

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 02:46:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618641.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_SRR618641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618641_1.fastq.gz SRR618641_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 02:46:43 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	61,115,288
Mapped reads	52,001,213 / 85.09%
Unmapped reads	9,114,075 / 14.91%
Mapped paired reads	52,001,213 / 85.09%
Mapped reads, first in pair	27,932,267 / 45.7%
Mapped reads, second in pair	24,068,946 / 39.38%
Mapped reads, both in pair	47,276,502 / 77.36%
Mapped reads, singletons	4,724,711 / 7.73%
Secondary alignments	0
Supplementary alignments	155,288 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	10,917,899 / 17.86%
Duplication rate	17.61%
Clipped reads	12,149,802 / 19.88%

2.2. ACGT Content

Number/percentage of A's	1,321,188,798 / 27.06%
Number/percentage of C's	1,086,090,280 / 22.25%
Number/percentage of T's	1,353,314,094 / 27.72%
Number/percentage of G's	1,120,734,482 / 22.96%
Number/percentage of N's	226,000 / 0%

GC Percentage	45.21%
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2.3. Coverage

Mean	1.578
Standard Deviation	7.5338

2.4. Mapping Quality

Mean Mapping Quality	53.07
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2.5. Insert size

Mean	123,333.91
Standard Deviation	3,546,631.93
P25/Median/P75	185 / 215 / 256

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	71,198,495
Insertions	899,387
Mapped reads with at least one insertion	1.7%
Deletions	2,440,543
Mapped reads with at least one deletion	4.57%
Homopolymer indels	52.44%

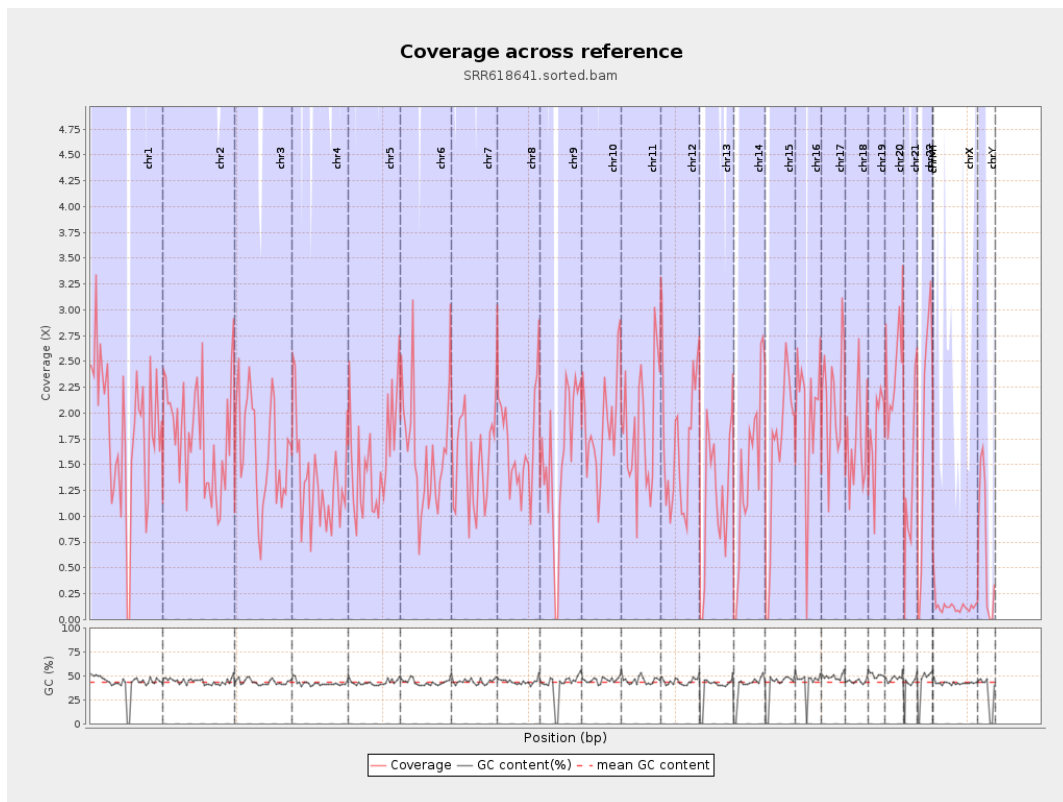
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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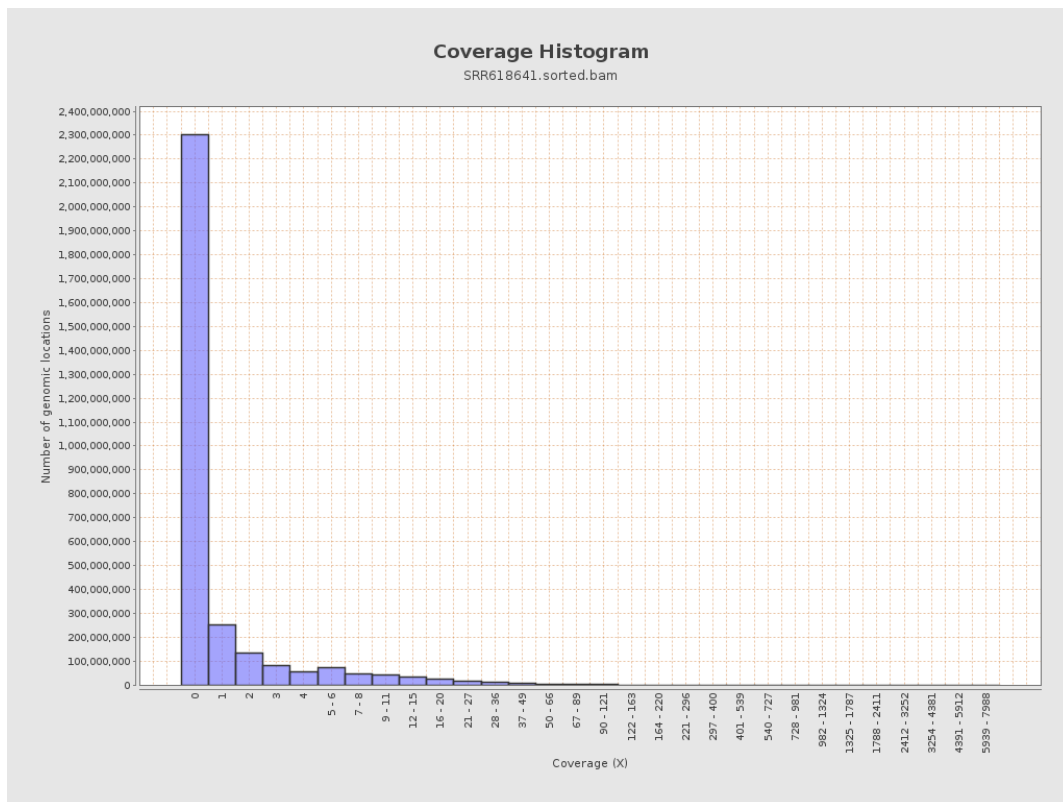
		bases	coverage	deviation
chr1	249250621	452390822	1.815	8.1864
chr2	243199373	429454171	1.7659	9.2566
chr3	198022430	320790122	1.62	6.2934
chr4	191154276	254192648	1.3298	6.2269
chr5	180915260	283150835	1.5651	6.9518
chr6	171115067	275175495	1.6081	6.3126
chr7	159138663	246068077	1.5462	6.3309
chr8	146364022	247837248	1.6933	6.9482
chr9	141213431	220306660	1.5601	7.1836
chr10	135534747	252164074	1.8605	7.4117
chr11	135006516	251033176	1.8594	7.7306
chr12	133851895	227117288	1.6968	7.6591
chr13	115169878	137313422	1.1923	5.3996
chr14	107349540	153718735	1.4319	6.2328
chr15	102531392	165950966	1.6185	7.189
chr16	90354753	178110578	1.9712	14.9206
chr17	81195210	173993583	2.1429	8.6174
chr18	78077248	130846633	1.6759	7.0996
chr19	59128983	106322940	1.7982	7.4733
chr20	63025520	153198802	2.4307	8.6148
chr21	48129895	66225149	1.376	9.9635
chr22	51304566	95855290	1.8684	8.2792
chrMT	16571	11356	0.6853	1.9992
chrX	155270560	19801657	0.1275	2.8711

chrY	59373566	43909720	0.7395	6.1446
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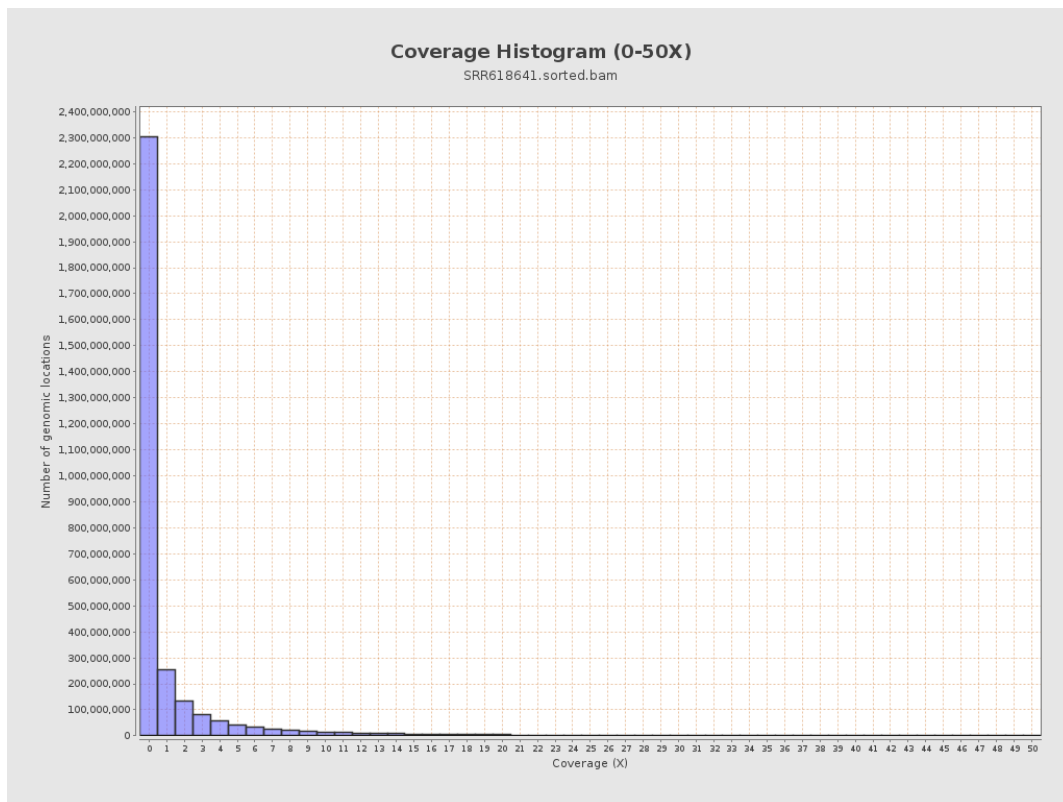
3. Results : Coverage across reference



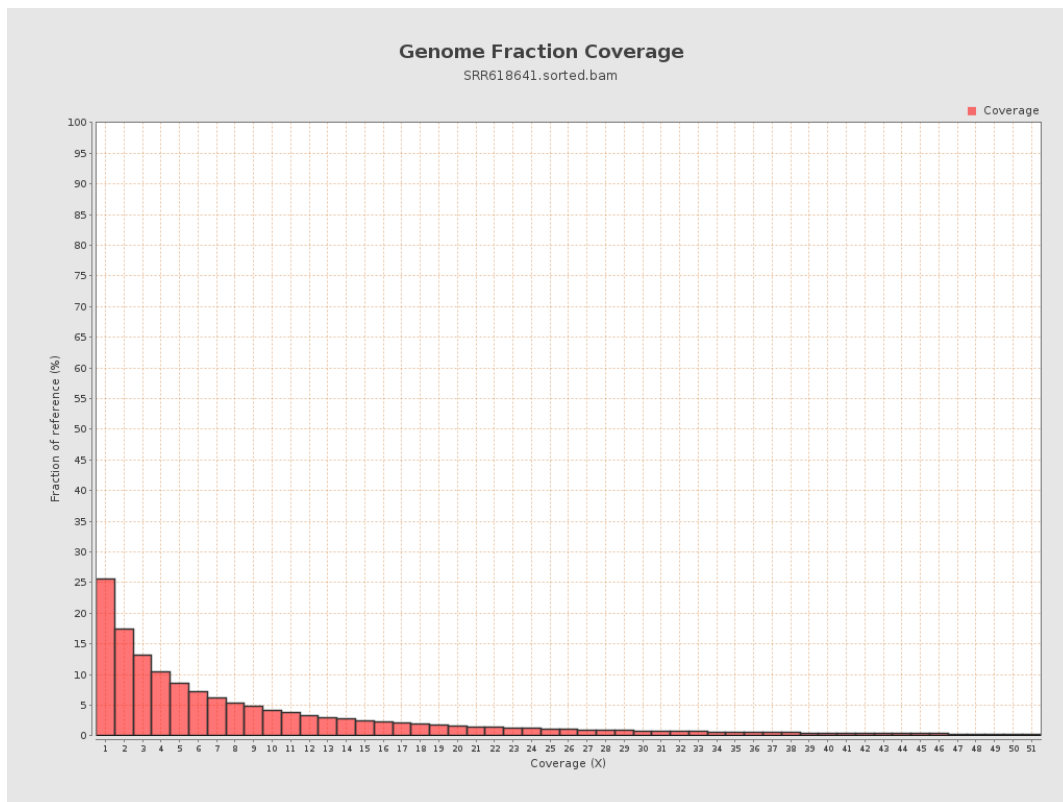
4. Results : Coverage Histogram



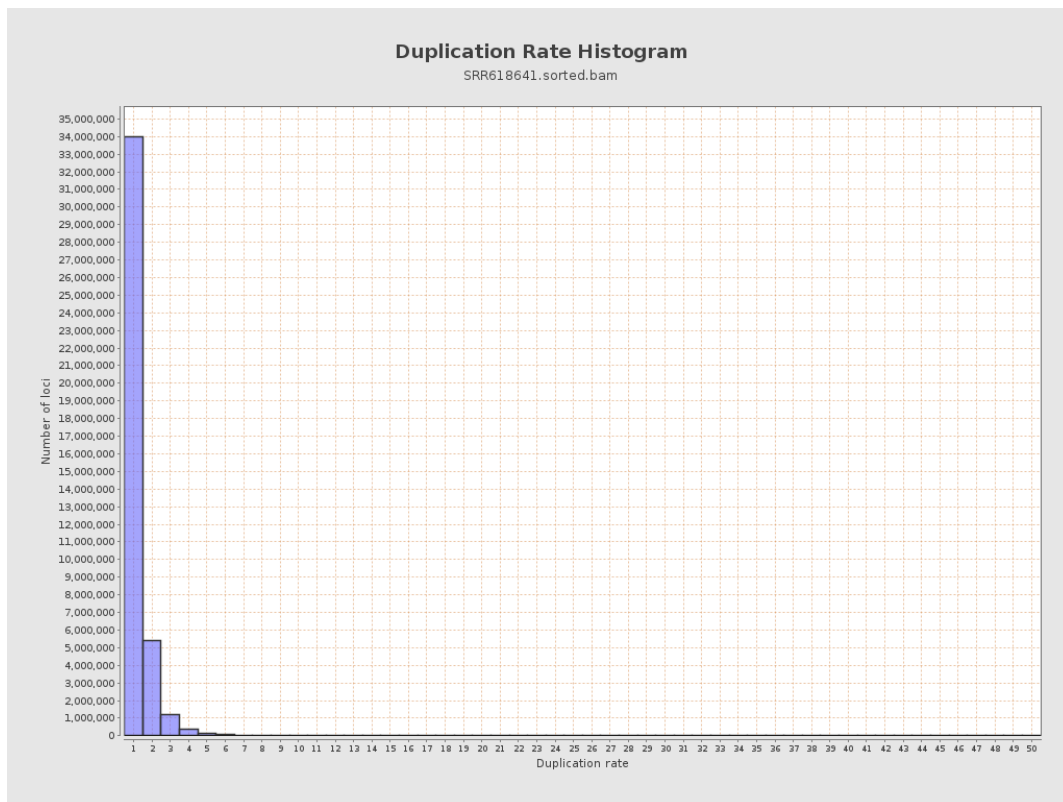
5. Results : Coverage Histogram (0-50X)



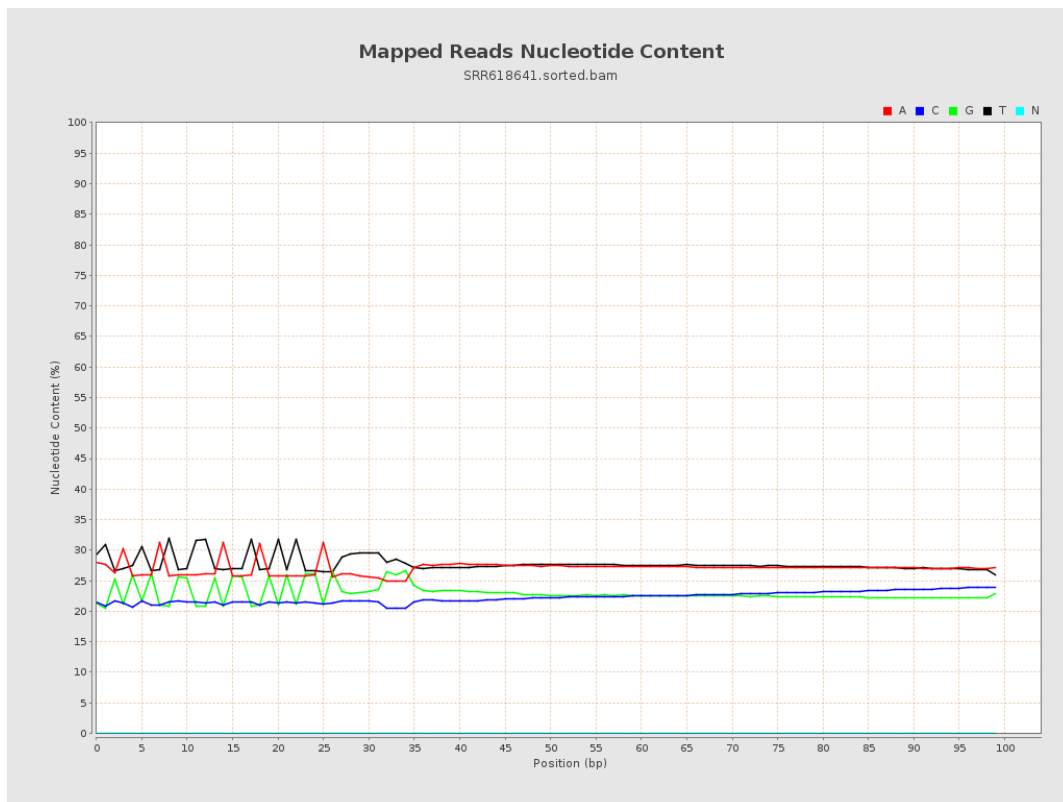
6. Results : Genome Fraction Coverage



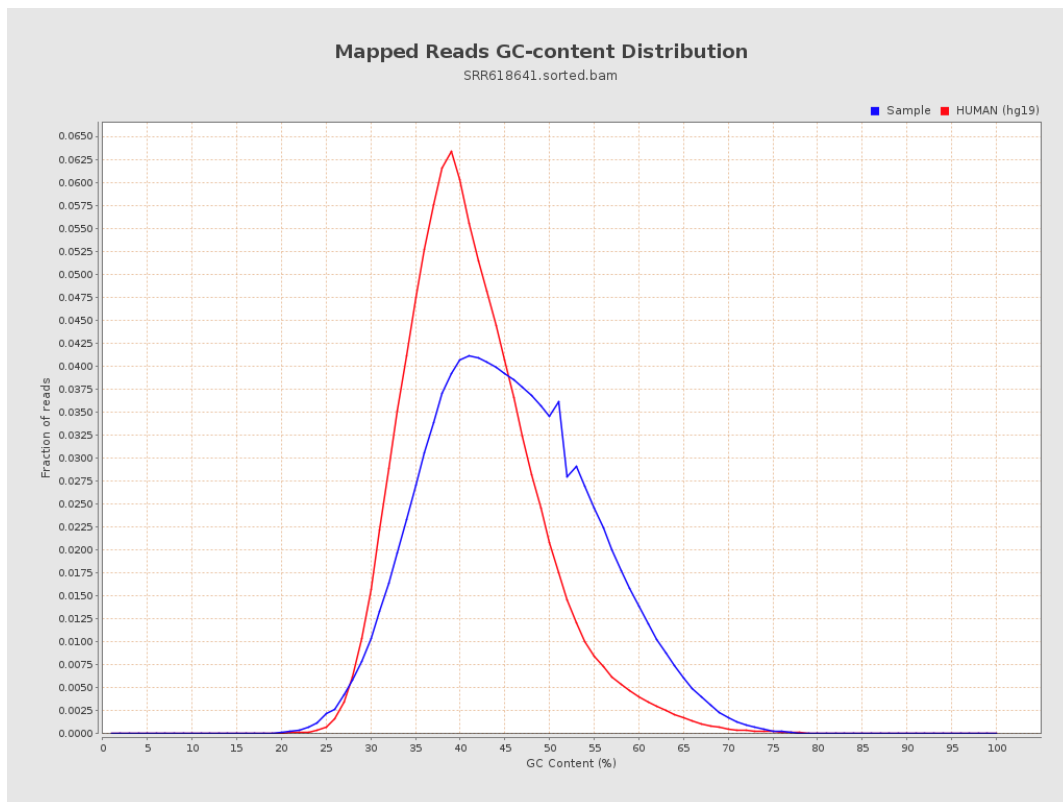
7. Results : Duplication Rate Histogram



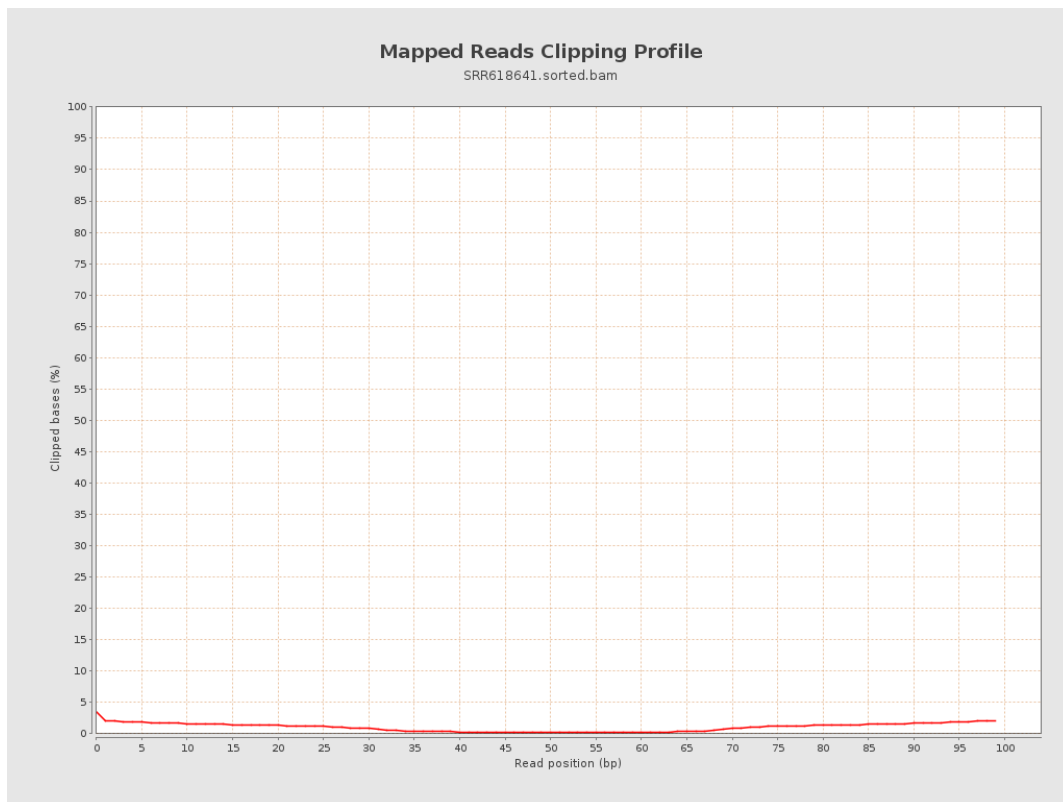
8. Results : Mapped Reads Nucleotide Content



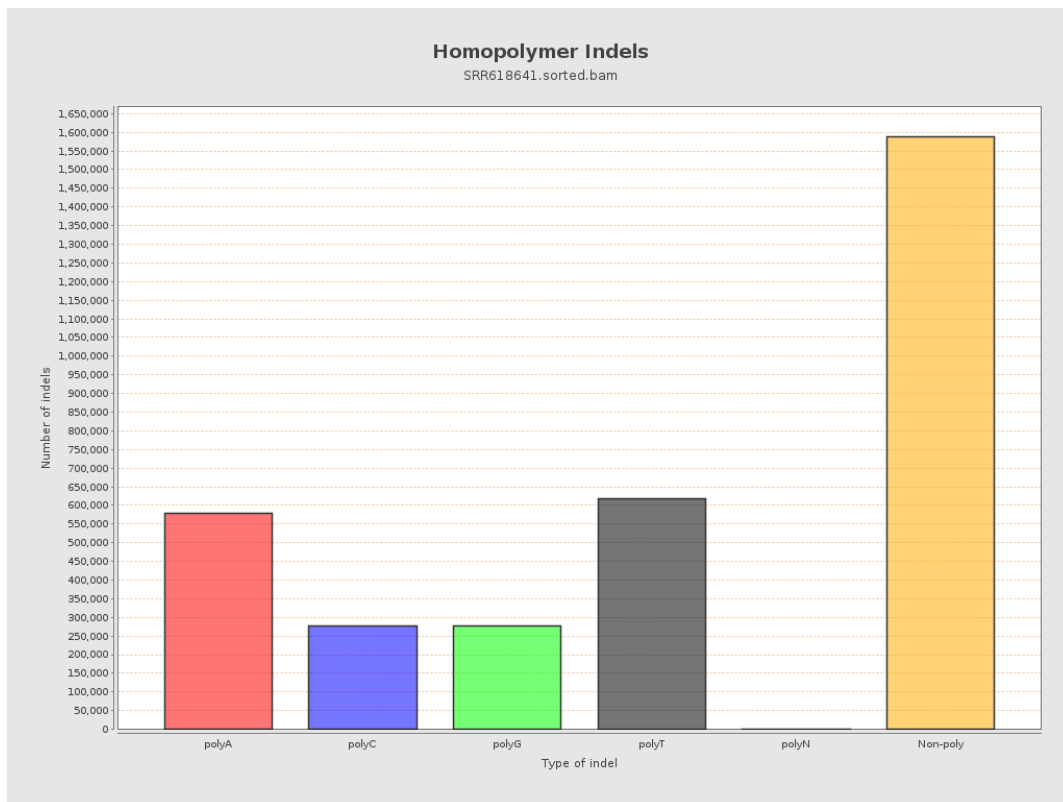
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



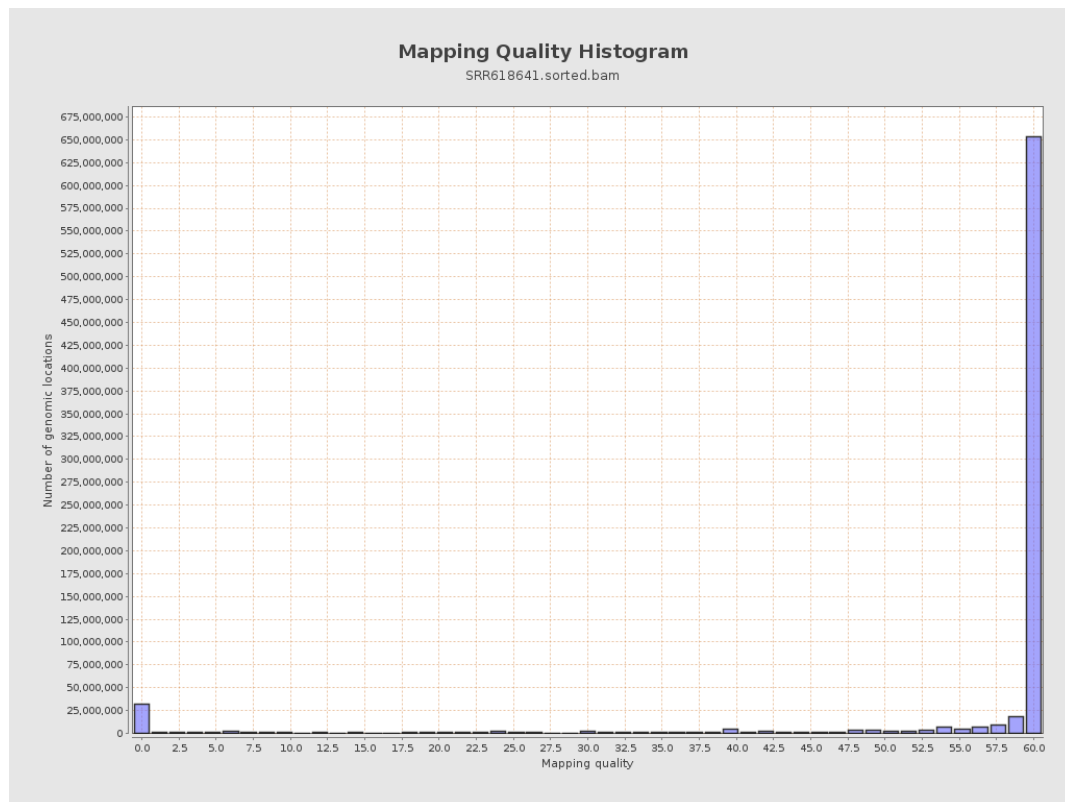
11. Results : Homopolymer Indels



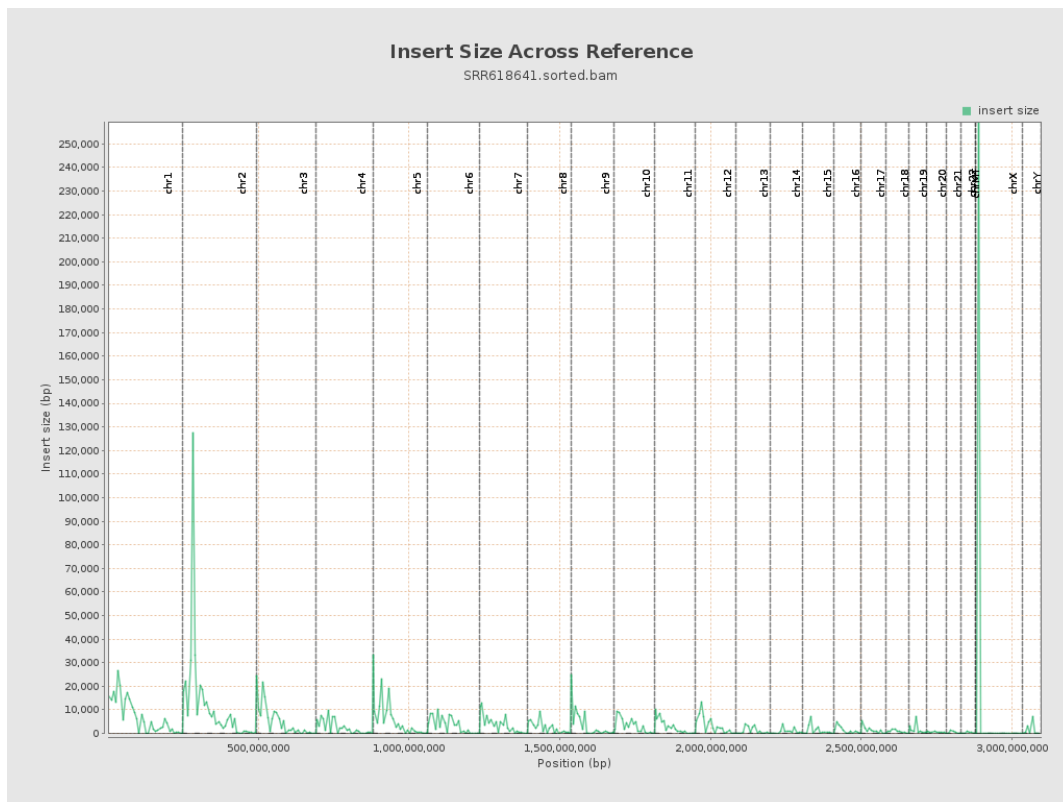
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

