Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:44:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714187.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_ERR9714187 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:44:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,548
Mapped reads	26,162 / 62.97%
Unmapped reads	15,386 / 37.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	913 / 2.2%
Read min/max/mean length	30 / 151 / 118.13
Duplicated reads (estimated)	18,096 / 43.55%
Duplication rate	39.58%
Clipped reads	24,211 / 58.27%

2.2. ACGT Content

Number/percentage of A's	895,687 / 27.2%
Number/percentage of C's	672,984 / 20.44%
Number/percentage of T's	849,936 / 25.81%
Number/percentage of G's	873,895 / 26.54%
Number/percentage of N's	62 / 0%
GC Percentage	46.98%

2.3. Coverage

Mean	0.0011

Standard Deviation	0.3048

2.4. Mapping Quality

Mean Mapping Quality	48.96

2.5. Mismatches and indels

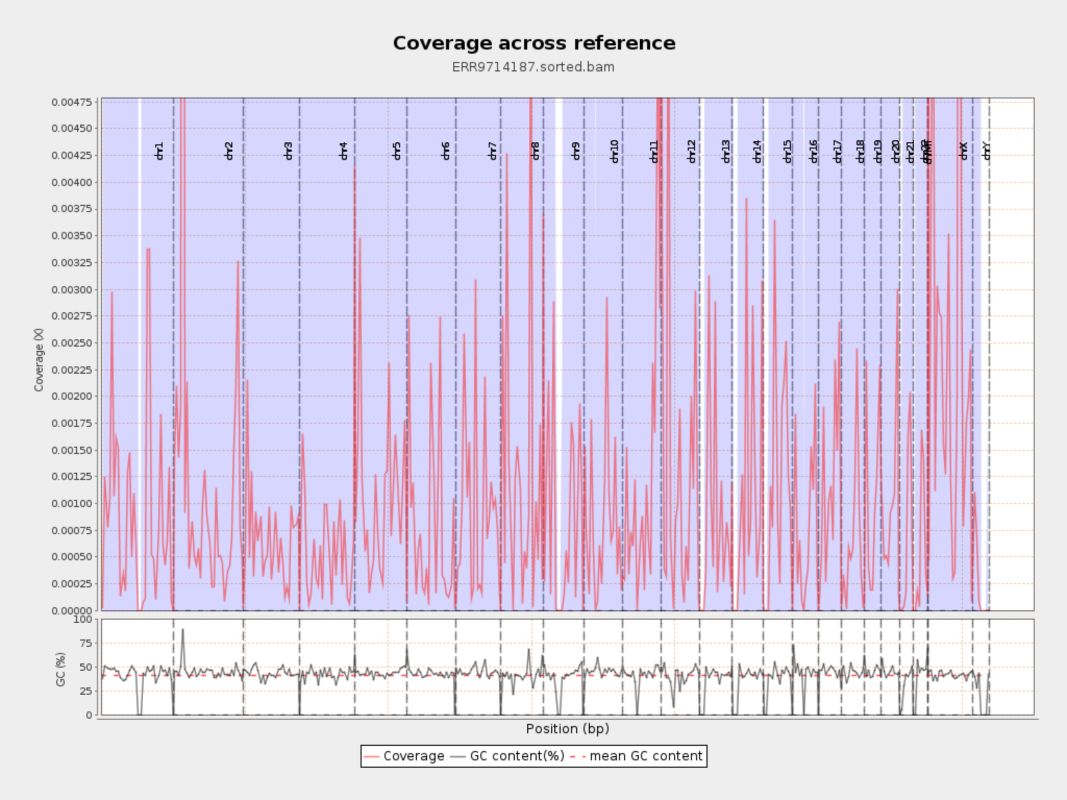
General error rate	4.64%
Mismatches	143,313
Insertions	3,569
Mapped reads with at least one insertion	12.98%
Deletions	12,549
Mapped reads with at least one deletion	43.83%
Homopolymer indels	30.93%

2.6. Chromosome stats

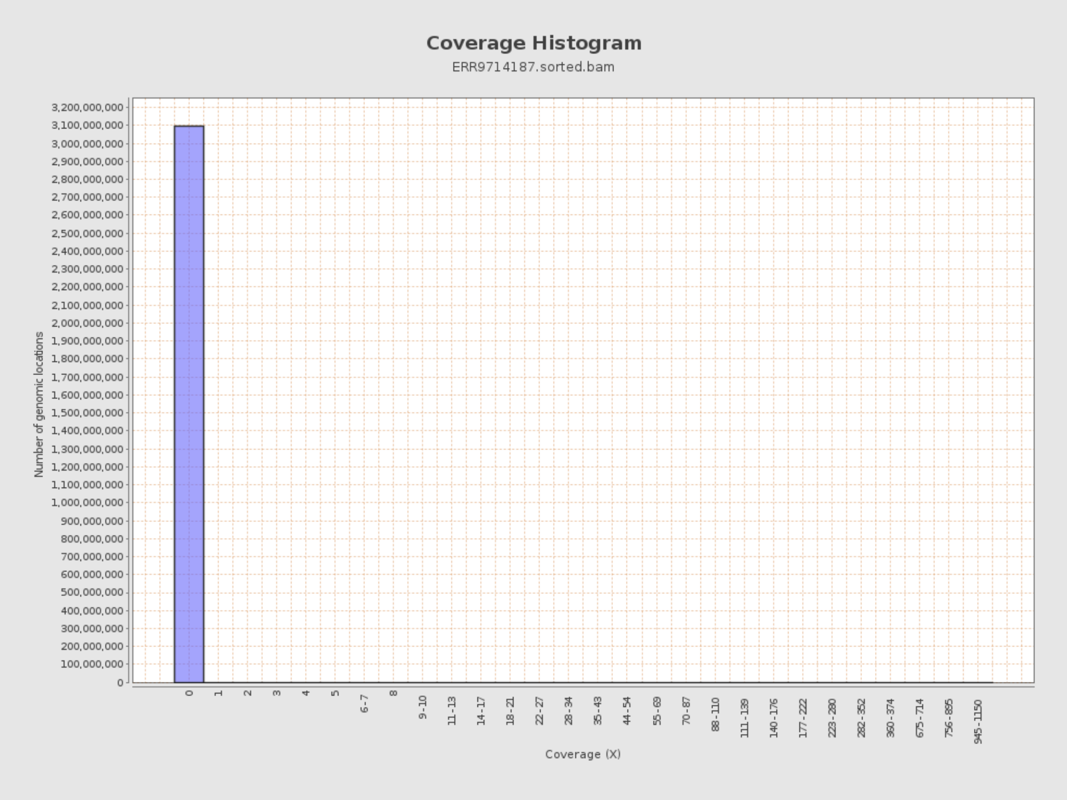
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	230143	0.0009	0.1747
chr2	243199373	441264	0.0018	0.7833
chr3	198022430	129258	0.0007	0.1115
chr4	191154276	103524	0.0005	0.1025
chr5	180915260	198672	0.0011	0.1737
chr6	171115067	133133	0.0008	0.1858
chr7	159138663	146532	0.0009	0.1732

chr8	146364022	193894	0.0013	0.3479
chr9	141213431	120825	0.0009	0.1688
chr10	135534747	117030	0.0009	0.1372
chr11	135006516	188507	0.0014	0.3292
chr12	133851895	184188	0.0014	0.3237
chr13	115169878	93518	0.0008	0.1692
chr14	107349540	120475	0.0011	0.2463
chr15	102531392	119834	0.0012	0.2148
chr16	90354753	68435	0.0008	0.1327
chr17	81195210	94628	0.0012	0.2136
chr18	78077248	54787	0.0007	0.1279
chr19	59128983	61360	0.001	0.1726
chr20	63025520	63544	0.001	0.189
chr21	48129895	32769	0.0007	0.1249
chr22	51304566	28600	0.0006	0.1133
chrMT	16571	27818	1.6787	12.1154
chrX	155270560	399098	0.0026	0.4219
chrY	59373566	16563	0.0003	0.098

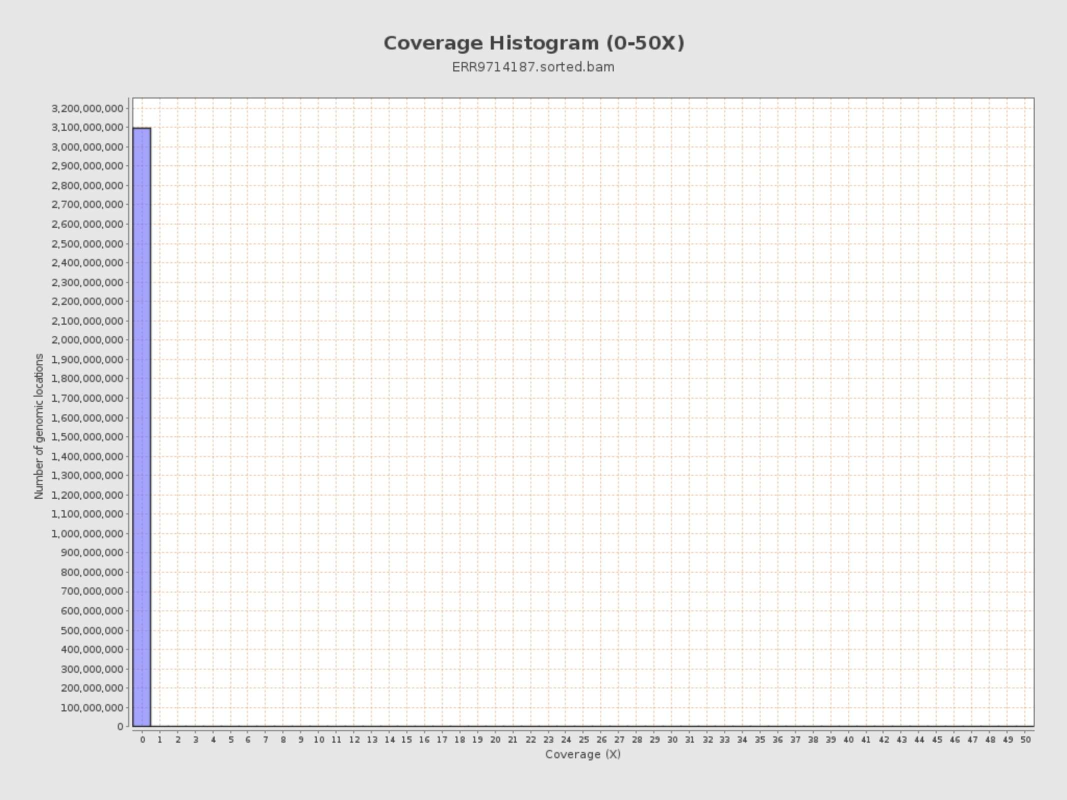
3. Results : Coverage across reference



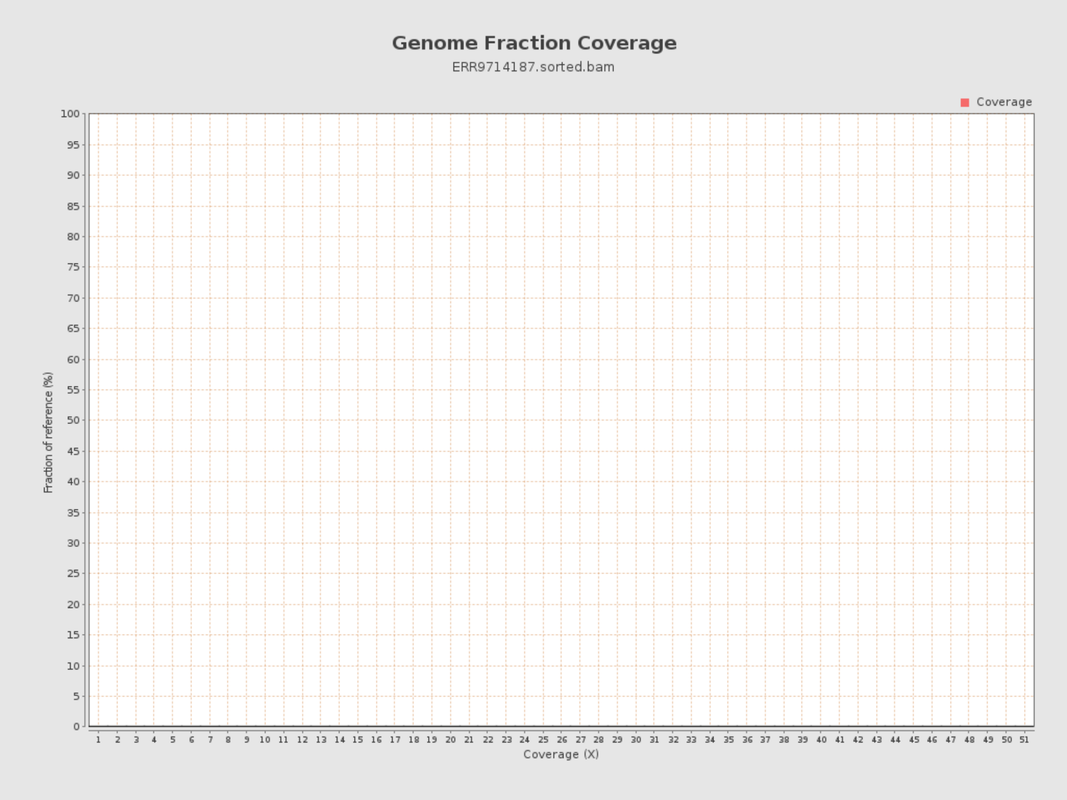
4. Results : Coverage Histogram



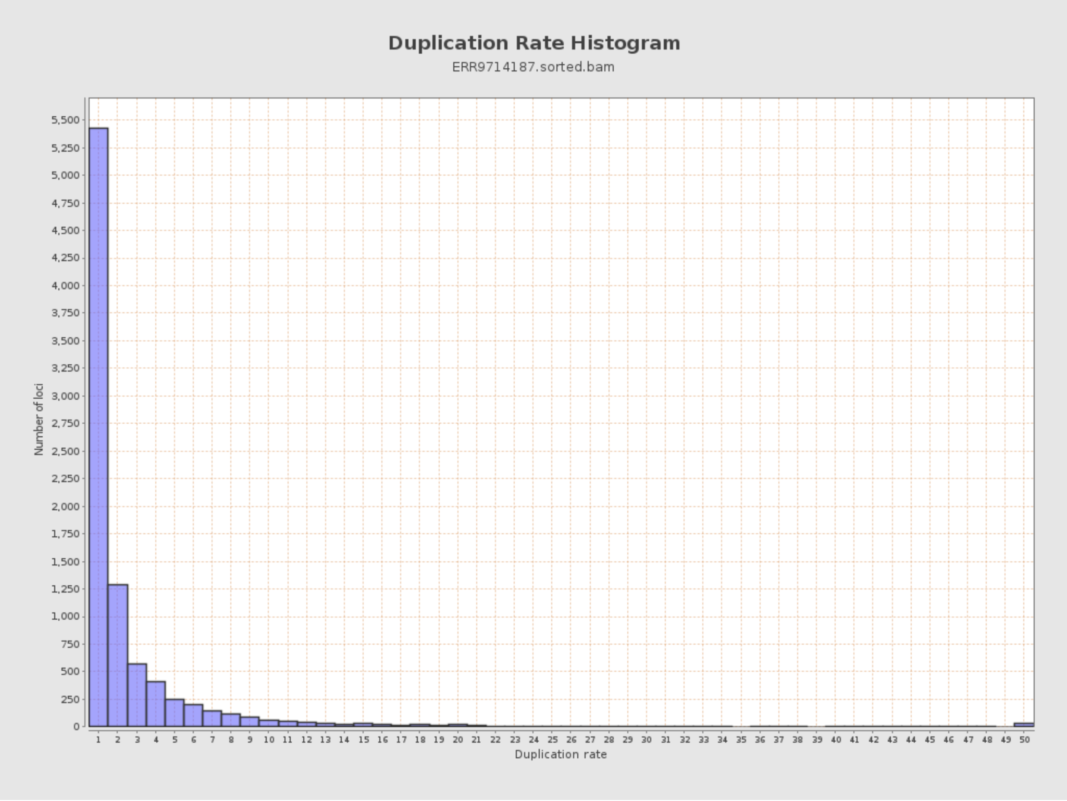
5. Results : Coverage Histogram (0-50X)



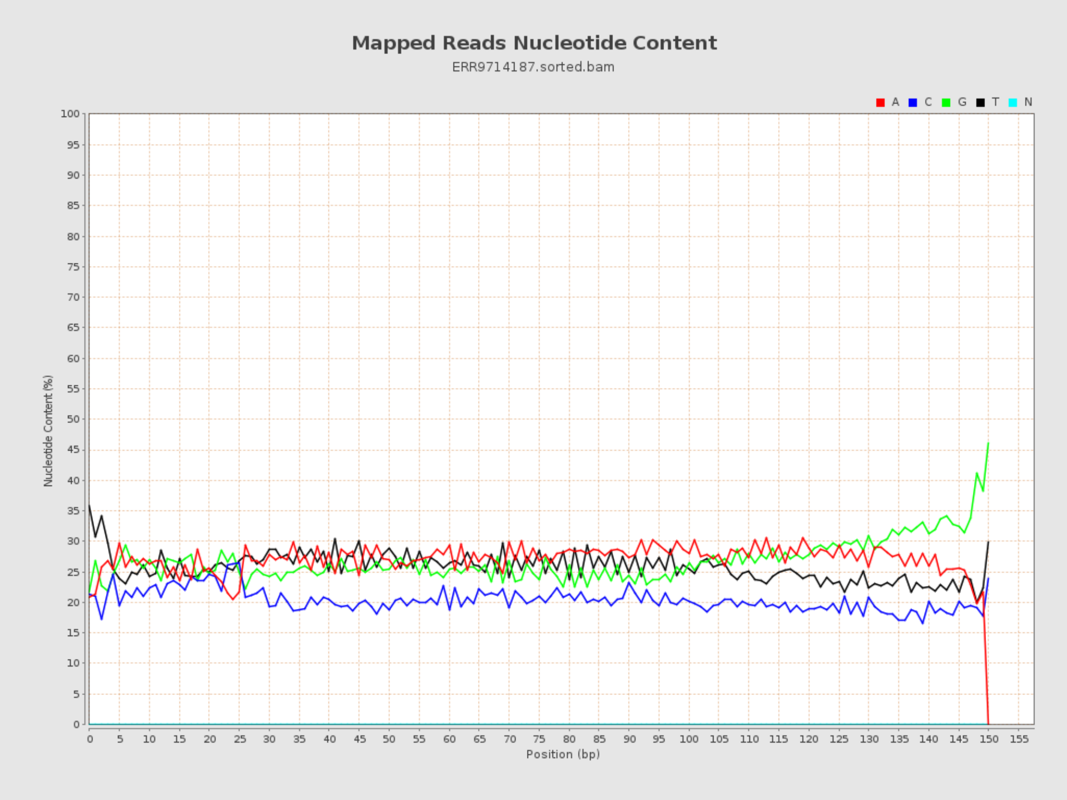
6. Results : Genome Fraction Coverage



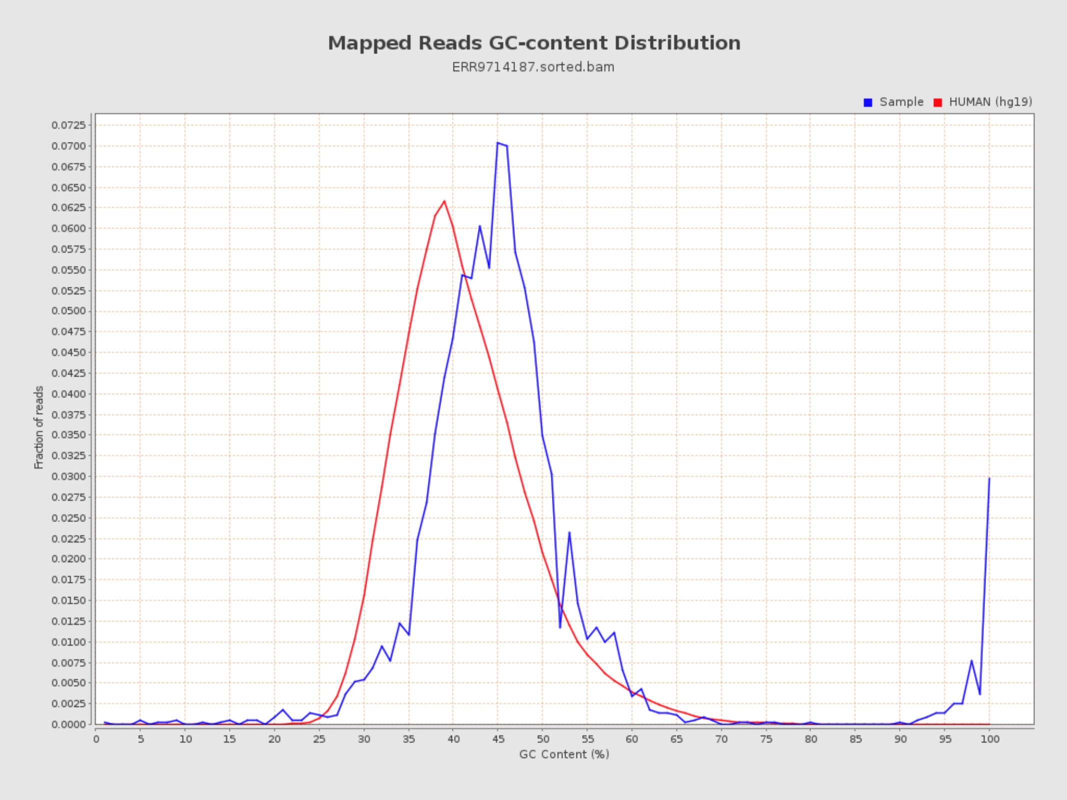
7. Results : Duplication Rate Histogram



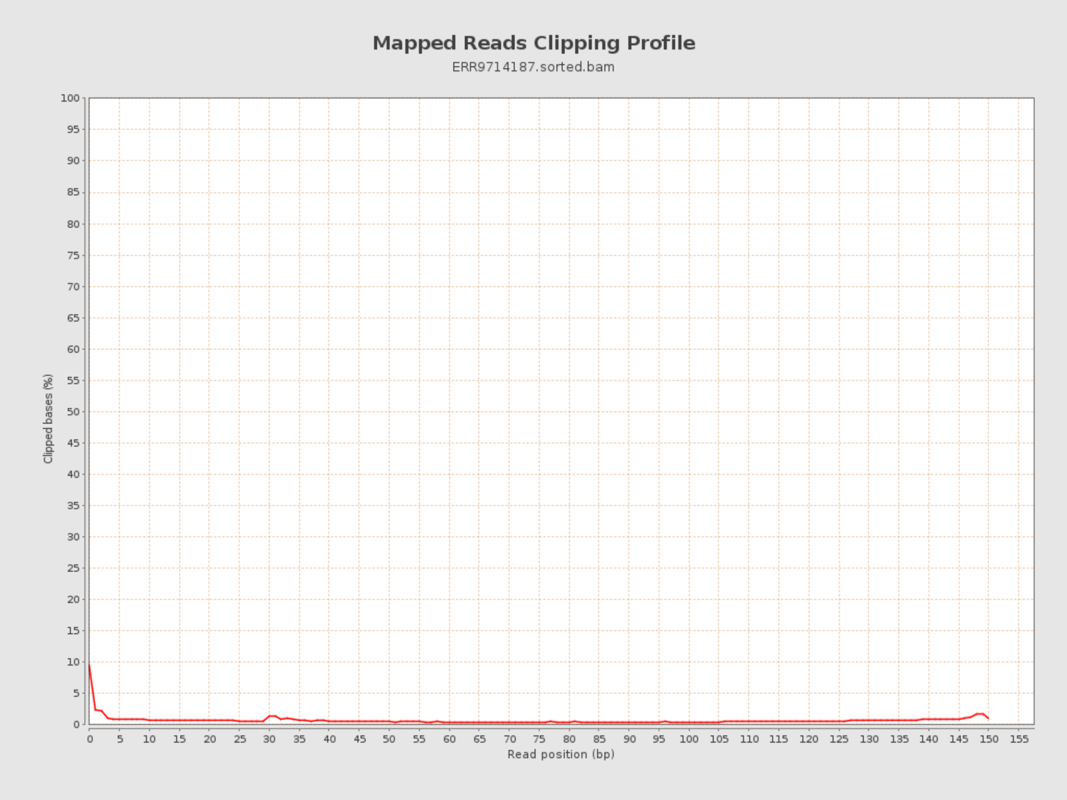
8. Results : Mapped Reads Nucleotide Content



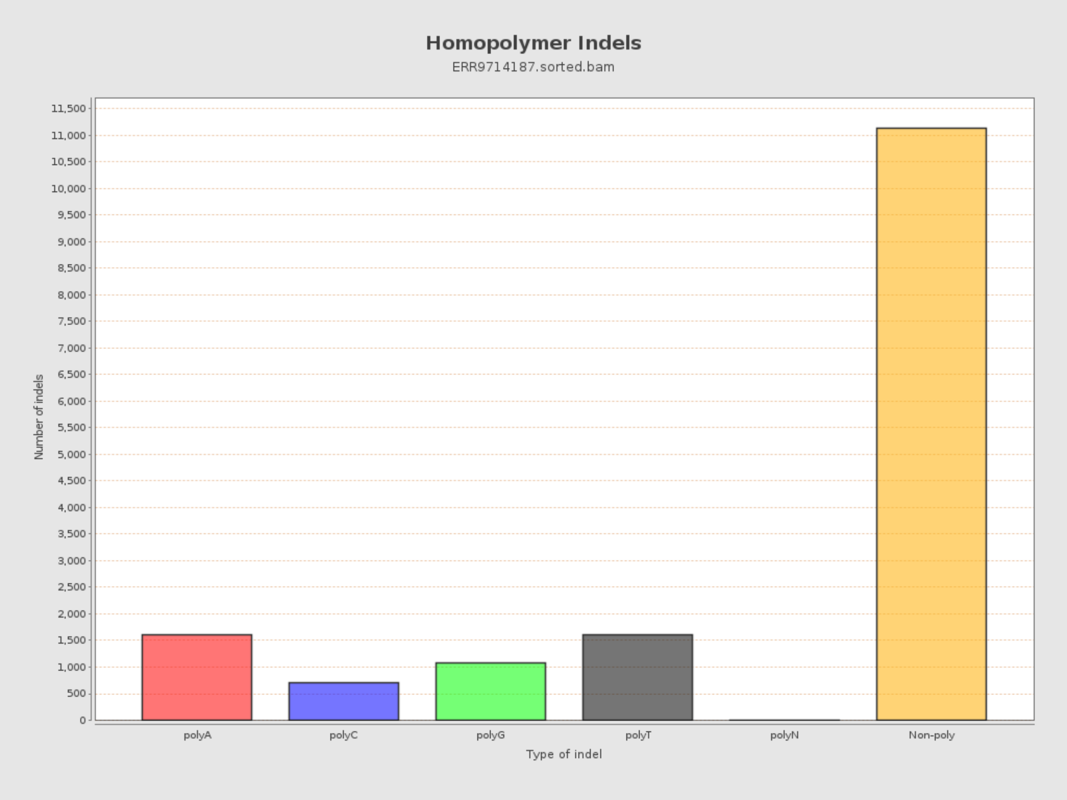
9. Results : Mapped Reads GC-content Distribution



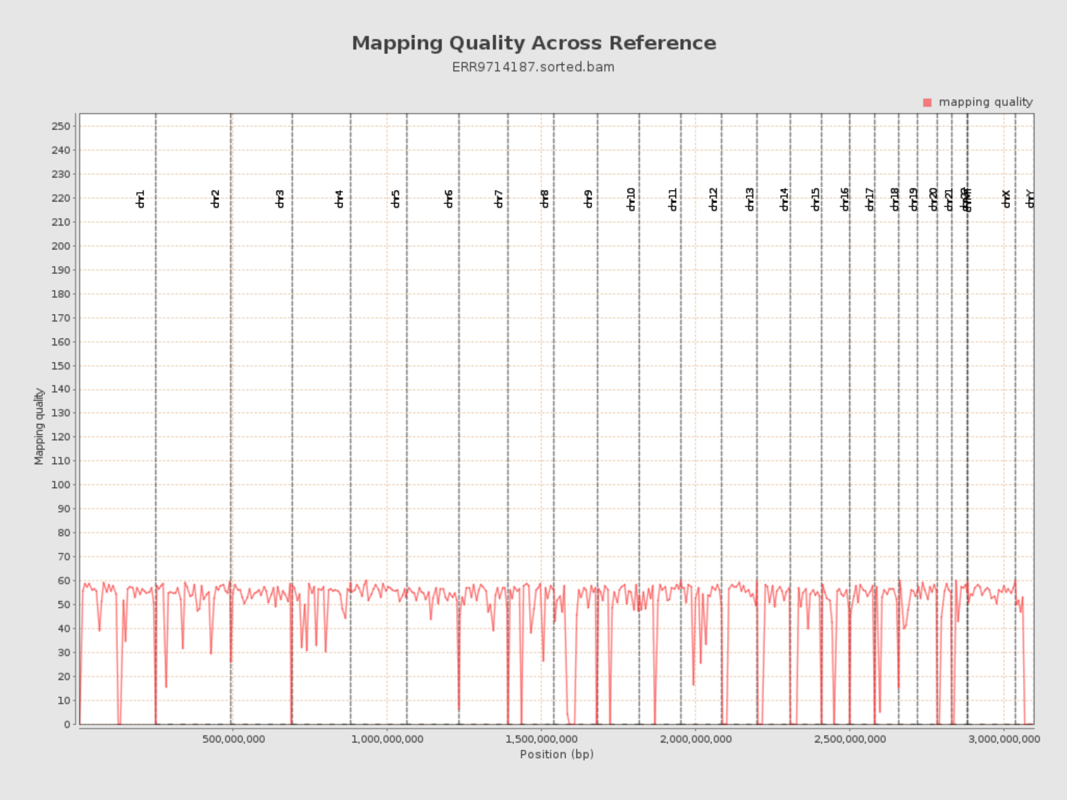
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram