

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 11:25:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438293.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_SRR8438293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438293_1.fastq.gz SRR8438293_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 11:25:00 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	691,439,774
Mapped reads	689,357,538 / 99.7%
Unmapped reads	2,082,236 / 0.3%
Mapped paired reads	689,357,538 / 99.7%
Mapped reads, first in pair	344,826,838 / 49.87%
Mapped reads, second in pair	344,530,700 / 49.83%
Mapped reads, both in pair	687,944,886 / 99.49%
Mapped reads, singletons	1,412,652 / 0.2%
Secondary alignments	0
Supplementary alignments	11,498,675 / 1.66%
Read min/max/mean length	28 / 151 / 144.96
Duplicated reads (estimated)	285,490,518 / 41.29%
Duplication rate	38.67%
Clipped reads	125,172,585 / 18.1%

2.2. ACGT Content

Number/percentage of A's	29,954,007,265 / 30.25%
Number/percentage of C's	19,792,788,026 / 19.99%
Number/percentage of T's	28,648,661,276 / 28.94%
Number/percentage of G's	20,609,170,701 / 20.82%
Number/percentage of N's	611,337 / 0%

GC Percentage	40.81%
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2.3. Coverage

Mean	31.99
Standard Deviation	92.1862

2.4. Mapping Quality

Mean Mapping Quality	55.05
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2.5. Insert size

Mean	38,310.27
Standard Deviation	1,901,928.37
P25/Median/P75	180 / 236 / 327

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	504,496,936
Insertions	12,063,270
Mapped reads with at least one insertion	1.72%
Deletions	10,654,922
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.26%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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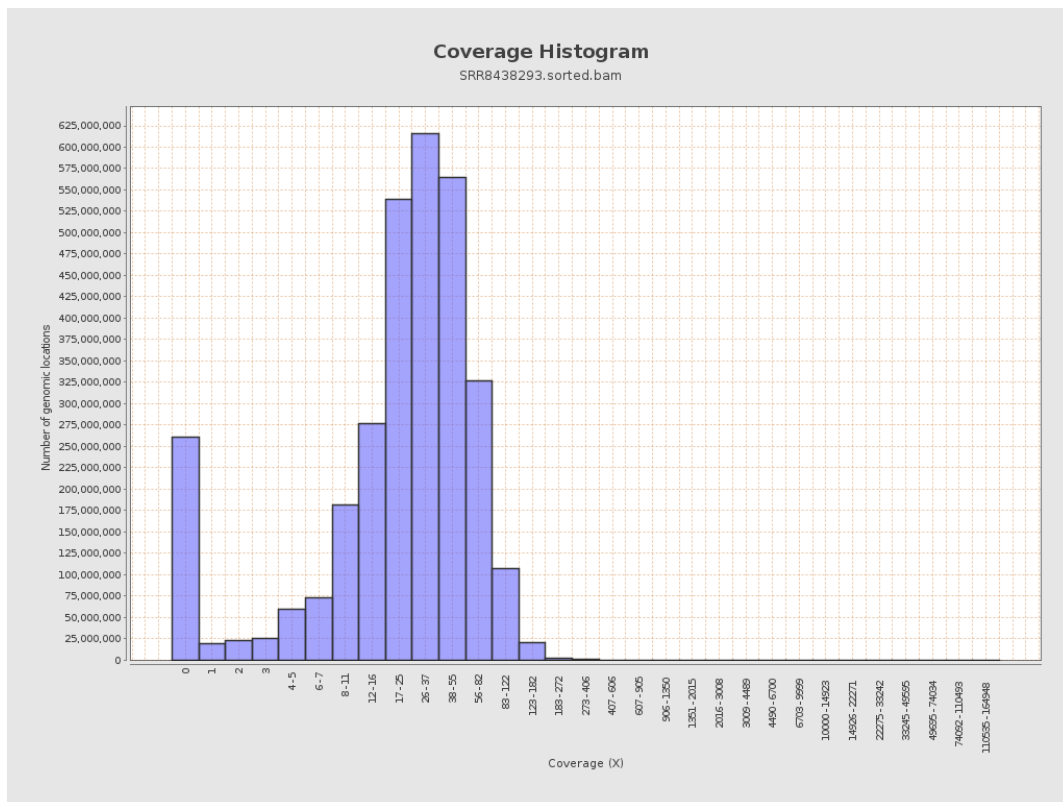
		bases	coverage	deviation
chr1	249250621	7949770601	31.8947	30.2353
chr2	243199373	8743040081	35.9501	116.8585
chr3	198022430	7212501051	36.4226	188.0641
chr4	191154276	6742010447	35.27	31.9097
chr5	180915260	6500823444	35.933	43.5287
chr6	171115067	5900015933	34.4798	30.4823
chr7	159138663	5359629298	33.679	30.5793
chr8	146364022	5246808295	35.8477	26.765
chr9	141213431	4179249408	29.5953	32.911
chr10	135534747	4738278329	34.9599	38.8626
chr11	135006516	4730349603	35.0379	26.99
chr12	133851895	4692736567	35.0592	26.5981
chr13	115169878	3460430240	30.0463	26.0418
chr14	107349540	3140961765	29.2592	29.2576
chr15	102531392	2891153722	28.1977	28.675
chr16	90354753	2713806992	30.035	50.0868
chr17	81195210	2339725981	28.8161	34.6629
chr18	78077248	2677826897	34.2971	26.4969
chr19	59128983	1528703197	25.8537	271.2653
chr20	63025520	2178156597	34.5599	30.2729
chr21	48129895	1251021997	25.9926	97.6106
chr22	51304566	1056801933	20.5986	26.3653
chrMT	16571	350192464	21,132.8504	7,878.2972
chrX	155270560	2951559826	19.0091	33.6125

chrY	59373566	495733207	8.3494	26.6184
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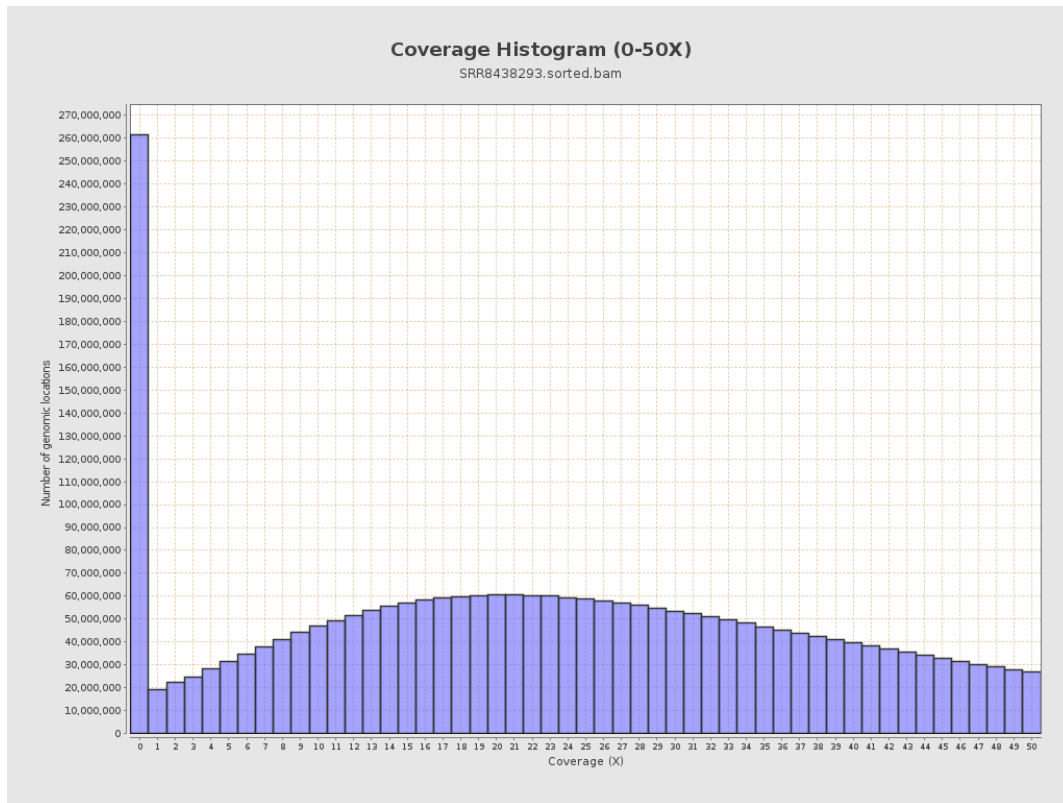
3. Results : Coverage across reference



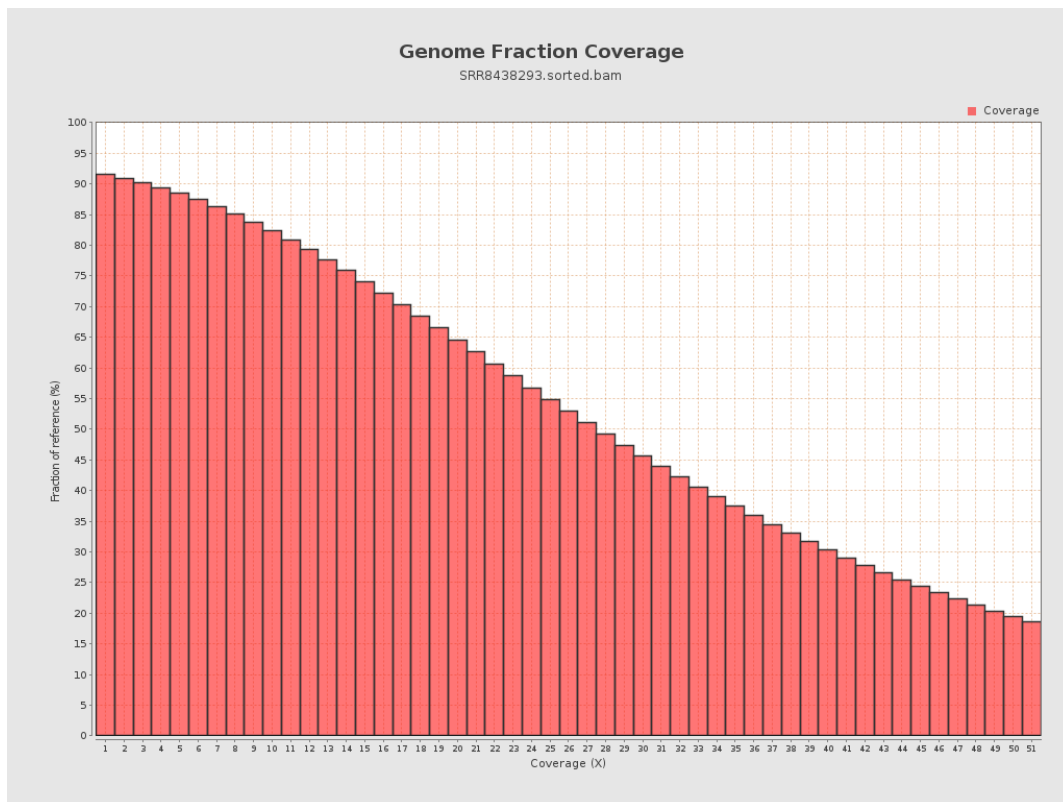
4. Results : Coverage Histogram



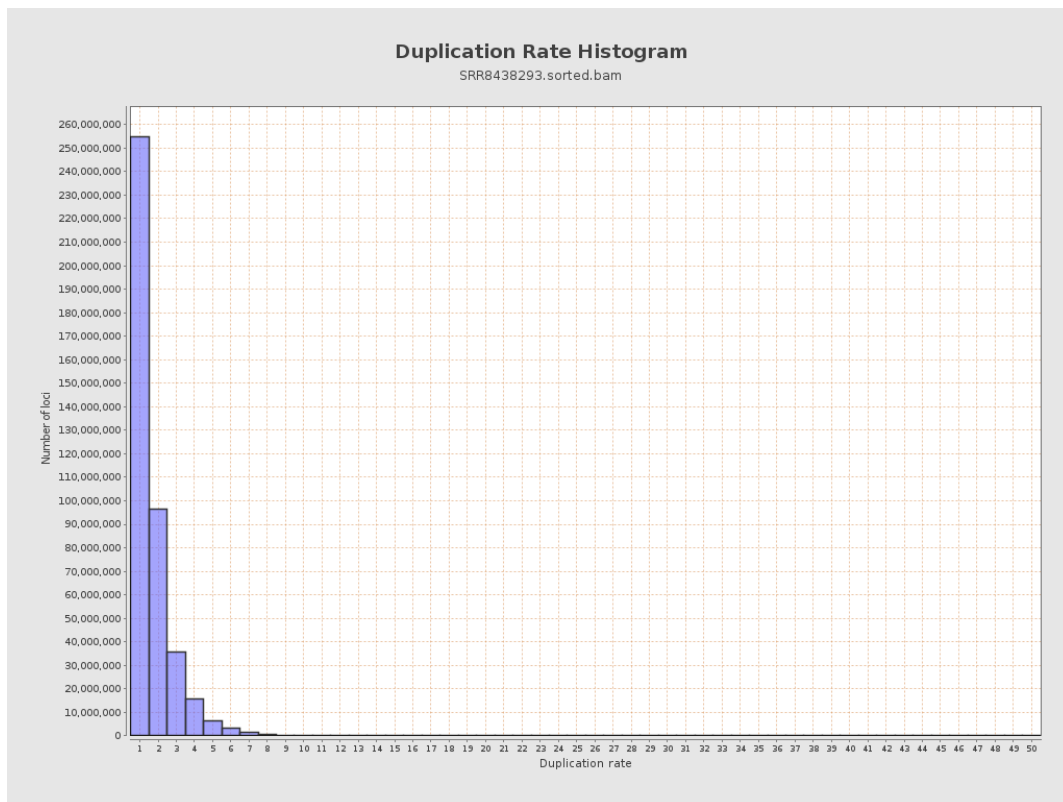
5. Results : Coverage Histogram (0-50X)



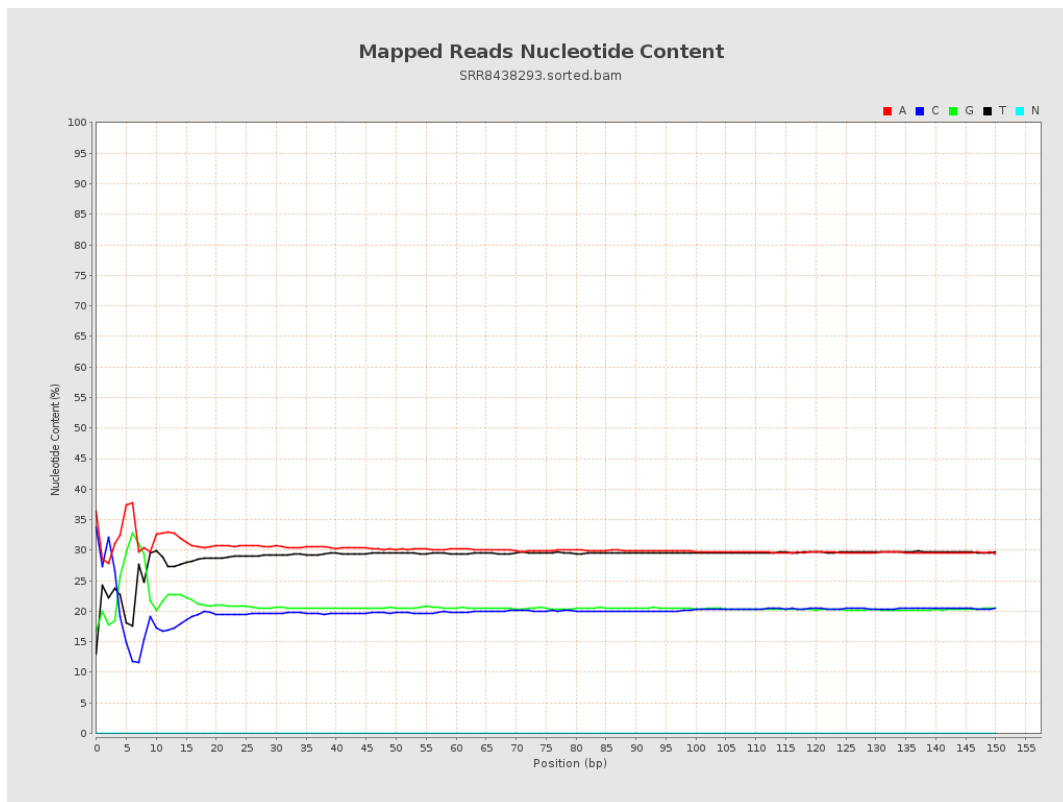
6. Results : Genome Fraction Coverage



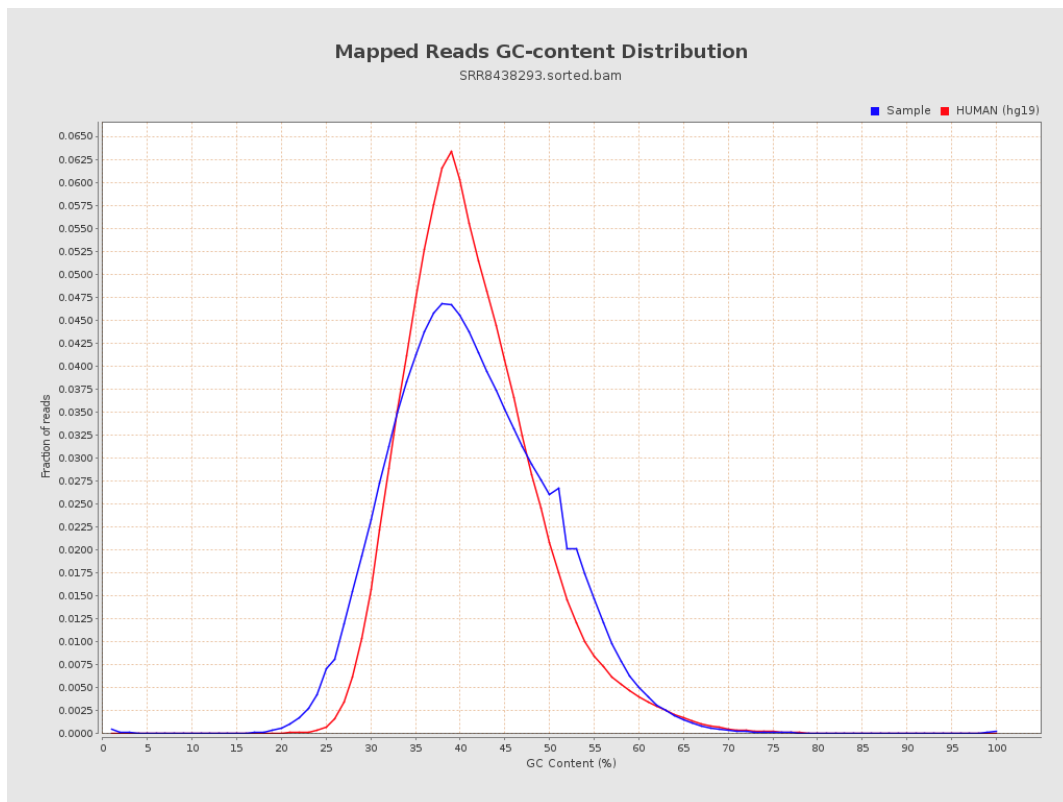
7. Results : Duplication Rate Histogram



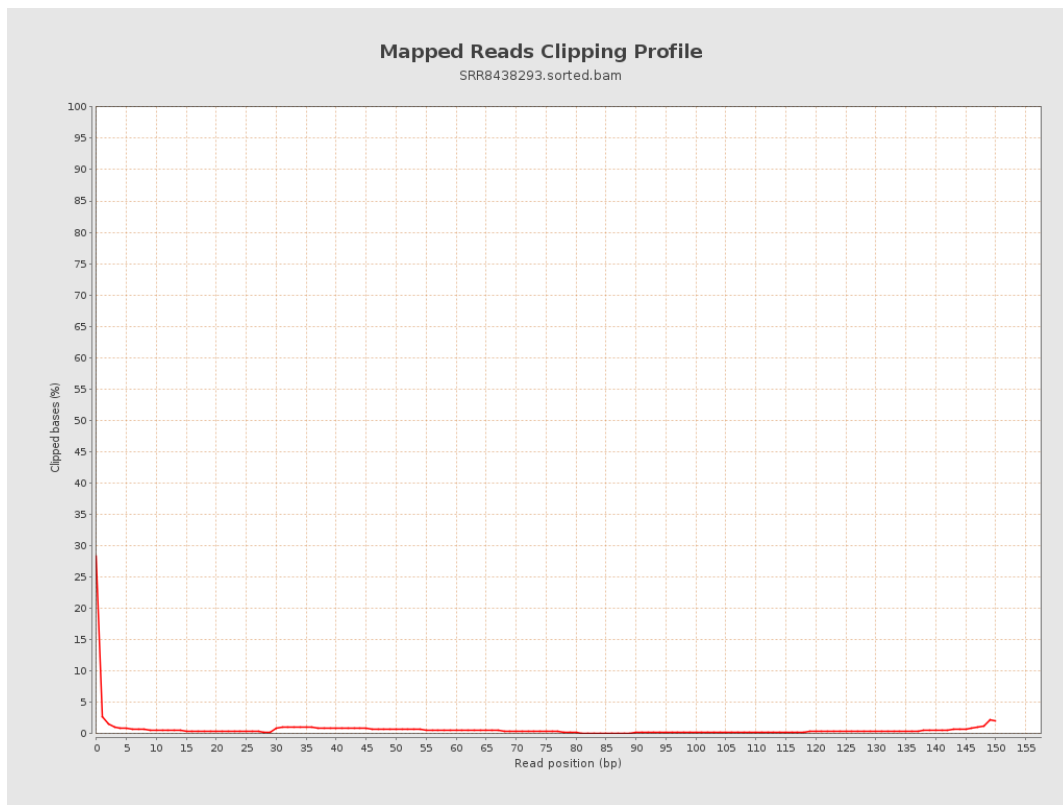
8. Results : Mapped Reads Nucleotide Content



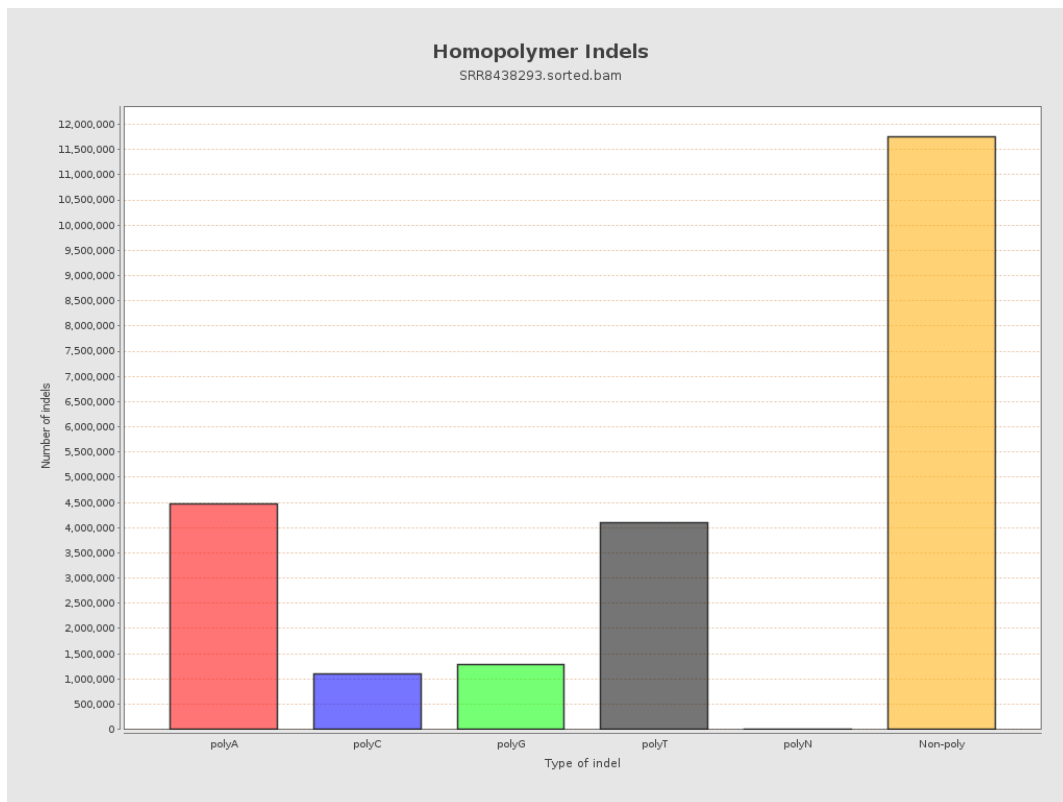
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



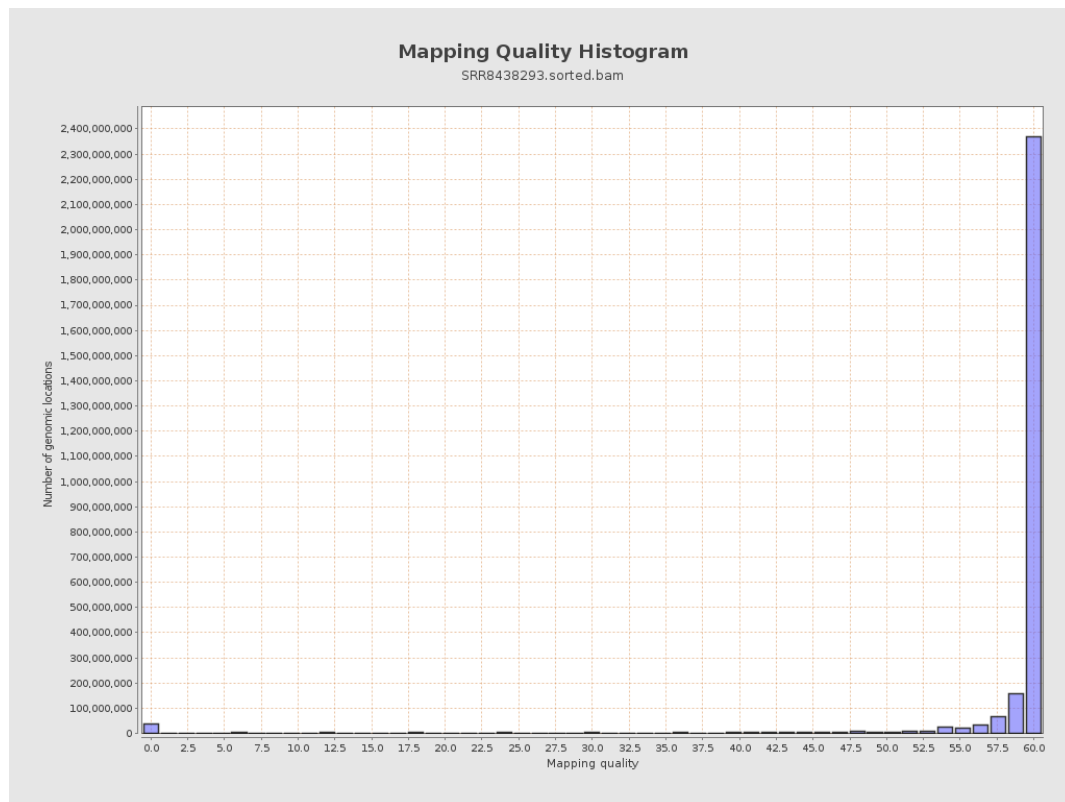
11. Results : Homopolymer Indels



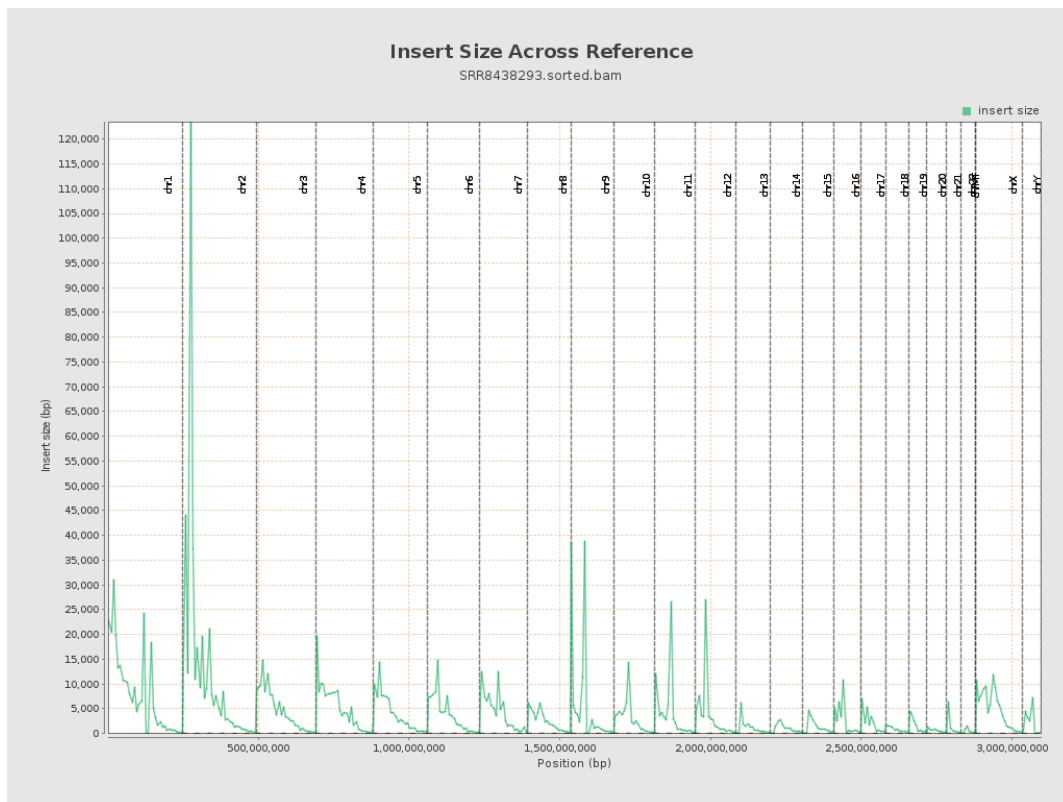
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

