Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:53:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714265.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_ERR9714265 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:53:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	293,344
Mapped reads	158,229 / 53.94%
Unmapped reads	135,115 / 46.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,047 / 1.72%
Read min/max/mean length	30 / 151 / 108.03
Duplicated reads (estimated)	131,700 / 44.9%
Duplication rate	43.15%
Clipped reads	141,103 / 48.1%

2.2. ACGT Content

Number/percentage of A's	4,960,591 / 25.26%
Number/percentage of C's	3,786,746 / 19.28%
Number/percentage of T's	4,716,865 / 24.02%
Number/percentage of G's	6,173,808 / 31.44%
Number/percentage of N's	200 / 0%
GC Percentage	50.72%

2.3. Coverage

Mean	0.0065

Standard Deviation	3.1884

2.4. Mapping Quality

Mean Mapping Quality	50.07

2.5. Mismatches and indels

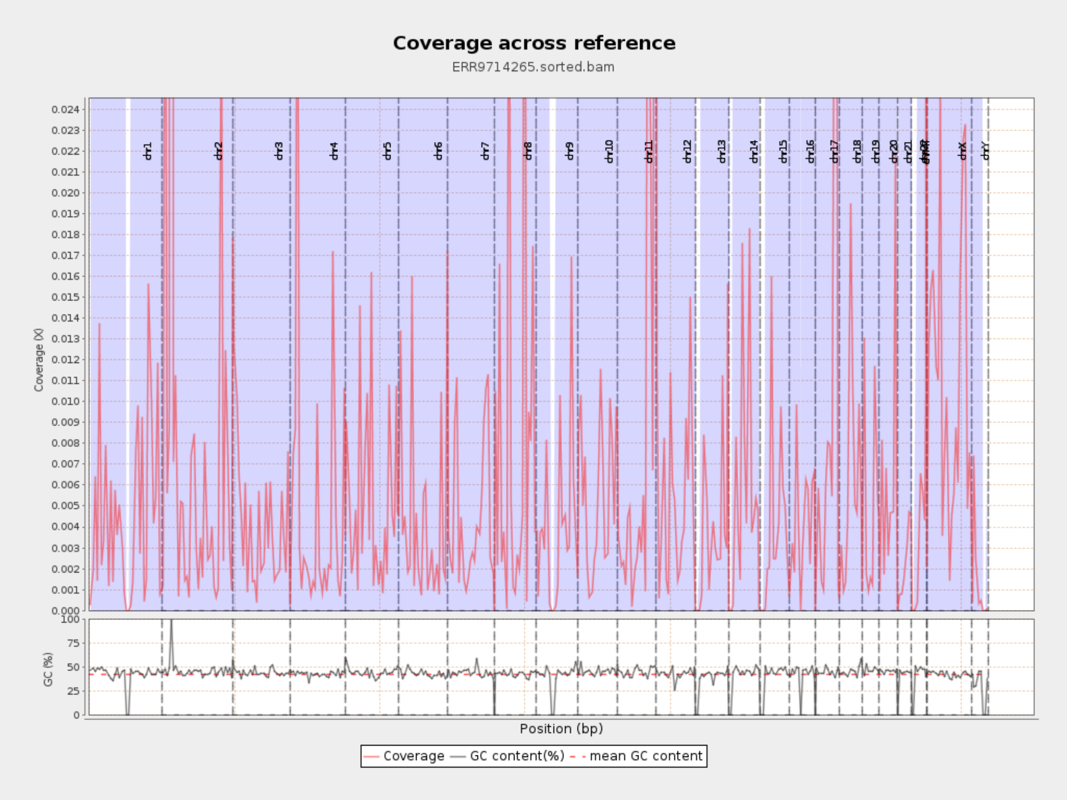
General error rate	4.52%
Mismatches	813,236
Insertions	23,329
Mapped reads with at least one insertion	13.75%
Deletions	69,667
Mapped reads with at least one deletion	40.06%
Homopolymer indels	32.13%

2.6. Chromosome stats

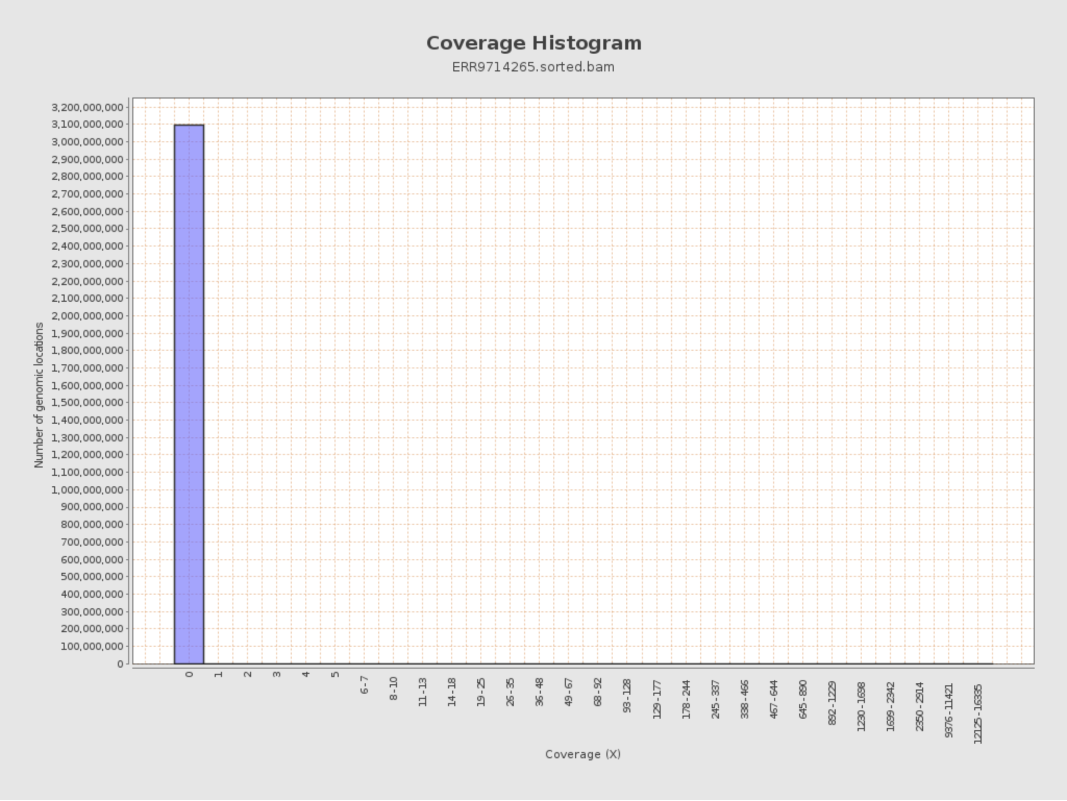
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1124318	0.0045	0.6905
chr2	243199373	3767716	0.0155	10.3658
chr3	198022430	853826	0.0043	0.8016
chr4	191154276	982993	0.0051	1.3478
chr5	180915260	974869	0.0054	1.036
chr6	171115067	738489	0.0043	0.7076
chr7	159138663	716353	0.0045	0.6883

chr8	146364022	1416678	0.0097	3.1533
chr9	141213431	571244	0.004	0.8118
chr10	135534747	770152	0.0057	0.8568
chr11	135006516	1269965	0.0094	2.7942
chr12	133851895	729316	0.0054	0.8427
chr13	115169878	404922	0.0035	0.7012
chr14	107349540	621735	0.0058	1.1267
chr15	102531392	408394	0.004	0.5425
chr16	90354753	387454	0.0043	0.5431
chr17	81195210	810903	0.01	2.1708
chr18	78077248	488079	0.0063	1.348
chr19	59128983	286186	0.0048	0.84
chr20	63025520	415201	0.0066	1.4303
chr21	48129895	106194	0.0022	0.2573
chr22	51304566	153102	0.003	0.4864
chrMT	16571	287408	17.344	131.8673
chrX	155270560	1691307	0.0109	1.4459
chrY	59373566	85286	0.0014	0.5238

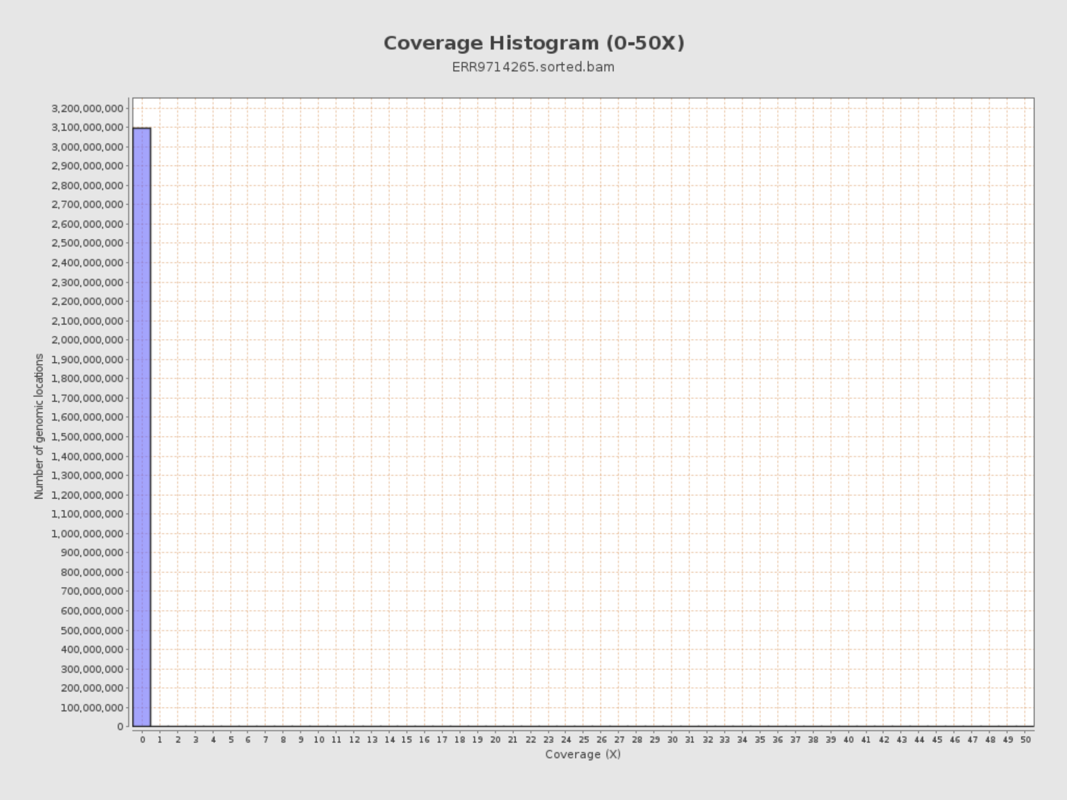
3. Results : Coverage across reference



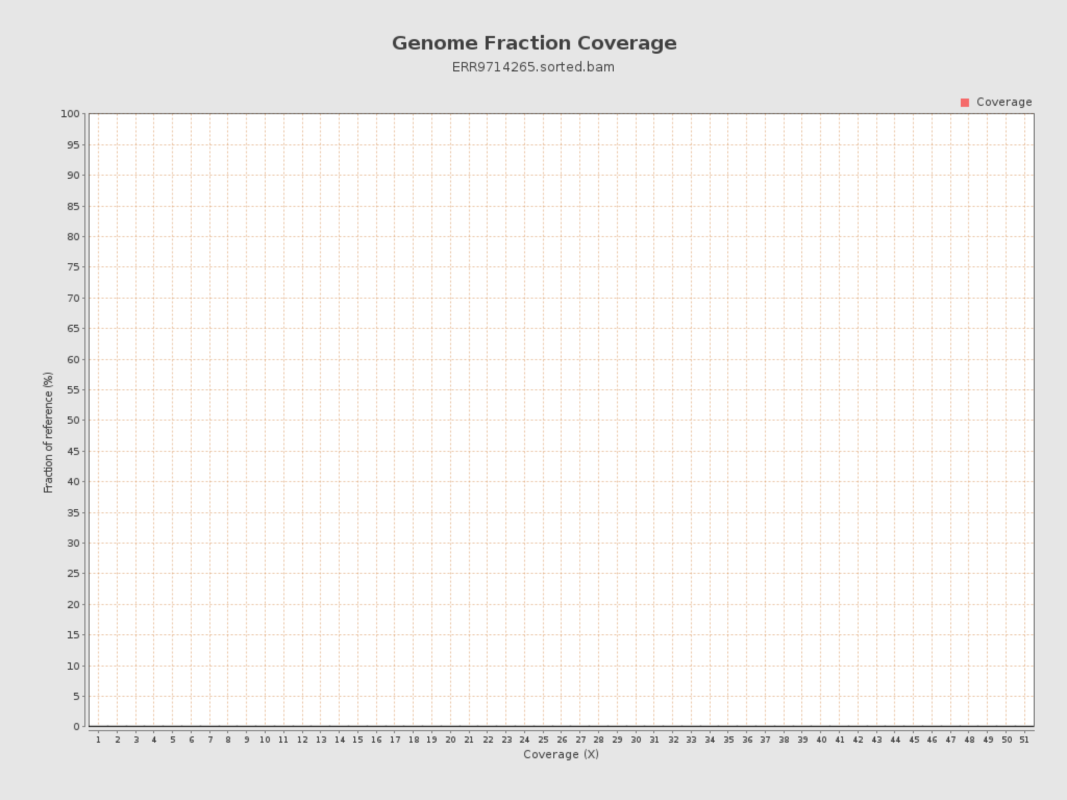
4. Results : Coverage Histogram



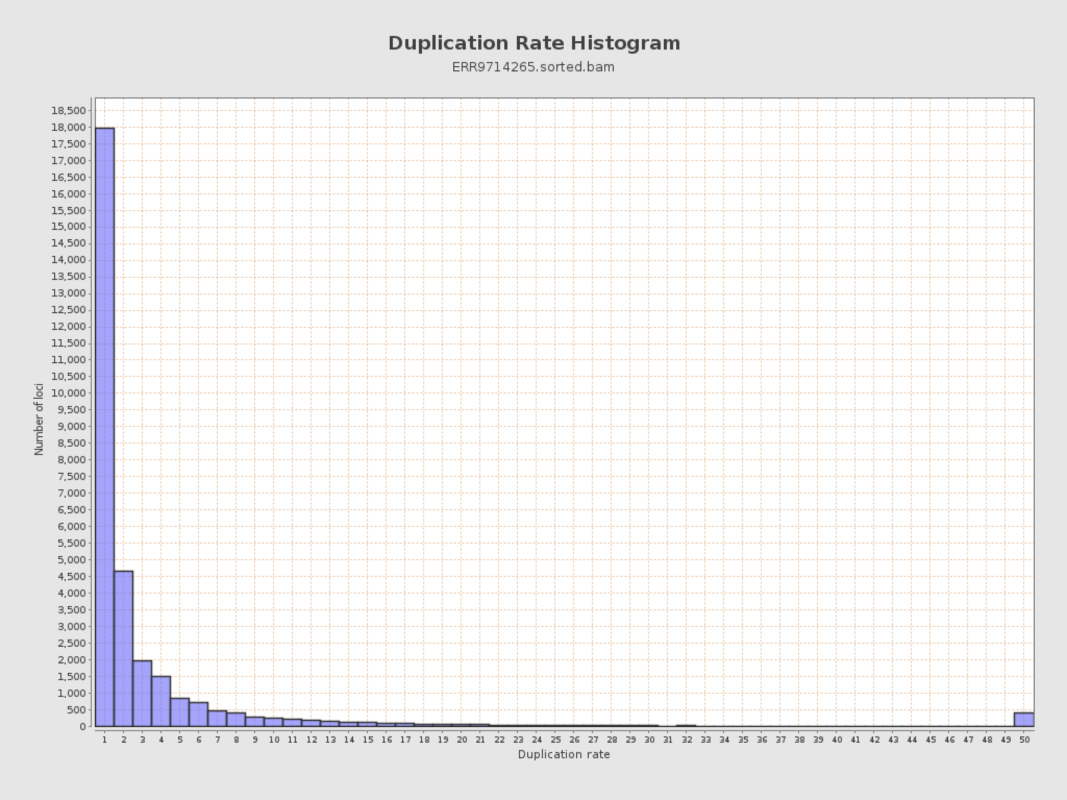
5. Results : Coverage Histogram (0-50X)



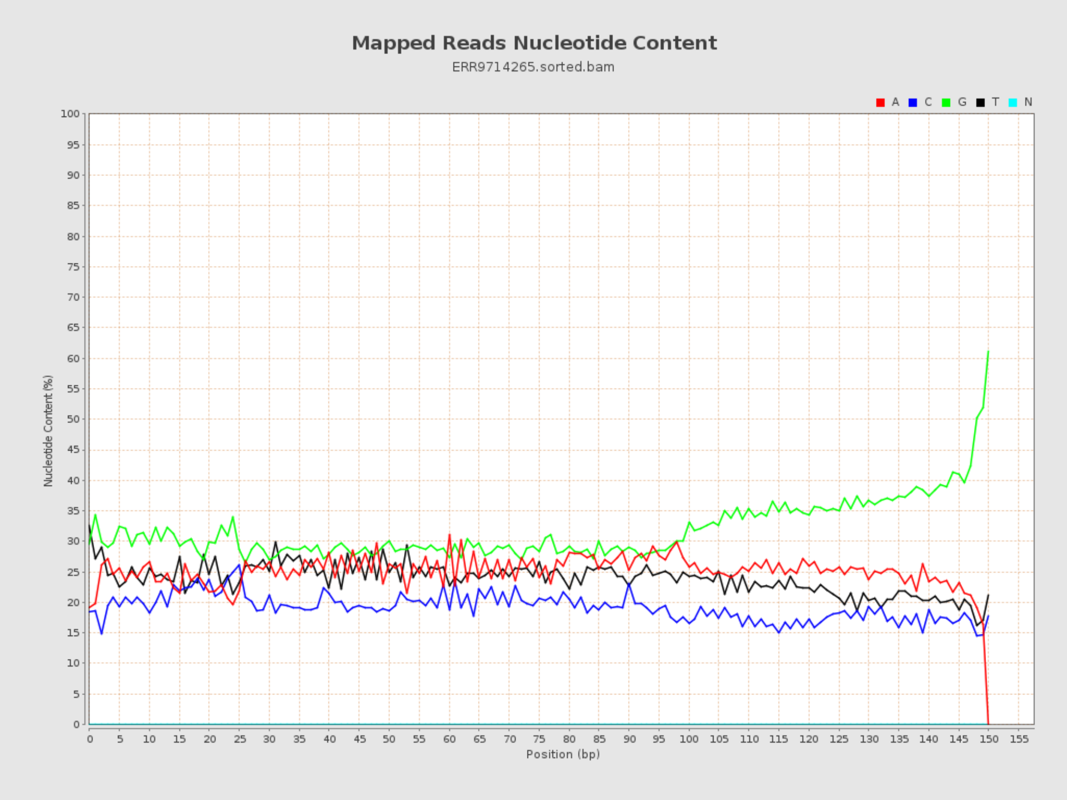
6. Results : Genome Fraction Coverage



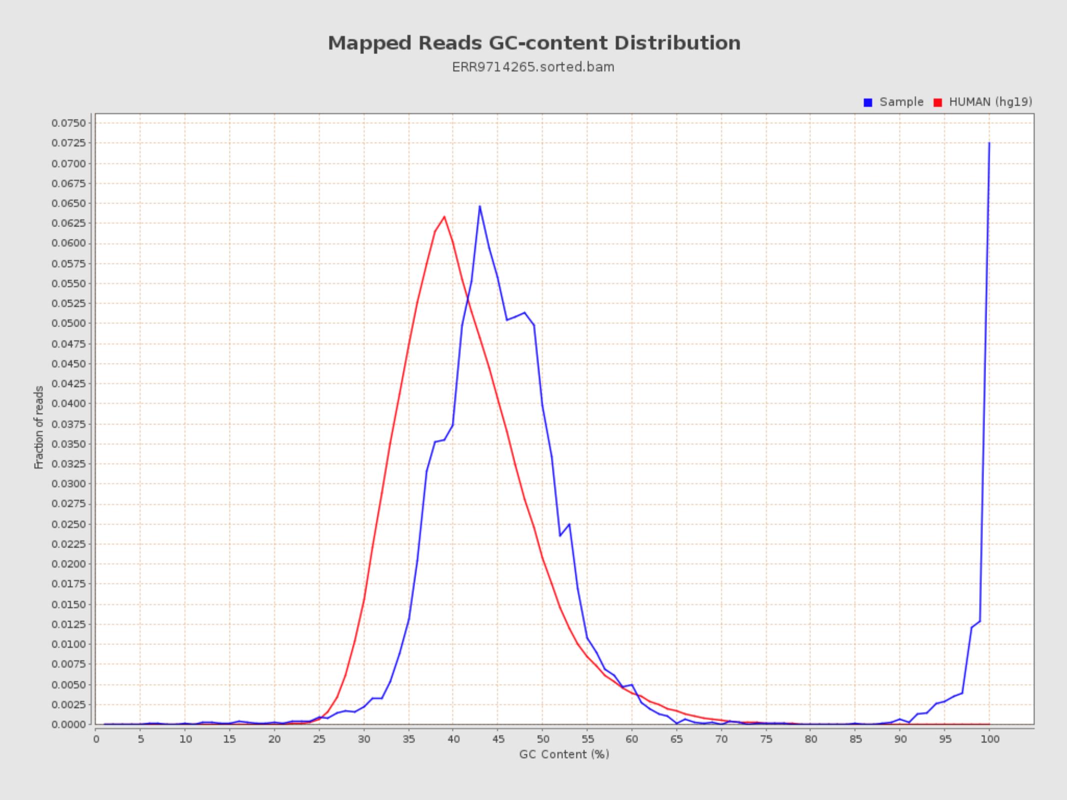
7. Results : Duplication Rate Histogram



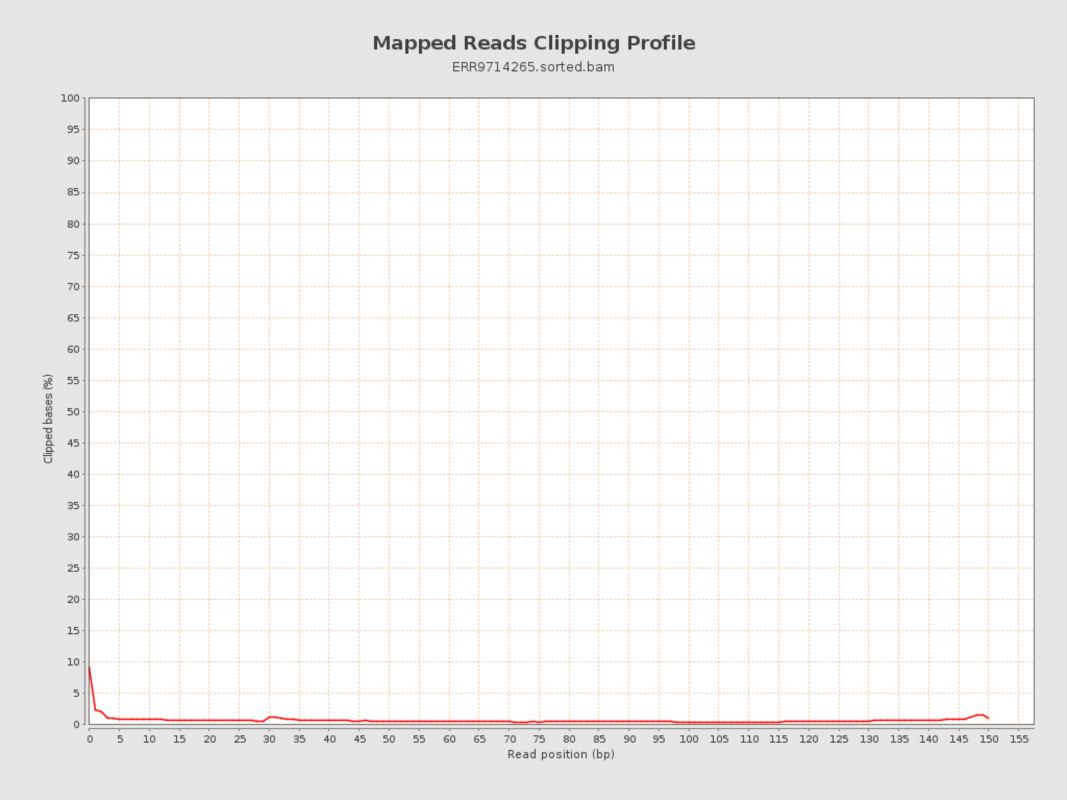
8. Results : Mapped Reads Nucleotide Content



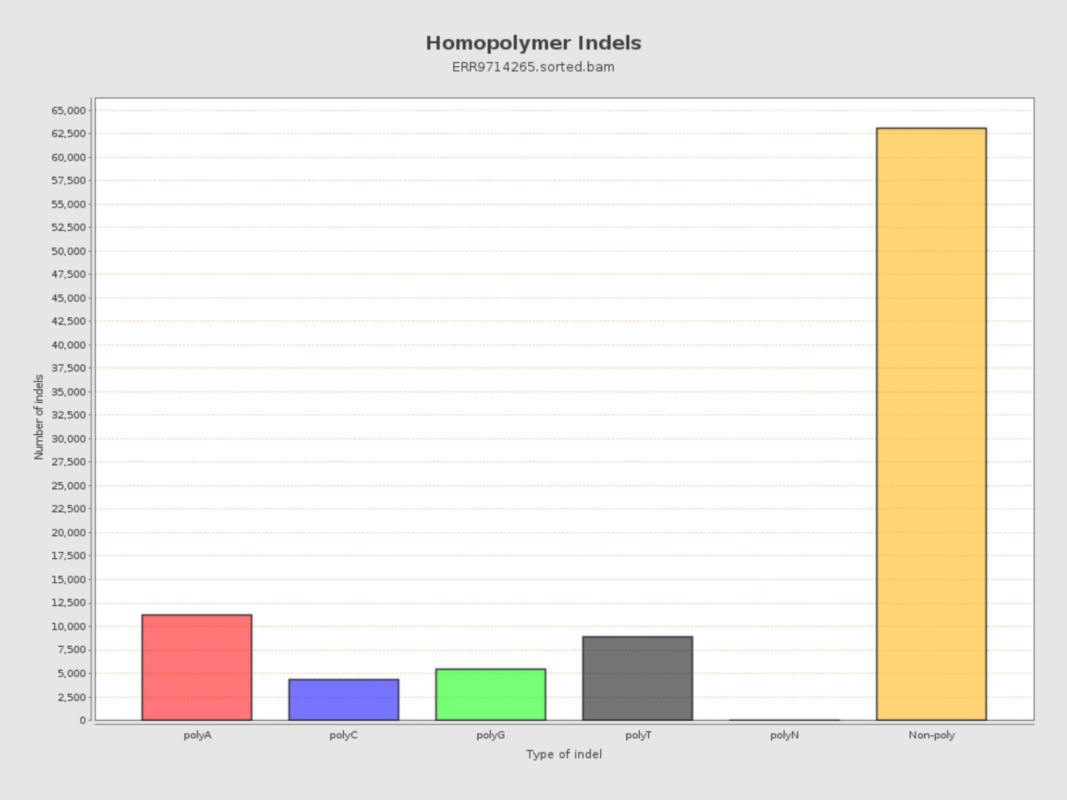
9. Results : Mapped Reads GC-content Distribution



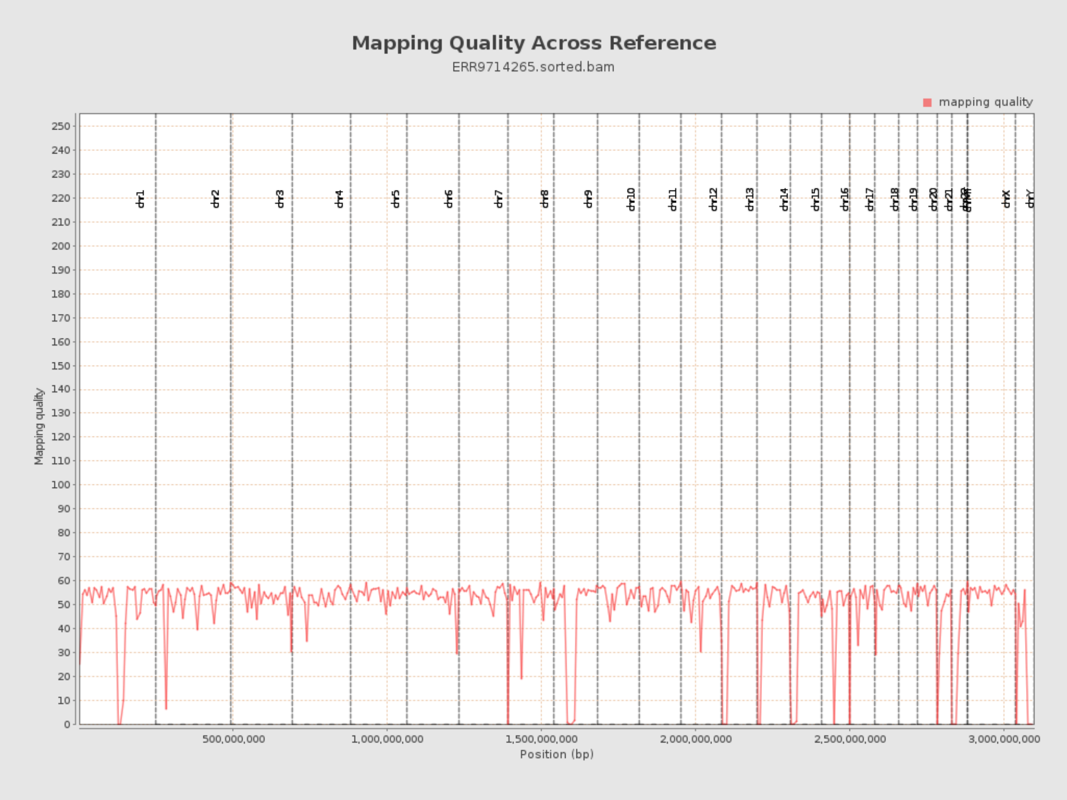
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram