Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:33:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714183.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_ERR9714183 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,139,164
Mapped reads	2,009,319 / 93.93%
Unmapped reads	129,845 / 6.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	118,662 / 5.55%
Read min/max/mean length	30 / 151 / 141.54
Duplicated reads (estimated)	1,914,084 / 89.48%
Duplication rate	46.97%
Clipped reads	1,971,836 / 92.18%

2.2. ACGT Content

Number/percentage of A's	74,004,110 / 29.46%
Number/percentage of C's	51,550,582 / 20.52%
Number/percentage of T's	69,413,258 / 27.63%
Number/percentage of G's	56,253,009 / 22.39%
Number/percentage of N's	1,959 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.083

Standard Deviation	15.5395

2.4. Mapping Quality

Mean Mapping Quality	50.94

2.5. Mismatches and indels

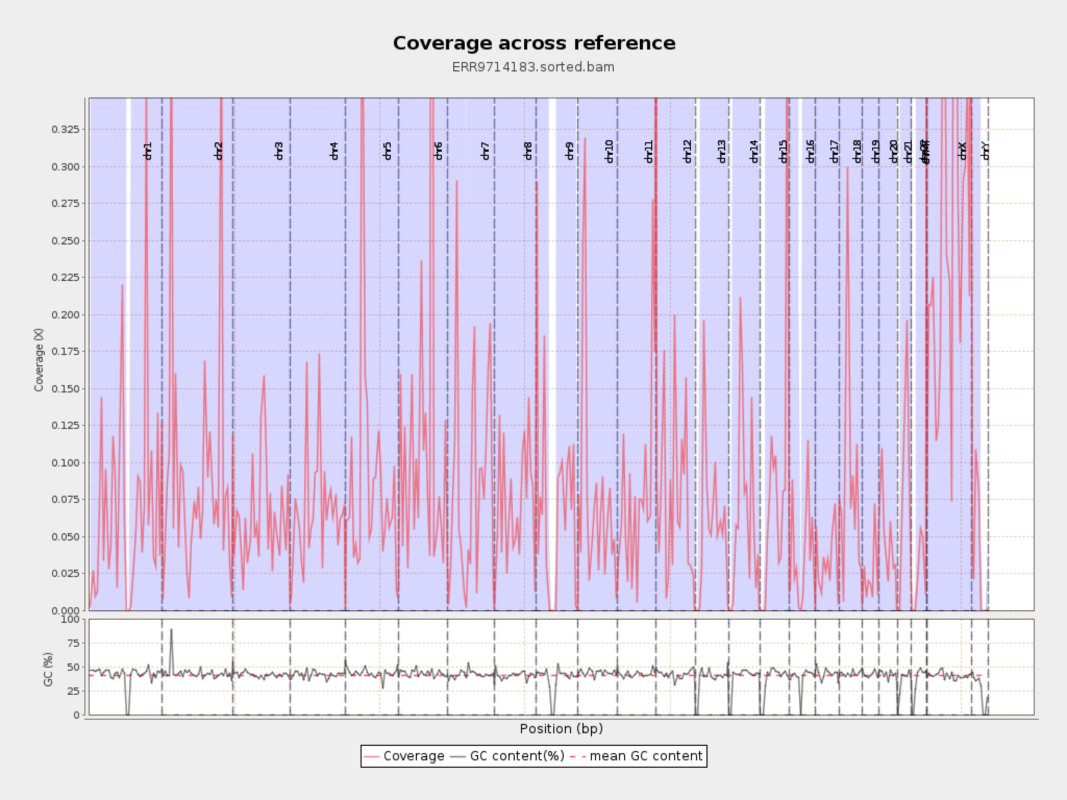
General error rate	4.05%
Mismatches	9,556,487
Insertions	244,607
Mapped reads with at least one insertion	11.82%
Deletions	809,798
Mapped reads with at least one deletion	38.43%
Homopolymer indels	25.54%

2.6. Chromosome stats

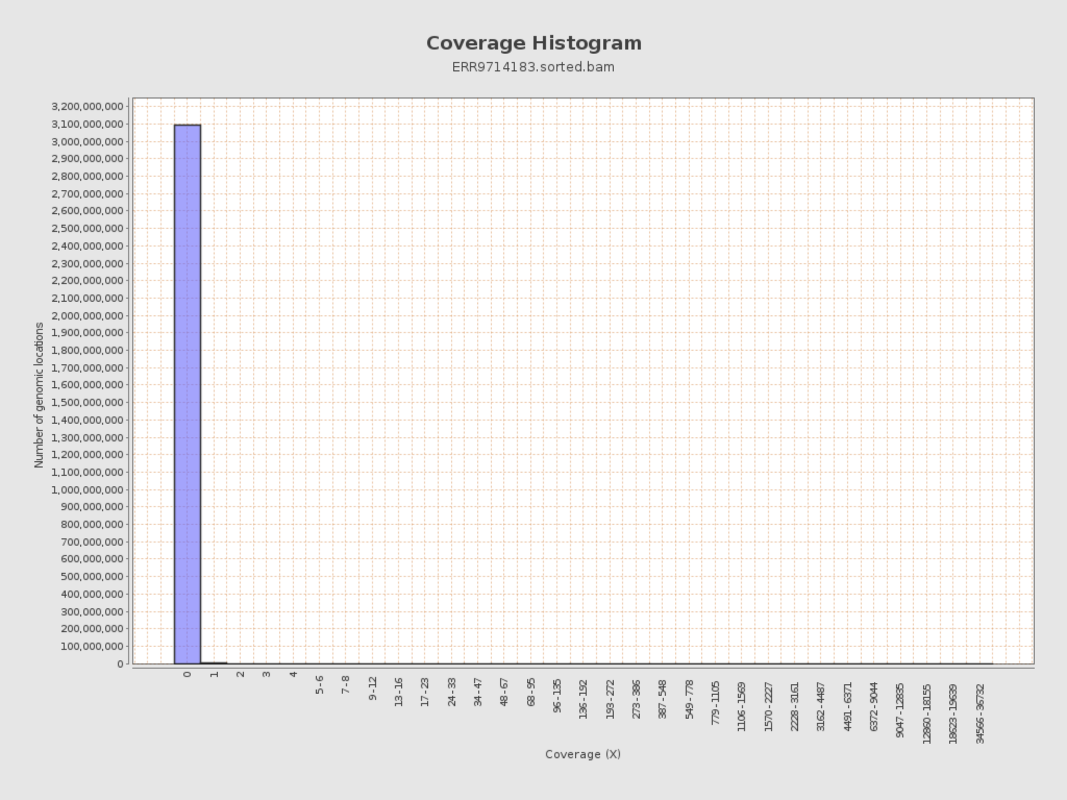
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17236215	0.0692	15.1926
chr2	243199373	22580678	0.0928	19.0946
chr3	198022430	12690250	0.0641	6.6691
chr4	191154276	13170259	0.0689	8.726
chr5	180915260	15927774	0.088	19.3836
chr6	171115067	20926712	0.1223	33.2154
chr7	159138663	13933249	0.0876	15.6961

chr8	146364022	10581902	0.0723	7.929
chr9	141213431	8994863	0.0637	8.4889
chr10	135534747	11050507	0.0815	16.4301
chr11	135006516	11211635	0.083	13.8272
chr12	133851895	10017609	0.0748	10.3441
chr13	115169878	6629873	0.0576	7.4716
chr14	107349540	7251150	0.0675	12.8679
chr15	102531392	8584991	0.0837	19.3669
chr16	90354753	3512002	0.0389	4.7273
chr17	81195210	2712148	0.0334	5.1698
chr18	78077248	7125129	0.0913	12.0115
chr19	59128983	1430701	0.0242	3.4525
chr20	63025520	3049640	0.0484	5.0824
chr21	48129895	3679151	0.0764	15.3075
chr22	51304566	1180345	0.023	3.0679
chrMT	16571	12615	0.7613	6.2876
chrX	155270560	41638387	0.2682	24.3514
chrY	59373566	1792916	0.0302	5.2239

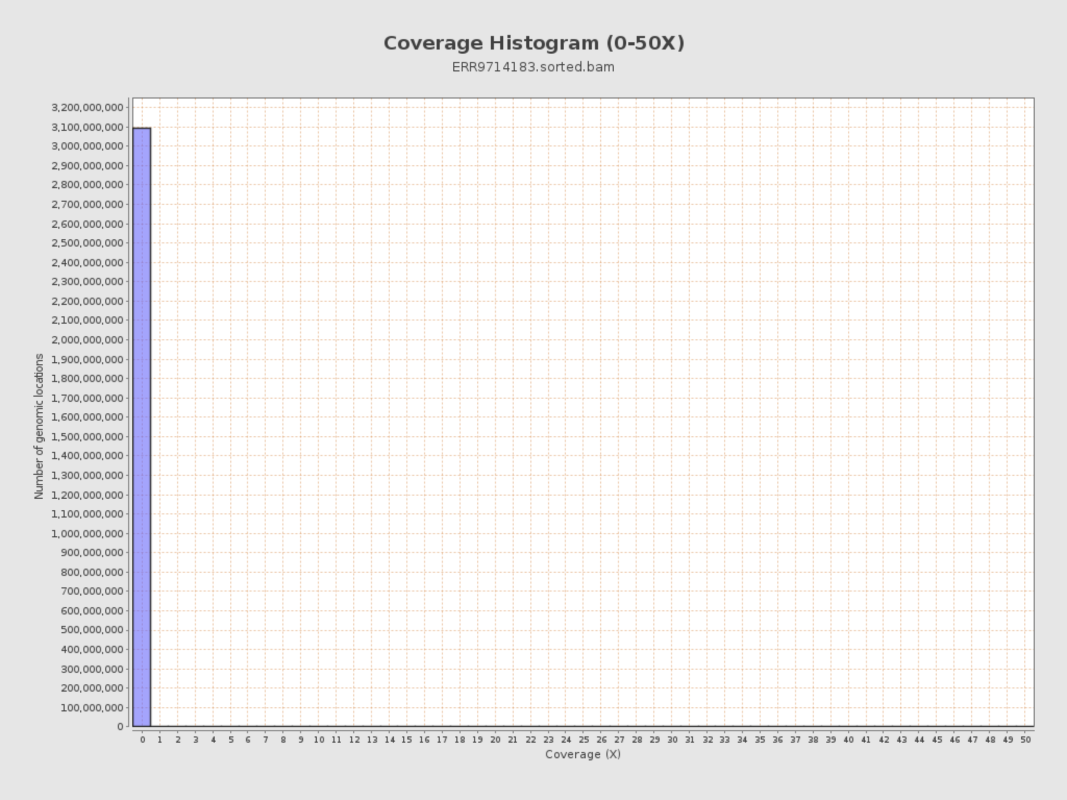
3. Results : Coverage across reference



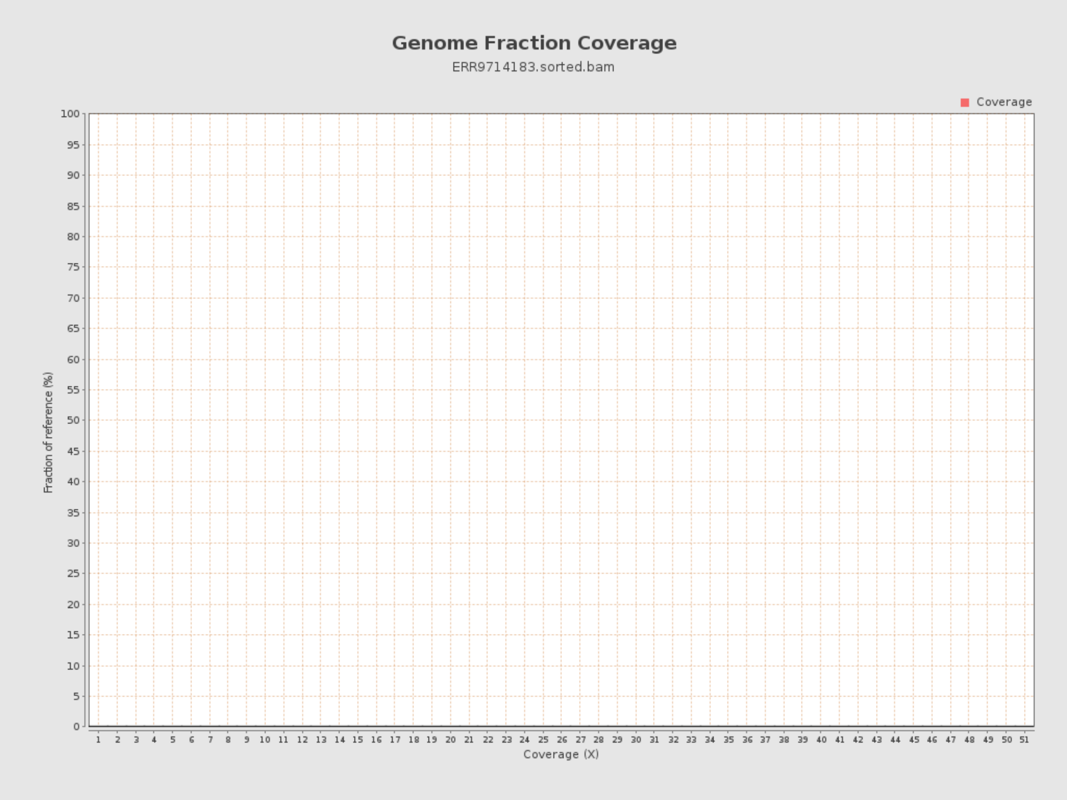
4. Results : Coverage Histogram



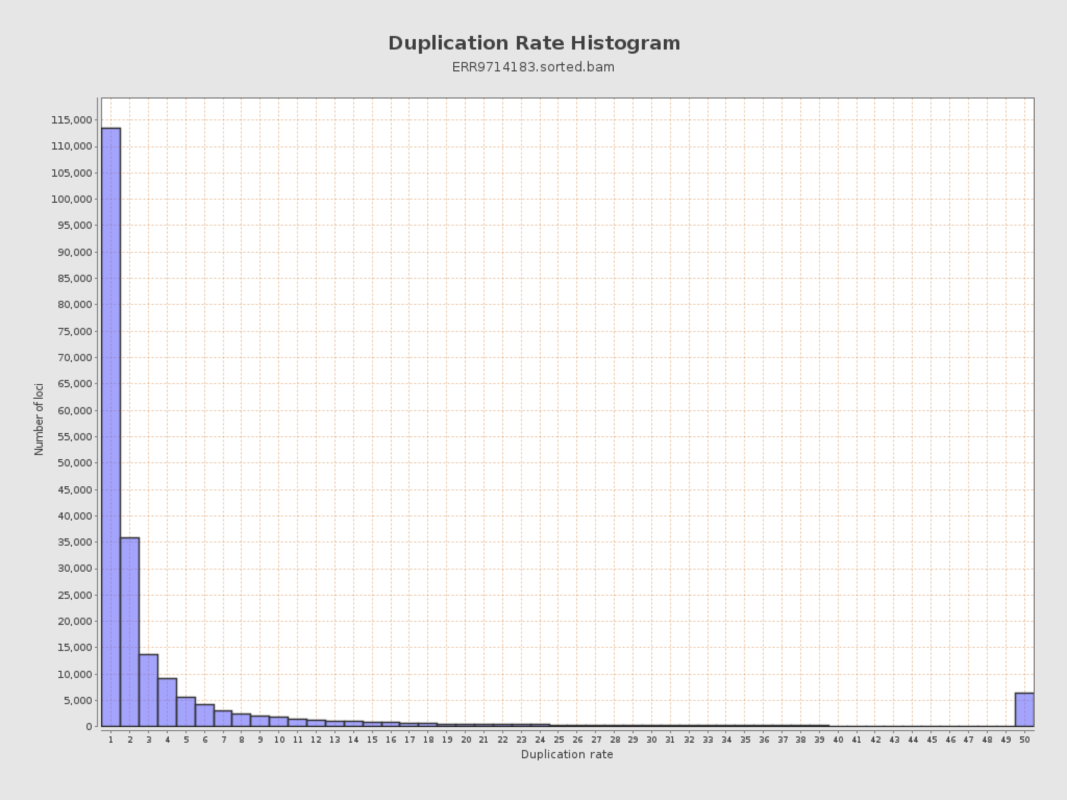
5. Results : Coverage Histogram (0-50X)



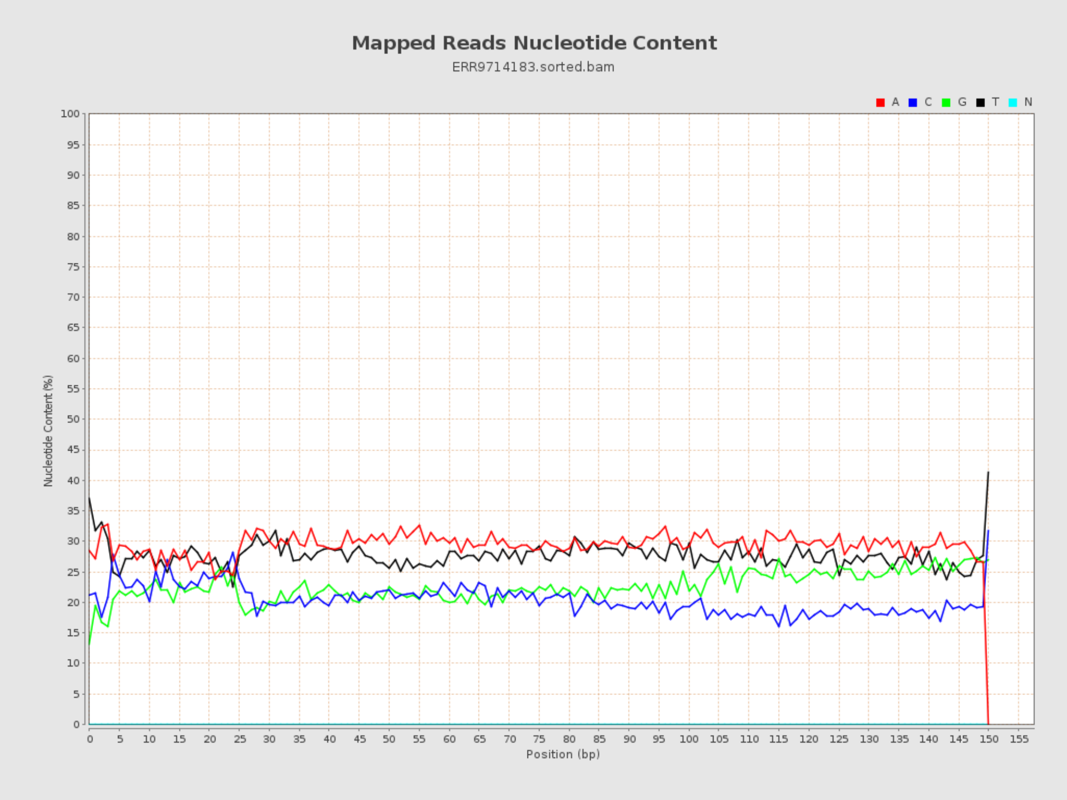
6. Results : Genome Fraction Coverage



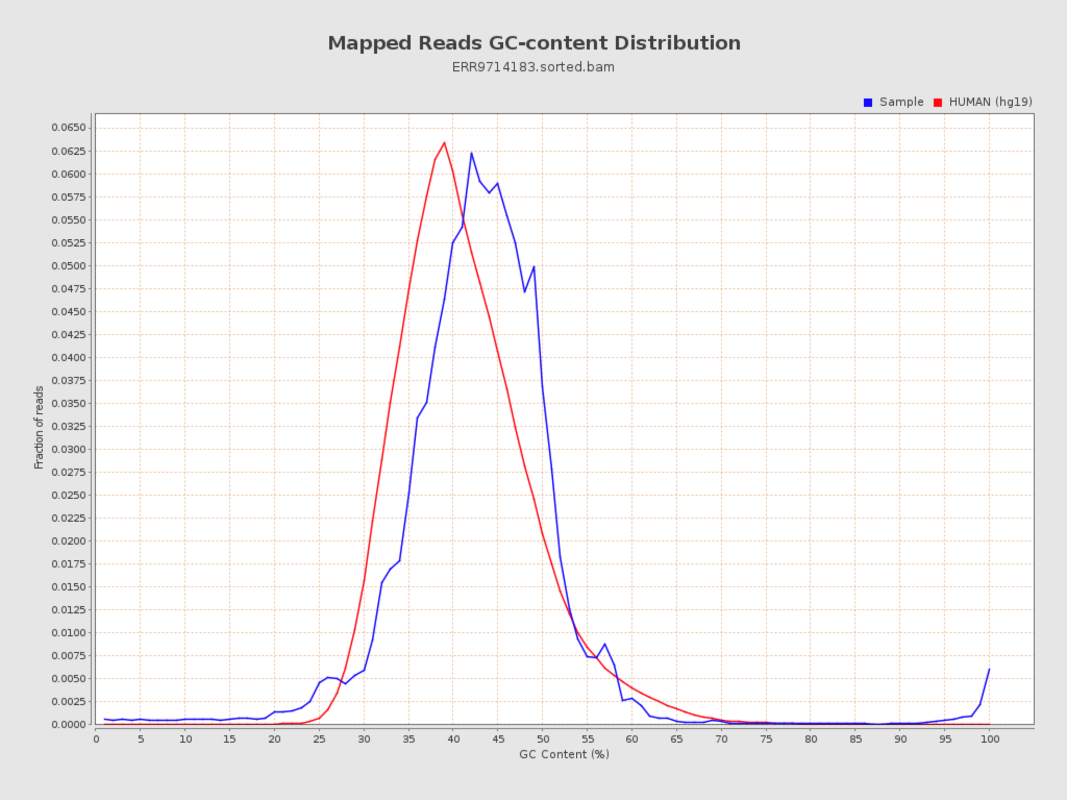
7. Results : Duplication Rate Histogram



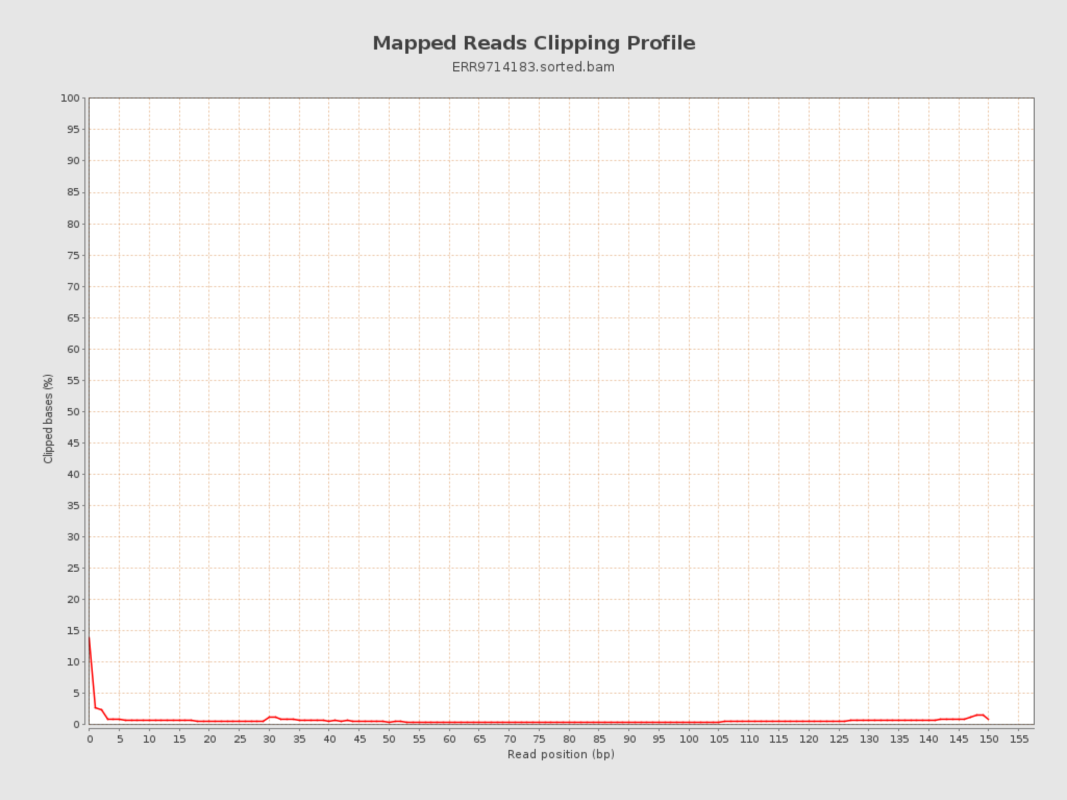
8. Results : Mapped Reads Nucleotide Content



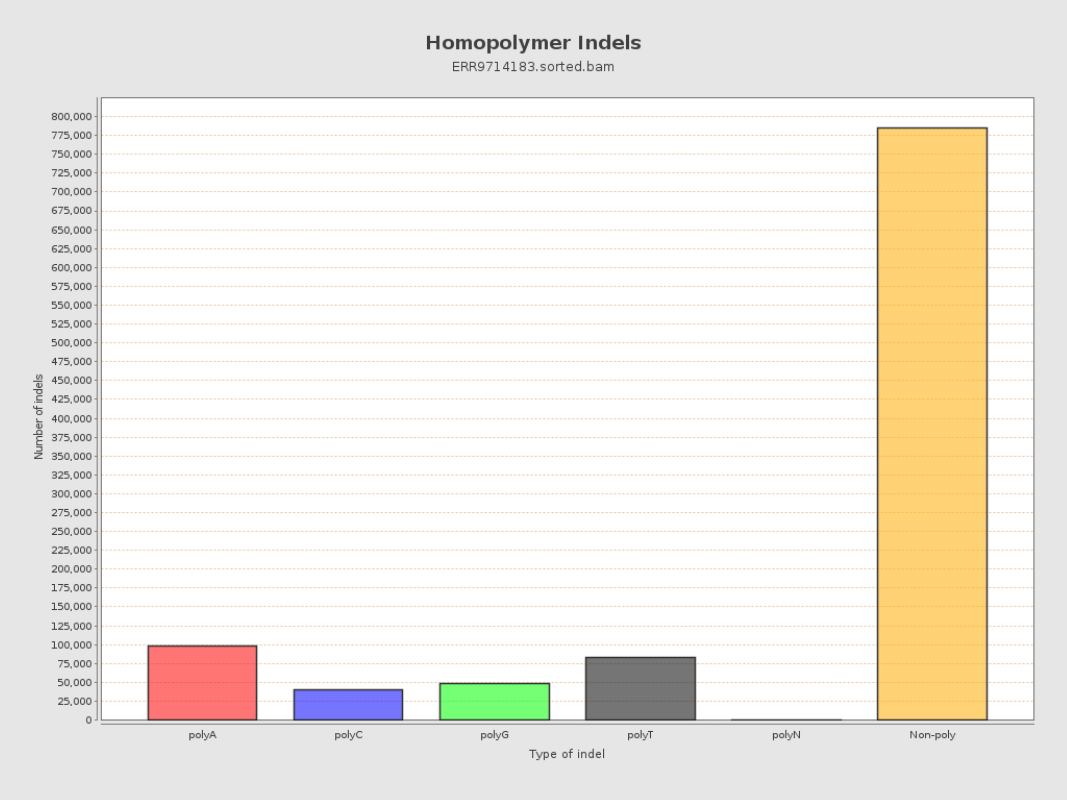
9. Results : Mapped Reads GC-content Distribution



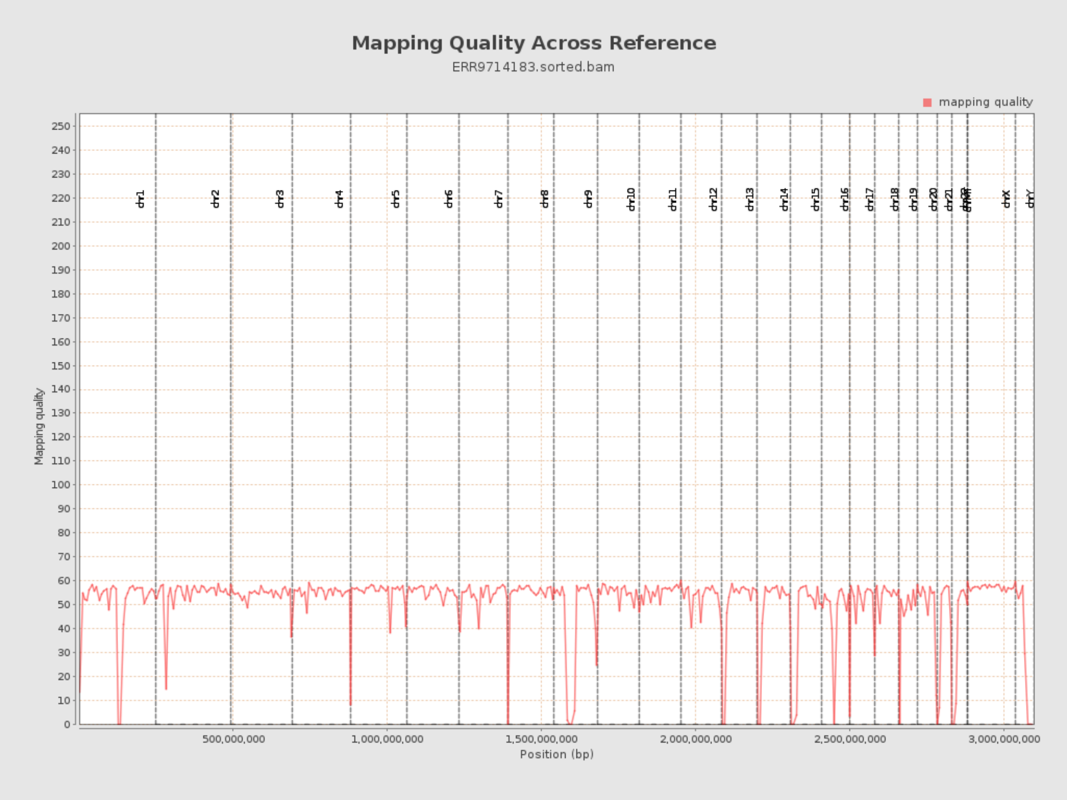
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram