

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/07 14:39:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362018.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_SRR16362018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362018_1.fastq.gz SRR16362018_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Feb 07 14:39:11 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	303,936,886
Mapped reads	293,958,191 / 96.72%
Unmapped reads	9,978,695 / 3.28%
Mapped paired reads	293,958,191 / 96.72%
Mapped reads, first in pair	147,997,183 / 48.69%
Mapped reads, second in pair	145,961,008 / 48.02%
Mapped reads, both in pair	291,298,238 / 95.84%
Mapped reads, singletons	2,659,953 / 0.88%
Secondary alignments	0
Supplementary alignments	13,160,330 / 4.33%
Read min/max/mean length	30 / 150 / 152.16
Duplicated reads (estimated)	108,522,469 / 35.71%
Duplication rate	32.04%
Clipped reads	192,556,898 / 63.35%

2.2. ACGT Content

Number/percentage of A's	11,810,974,344 / 28.92%
Number/percentage of C's	8,583,087,231 / 21.01%
Number/percentage of T's	11,749,840,872 / 28.77%
Number/percentage of G's	8,695,867,289 / 21.29%
Number/percentage of N's	3,091,303 / 0.01%

GC Percentage	42.31%
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2.3. Coverage

Mean	13.2047
Standard Deviation	124.6877

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	155,389.45
Standard Deviation	3,821,711.53
P25/Median/P75	188 / 249 / 350

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	360,691,581
Insertions	7,236,242
Mapped reads with at least one insertion	2.34%
Deletions	19,067,953
Mapped reads with at least one deletion	6.22%
Homopolymer indels	44.81%

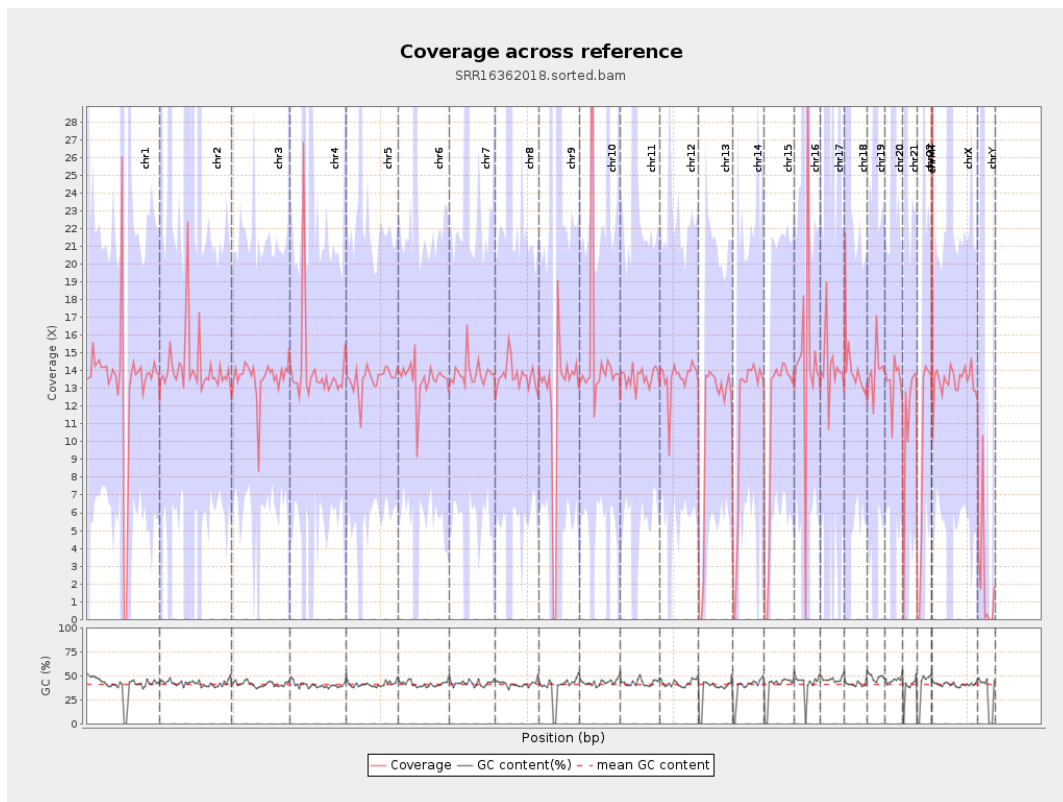
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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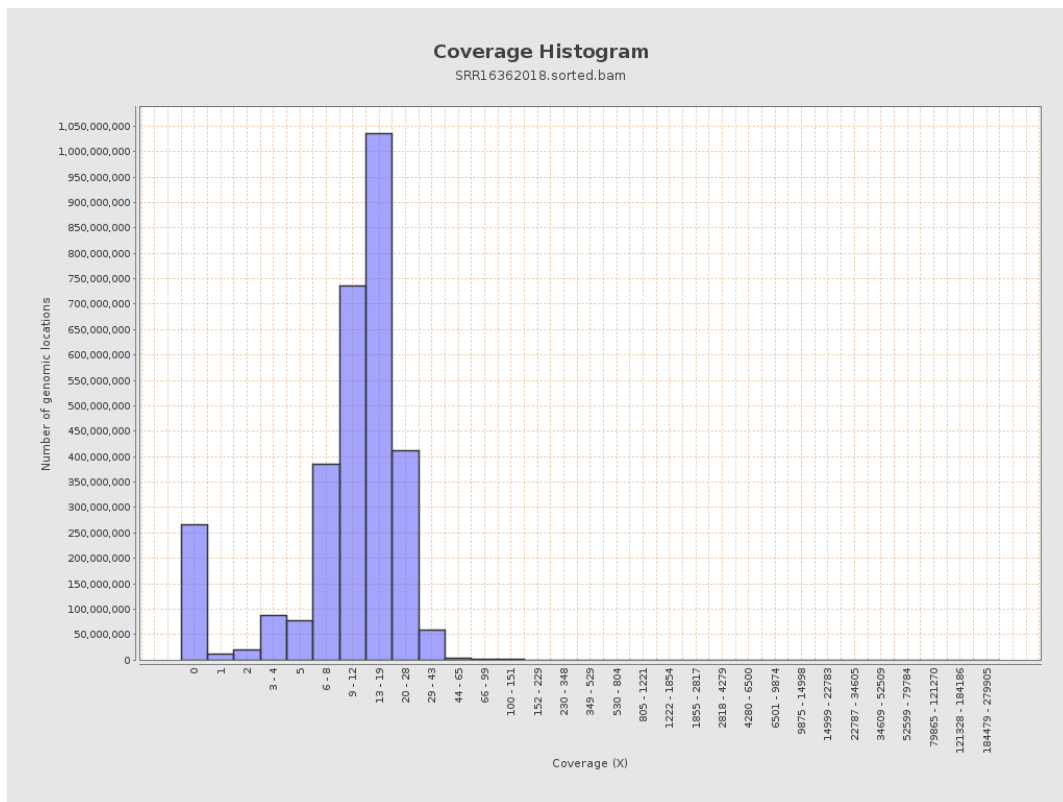
		bases	coverage	deviation
chr1	249250621	3337103829	13.3885	279.8326
chr2	243199373	3463044000	14.2395	93.1775
chr3	198022430	2685177736	13.56	12.4117
chr4	191154276	2670166888	13.9686	122.3935
chr5	180915260	2447555878	13.5287	10.3199
chr6	171115067	2314613278	13.5266	29.2556
chr7	159138663	2205154316	13.8568	85.4431
chr8	146364022	2009412520	13.7289	169.1845
chr9	141213431	1748430283	12.3815	139.0121
chr10	135534747	2056160977	15.1707	225.7897
chr11	135006516	1839812274	13.6276	57.0831
chr12	133851895	1816526421	13.5712	8.8642
chr13	115169878	1276478491	11.0834	8.2494
chr14	107349540	1222025569	11.3836	11.0632
chr15	102531392	1138709552	11.106	8.4277
chr16	90354753	1329395134	14.7131	125.0748
chr17	81195210	1146785955	14.1238	70.9409
chr18	78077248	1099898625	14.0873	134.5534
chr19	59128983	828853941	14.0177	170.5037
chr20	63025520	841357550	13.3495	35.5761
chr21	48129895	552494871	11.4792	57.9643
chr22	51304566	489582678	9.5427	11.8001
chrMT	16571	151059986	9,115.9246	1,459.1881
chrX	155270560	2078937149	13.3891	28.7216

chrY	59373566	128957911	2.172	143.4592
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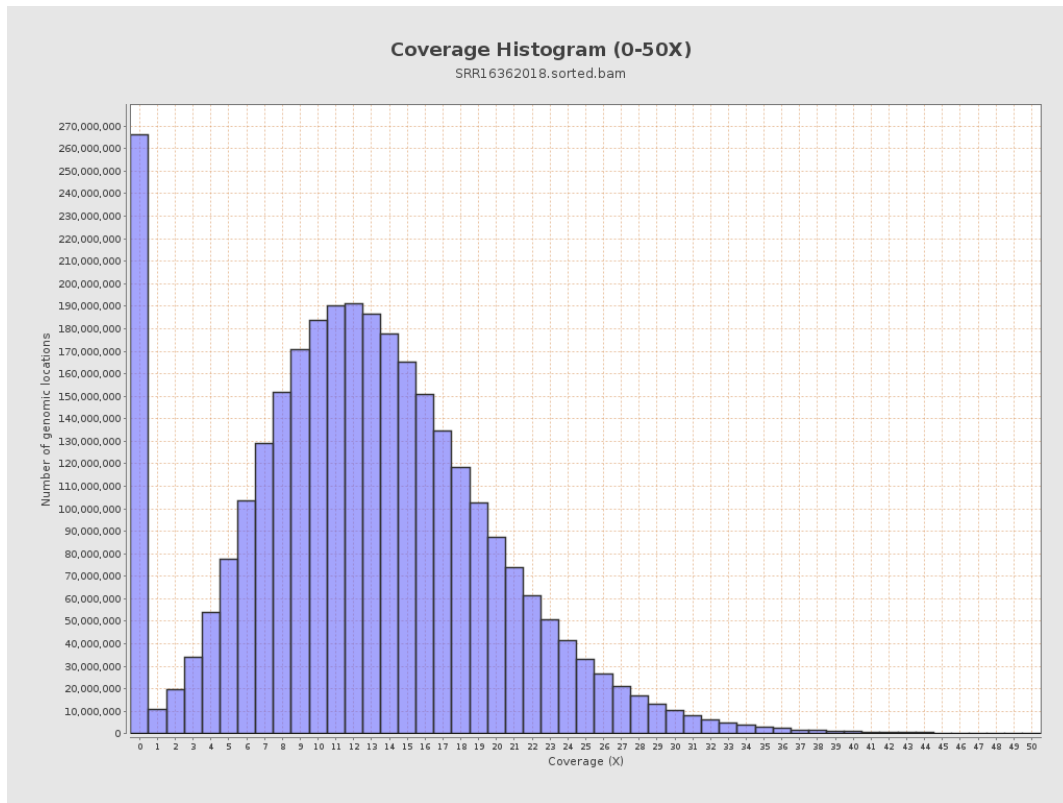
3. Results : Coverage across reference



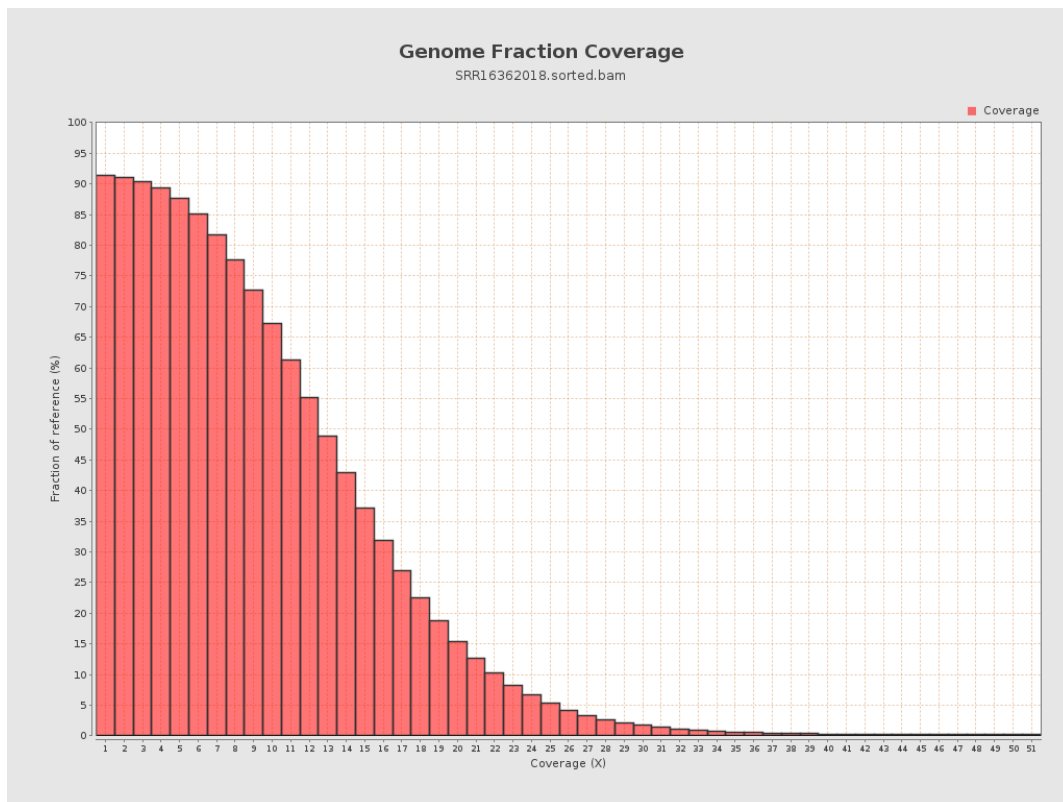
4. Results : Coverage Histogram



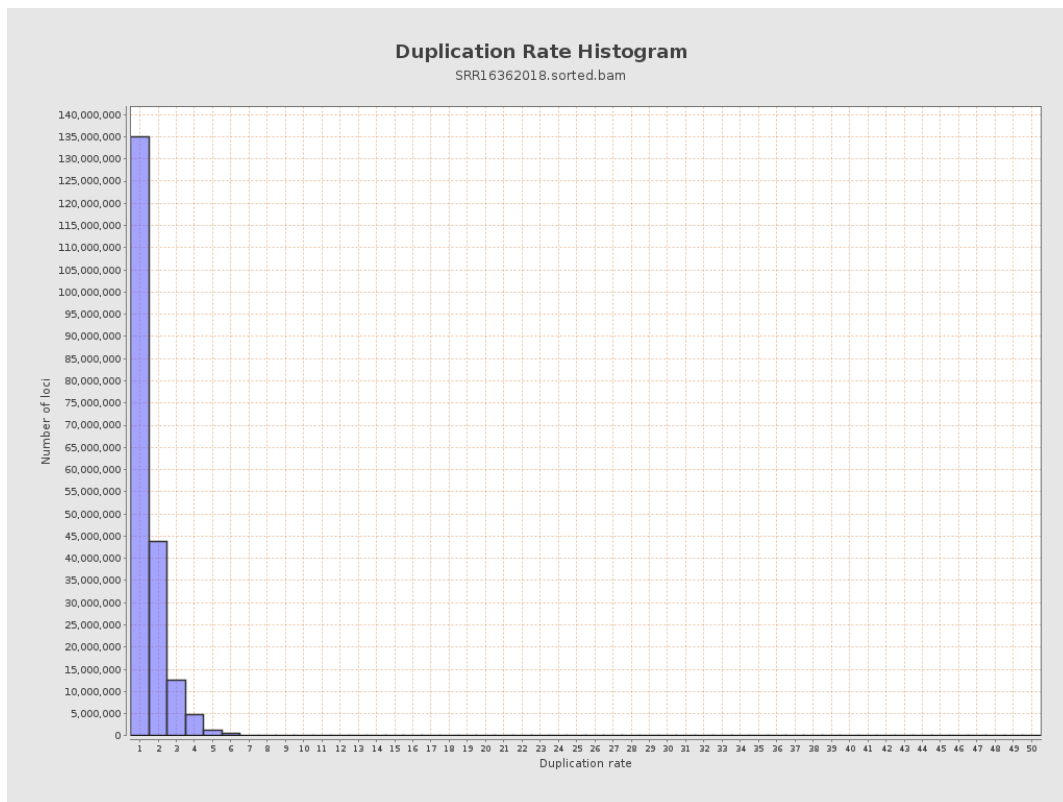
5. Results : Coverage Histogram (0-50X)



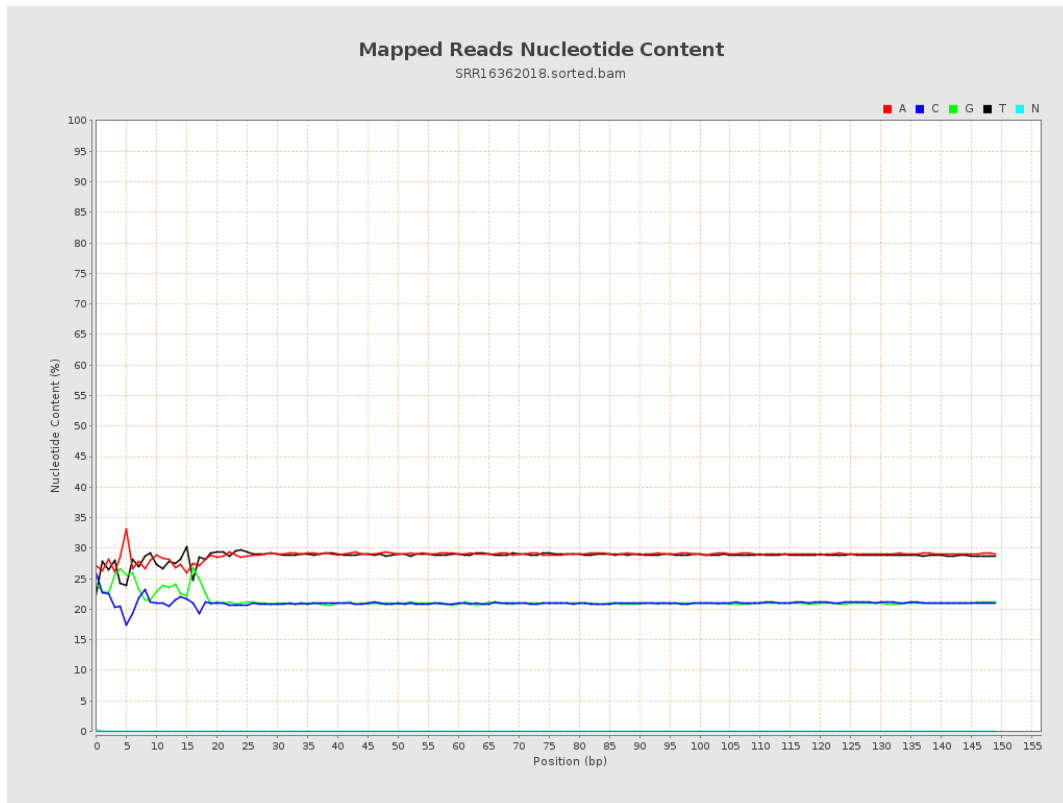
6. Results : Genome Fraction Coverage



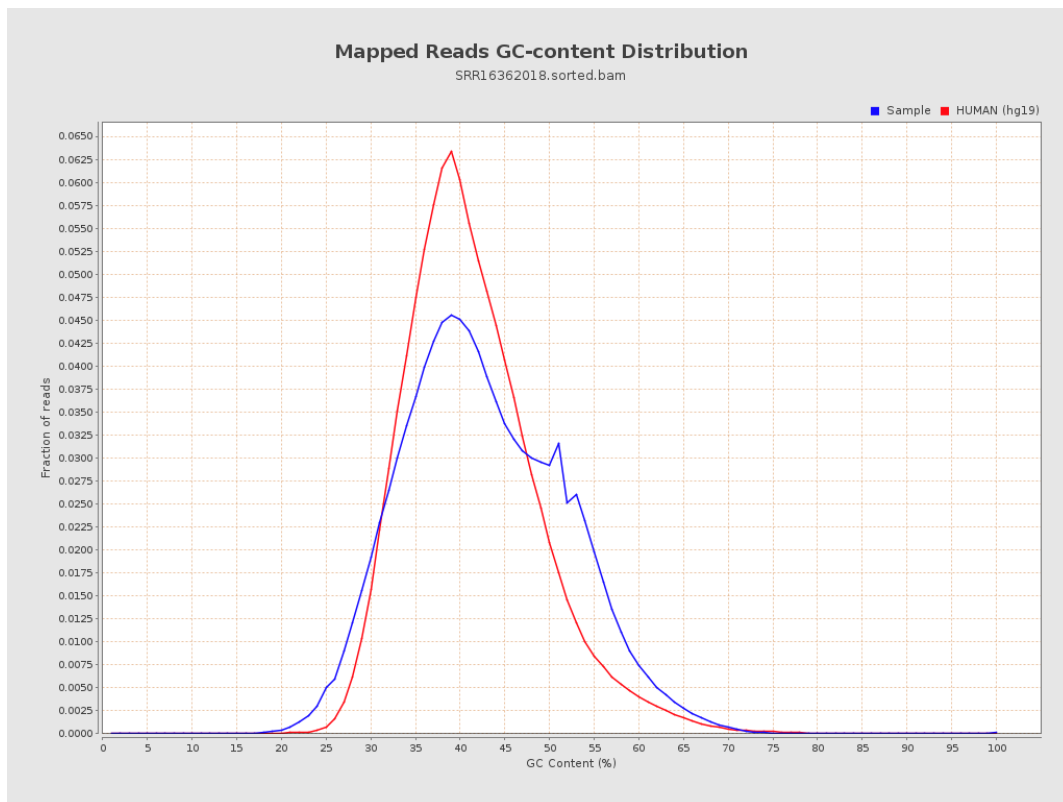
7. Results : Duplication Rate Histogram



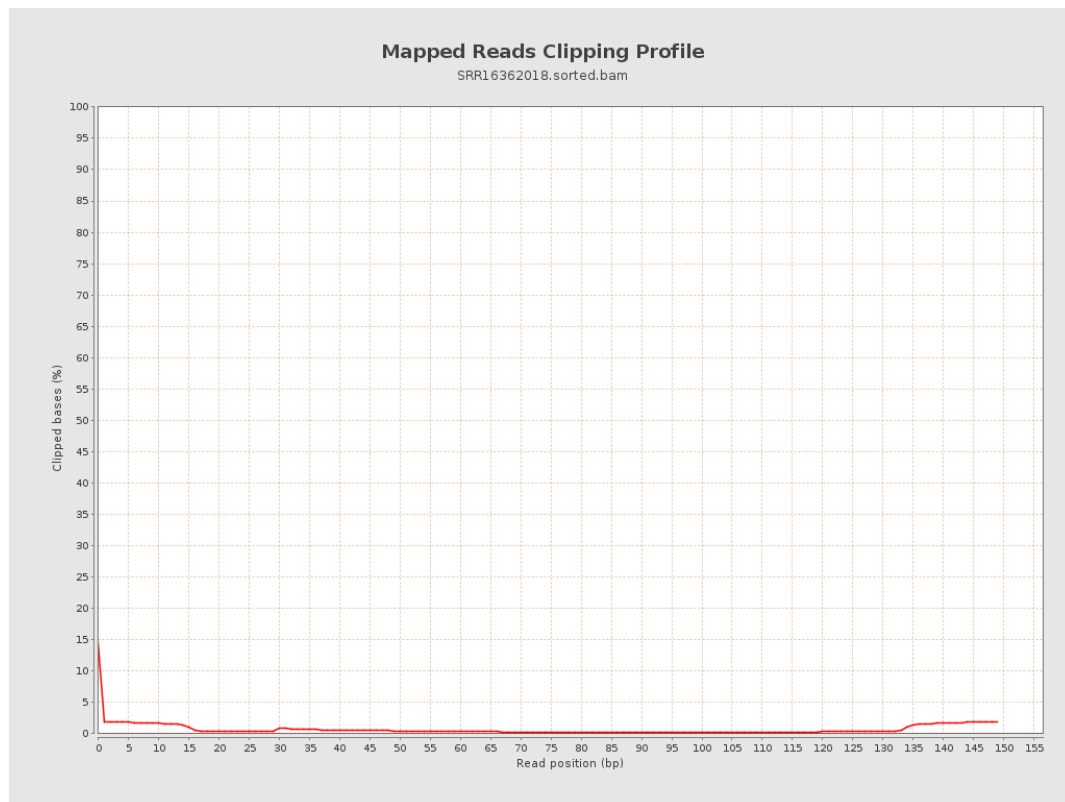
8. Results : Mapped Reads Nucleotide Content



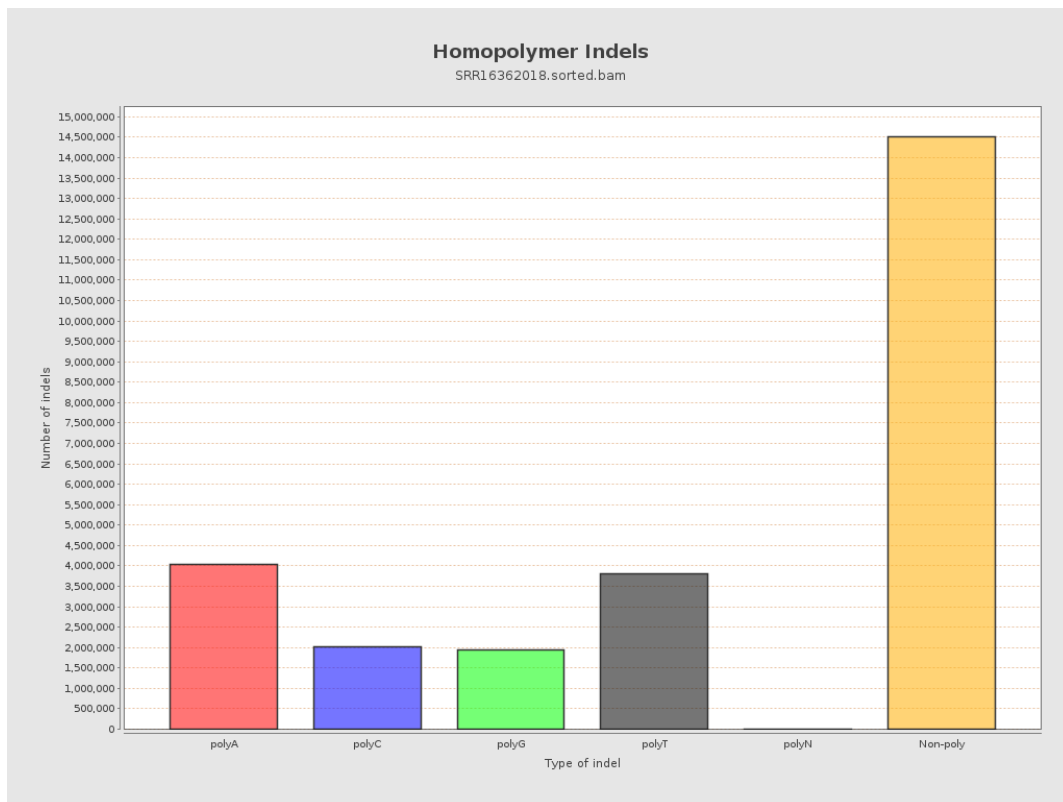
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



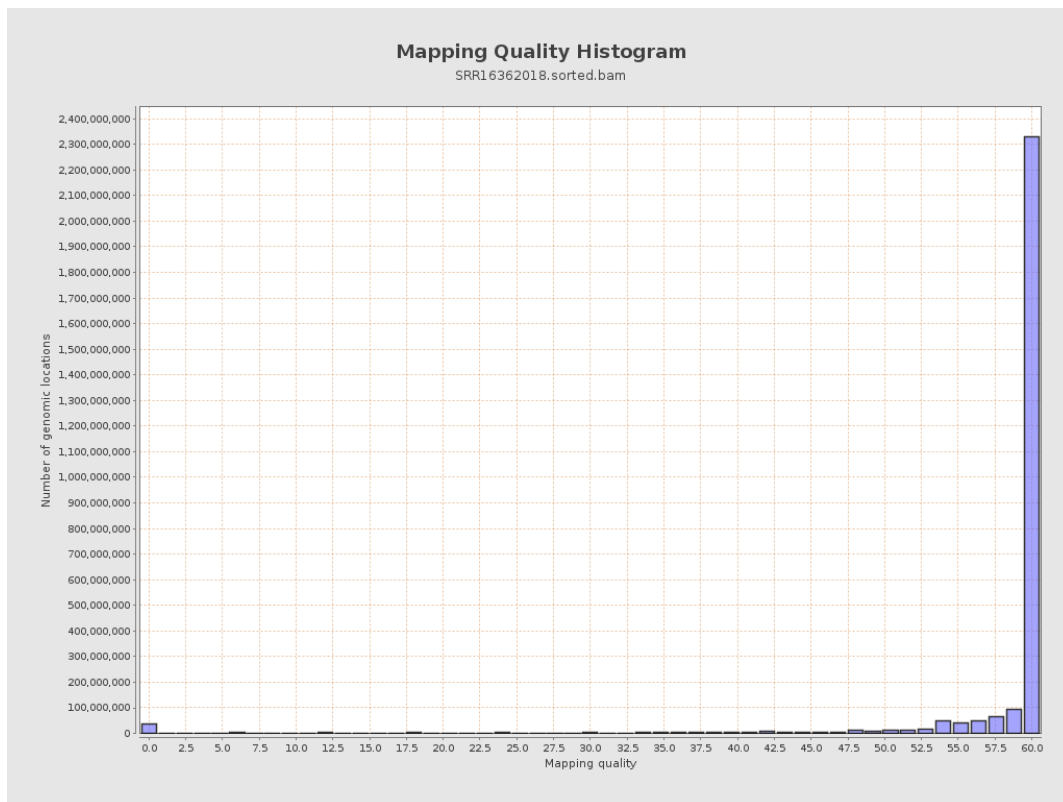
11. Results : Homopolymer Indels



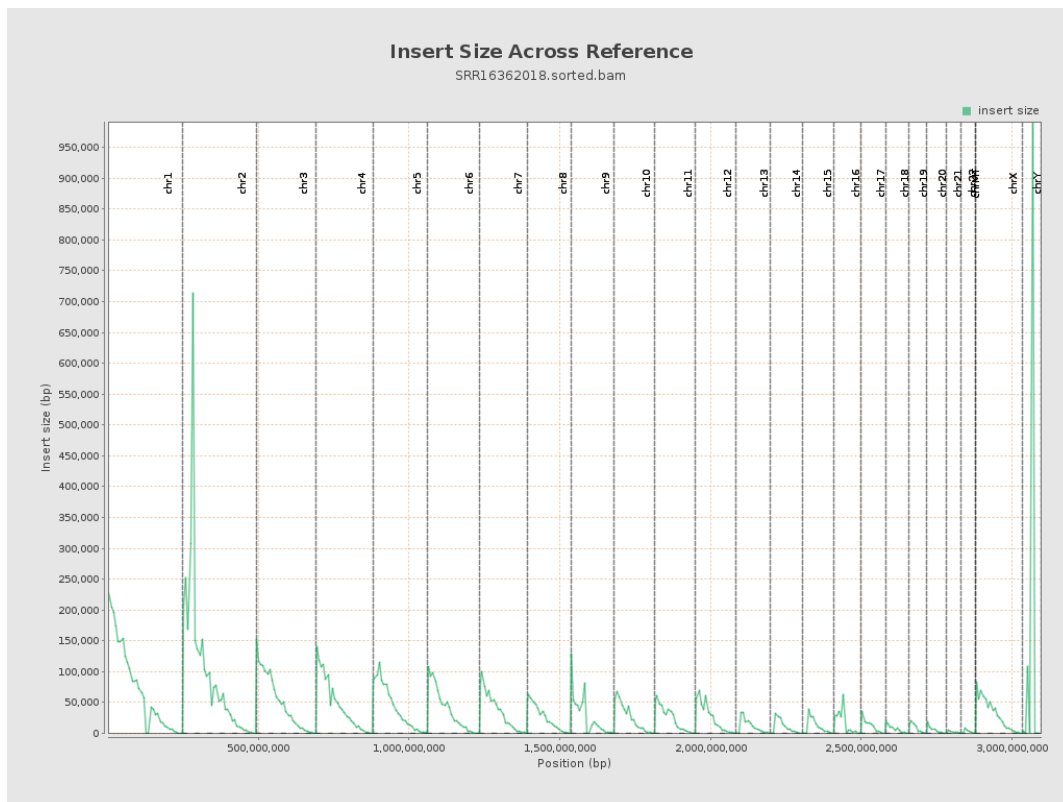
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

