

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 18:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618630.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_SRR618630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618630_1.fastq.gz SRR618630_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 18:07:05 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,985,524
Mapped reads	22,205,560 / 96.61%
Unmapped reads	779,964 / 3.39%
Mapped paired reads	22,205,560 / 96.61%
Mapped reads, first in pair	11,214,972 / 48.79%
Mapped reads, second in pair	10,990,588 / 47.82%
Mapped reads, both in pair	21,796,274 / 94.83%
Mapped reads, singletons	409,286 / 1.78%
Secondary alignments	0
Supplementary alignments	29,844 / 0.13%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	7,721,601 / 33.59%
Duplication rate	29.32%
Clipped reads	3,840,285 / 16.71%

2.2. ACGT Content

Number/percentage of A's	569,650,682 / 26.82%
Number/percentage of C's	482,483,693 / 22.72%
Number/percentage of T's	572,806,810 / 26.97%
Number/percentage of G's	499,013,781 / 23.49%
Number/percentage of N's	96,337 / 0%

GC Percentage	46.21%
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2.3. Coverage

Mean	0.6866
Standard Deviation	3.2254

2.4. Mapping Quality

Mean Mapping Quality	53.98
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2.5. Insert size

Mean	26,082.86
Standard Deviation	1,597,077.98
P25/Median/P75	167 / 195 / 234

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	27,246,058
Insertions	361,922
Mapped reads with at least one insertion	1.6%
Deletions	961,799
Mapped reads with at least one deletion	4.23%
Homopolymer indels	51.69%

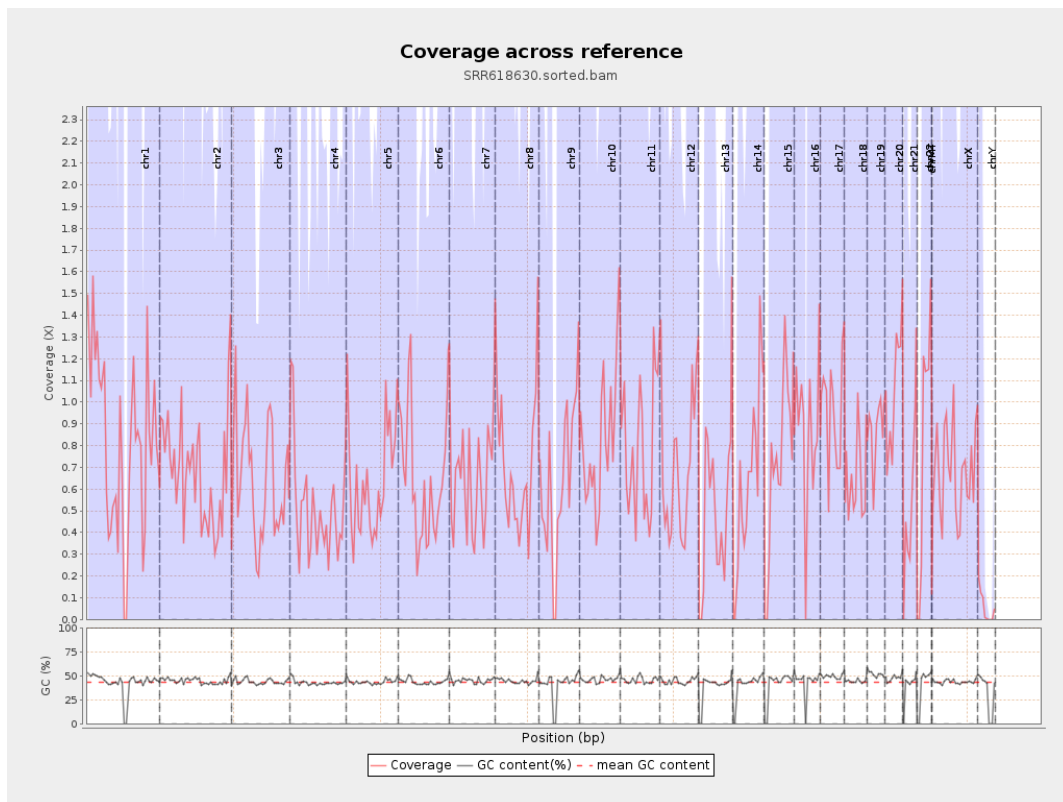
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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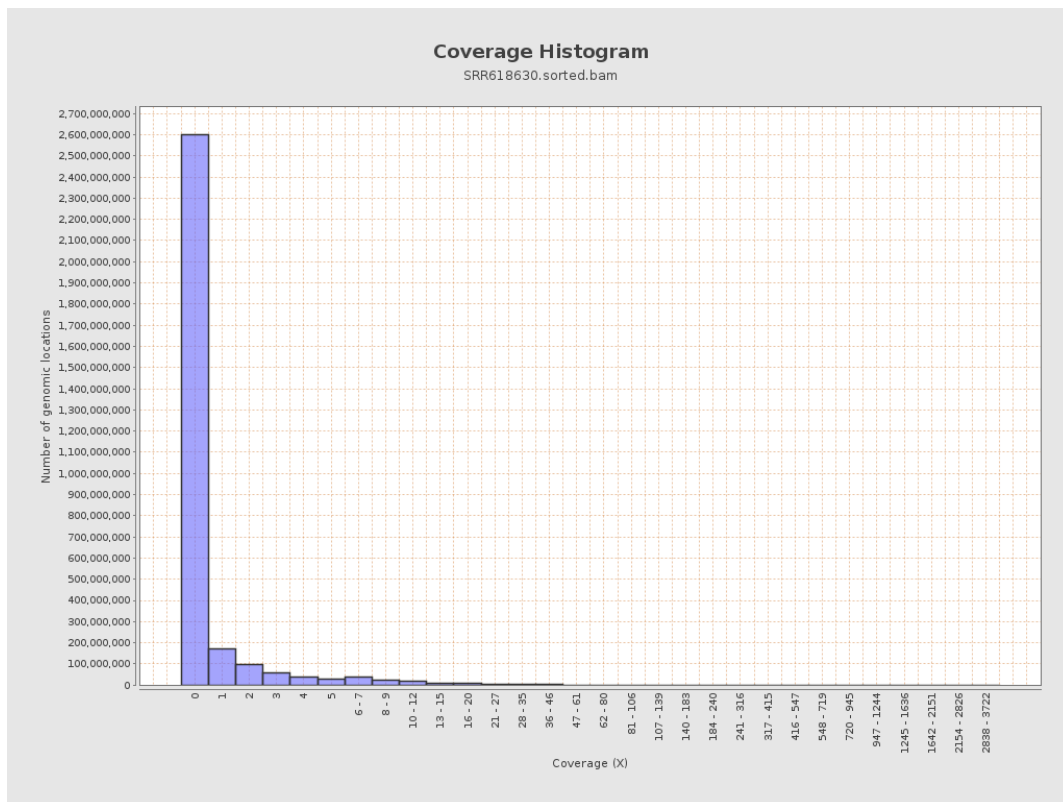
		bases	coverage	deviation
chr1	249250621	202075308	0.8107	3.6153
chr2	243199373	164657666	0.677	3.7187
chr3	198022430	127765409	0.6452	2.6375
chr4	191154276	95450898	0.4993	2.6178
chr5	180915260	117356515	0.6487	2.5734
chr6	171115067	110205698	0.644	2.6262
chr7	159138663	103392911	0.6497	2.616
chr8	146364022	100999389	0.6901	2.7836
chr9	141213431	91923433	0.651	3.0145
chr10	135534747	112222544	0.828	3.2854
chr11	135006516	107632078	0.7972	3.2864
chr12	133851895	92688008	0.6925	2.8293
chr13	115169878	56196648	0.4879	2.2356
chr14	107349540	67496160	0.6288	2.6882
chr15	102531392	72735844	0.7094	2.8854
chr16	90354753	78201111	0.8655	7.0946
chr17	81195210	78117271	0.9621	3.5787
chr18	78077248	51350750	0.6577	2.8876
chr19	59128983	51290644	0.8674	3.6571
chr20	63025520	65951807	1.0464	3.6999
chr21	48129895	26641321	0.5535	4.0954
chr22	51304566	43117730	0.8404	3.5423
chrMT	16571	1878	0.1133	0.7647
chrX	155270560	104699511	0.6743	2.6606

chrY	59373566	3216903	0.0542	2.2705
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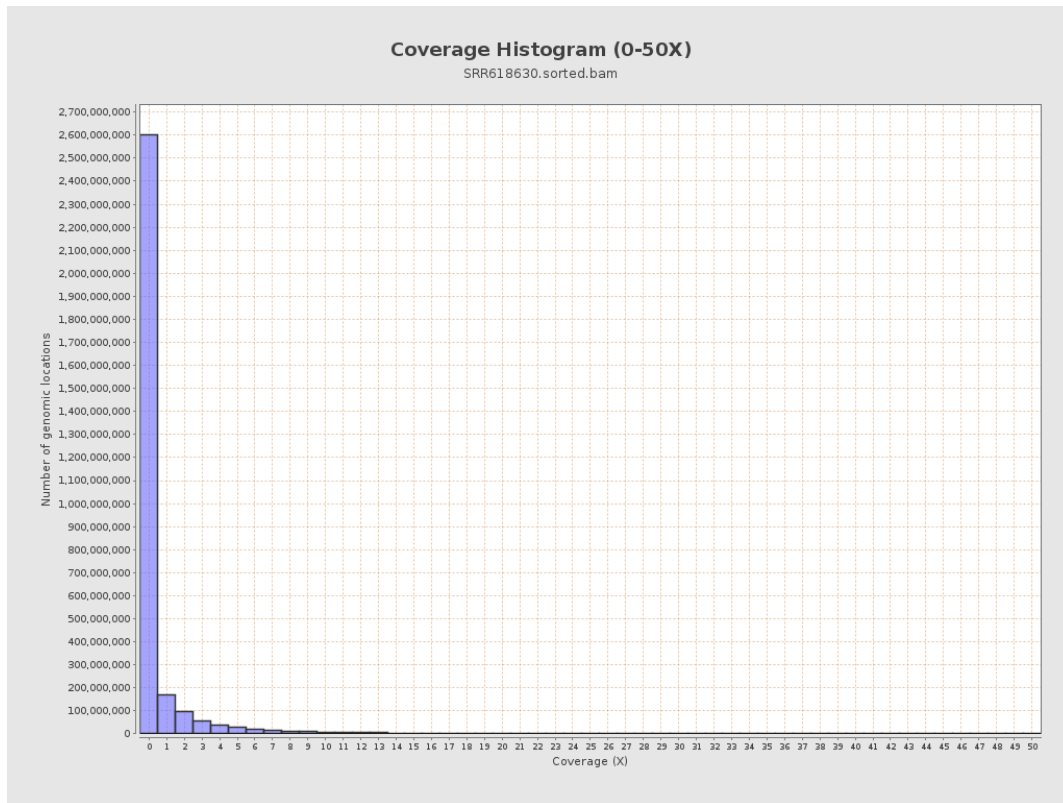
3. Results : Coverage across reference



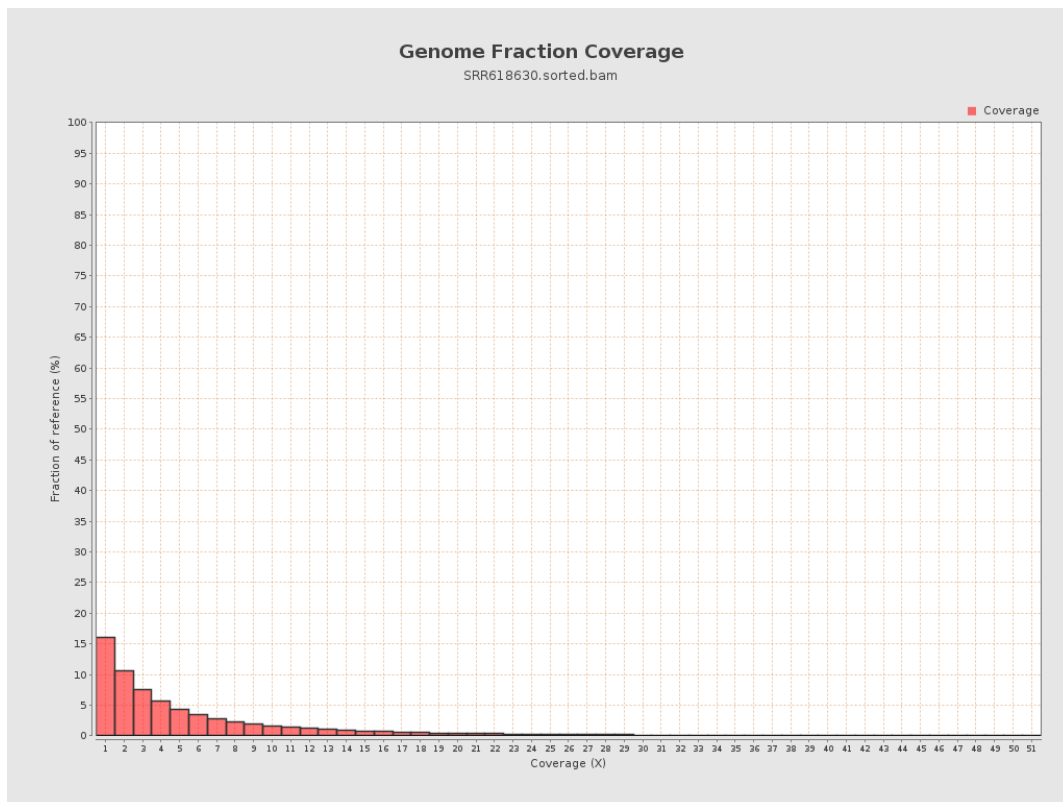
4. Results : Coverage Histogram



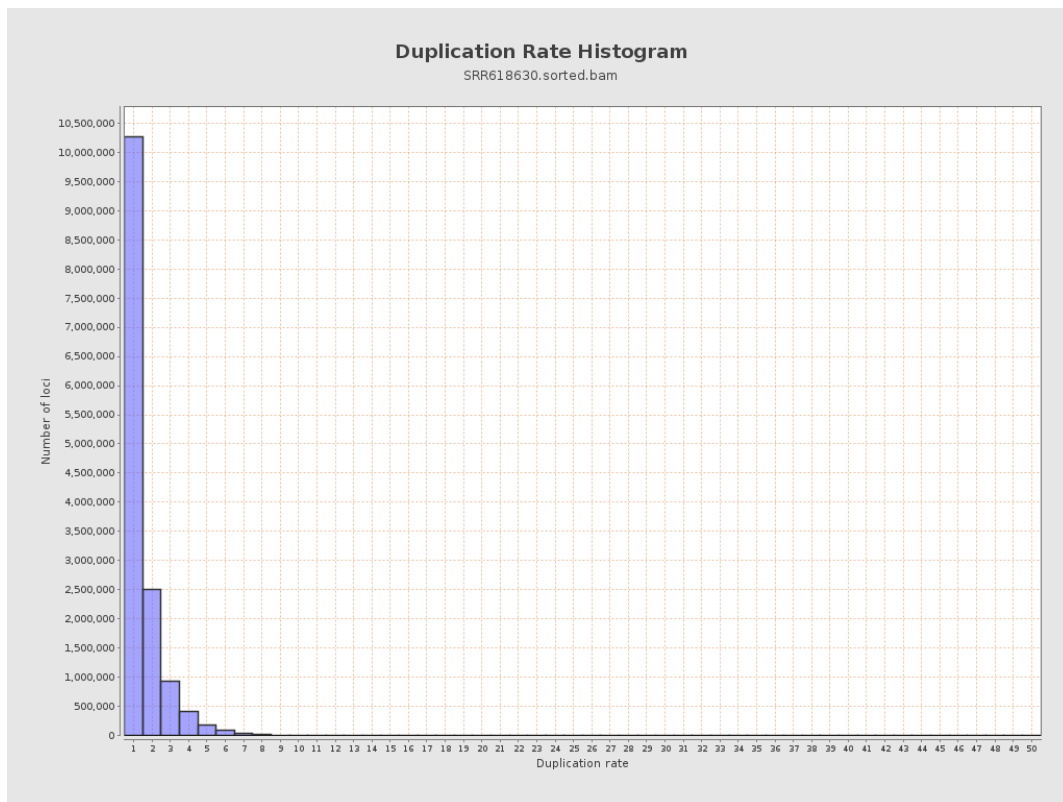
5. Results : Coverage Histogram (0-50X)



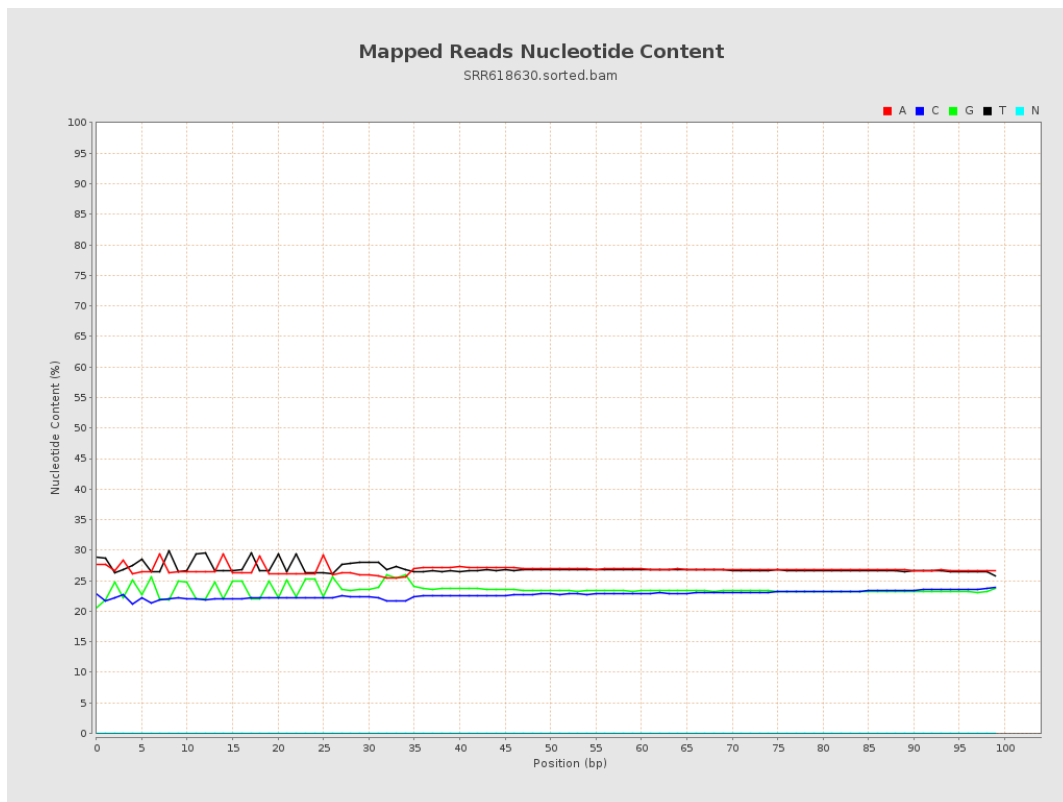
6. Results : Genome Fraction Coverage



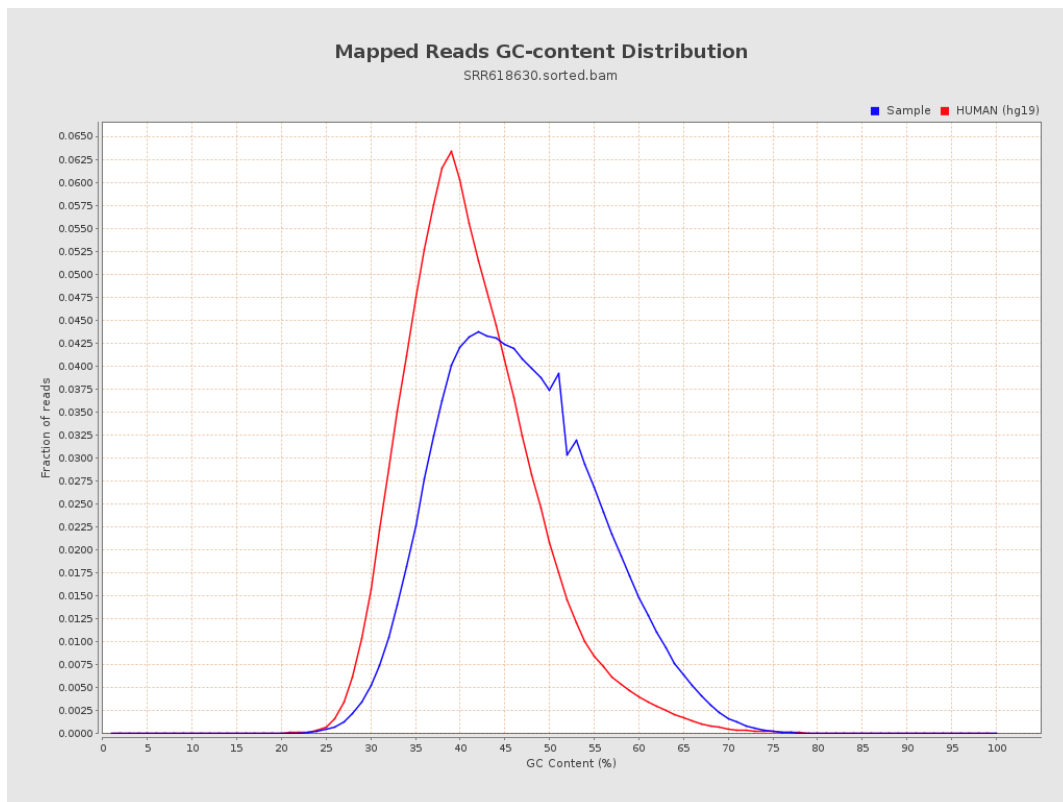
7. Results : Duplication Rate Histogram



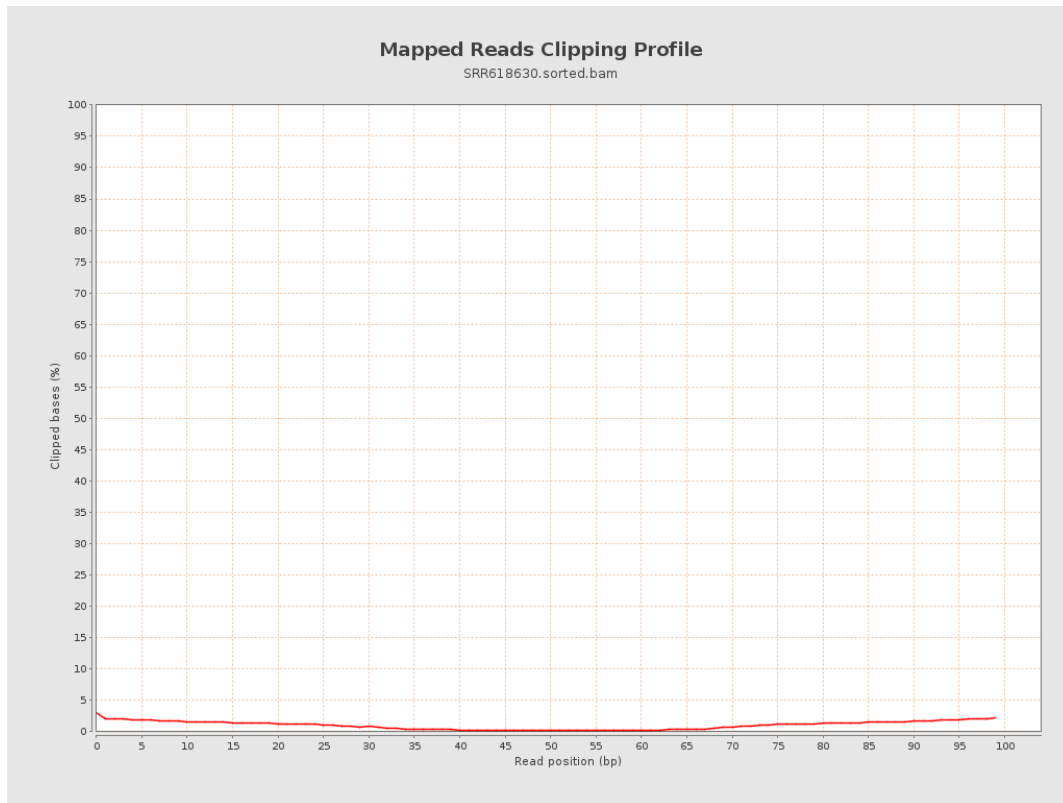
8. Results : Mapped Reads Nucleotide Content



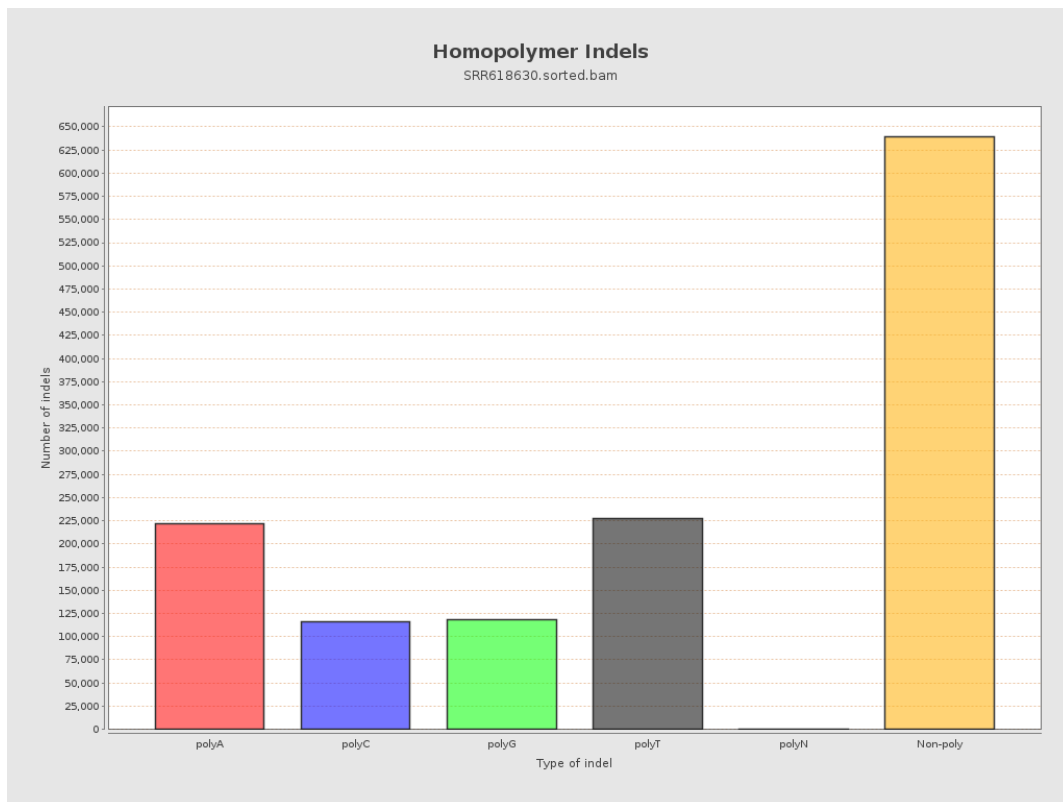
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



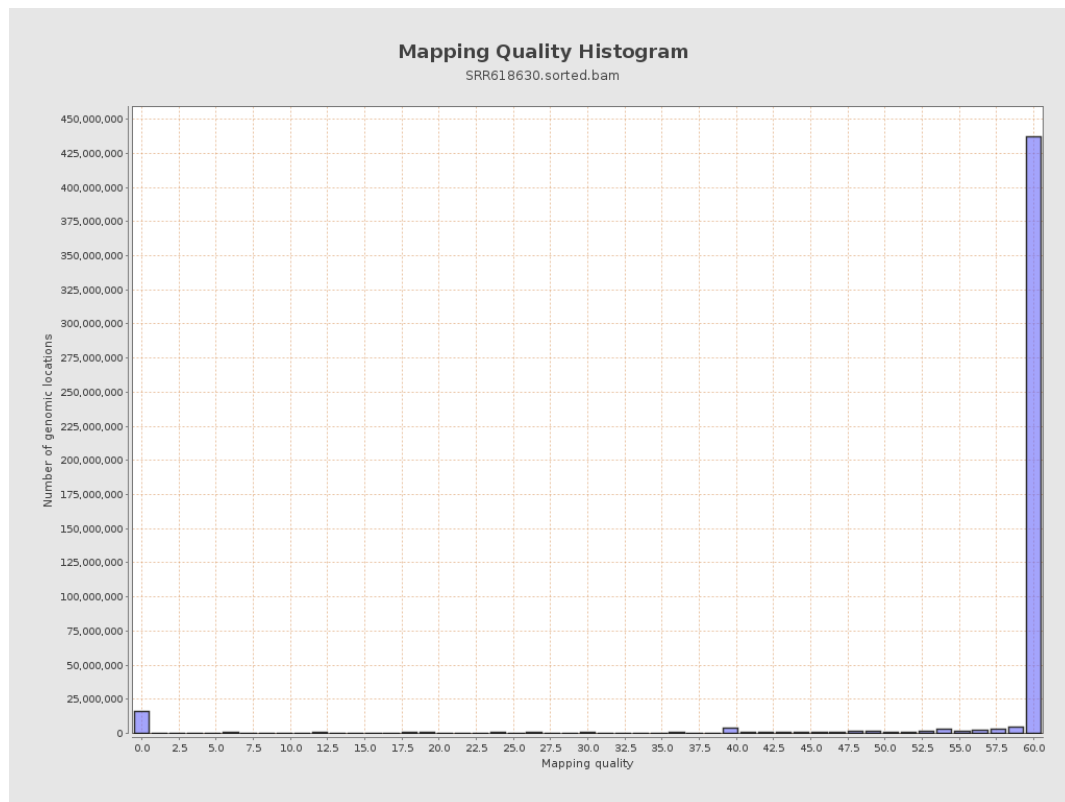
11. Results : Homopolymer Indels



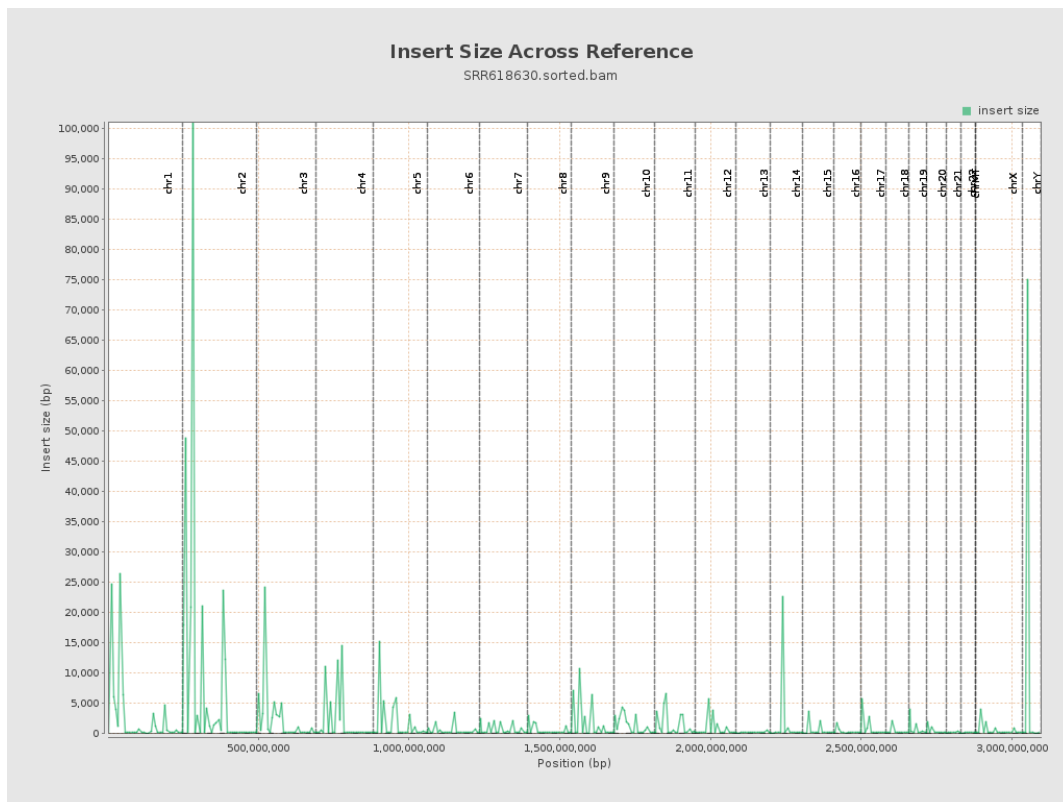
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

