

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:55:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714266.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_ERR9714266 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:55:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	256,614
Mapped reads	208,136 / 81.11%
Unmapped reads	48,478 / 18.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,304 / 2.46%
Read min/max/mean length	30 / 151 / 131.2
Duplicated reads (estimated)	170,633 / 66.49%
Duplication rate	42.76%
Clipped reads	195,500 / 76.18%

2.2. ACGT Content

Number/percentage of A's	6,936,279 / 26.38%
Number/percentage of C's	5,790,723 / 22.02%
Number/percentage of T's	6,572,179 / 25%
Number/percentage of G's	6,992,723 / 26.6%
Number/percentage of N's	187 / 0%
GC Percentage	48.62%

2.3. Coverage

Mean	0.0087

Standard Deviation	2.2573
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2.4. Mapping Quality

Mean Mapping Quality	51.21
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2.5. Mismatches and indels

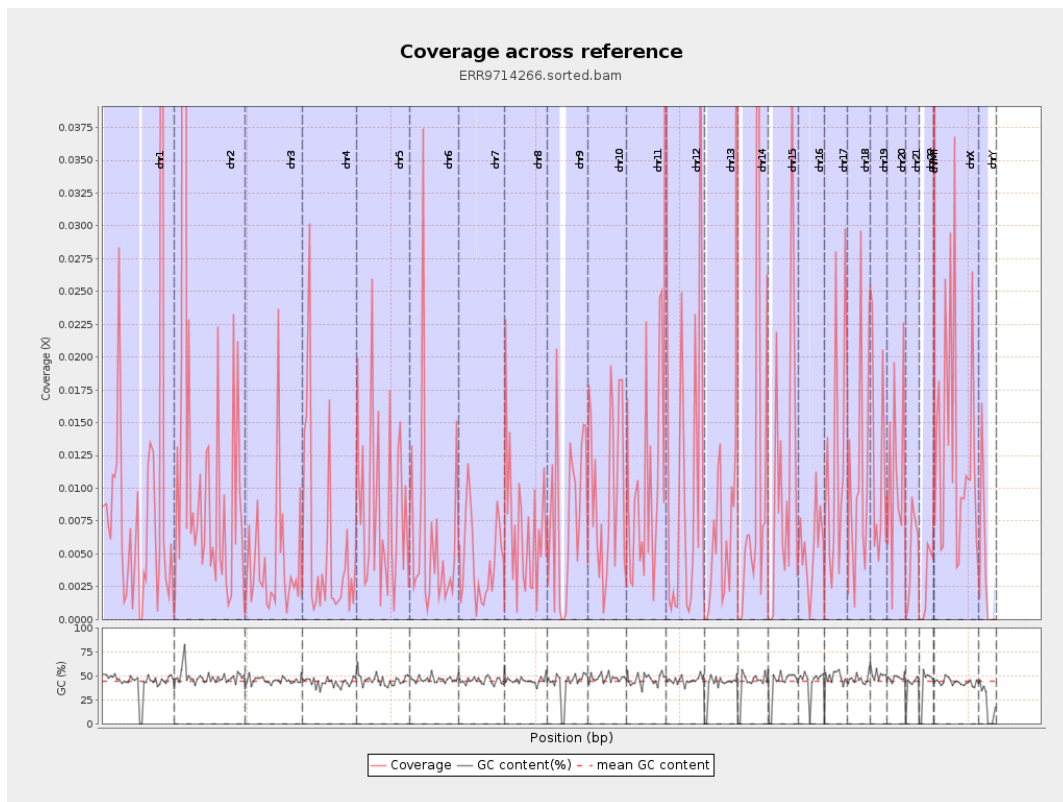
General error rate	4.42%
Mismatches	1,079,137
Insertions	29,017
Mapped reads with at least one insertion	13.42%
Deletions	91,223
Mapped reads with at least one deletion	41.61%
Homopolymer indels	31.09%

2.6. Chromosome stats

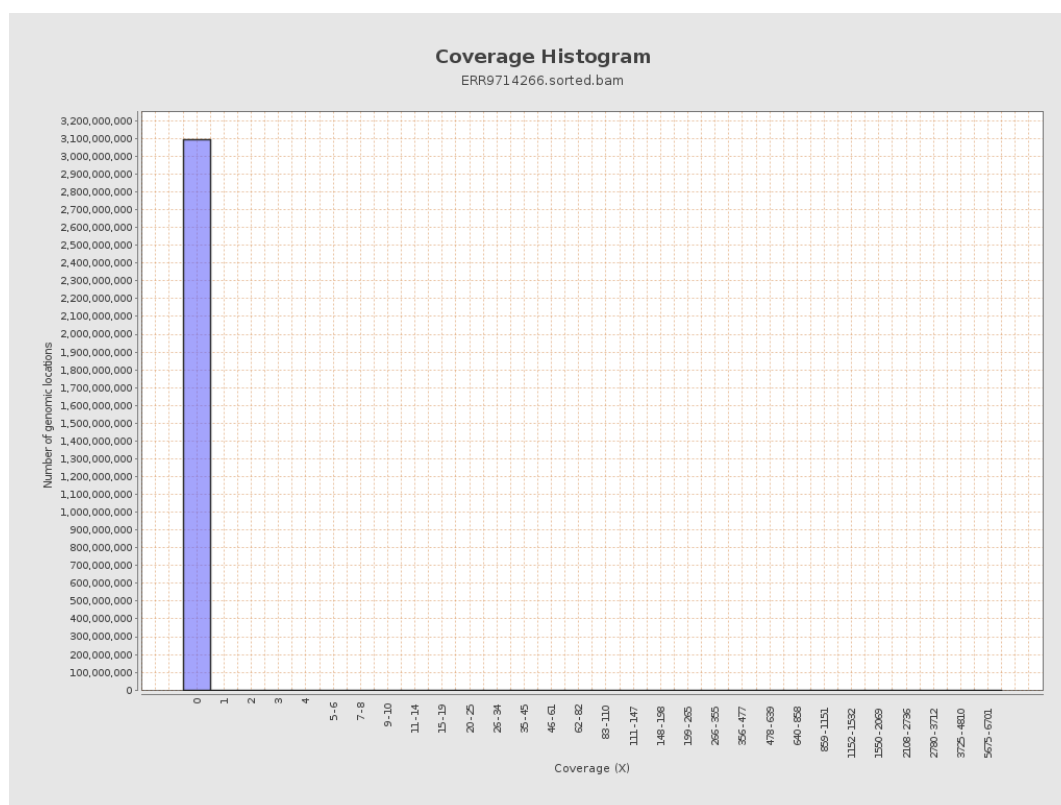
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2381144	0.0096	3.0093
chr2	243199373	3501221	0.0144	4.7666
chr3	198022430	848881	0.0043	0.7623
chr4	191154276	993497	0.0052	1.2264
chr5	180915260	1459360	0.0081	1.6311
chr6	171115067	1064938	0.0062	1.3455
chr7	159138663	725843	0.0046	0.658

chr8	146364022	1013296	0.0069	1.2536
chr9	141213431	1093753	0.0077	1.3979
chr10	135534747	1303704	0.0096	1.4407
chr11	135006516	1374755	0.0102	1.6026
chr12	133851895	1398172	0.0104	2.5111
chr13	115169878	1077481	0.0094	3.4503
chr14	107349540	1127292	0.0105	3.8258
chr15	102531392	1090431	0.0106	2.0801
chr16	90354753	490811	0.0054	0.6076
chr17	81195210	971309	0.012	1.8642
chr18	78077248	830464	0.0106	2.3756
chr19	59128983	670108	0.0113	1.1604
chr20	63025520	719014	0.0114	1.4691
chr21	48129895	244782	0.0051	0.7518
chr22	51304566	154849	0.003	0.3896
chrMT	16571	25514	1.5397	12.227
chrX	155270560	2089923	0.0135	1.4138
chrY	59373566	230508	0.0039	0.8669

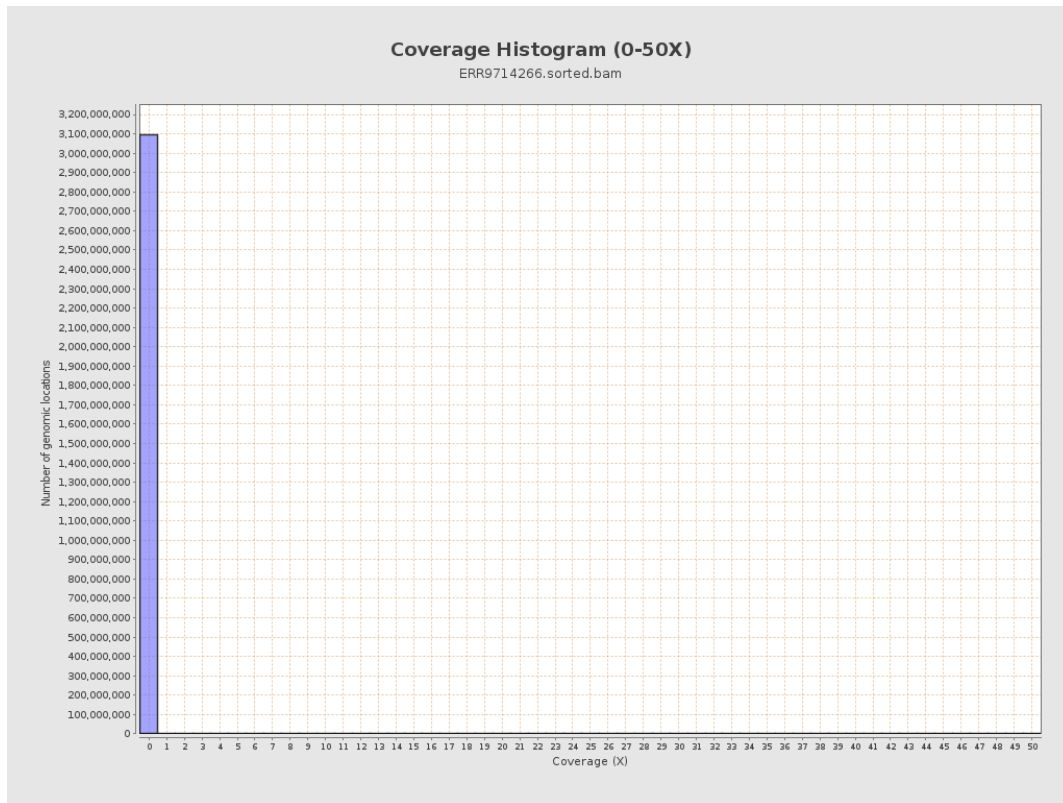
3. Results : Coverage across reference



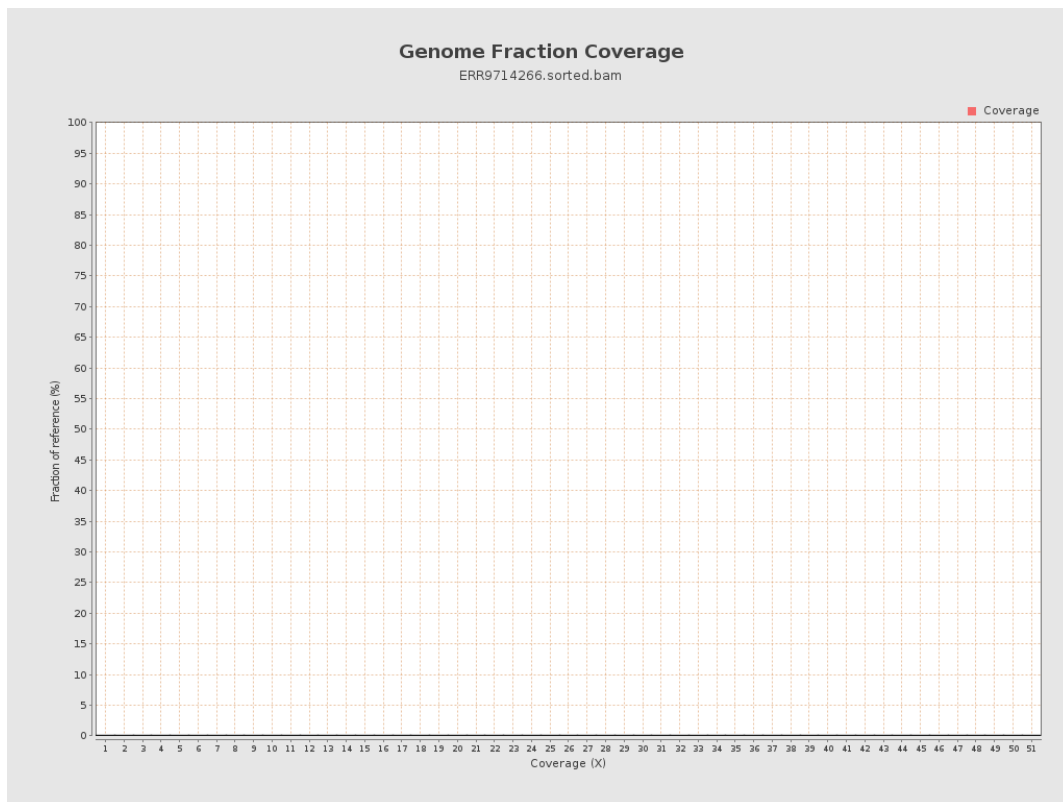
4. Results : Coverage Histogram



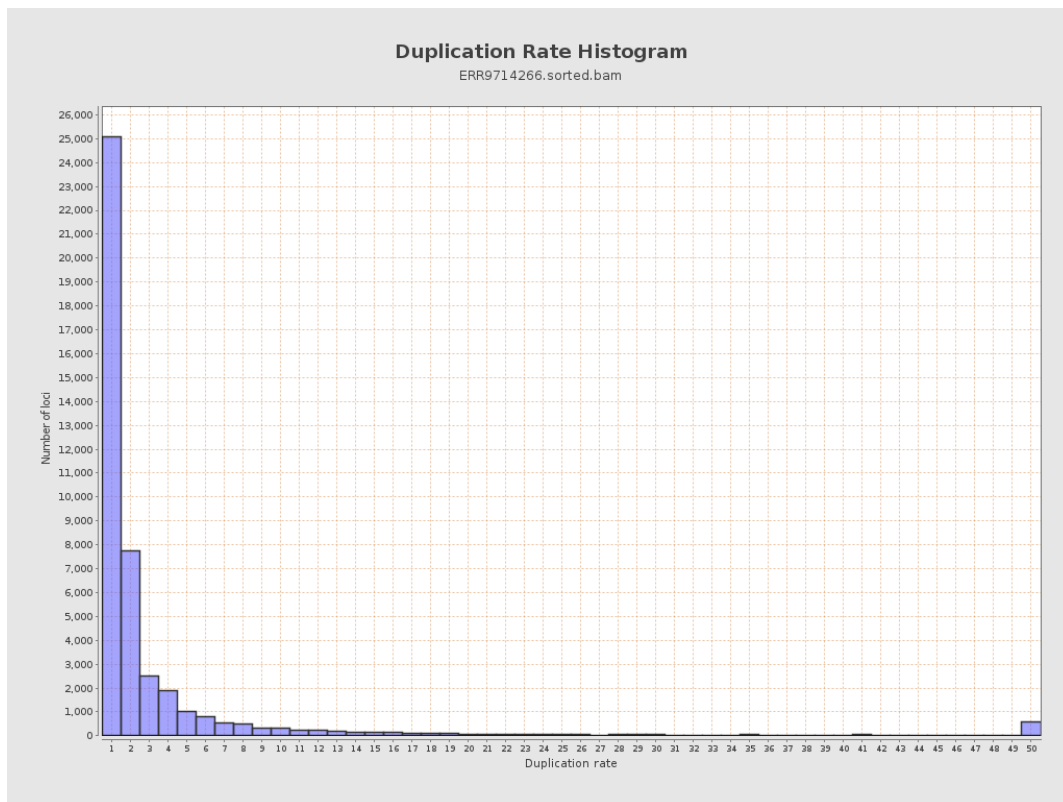
5. Results : Coverage Histogram (0-50X)



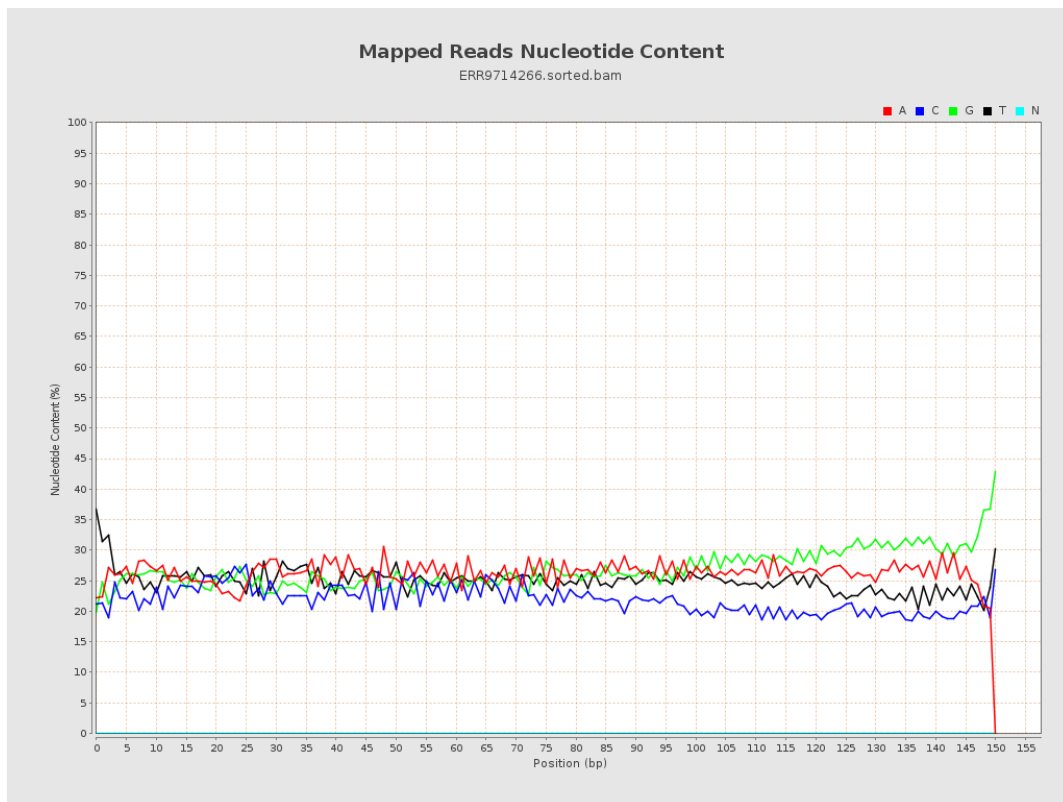
6. Results : Genome Fraction Coverage



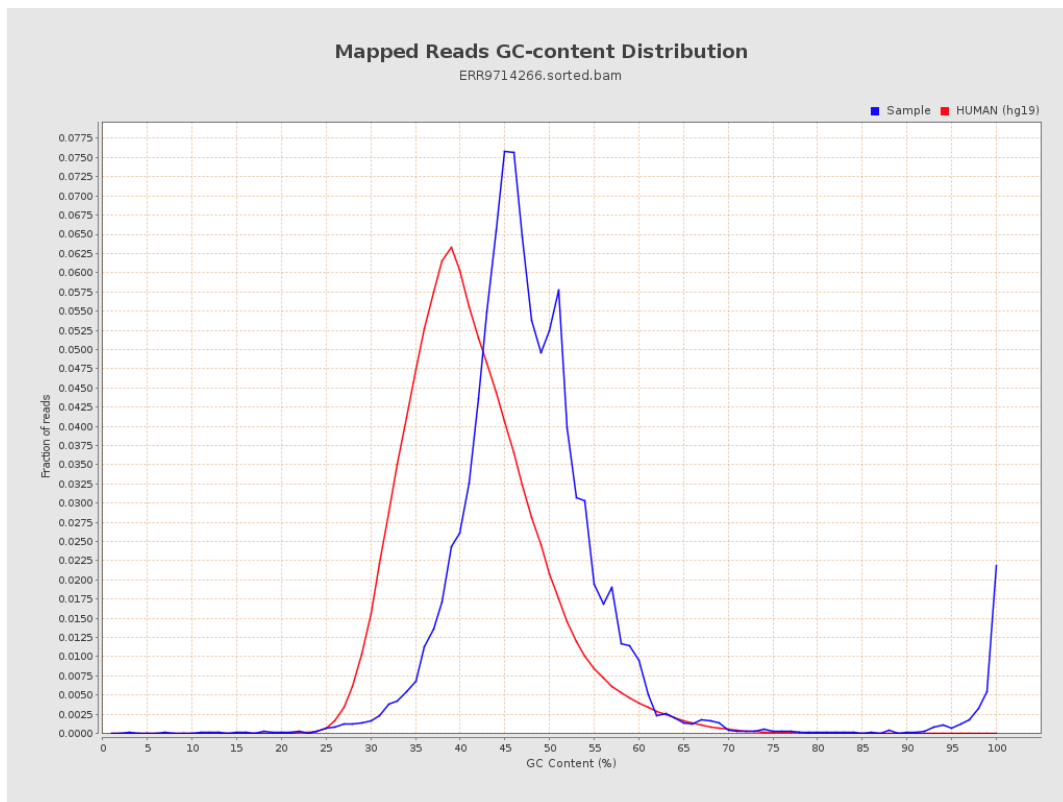
7. Results : Duplication Rate Histogram



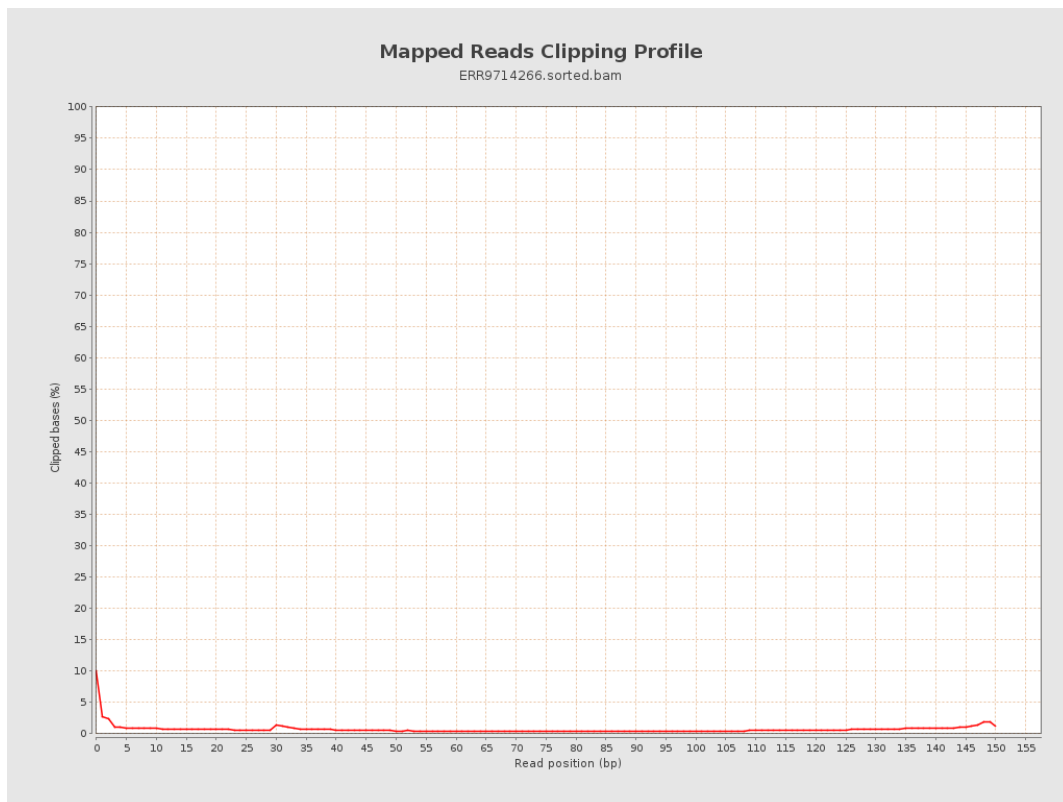
8. Results : Mapped Reads Nucleotide Content



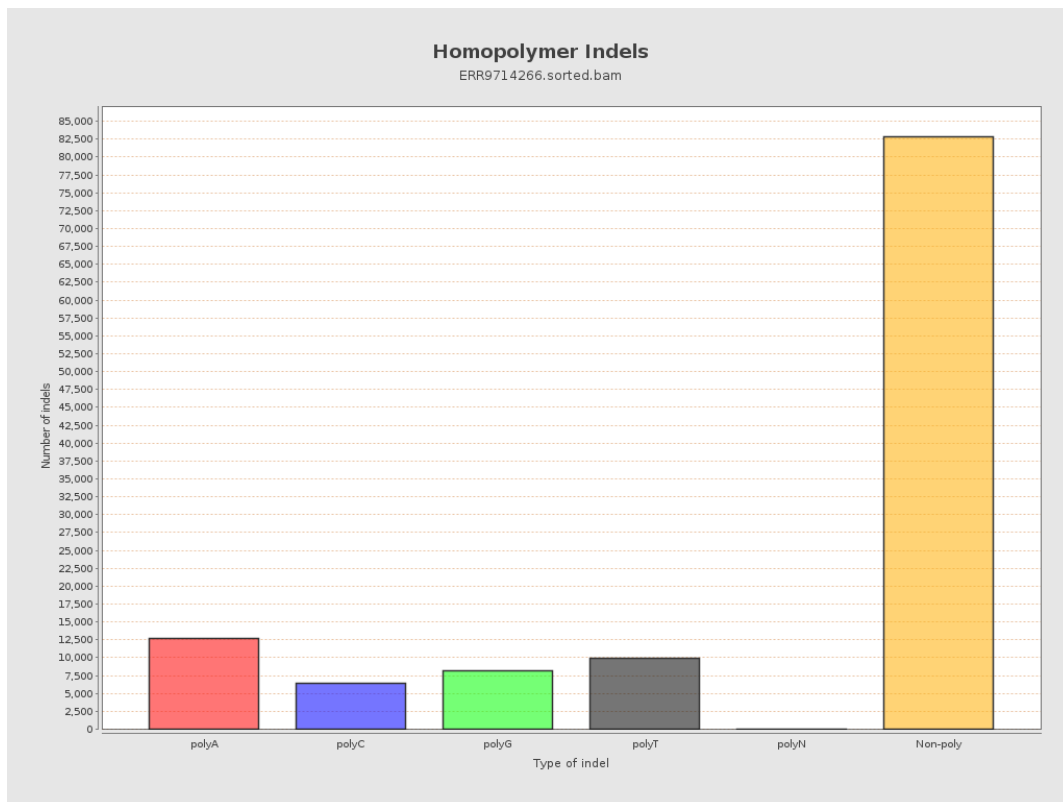
9. Results : Mapped Reads GC-content Distribution



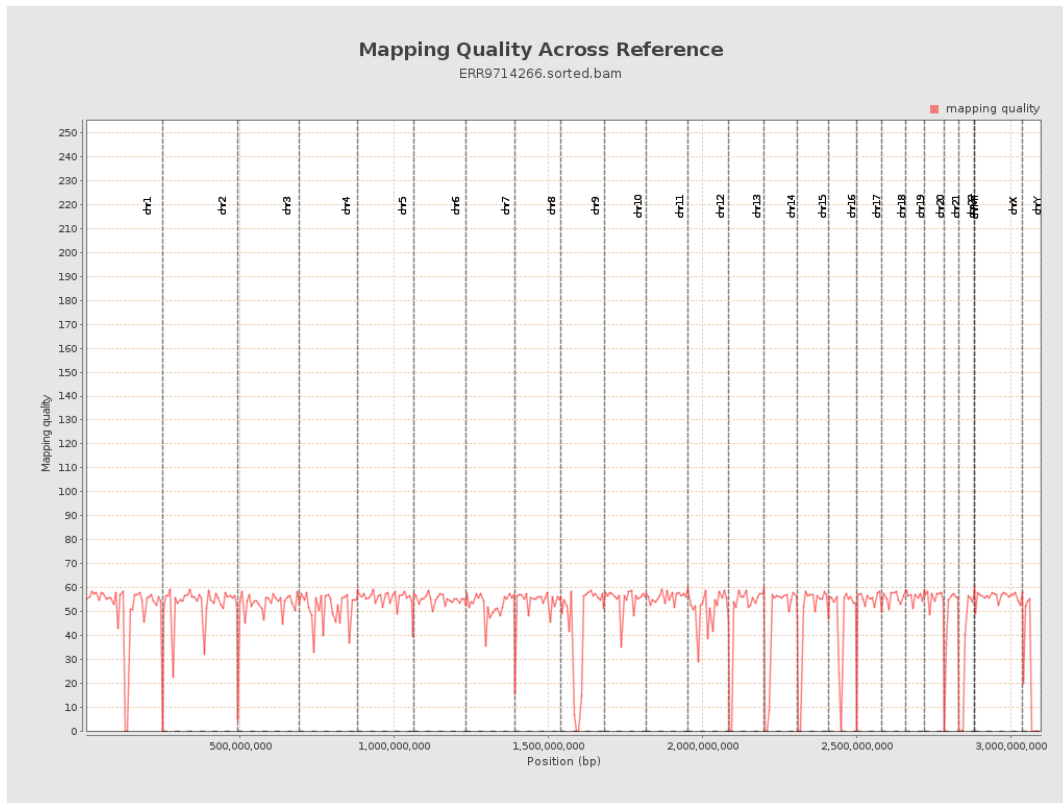
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

