

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 11:38:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618672.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_SRR618672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618672_1.fastq.gz SRR618672_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 11:38:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	221,100,314
Mapped reads	213,259,345 / 96.45%
Unmapped reads	7,840,969 / 3.55%
Mapped paired reads	213,259,345 / 96.45%
Mapped reads, first in pair	106,727,095 / 48.27%
Mapped reads, second in pair	106,532,250 / 48.18%
Mapped reads, both in pair	210,086,484 / 95.02%
Mapped reads, singletons	3,172,861 / 1.44%
Secondary alignments	0
Supplementary alignments	552,992 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	35,083,775 / 15.87%
Duplication rate	12.04%
Clipped reads	29,653,323 / 13.41%

2.2. ACGT Content

Number/percentage of A's	6,112,310,305 / 29.6%
Number/percentage of C's	4,241,629,107 / 20.54%
Number/percentage of T's	6,081,329,204 / 29.45%
Number/percentage of G's	4,214,728,487 / 20.41%
Number/percentage of N's	2,878,441 / 0.01%

GC Percentage	40.95%
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2.3. Coverage

Mean	6.6734
Standard Deviation	62.828

2.4. Mapping Quality

Mean Mapping Quality	53.66
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2.5. Insert size

Mean	42,092.27
Standard Deviation	1,960,380.87
P25/Median/P75	227 / 256 / 295

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	225,999,332
Insertions	2,305,458
Mapped reads with at least one insertion	1.06%
Deletions	2,631,544
Mapped reads with at least one deletion	1.2%
Homopolymer indels	41.1%

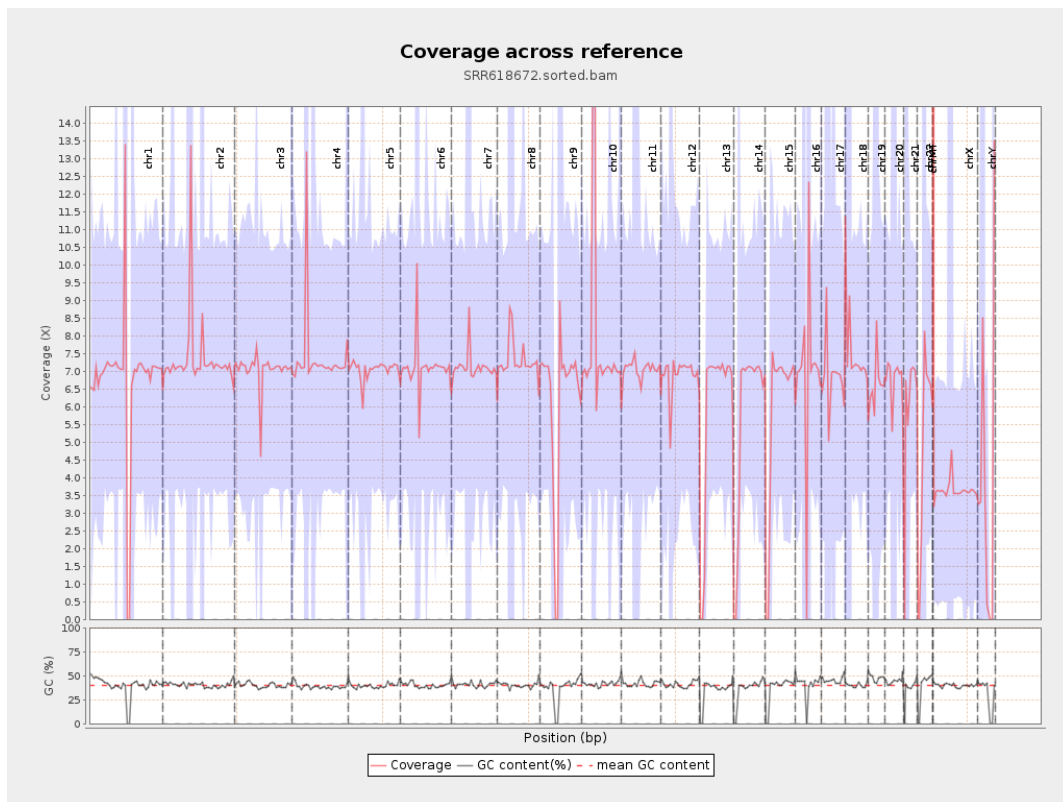
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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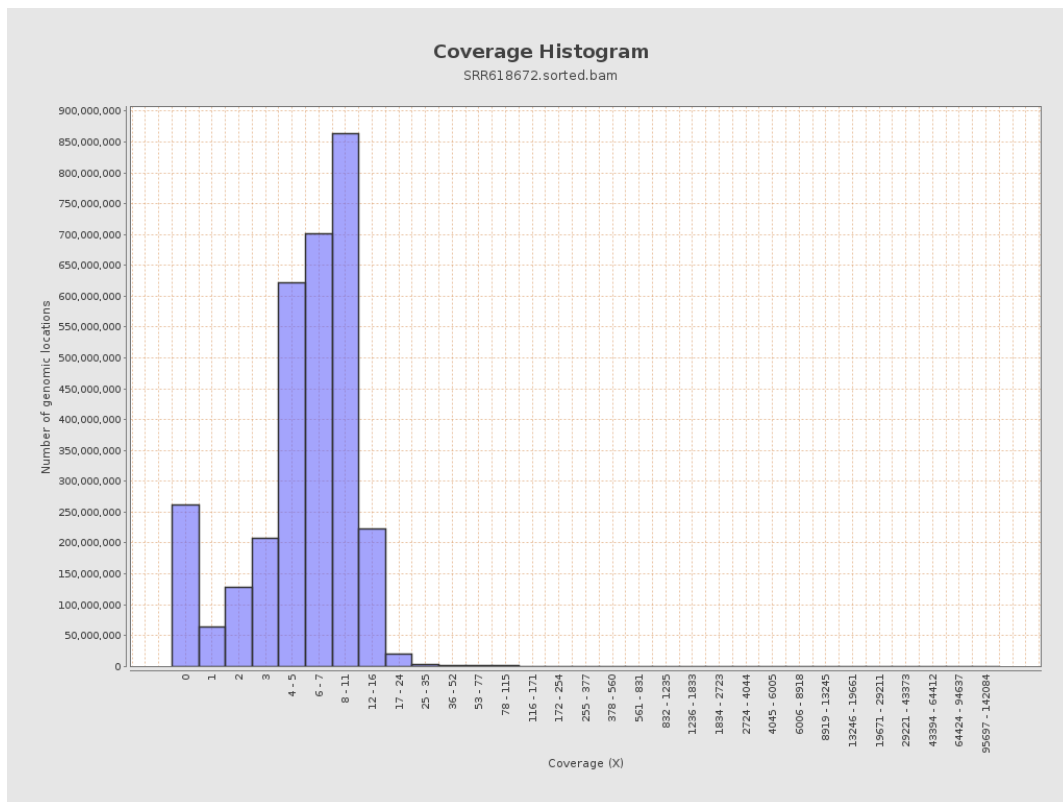
		bases	coverage	deviation
chr1	249250621	1688792887	6.7755	148.3451
chr2	243199373	1792474198	7.3704	38.8822
chr3	198022430	1395185920	7.0456	4.5446
chr4	191154276	1411914135	7.3863	44.2456
chr5	180915260	1273502288	7.0392	6.0849
chr6	171115067	1218774496	7.1225	34.2356
chr7	159138663	1132571697	7.1169	44.4868
chr8	146364022	1069457723	7.3068	98.8939
chr9	141213431	876998874	6.2104	64.6748
chr10	135534747	1067548439	7.8766	115.5401
chr11	135006516	952833991	7.0577	29.6395
chr12	133851895	925067848	6.9111	5.5481
chr13	115169878	679021775	5.8958	4.2123
chr14	107349540	628330498	5.8531	5.9965
chr15	102531392	596966851	5.8223	4.677
chr16	90354753	627364388	6.9433	43.4707
chr17	81195210	558946367	6.884	35.6827
chr18	78077248	584696506	7.4887	83.8111
chr19	59128983	393375542	6.6528	67.8649
chr20	63025520	426226780	6.7628	13.2253
chr21	48129895	290717276	6.0403	26.4315
chr22	51304566	250242675	4.8776	32.2983
chrMT	16571	5986757	361.2792	48.8624
chrX	155270560	567198233	3.653	12.6973

chrY	59373566	244732010	4.1219	68.8078
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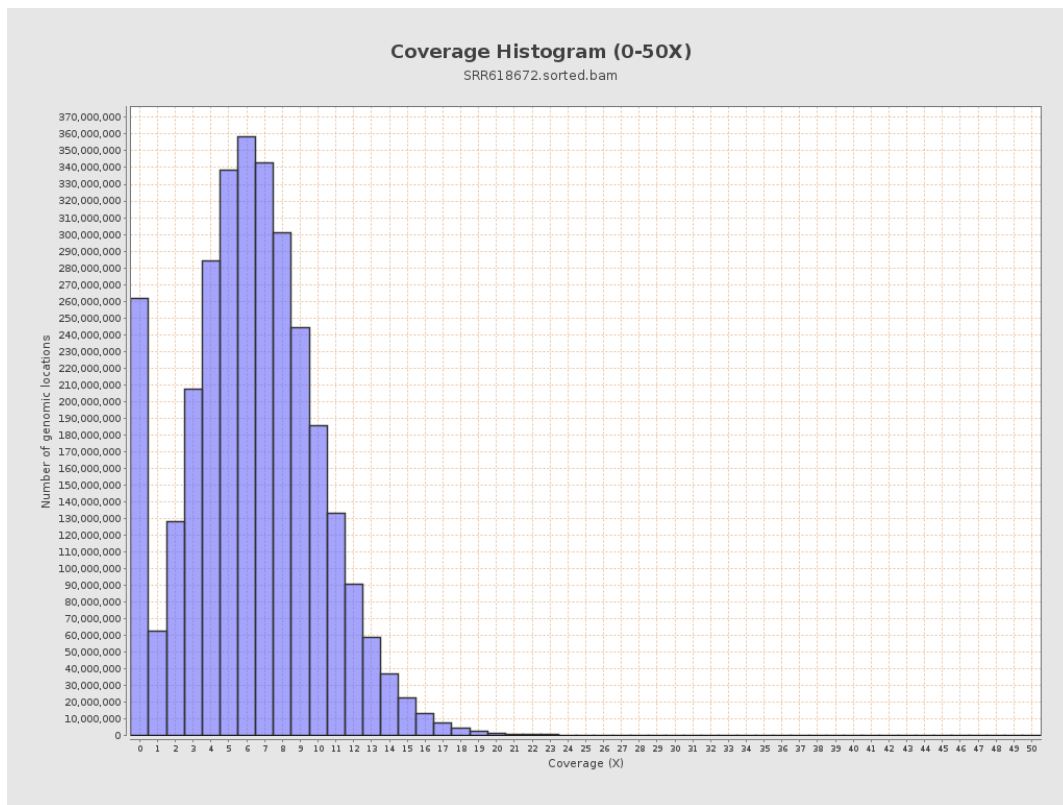
3. Results : Coverage across reference



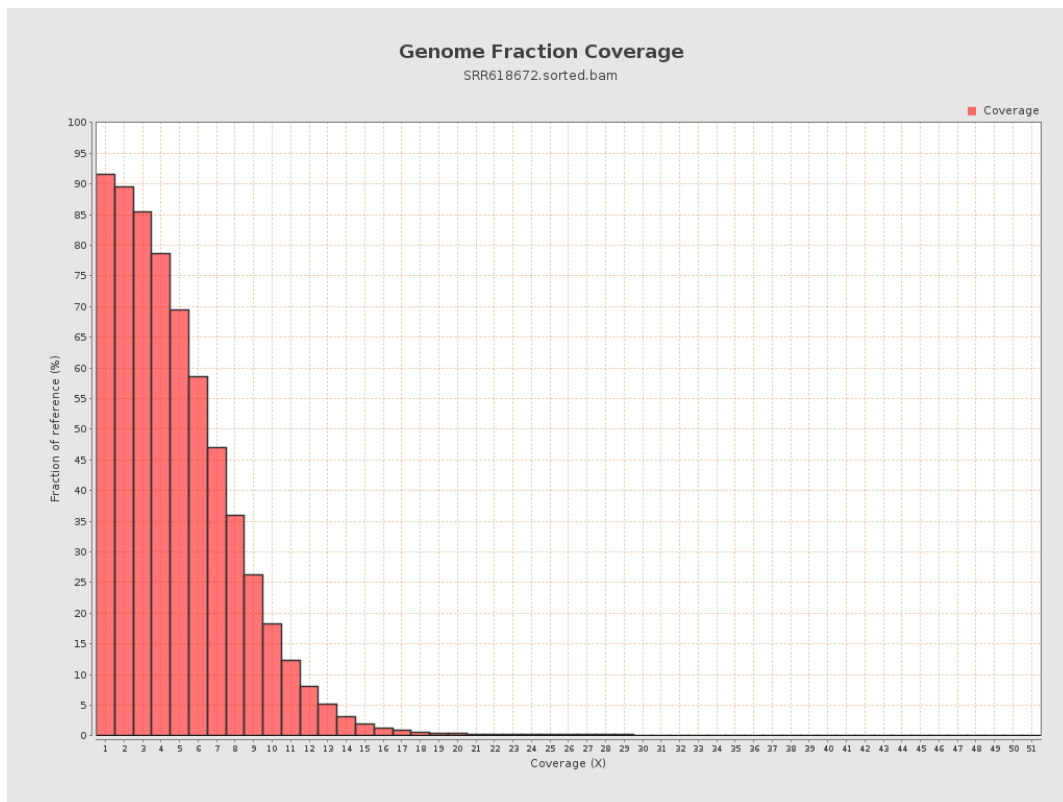
4. Results : Coverage Histogram



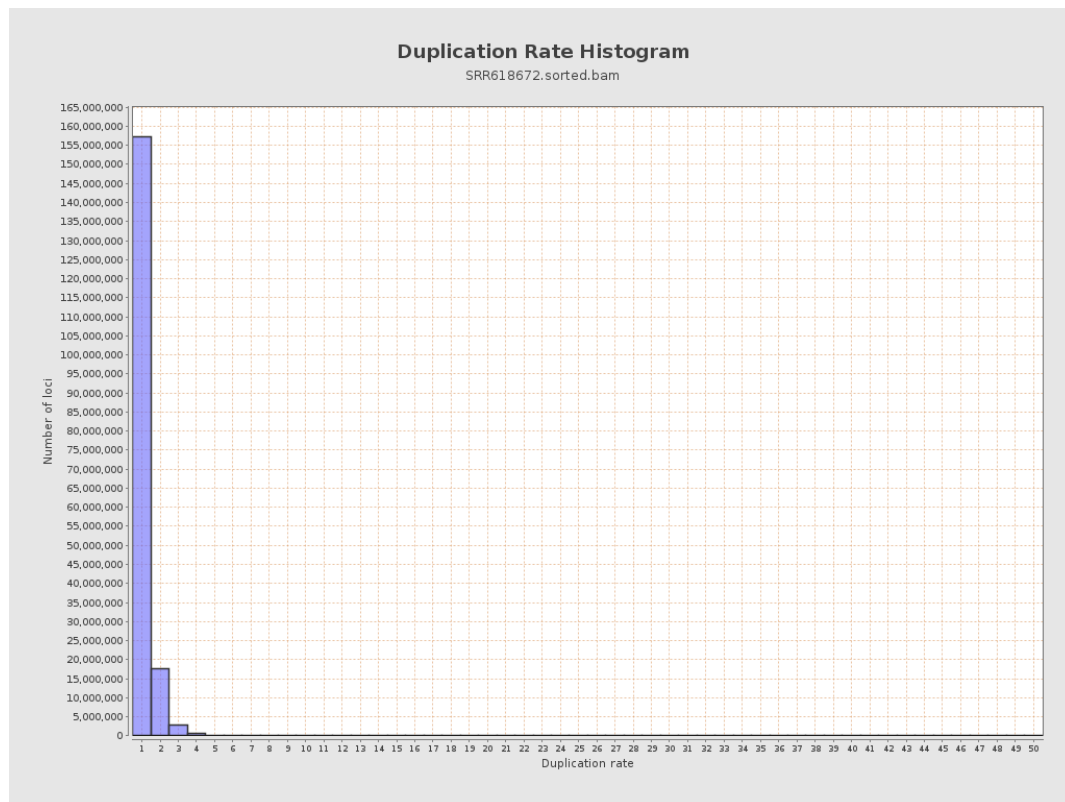
5. Results : Coverage Histogram (0-50X)



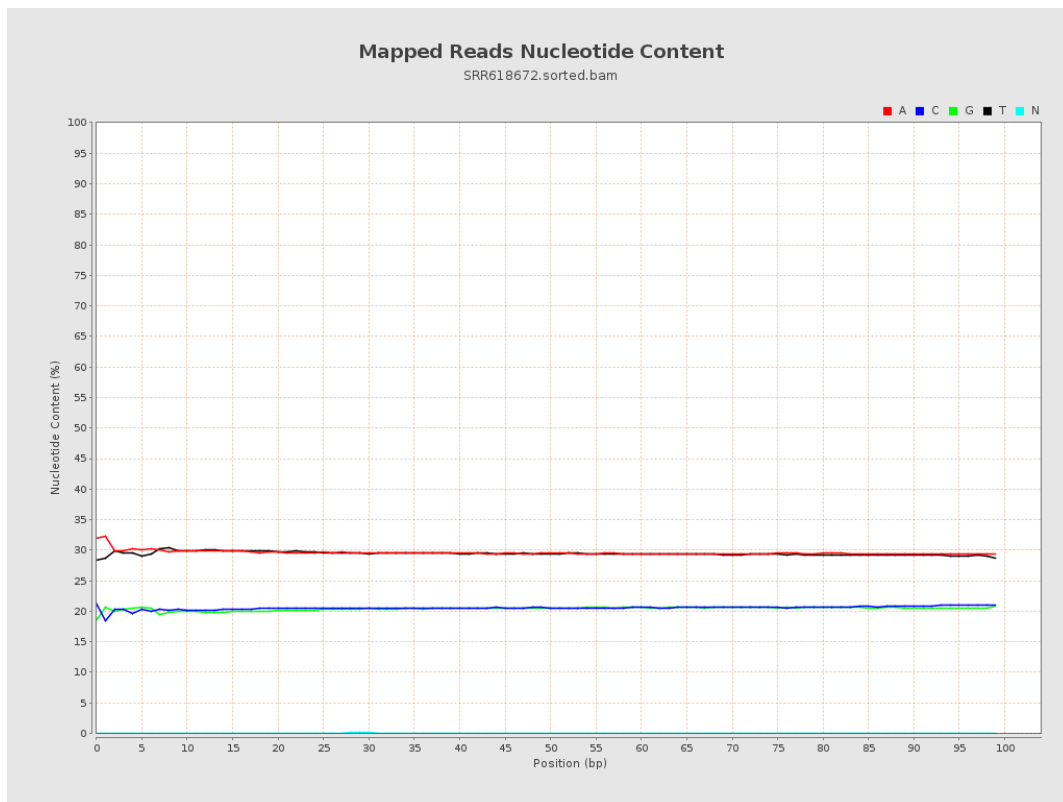
6. Results : Genome Fraction Coverage



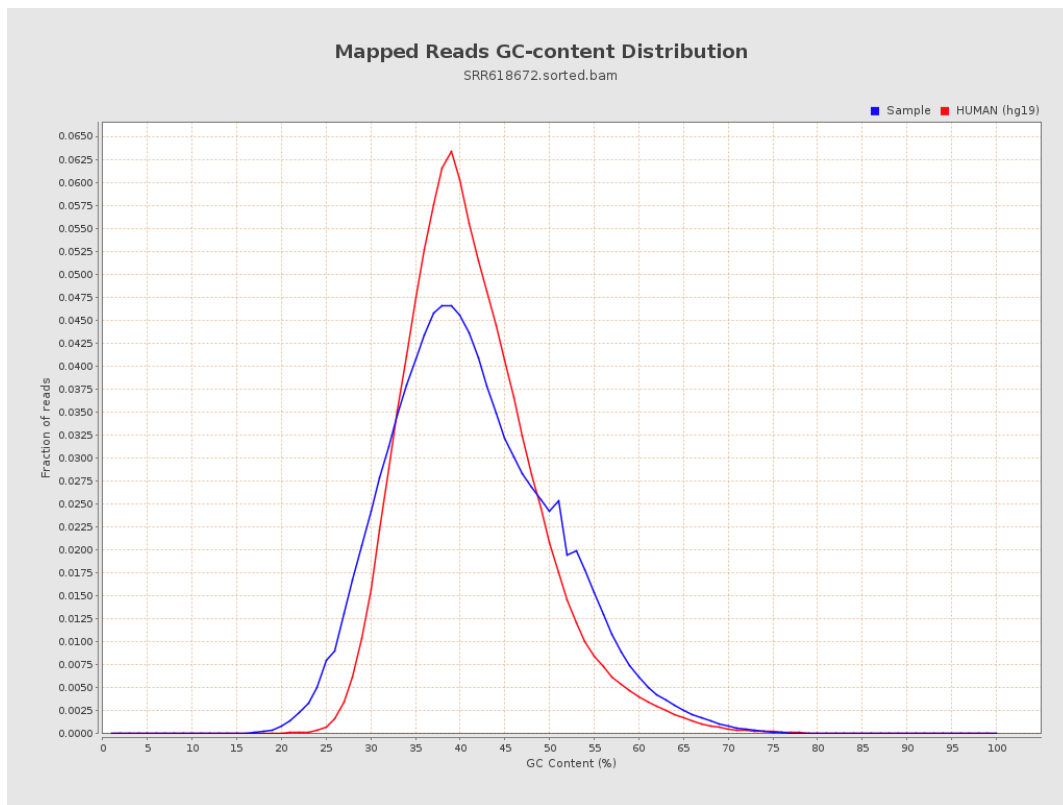
7. Results : Duplication Rate Histogram



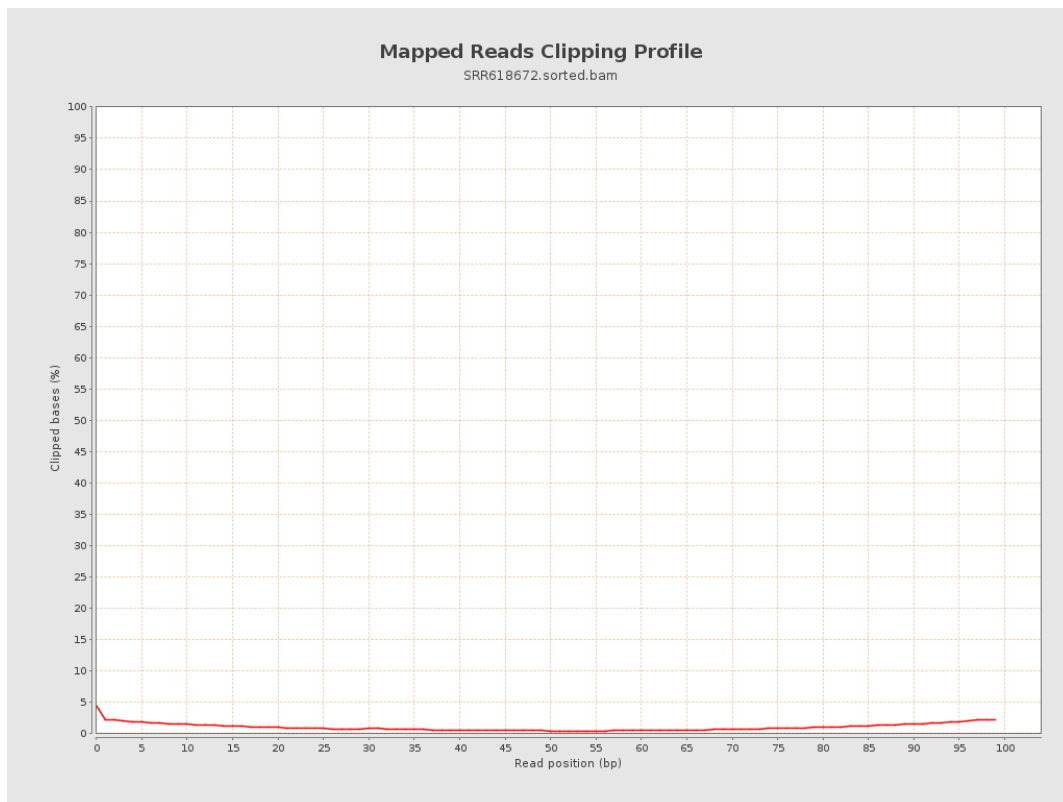
8. Results : Mapped Reads Nucleotide Content



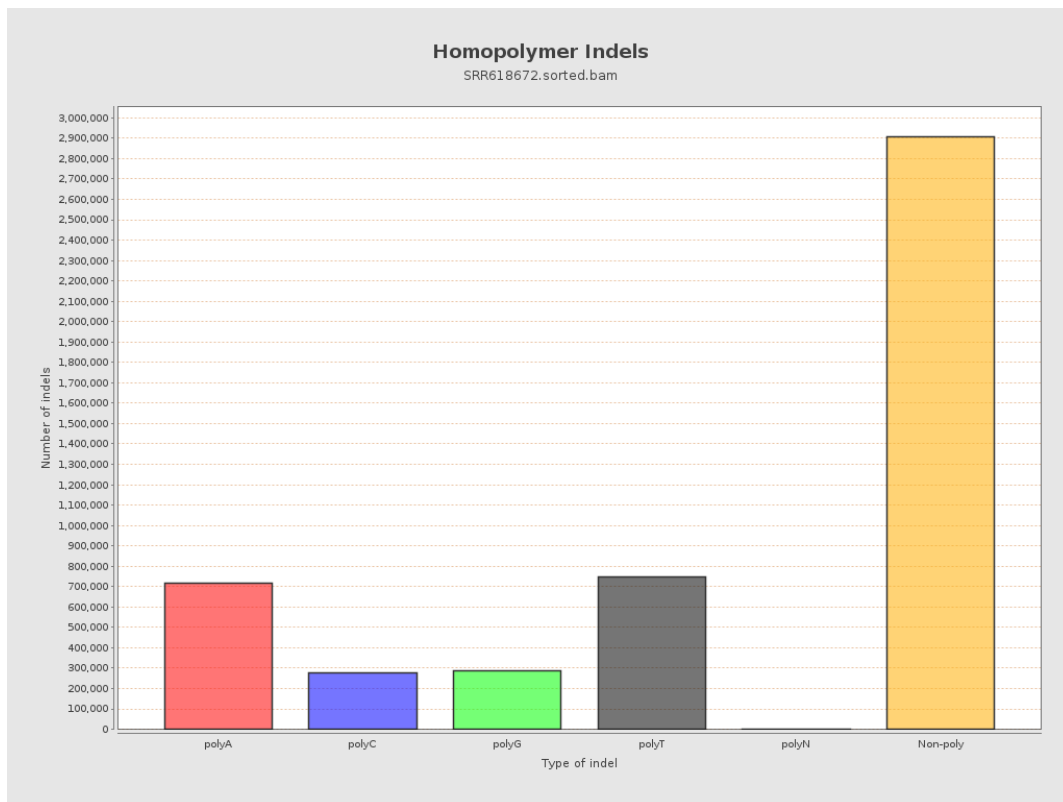
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



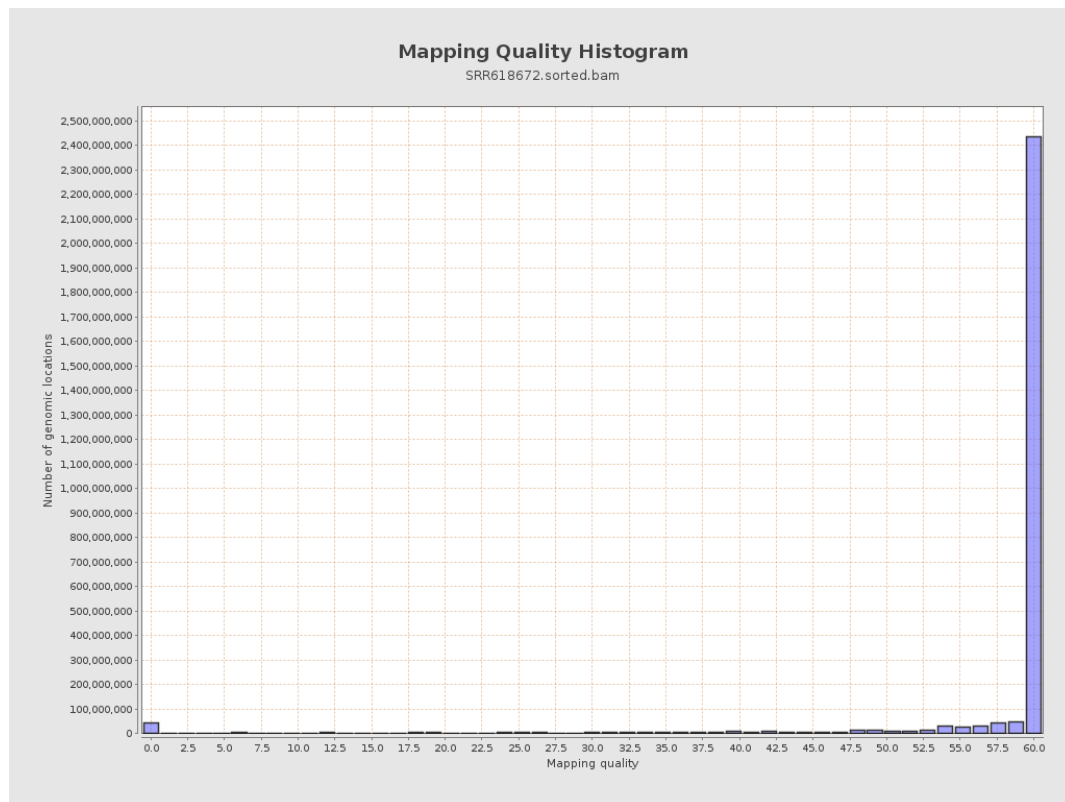
11. Results : Homopolymer Indels



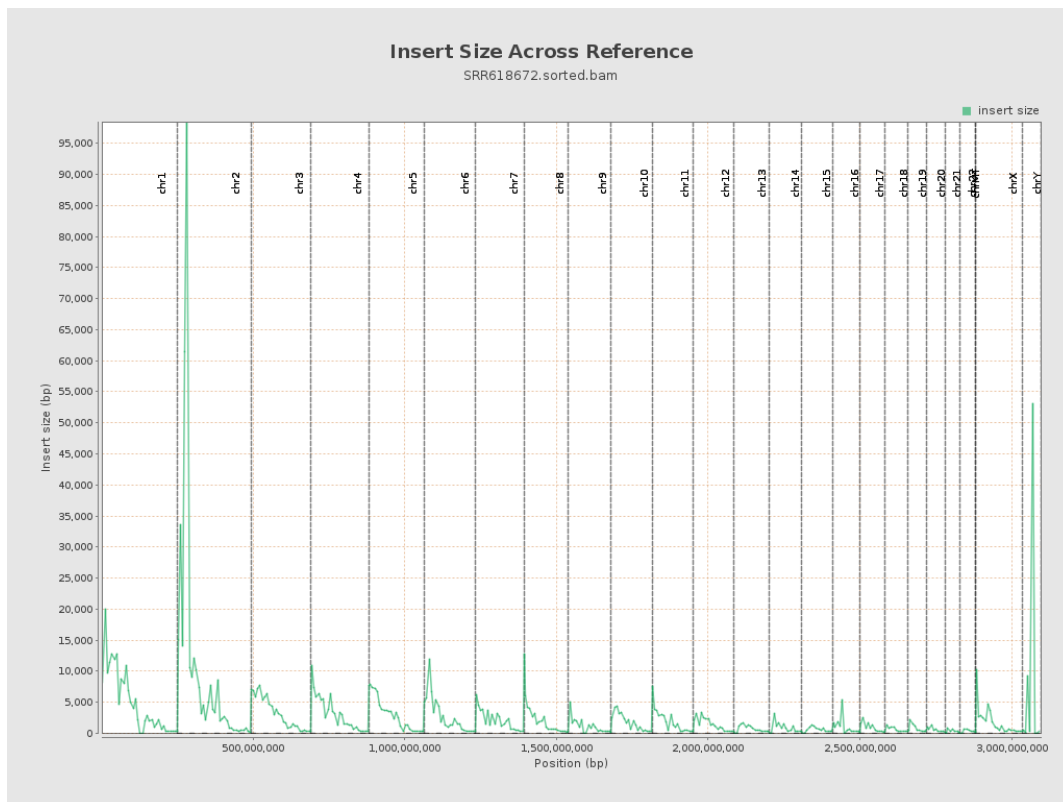
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

