

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 13:46:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438299.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_SRR8438299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 13:46:13 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	873,783,930
Mapped reads	861,604,280 / 98.61%
Unmapped reads	12,179,650 / 1.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,063,786 / 0.35%
Read min/max/mean length	30 / 151 / 140.71
Duplicated reads (estimated)	256,800,481 / 29.39%
Duplication rate	25.52%
Clipped reads	31,169,387 / 3.57%

2.2. ACGT Content

Number/percentage of A's	36,105,592,654 / 29.9%
Number/percentage of C's	24,362,791,813 / 20.18%
Number/percentage of T's	35,925,366,224 / 29.75%
Number/percentage of G's	24,354,048,945 / 20.17%
Number/percentage of N's	630,059 / 0%
GC Percentage	40.35%

2.3. Coverage

Mean	39.0176

Standard Deviation	359.3236
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2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Mismatches and indels

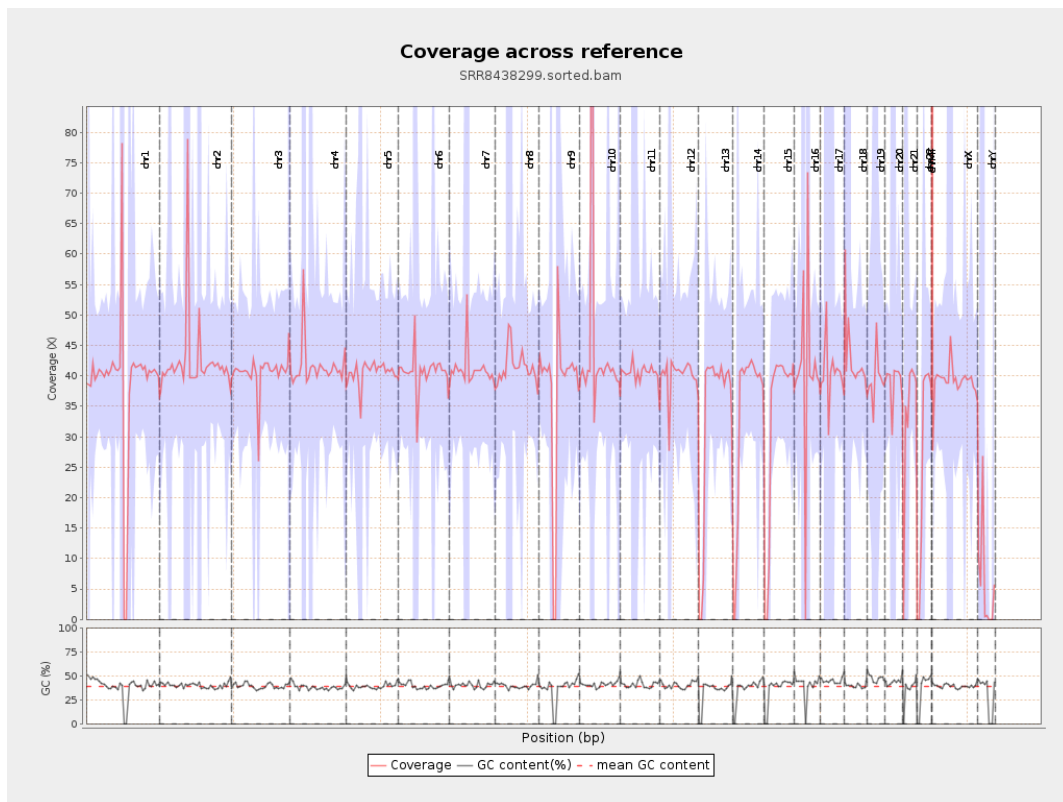
General error rate	0.42%
Mismatches	479,139,542
Insertions	12,394,604
Mapped reads with at least one insertion	1.37%
Deletions	13,648,186
Mapped reads with at least one deletion	1.51%
Homopolymer indels	42.51%

2.6. Chromosome stats

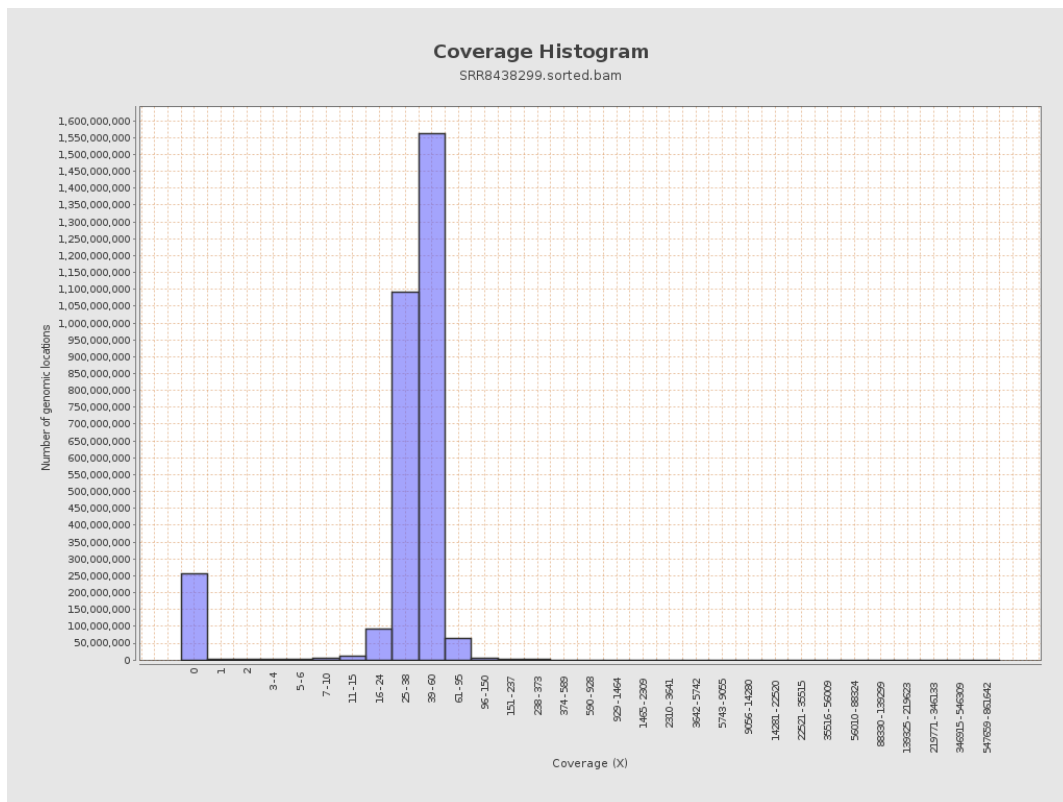
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9780684497	39.2404	853.3503
chr2	243199373	10321499384	42.4405	257.2702
chr3	198022430	8008662243	40.4432	62.7969
chr4	191154276	7923076528	41.4486	128.3168
chr5	180915260	7328318967	40.5069	30.3843
chr6	171115067	6972115666	40.7452	115.3638
chr7	159138663	6525561509	41.0055	295.0005

chr8	146364022	6069716724	41.47	496.9756
chr9	141213431	5263817762	37.2756	354.7201
chr10	135534747	6111855793	45.0944	751.1466
chr11	135006516	5475356052	40.5562	175.1605
chr12	133851895	5356745026	40.0199	26.2565
chr13	115169878	3872671356	33.6257	21.6955
chr14	107349540	3628611145	33.8018	31.268
chr15	102531392	3330518122	32.4829	20.6304
chr16	90354753	3707126389	41.0286	274.2383
chr17	81195210	3275579879	40.342	187.93
chr18	78077248	3290074735	42.1387	432.2772
chr19	59128983	2331782908	39.4355	444.9893
chr20	63025520	2450977424	38.8887	59.212
chr21	48129895	1645377807	34.1862	101.9359
chr22	51304566	1403959213	27.3652	31.2639
chrMT	16571	289091386	17,445.621	2,160.81
chrX	155270560	6068295981	39.0821	105.5509
chrY	59373566	355057312	5.9801	238.832

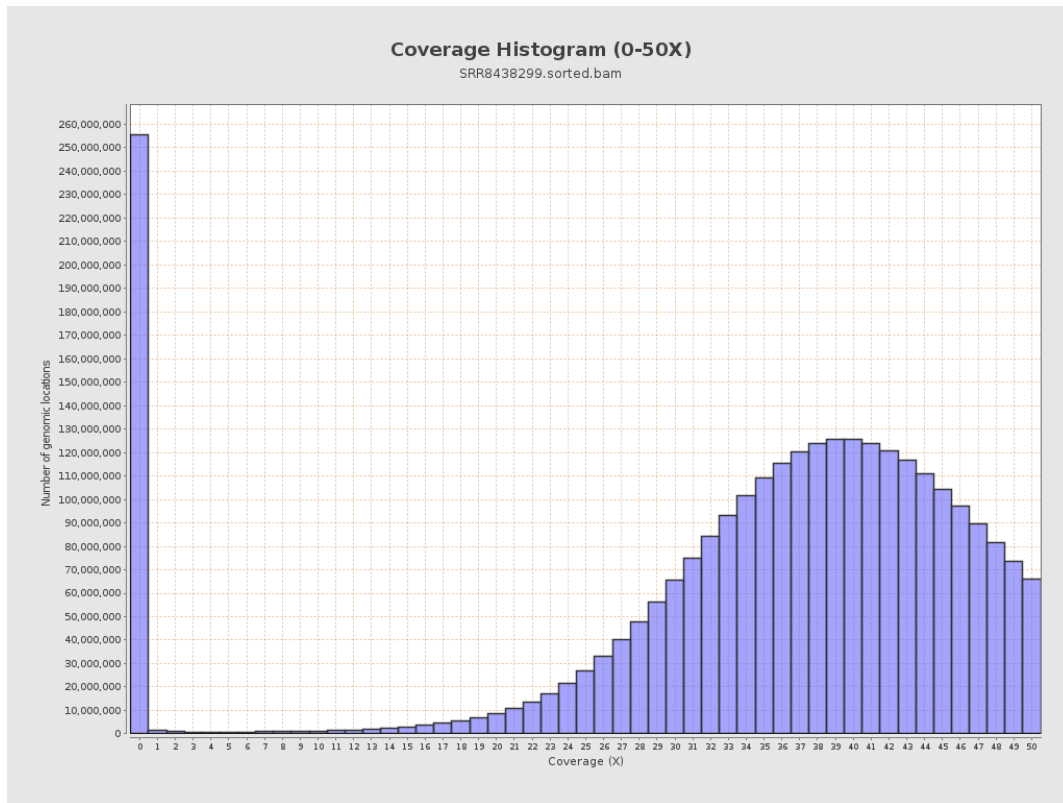
3. Results : Coverage across reference



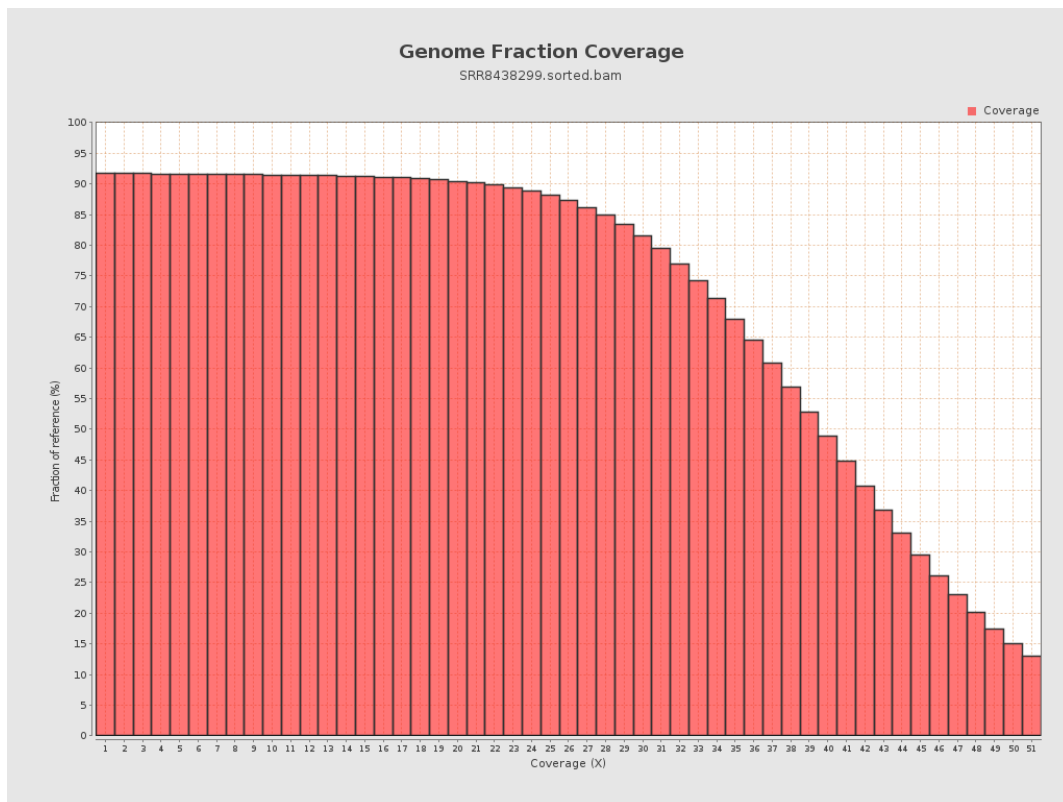
4. Results : Coverage Histogram



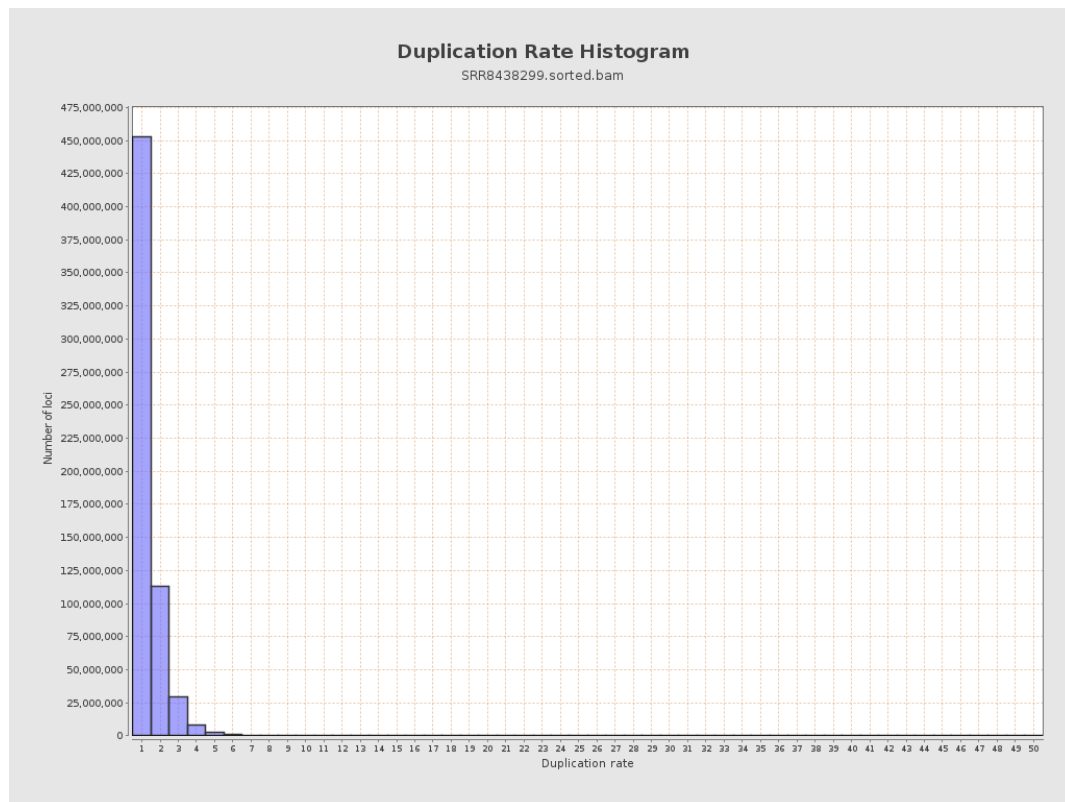
5. Results : Coverage Histogram (0-50X)



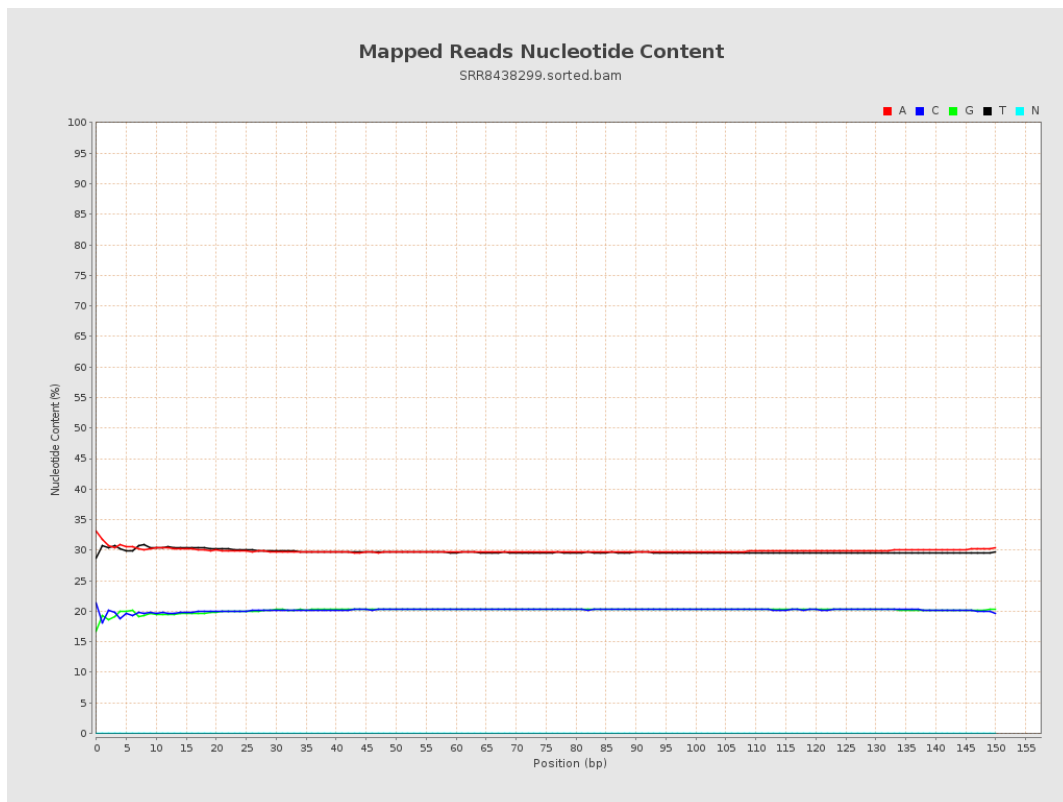
6. Results : Genome Fraction Coverage



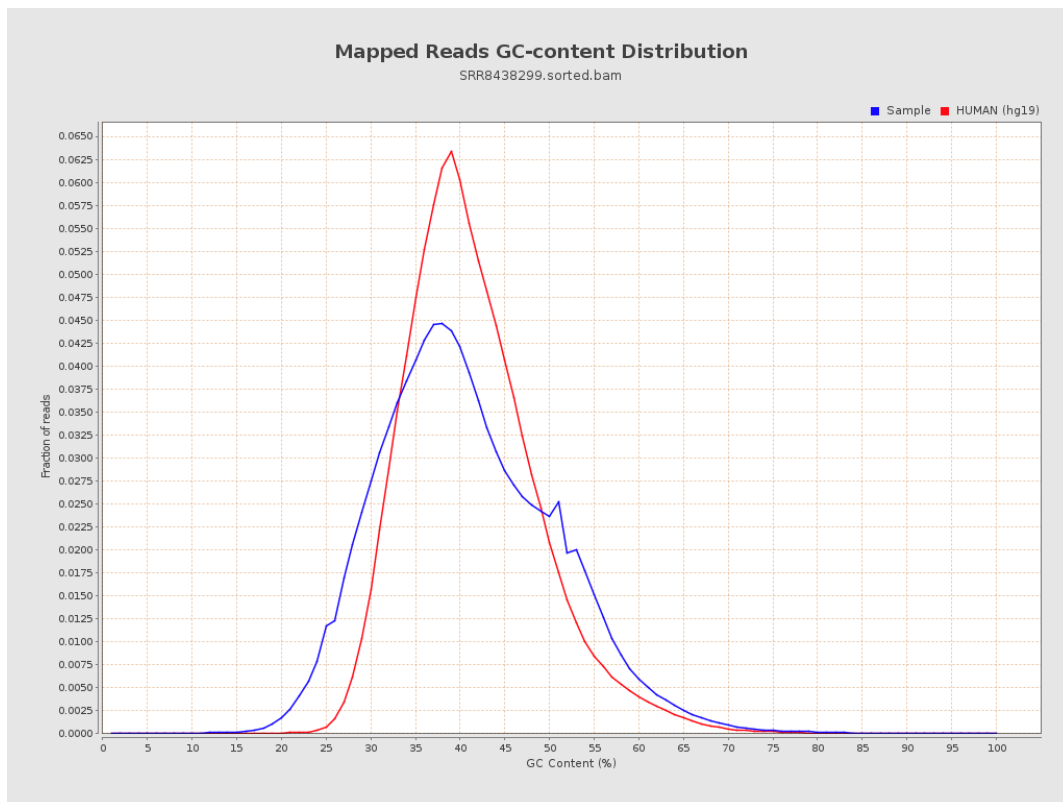
7. Results : Duplication Rate Histogram



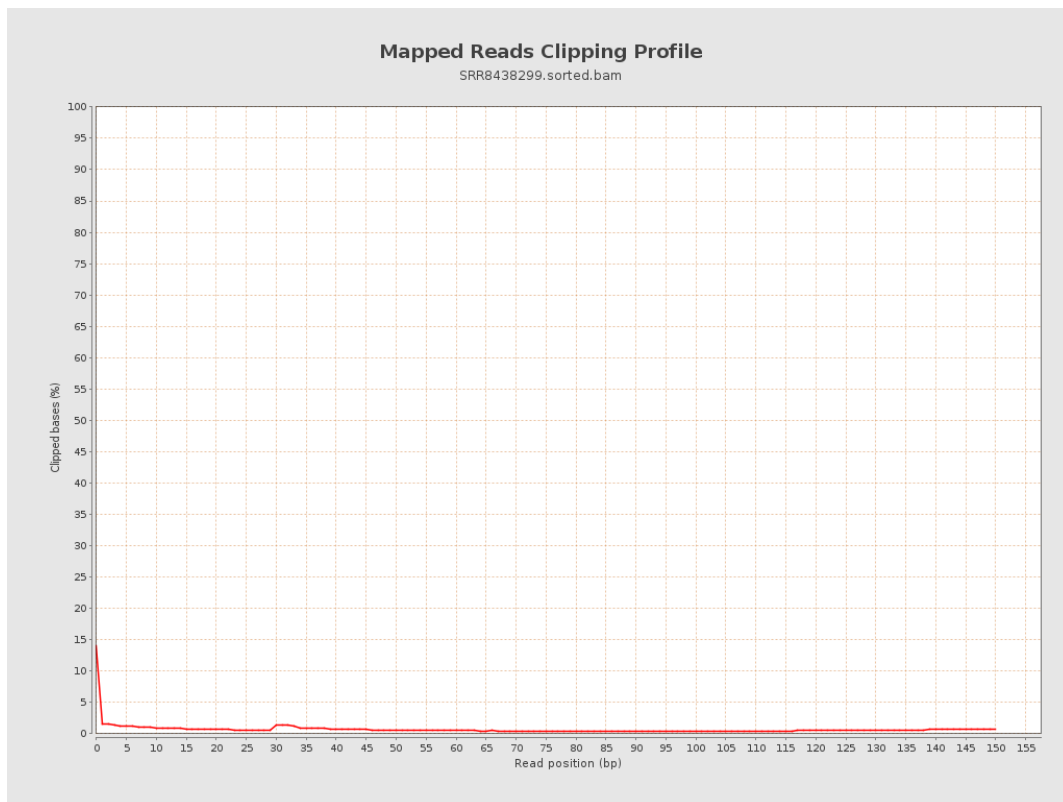
8. Results : Mapped Reads Nucleotide Content



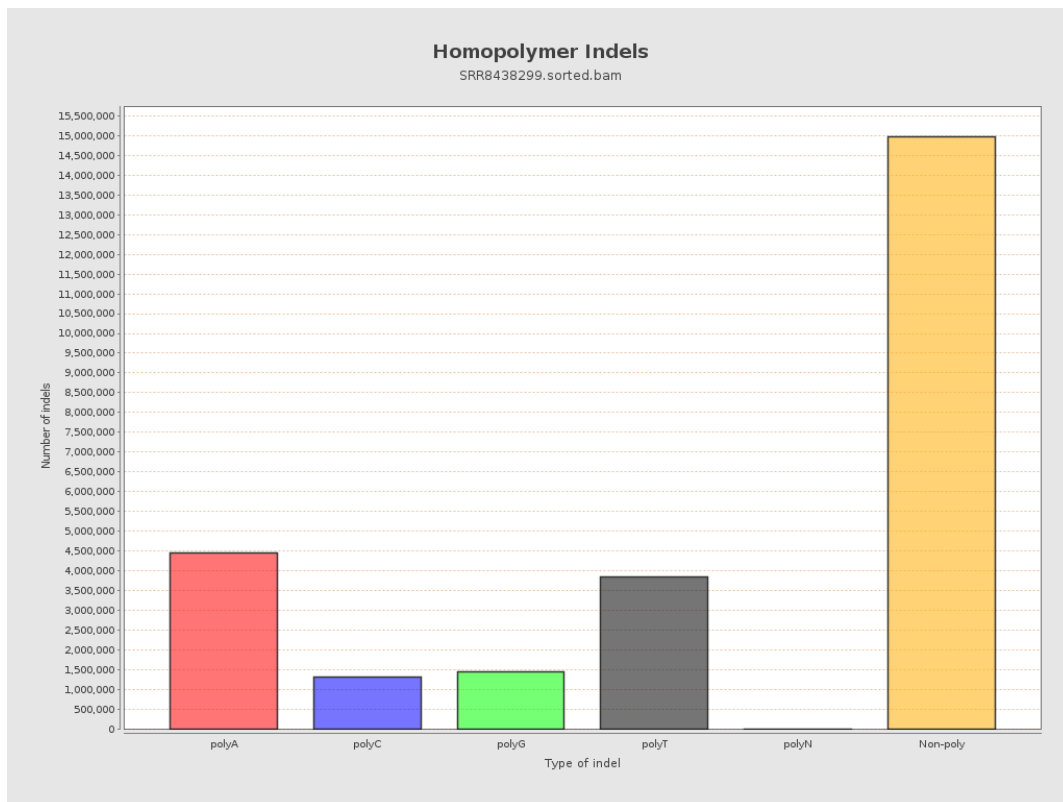
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

