

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 23:46:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618601.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_SRR618601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618601_1.fastq.gz SRR618601_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 23:46:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,638,376
Mapped reads	43,071,438 / 96.49%
Unmapped reads	1,566,938 / 3.51%
Mapped paired reads	43,071,438 / 96.49%
Mapped reads, first in pair	21,750,740 / 48.73%
Mapped reads, second in pair	21,320,698 / 47.76%
Mapped reads, both in pair	42,265,594 / 94.68%
Mapped reads, singletons	805,844 / 1.81%
Secondary alignments	0
Supplementary alignments	141,407 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,205,930 / 20.62%
Duplication rate	18.64%
Clipped reads	9,054,697 / 20.28%

2.2. ACGT Content

Number/percentage of A's	1,120,888,935 / 27.55%
Number/percentage of C's	878,495,951 / 21.59%
Number/percentage of T's	1,132,512,150 / 27.83%
Number/percentage of G's	936,711,423 / 23.02%
Number/percentage of N's	203,116 / 0%

GC Percentage	44.61%
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2.3. Coverage

Mean	1.3153
Standard Deviation	5.1827

2.4. Mapping Quality

Mean Mapping Quality	53.65
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2.5. Insert size

Mean	63,749.07
Standard Deviation	2,509,133.24
P25/Median/P75	168 / 197 / 236

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	50,694,285
Insertions	733,795
Mapped reads with at least one insertion	1.68%
Deletions	2,056,902
Mapped reads with at least one deletion	4.65%
Homopolymer indels	52.82%

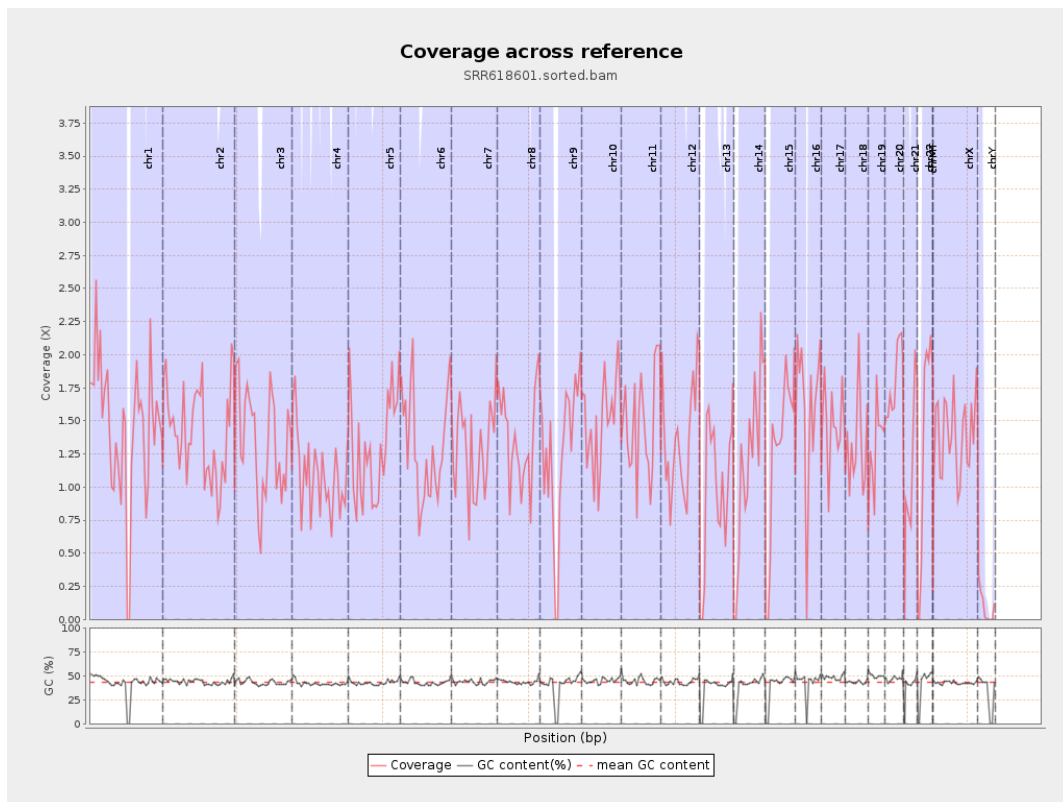
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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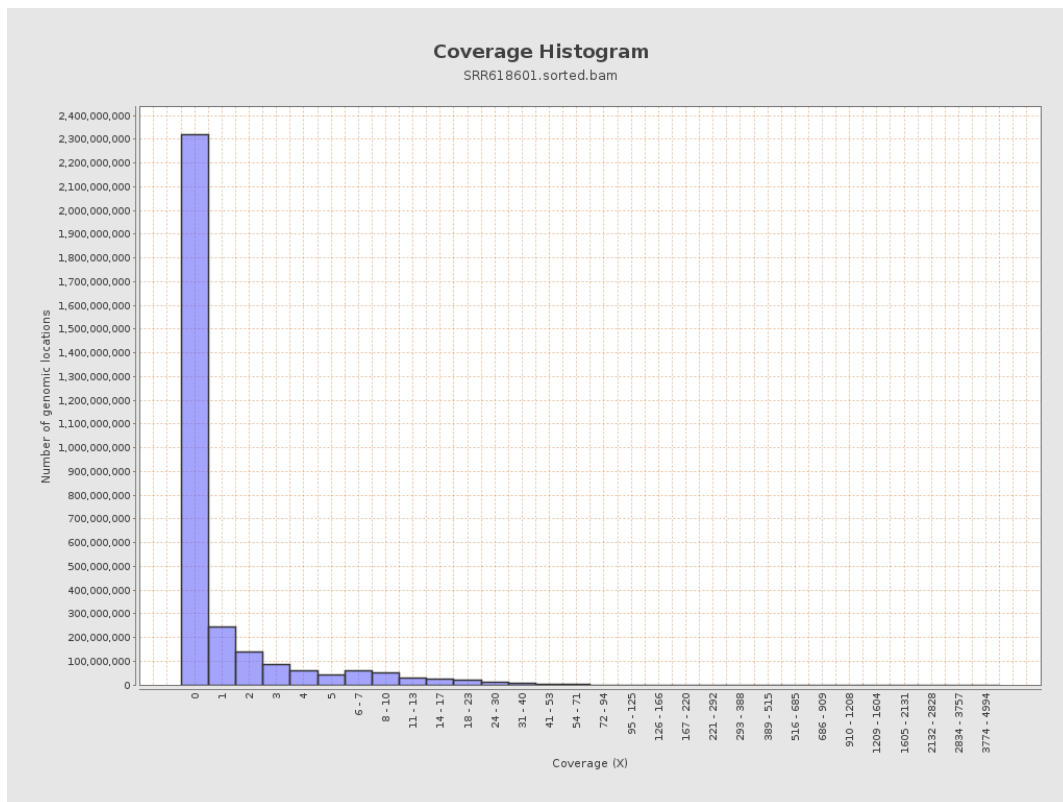
		bases	coverage	deviation
chr1	249250621	358797524	1.4395	5.7722
chr2	243199373	342660473	1.409	6.0919
chr3	198022430	262489838	1.3256	4.3731
chr4	191154276	208338620	1.0899	4.3169
chr5	180915260	237888748	1.3149	4.3704
chr6	171115067	221968442	1.2972	4.5198
chr7	159138663	205707388	1.2926	4.317
chr8	146364022	199676086	1.3642	4.4963
chr9	141213431	176840416	1.2523	5.2965
chr10	135534747	203064464	1.4982	4.933
chr11	135006516	199473851	1.4775	6.023
chr12	133851895	183671887	1.3722	4.6432
chr13	115169878	112277861	0.9749	3.6173
chr14	107349540	127858781	1.1911	4.4198
chr15	102531392	129712067	1.2651	4.6096
chr16	90354753	141946423	1.571	9.9104
chr17	81195210	120257202	1.4811	5.4143
chr18	78077248	101447455	1.2993	5.065
chr19	59128983	77598067	1.3124	5.1655
chr20	63025520	114217952	1.8122	5.8162
chr21	48129895	54261698	1.1274	6.6515
chr22	51304566	69085485	1.3466	5.4798
chrMT	16571	3546	0.214	0.9066
chrX	155270560	216713265	1.3957	4.5865

chrY	59373566	5665034	0.0954	3.4598
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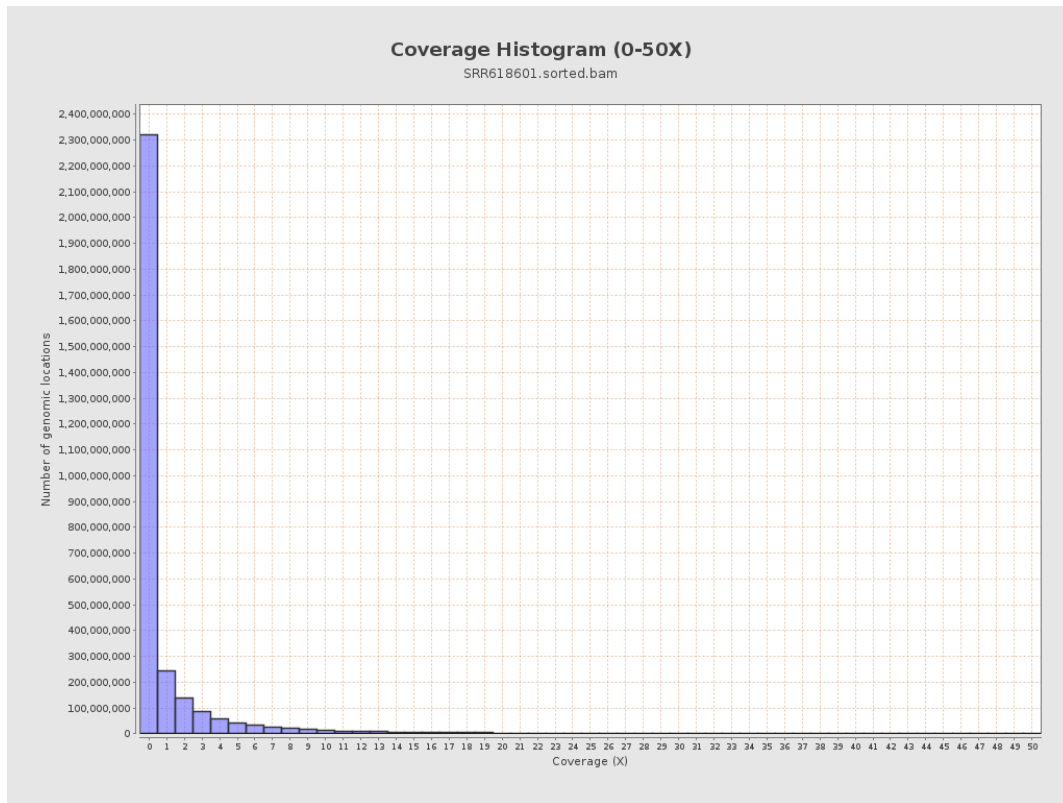
3. Results : Coverage across reference



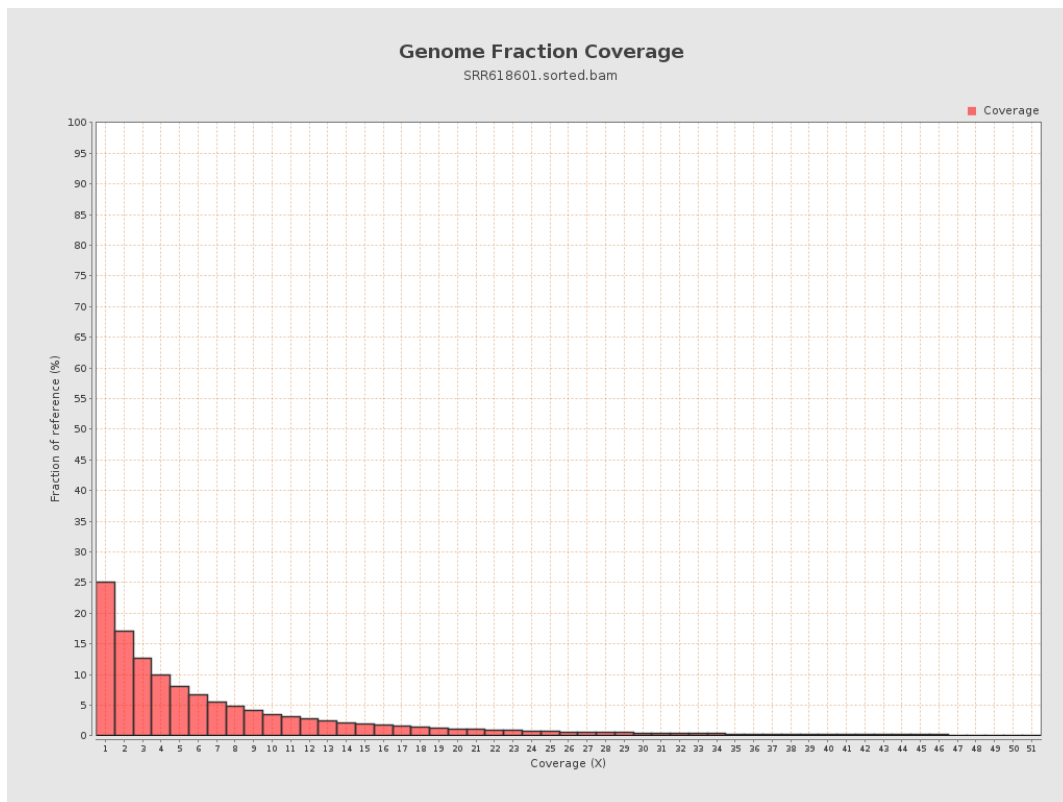
4. Results : Coverage Histogram



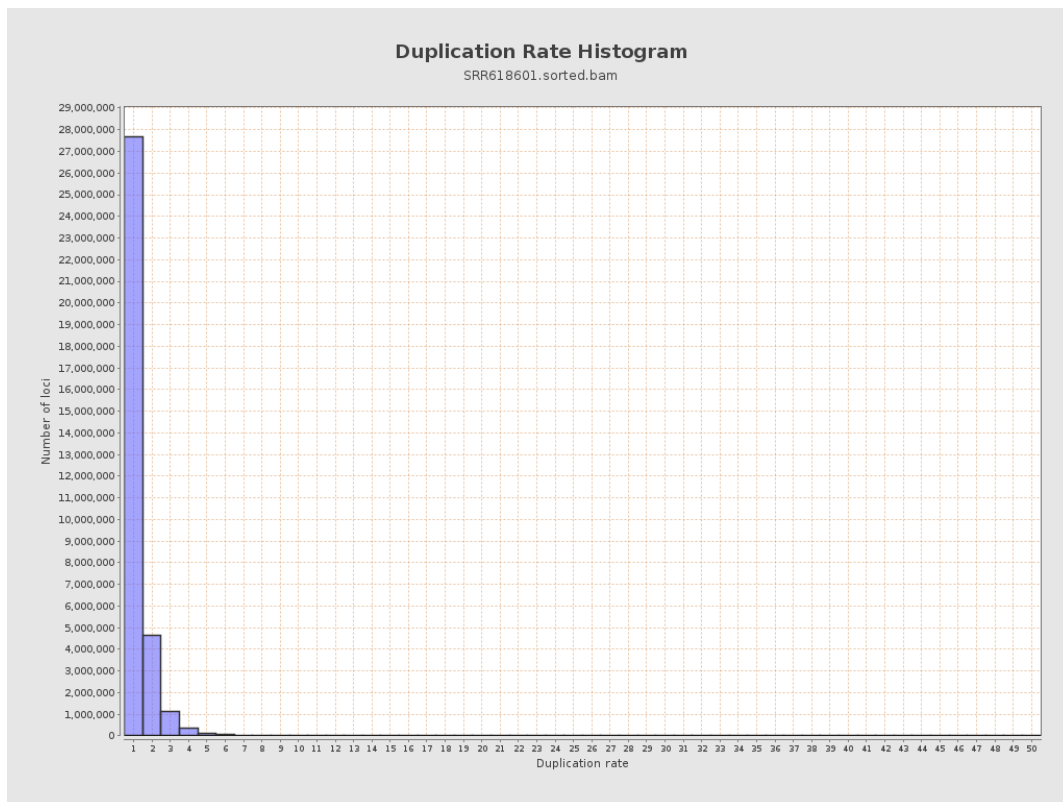
5. Results : Coverage Histogram (0-50X)



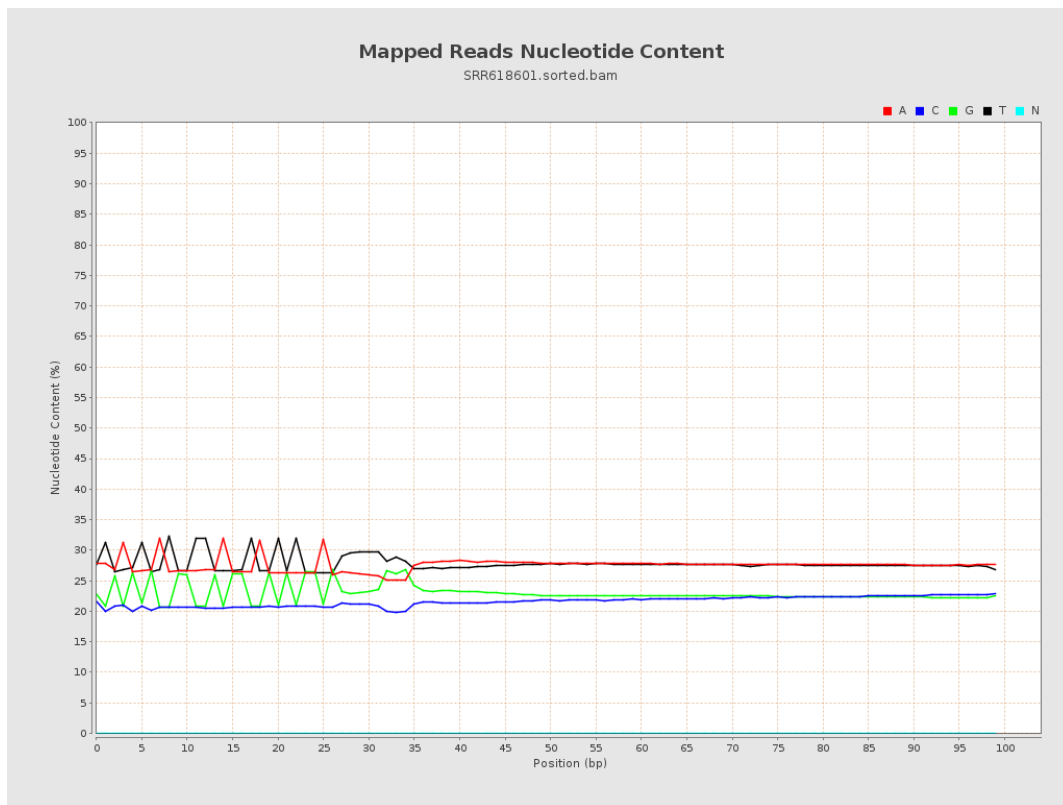
6. Results : Genome Fraction Coverage



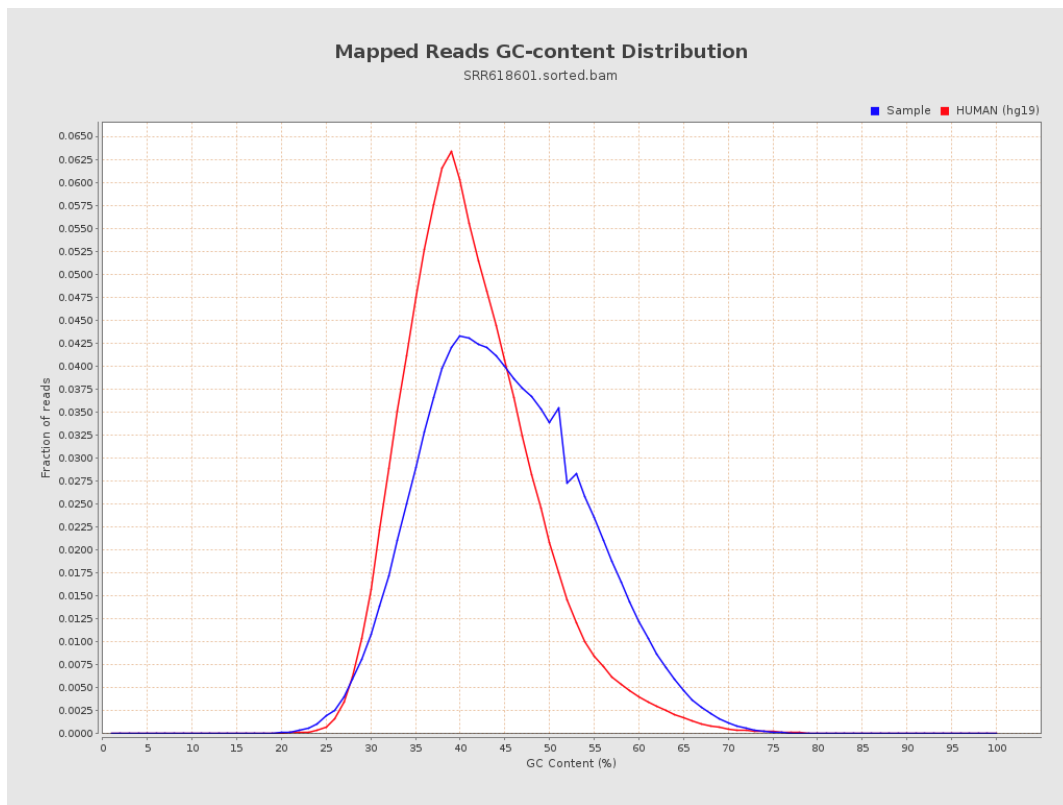
7. Results : Duplication Rate Histogram



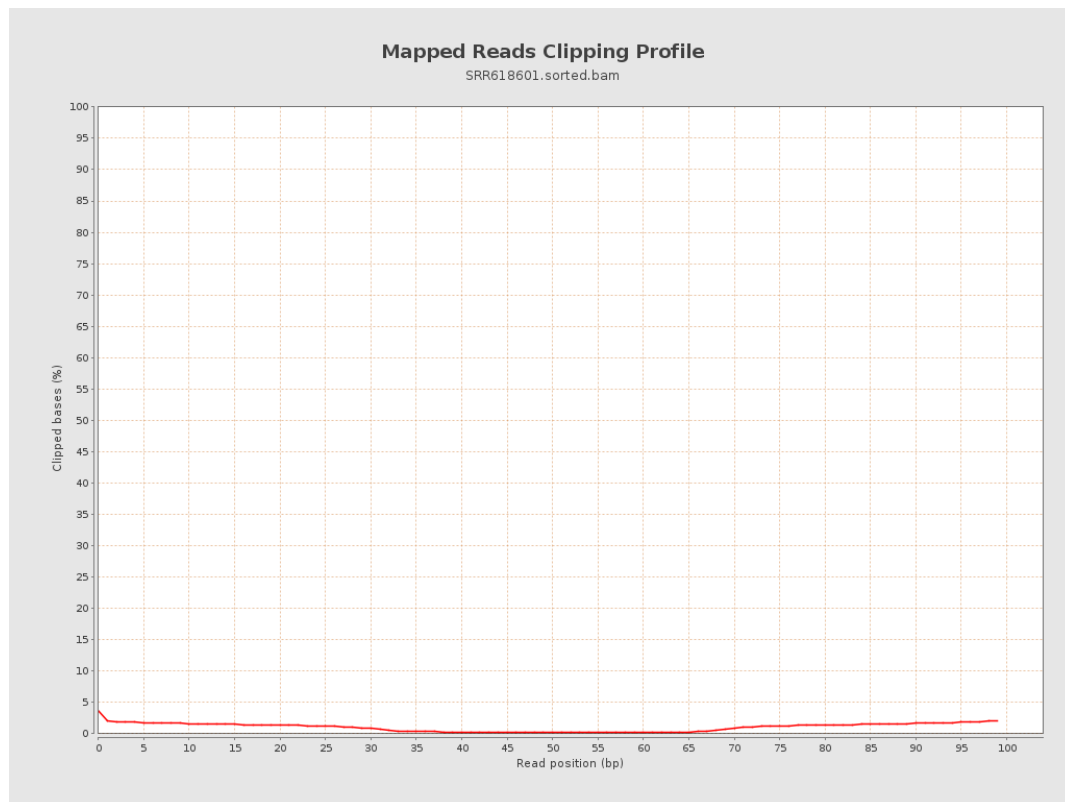
8. Results : Mapped Reads Nucleotide Content



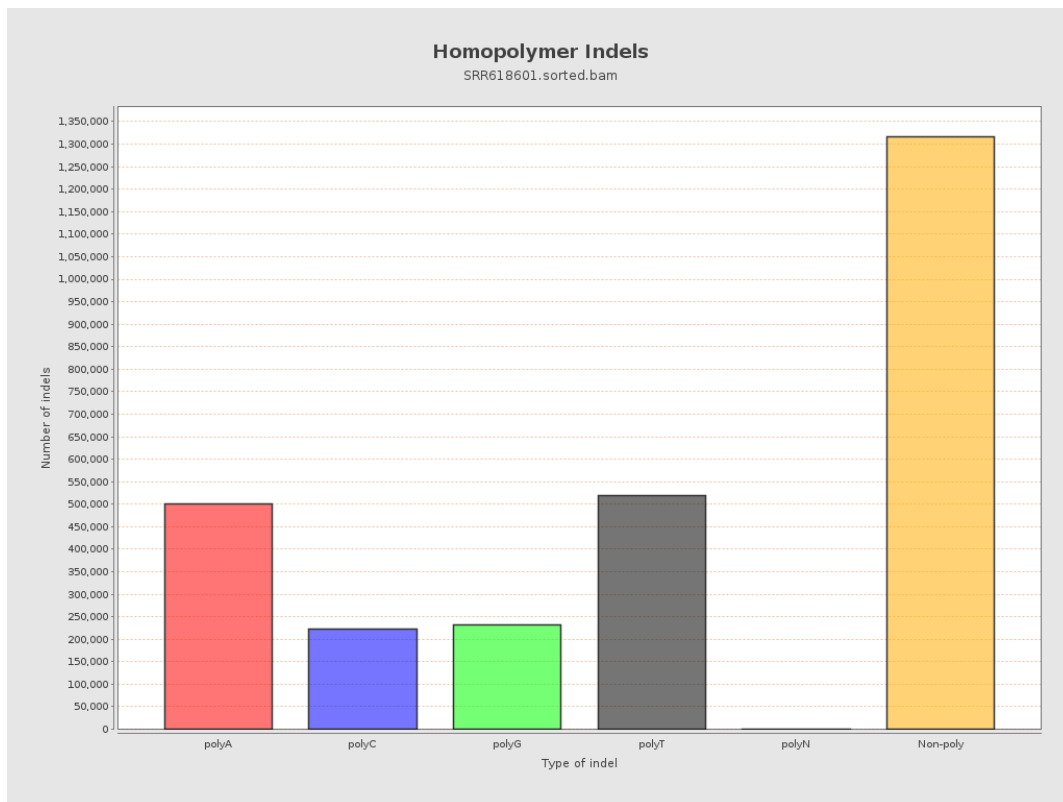
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



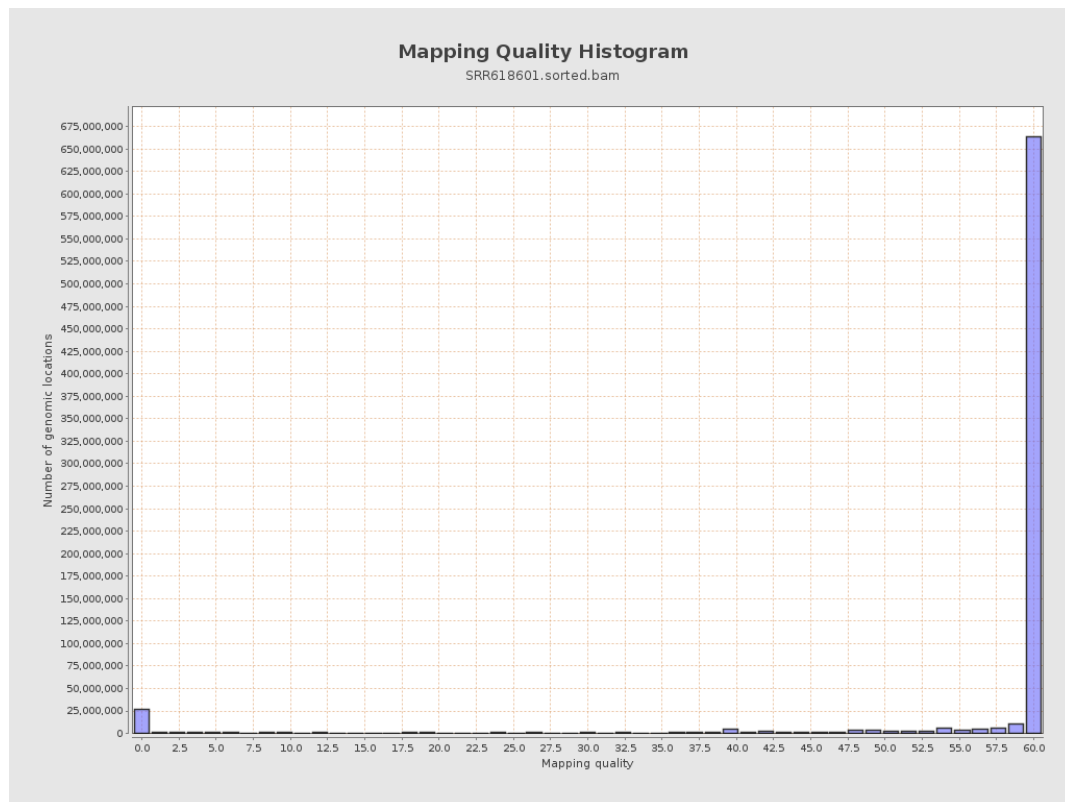
11. Results : Homopolymer Indels



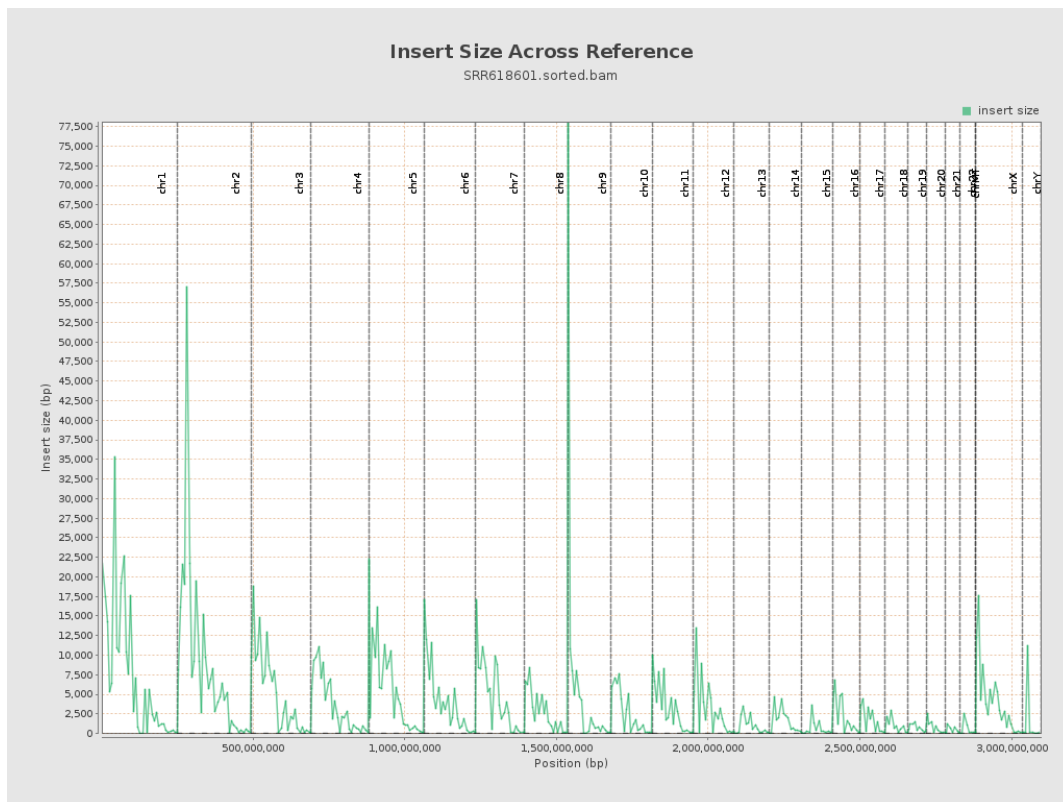
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

