

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 00:34:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618602.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_SRR618602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618602_1.fastq.gz SRR618602_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 00:34:58 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	58,190,958
Mapped reads	53,093,407 / 91.24%
Unmapped reads	5,097,551 / 8.76%
Mapped paired reads	53,093,407 / 91.24%
Mapped reads, first in pair	27,161,128 / 46.68%
Mapped reads, second in pair	25,932,279 / 44.56%
Mapped reads, both in pair	51,209,814 / 88%
Mapped reads, singletons	1,883,593 / 3.24%
Secondary alignments	0
Supplementary alignments	141,643 / 0.24%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	26,383,334 / 45.34%
Duplication rate	38.19%
Clipped reads	11,365,481 / 19.53%

2.2. ACGT Content

Number/percentage of A's	1,309,473,598 / 26.14%
Number/percentage of C's	1,155,093,980 / 23.06%
Number/percentage of T's	1,324,222,019 / 26.44%
Number/percentage of G's	1,219,549,440 / 24.35%
Number/percentage of N's	179,046 / 0%

GC Percentage	47.41%
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2.3. Coverage

Mean	1.6189
Standard Deviation	8.0351

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	71,551.89
Standard Deviation	2,701,591.64
P25/Median/P75	177 / 207 / 248

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	62,599,362
Insertions	875,470
Mapped reads with at least one insertion	1.62%
Deletions	2,226,932
Mapped reads with at least one deletion	4.1%
Homopolymer indels	52.62%

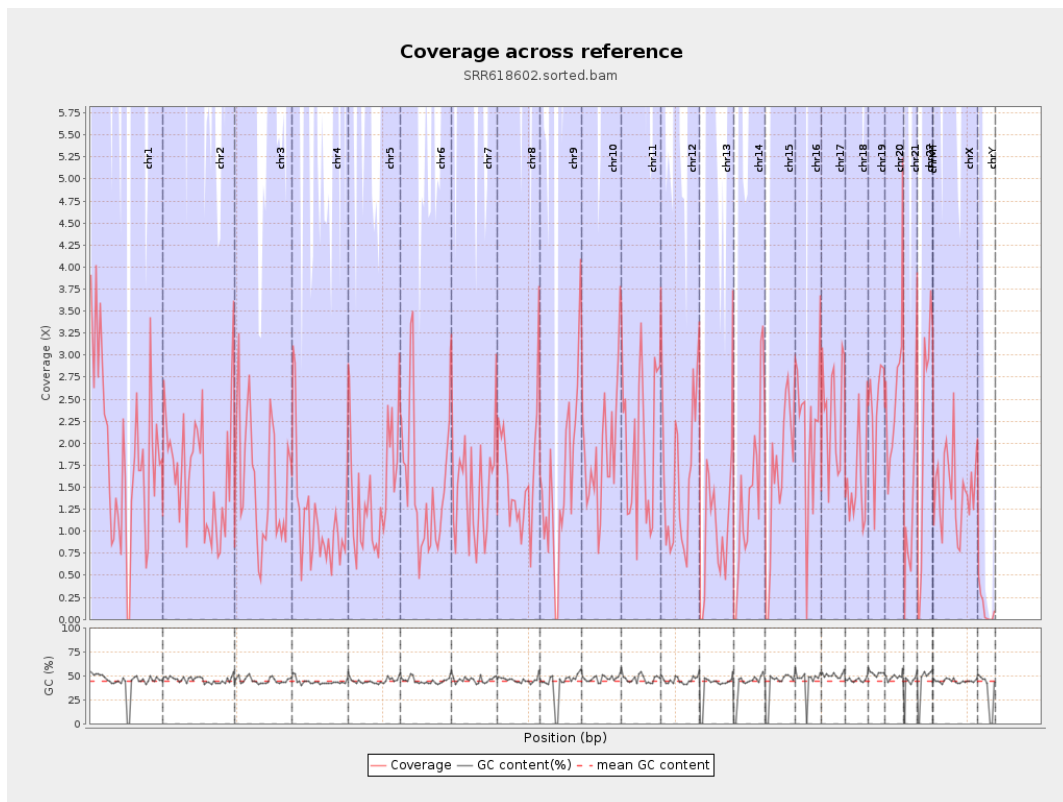
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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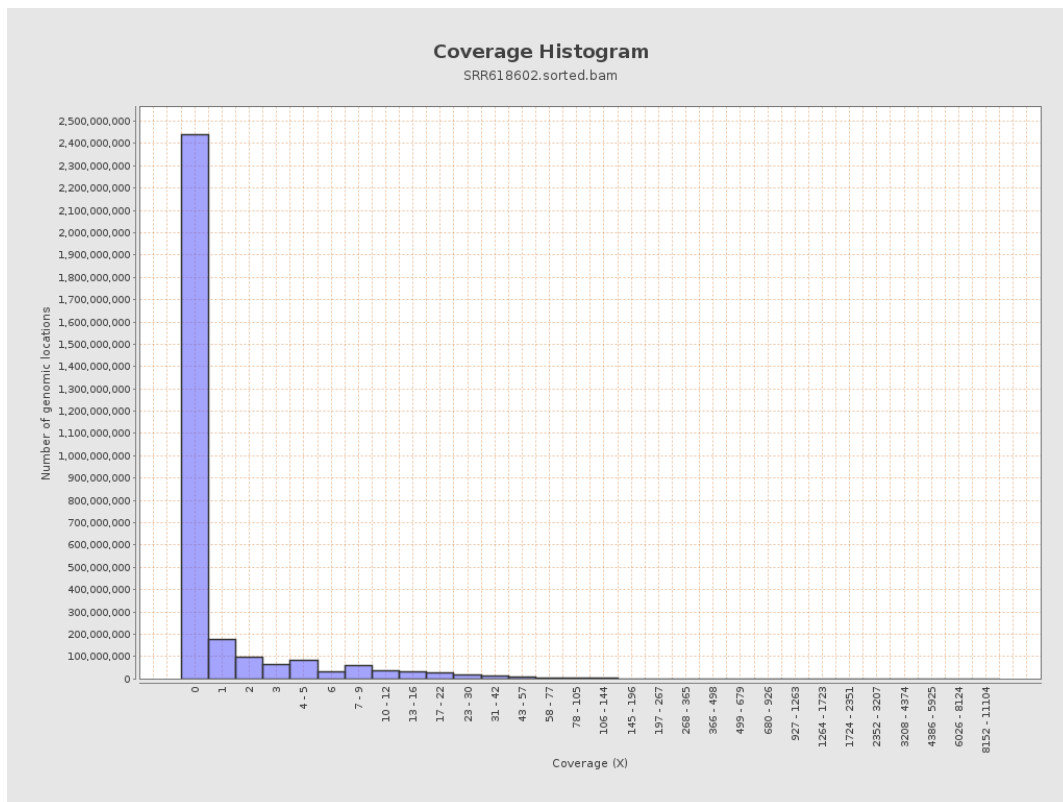
		bases	coverage	deviation
chr1	249250621	464889357	1.8651	8.5083
chr2	243199373	403352720	1.6585	8.9554
chr3	198022430	307018812	1.5504	6.5965
chr4	191154276	214939672	1.1244	7.3998
chr5	180915260	264556420	1.4623	6.2057
chr6	171115067	256230557	1.4974	6.274
chr7	159138663	239421979	1.5045	6.7105
chr8	146364022	238702711	1.6309	10.5155
chr9	141213431	221073092	1.5655	7.7042
chr10	135534747	256101479	1.8896	7.9032
chr11	135006516	268775102	1.9908	8.2141
chr12	133851895	218988742	1.6361	7.0469
chr13	115169878	118929182	1.0326	5.0706
chr14	107349540	153776102	1.4325	6.5565
chr15	102531392	164889083	1.6082	7.0544
chr16	90354753	197461860	2.1854	15.8514
chr17	81195210	191272907	2.3557	8.8131
chr18	78077248	118868633	1.5224	7.0115
chr19	59128983	141841764	2.3989	9.6054
chr20	63025520	158242706	2.5108	9.1374
chr21	48129895	66151159	1.3744	11.0444
chr22	51304566	109595975	2.1362	8.9591
chrMT	16571	51253	3.0929	18.4111
chrX	155270560	229137136	1.4757	5.9981

chrY	59373566	7336650	0.1236	4.6757
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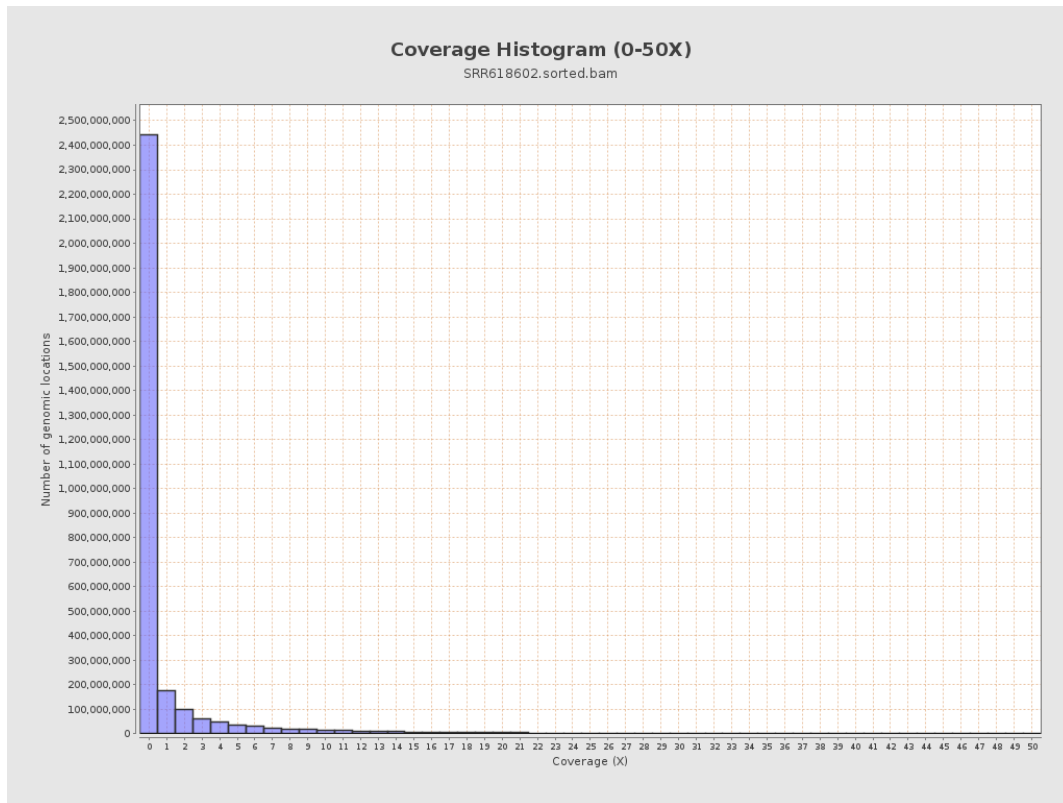
3. Results : Coverage across reference



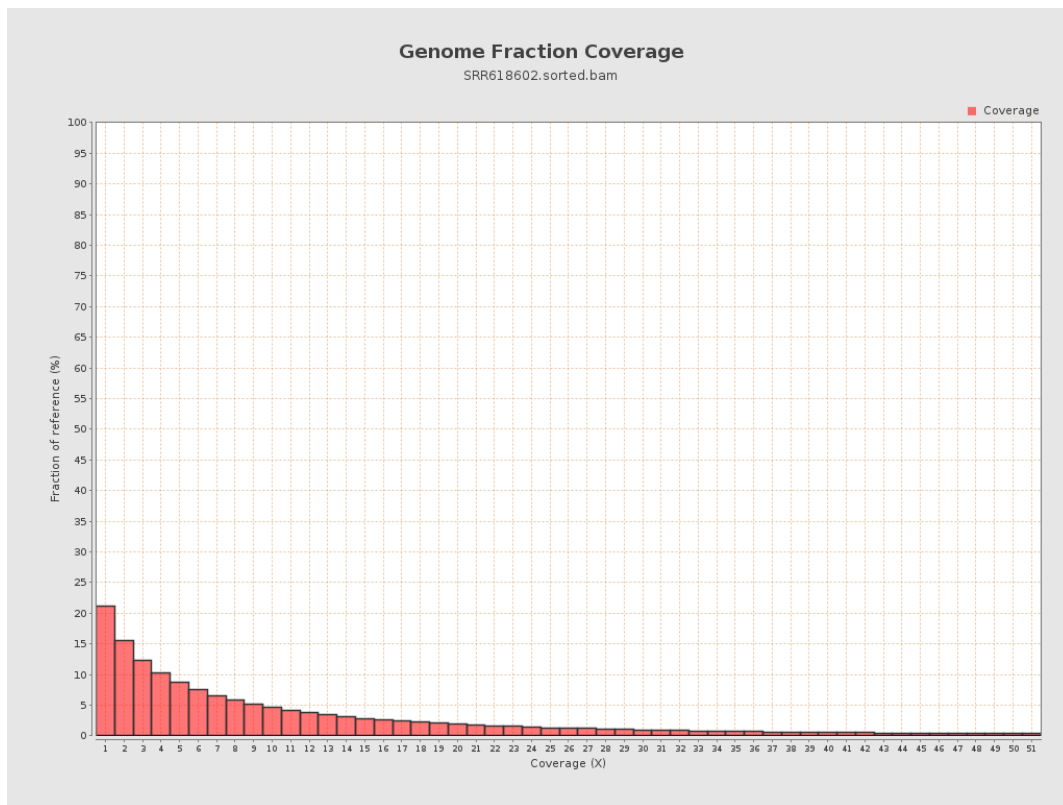
4. Results : Coverage Histogram



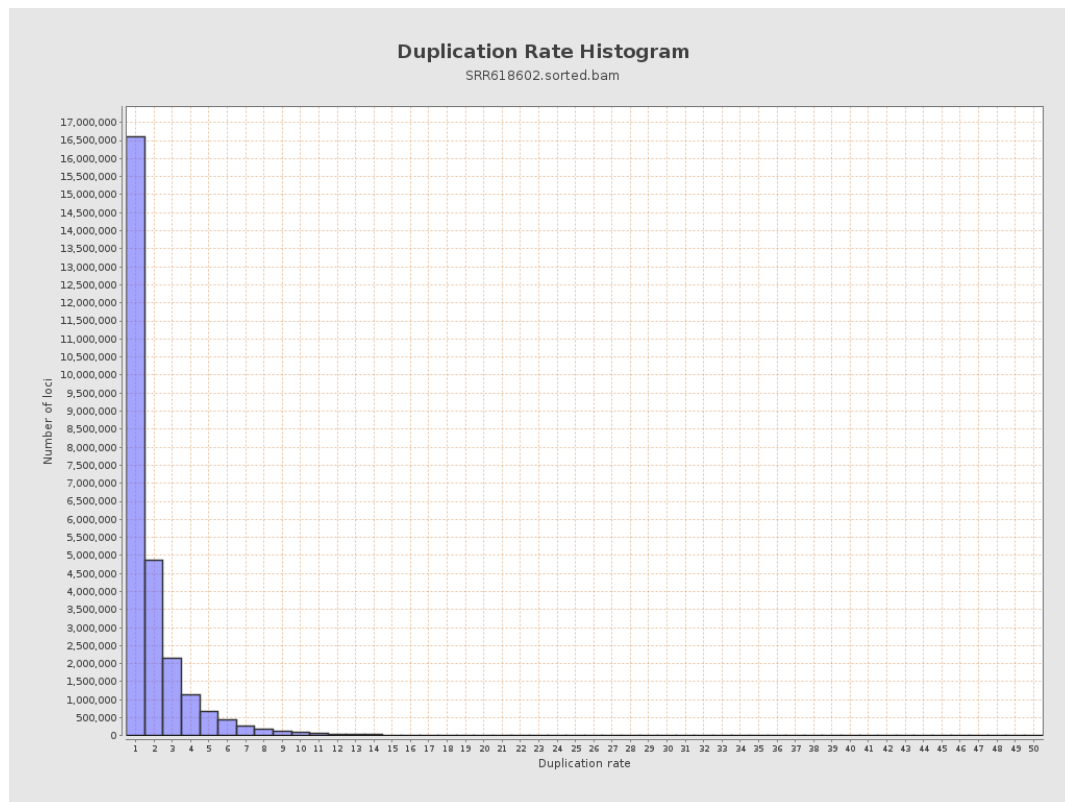
5. Results : Coverage Histogram (0-50X)



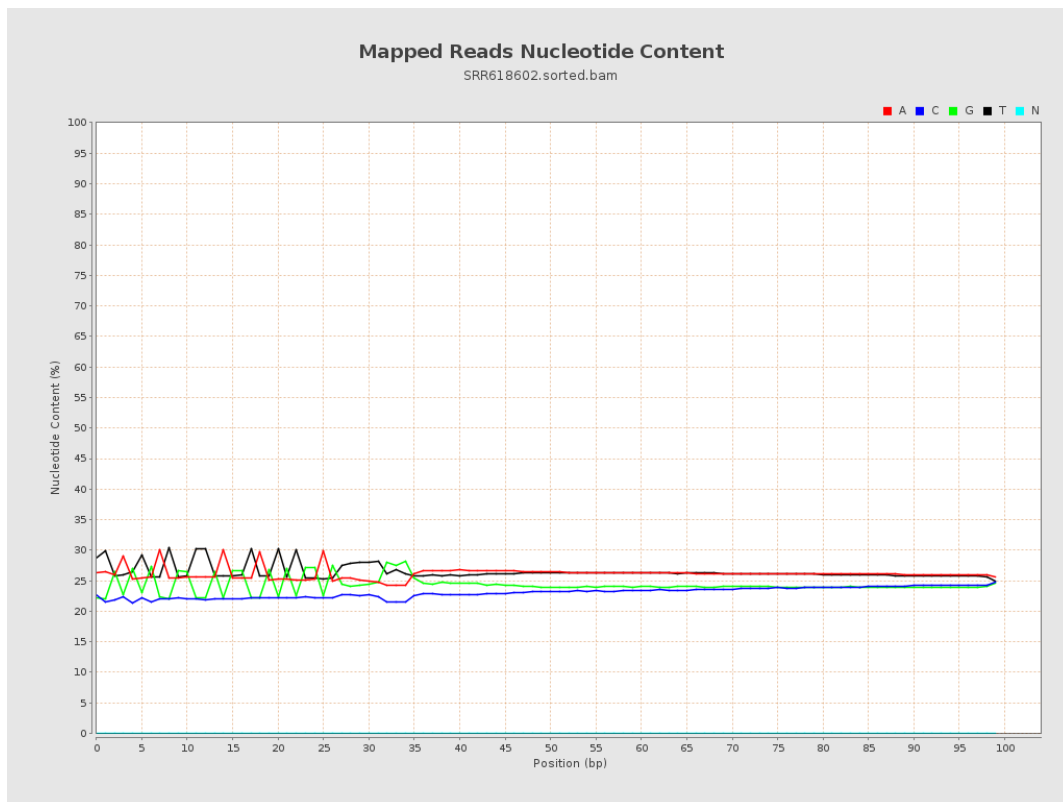
6. Results : Genome Fraction Coverage



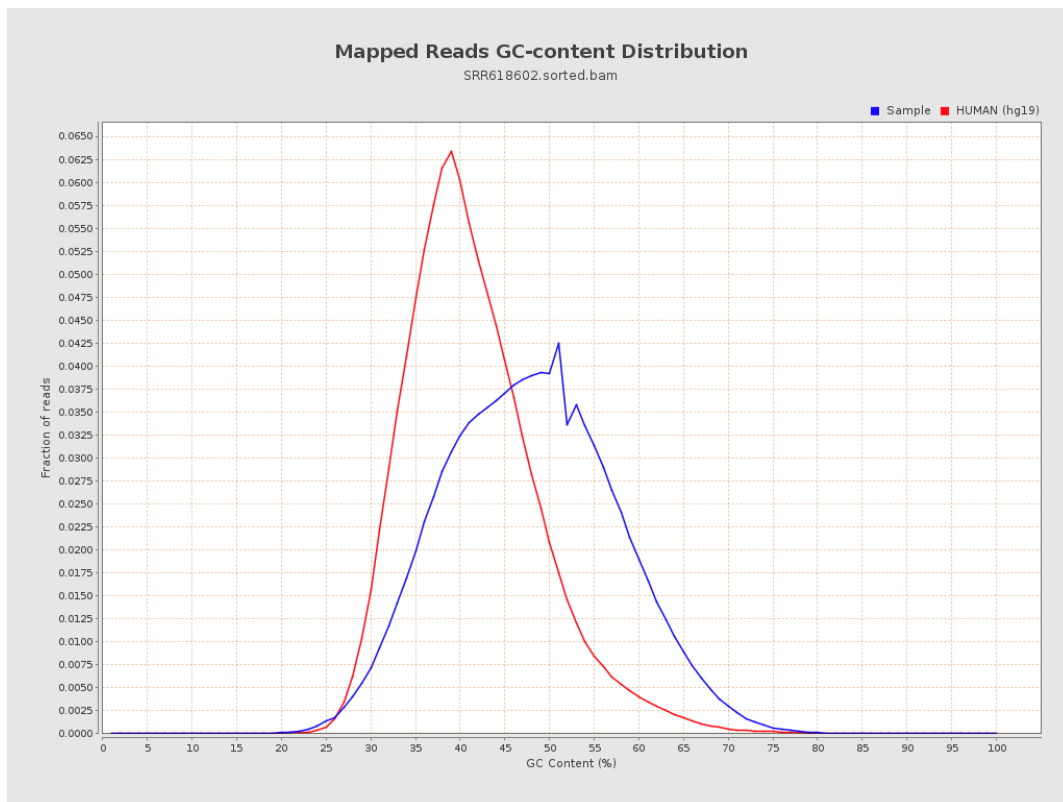
7. Results : Duplication Rate Histogram



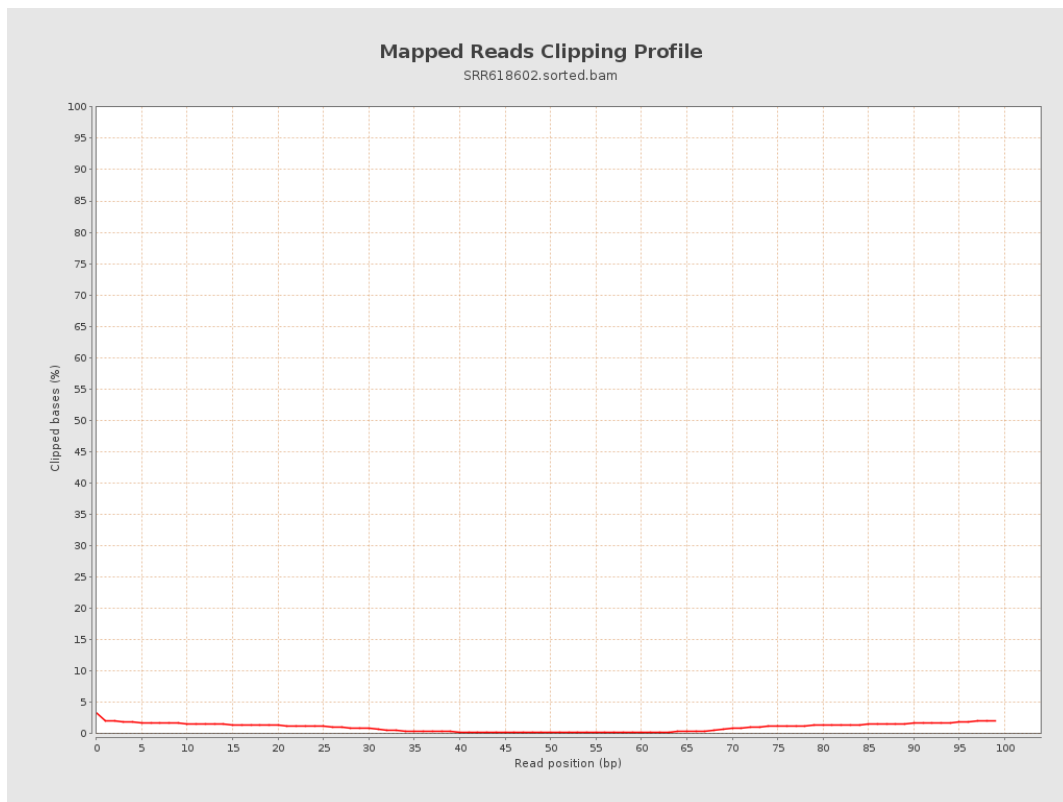
8. Results : Mapped Reads Nucleotide Content



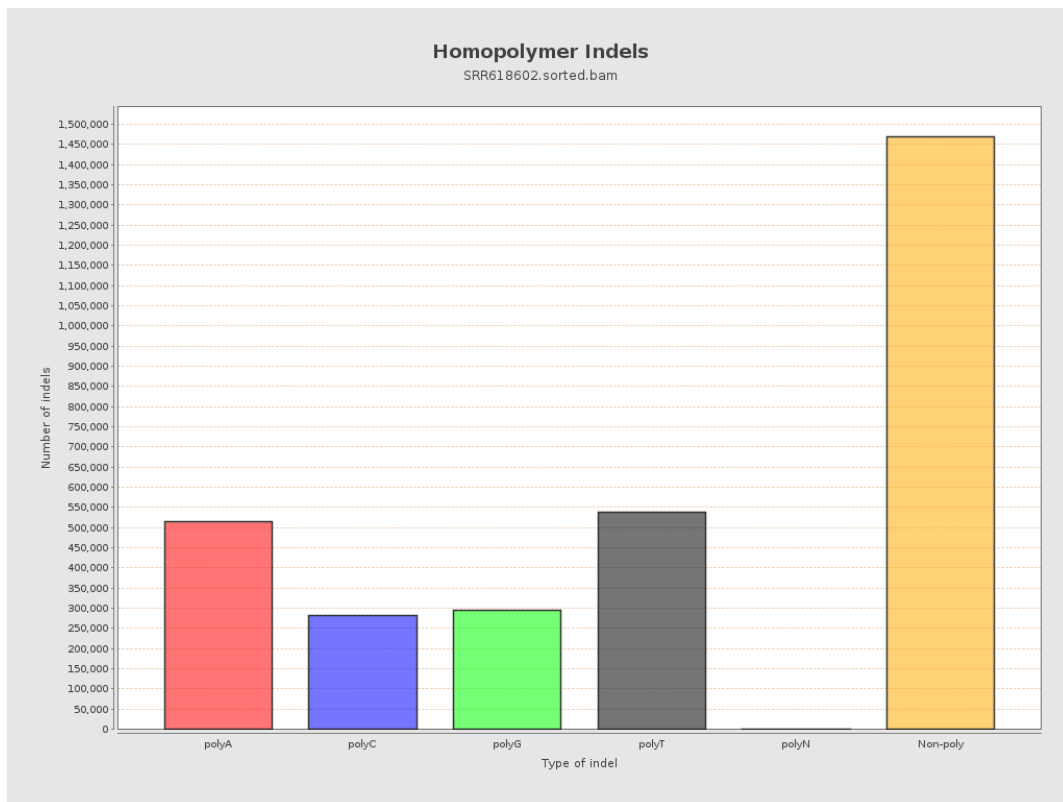
9. Results : Mapped Reads GC-content Distribution



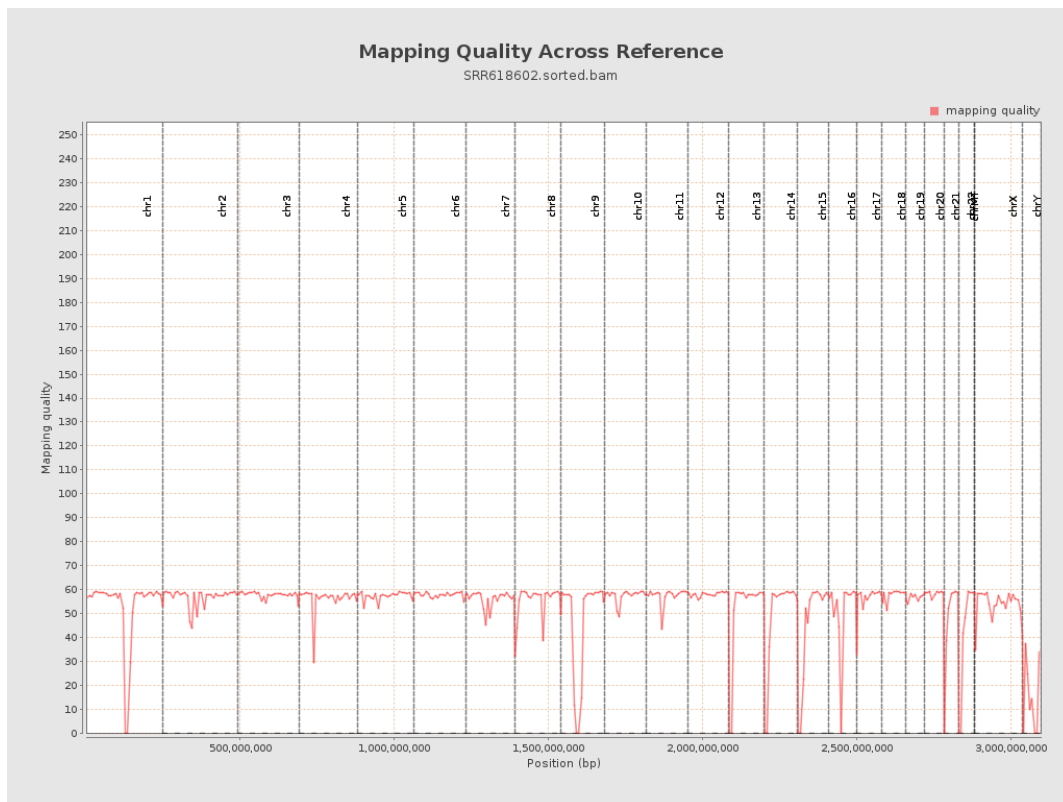
10. Results : Mapped Reads Clipping Profile



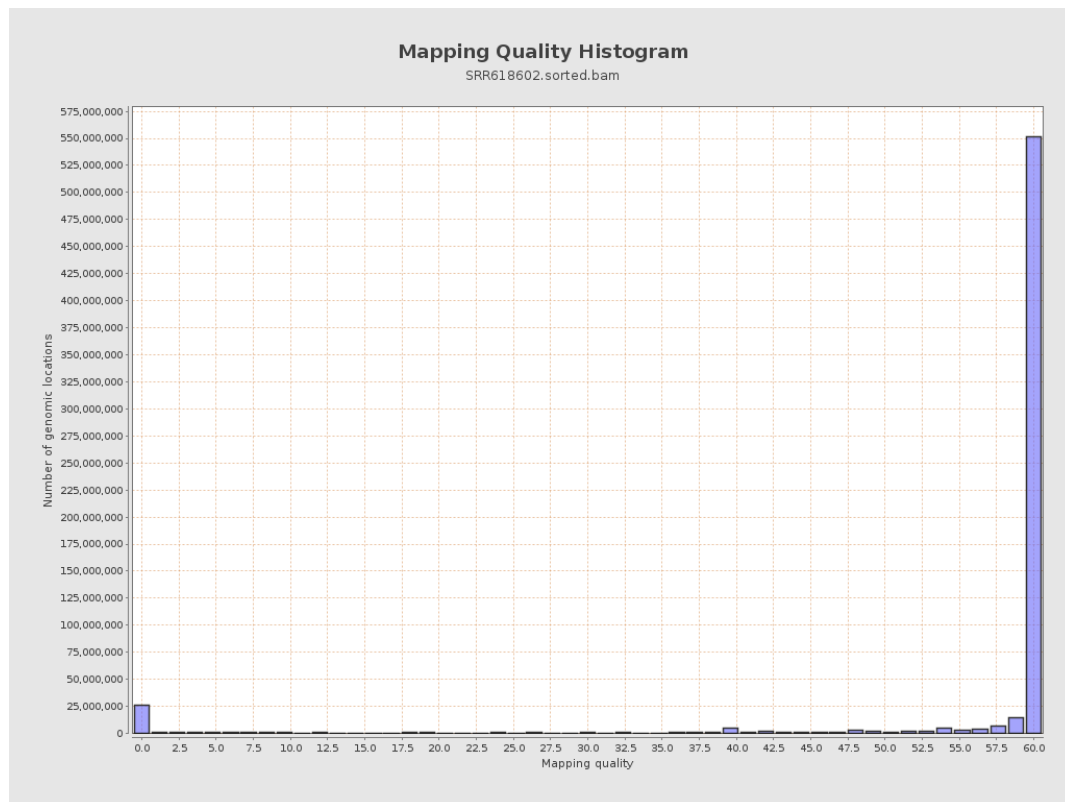
11. Results : Homopolymer Indels



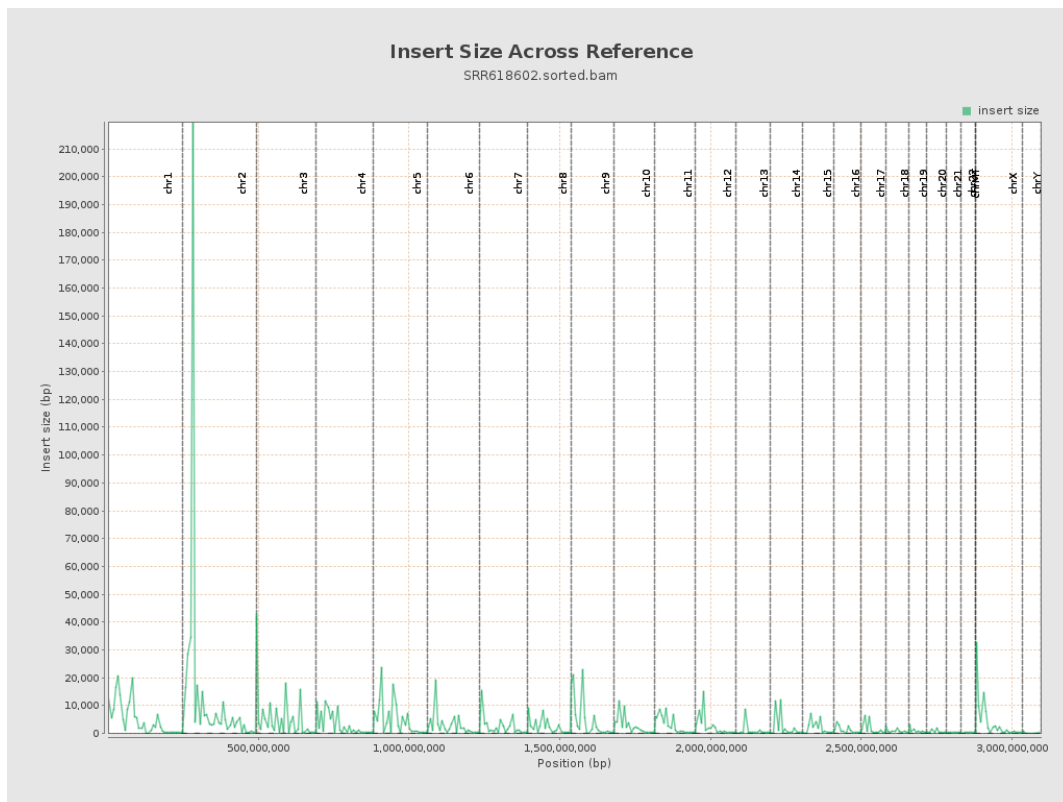
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

