

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/31 23:39:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438292.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_SRR8438292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438292_1.fastq.gz SRR8438292_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 31 23:39:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	695,713,054
Mapped reads	693,627,482 / 99.7%
Unmapped reads	2,085,572 / 0.3%
Mapped paired reads	693,627,482 / 99.7%
Mapped reads, first in pair	347,009,320 / 49.88%
Mapped reads, second in pair	346,618,162 / 49.82%
Mapped reads, both in pair	692,193,552 / 99.49%
Mapped reads, singletons	1,433,930 / 0.21%
Secondary alignments	0
Supplementary alignments	11,587,825 / 1.67%
Read min/max/mean length	28 / 151 / 145.29
Duplicated reads (estimated)	299,623,288 / 43.07%
Duplication rate	40.56%
Clipped reads	125,800,191 / 18.08%

2.2. ACGT Content

Number/percentage of A's	30,167,686,560 / 30.21%
Number/percentage of C's	19,985,856,421 / 20.01%
Number/percentage of T's	28,845,308,459 / 28.89%
Number/percentage of G's	20,857,339,491 / 20.89%
Number/percentage of N's	613,990 / 0%

GC Percentage	40.9%
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2.3. Coverage

Mean	32.2654
Standard Deviation	80.2486

2.4. Mapping Quality

Mean Mapping Quality	55.06
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2.5. Insert size

Mean	42,491.52
Standard Deviation	2,012,802.19
P25/Median/P75	181 / 236 / 326

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	508,438,641
Insertions	12,459,806
Mapped reads with at least one insertion	1.77%
Deletions	11,013,020
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.36%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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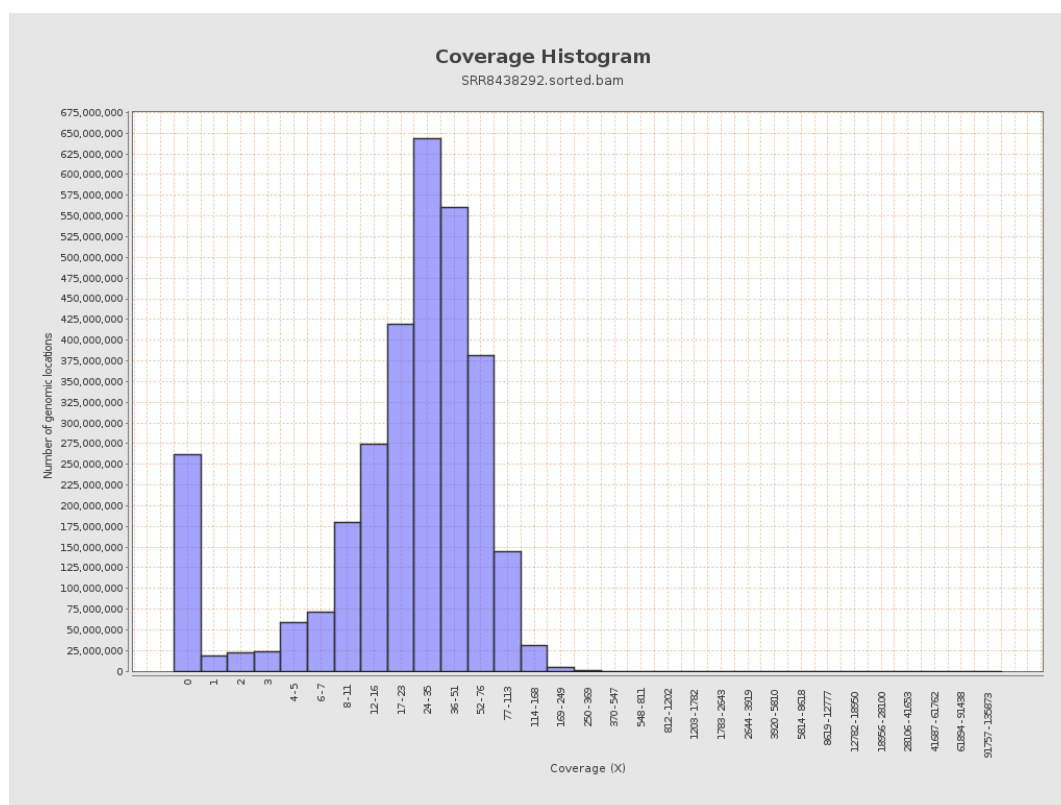
		bases	coverage	deviation
chr1	249250621	8092929612	32.469	30.2972
chr2	243199373	8910209410	36.6375	134.3803
chr3	198022430	7081278852	35.76	123.5204
chr4	191154276	6725491882	35.1836	27.5073
chr5	180915260	6534103321	36.1169	35.6375
chr6	171115067	6024624673	35.208	27.1481
chr7	159138663	5417694944	34.0439	27.394
chr8	146364022	5215513251	35.6338	26.2663
chr9	141213431	4379025913	31.01	32.8273
chr10	135534747	4753351790	35.0711	36.6802
chr11	135006516	4708482782	34.876	26.6717
chr12	133851895	4771887010	35.6505	26.23
chr13	115169878	3438116943	29.8526	26.0581
chr14	107349540	3144390237	29.2911	28.97
chr15	102531392	2975667449	29.022	28.7812
chr16	90354753	2751003412	30.4467	49.6292
chr17	81195210	2385194128	29.376	34.6673
chr18	78077248	2731581422	34.9856	26.751
chr19	59128983	1519465487	25.6975	171.7976
chr20	63025520	2200108544	34.9082	29.4414
chr21	48129895	1257527509	26.1278	61.1857
chr22	51304566	1062500049	20.7097	26.8208
chrMT	16571	344434479	20,785.3768	7,957.3756
chrX	155270560	2950260446	19.0008	23.3715

chrY	59373566	509034924	8.5734	25.6571
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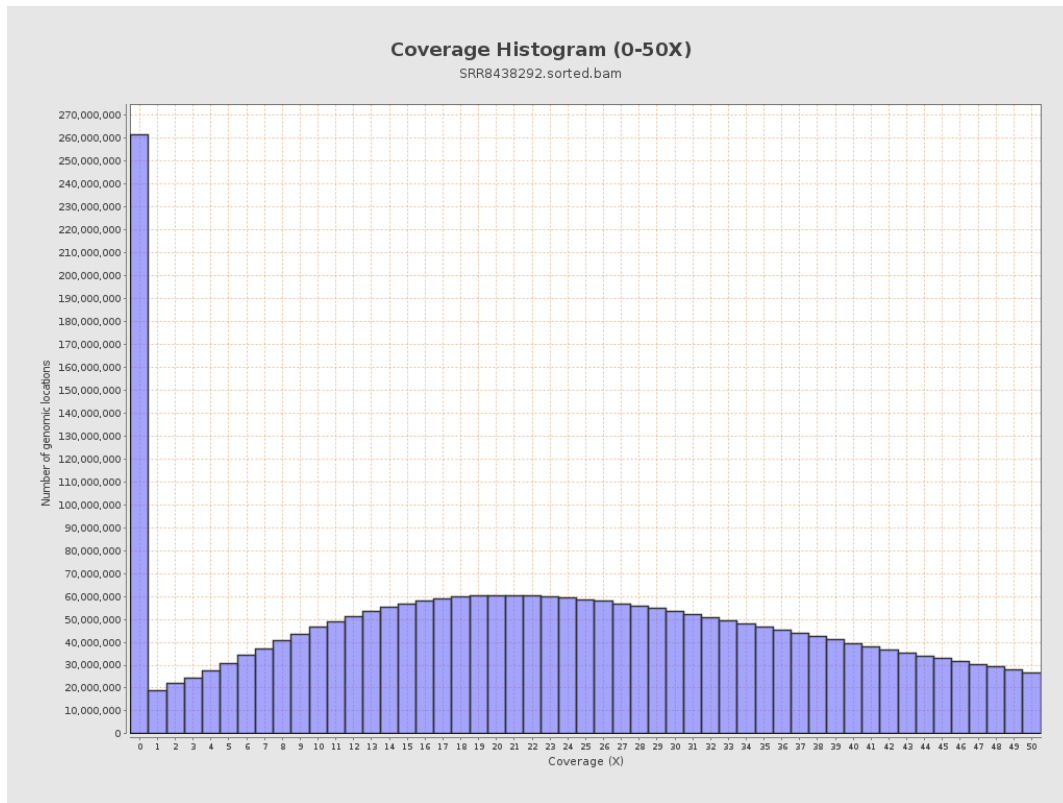
3. Results : Coverage across reference



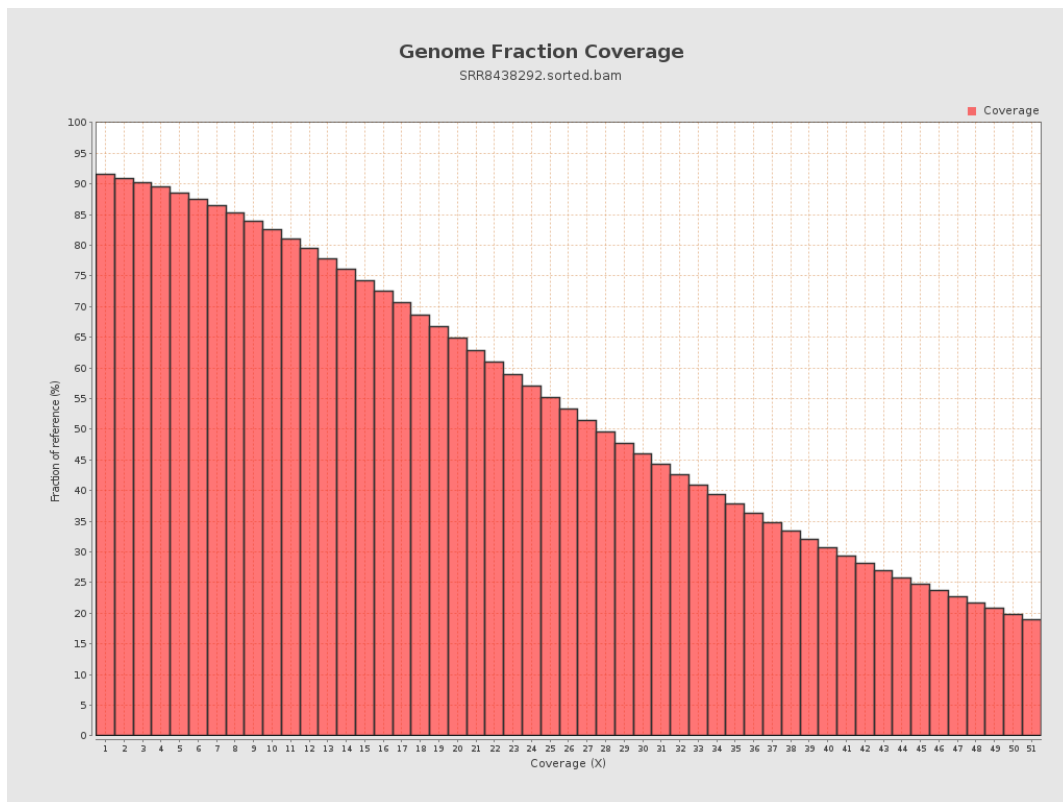
4. Results : Coverage Histogram



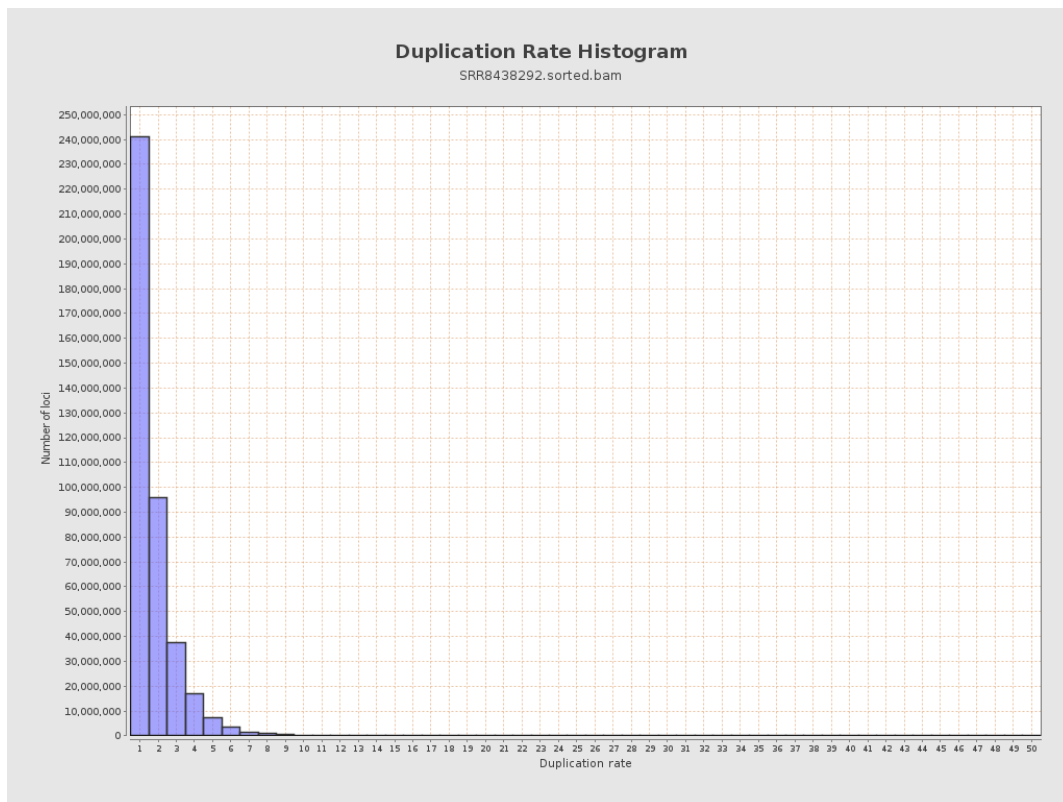
5. Results : Coverage Histogram (0-50X)



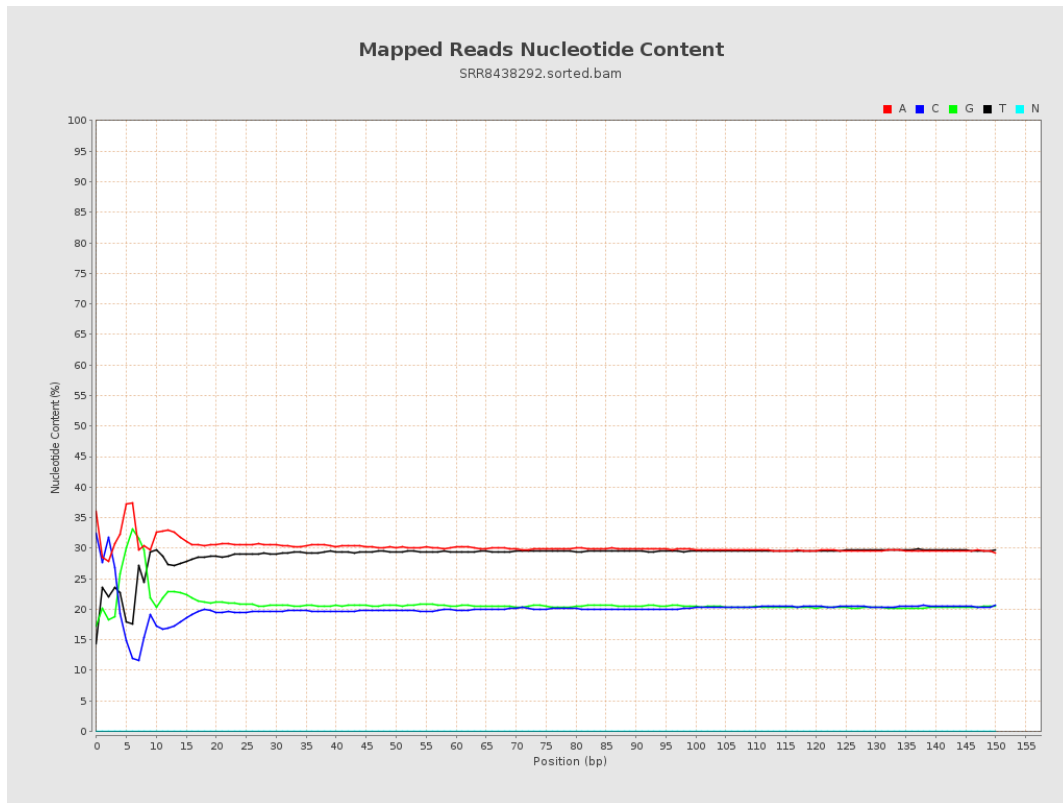
6. Results : Genome Fraction Coverage



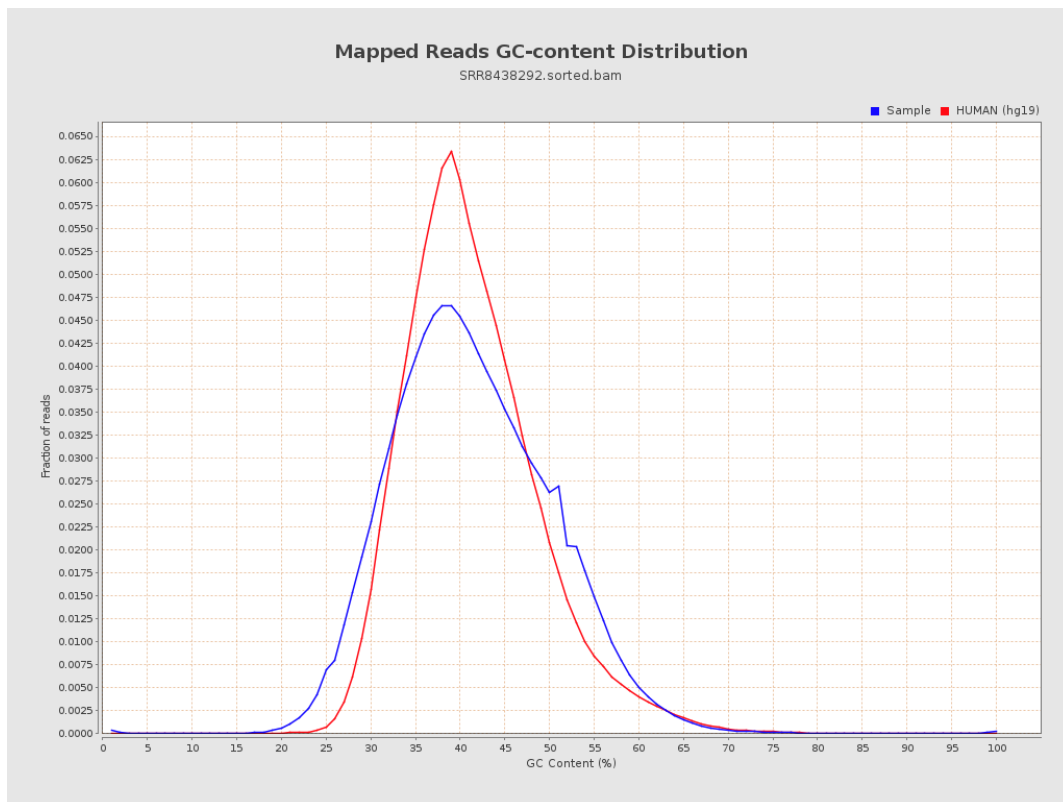
7. Results : Duplication Rate Histogram



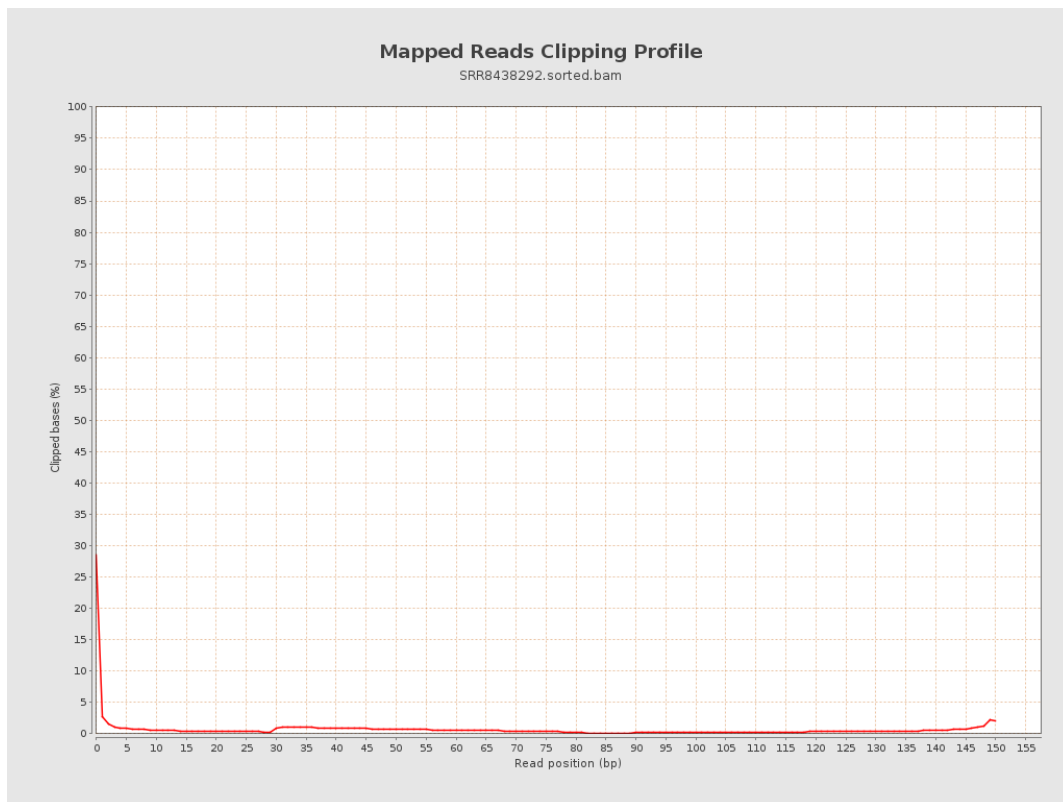
8. Results : Mapped Reads Nucleotide Content



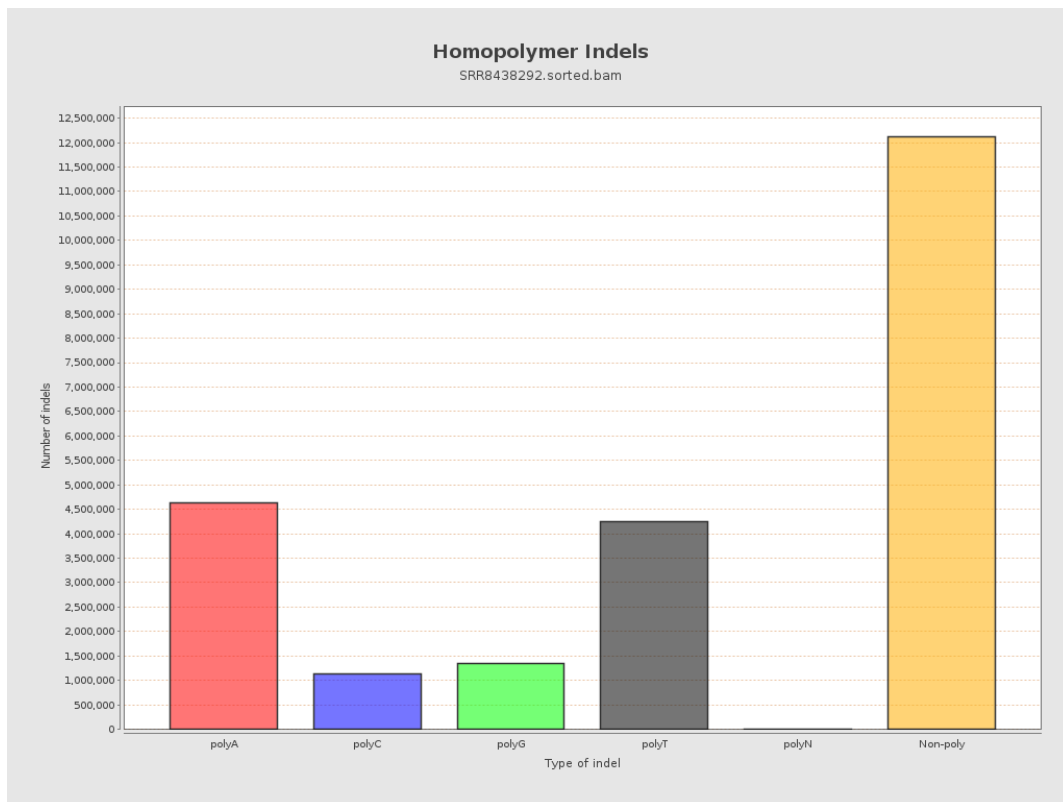
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



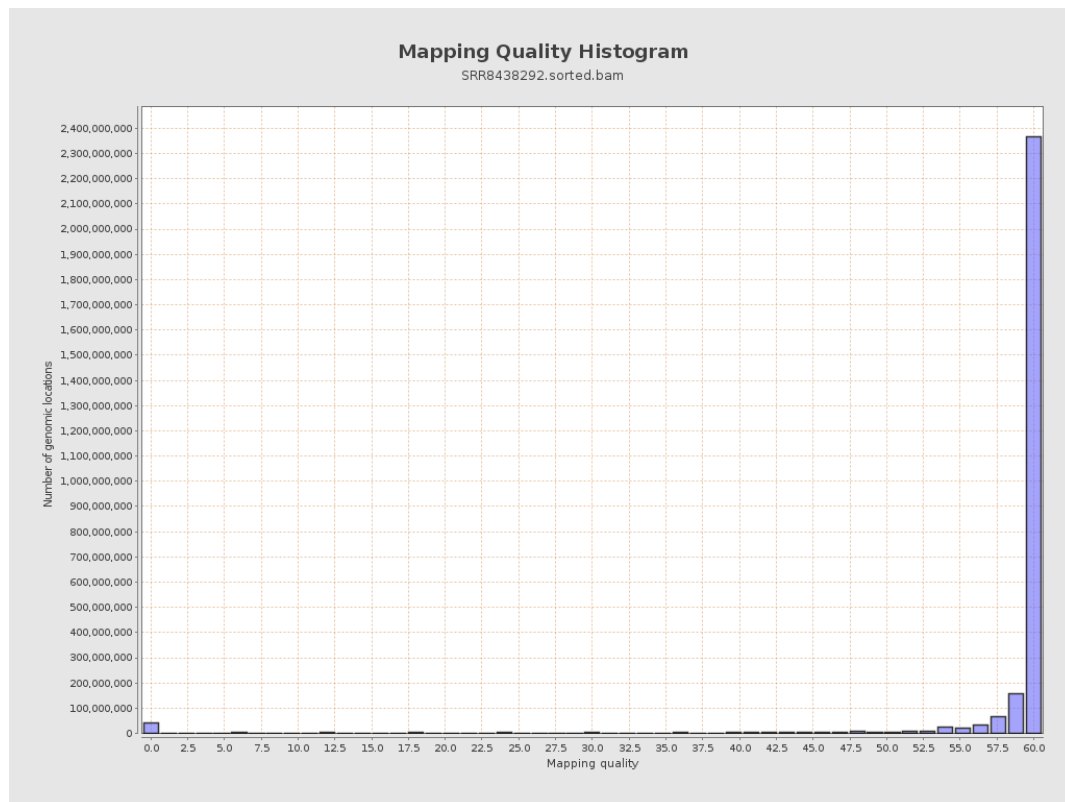
11. Results : Homopolymer Indels



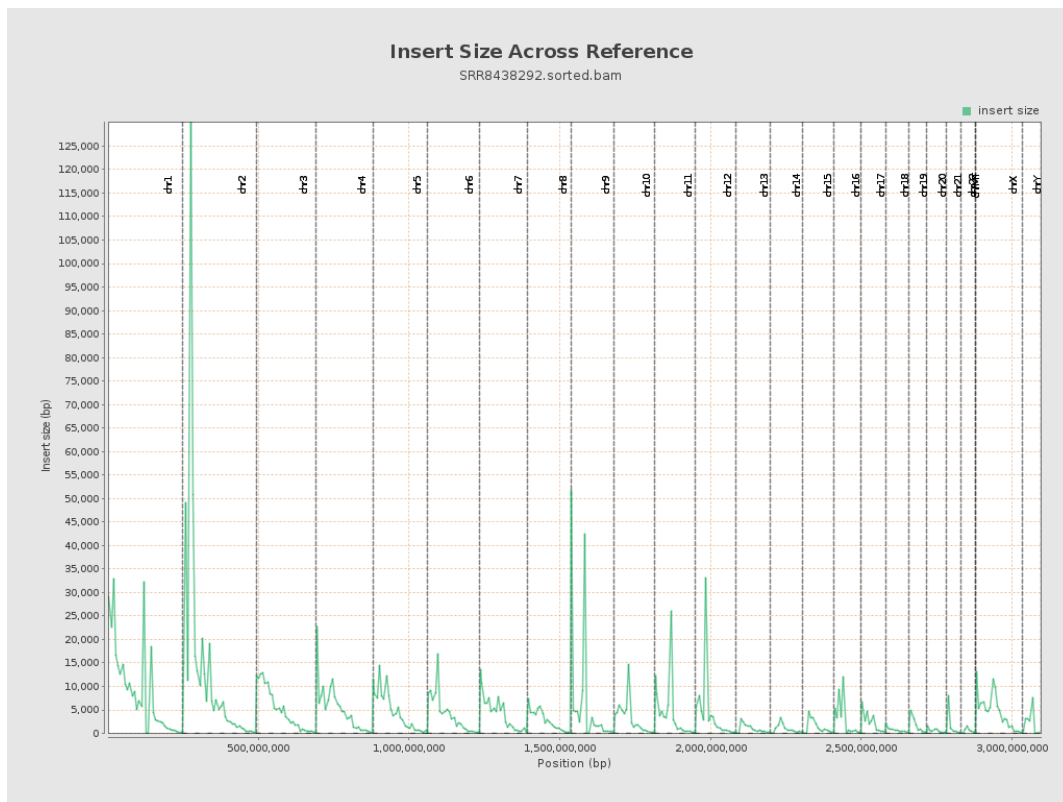
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

