

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:12:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054610.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_SRR054610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:12:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,778,203
Mapped reads	11,617,588 / 73.63%
Unmapped reads	4,160,615 / 26.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	318 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,012,756 / 19.09%
Duplication rate	18.49%
Clipped reads	1,064,247 / 6.75%

2.2. ACGT Content

Number/percentage of A's	165,176,619 / 30.15%
Number/percentage of C's	103,537,232 / 18.9%
Number/percentage of T's	166,007,490 / 30.3%
Number/percentage of G's	113,205,008 / 20.66%
Number/percentage of N's	2,492 / 0%
GC Percentage	39.56%

2.3. Coverage

Mean	0.177

Standard Deviation	1.2946
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2.4. Mapping Quality

Mean Mapping Quality	45.4
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2.5. Mismatches and indels

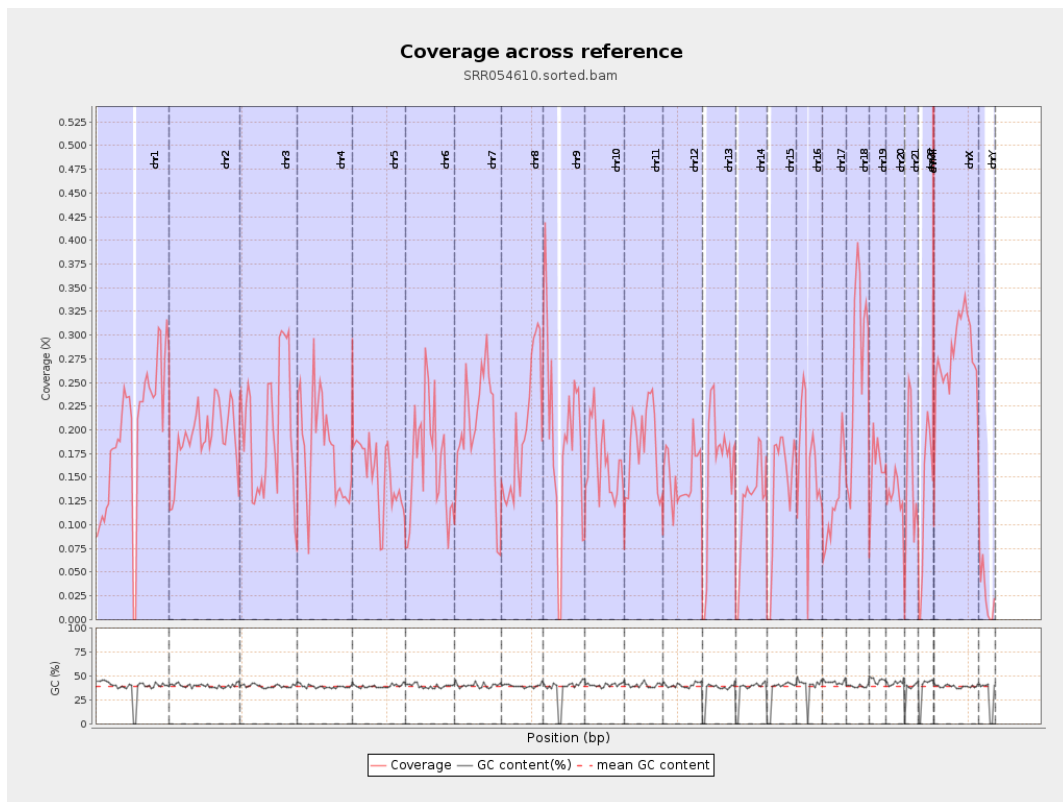
General error rate	0.56%
Mismatches	3,057,752
Insertions	22,221
Mapped reads with at least one insertion	0.19%
Deletions	73,905
Mapped reads with at least one deletion	0.63%
Homopolymer indels	47.46%

2.6. Chromosome stats

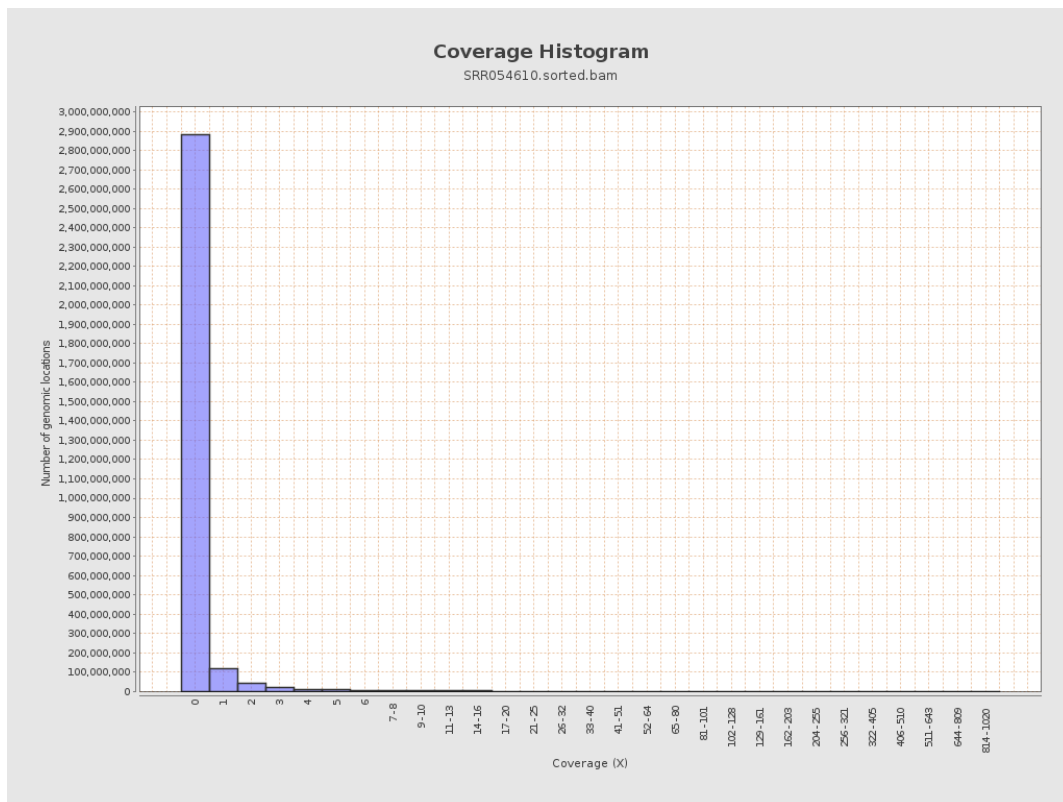
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	48774834	0.1957	1.4053
chr2	243199373	46820445	0.1925	1.4914
chr3	198022430	39746400	0.2007	1.2837
chr4	191154276	33951900	0.1776	1.2248
chr5	180915260	27582810	0.1525	1.0327
chr6	171115067	27694435	0.1618	1.224
chr7	159138663	32402536	0.2036	1.5294

chr8	146364022	29138529	0.1991	1.3806
chr9	141213431	27289842	0.1933	1.4159
chr10	135534747	22720557	0.1676	1.242
chr11	135006516	24821297	0.1839	1.3232
chr12	133851895	20043951	0.1497	1.0424
chr13	115169878	18177481	0.1578	1.0742
chr14	107349540	12832938	0.1195	1.0621
chr15	102531392	14162919	0.1381	0.9772
chr16	90354753	14840644	0.1642	1.2854
chr17	81195210	10029193	0.1235	0.9069
chr18	78077248	20924074	0.268	1.7952
chr19	59128983	9664714	0.1635	1.2869
chr20	63025520	8215995	0.1304	1.0309
chr21	48129895	6982289	0.1451	1.2308
chr22	51304566	6509977	0.1269	0.9491
chrMT	16571	33174	2.0019	3.9338
chrX	155270560	43106411	0.2776	1.6798
chrY	59373566	1570557	0.0265	0.5801

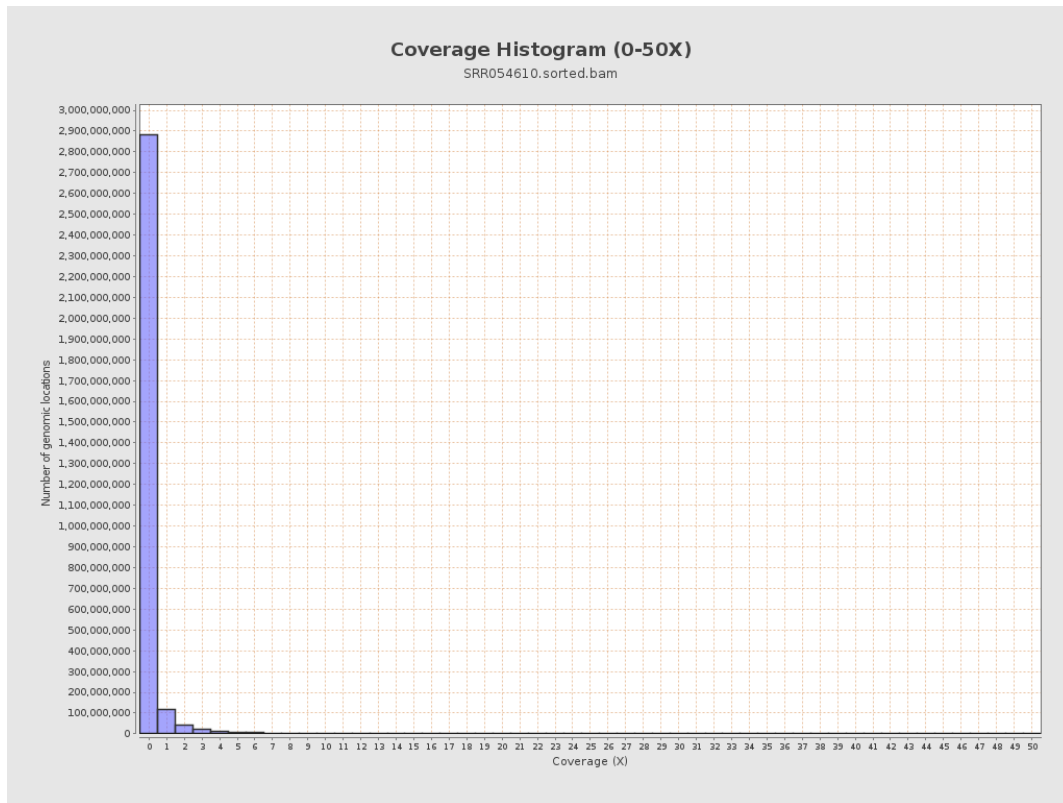
3. Results : Coverage across reference



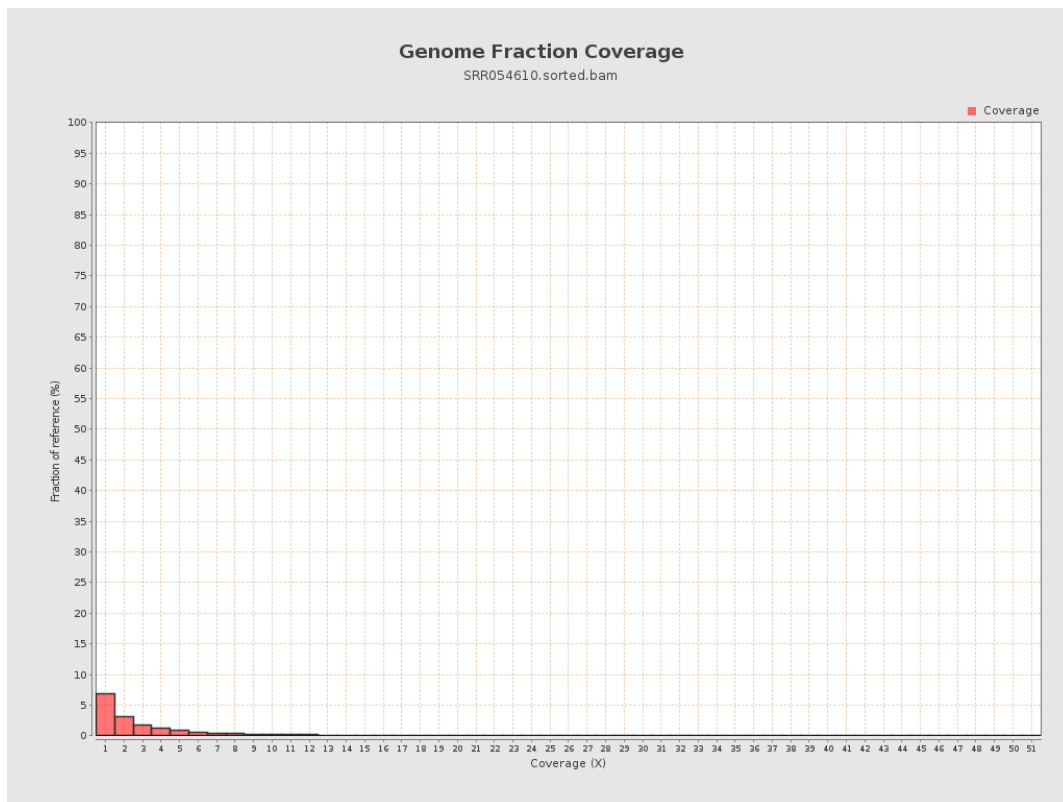
4. Results : Coverage Histogram



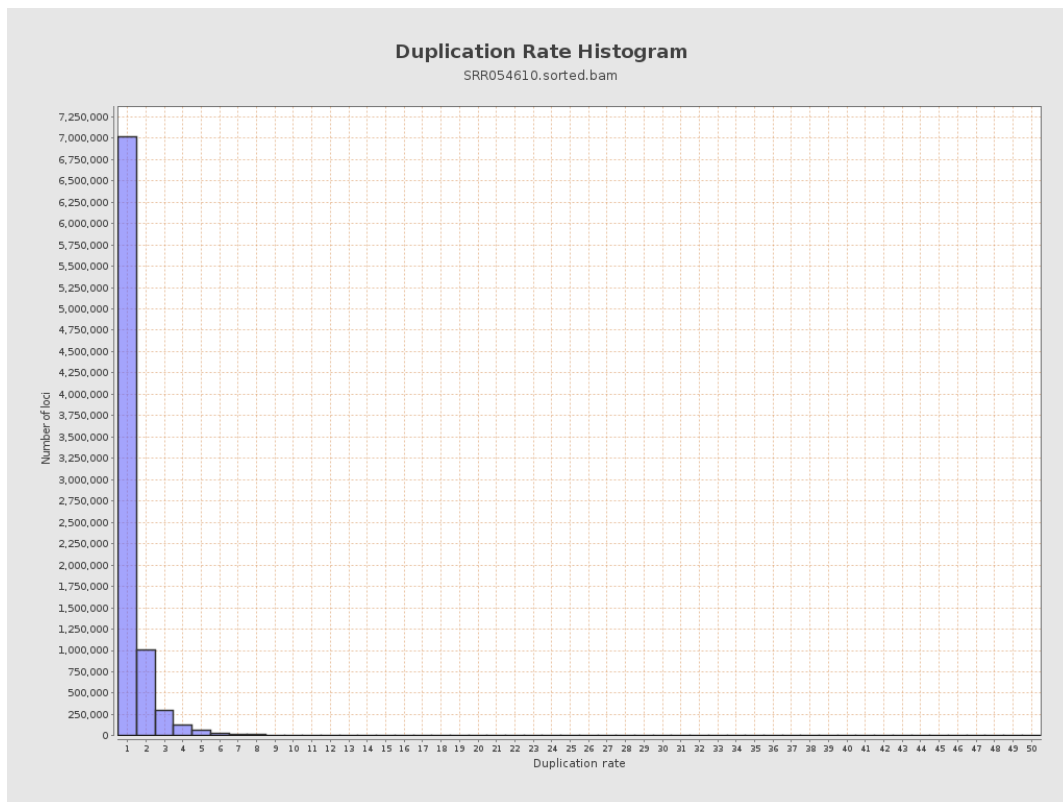
5. Results : Coverage Histogram (0-50X)



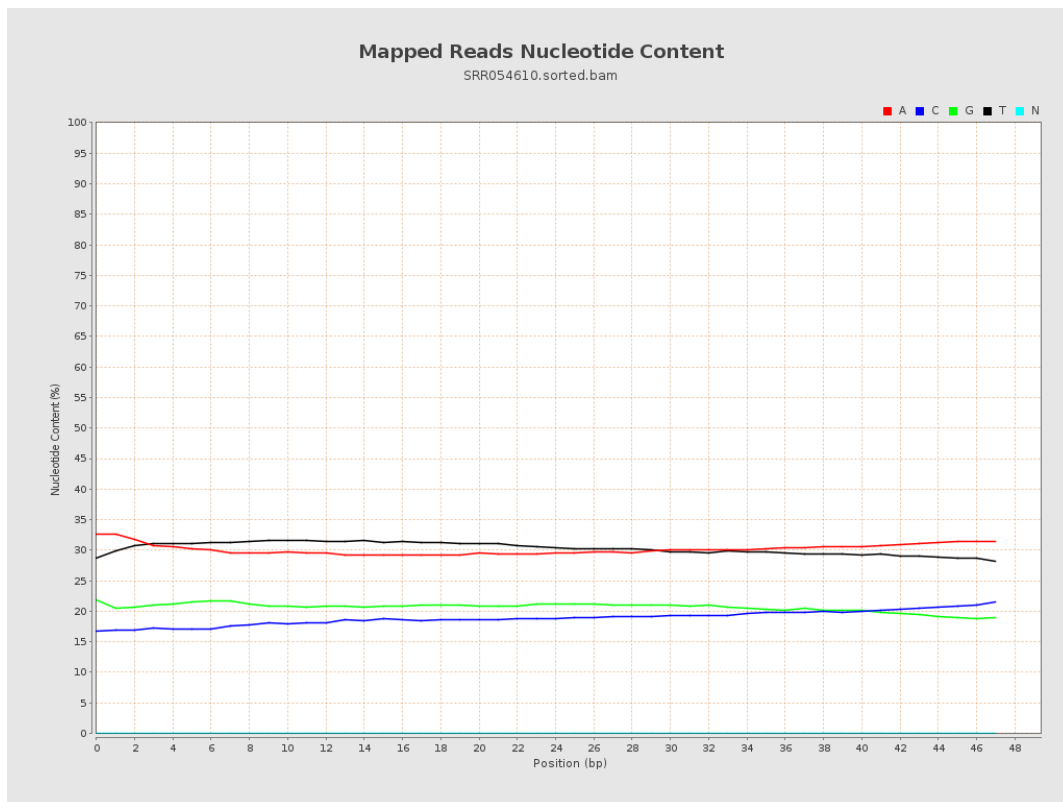
6. Results : Genome Fraction Coverage



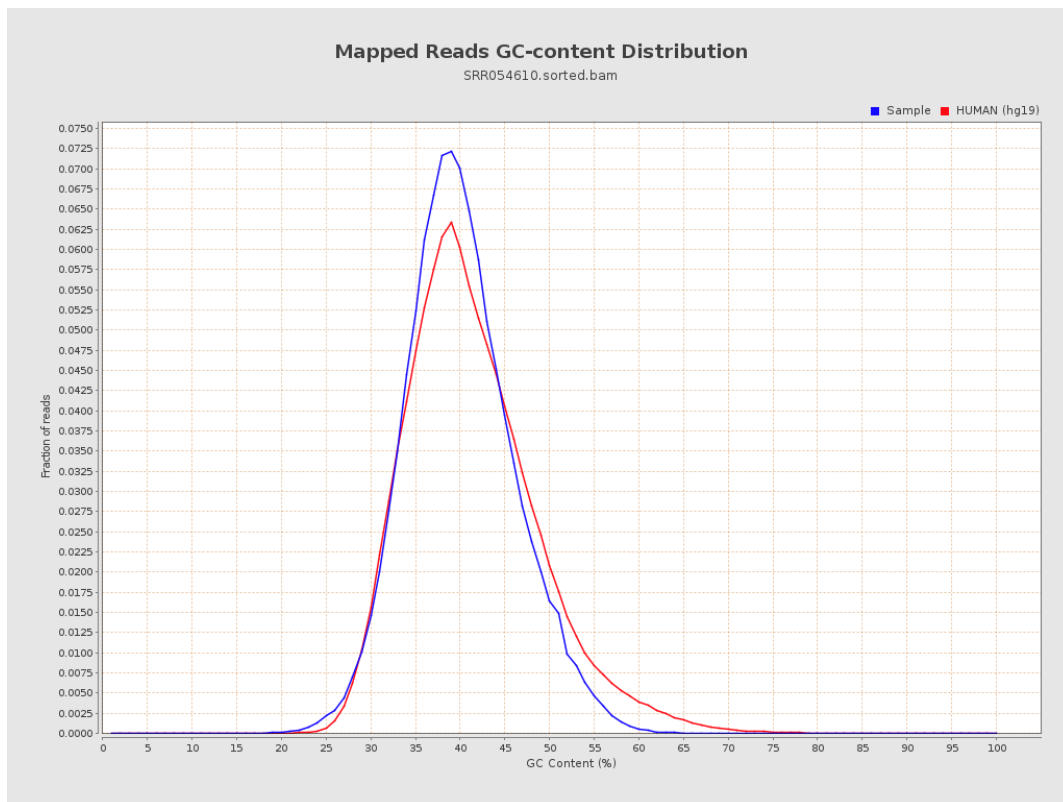
7. Results : Duplication Rate Histogram



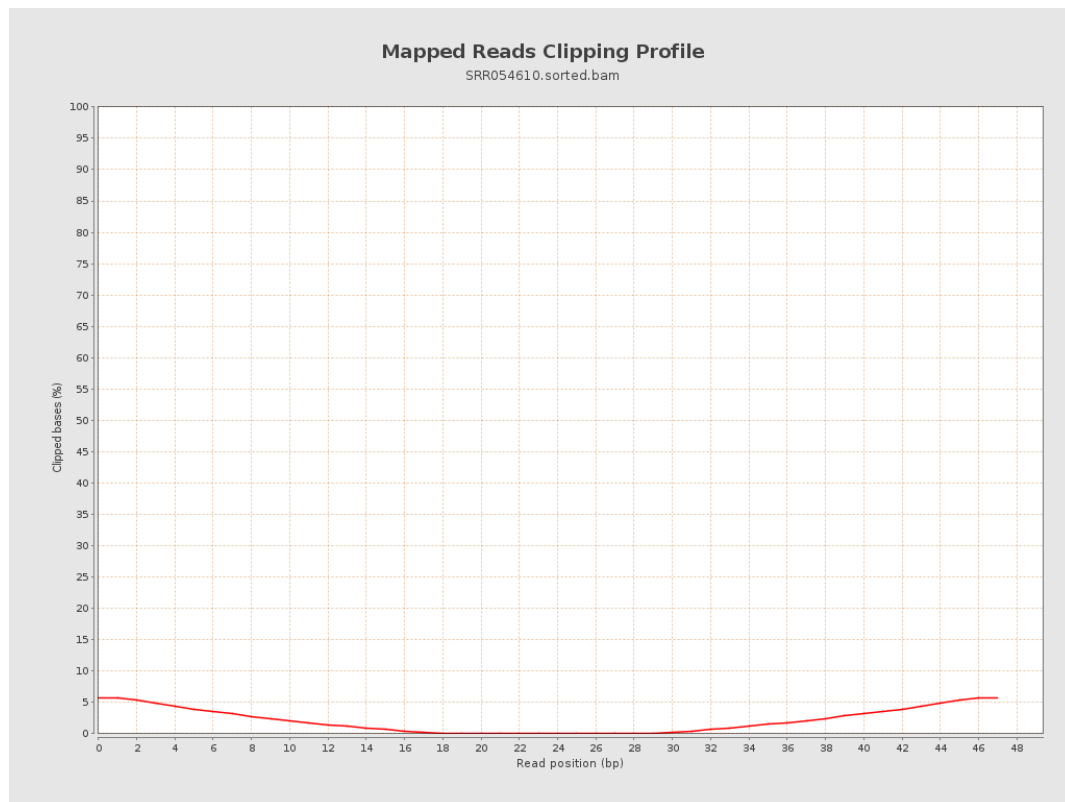
8. Results : Mapped Reads Nucleotide Content



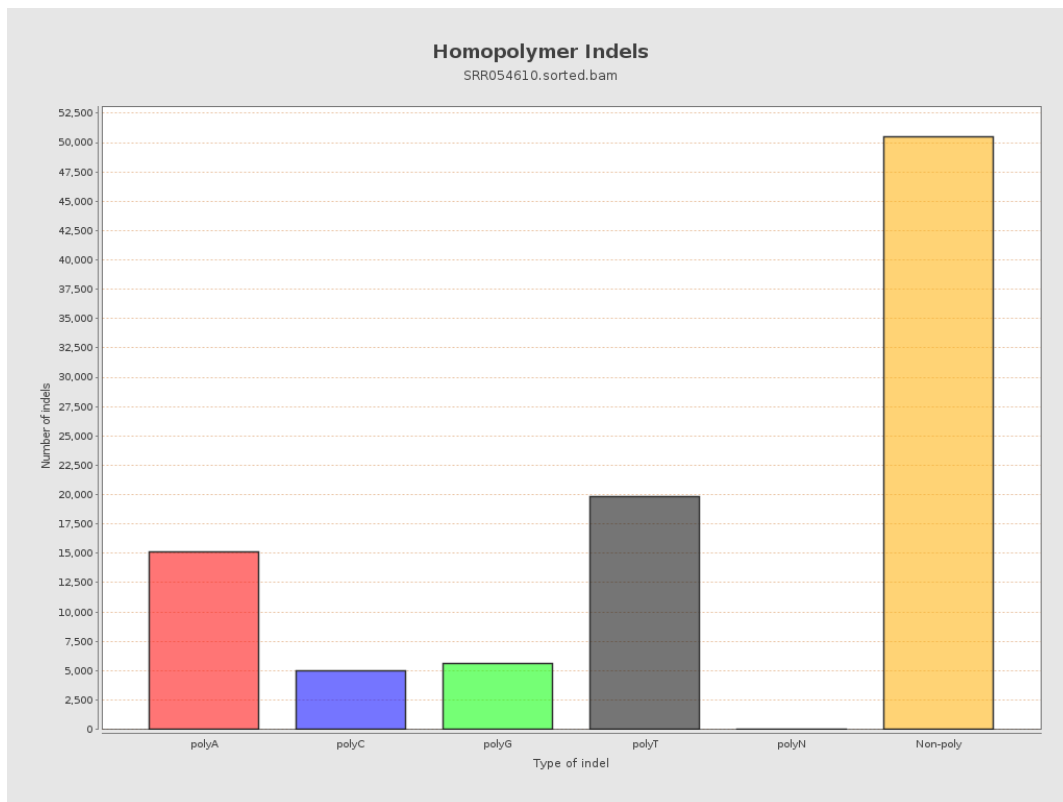
9. Results : Mapped Reads GC-content Distribution



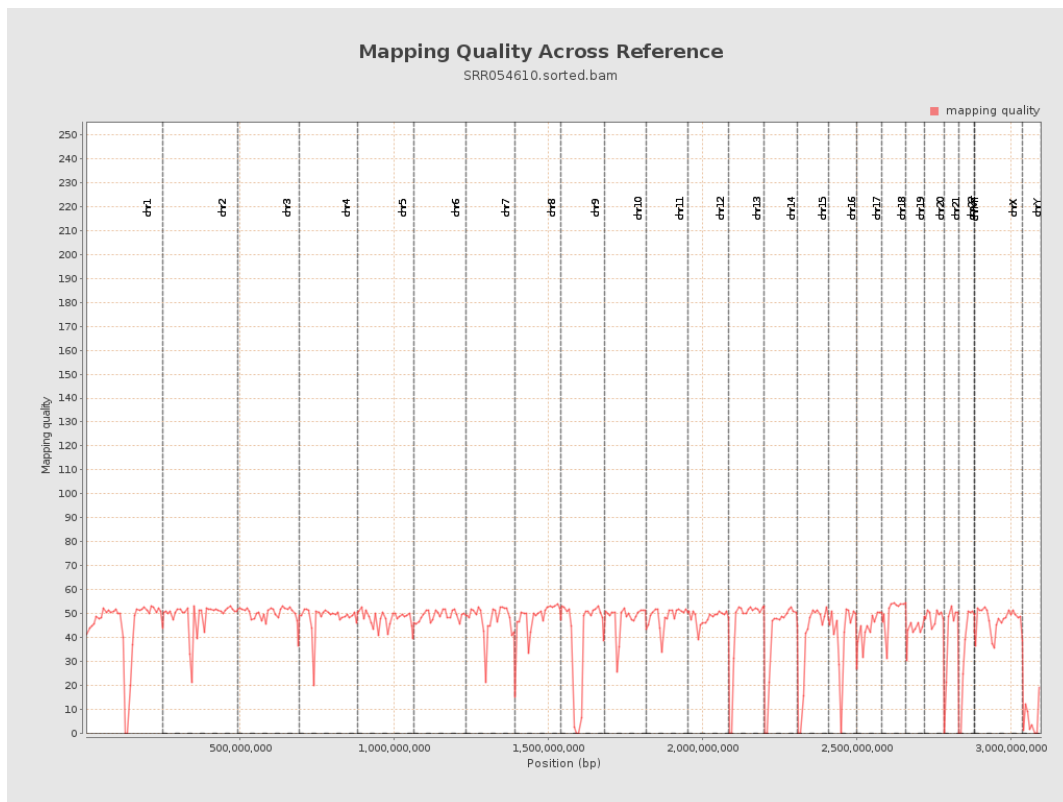
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

