

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:19:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714099.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_ERR9714099 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:19:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	579,502
Mapped reads	374,646 / 64.65%
Unmapped reads	204,856 / 35.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,895 / 2.05%
Read min/max/mean length	30 / 151 / 118.72
Duplicated reads (estimated)	320,106 / 55.24%
Duplication rate	43.33%
Clipped reads	343,015 / 59.19%

2.2. ACGT Content

Number/percentage of A's	12,717,306 / 27.05%
Number/percentage of C's	9,307,706 / 19.8%
Number/percentage of T's	12,054,807 / 25.64%
Number/percentage of G's	12,928,879 / 27.5%
Number/percentage of N's	448 / 0%
GC Percentage	47.3%

2.3. Coverage

Mean	0.0155

Standard Deviation	4.8954
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2.4. Mapping Quality

Mean Mapping Quality	51.22
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2.5. Mismatches and indels

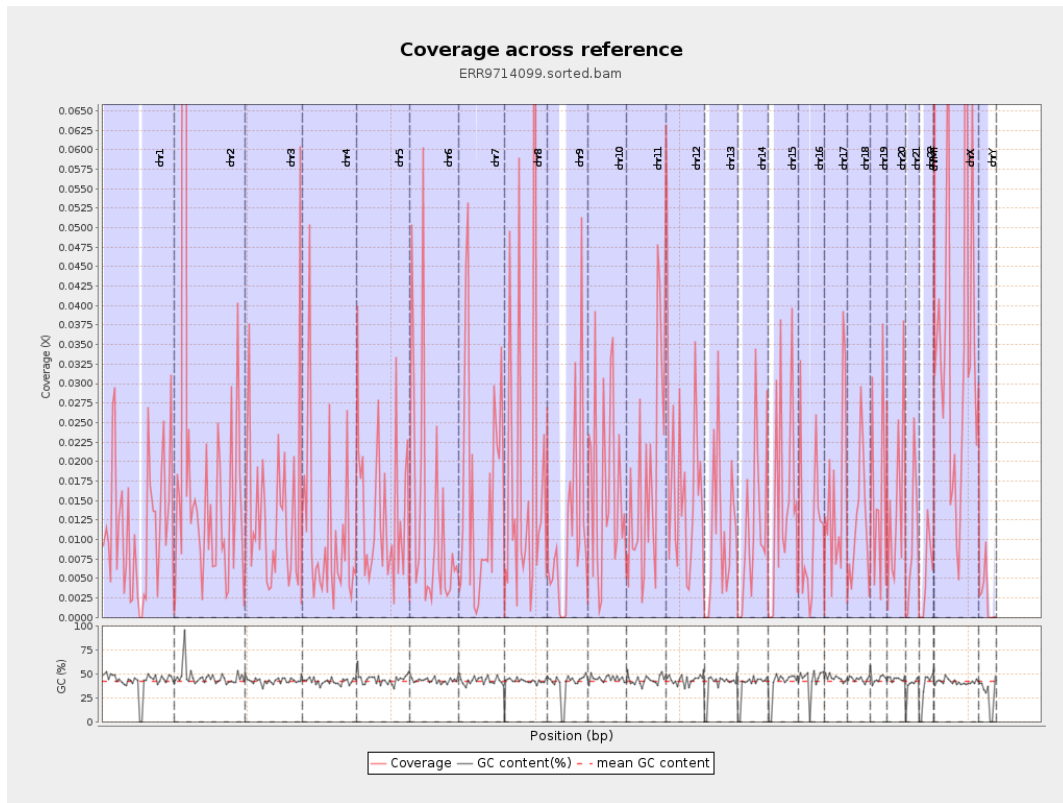
General error rate	4.63%
Mismatches	2,033,464
Insertions	53,036
Mapped reads with at least one insertion	13.44%
Deletions	181,211
Mapped reads with at least one deletion	44.58%
Homopolymer indels	30.39%

2.6. Chromosome stats

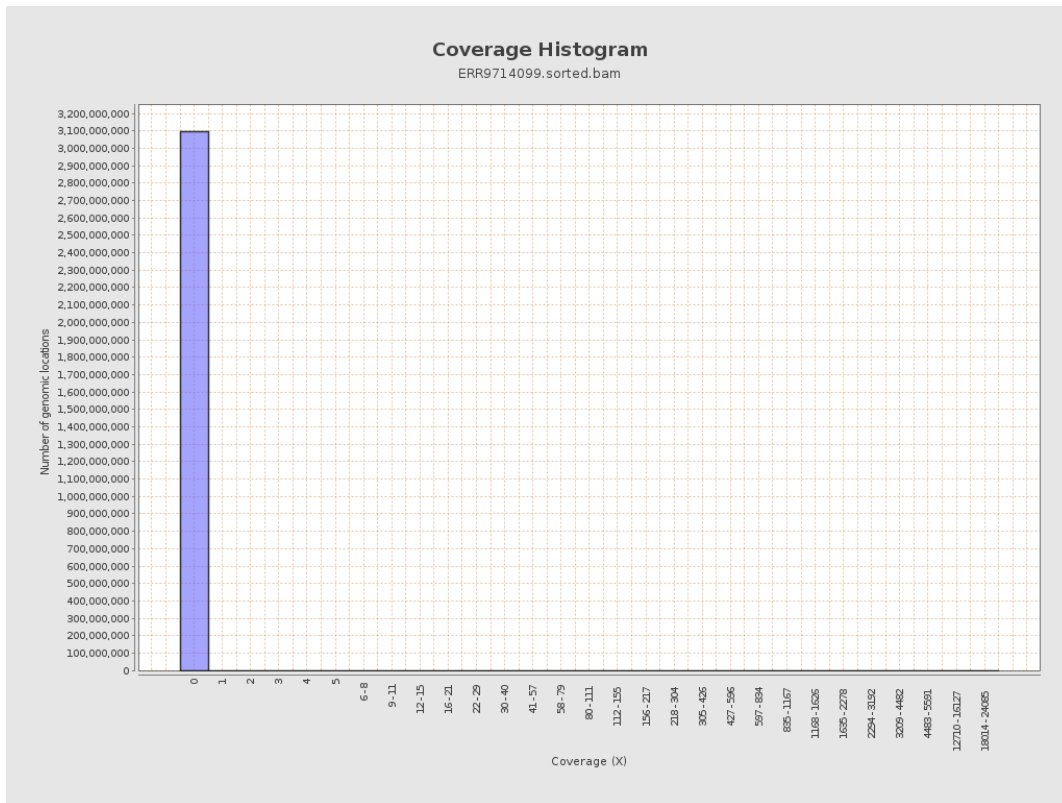
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2823057	0.0113	1.5857
chr2	243199373	6638904	0.0273	14.7323
chr3	198022430	2797797	0.0141	2.978
chr4	191154276	1960930	0.0103	1.5397
chr5	180915260	2372945	0.0131	1.7354
chr6	171115067	2168445	0.0127	2.4138
chr7	159138663	2481692	0.0156	2.8089

chr8	146364022	2778428	0.019	6.1133
chr9	141213431	1538295	0.0109	1.9284
chr10	135534747	2246505	0.0166	2.4307
chr11	135006516	2382617	0.0176	3.1859
chr12	133851895	2279228	0.017	2.3107
chr13	115169878	1257430	0.0109	1.9362
chr14	107349540	1226248	0.0114	1.6614
chr15	102531392	1474306	0.0144	2.1497
chr16	90354753	1008120	0.0112	1.555
chr17	81195210	1256367	0.0155	2.4706
chr18	78077248	998010	0.0128	1.4109
chr19	59128983	900257	0.0152	2.1562
chr20	63025520	936942	0.0149	2.198
chr21	48129895	441264	0.0092	1.7119
chr22	51304566	287213	0.0056	0.7446
chrMT	16571	218379	13.1784	95.2256
chrX	155270560	5483571	0.0353	4.9962
chrY	59373566	151691	0.0026	0.8092

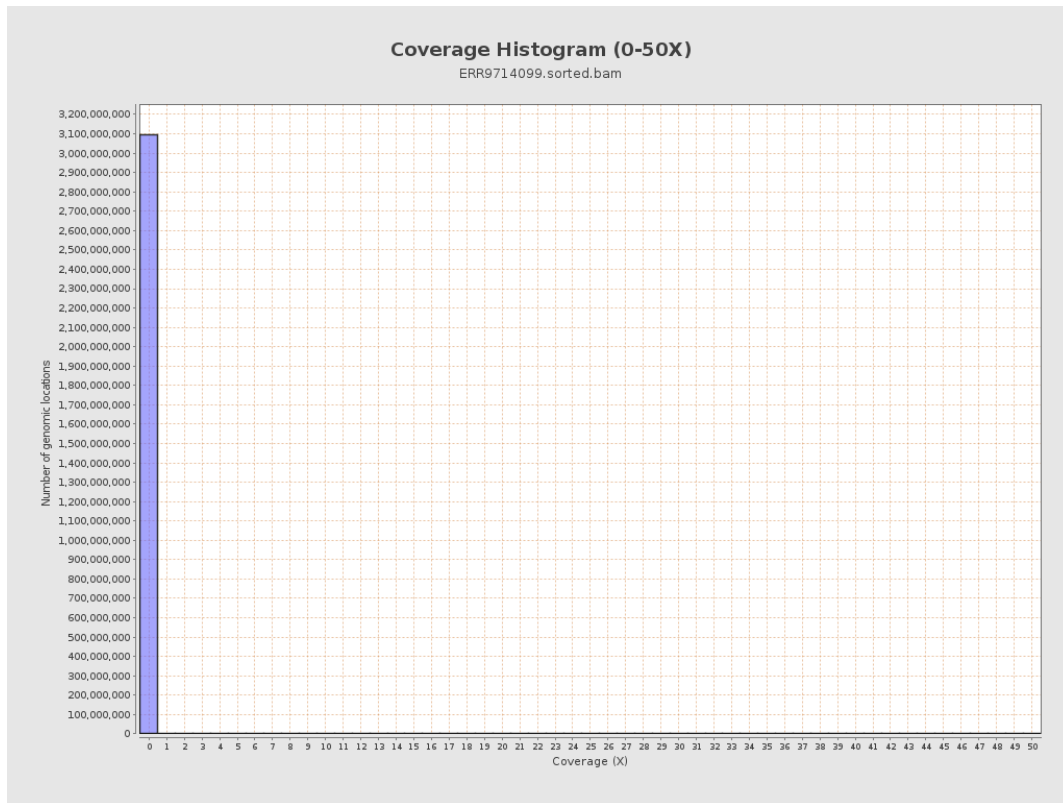
3. Results : Coverage across reference



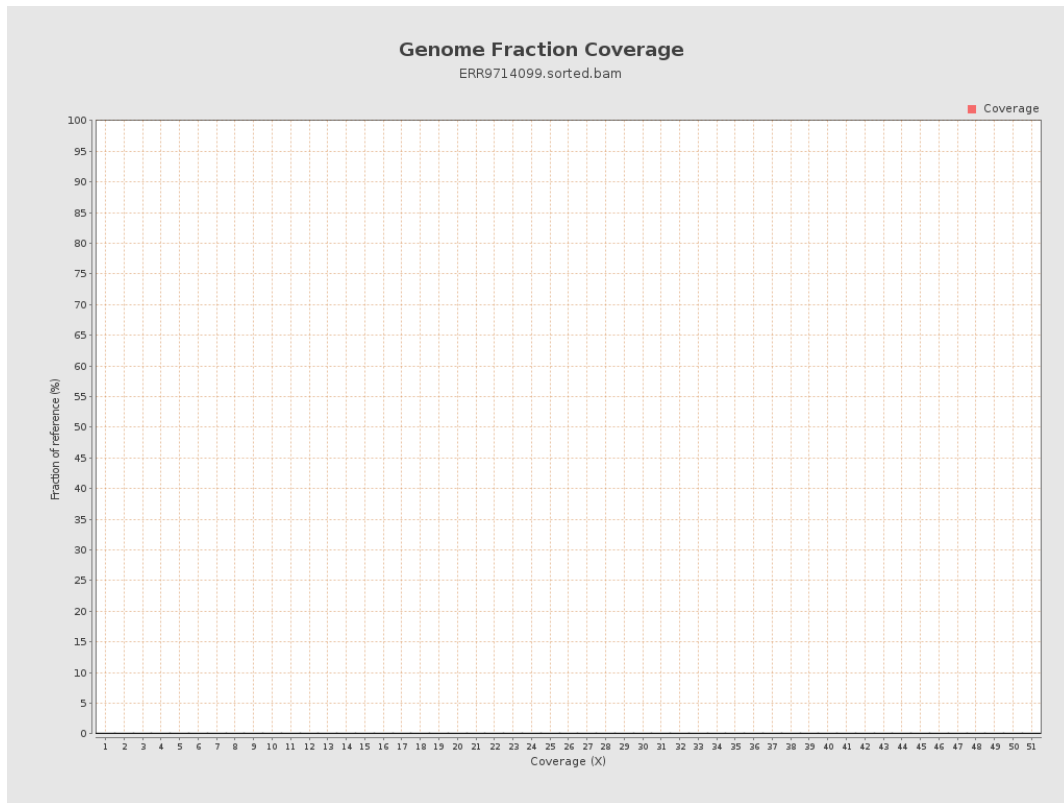
4. Results : Coverage Histogram



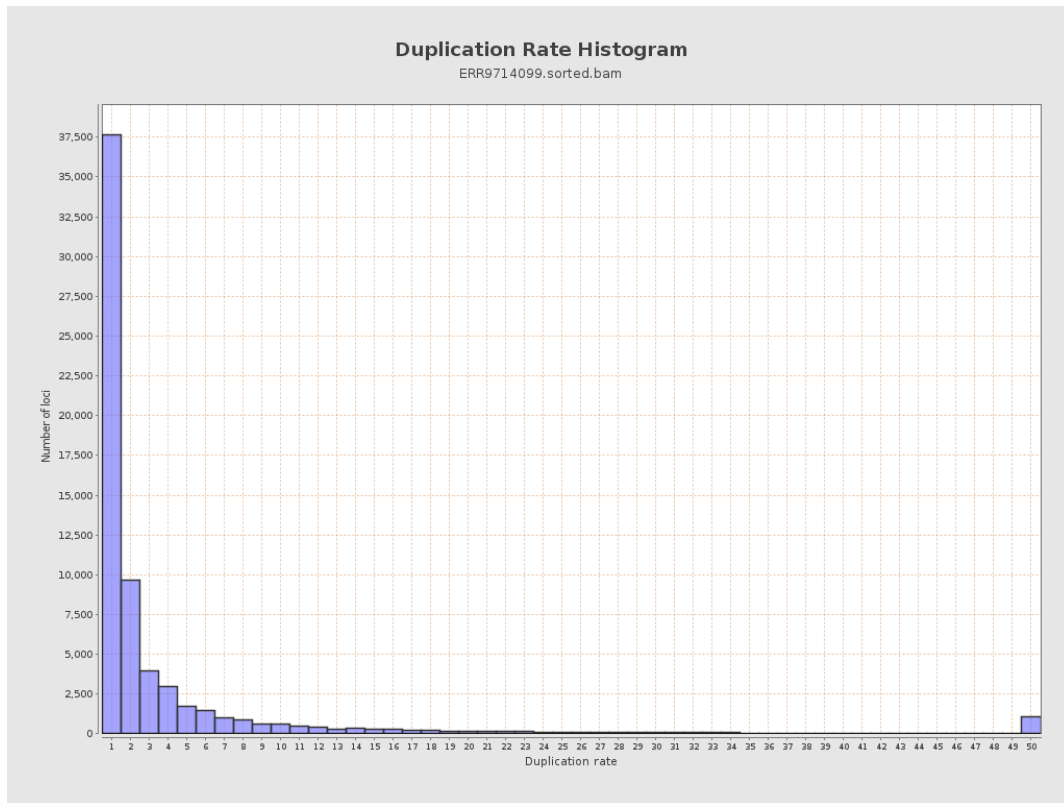
5. Results : Coverage Histogram (0-50X)



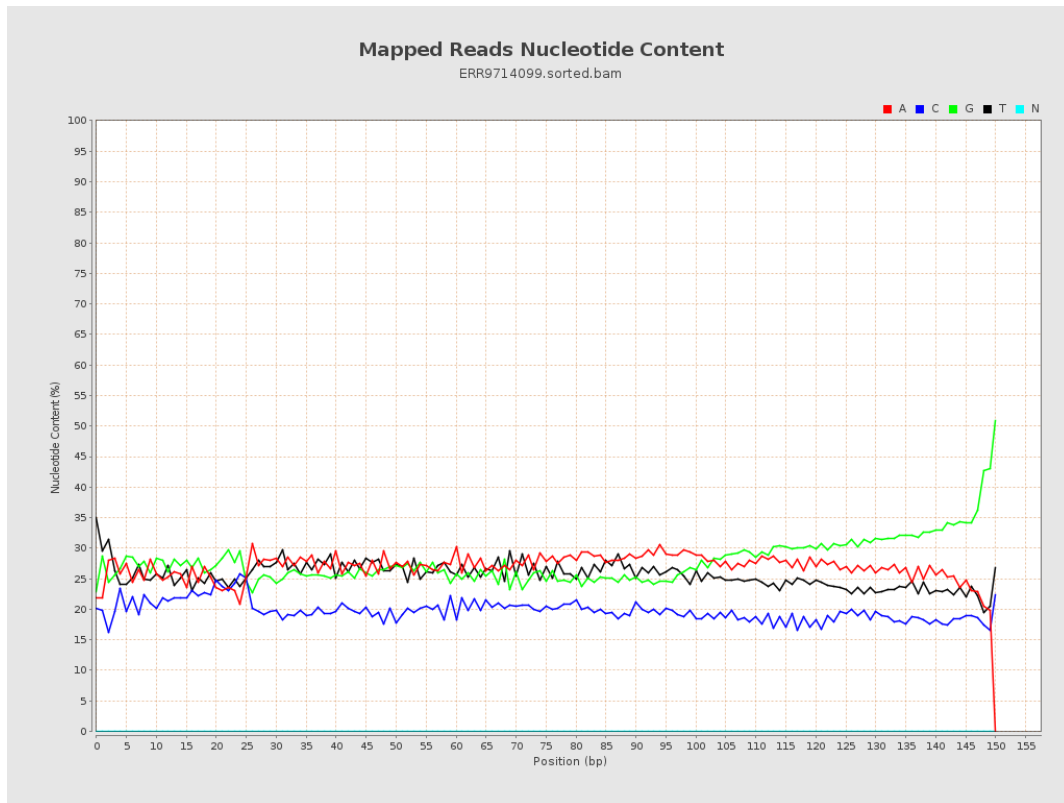
6. Results : Genome Fraction Coverage



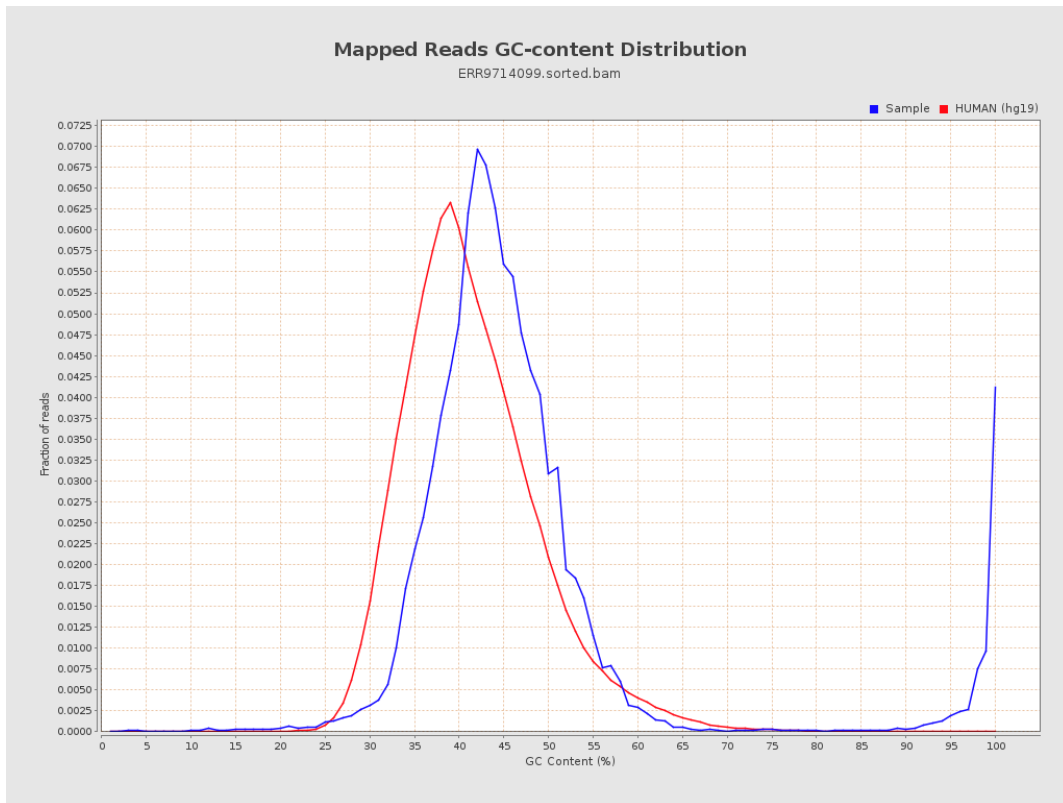
7. Results : Duplication Rate Histogram



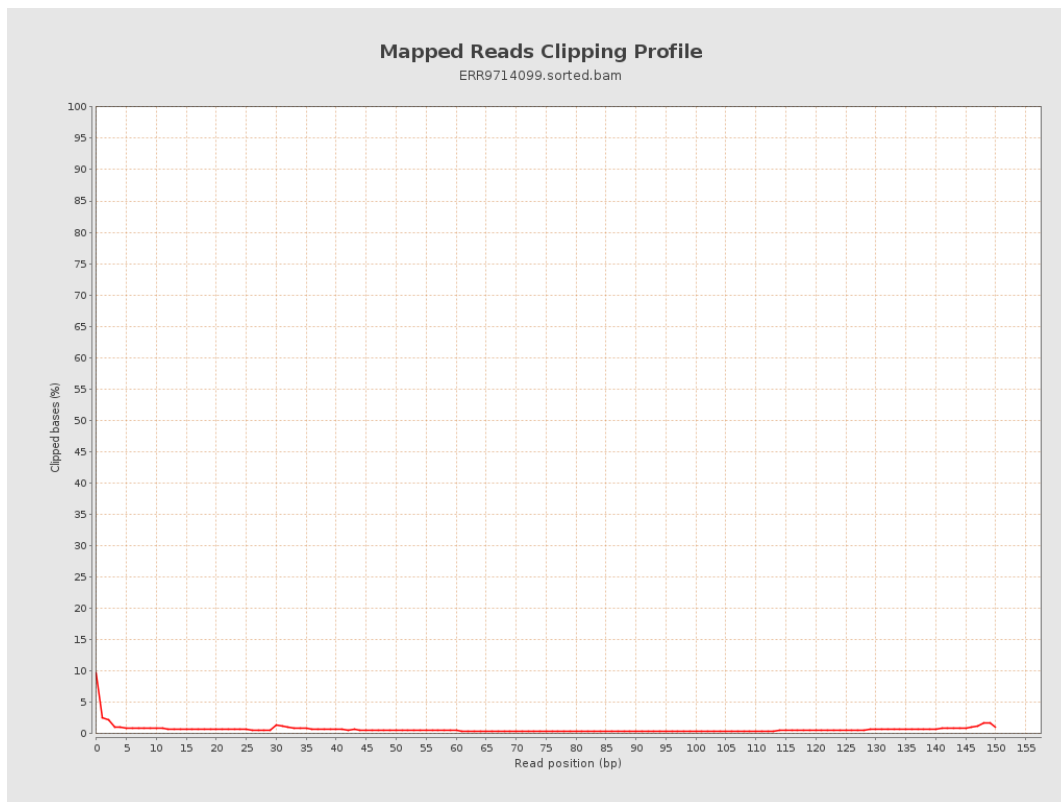
8. Results : Mapped Reads Nucleotide Content



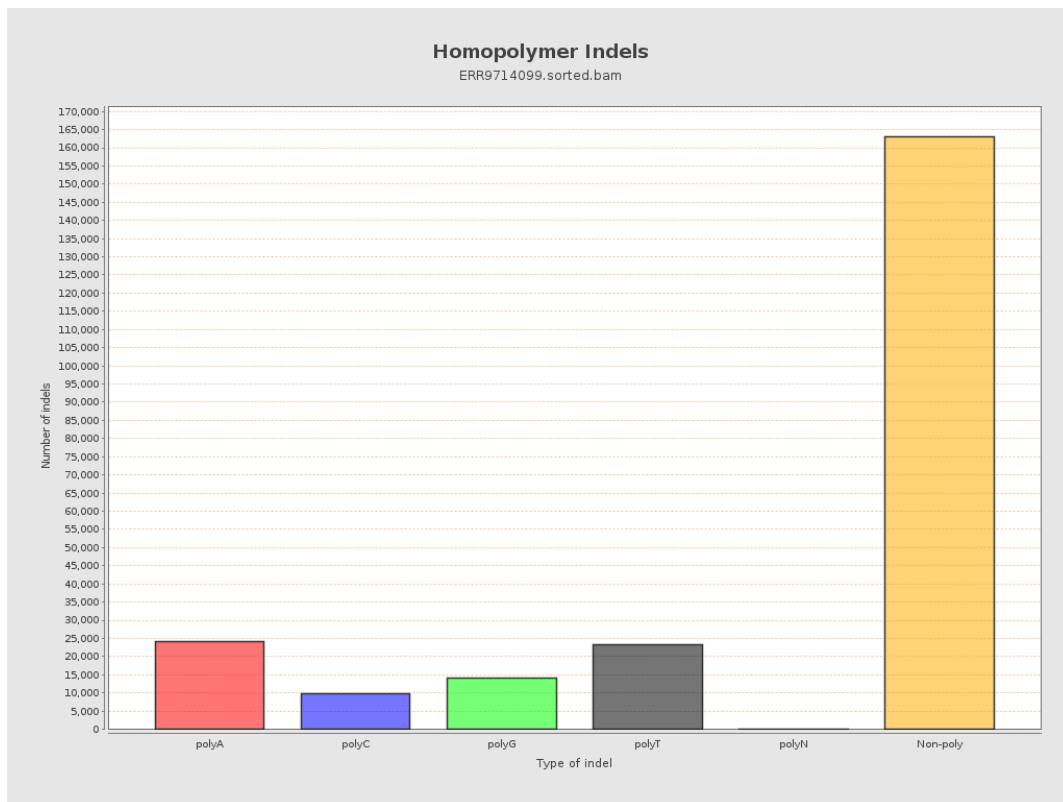
9. Results : Mapped Reads GC-content Distribution



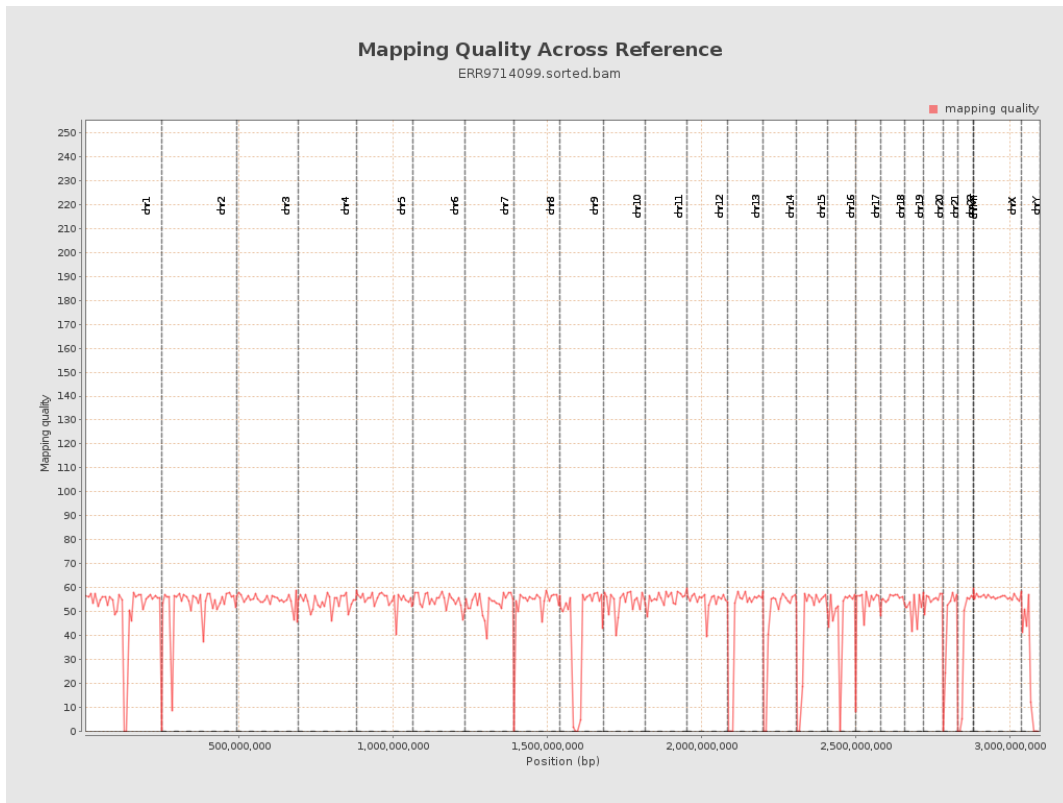
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

