

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 23:19:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438296.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_SRR8438296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438296_1.fastq.gz SRR8438296_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 23:19:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	743,425,010
Mapped reads	741,093,010 / 99.69%
Unmapped reads	2,332,000 / 0.31%
Mapped paired reads	741,093,010 / 99.69%
Mapped reads, first in pair	370,714,160 / 49.87%
Mapped reads, second in pair	370,378,850 / 49.82%
Mapped reads, both in pair	739,497,778 / 99.47%
Mapped reads, singletons	1,595,232 / 0.21%
Secondary alignments	0
Supplementary alignments	12,102,503 / 1.63%
Read min/max/mean length	28 / 151 / 145.51
Duplicated reads (estimated)	328,092,554 / 44.13%
Duplication rate	41.35%
Clipped reads	138,264,207 / 18.6%

2.2. ACGT Content

Number/percentage of A's	31,998,729,695 / 29.95%
Number/percentage of C's	21,651,798,989 / 20.26%
Number/percentage of T's	30,565,646,950 / 28.61%
Number/percentage of G's	22,629,122,885 / 21.18%
Number/percentage of N's	653,268 / 0%

GC Percentage	41.44%
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2.3. Coverage

Mean	34.524
Standard Deviation	81.8748

2.4. Mapping Quality

Mean Mapping Quality	55.16
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2.5. Insert size

Mean	42,319.75
Standard Deviation	2,015,400.83
P25/Median/P75	181 / 236 / 328

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	545,349,918
Insertions	13,739,326
Mapped reads with at least one insertion	1.82%
Deletions	12,154,074
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.57%

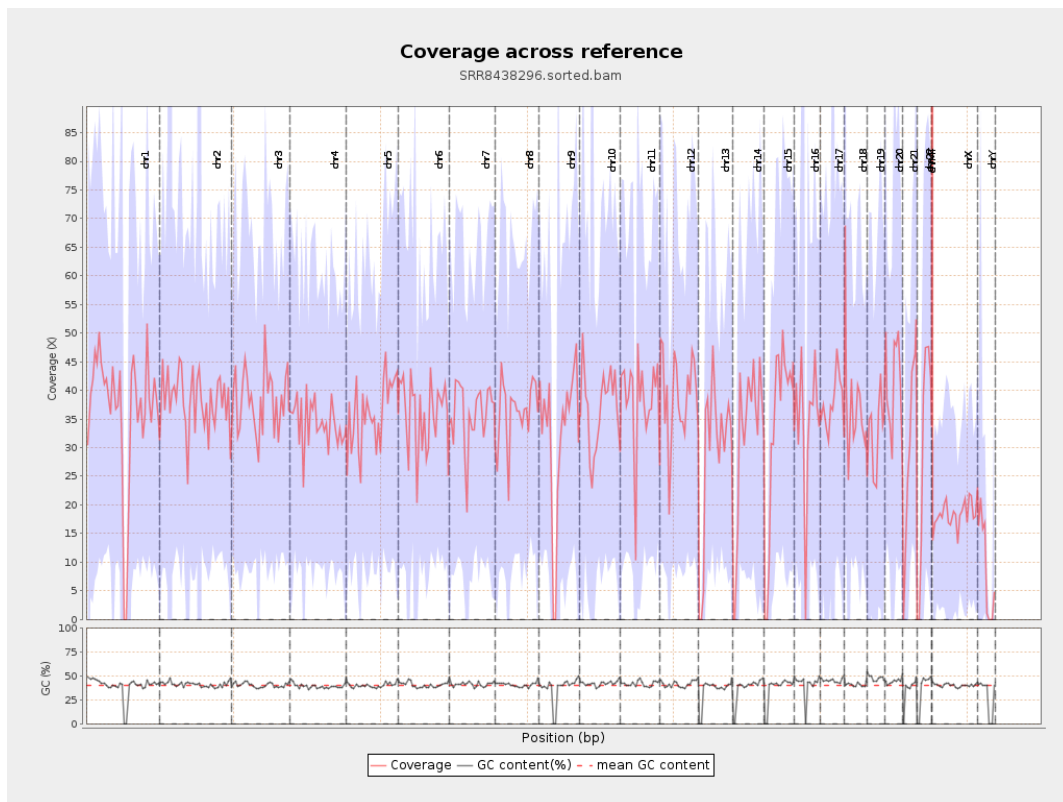
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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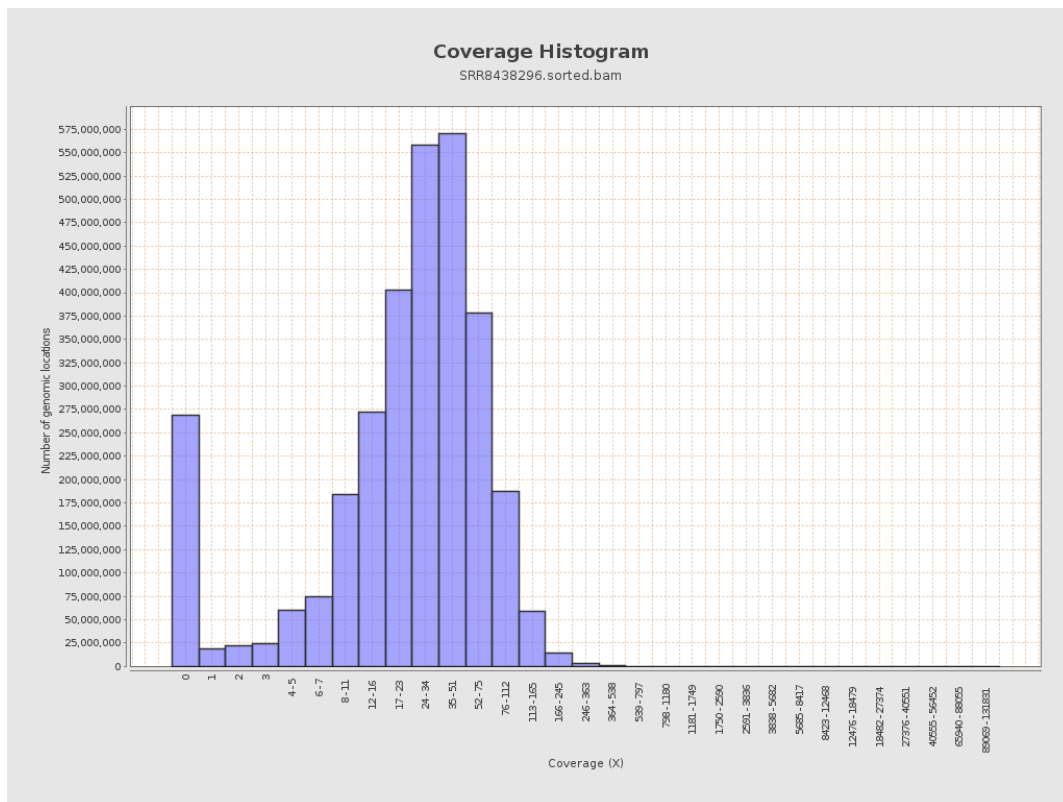
		bases	coverage	deviation
chr1	249250621	9202682876	36.9214	36.6114
chr2	243199373	9284003014	38.1745	134.1216
chr3	198022430	7588867052	38.3233	30.0833
chr4	191154276	6572084196	34.381	26.8658
chr5	180915260	6474326993	35.7865	28.3498
chr6	171115067	6163493535	36.0196	30.3457
chr7	159138663	5717108144	35.9253	29.13
chr8	146364022	5348333170	36.5413	29.0499
chr9	141213431	4543092391	32.1718	35.5001
chr10	135534747	4991230493	36.8262	40.5449
chr11	135006516	5215555887	38.6319	32.1518
chr12	133851895	5223222531	39.0224	31.8052
chr13	115169878	3366991742	29.235	27.9978
chr14	107349540	3411388812	31.7783	33.1914
chr15	102531392	3398289041	33.1439	34.4386
chr16	90354753	3073225493	34.0129	56.9539
chr17	81195210	3065299789	37.7522	43.6002
chr18	78077248	2860873557	36.6416	32.8776
chr19	59128983	1934413388	32.7151	35.1993
chr20	63025520	2597847128	41.219	36.3045
chr21	48129895	1473506984	30.6152	36.4161
chr22	51304566	1540864303	30.0337	38.5757
chrMT	16571	435086962	26,255.9267	10,226.8328
chrX	155270560	2848995659	18.3486	17.2352

chrY	59373566	544924301	9.1779	30.3056
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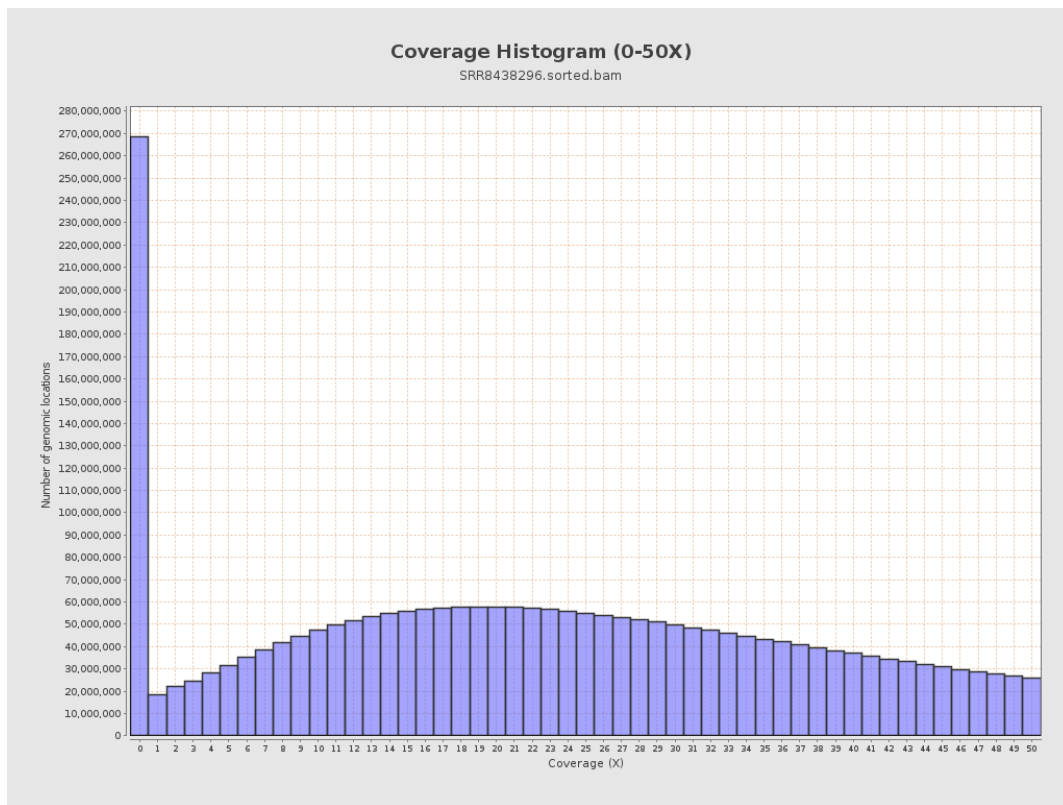
3. Results : Coverage across reference



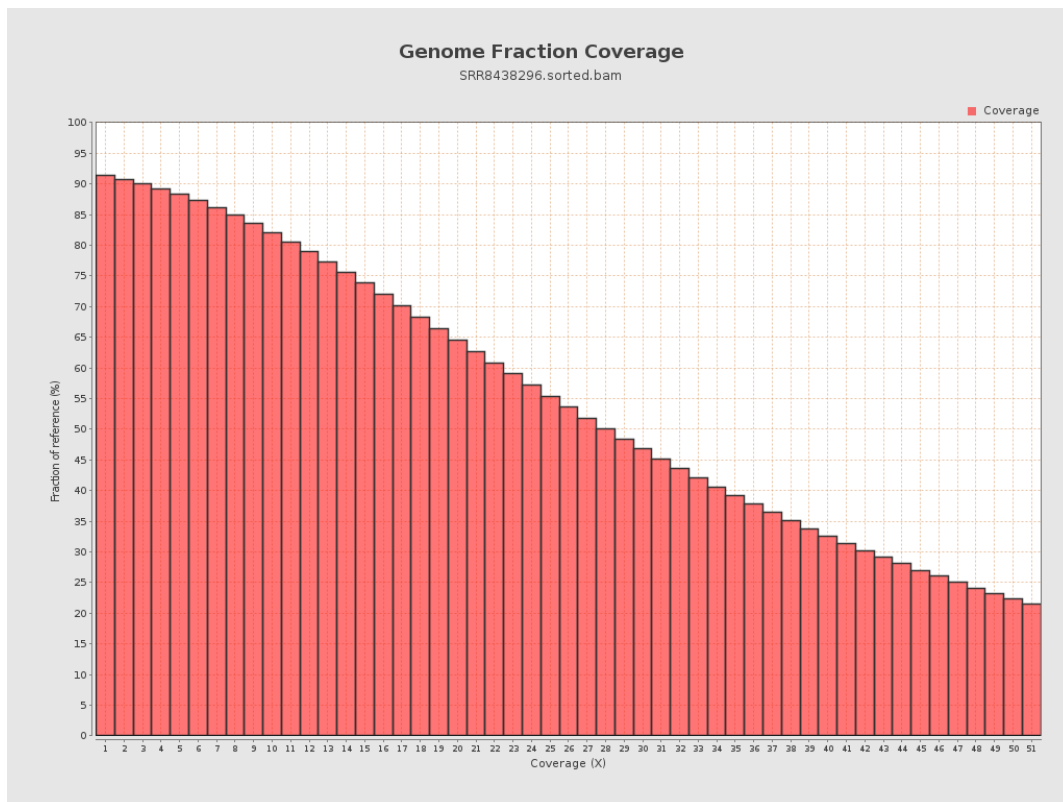
4. Results : Coverage Histogram



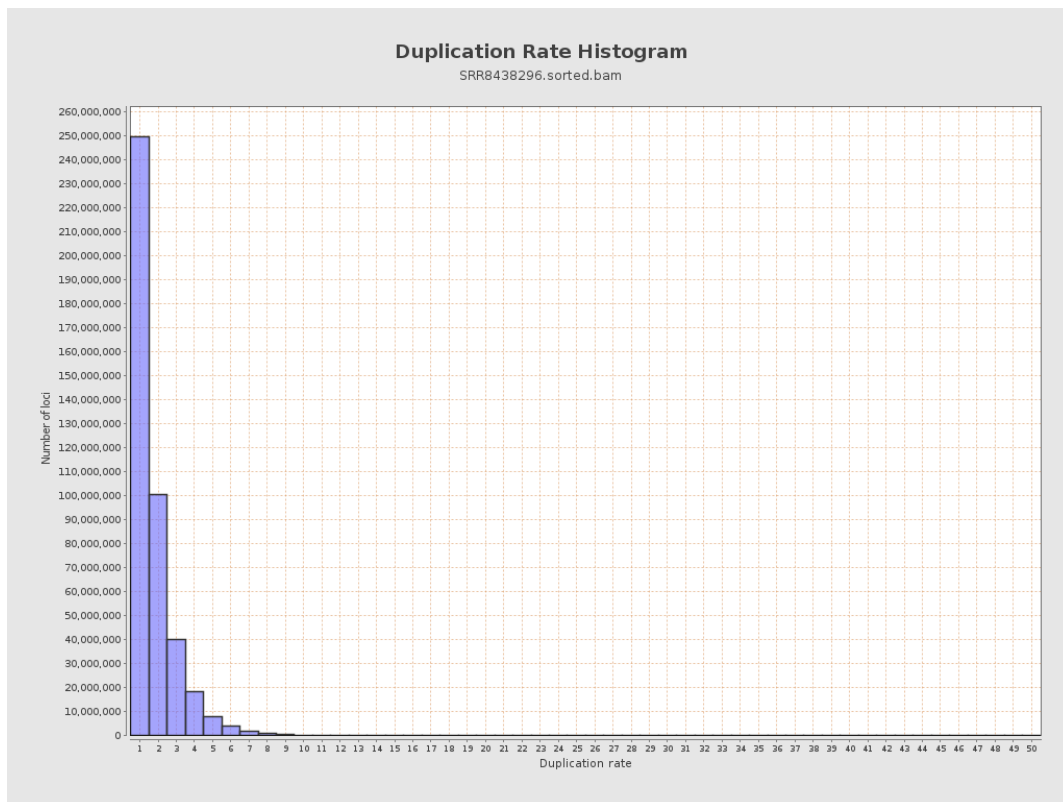
5. Results : Coverage Histogram (0-50X)



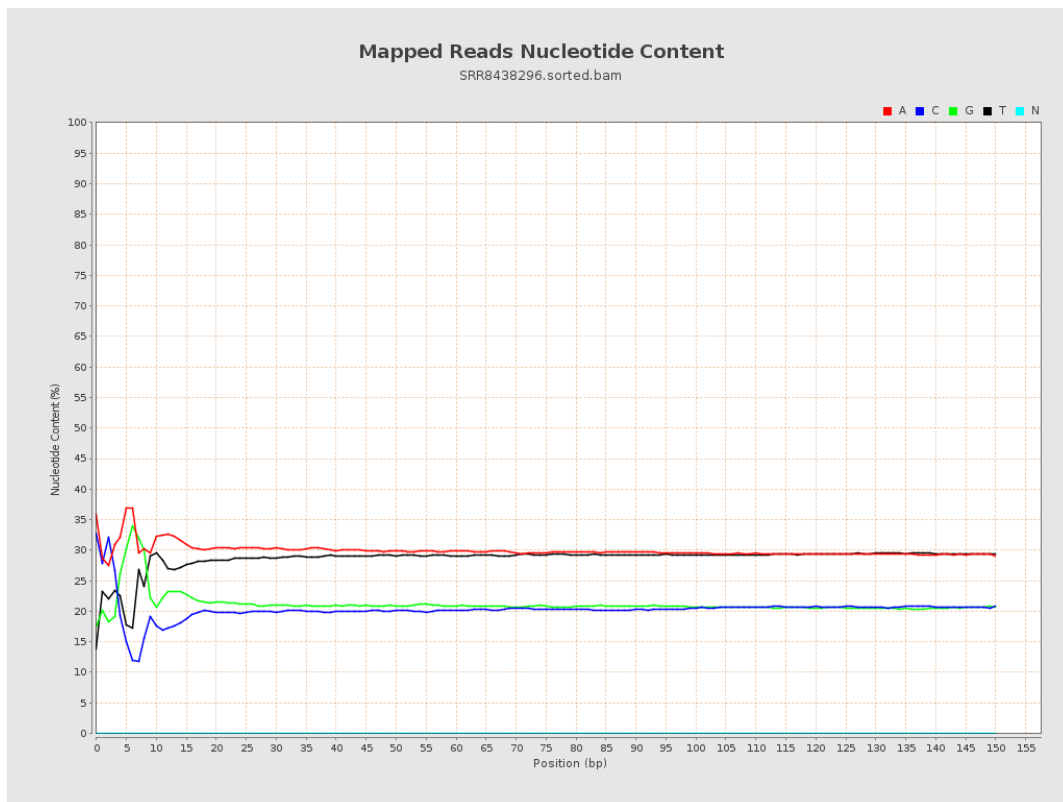
6. Results : Genome Fraction Coverage



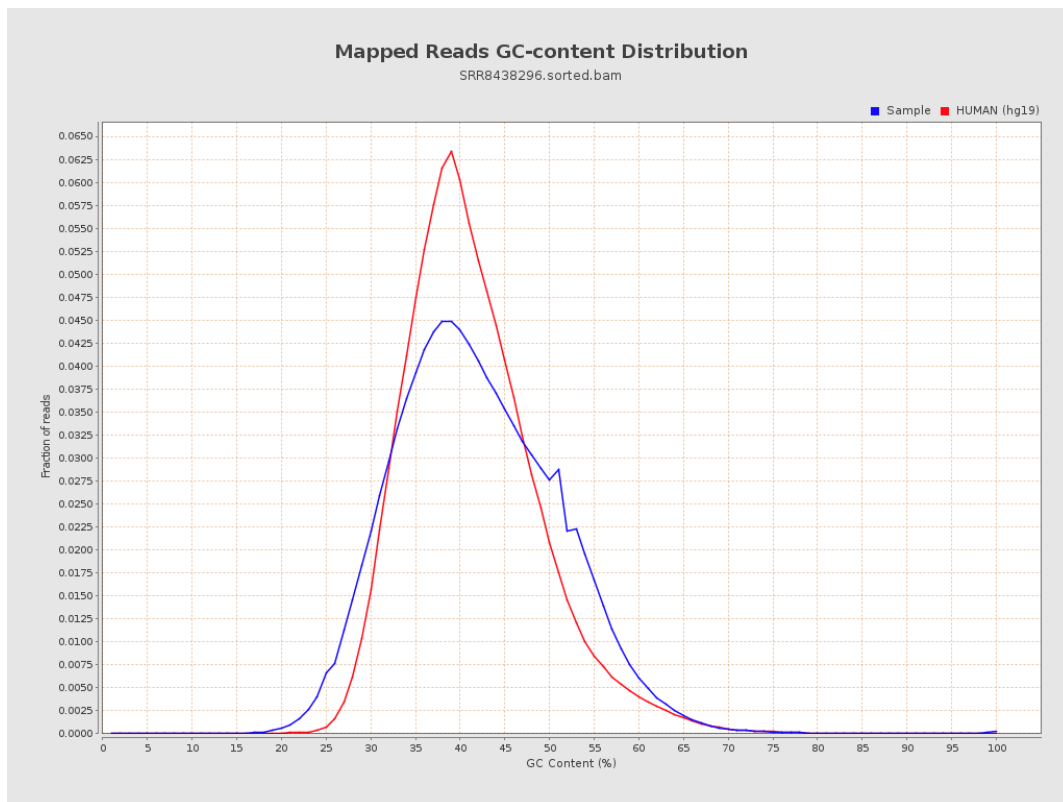
7. Results : Duplication Rate Histogram



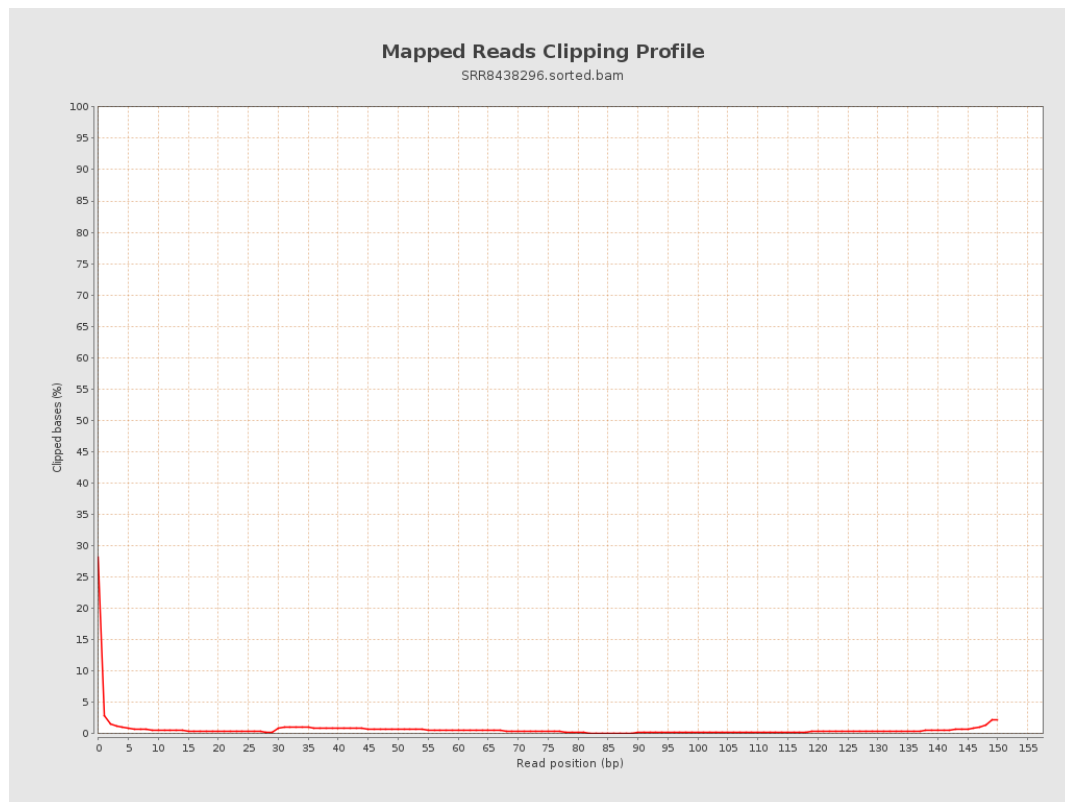
8. Results : Mapped Reads Nucleotide Content



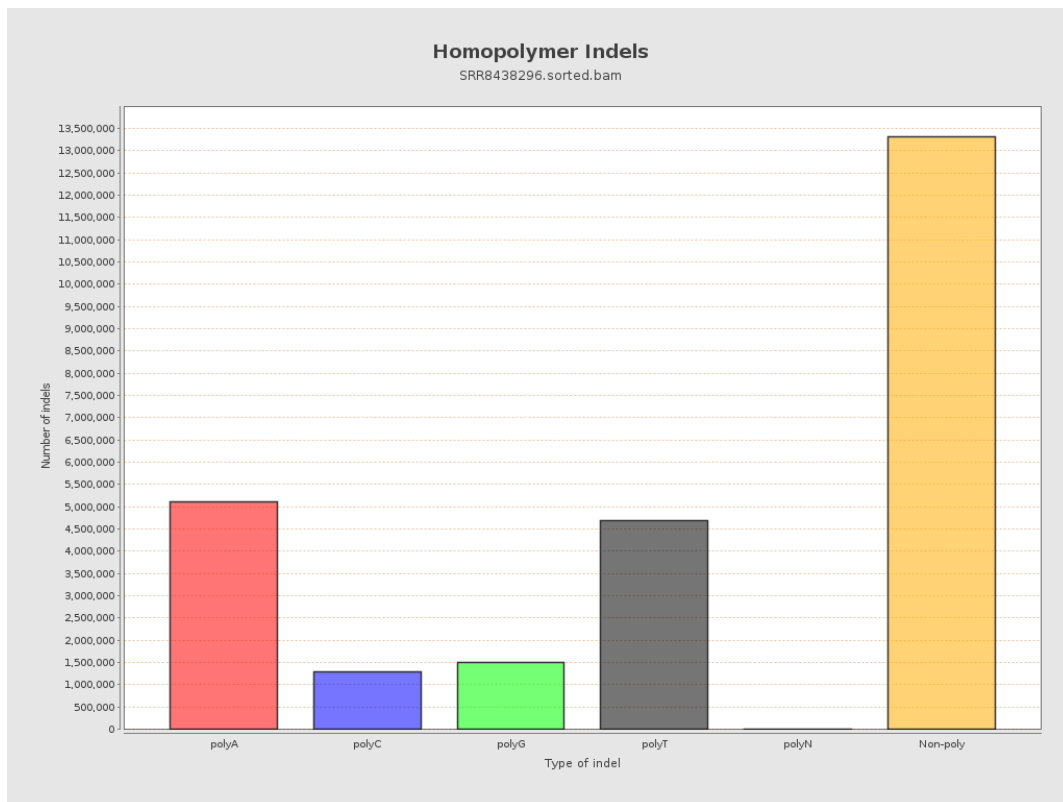
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



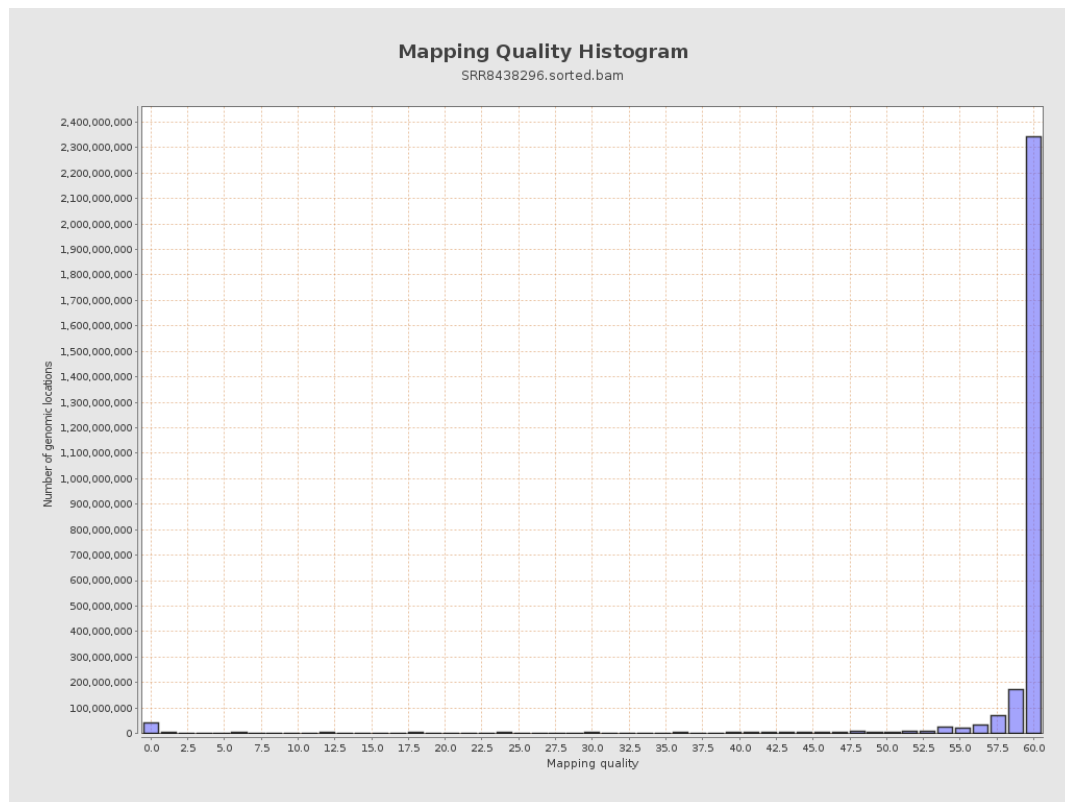
11. Results : Homopolymer Indels



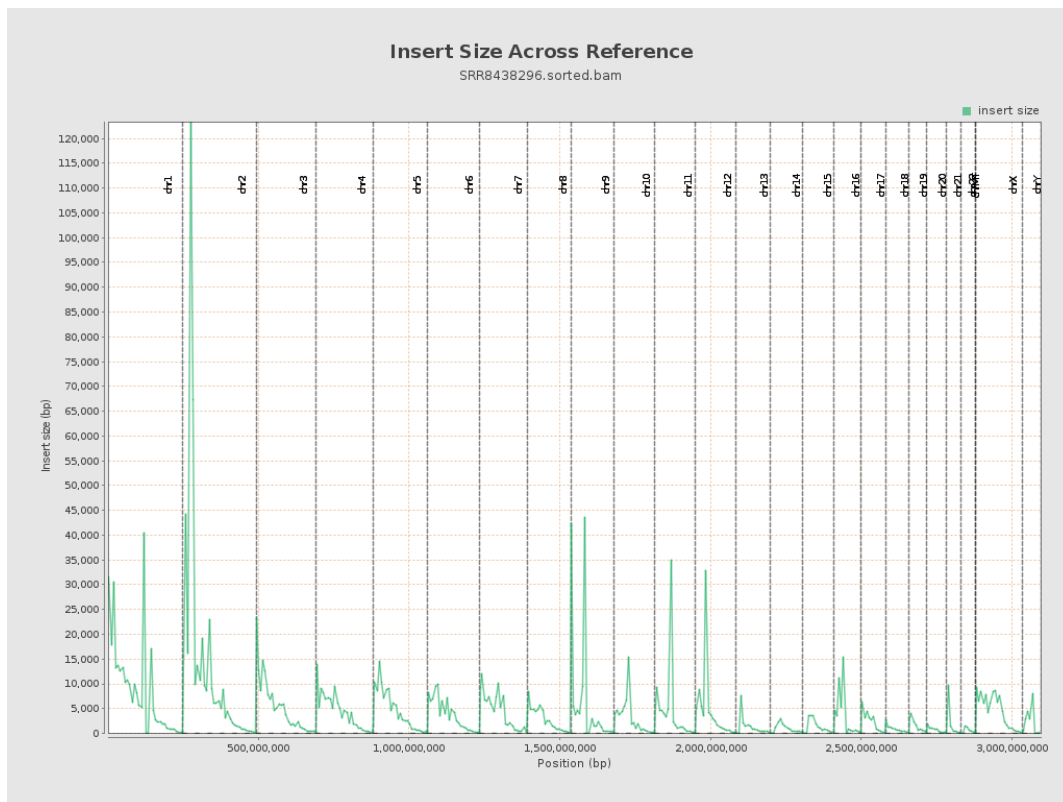
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

