

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 12:27:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695915.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695915 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695915_1.fastq.gz SRR1695915_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 12:27:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	366,910,526
Mapped reads	360,388,715 / 98.22%
Unmapped reads	6,521,811 / 1.78%
Mapped paired reads	360,388,715 / 98.22%
Mapped reads, first in pair	181,362,260 / 49.43%
Mapped reads, second in pair	179,026,455 / 48.79%
Mapped reads, both in pair	356,690,572 / 97.21%
Mapped reads, singletons	3,698,143 / 1.01%
Secondary alignments	0
Supplementary alignments	808,593 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	52,734,951 / 14.37%
Duplication rate	9.36%
Clipped reads	17,316,844 / 4.72%

2.2. ACGT Content

Number/percentage of A's	10,406,036,729 / 29.21%
Number/percentage of C's	7,395,043,775 / 20.76%
Number/percentage of T's	10,386,379,608 / 29.16%
Number/percentage of G's	7,428,159,151 / 20.85%
Number/percentage of N's	7,747,728 / 0.02%

GC Percentage	41.61%
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2.3. Coverage

Mean	11.5108
Standard Deviation	126.4264

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	37,021.26
Standard Deviation	1,783,881.23
P25/Median/P75	301 / 308 / 316

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	222,061,962
Insertions	3,573,279
Mapped reads with at least one insertion	0.96%
Deletions	4,283,283
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.03%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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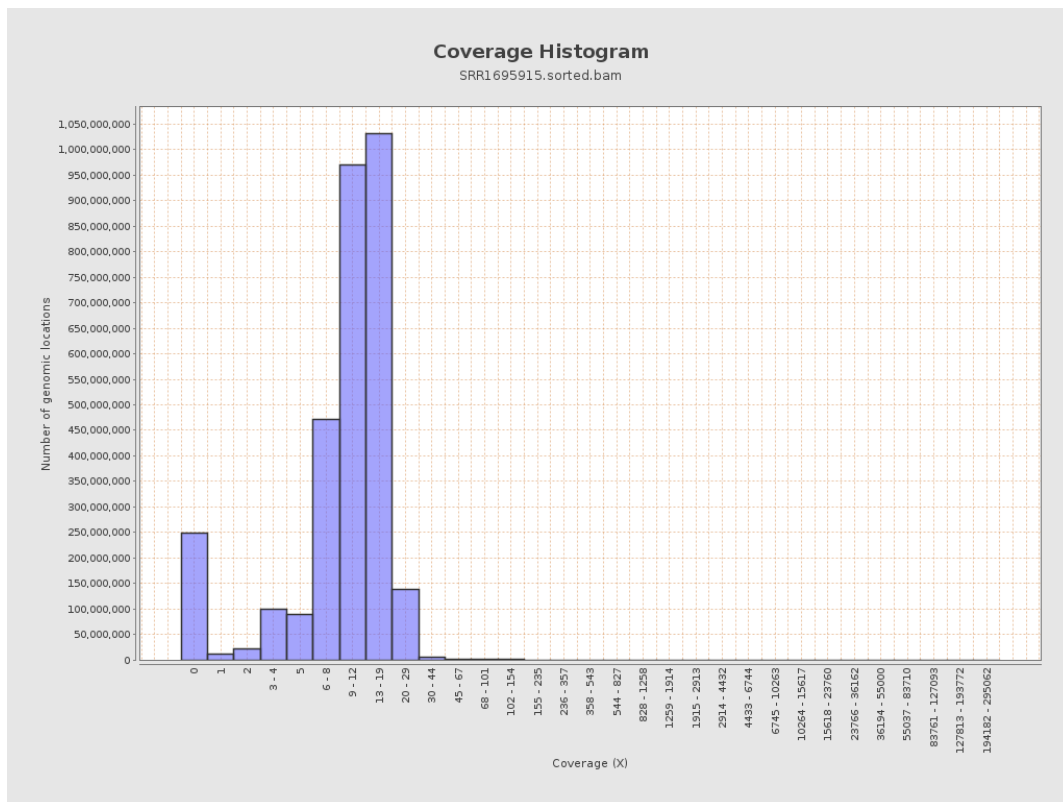
		bases	coverage	deviation
chr1	249250621	2971388815	11.9213	287.9931
chr2	243199373	3100527942	12.7489	80.1305
chr3	198022430	2332741528	11.7802	12.7138
chr4	191154276	2308464499	12.0764	88.1649
chr5	180915260	2117636549	11.7051	11.0566
chr6	171115067	2033513326	11.8839	47.9663
chr7	159138663	1923863000	12.0892	104.5119
chr8	146364022	1769723597	12.0912	70.5732
chr9	141213431	1506550953	10.6686	107.4807
chr10	135534747	1971722777	14.5477	330.8116
chr11	135006516	1648111183	12.2076	57.09
chr12	133851895	1588016662	11.864	10.1319
chr13	115169878	1094130313	9.5001	7.1261
chr14	107349540	1083210047	10.0905	10.1204
chr15	102531392	1032204018	10.0672	7.4884
chr16	90354753	1165924761	12.9039	90.4295
chr17	81195210	1048682636	12.9156	53.3184
chr18	78077248	967165103	12.3873	138.613
chr19	59128983	762143386	12.8895	153.6461
chr20	63025520	772938140	12.2639	42.099
chr21	48129895	493801212	10.2598	51.4424
chr22	51304566	476943984	9.2963	48.6246
chrMT	16571	100881557	6,087.8376	922.3763
chrX	155270560	925255406	5.959	22.0022

chrY	59373566	438318500	7.3824	127.71
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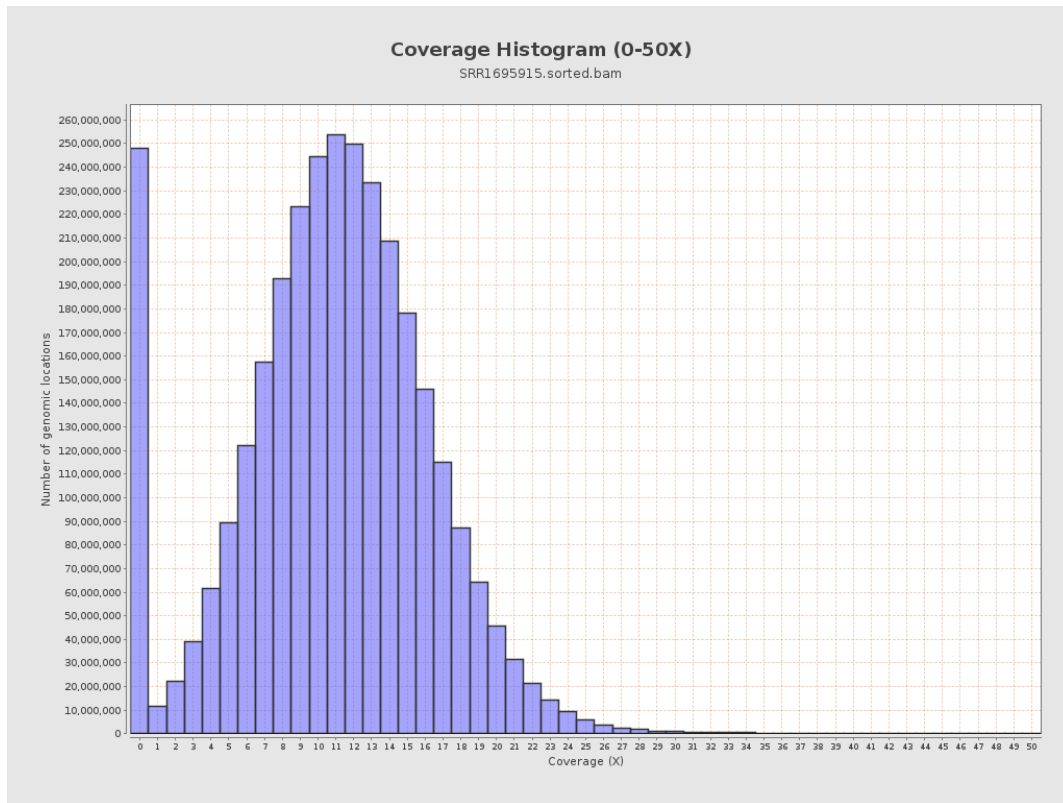
3. Results : Coverage across reference



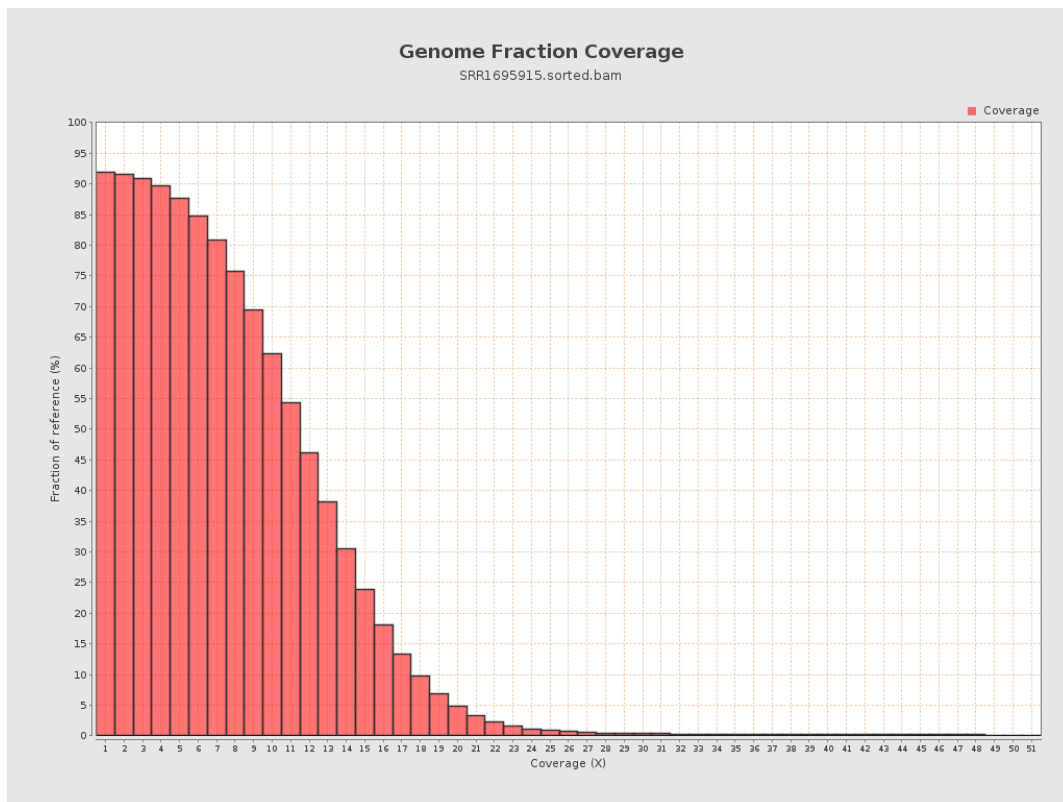
4. Results : Coverage Histogram



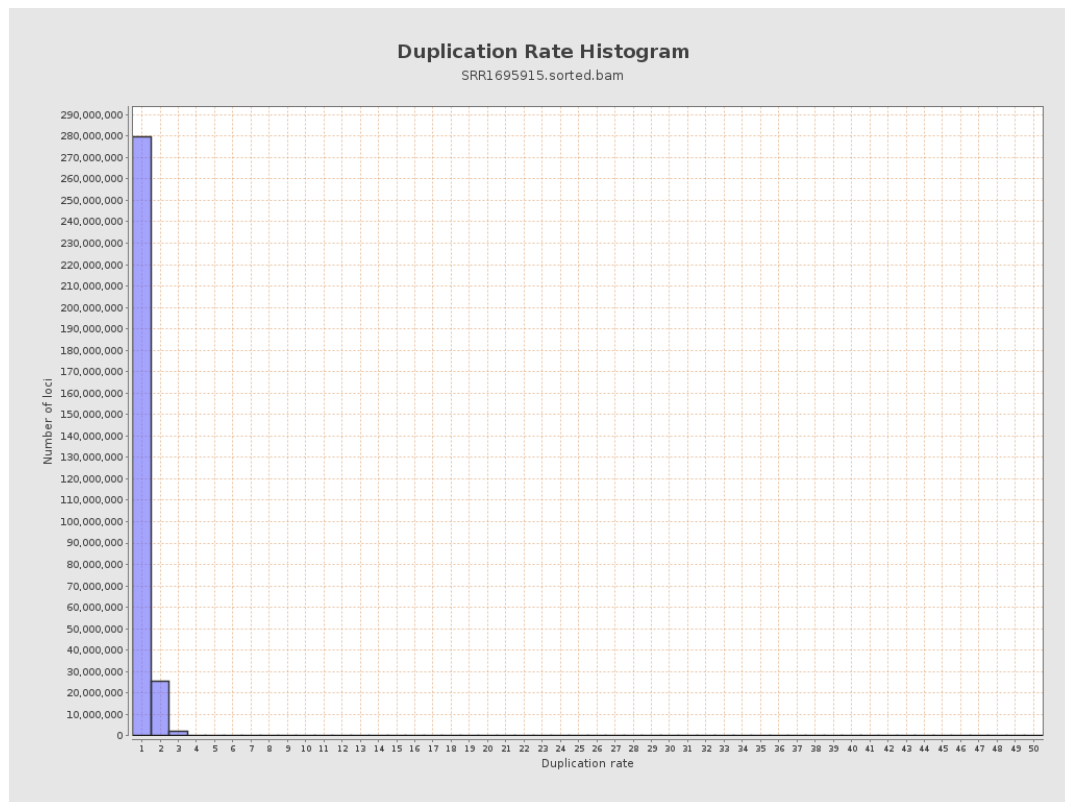
5. Results : Coverage Histogram (0-50X)



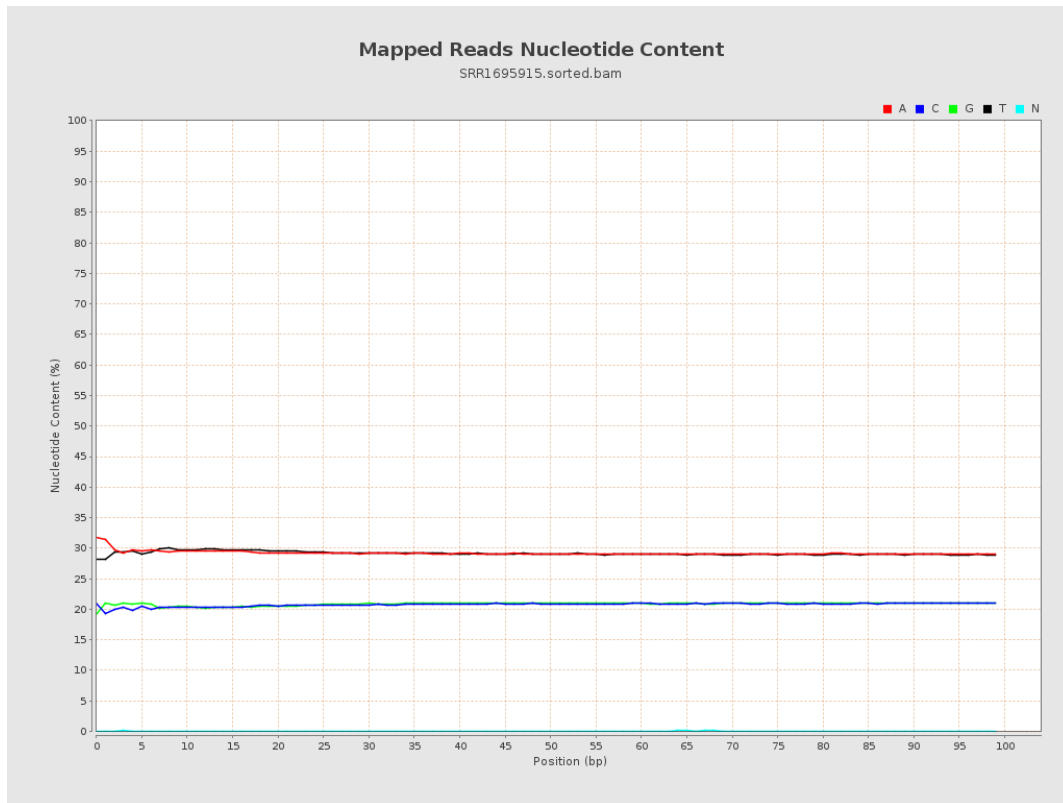
6. Results : Genome Fraction Coverage



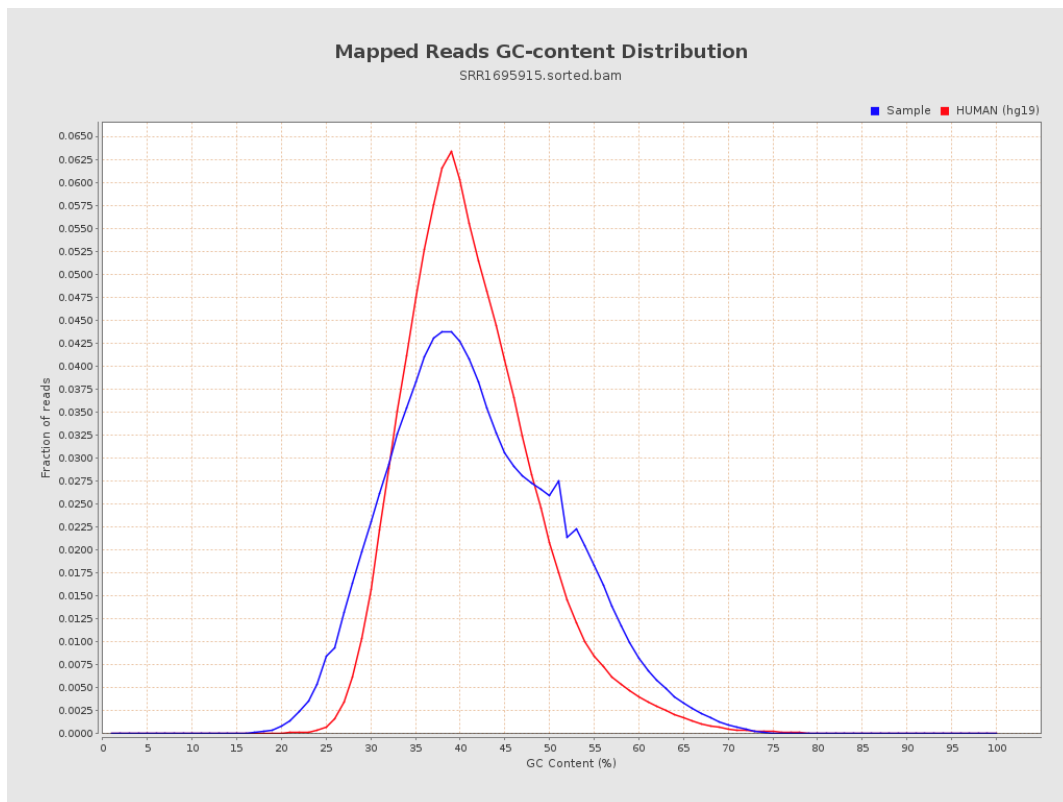
7. Results : Duplication Rate Histogram



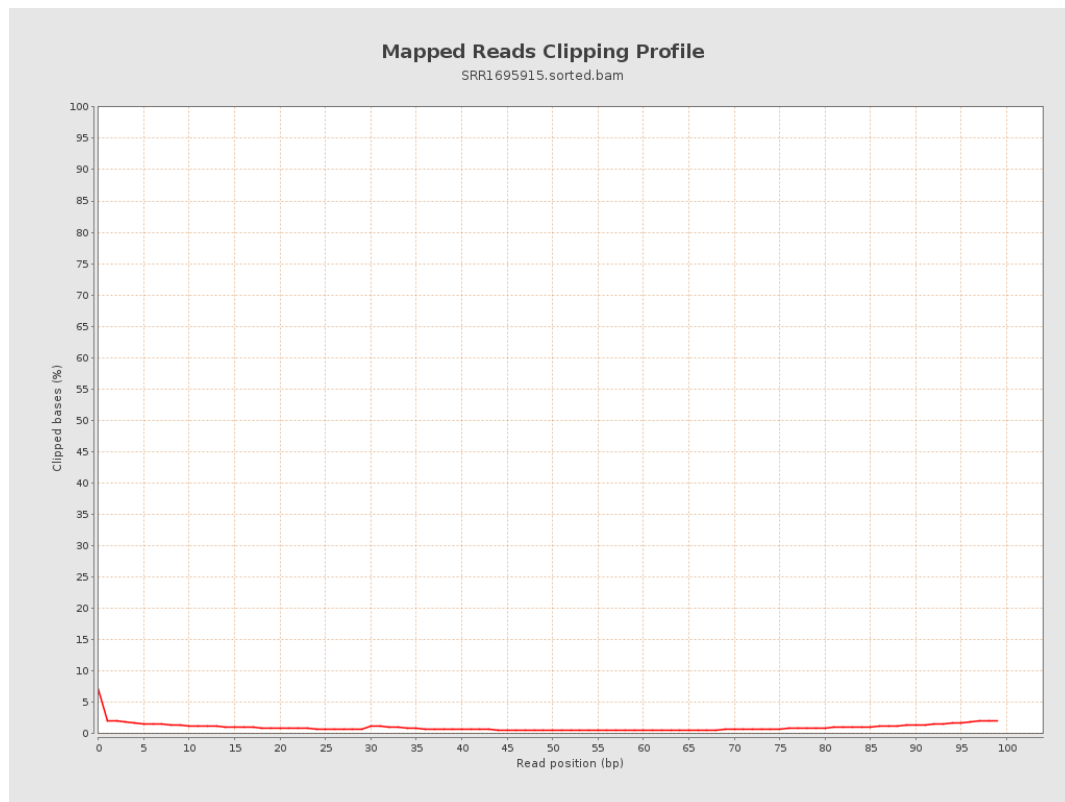
8. Results : Mapped Reads Nucleotide Content



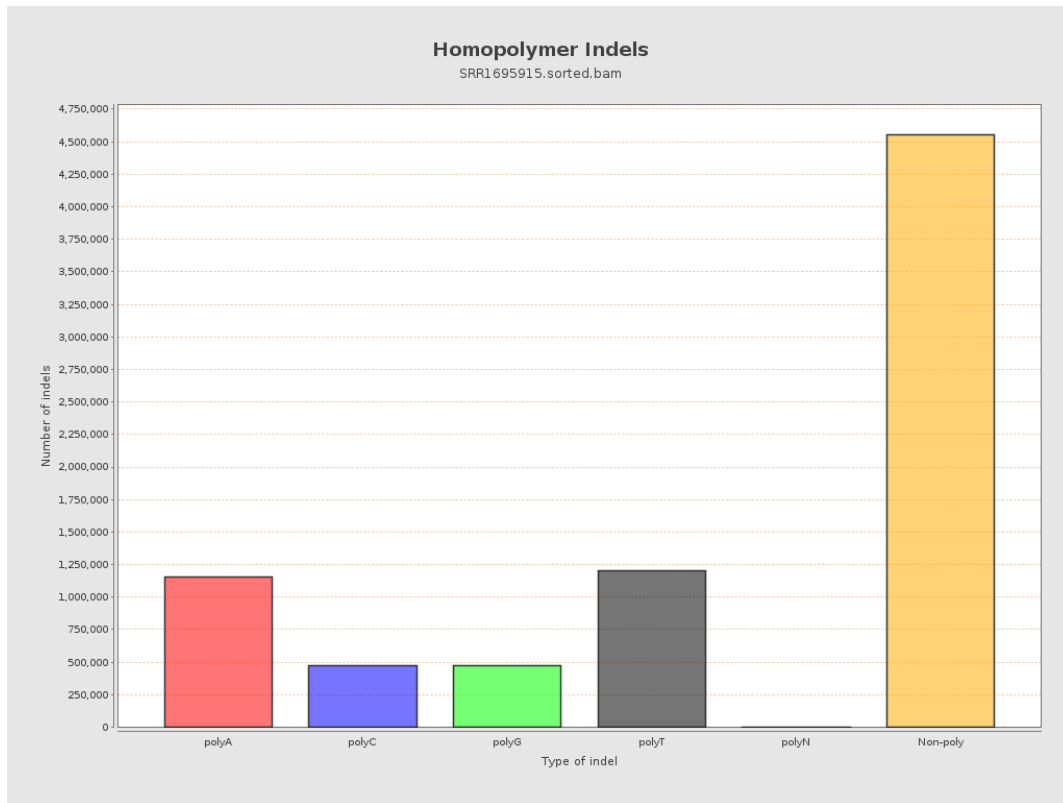
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



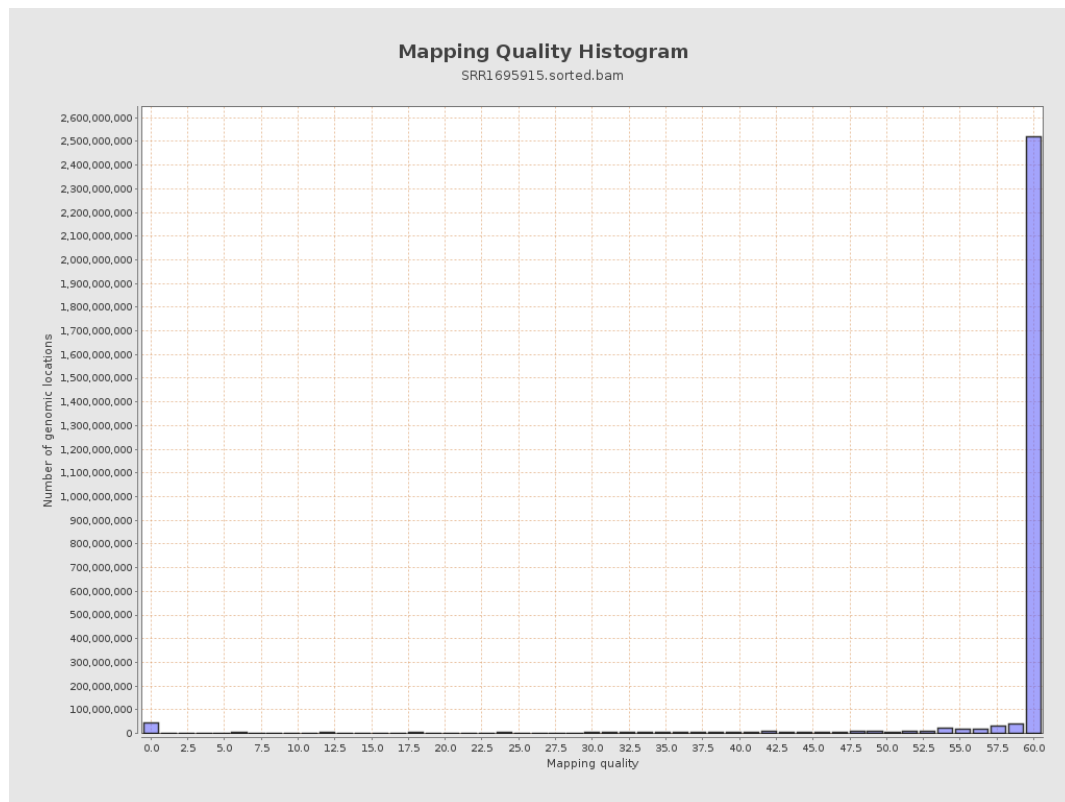
11. Results : Homopolymer Indels



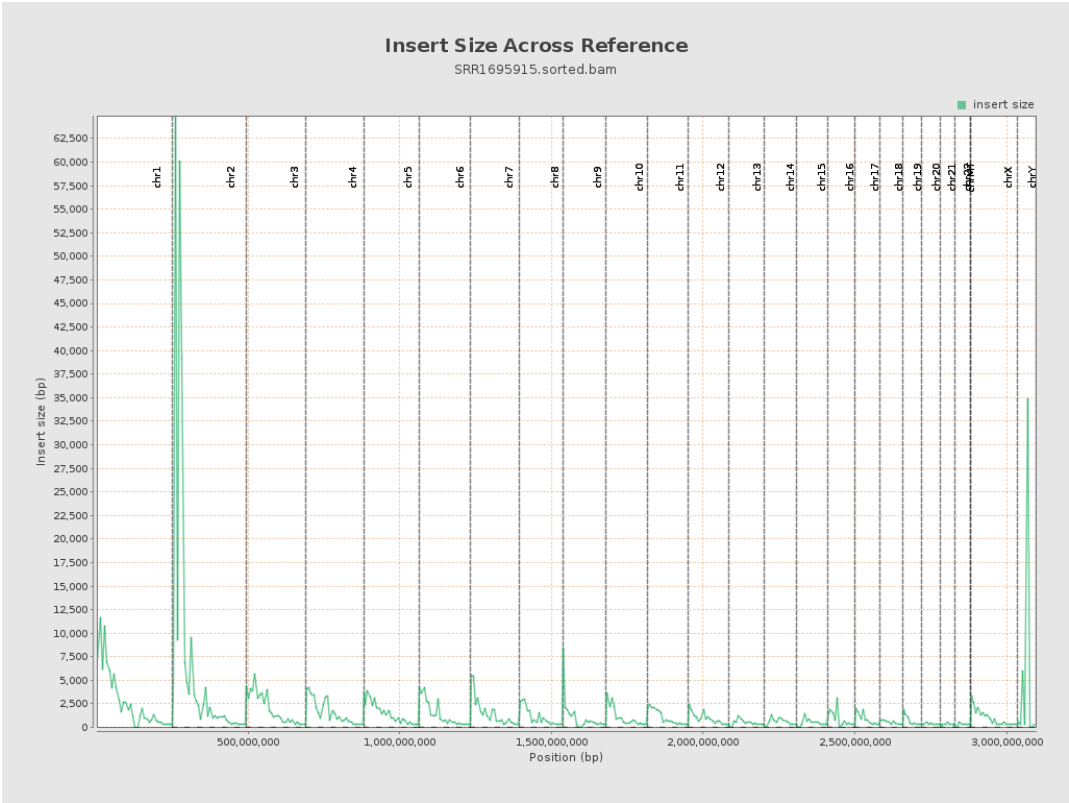
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

