

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 03:40:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618606.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_SRR618606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618606_1.fastq.gz SRR618606_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 03:40:06 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,822,476
Mapped reads	43,137,706 / 96.24%
Unmapped reads	1,684,770 / 3.76%
Mapped paired reads	43,137,706 / 96.24%
Mapped reads, first in pair	21,736,498 / 48.49%
Mapped reads, second in pair	21,401,208 / 47.75%
Mapped reads, both in pair	42,416,442 / 94.63%
Mapped reads, singletons	721,264 / 1.61%
Secondary alignments	0
Supplementary alignments	132,317 / 0.3%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	9,372,854 / 20.91%
Duplication rate	18.71%
Clipped reads	9,672,977 / 21.58%

2.2. ACGT Content

Number/percentage of A's	1,103,725,242 / 27.22%
Number/percentage of C's	879,043,476 / 21.68%
Number/percentage of T's	1,119,910,536 / 27.62%
Number/percentage of G's	951,227,103 / 23.46%
Number/percentage of N's	319,262 / 0.01%

GC Percentage	45.14%
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2.3. Coverage

Mean	1.3106
Standard Deviation	4.8255

2.4. Mapping Quality

Mean Mapping Quality	53.23
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2.5. Insert size

Mean	63,259.84
Standard Deviation	2,508,772.47
P25/Median/P75	159 / 189 / 229

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	46,195,329
Insertions	726,402
Mapped reads with at least one insertion	1.66%
Deletions	2,079,939
Mapped reads with at least one deletion	4.7%
Homopolymer indels	53.09%

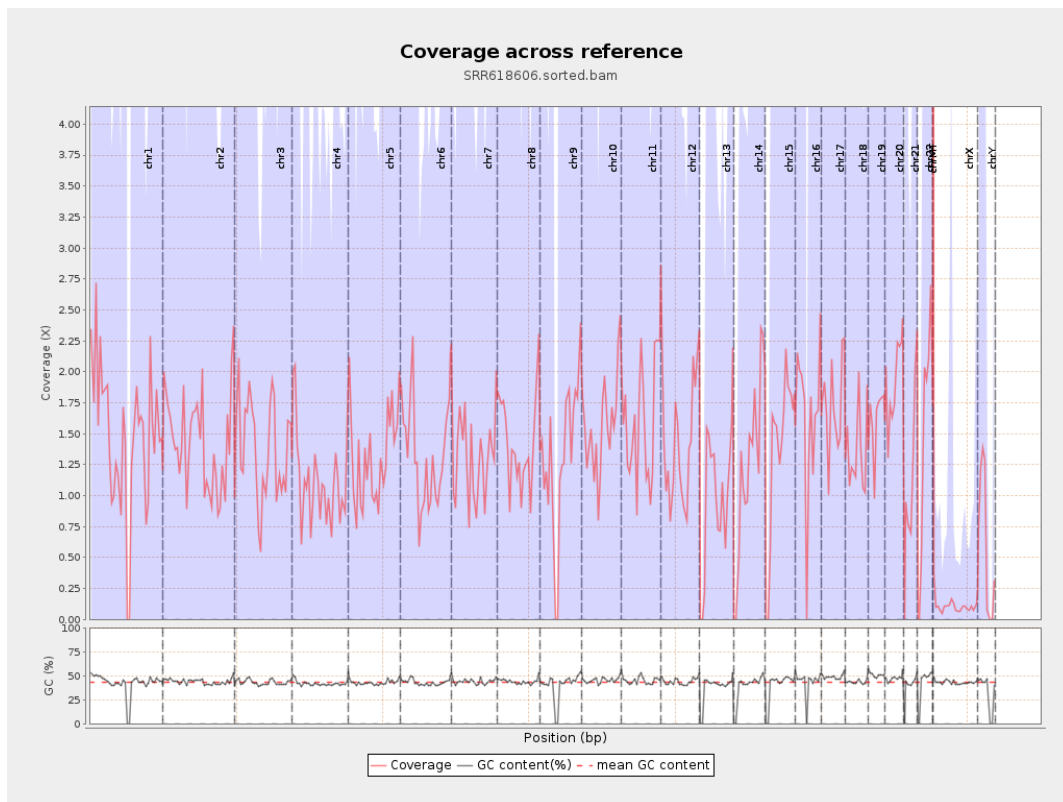
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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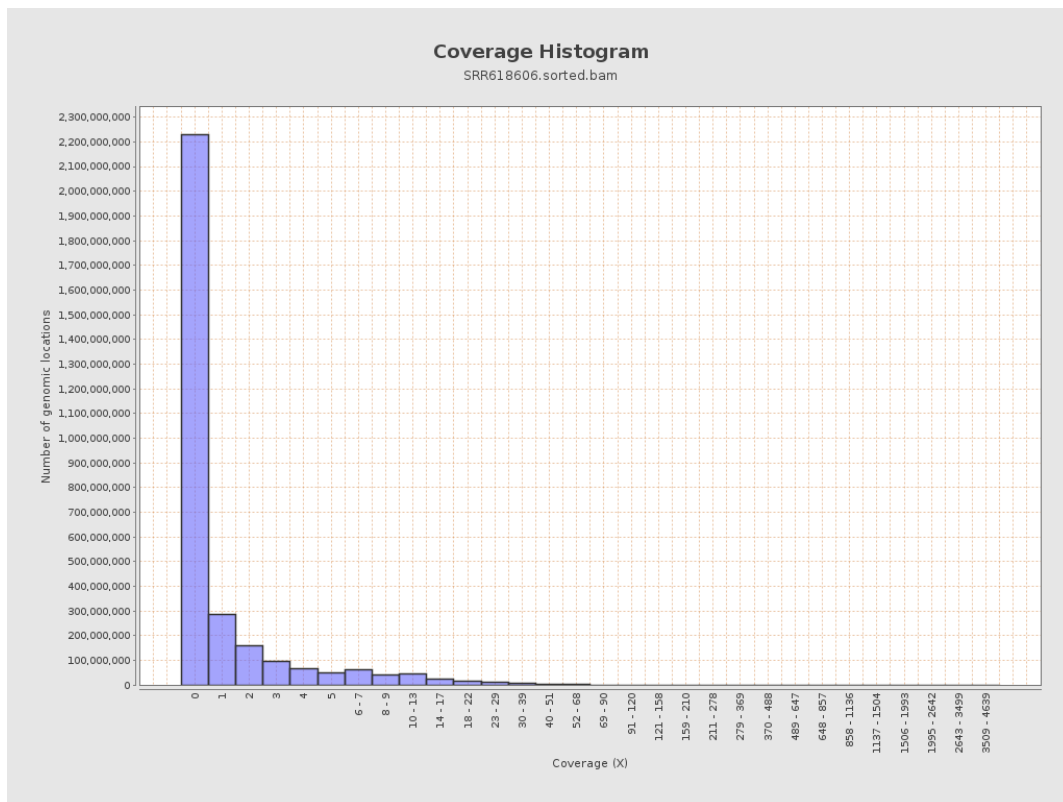
		bases	coverage	deviation
chr1	249250621	366801352	1.4716	5.4042
chr2	243199373	347399689	1.4285	5.7512
chr3	198022430	271109409	1.3691	3.9605
chr4	191154276	211729271	1.1076	3.9249
chr5	180915260	239912348	1.3261	3.9549
chr6	171115067	225834100	1.3198	4.0837
chr7	159138663	209700990	1.3177	4.0749
chr8	146364022	207751722	1.4194	4.2792
chr9	141213431	184631398	1.3075	5.5903
chr10	135534747	210309227	1.5517	4.5558
chr11	135006516	214538594	1.5891	5.6142
chr12	133851895	192131781	1.4354	4.2937
chr13	115169878	112022197	0.9727	3.2113
chr14	107349540	132734912	1.2365	4.3488
chr15	102531392	139078329	1.3564	4.2057
chr16	90354753	147544133	1.6329	9.3903
chr17	81195210	138831332	1.7098	5.0645
chr18	78077248	104095579	1.3332	5.5321
chr19	59128983	94858916	1.6043	5.2572
chr20	63025520	120498113	1.9119	5.3185
chr21	48129895	55851590	1.1604	6.1263
chr22	51304566	75268611	1.4671	4.9675
chrMT	16571	330297	19.9322	62.3745
chrX	155270560	17012134	0.1096	1.3958

chrY	59373566	37089723	0.6247	4.2301
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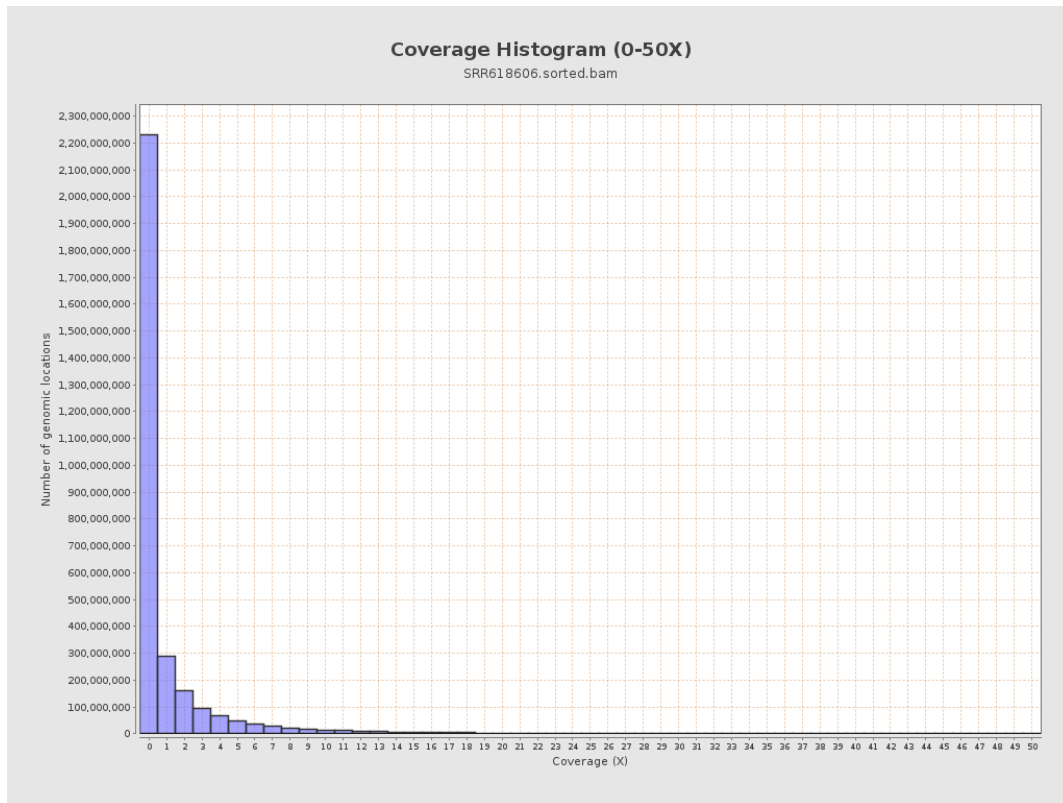
3. Results : Coverage across reference



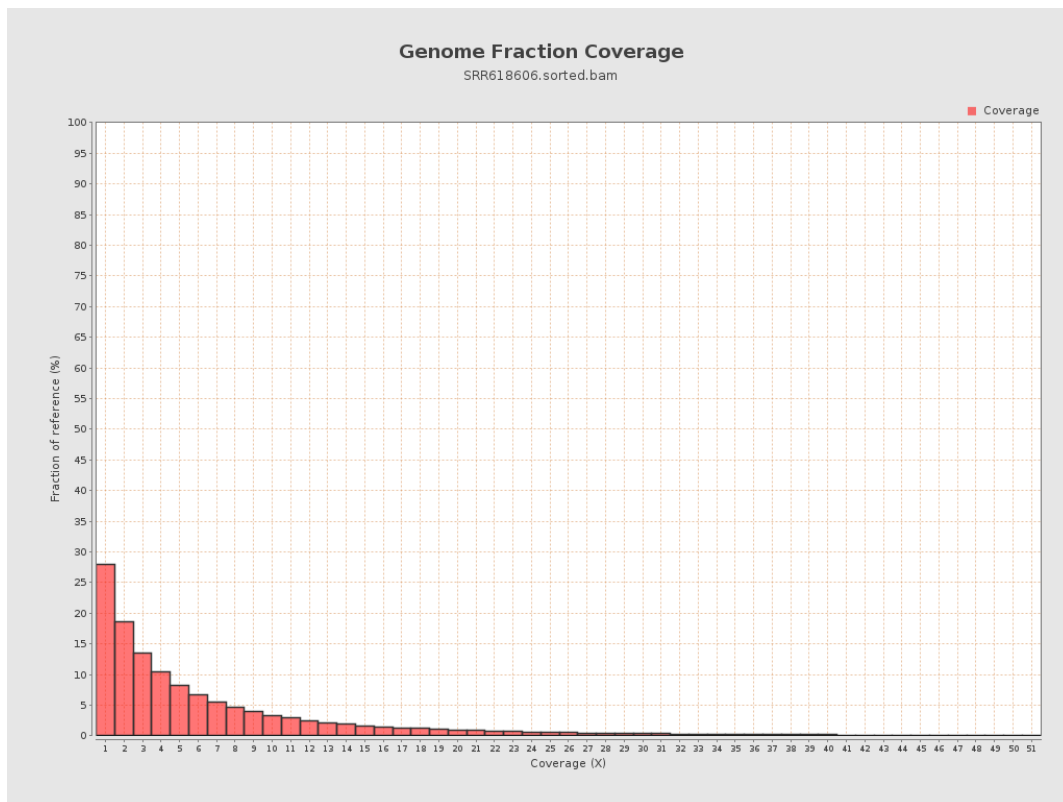
4. Results : Coverage Histogram



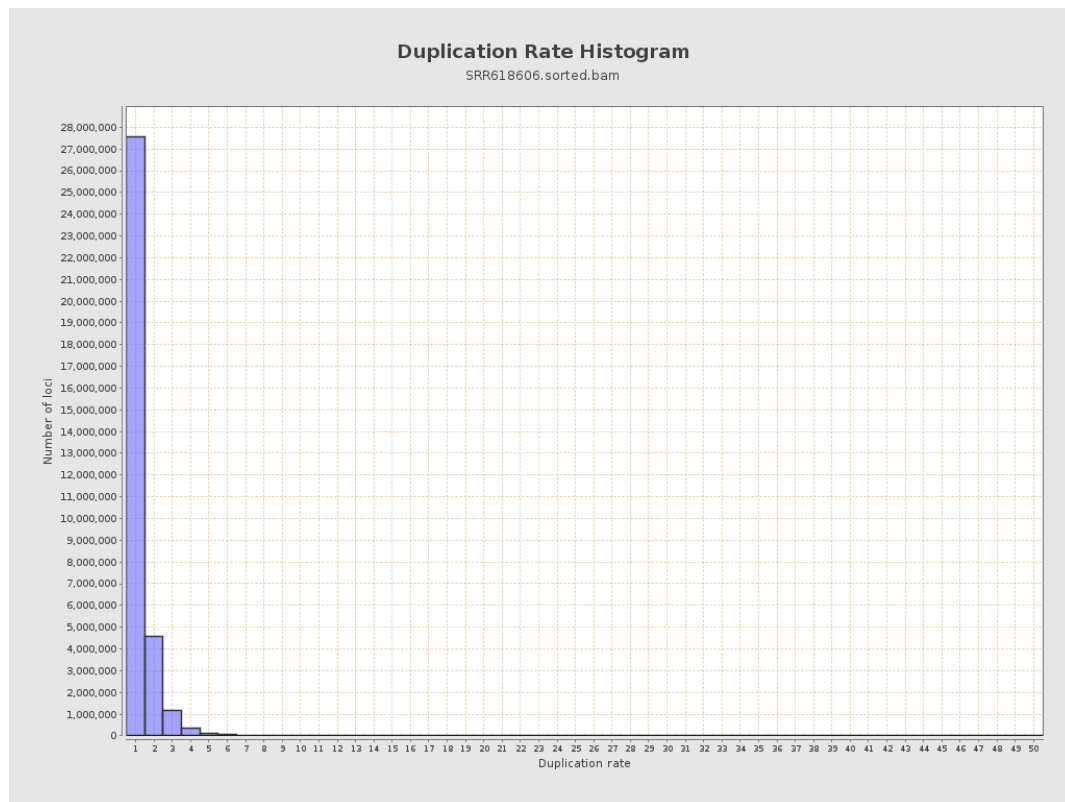
5. Results : Coverage Histogram (0-50X)



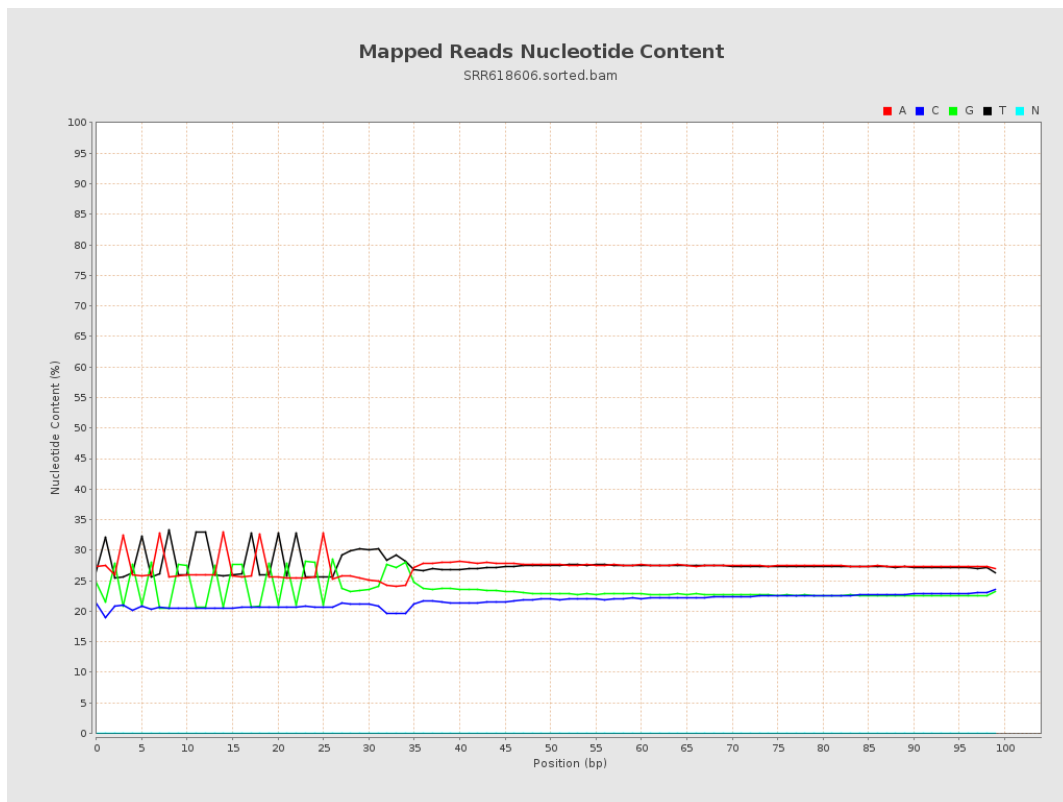
6. Results : Genome Fraction Coverage



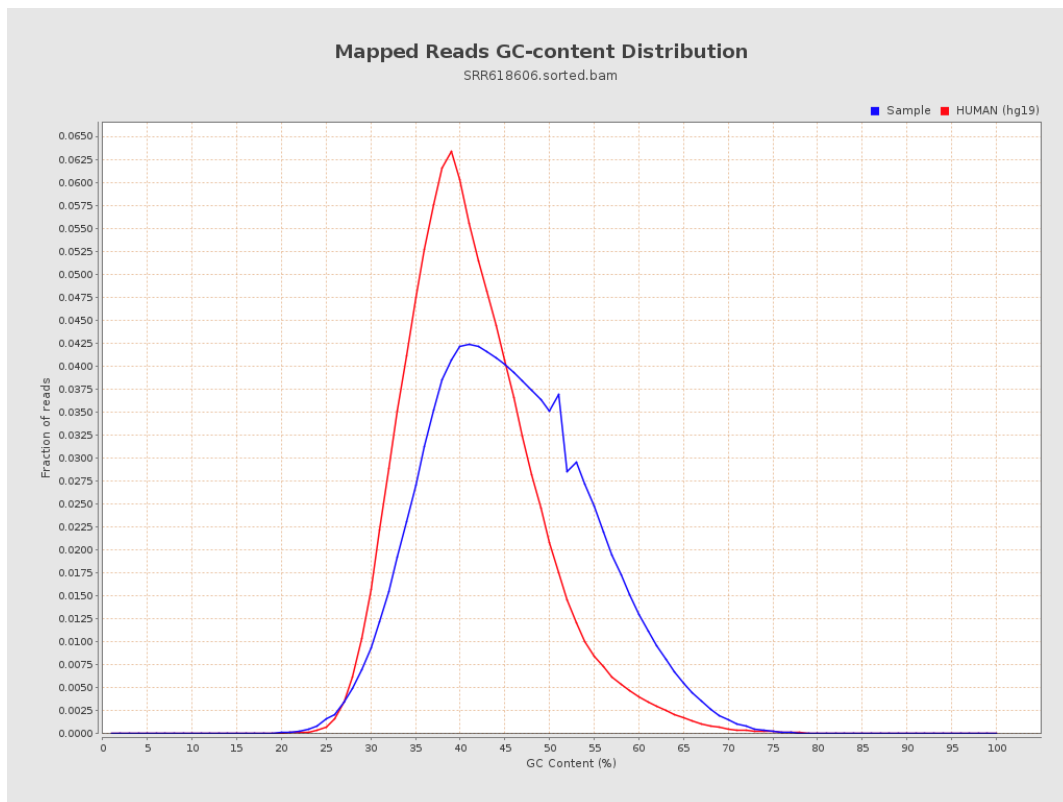
7. Results : Duplication Rate Histogram



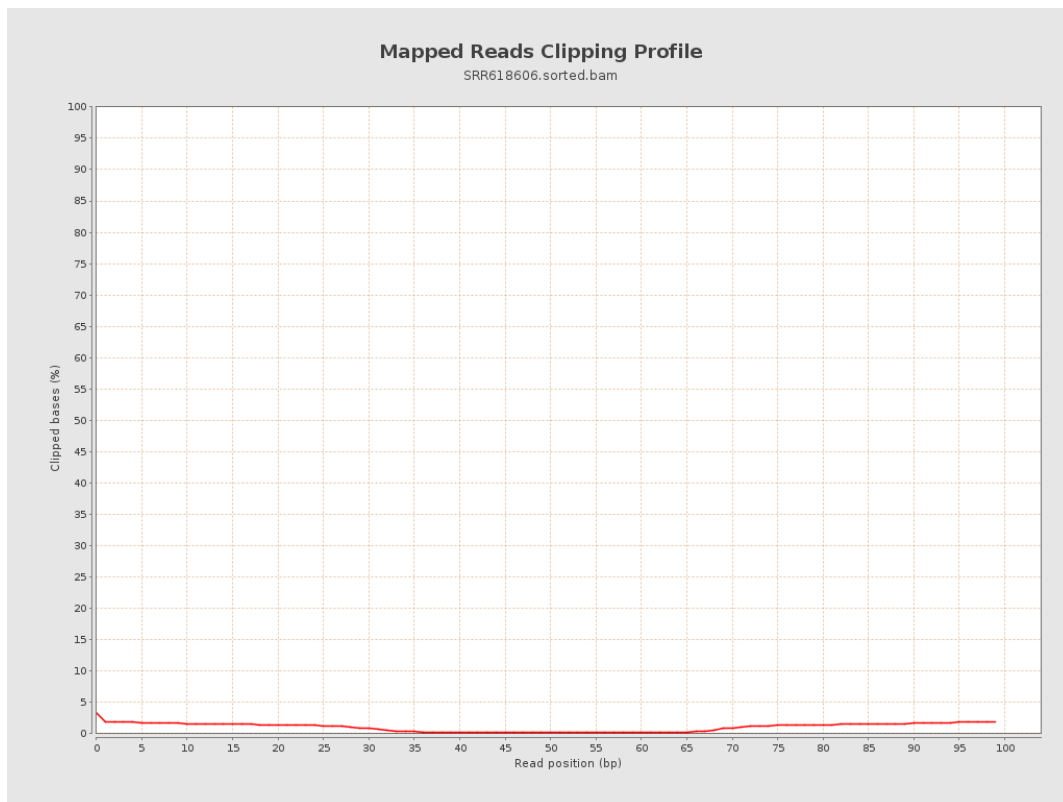
8. Results : Mapped Reads Nucleotide Content



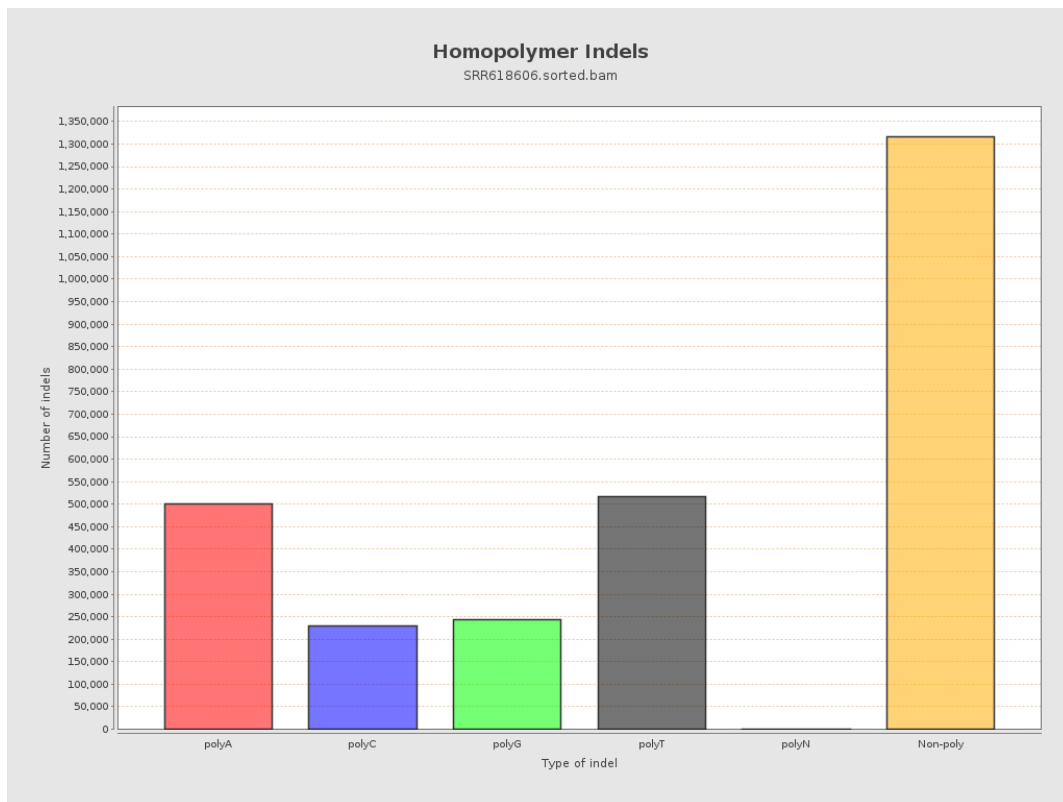
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



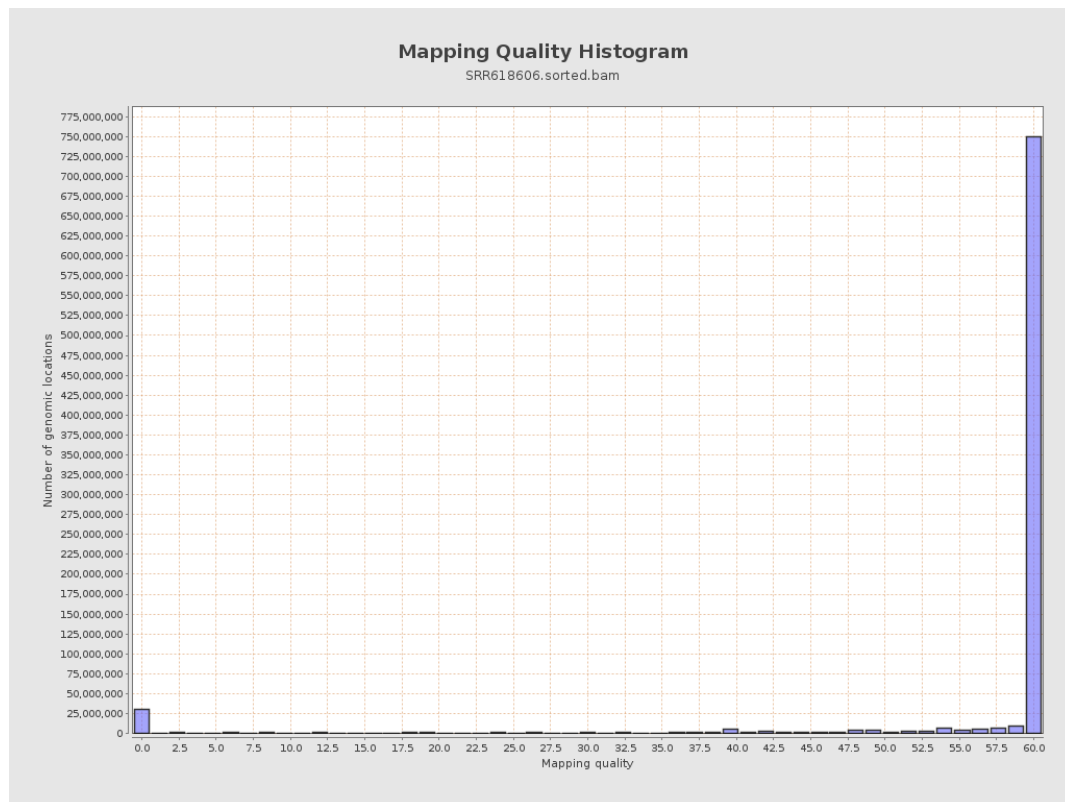
11. Results : Homopolymer Indels



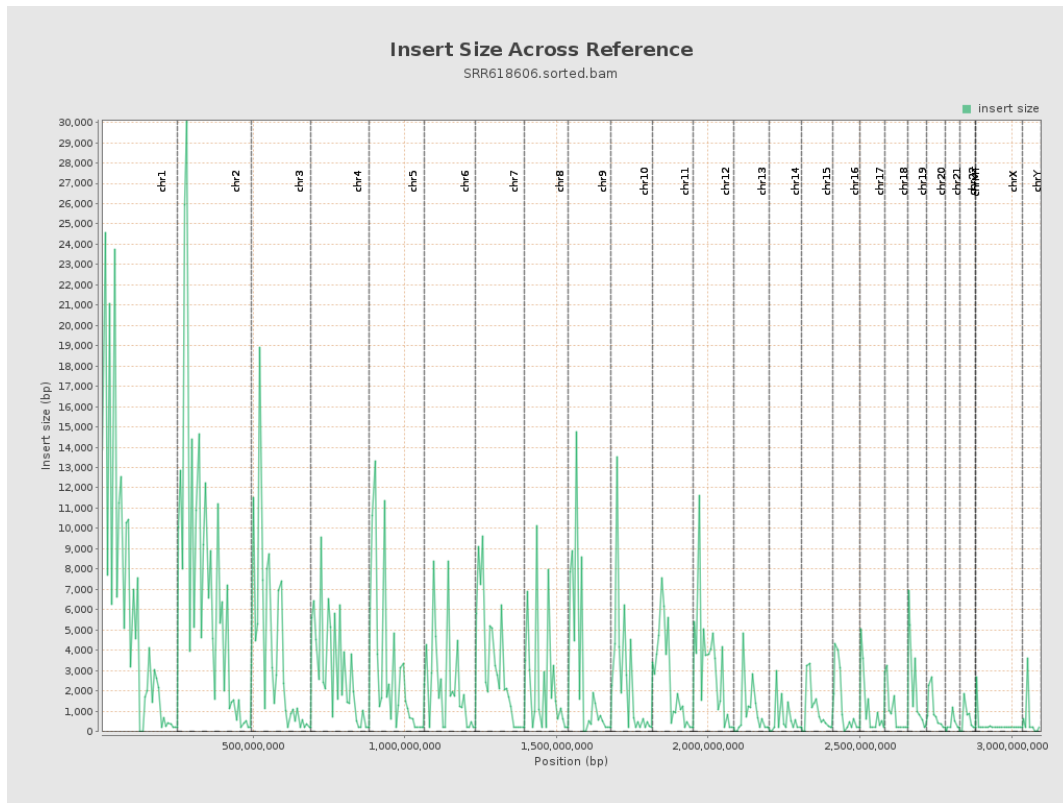
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

