

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 01:38:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438298.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_SRR8438298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438298_1.fastq.gz SRR8438298_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 01:38:43 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	780,930,134
Mapped reads	776,744,186 / 99.46%
Unmapped reads	4,185,948 / 0.54%
Mapped paired reads	776,744,186 / 99.46%
Mapped reads, first in pair	388,628,729 / 49.76%
Mapped reads, second in pair	388,115,457 / 49.7%
Mapped reads, both in pair	774,154,076 / 99.13%
Mapped reads, singletons	2,590,110 / 0.33%
Secondary alignments	0
Supplementary alignments	20,611,699 / 2.64%
Read min/max/mean length	30 / 149 / 143.19
Duplicated reads (estimated)	320,948,461 / 41.1%
Duplication rate	36.43%
Clipped reads	106,558,711 / 13.65%

2.2. ACGT Content

Number/percentage of A's	33,865,364,442 / 30.79%
Number/percentage of C's	20,791,882,980 / 18.9%
Number/percentage of T's	31,886,674,770 / 28.99%
Number/percentage of G's	23,443,222,713 / 21.31%
Number/percentage of N's	204,060 / 0%

GC Percentage	40.22%
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2.3. Coverage

Mean	35.5405
Standard Deviation	106.6368

2.4. Mapping Quality

Mean Mapping Quality	54.24
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2.5. Insert size

Mean	103,785.96
Standard Deviation	3,109,422.54
P25/Median/P75	385 / 459 / 578

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	613,826,323
Insertions	14,587,965
Mapped reads with at least one insertion	1.83%
Deletions	12,941,529
Mapped reads with at least one deletion	1.62%
Homopolymer indels	48.07%

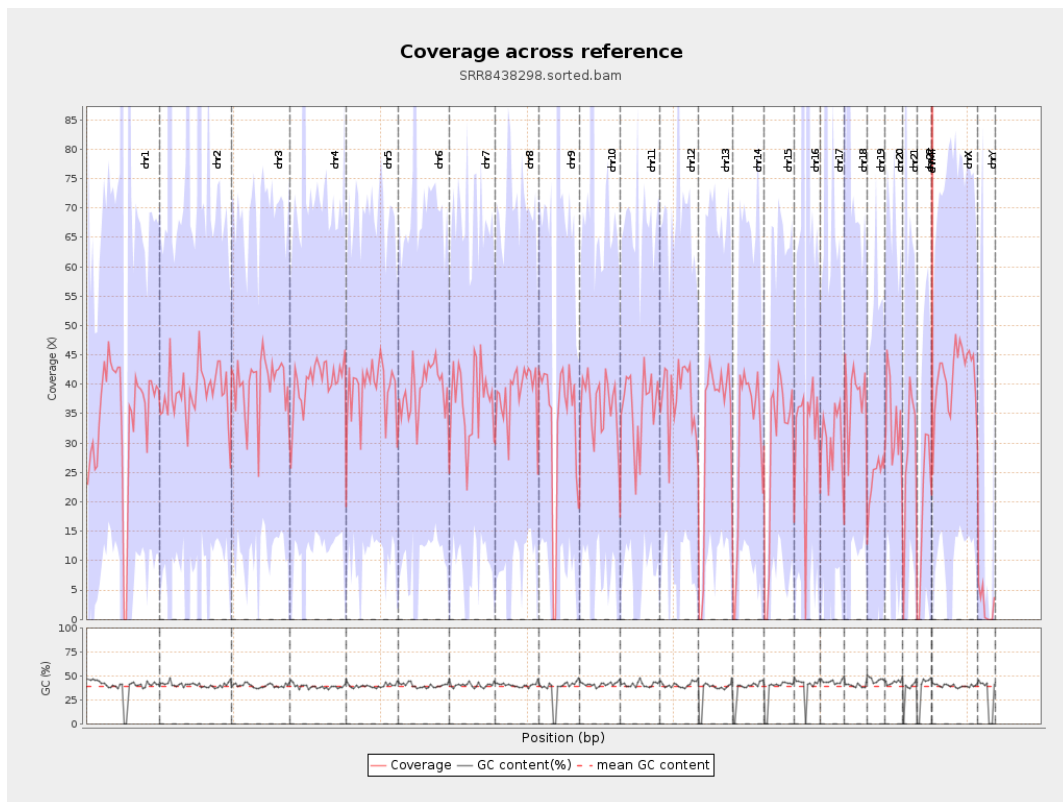
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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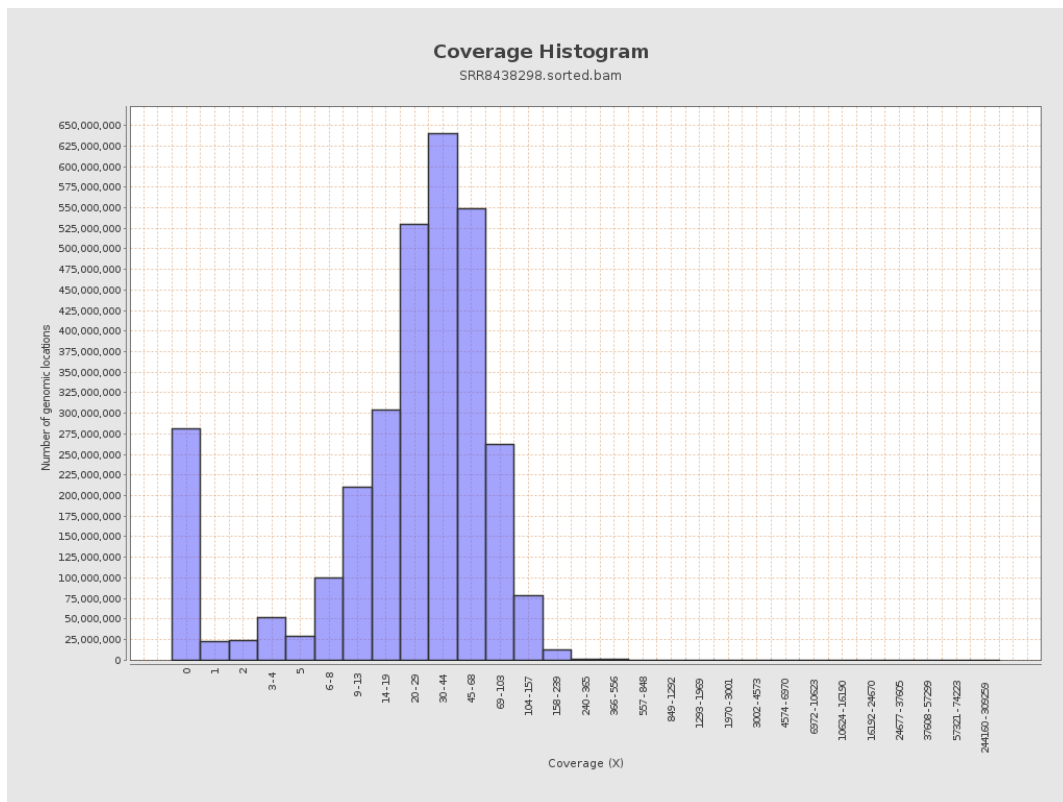
		bases	coverage	deviation
chr1	249250621	8616289831	34.5688	42.4993
chr2	243199373	9393777701	38.6258	228.5149
chr3	198022430	7936668837	40.0796	28.8968
chr4	191154276	7733530971	40.457	37.6318
chr5	180915260	7064823820	39.0505	28.8034
chr6	171115067	6735581043	39.3629	33.5437
chr7	159138663	5905978665	37.1122	31.4329
chr8	146364022	5654271764	38.6316	32.2327
chr9	141213431	4648181120	32.916	56.5048
chr10	135534747	4943598793	36.4748	81.6956
chr11	135006516	4870813169	36.0784	31.5633
chr12	133851895	5069301579	37.8725	31.0279
chr13	115169878	3804511010	33.0339	29.591
chr14	107349540	3322086414	30.9464	30.299
chr15	102531392	3022272165	29.4766	29.0638
chr16	90354753	2838310283	31.413	90.3411
chr17	81195210	2426886354	29.8895	51.7383
chr18	78077248	3000763854	38.4333	68.2626
chr19	59128983	1428267892	24.1551	30.4395
chr20	63025520	2106931705	33.4298	33.1313
chr21	48129895	1408090028	29.256	45.6082
chr22	51304566	983969626	19.179	26.7275
chrMT	16571	500719723	30,216.6268	11,026.7872
chrX	155270560	6467827279	41.6552	32.5005

chrY	59373566	139039994	2.3418	37.7532
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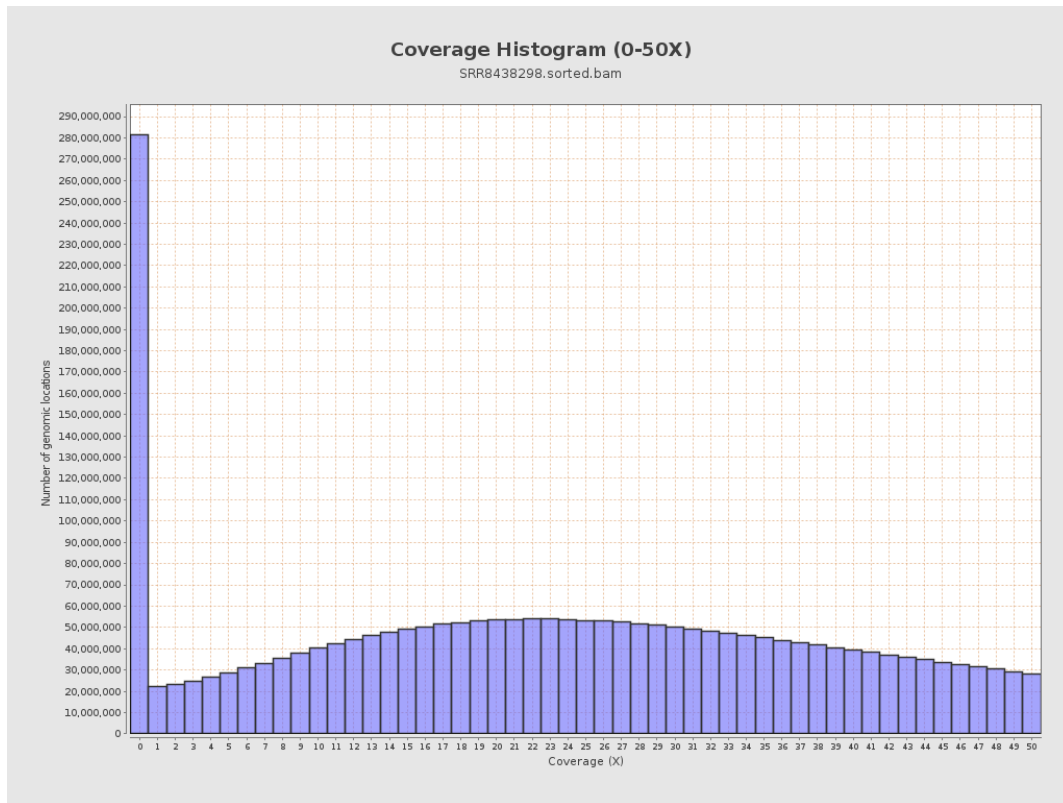
3. Results : Coverage across reference



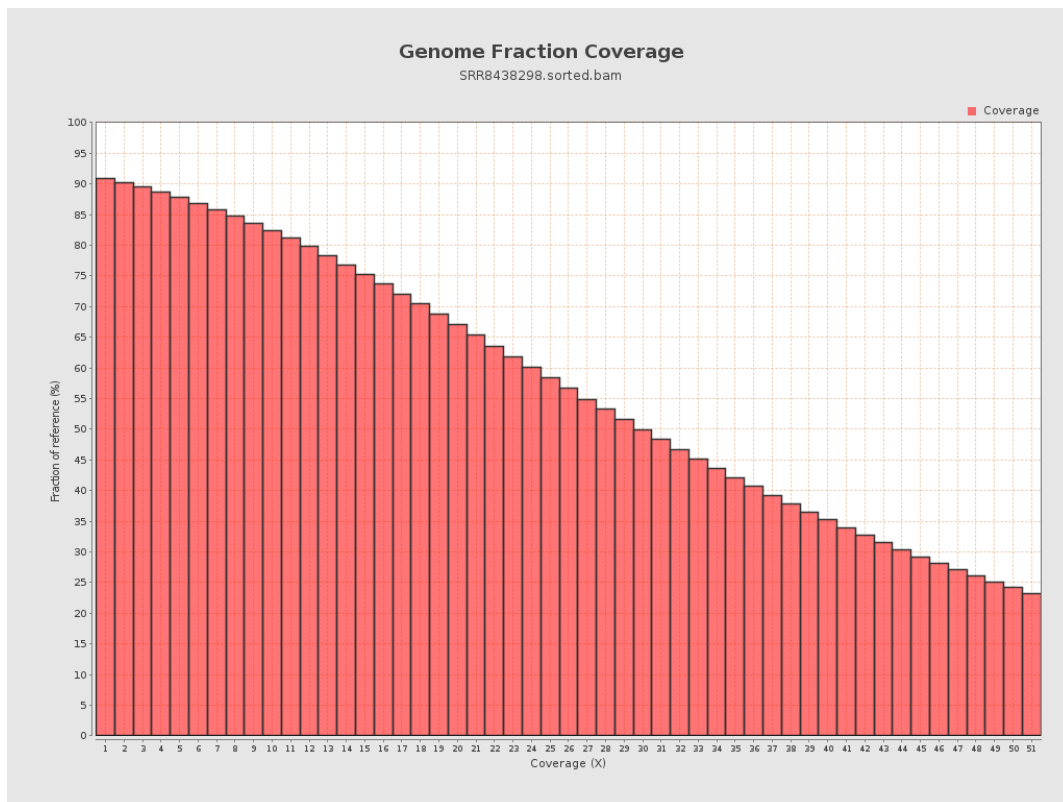
4. Results : Coverage Histogram



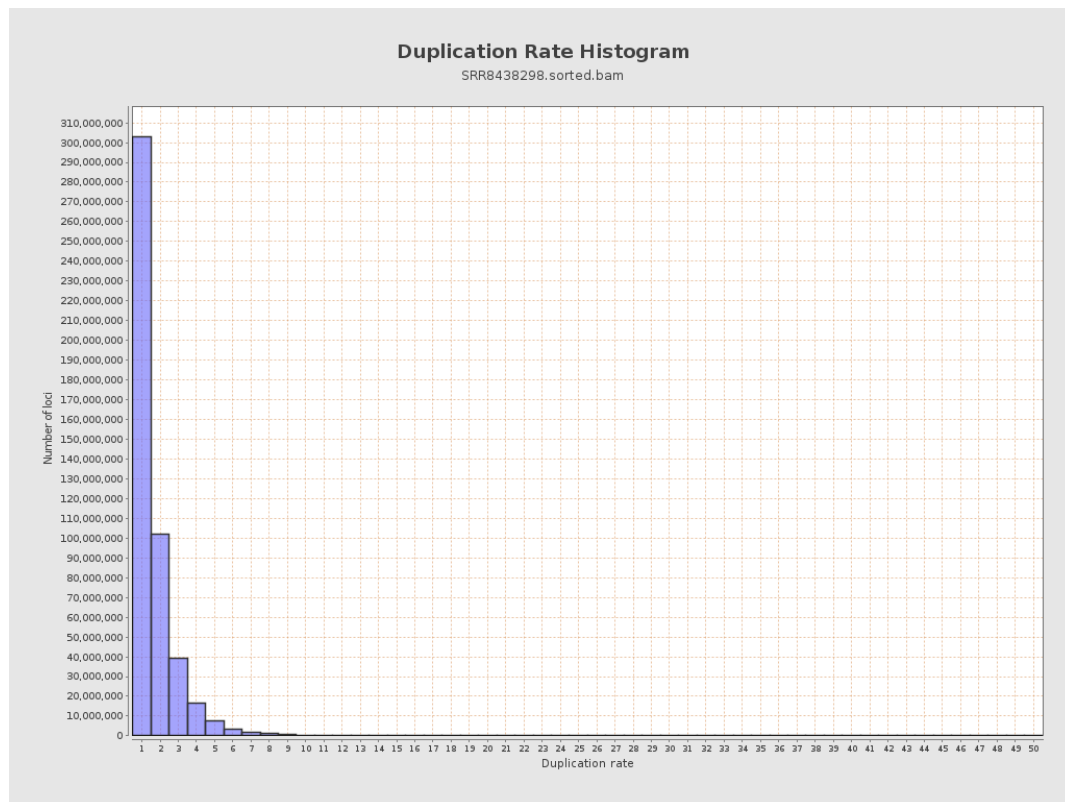
5. Results : Coverage Histogram (0-50X)



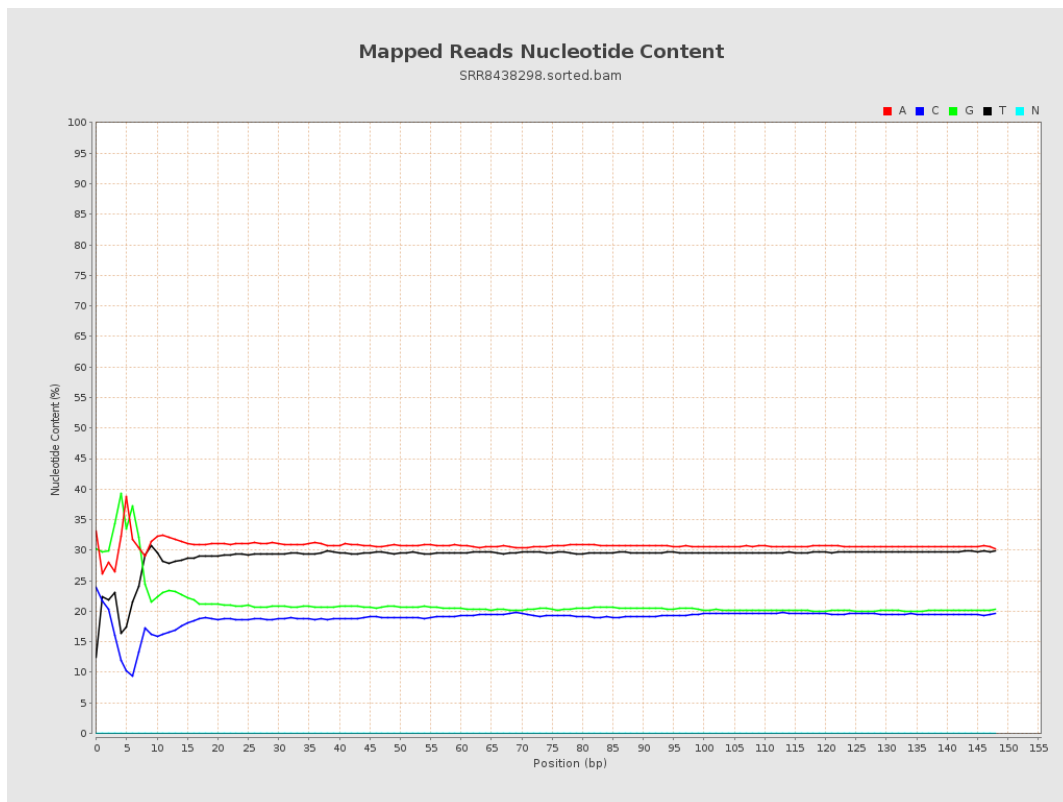
6. Results : Genome Fraction Coverage



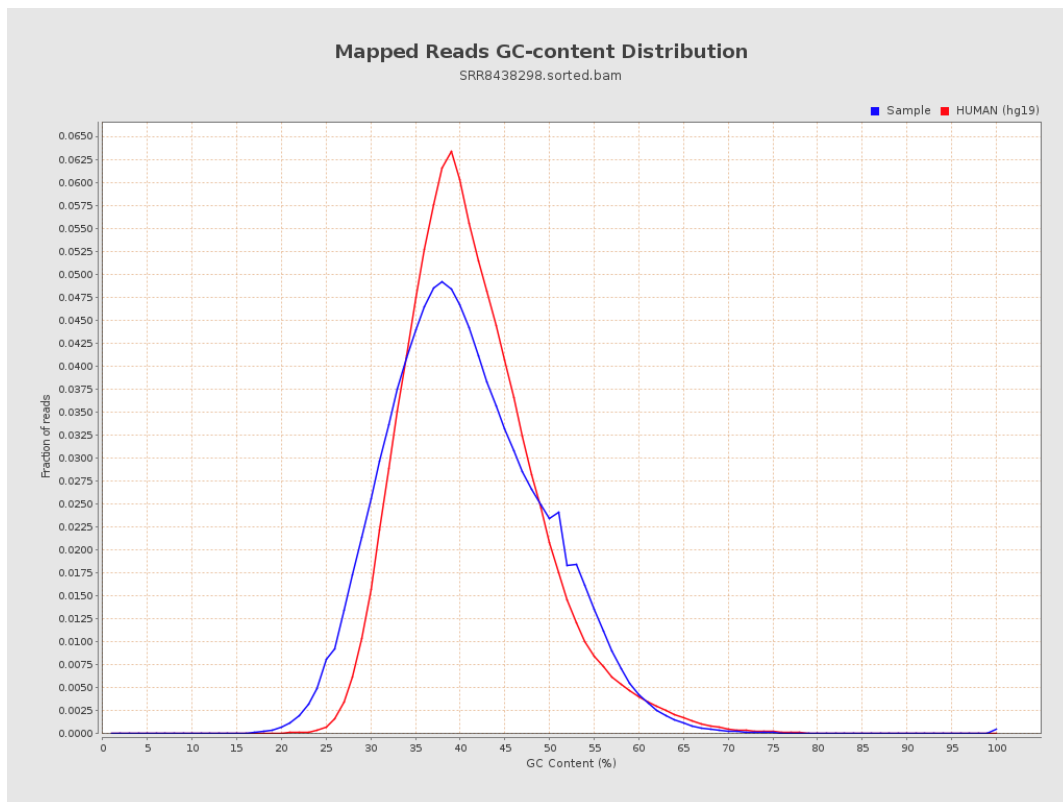
7. Results : Duplication Rate Histogram



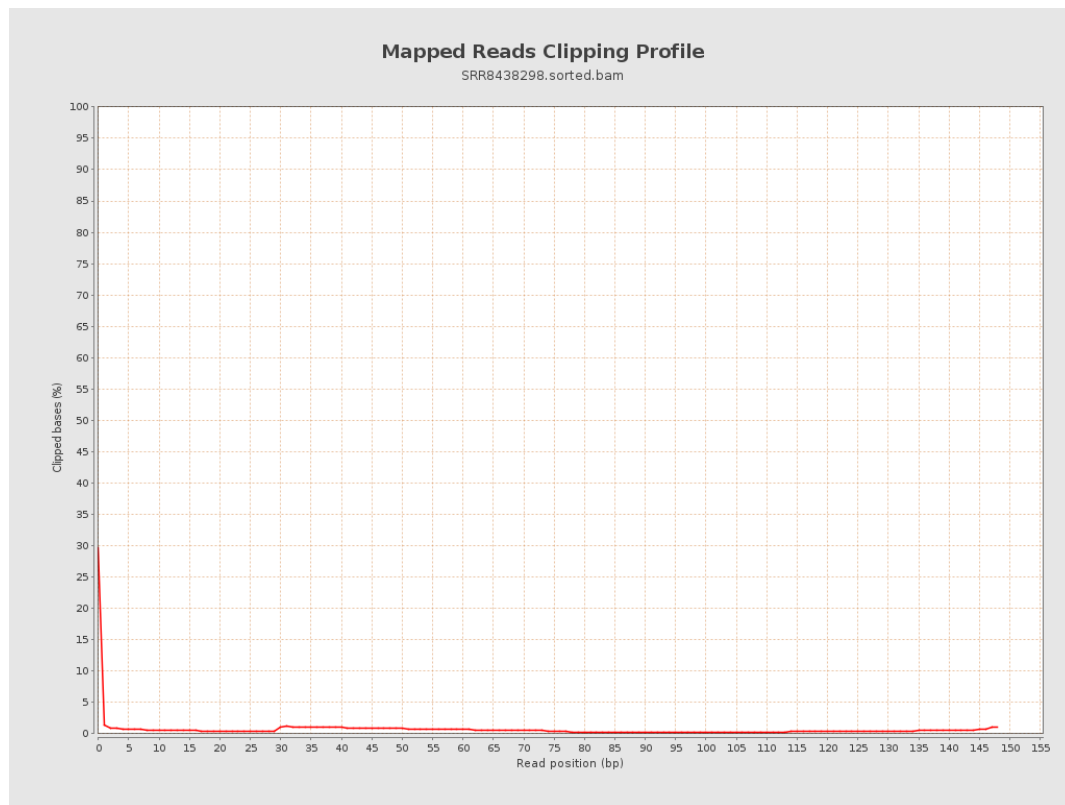
8. Results : Mapped Reads Nucleotide Content



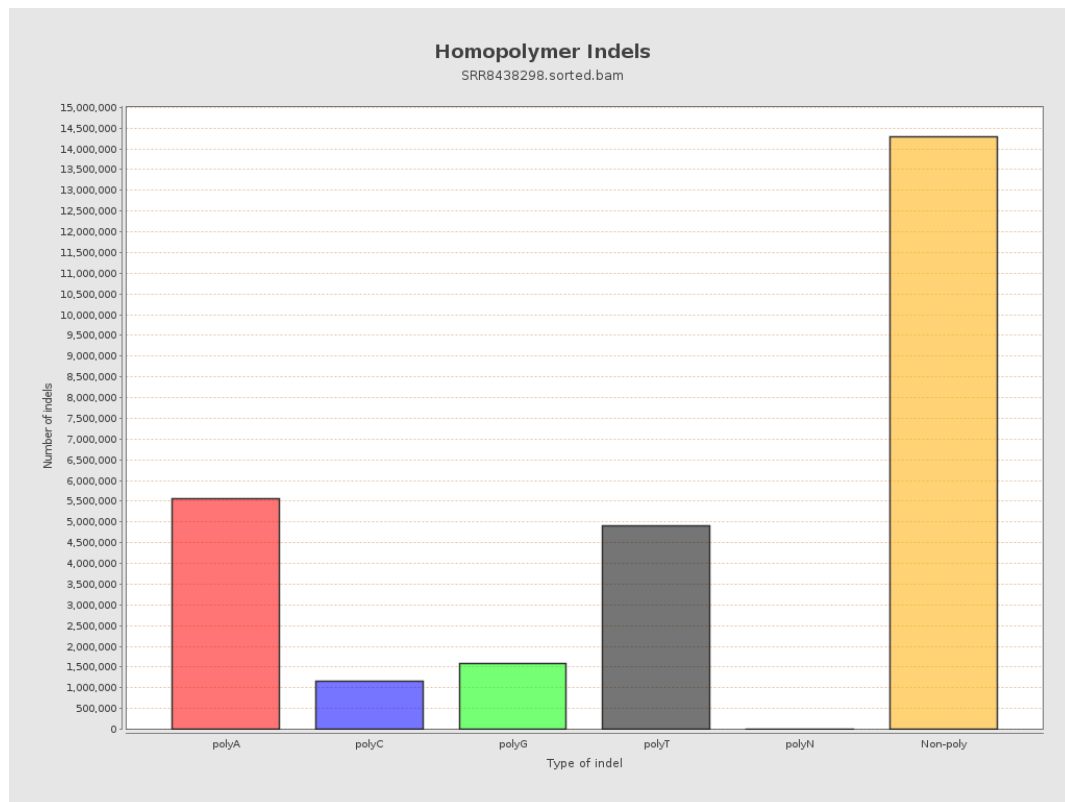
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



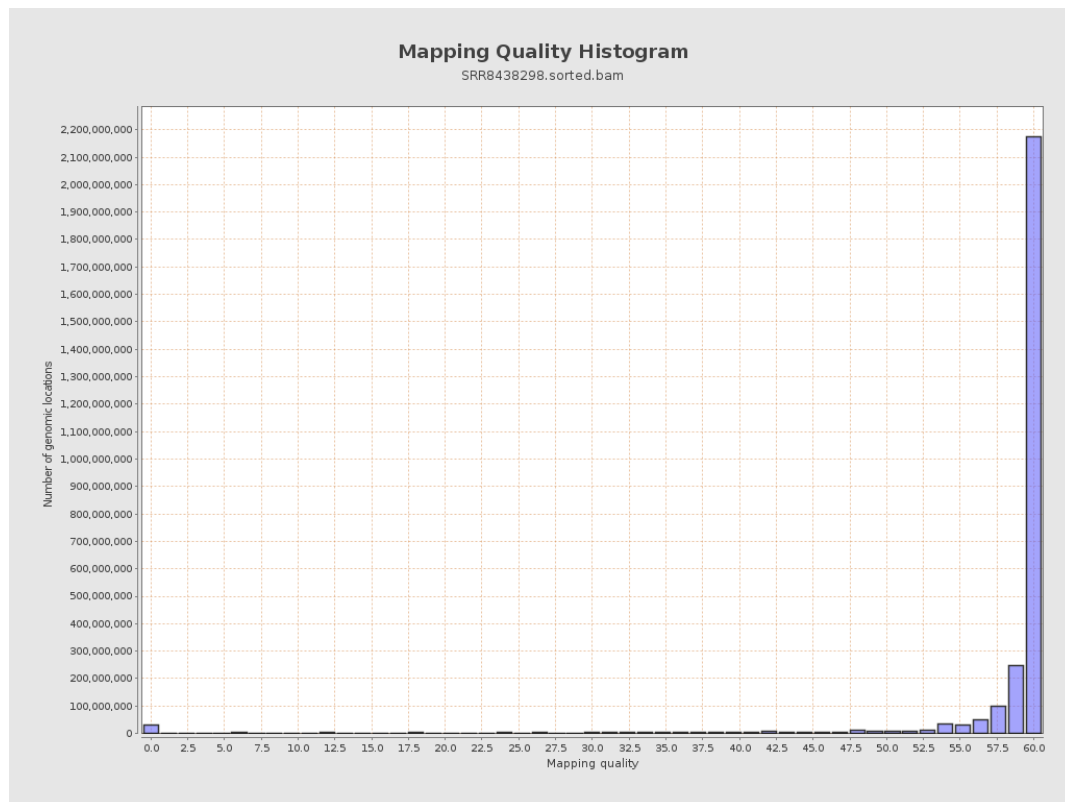
11. Results : Homopolymer Indels



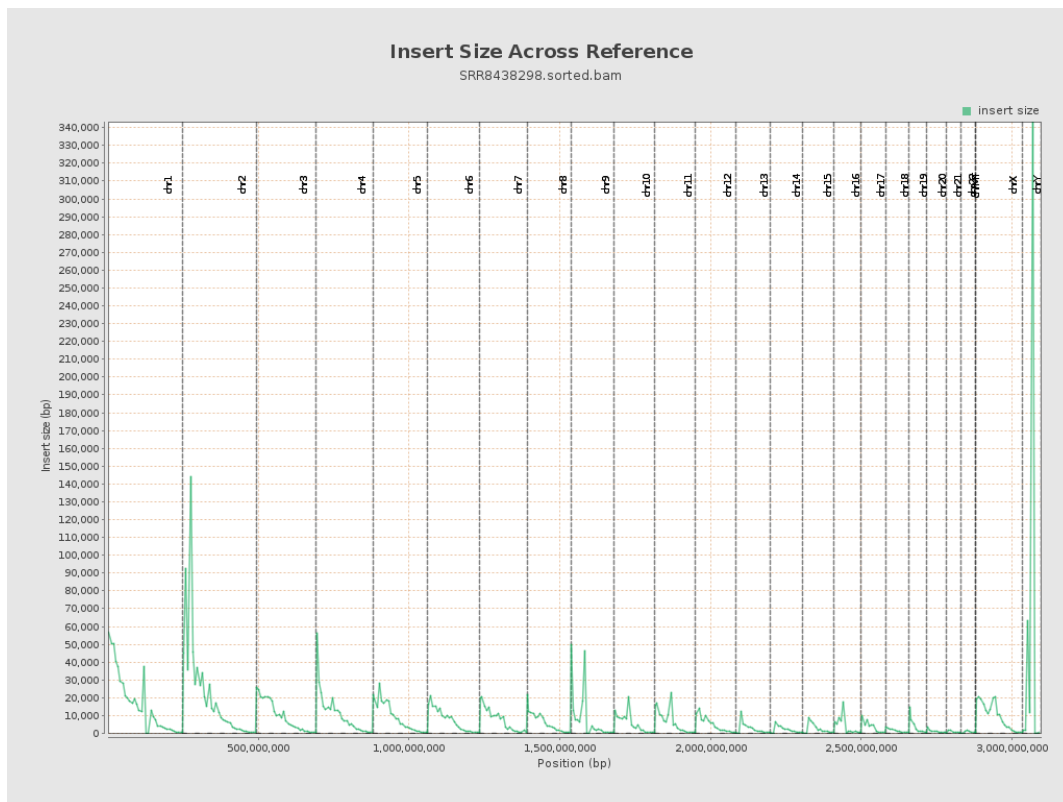
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

