Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:42:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054592.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_SRR054592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:42:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,294,577
Mapped reads	5,745,514 / 78.76%
Unmapped reads	1,549,063 / 21.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	129 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,840,528 / 25.23%
Duplication rate	21.88%
Clipped reads	1,024,511 / 14.04%

2.2. ACGT Content

Number/percentage of A's	83,507,412 / 31.36%
Number/percentage of C's	54,924,349 / 20.63%
Number/percentage of T's	73,046,449 / 27.43%
Number/percentage of G's	54,788,596 / 20.58%
Number/percentage of N's	952 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.086

Standard Deviation	0.9135

2.4. Mapping Quality

Mean Mapping Quality	43.69

2.5. Mismatches and indels

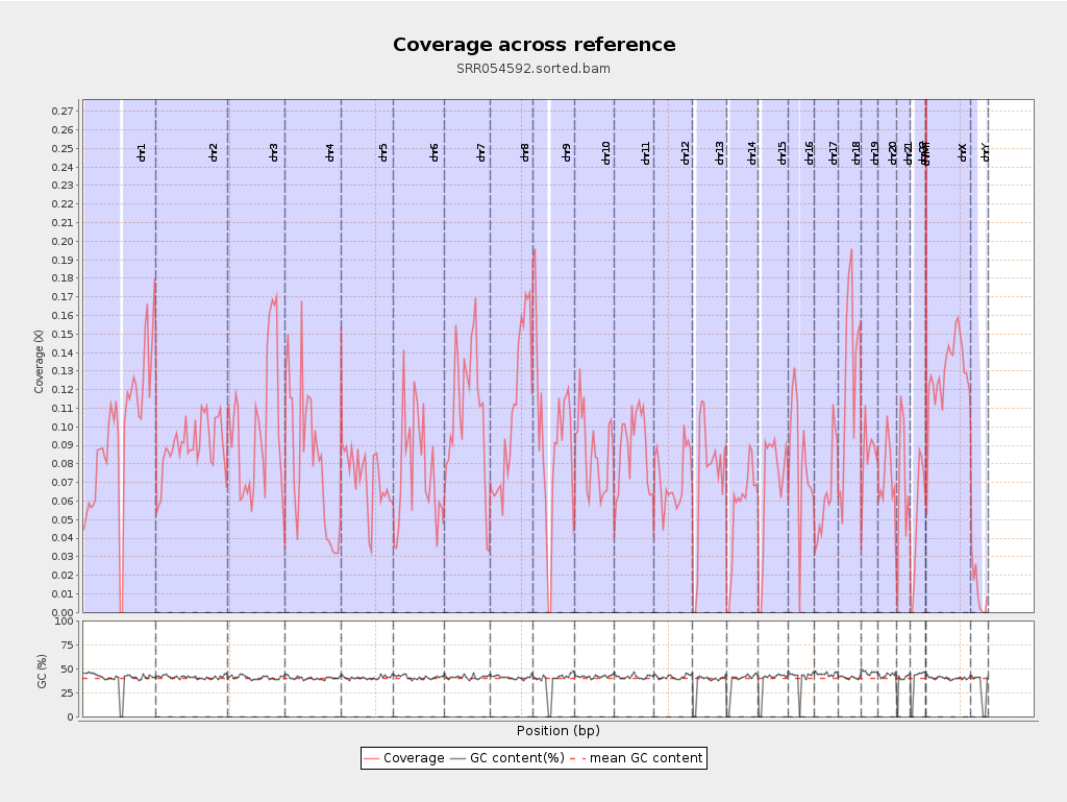
General error rate	0.56%
Mismatches	1,487,619
Insertions	11,380
Mapped reads with at least one insertion	0.2%
Deletions	35,240
Mapped reads with at least one deletion	0.61%
Homopolymer indels	41.67%

2.6. Chromosome stats

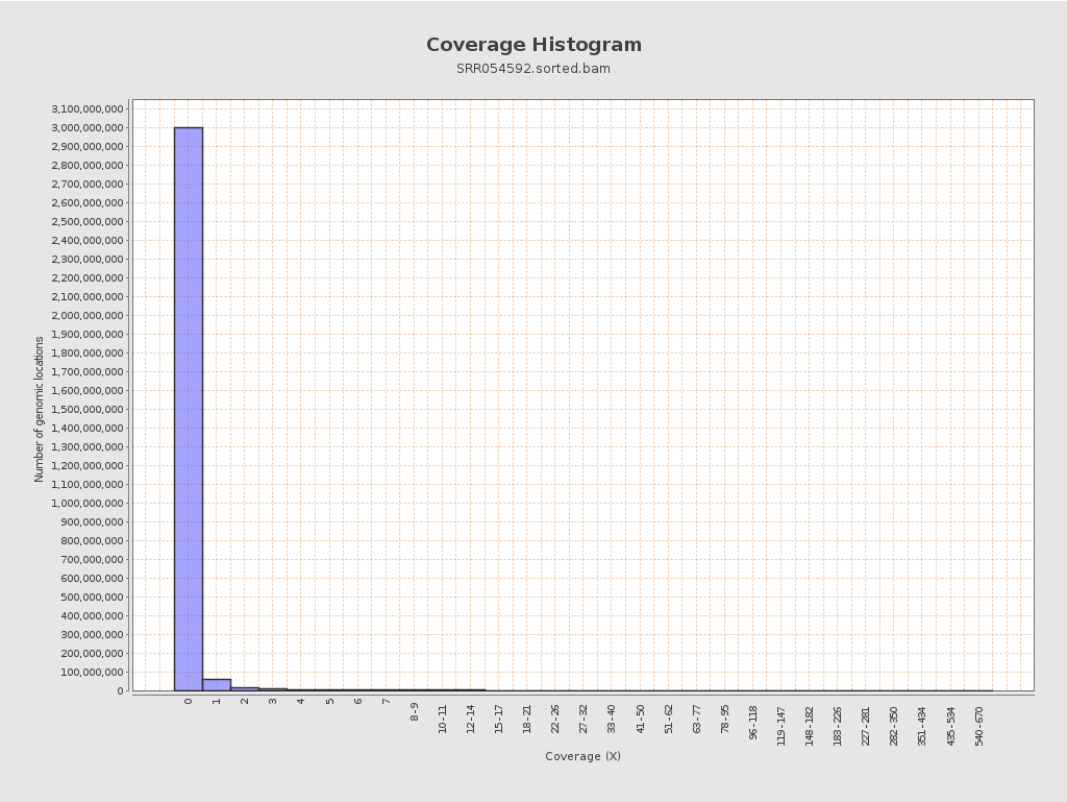
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24193331	0.0971	0.9922
chr2	243199373	21774603	0.0895	0.931
chr3	198022430	19413595	0.098	0.9625
chr4	191154276	15426299	0.0807	0.8844
chr5	180915260	13040987	0.0721	0.7658
chr6	171115067	13136450	0.0768	0.9075
chr7	159138663	17175868	0.1079	1.0593

chr8	146364022	15805269	0.108	1.0346
chr9	141213431	12971464	0.0919	0.9746
chr10	135534747	11761739	0.0868	0.8831
chr11	135006516	11889190	0.0881	0.9504
chr12	133851895	9692715	0.0724	0.769
chr13	115169878	8435622	0.0732	0.7979
chr14	107349540	6086078	0.0567	0.7148
chr15	102531392	6974241	0.068	0.7536
chr16	90354753	7410497	0.082	0.9284
chr17	81195210	5139593	0.0633	0.7095
chr18	78077248	9751725	0.1249	1.1227
chr19	59128983	5127420	0.0867	0.8788
chr20	63025520	4562651	0.0724	0.8308
chr21	48129895	3187172	0.0662	0.9408
chr22	51304566	2624183	0.0511	0.6206
chrMT	16571	17443	1.0526	3.6055
chrX	155270560	20053044	0.1291	1.1597
chrY	59373566	668708	0.0113	0.2963

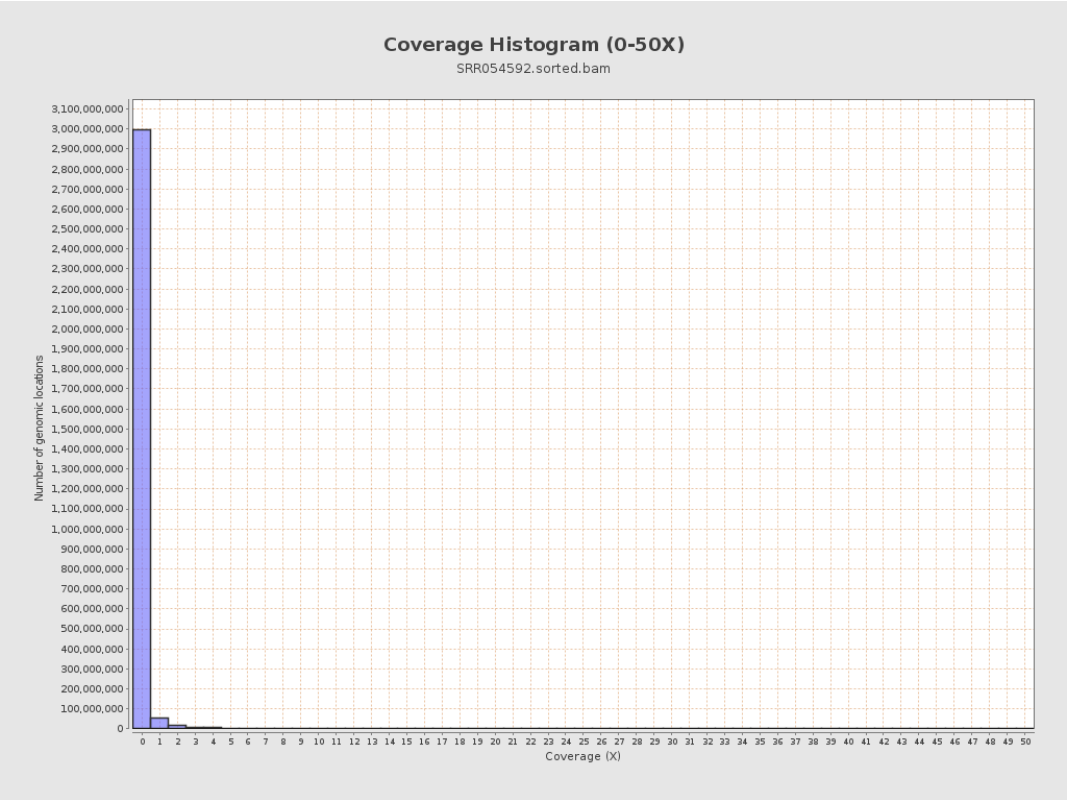
3. Results : Coverage across reference



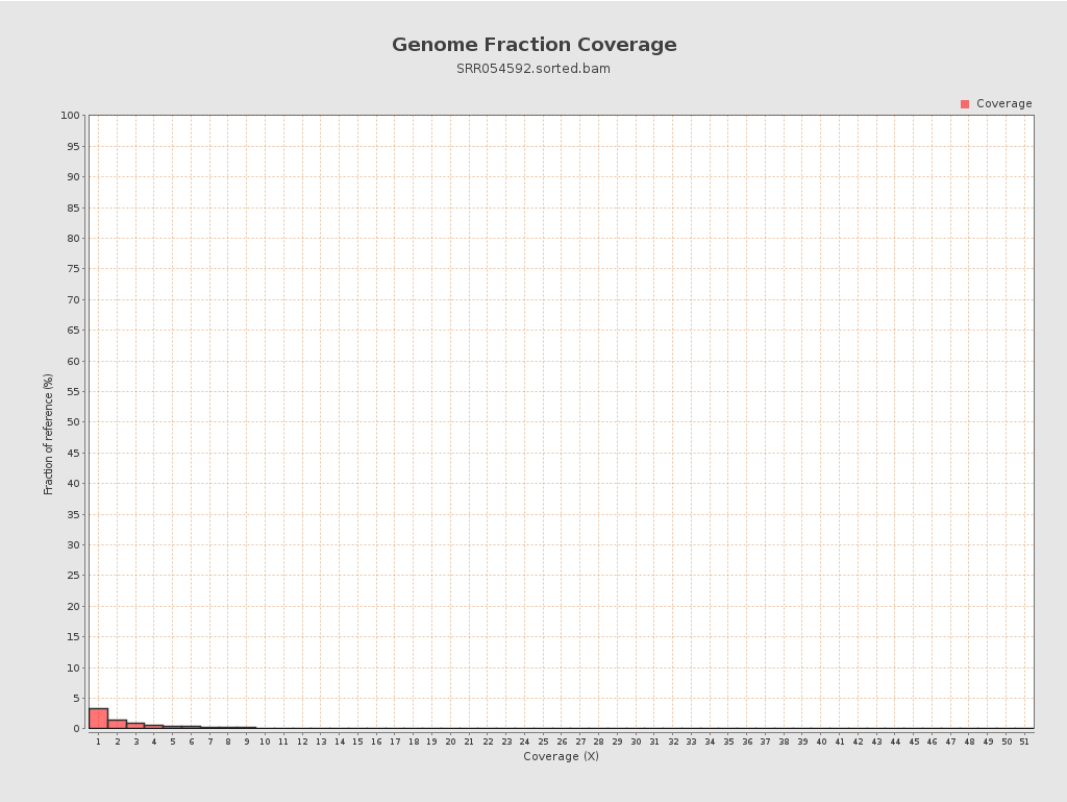
4. Results : Coverage Histogram



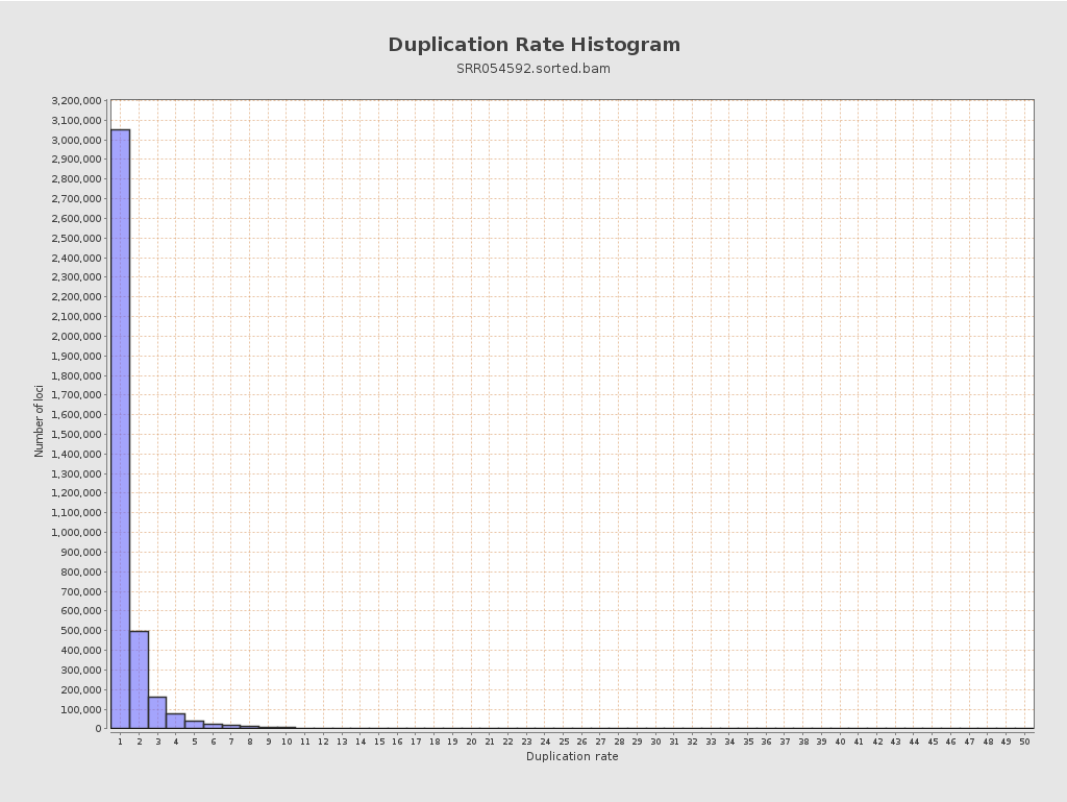
5. Results : Coverage Histogram (0-50X)



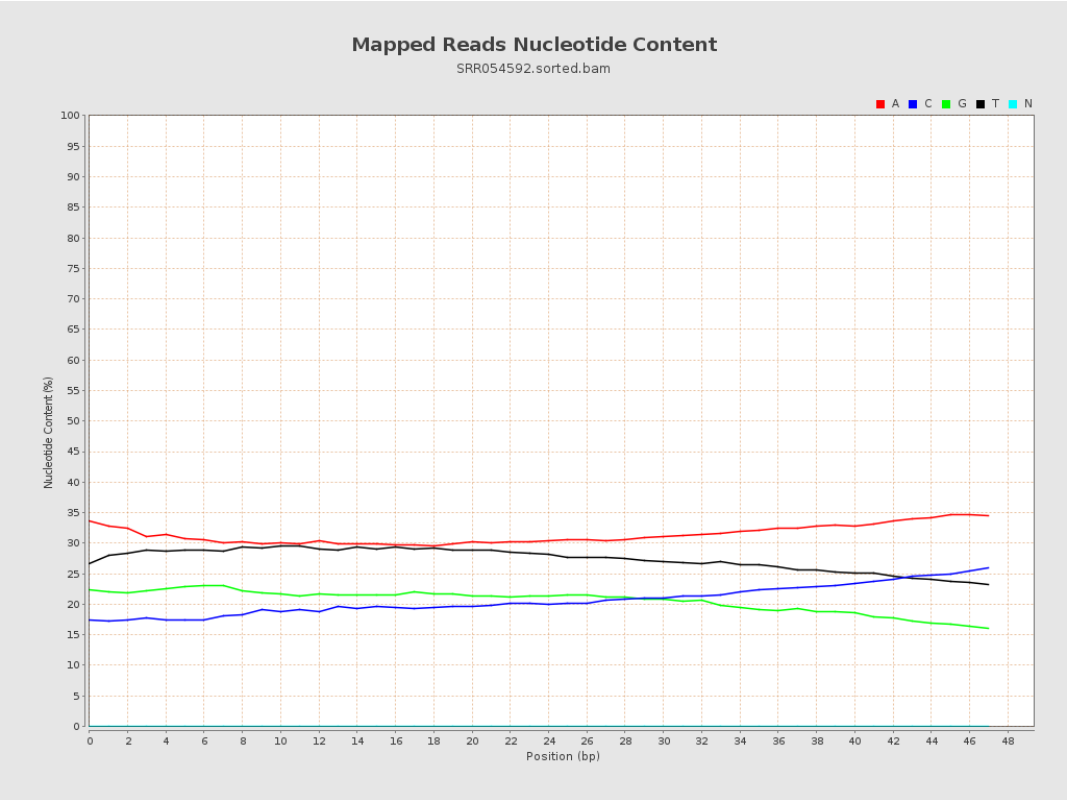
6. Results : Genome Fraction Coverage



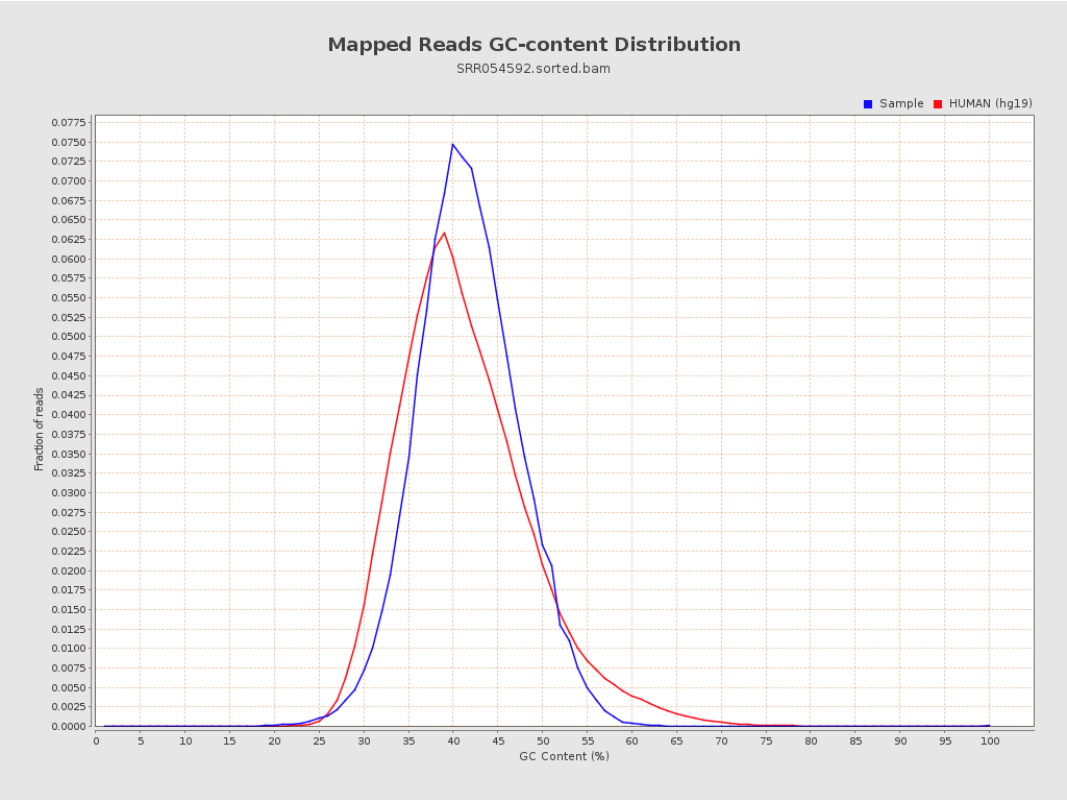
7. Results : Duplication Rate Histogram



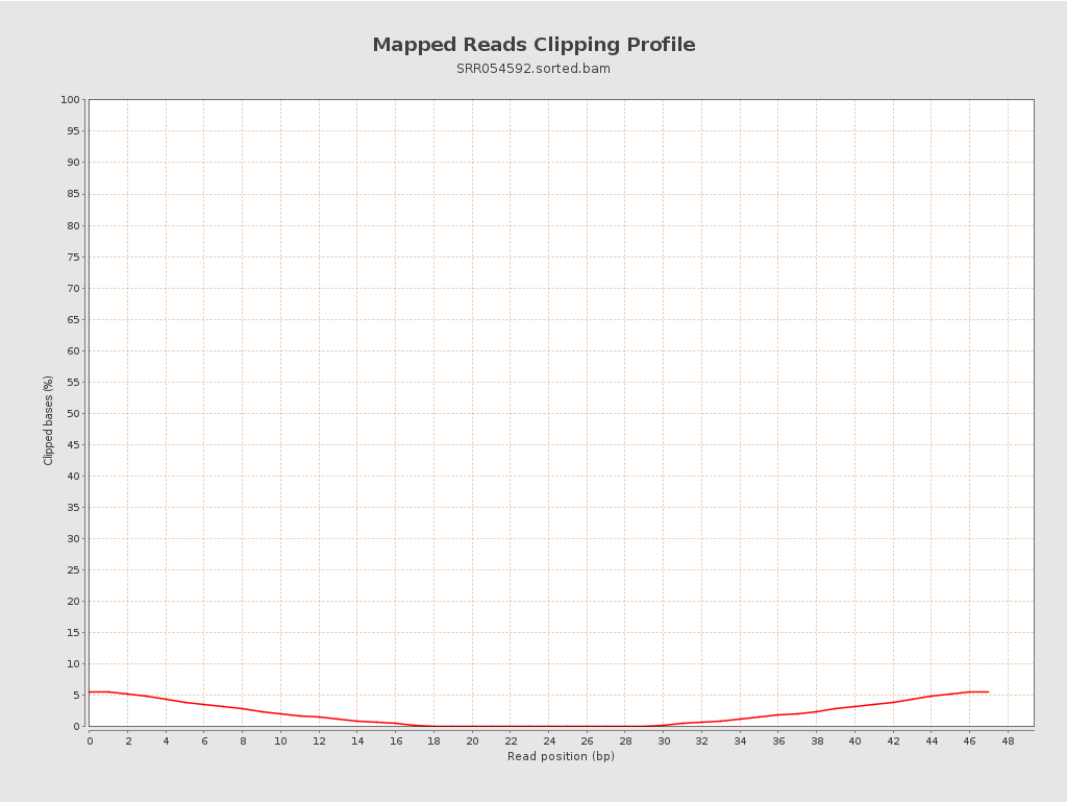
8. Results : Mapped Reads Nucleotide Content



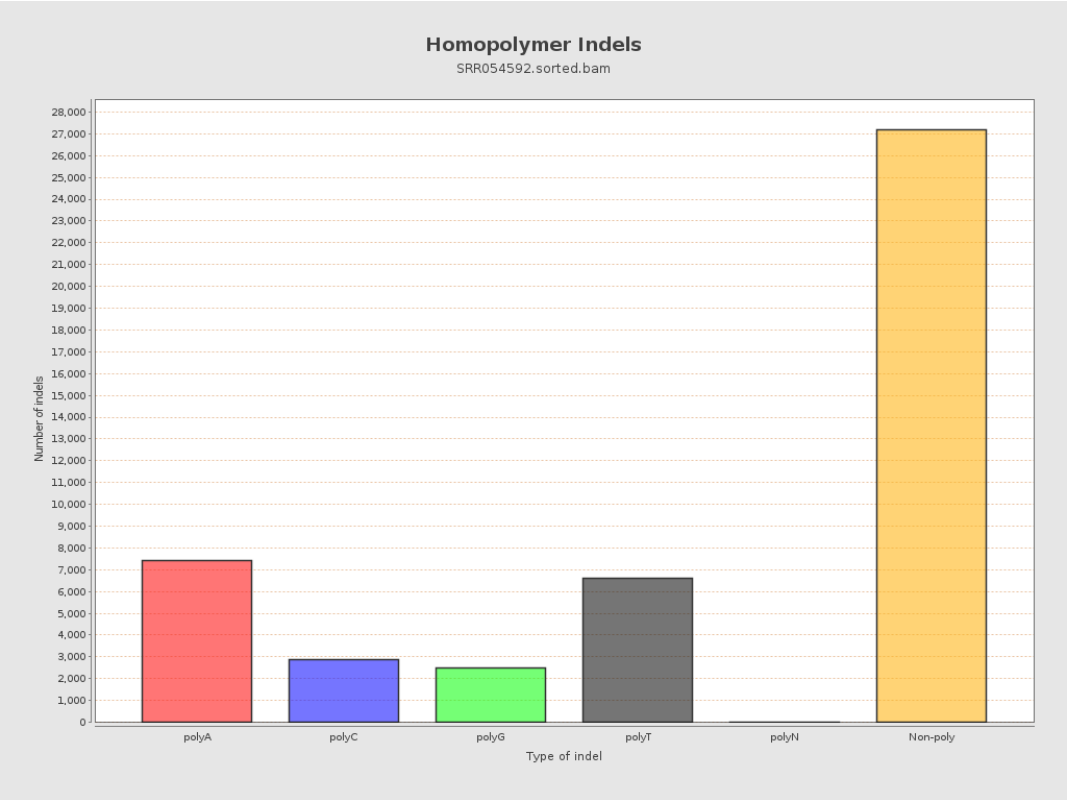
9. Results : Mapped Reads GC-content Distribution



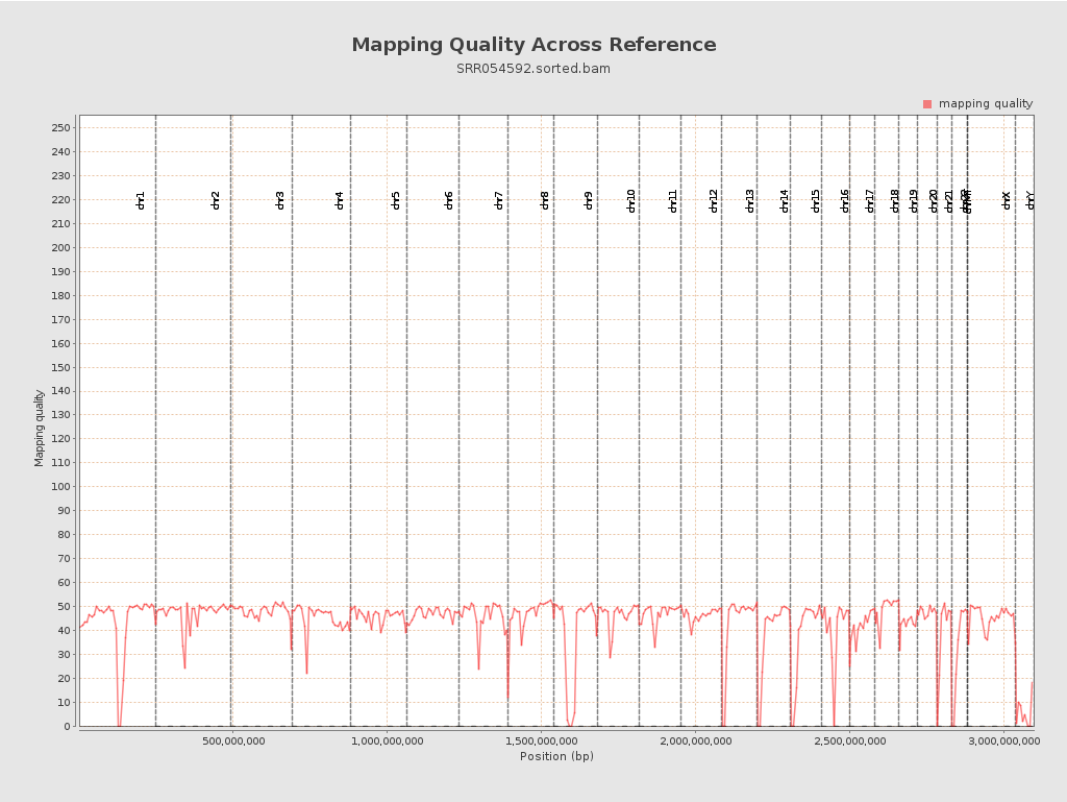
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram