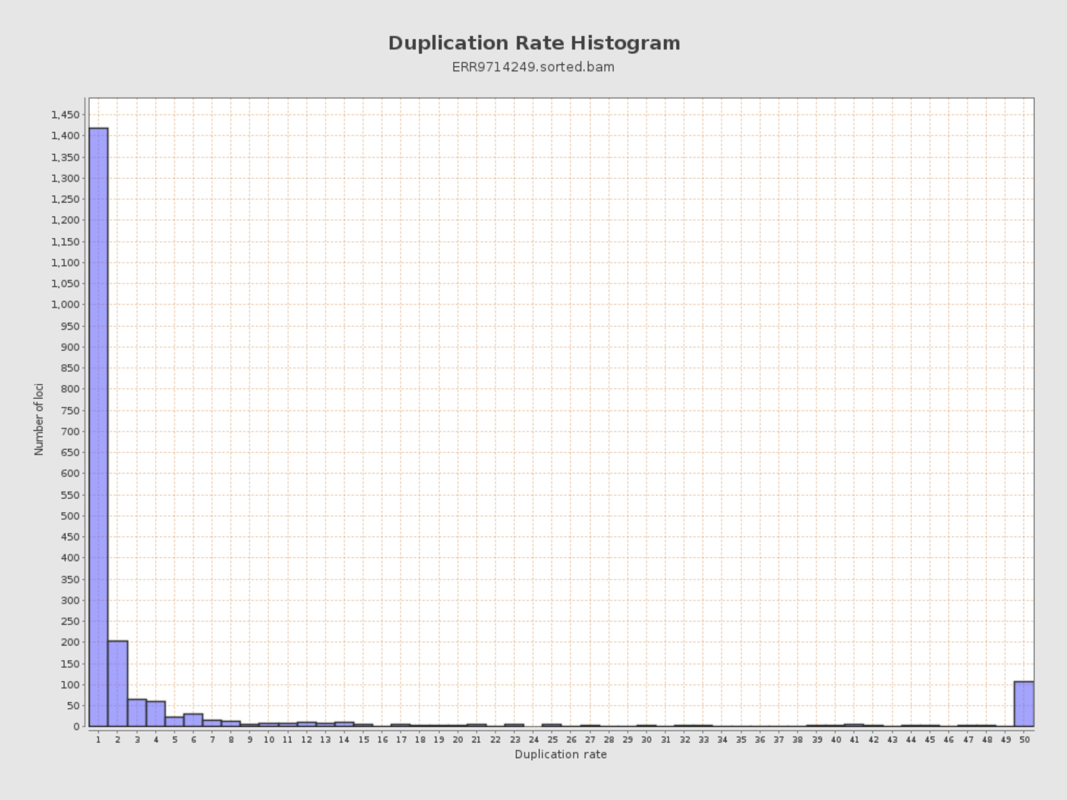
5. Results : Coverage Histogram (0-50X)



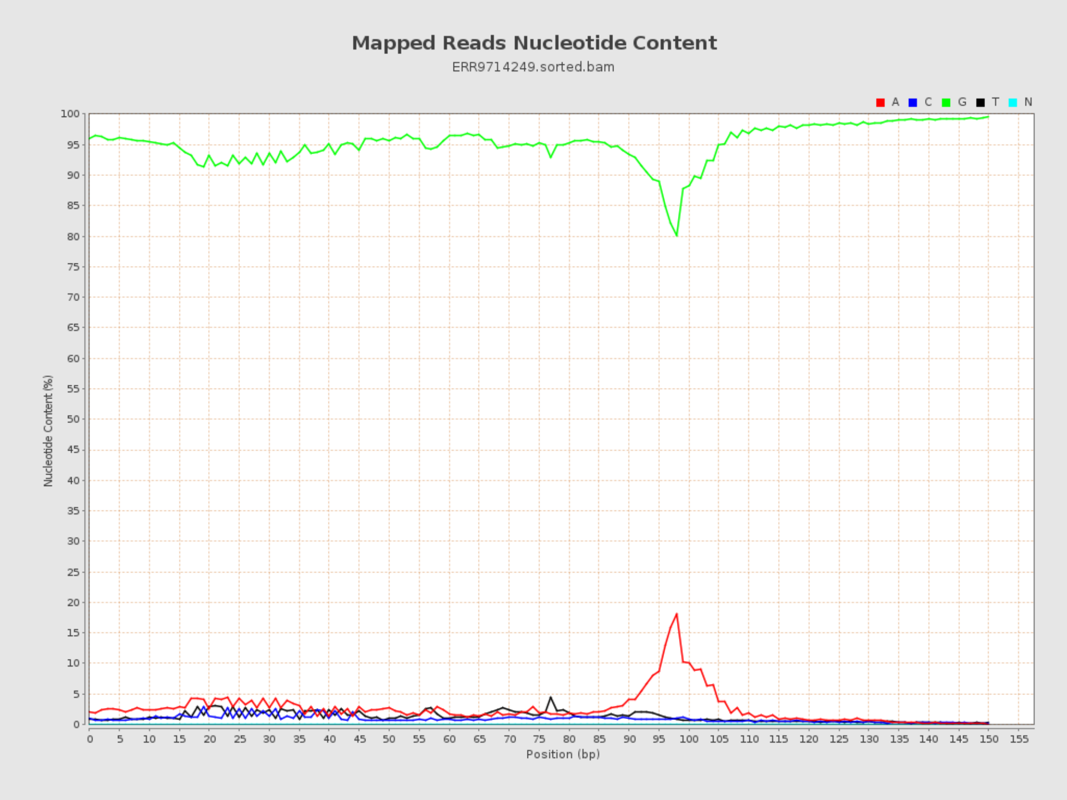
6. Results : Genome Fraction Coverage



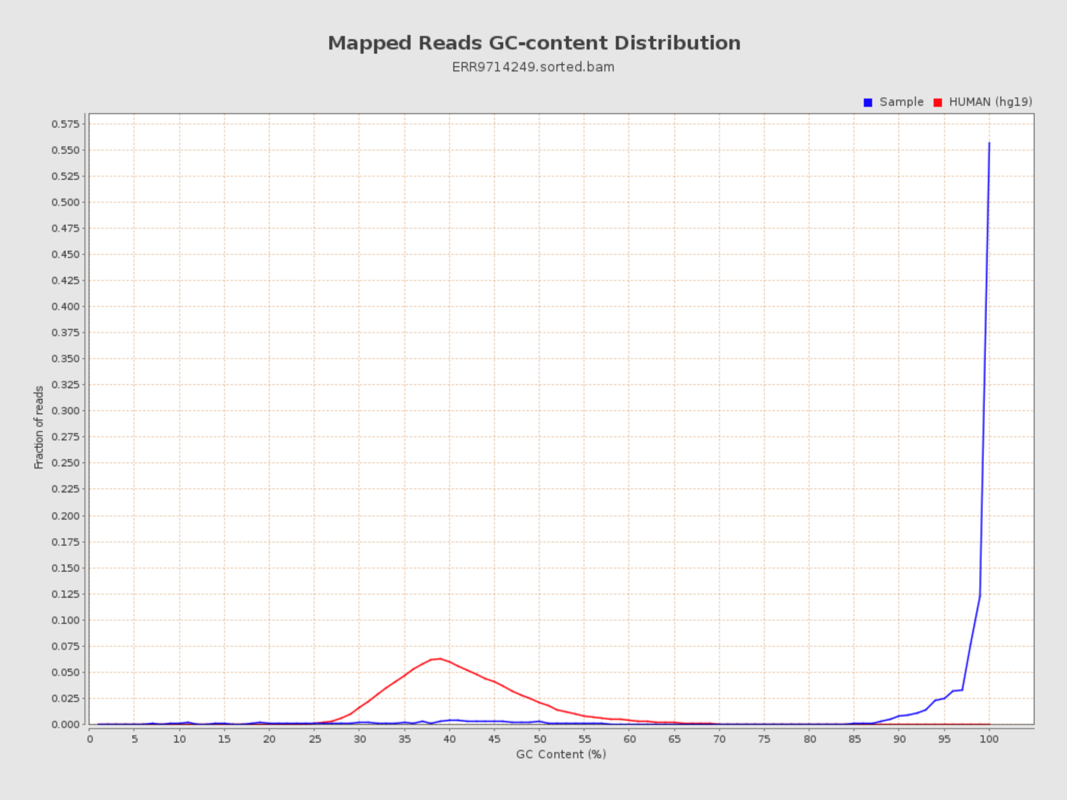
7. Results : Duplication Rate Histogram



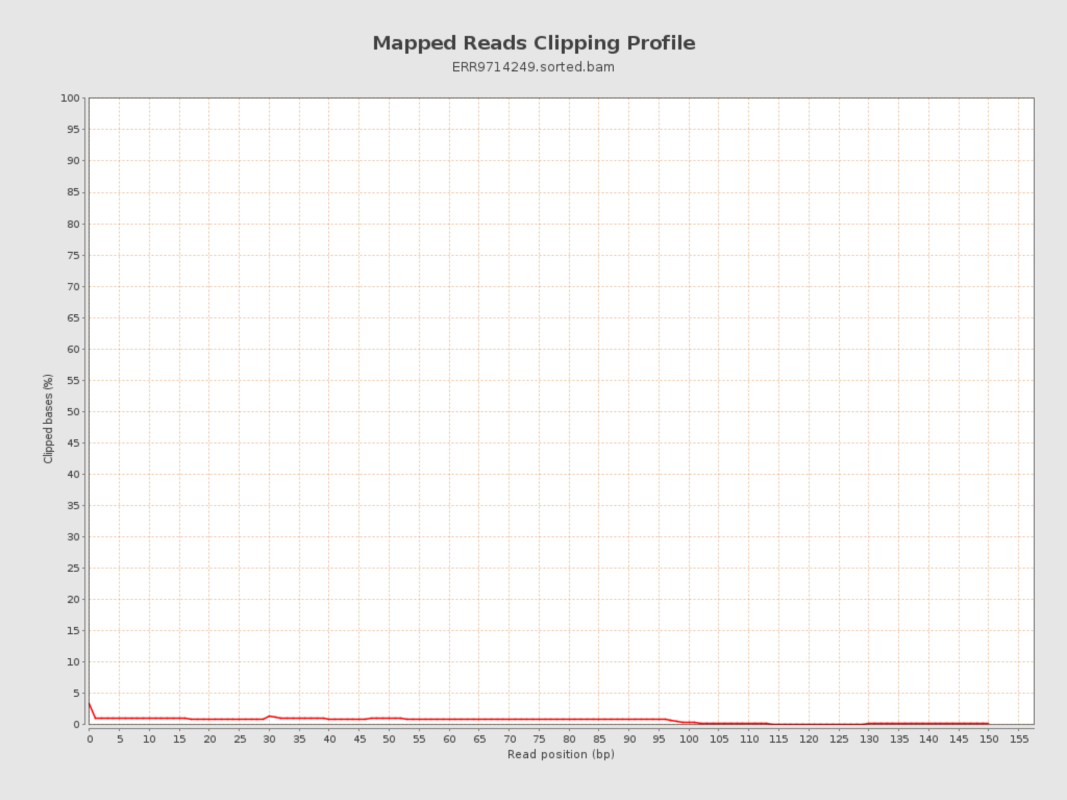
8. Results : Mapped Reads Nucleotide Content



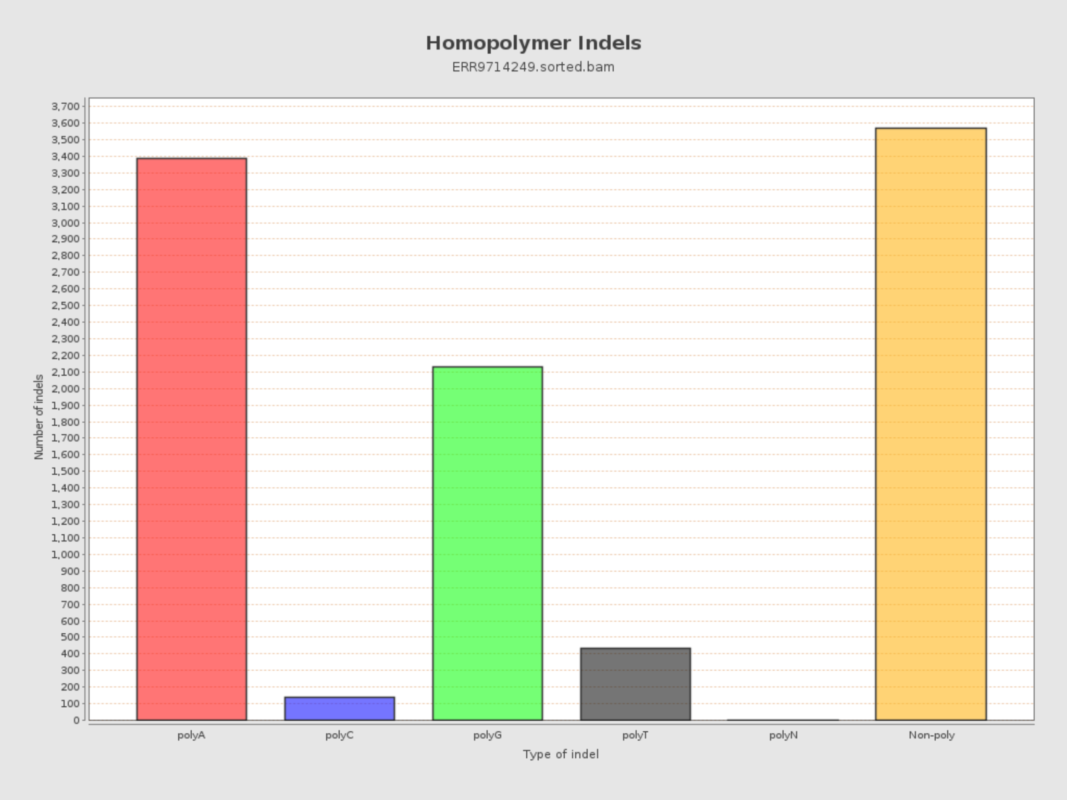
9. Results : Mapped Reads GC-content Distribution



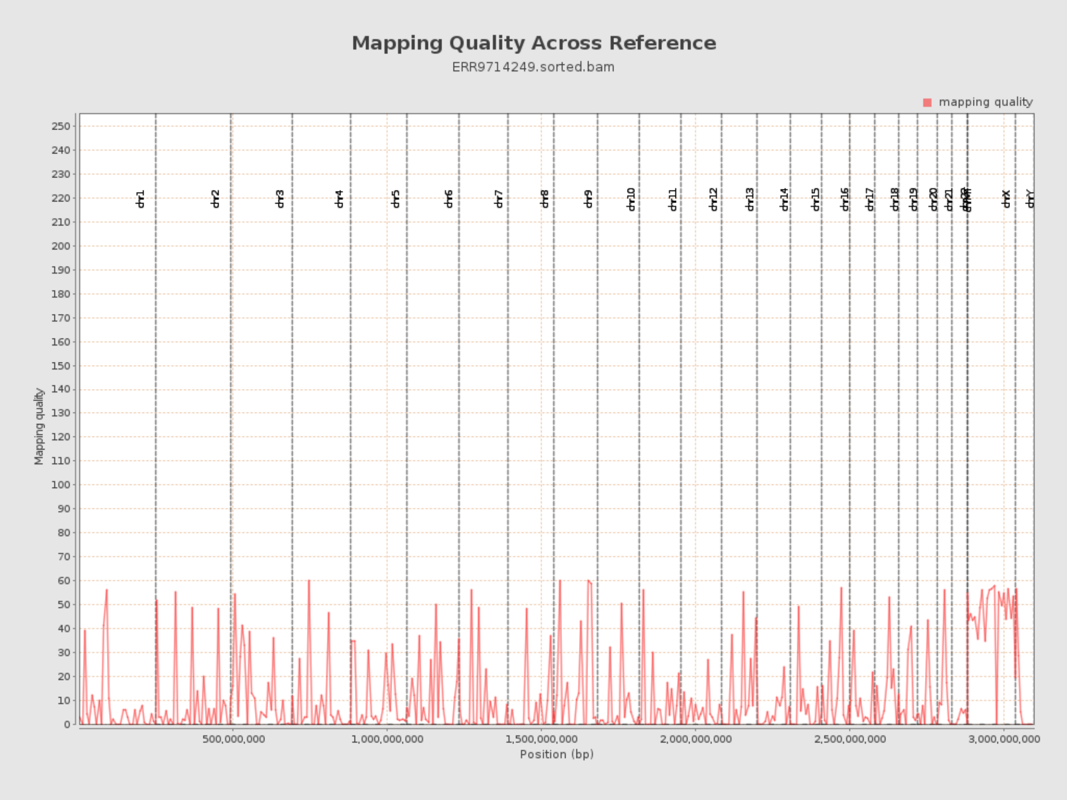
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram