

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:04:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714176.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_ERR9714176 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:04:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,623,584
Mapped reads	1,306,044 / 80.44%
Unmapped reads	317,540 / 19.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,582 / 2.62%
Read min/max/mean length	30 / 151 / 130.35
Duplicated reads (estimated)	1,166,018 / 71.82%
Duplication rate	45.49%
Clipped reads	1,239,770 / 76.36%

2.2. ACGT Content

Number/percentage of A's	44,970,987 / 27.27%
Number/percentage of C's	36,538,197 / 22.16%
Number/percentage of T's	42,733,654 / 25.91%
Number/percentage of G's	40,662,253 / 24.66%
Number/percentage of N's	1,124 / 0%
GC Percentage	46.81%

2.3. Coverage

Mean	0.0545

Standard Deviation	6.3908
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2.4. Mapping Quality

Mean Mapping Quality	52.56
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2.5. Mismatches and indels

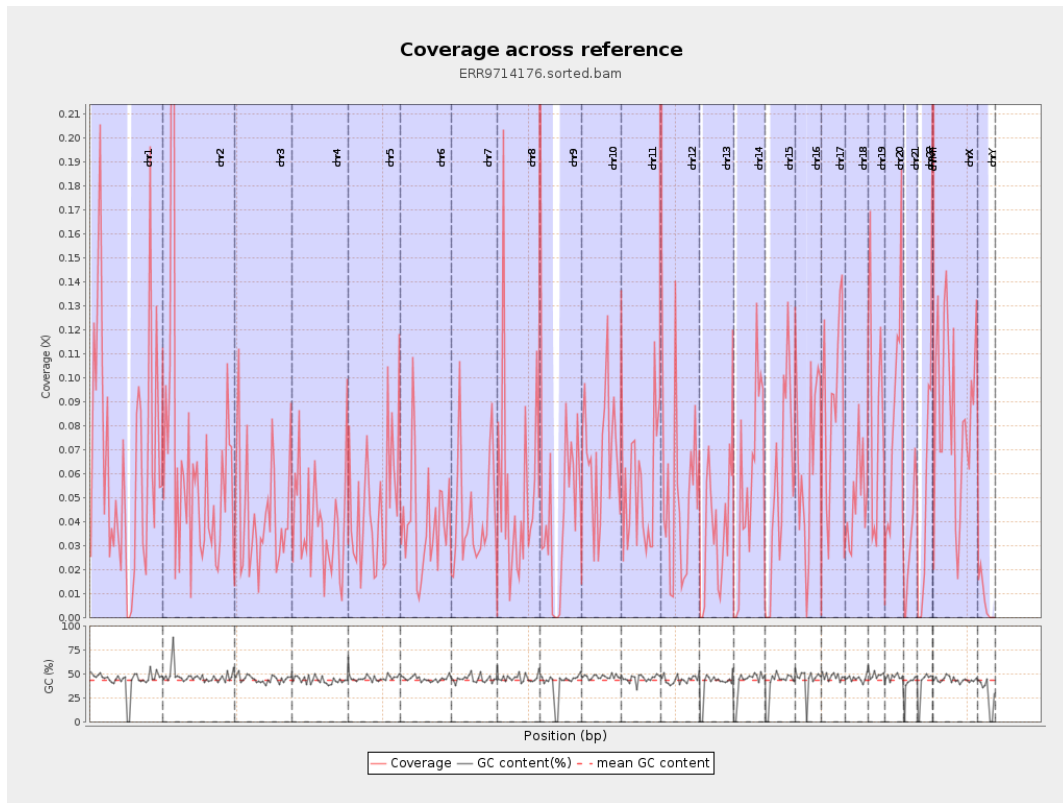
General error rate	4.47%
Mismatches	6,862,114
Insertions	180,152
Mapped reads with at least one insertion	13.39%
Deletions	630,391
Mapped reads with at least one deletion	45.89%
Homopolymer indels	28.96%

2.6. Chromosome stats

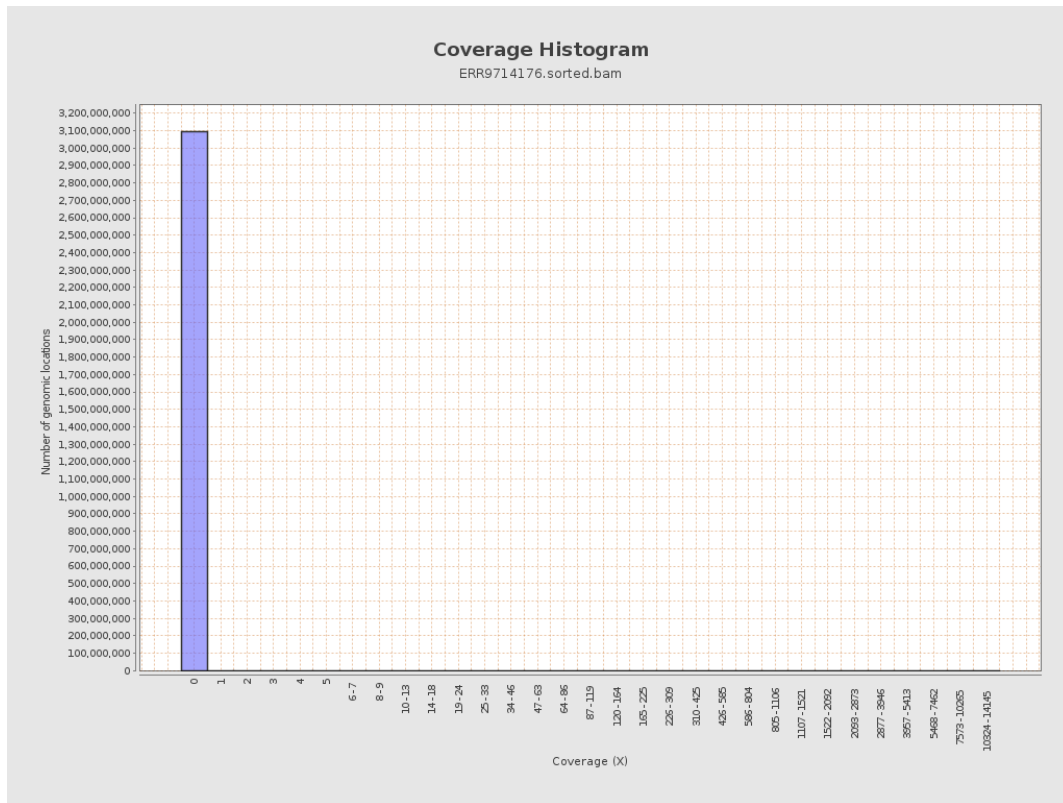
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16436198	0.0659	8.0117
chr2	243199373	15527255	0.0638	11.4642
chr3	198022430	8436189	0.0426	4.146
chr4	191154276	7582774	0.0397	4.4843
chr5	180915260	8702951	0.0481	4.7025
chr6	171115067	6786348	0.0397	3.8085
chr7	159138663	6682258	0.042	4.4256

chr8	146364022	7686946	0.0525	6.4432
chr9	141213431	5817504	0.0412	4.4686
chr10	135534747	9174816	0.0677	5.9945
chr11	135006516	7931169	0.0587	6.4959
chr12	133851895	7111976	0.0531	6.4912
chr13	115169878	4148343	0.036	4.4878
chr14	107349540	6159215	0.0574	6.3334
chr15	102531392	5438678	0.053	4.8168
chr16	90354753	6082583	0.0673	6.3826
chr17	81195210	7364789	0.0907	9.03
chr18	78077248	3816496	0.0489	4.4005
chr19	59128983	4607130	0.0779	7.9836
chr20	63025520	5370662	0.0852	8.2627
chr21	48129895	1534741	0.0319	3.1532
chr22	51304566	2610578	0.0509	5.7568
chrMT	16571	258193	15.581	142.435
chrX	155270560	13084176	0.0843	5.7026
chrY	59373566	424109	0.0071	1.0336

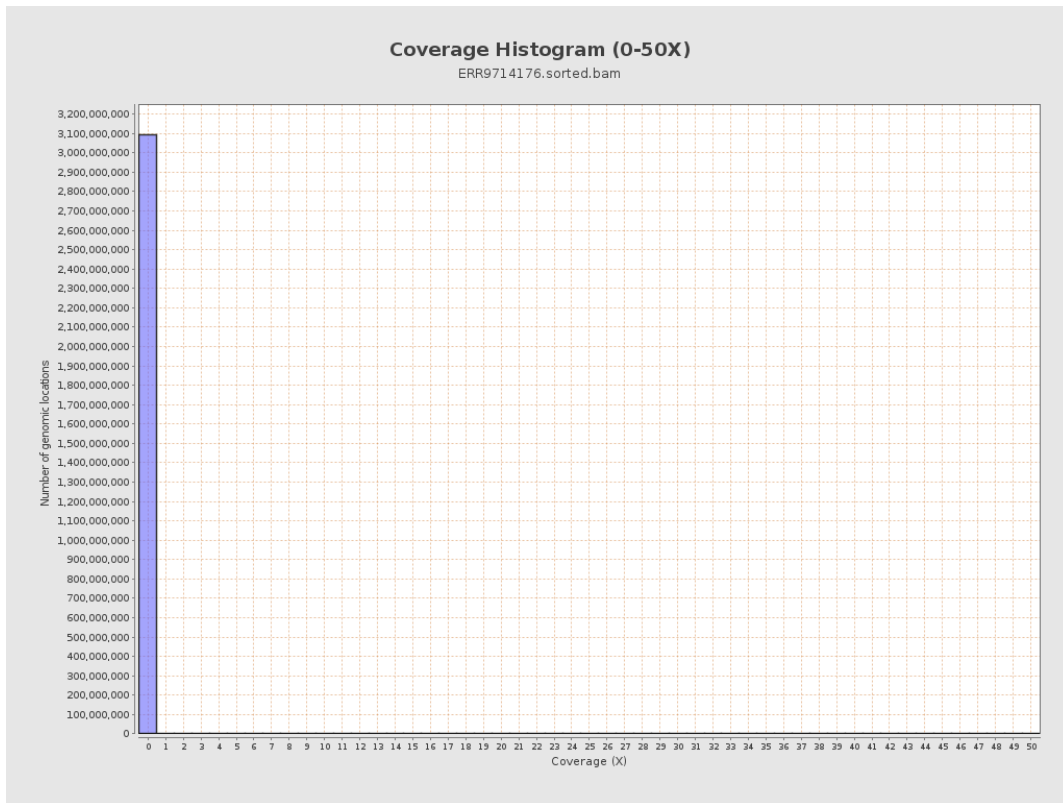
3. Results : Coverage across reference



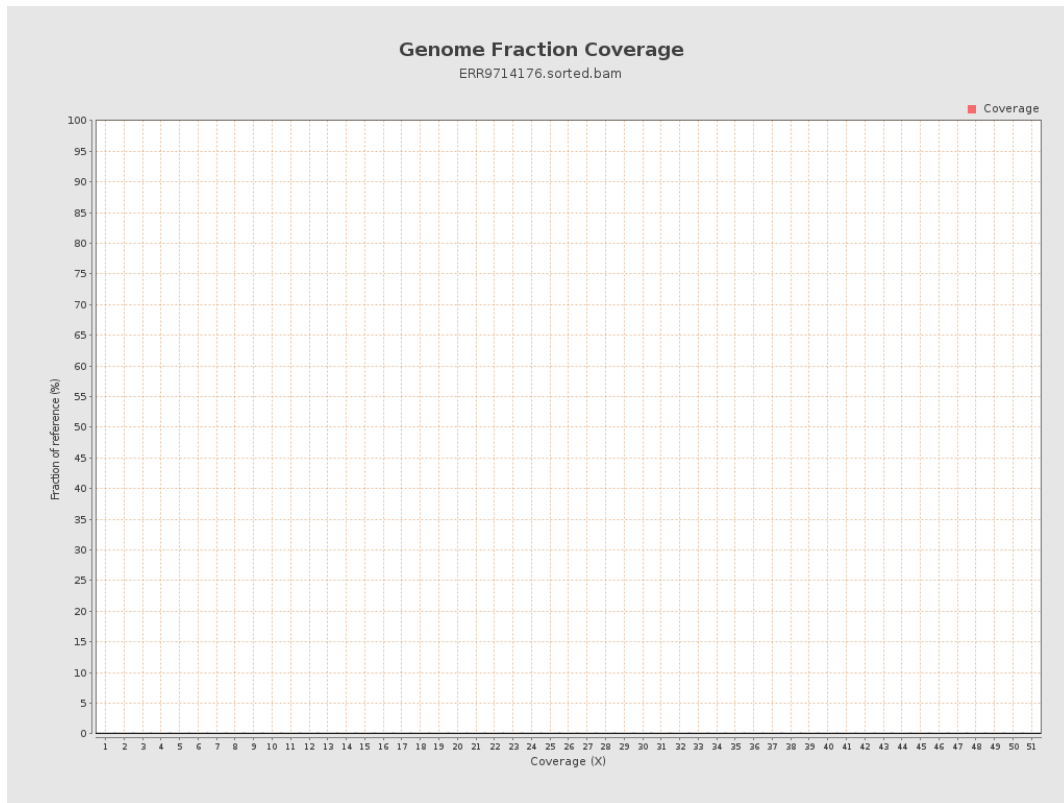
4. Results : Coverage Histogram



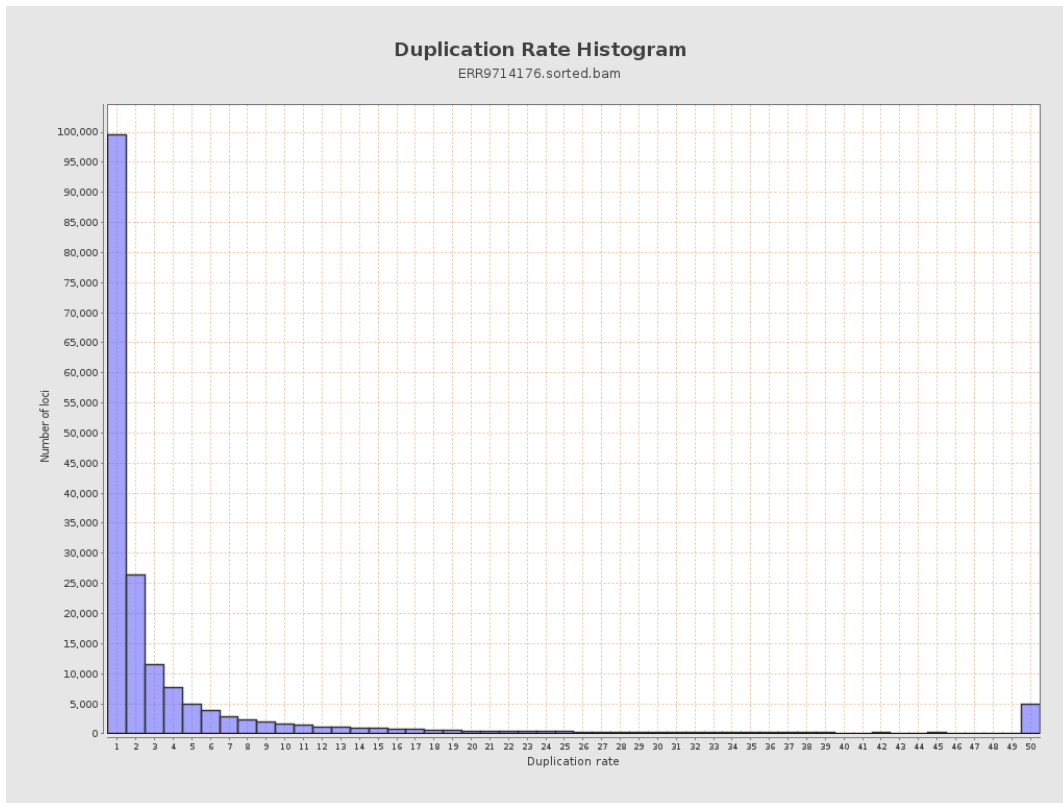
5. Results : Coverage Histogram (0-50X)



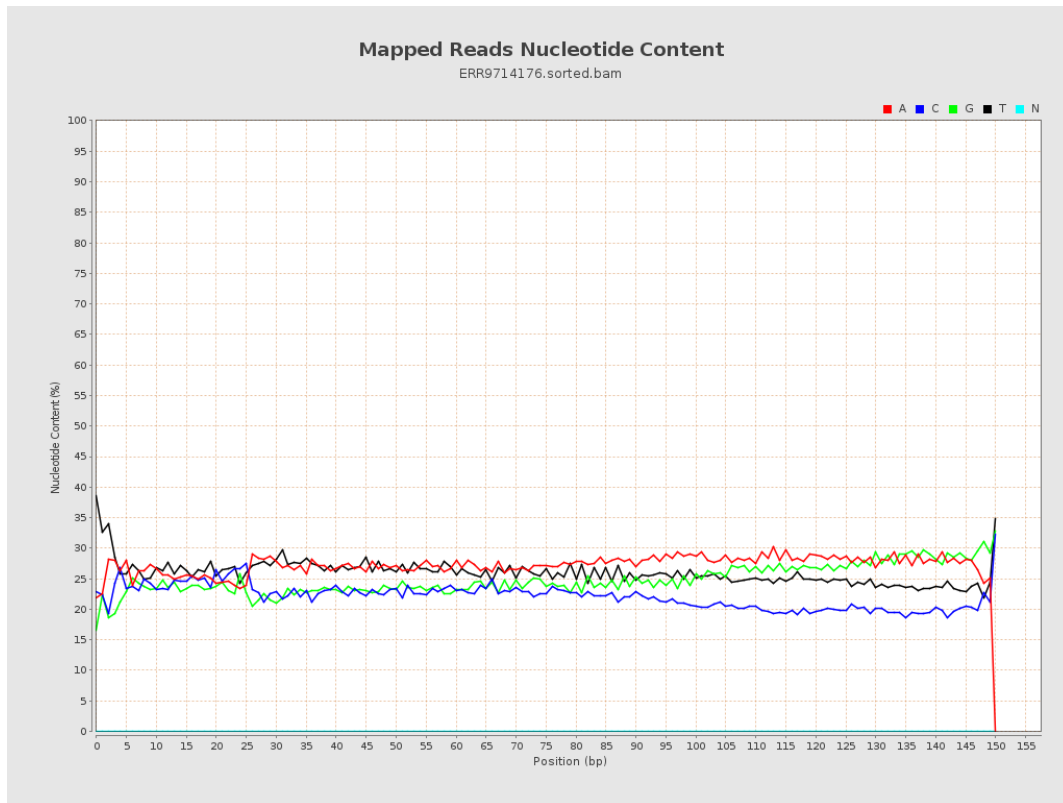
6. Results : Genome Fraction Coverage



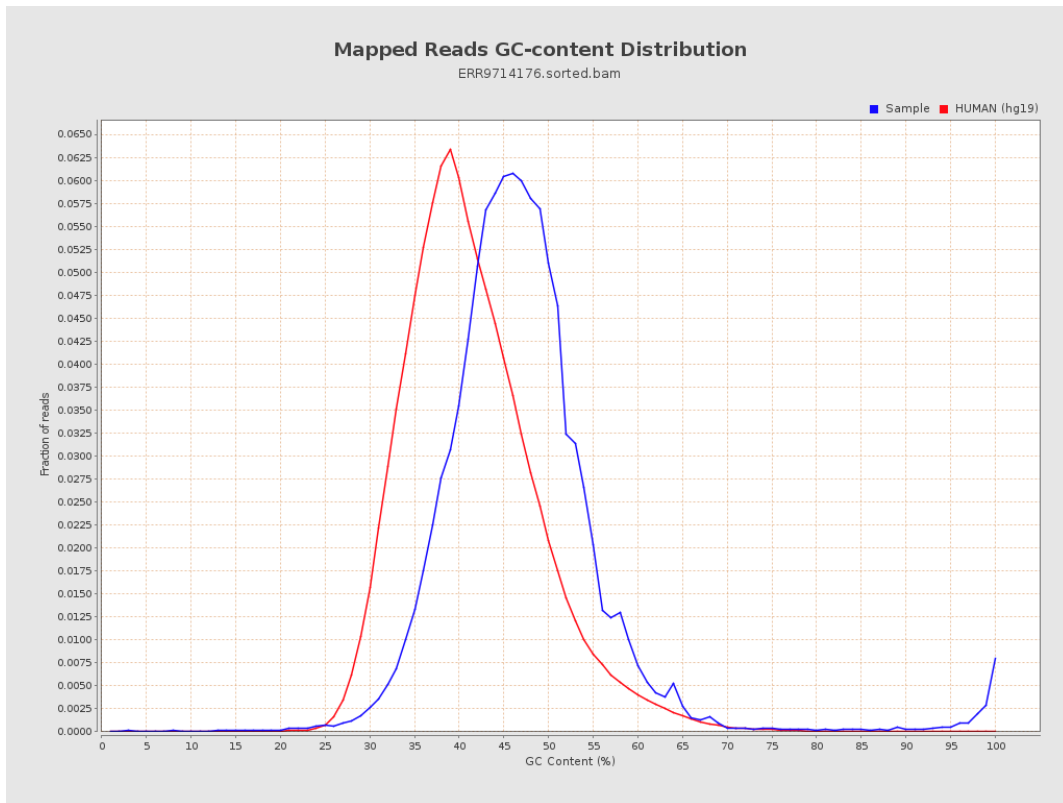
7. Results : Duplication Rate Histogram



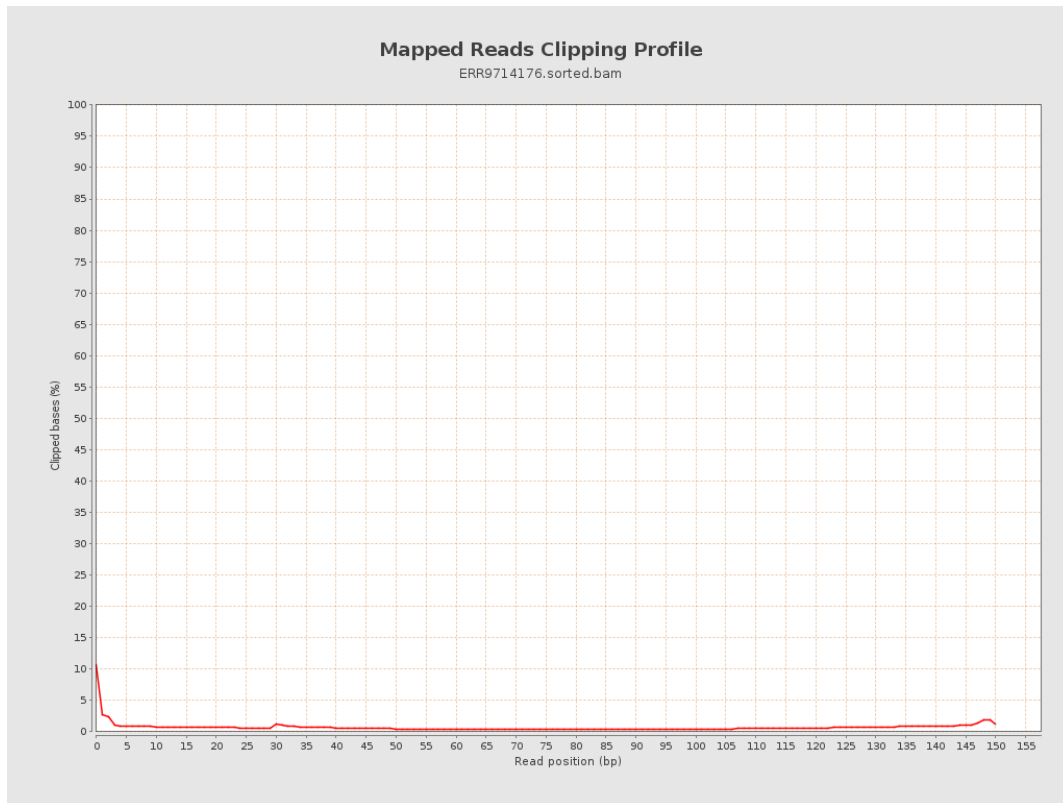
8. Results : Mapped Reads Nucleotide Content



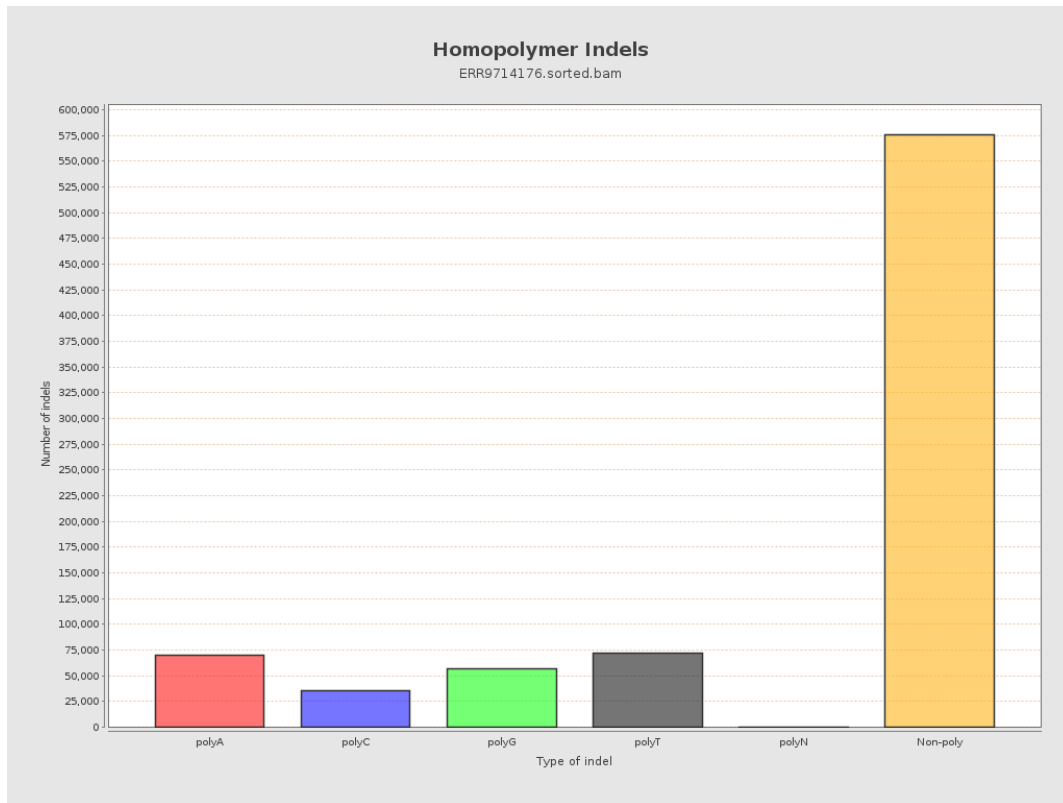
9. Results : Mapped Reads GC-content Distribution



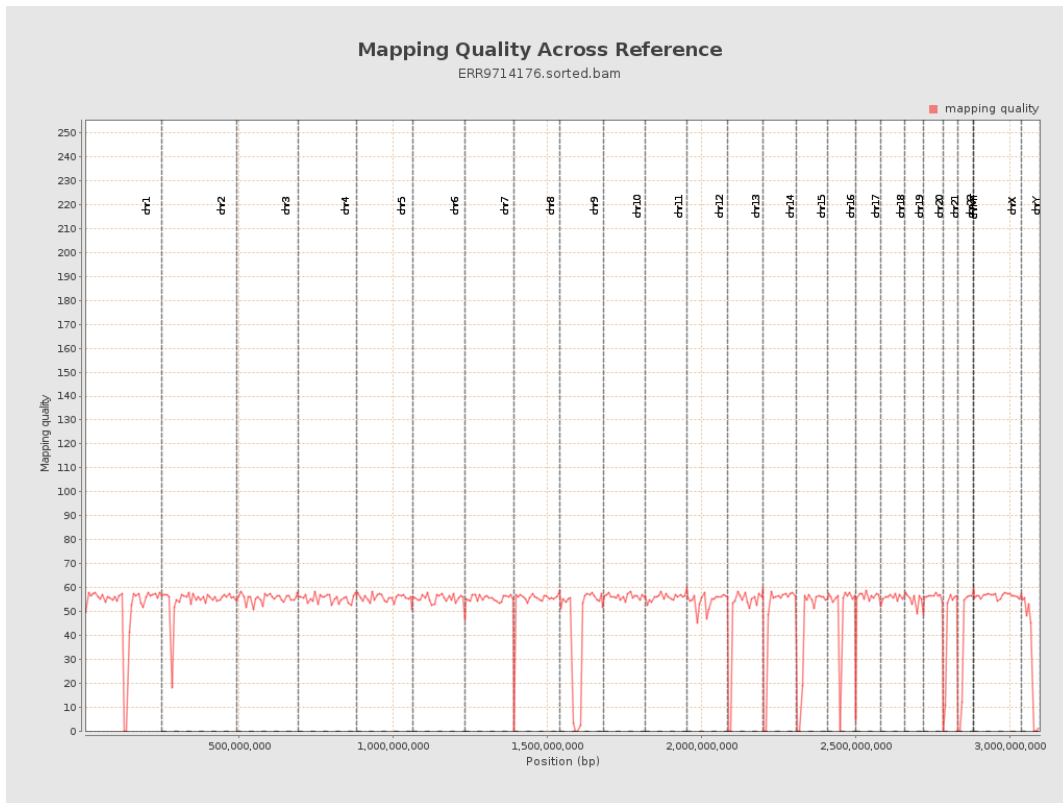
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

