

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:43:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524814.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_SRR10524814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:43:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,076,017
Mapped reads	987,090 / 91.74%
Unmapped reads	88,927 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,976 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,652 / 2.48%
Duplication rate	2.03%
Clipped reads	988,344 / 91.85%

2.2. ACGT Content

Number/percentage of A's	13,756,215 / 24.2%
Number/percentage of C's	10,610,481 / 18.67%
Number/percentage of T's	18,327,309 / 32.24%
Number/percentage of G's	14,143,286 / 24.88%
Number/percentage of N's	7,484 / 0.01%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1807
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2.4. Mapping Quality

Mean Mapping Quality	44.62
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2.5. Mismatches and indels

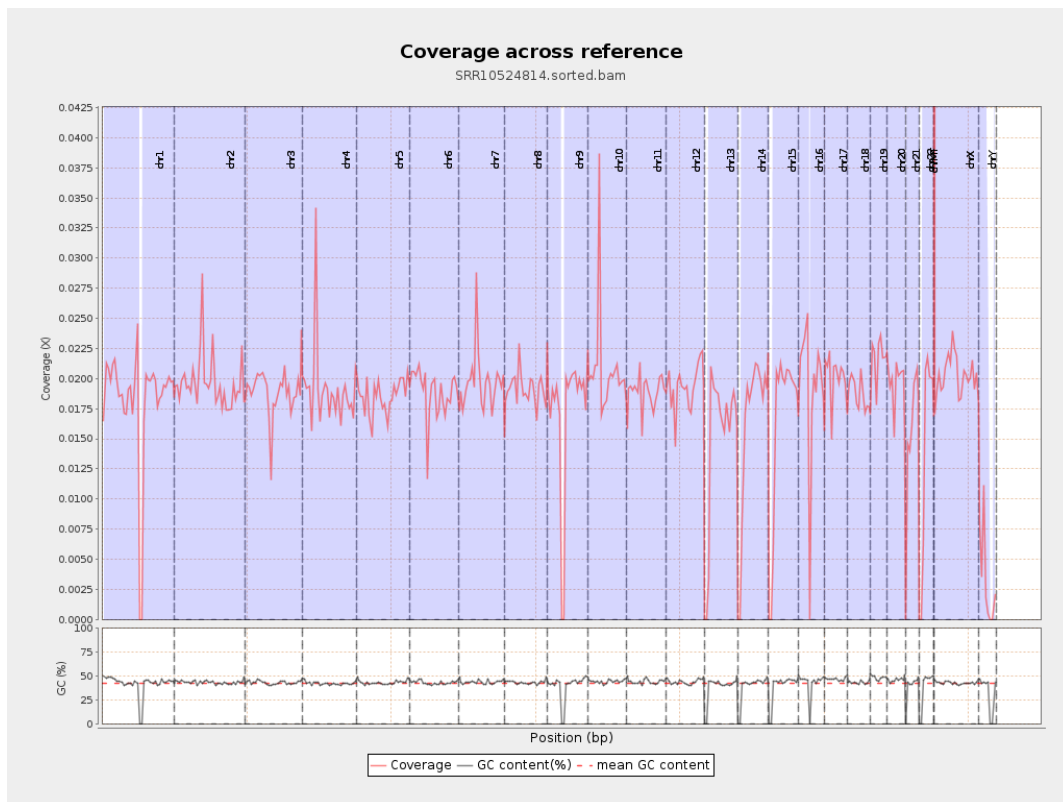
General error rate	0.52%
Mismatches	288,210
Insertions	4,068
Mapped reads with at least one insertion	0.41%
Deletions	11,806
Mapped reads with at least one deletion	1.19%
Homopolymer indels	42.23%

2.6. Chromosome stats

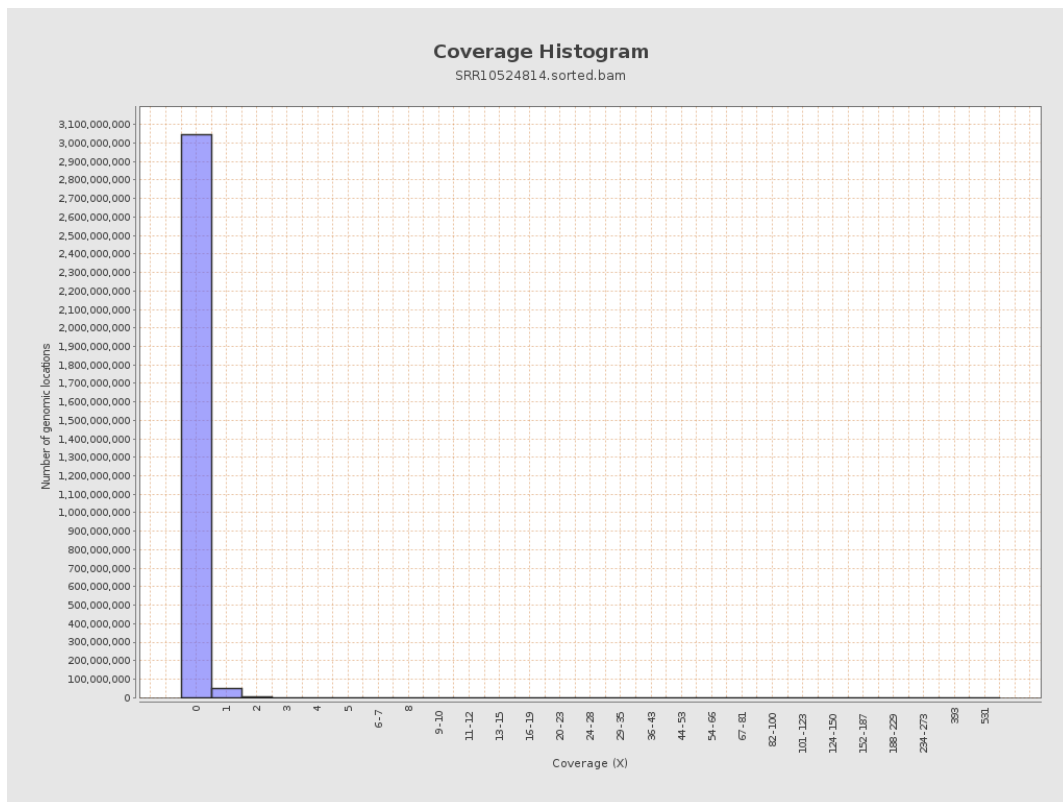
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4530899	0.0182	0.2368
chr2	243199373	4773127	0.0196	0.2709
chr3	198022430	3733235	0.0189	0.1474
chr4	191154276	3651493	0.0191	0.1636
chr5	180915260	3352936	0.0185	0.1449
chr6	171115067	3220616	0.0188	0.1558
chr7	159138663	3140799	0.0197	0.2152

chr8	146364022	2802478	0.0191	0.1665
chr9	141213431	2402580	0.017	0.1584
chr10	135534747	2819769	0.0208	0.2096
chr11	135006516	2558279	0.0189	0.1632
chr12	133851895	2585102	0.0193	0.149
chr13	115169878	1724569	0.015	0.1295
chr14	107349540	1739707	0.0162	0.1373
chr15	102531392	1659955	0.0162	0.1372
chr16	90354753	1723322	0.0191	0.1589
chr17	81195210	1630636	0.0201	0.1547
chr18	78077248	1467757	0.0188	0.2291
chr19	59128983	1279662	0.0216	0.2017
chr20	63025520	1231534	0.0195	0.1527
chr21	48129895	751211	0.0156	0.1418
chr22	51304566	724936	0.0141	0.1269
chrMT	16571	16537	0.9979	1.1216
chrX	155270560	3153069	0.0203	0.1577
chrY	59373566	189506	0.0032	0.0974

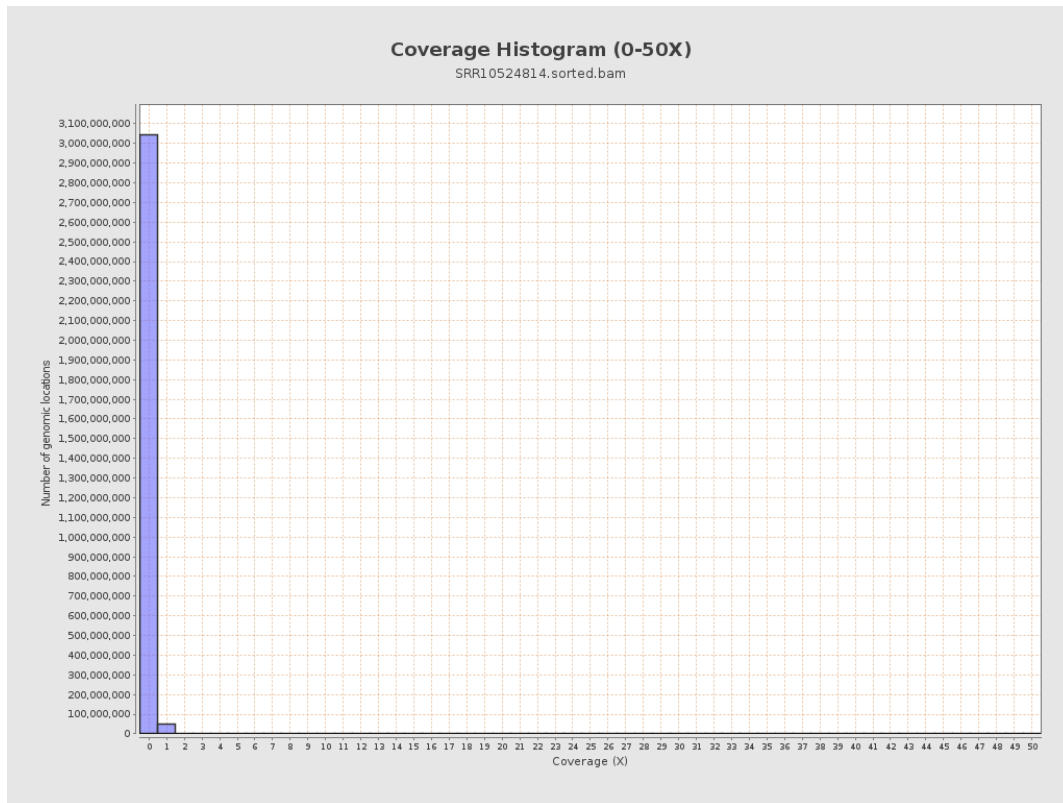
3. Results : Coverage across reference



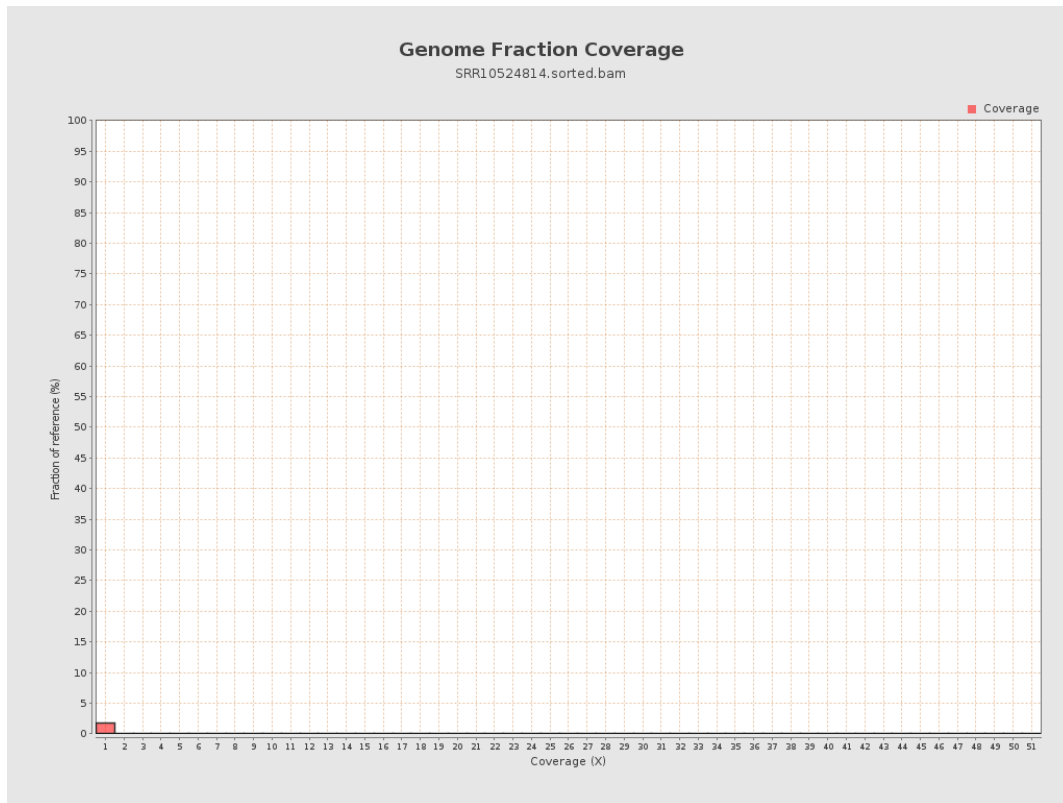
4. Results : Coverage Histogram



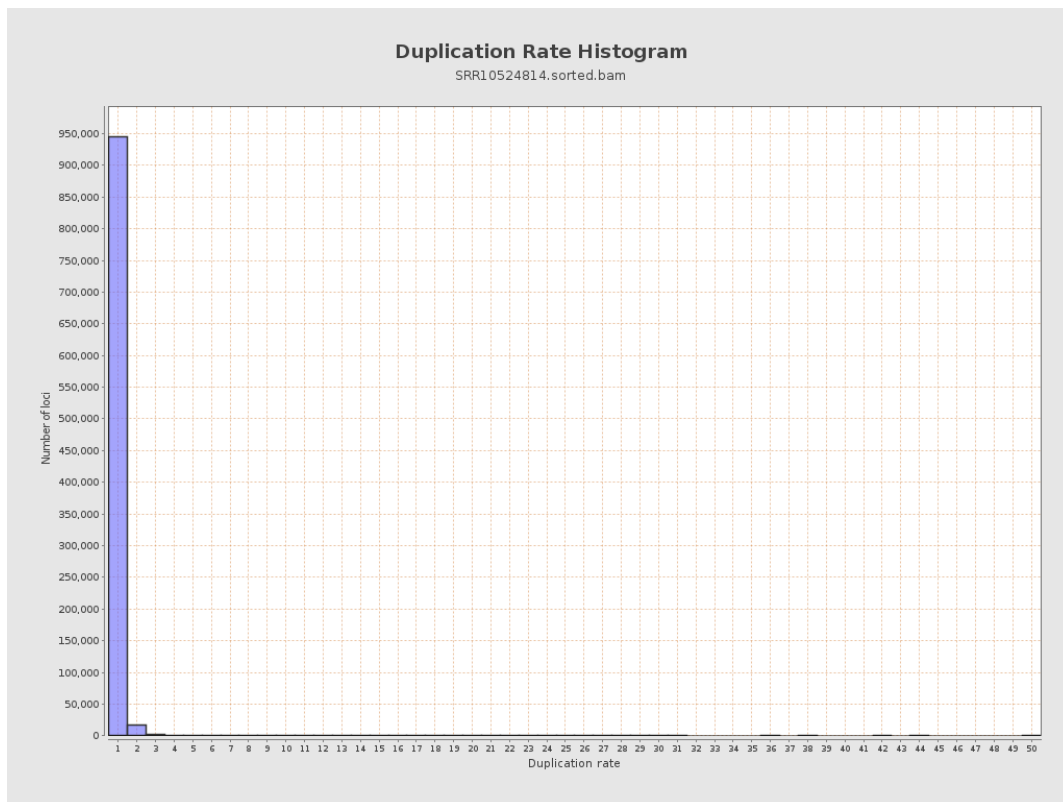
5. Results : Coverage Histogram (0-50X)



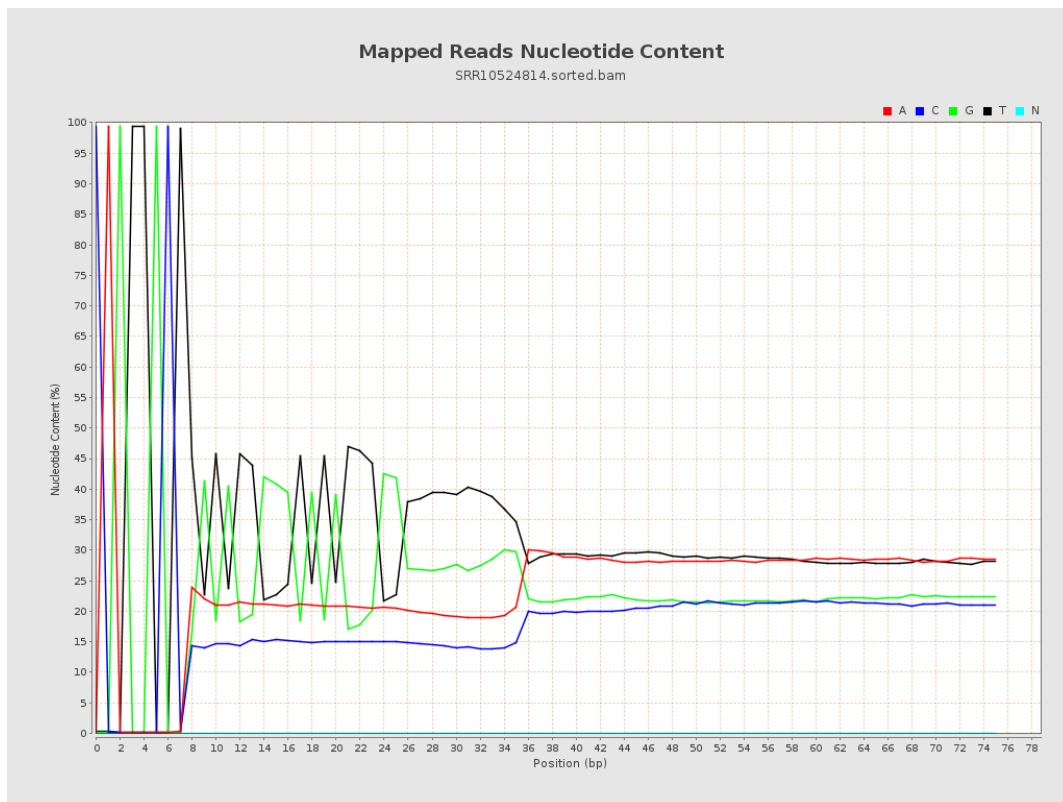
6. Results : Genome Fraction Coverage



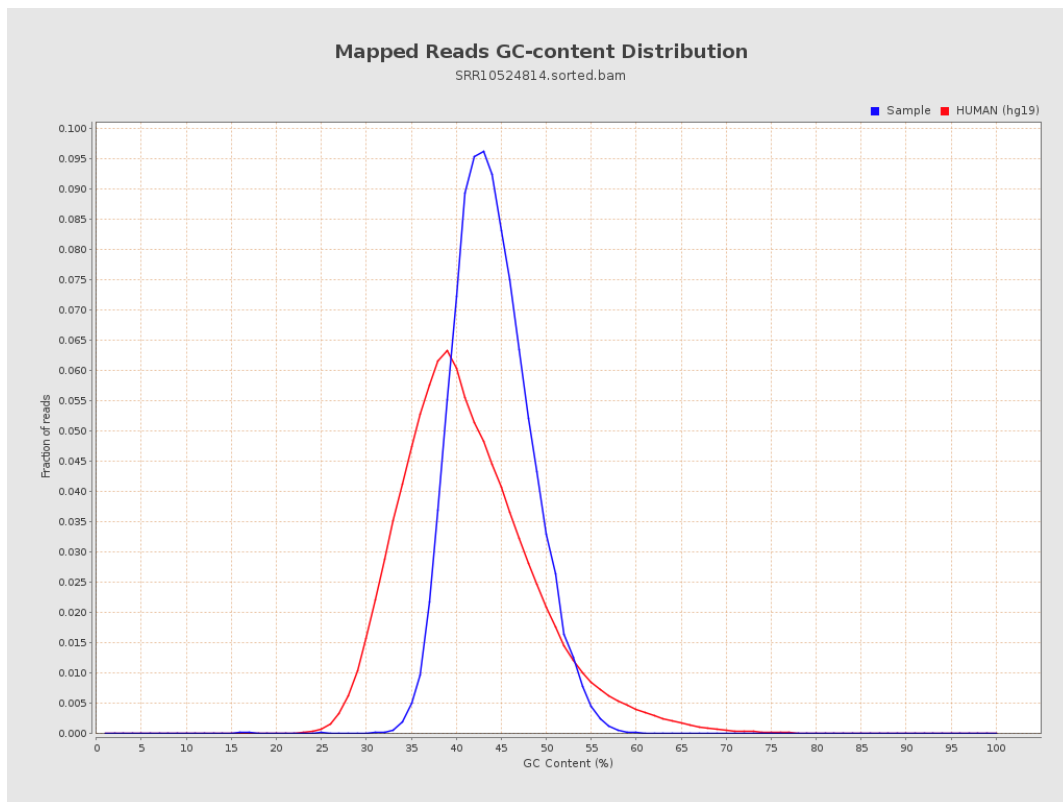
7. Results : Duplication Rate Histogram



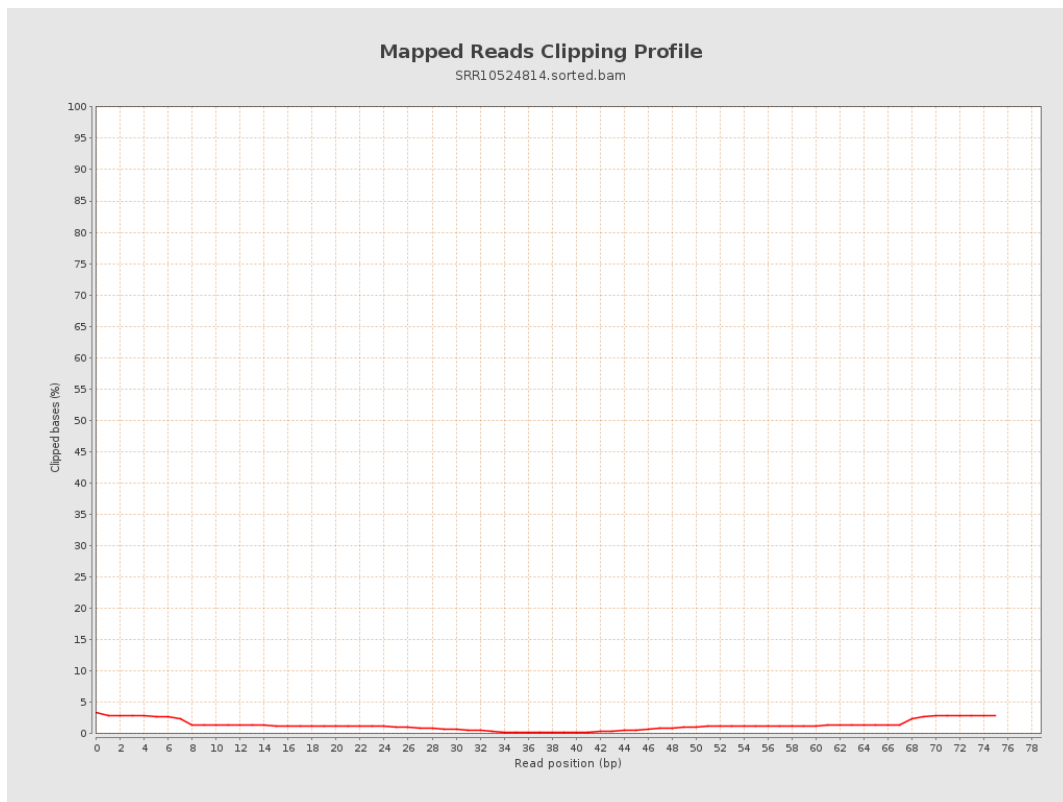
8. Results : Mapped Reads Nucleotide Content



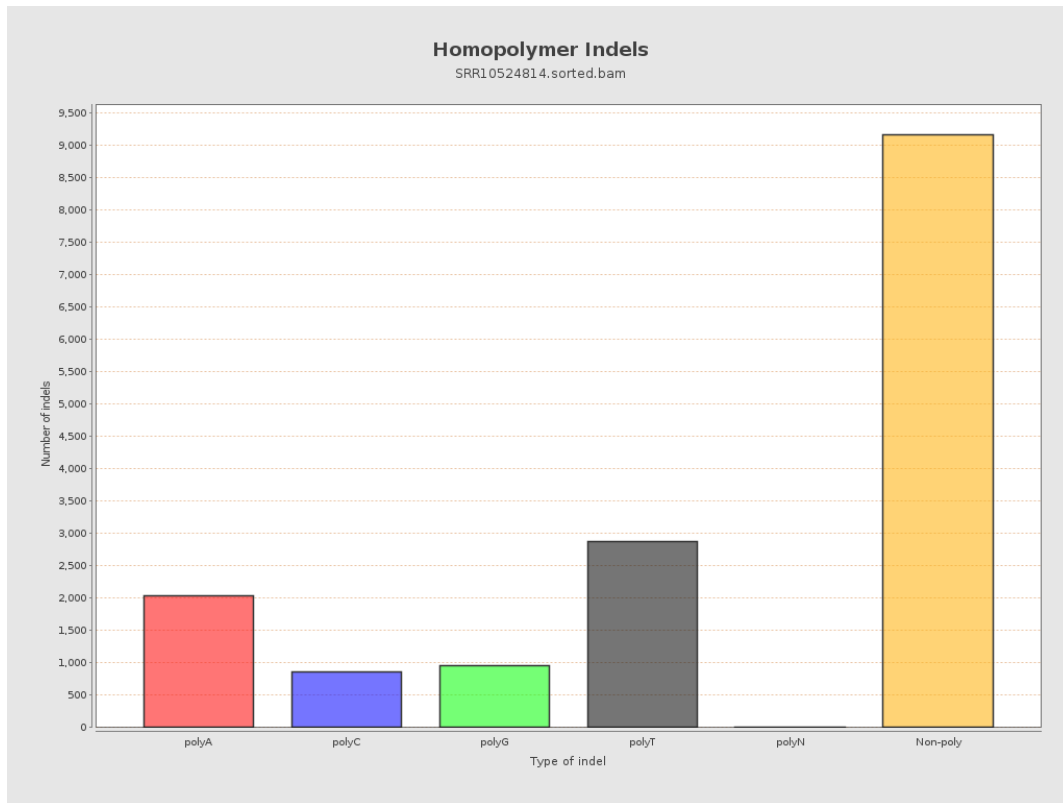
9. Results : Mapped Reads GC-content Distribution



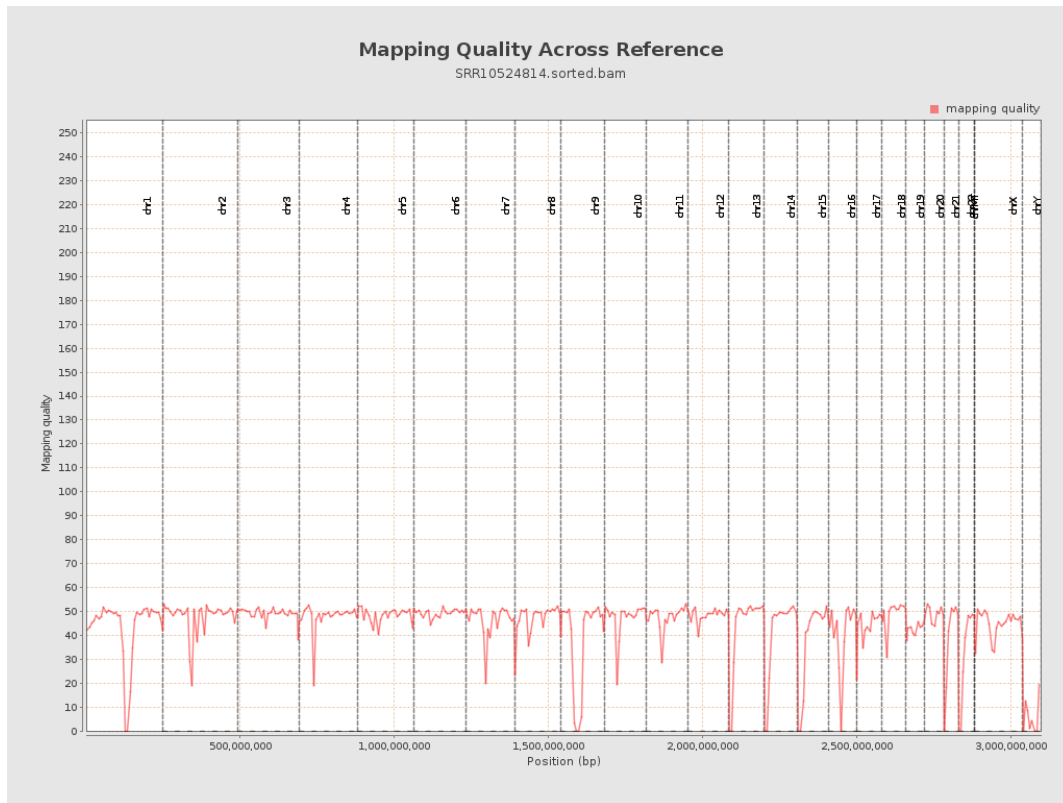
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

