

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/18 23:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362020.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_SRR16362020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362020_1.fastq.gz SRR16362020_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Feb 18 23:36:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	689,432,486
Mapped reads	675,218,925 / 97.94%
Unmapped reads	14,213,561 / 2.06%
Mapped paired reads	675,218,925 / 97.94%
Mapped reads, first in pair	339,053,542 / 49.18%
Mapped reads, second in pair	336,165,383 / 48.76%
Mapped reads, both in pair	670,835,416 / 97.3%
Mapped reads, singletons	4,383,509 / 0.64%
Secondary alignments	0
Supplementary alignments	28,784,995 / 4.18%
Read min/max/mean length	30 / 150 / 152.06
Duplicated reads (estimated)	227,270,790 / 32.96%
Duplication rate	28.58%
Clipped reads	437,042,665 / 63.39%

2.2. ACGT Content

Number/percentage of A's	27,007,038,330 / 28.79%
Number/percentage of C's	19,761,098,019 / 21.07%
Number/percentage of T's	26,942,695,228 / 28.73%
Number/percentage of G's	20,076,116,694 / 21.4%
Number/percentage of N's	8,091,559 / 0.01%

GC Percentage	42.47%
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2.3. Coverage

Mean	30.3284
Standard Deviation	293.9482

2.4. Mapping Quality

Mean Mapping Quality	53.95
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2.5. Insert size

Mean	80,330.11
Standard Deviation	2,763,197.29
P25/Median/P75	203 / 273 / 392

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	826,271,506
Insertions	16,588,590
Mapped reads with at least one insertion	2.32%
Deletions	55,592,526
Mapped reads with at least one deletion	7.86%
Homopolymer indels	45.31%

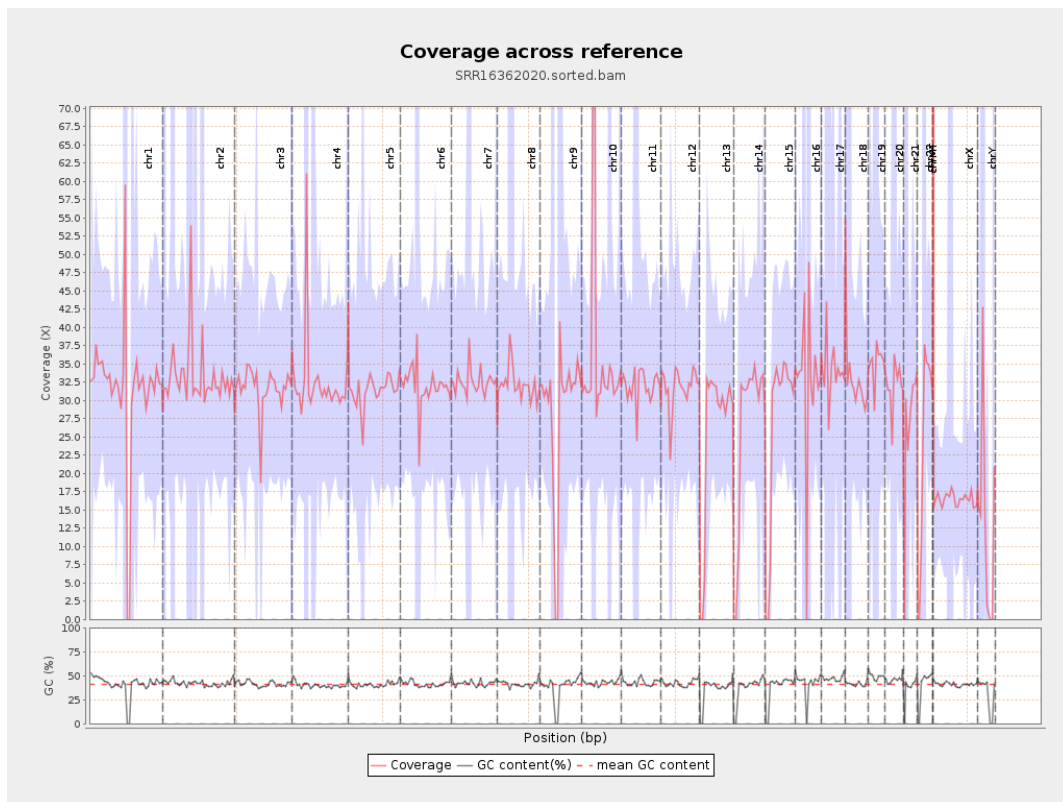
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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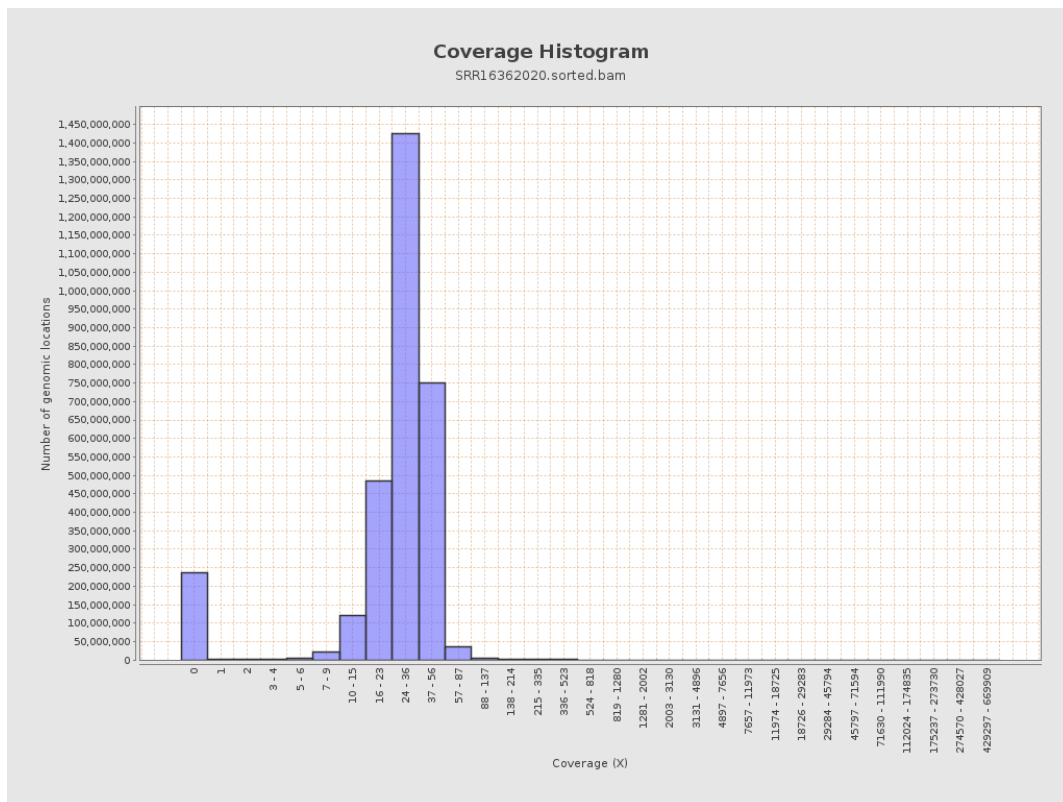
		bases	coverage	deviation
chr1	249250621	7853624453	31.5089	660.8918
chr2	243199373	8094044799	33.2815	258.2015
chr3	198022430	6256267360	31.5937	29.1026
chr4	191154276	6213624187	32.5058	280.0238
chr5	180915260	5682645218	31.4105	26.0392
chr6	171115067	5453647060	31.8712	101.286
chr7	159138663	5184289142	32.5772	198.5792
chr8	146364022	4710305855	32.1821	411.8944
chr9	141213431	4035385315	28.5765	314.6334
chr10	135534747	4873149501	35.955	603.3684
chr11	135006516	4304951577	31.887	87.8204
chr12	133851895	4271525447	31.9123	18.5661
chr13	115169878	2969874193	25.7869	17.5646
chr14	107349540	2867210589	26.7091	24.2041
chr15	102531392	2700999420	26.3431	17.9608
chr16	90354753	2946798986	32.6137	165.034
chr17	81195210	2772222186	34.1427	129.9825
chr18	78077248	2545511694	32.6025	302.4194
chr19	59128983	2074067888	35.077	380.501
chr20	63025520	2009112951	31.8778	78.0371
chr21	48129895	1303822140	27.0897	140.5028
chr22	51304566	1235451877	24.0807	91.0818
chrMT	16571	160070810	9,659.6953	1,308.3419
chrX	155270560	2558416722	16.4772	41.581

chrY	59373566	810294407	13.6474	331.5862
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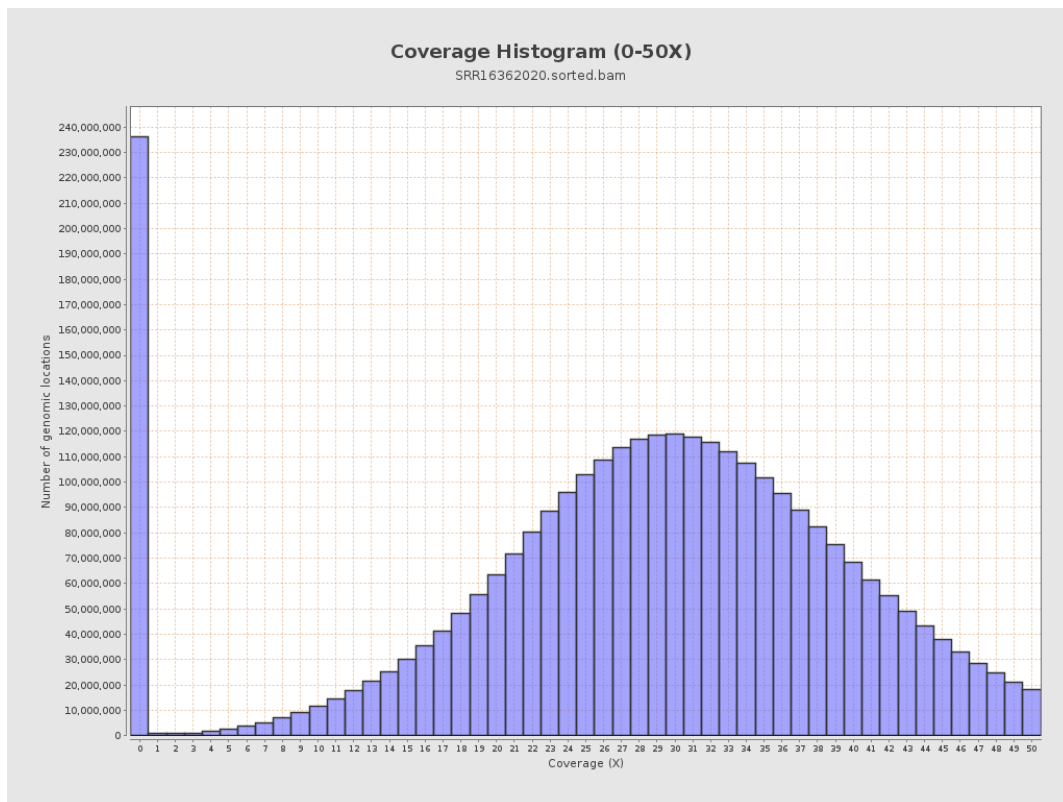
3. Results : Coverage across reference



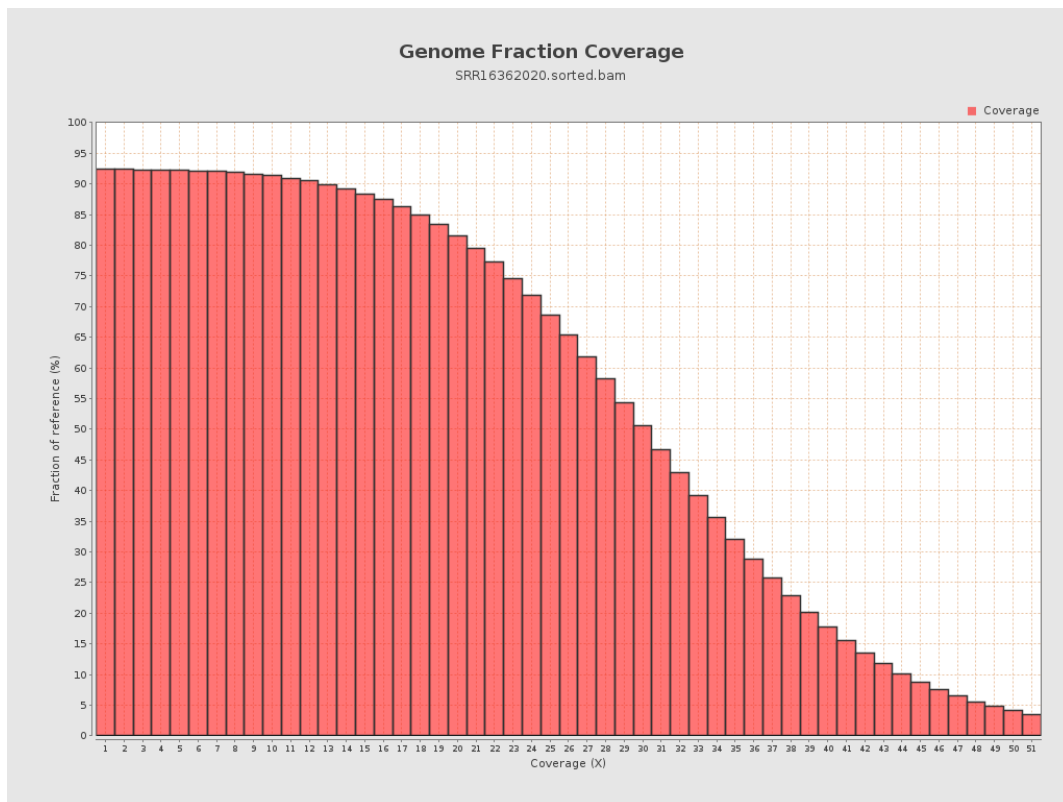
4. Results : Coverage Histogram



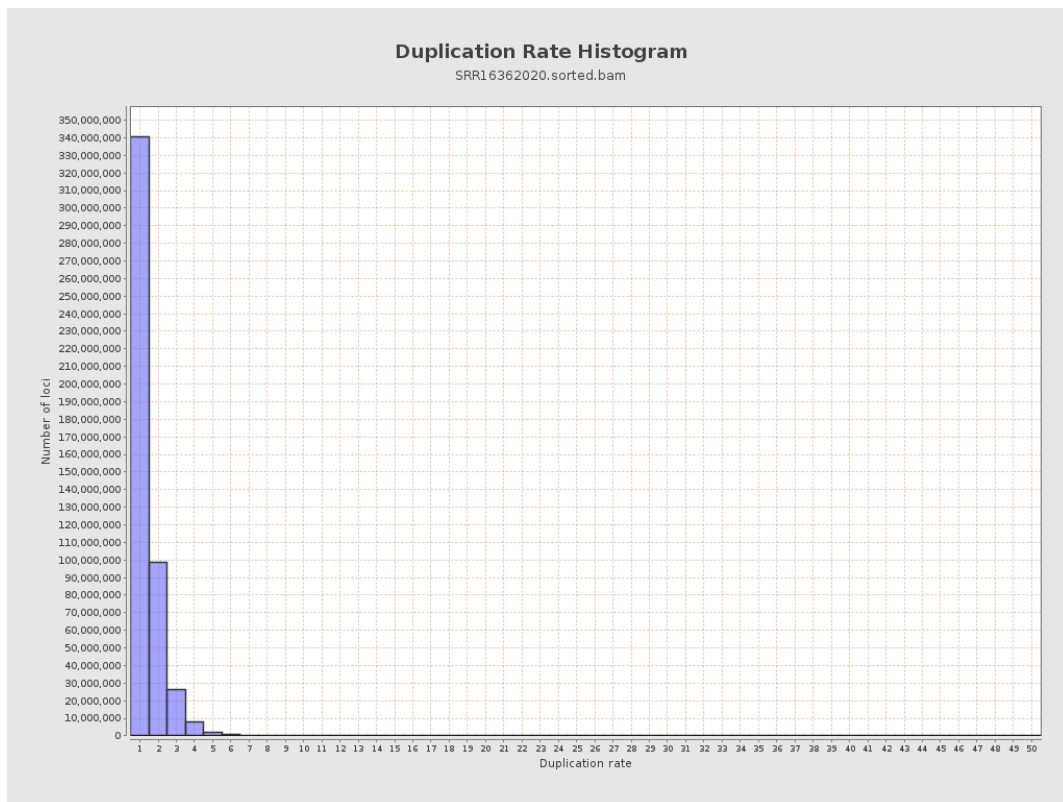
5. Results : Coverage Histogram (0-50X)



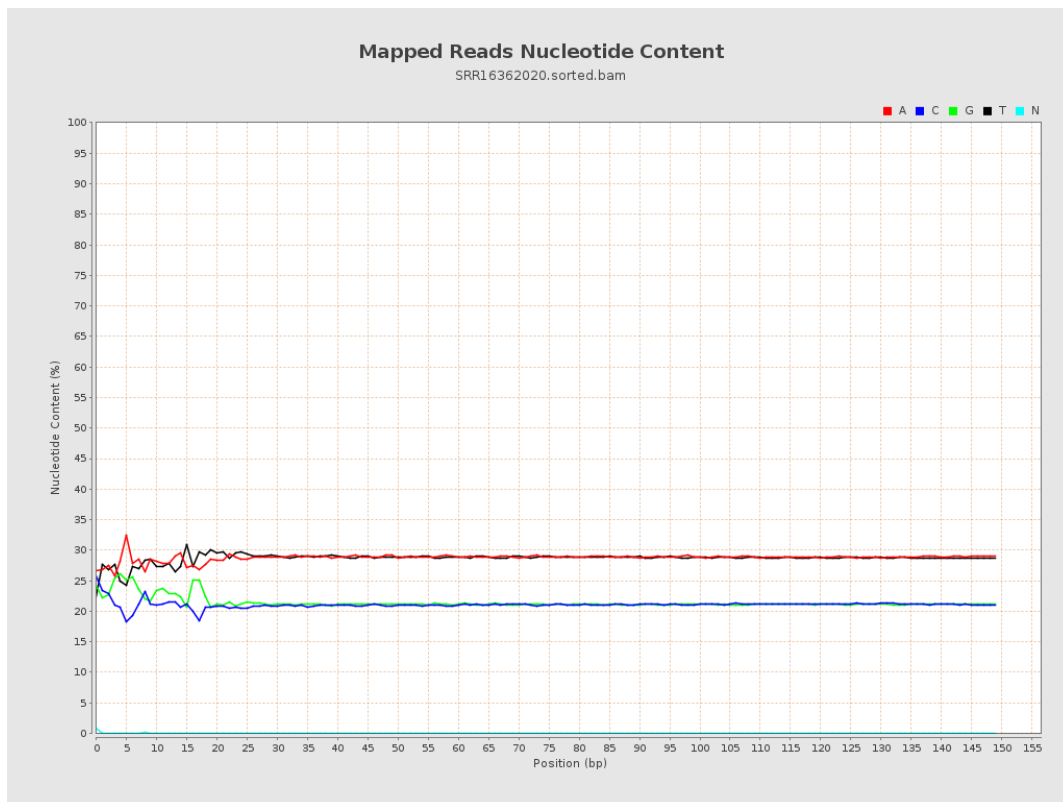
6. Results : Genome Fraction Coverage



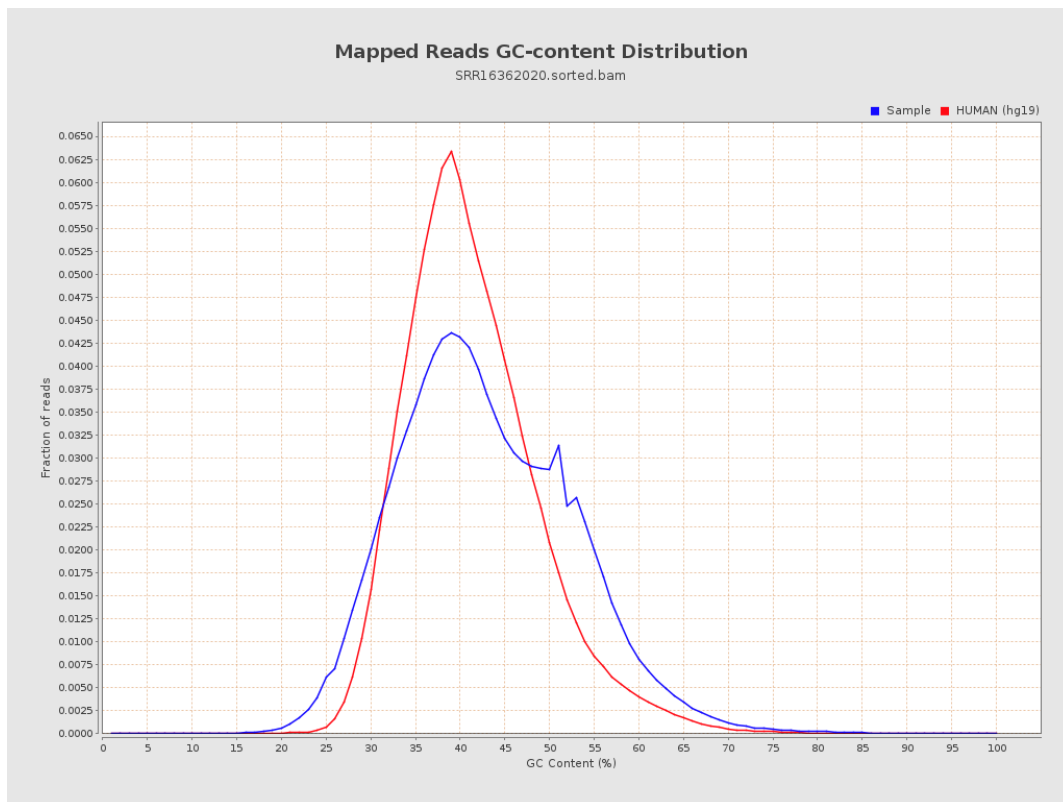
7. Results : Duplication Rate Histogram



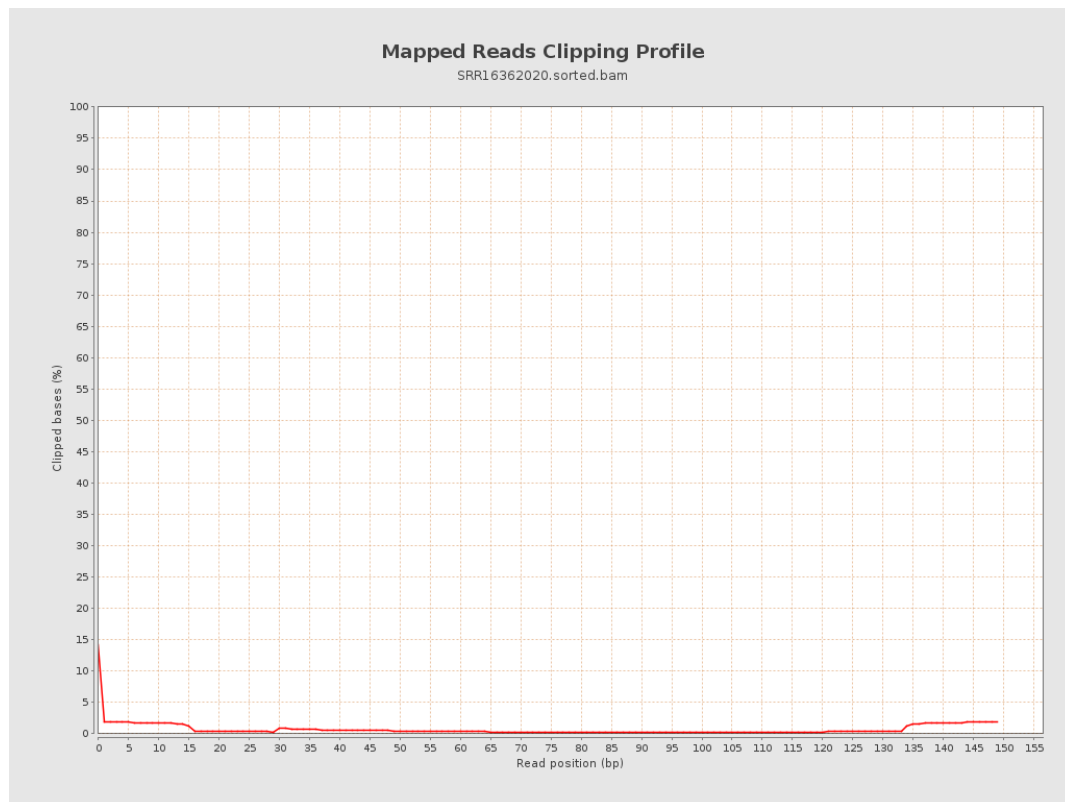
8. Results : Mapped Reads Nucleotide Content



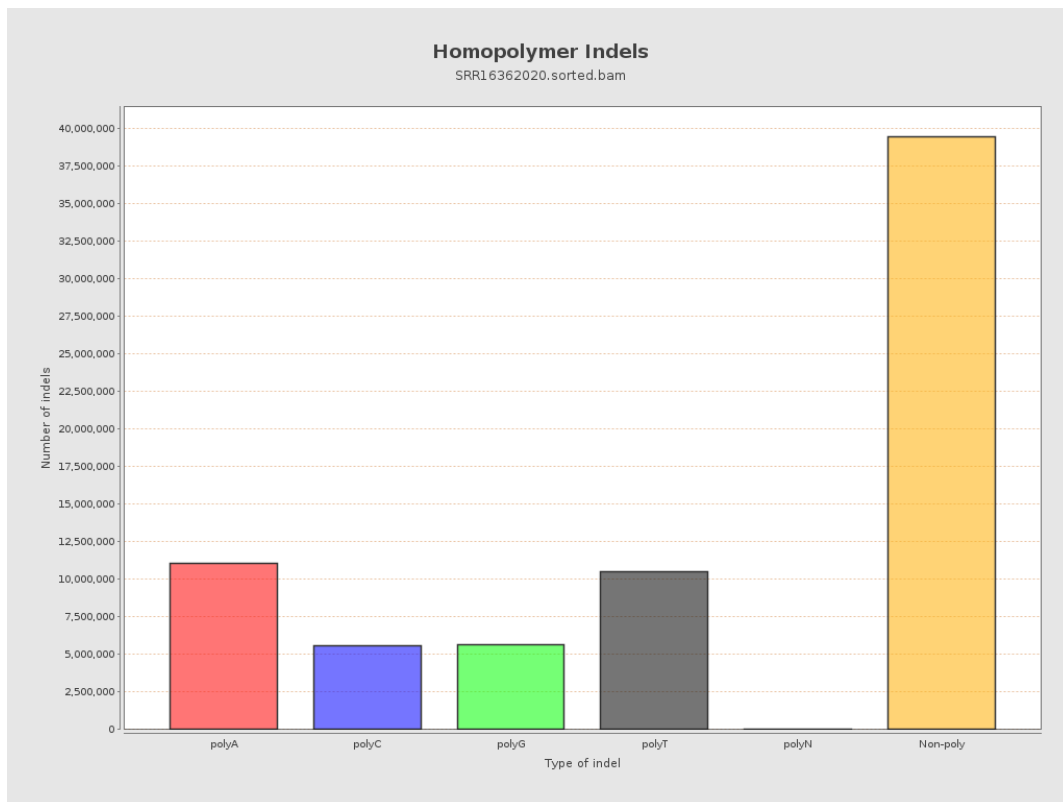
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



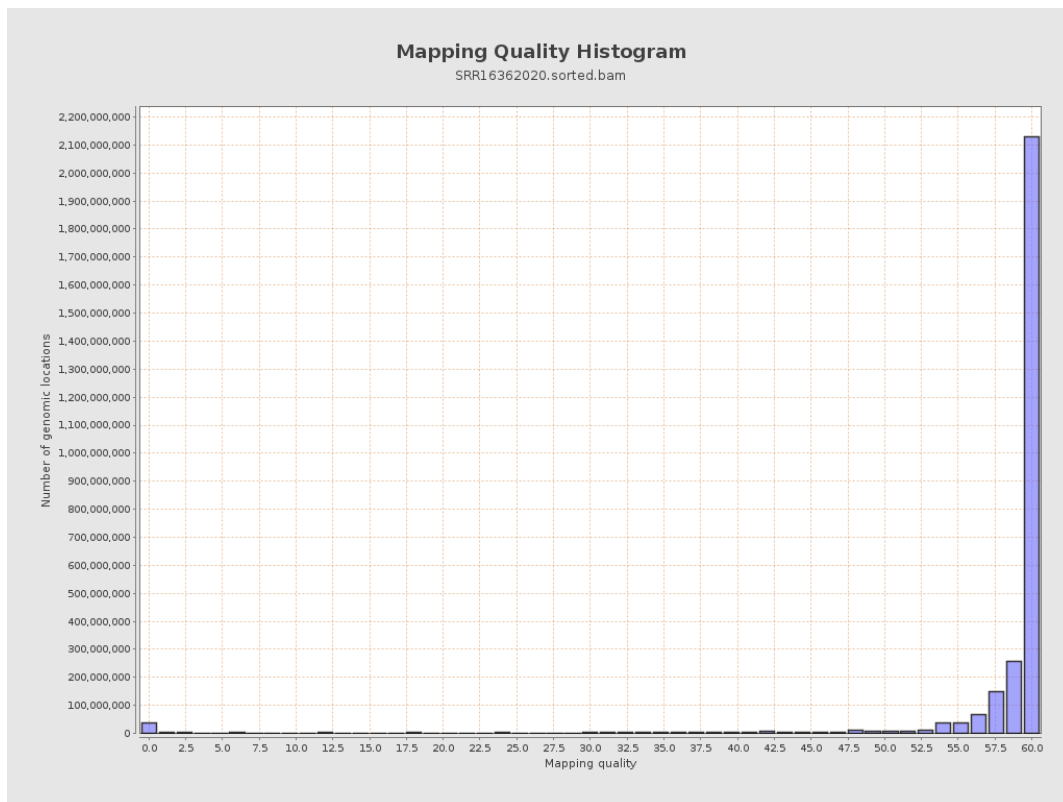
11. Results : Homopolymer Indels



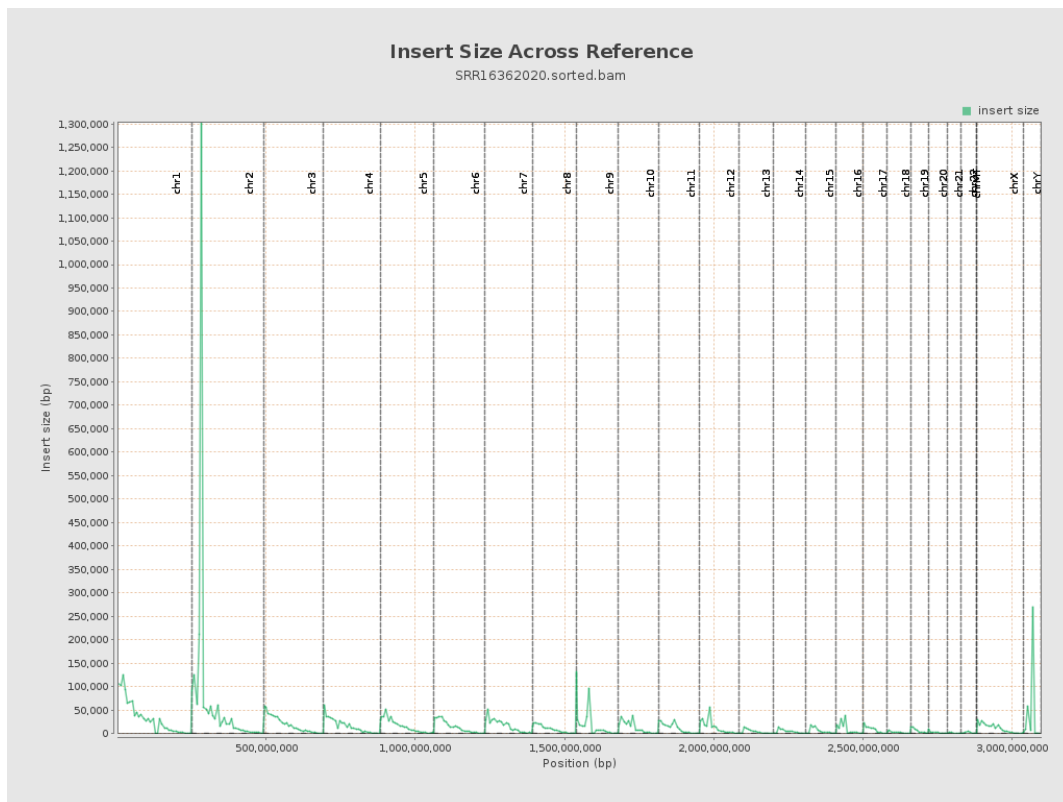
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

