

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 23:02:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618600.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_SRR618600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618600_1.fastq.gz SRR618600_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 23:02:55 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	45,291,598
Mapped reads	43,504,994 / 96.06%
Unmapped reads	1,786,604 / 3.94%
Mapped paired reads	43,504,994 / 96.06%
Mapped reads, first in pair	21,961,161 / 48.49%
Mapped reads, second in pair	21,543,833 / 47.57%
Mapped reads, both in pair	42,851,206 / 94.61%
Mapped reads, singletons	653,788 / 1.44%
Secondary alignments	0
Supplementary alignments	144,224 / 0.32%
Read min/max/mean length	30 / 101 / 100.13
Duplicated reads (estimated)	11,849,581 / 26.16%
Duplication rate	23.83%
Clipped reads	9,829,274 / 21.7%

2.2. ACGT Content

Number/percentage of A's	1,125,555,285 / 27.21%
Number/percentage of C's	906,266,173 / 21.91%
Number/percentage of T's	1,133,664,624 / 27.41%
Number/percentage of G's	970,846,071 / 23.47%
Number/percentage of N's	196,770 / 0%

GC Percentage	45.38%
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2.3. Coverage

Mean	1.3373
Standard Deviation	5.377

2.4. Mapping Quality

Mean Mapping Quality	52.91
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2.5. Insert size

Mean	65,959.61
Standard Deviation	2,550,705.95
P25/Median/P75	191 / 217 / 256

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	66,176,897
Insertions	793,487
Mapped reads with at least one insertion	1.79%
Deletions	2,478,999
Mapped reads with at least one deletion	5.54%
Homopolymer indels	53.41%

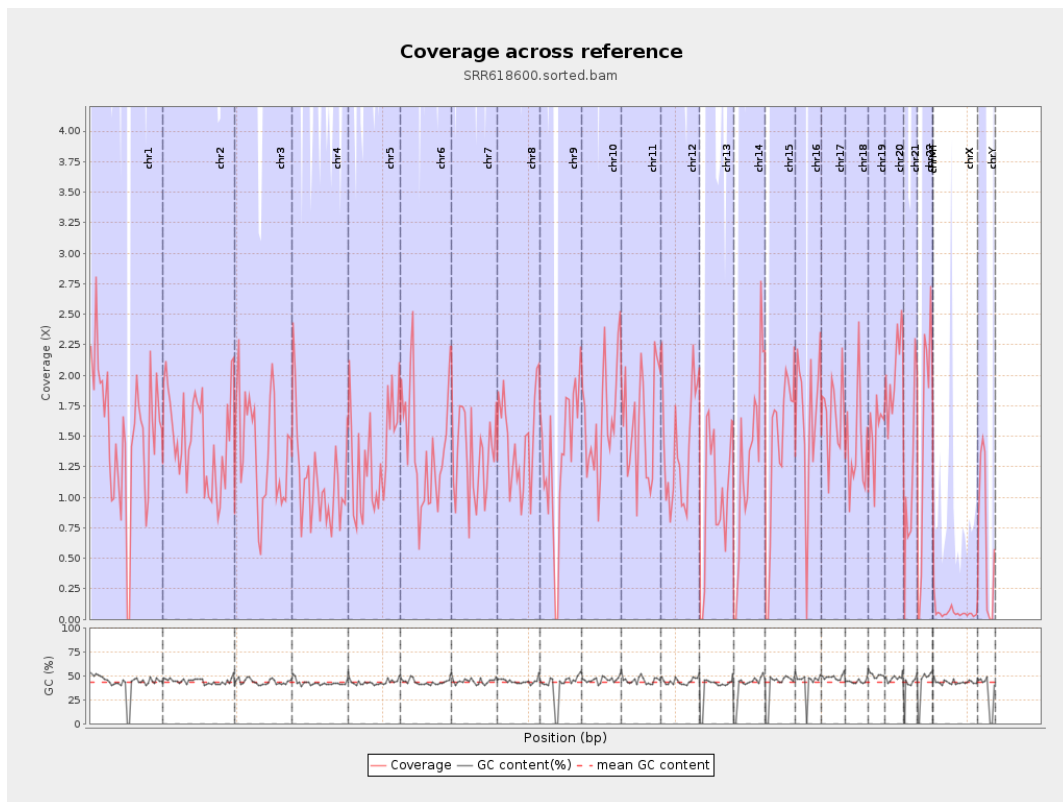
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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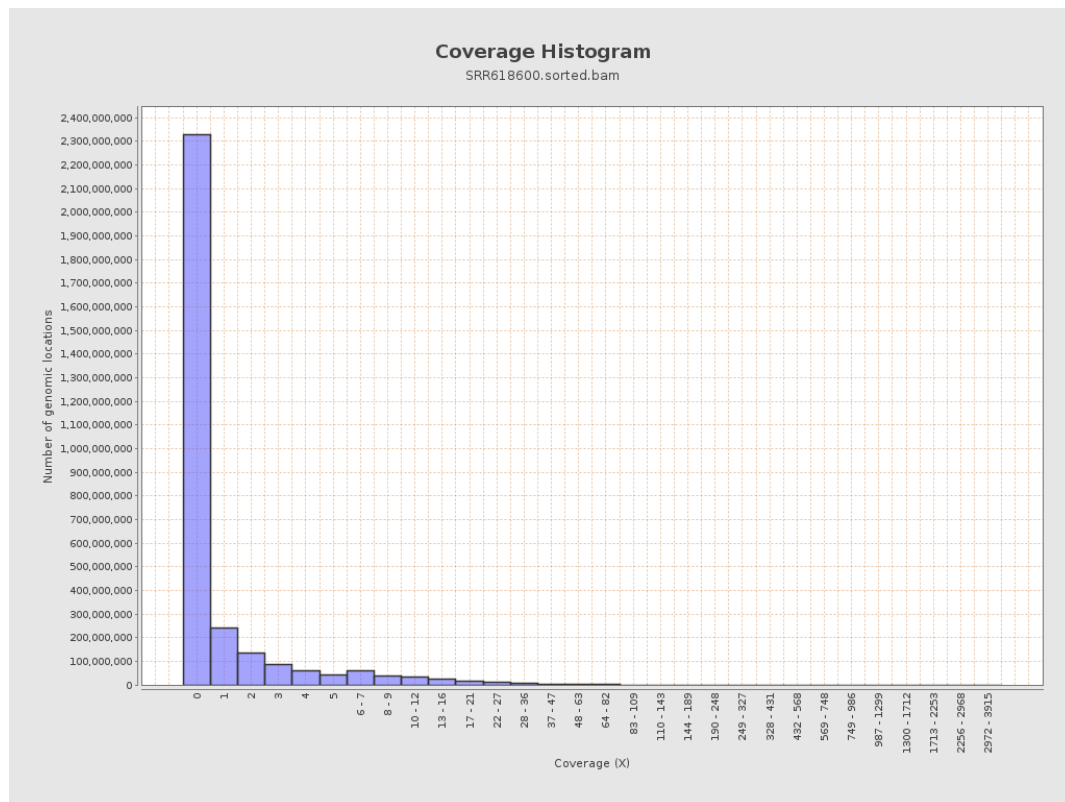
		bases	coverage	deviation
chr1	249250621	376864942	1.512	6.5831
chr2	243199373	359395498	1.4778	5.9694
chr3	198022430	272005353	1.3736	4.6663
chr4	191154276	217106159	1.1358	4.3524
chr5	180915260	242598757	1.341	4.5216
chr6	171115067	238466802	1.3936	4.9031
chr7	159138663	213578727	1.3421	4.61
chr8	146364022	212850501	1.4543	4.8934
chr9	141213431	186223598	1.3187	5.5287
chr10	135534747	218794378	1.6143	5.5345
chr11	135006516	215731595	1.5979	6.3371
chr12	133851895	189803656	1.418	4.9788
chr13	115169878	115166823	1	3.804
chr14	107349540	140001669	1.3042	4.8594
chr15	102531392	142722033	1.392	5.1759
chr16	90354753	148223809	1.6405	8.249
chr17	81195210	137340771	1.6915	6.151
chr18	78077248	108863592	1.3943	5.6281
chr19	59128983	90804887	1.5357	6.0301
chr20	63025520	128229201	2.0346	6.5113
chr21	48129895	56603442	1.1761	7.7703
chr22	51304566	77189424	1.5045	6.026
chrMT	16571	19426	1.1723	3.9225
chrX	155270560	9169457	0.0591	1.1798

chrY	59373566	42063461	0.7085	4.7807
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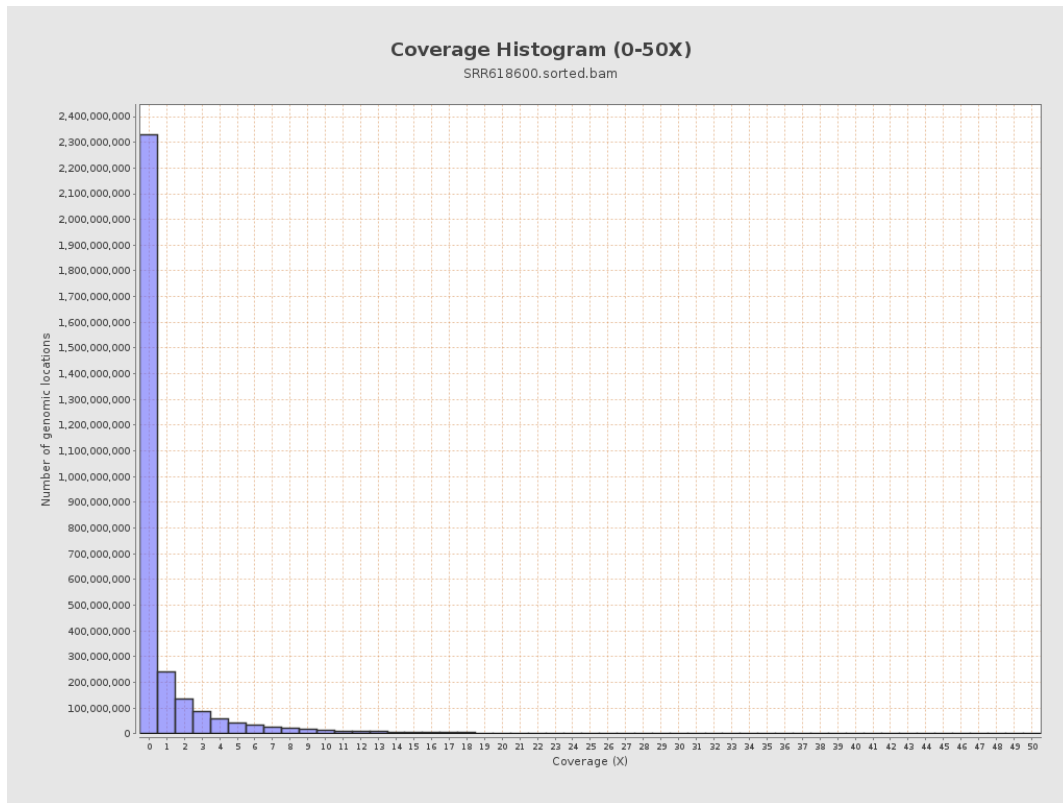
3. Results : Coverage across reference



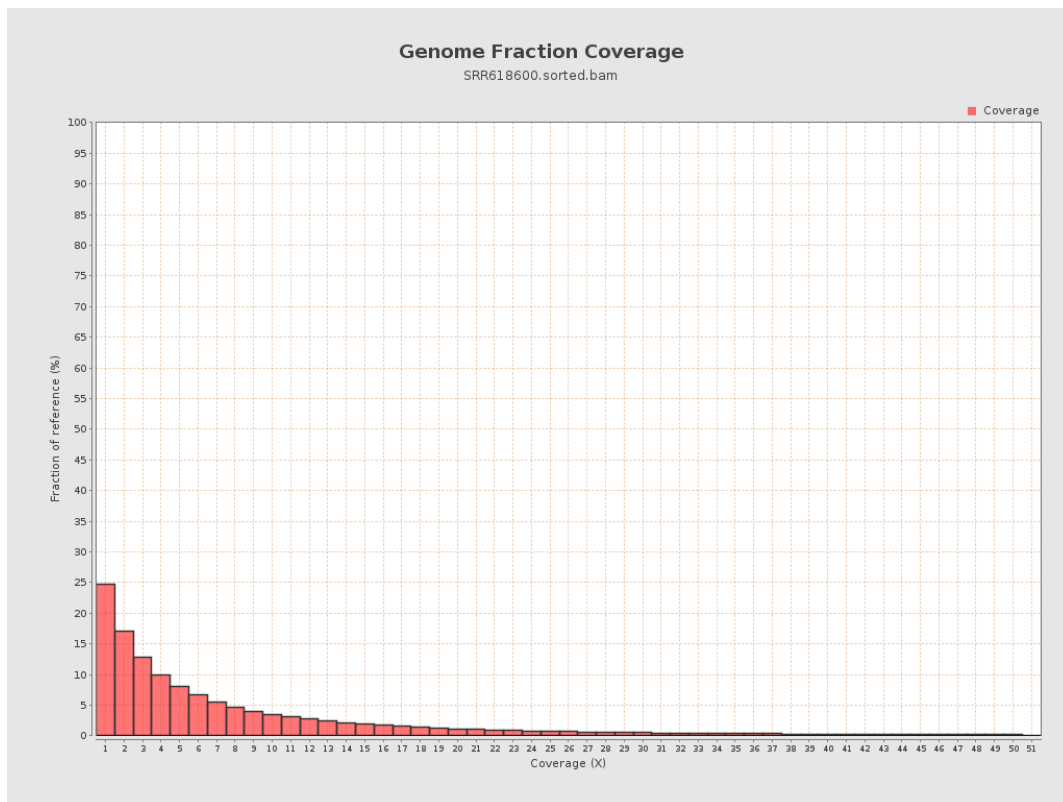
4. Results : Coverage Histogram



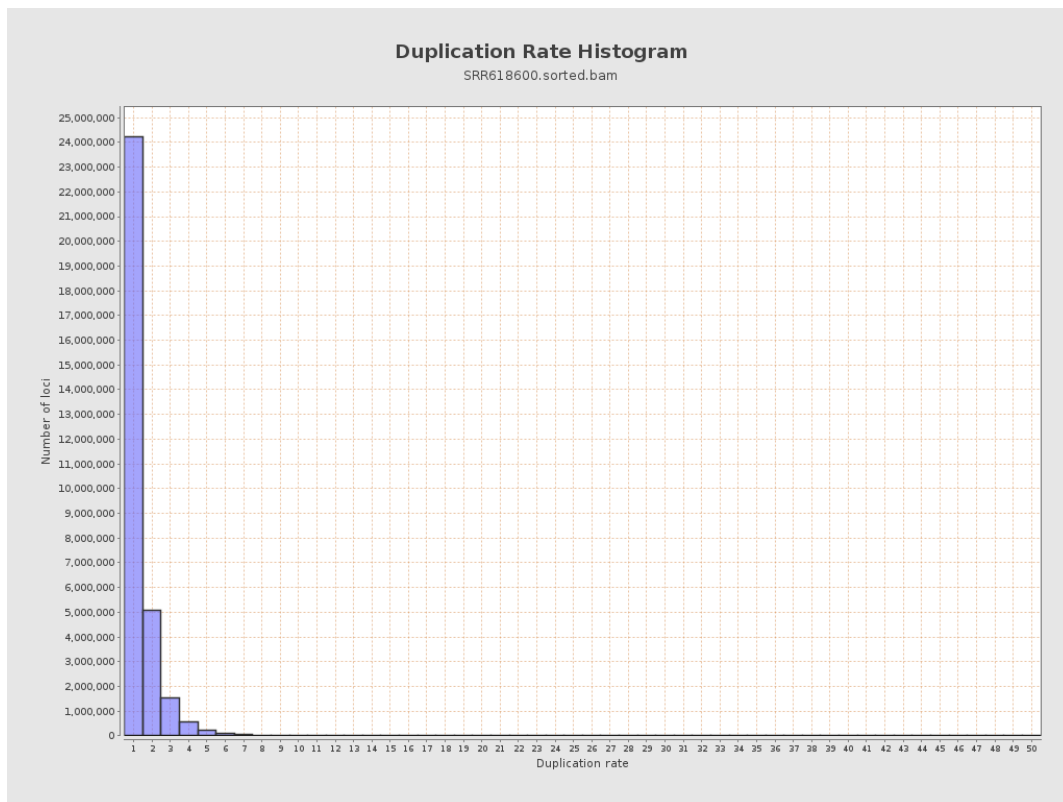
5. Results : Coverage Histogram (0-50X)



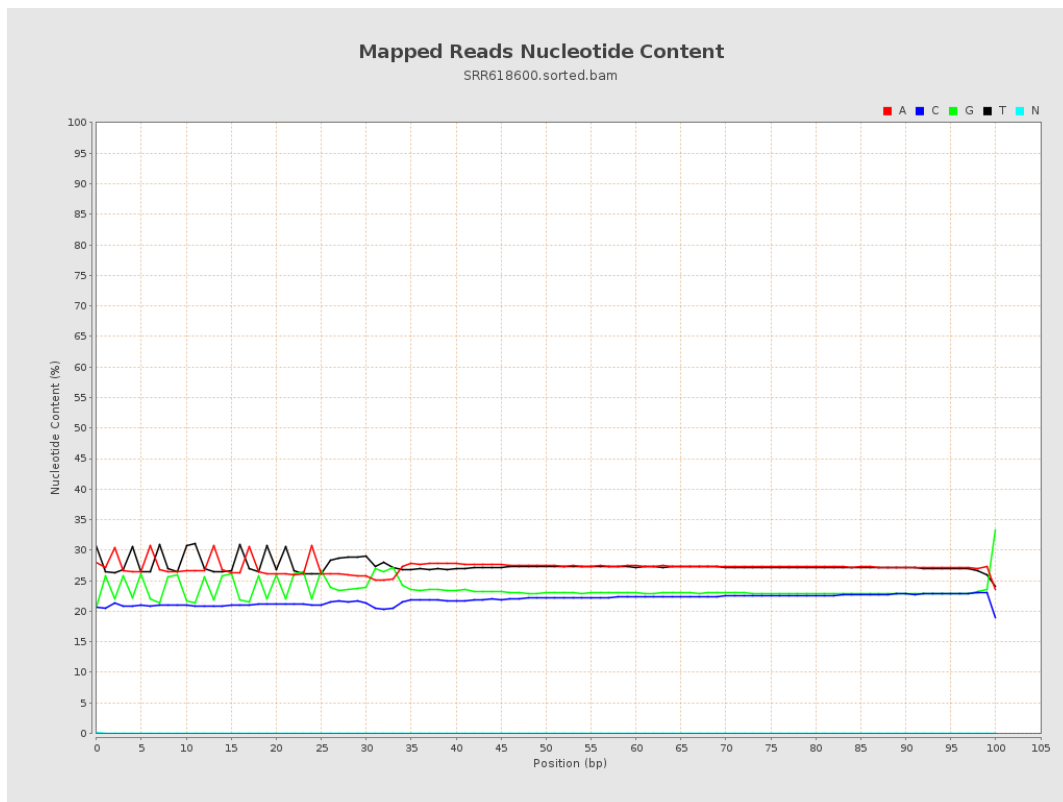
6. Results : Genome Fraction Coverage



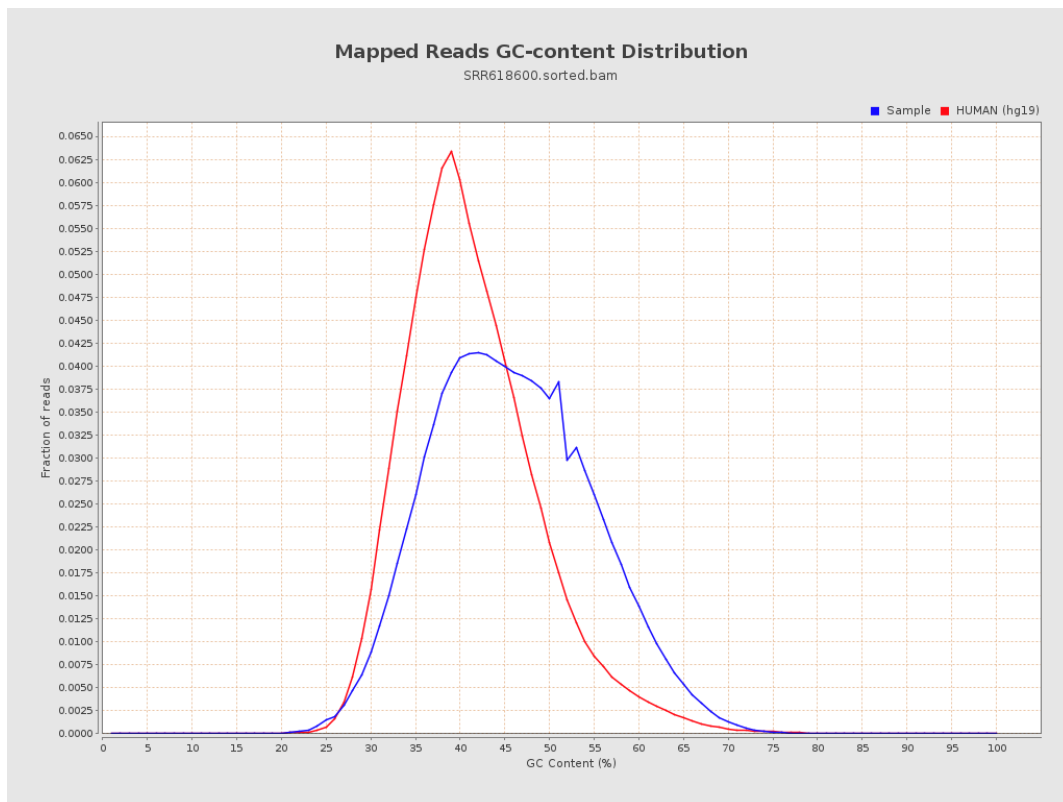
7. Results : Duplication Rate Histogram



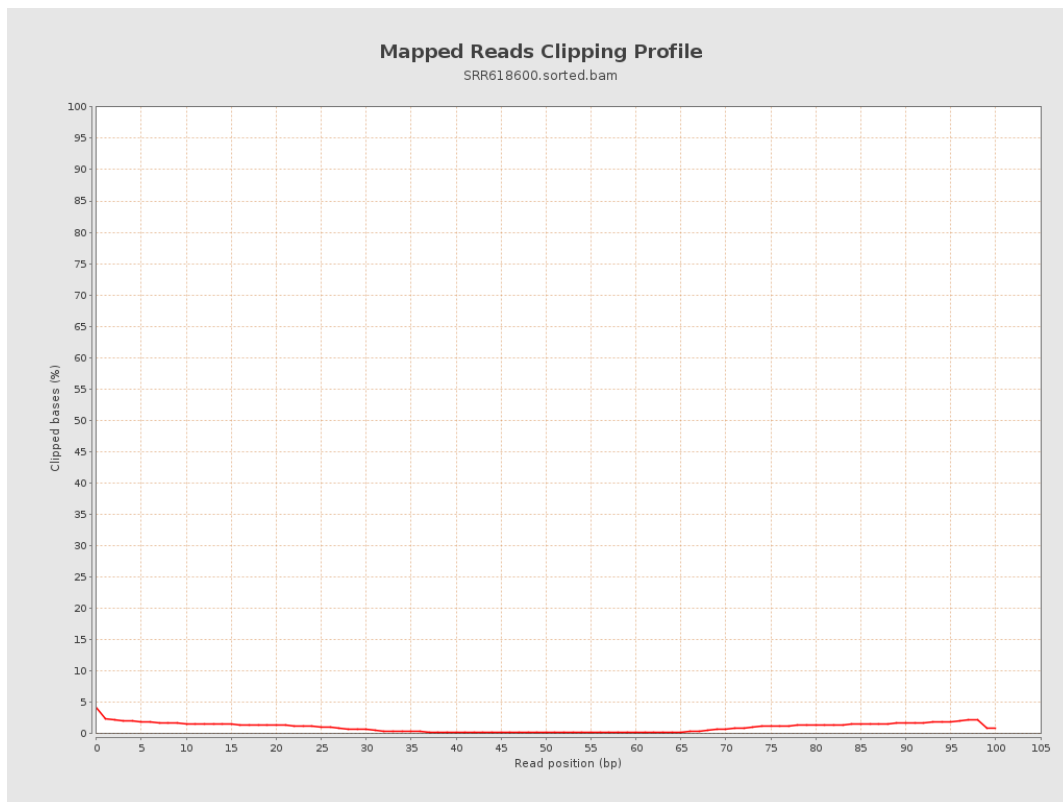
8. Results : Mapped Reads Nucleotide Content



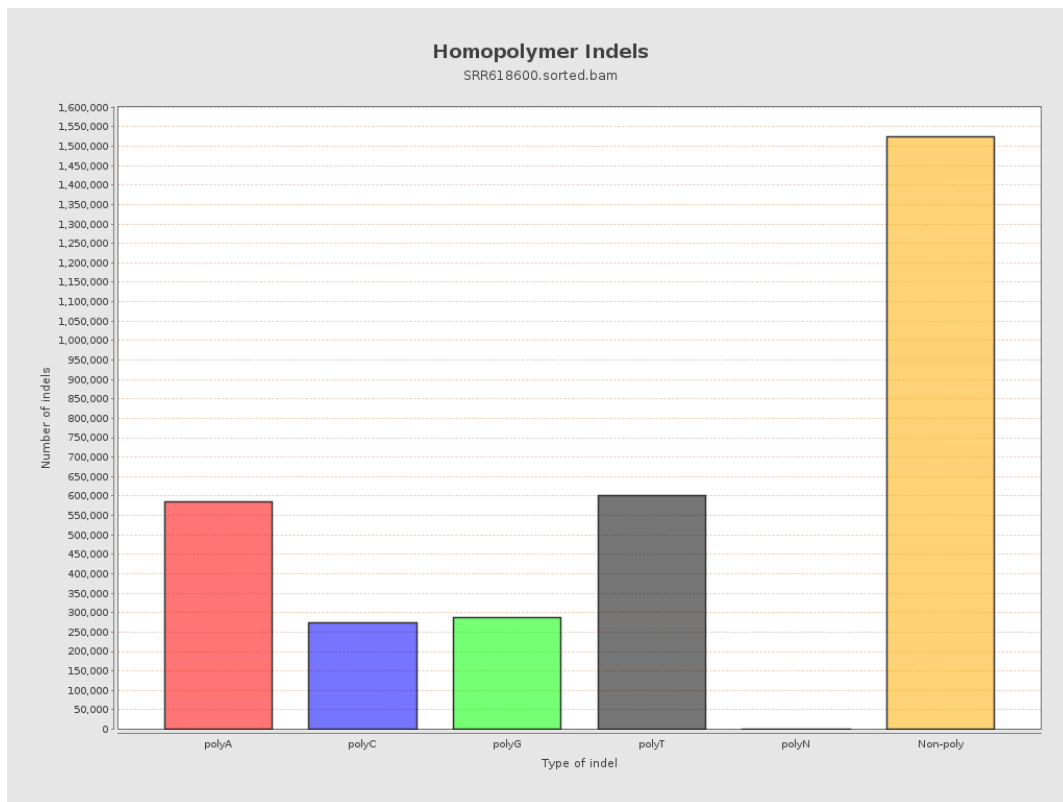
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



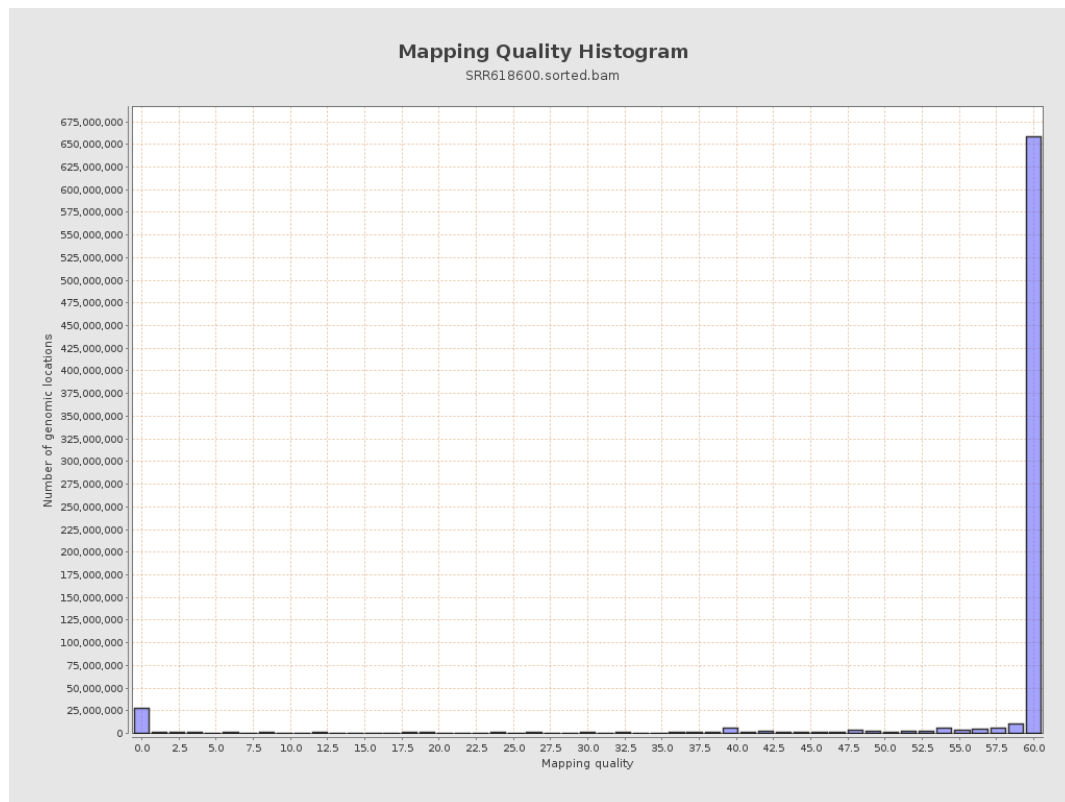
11. Results : Homopolymer Indels



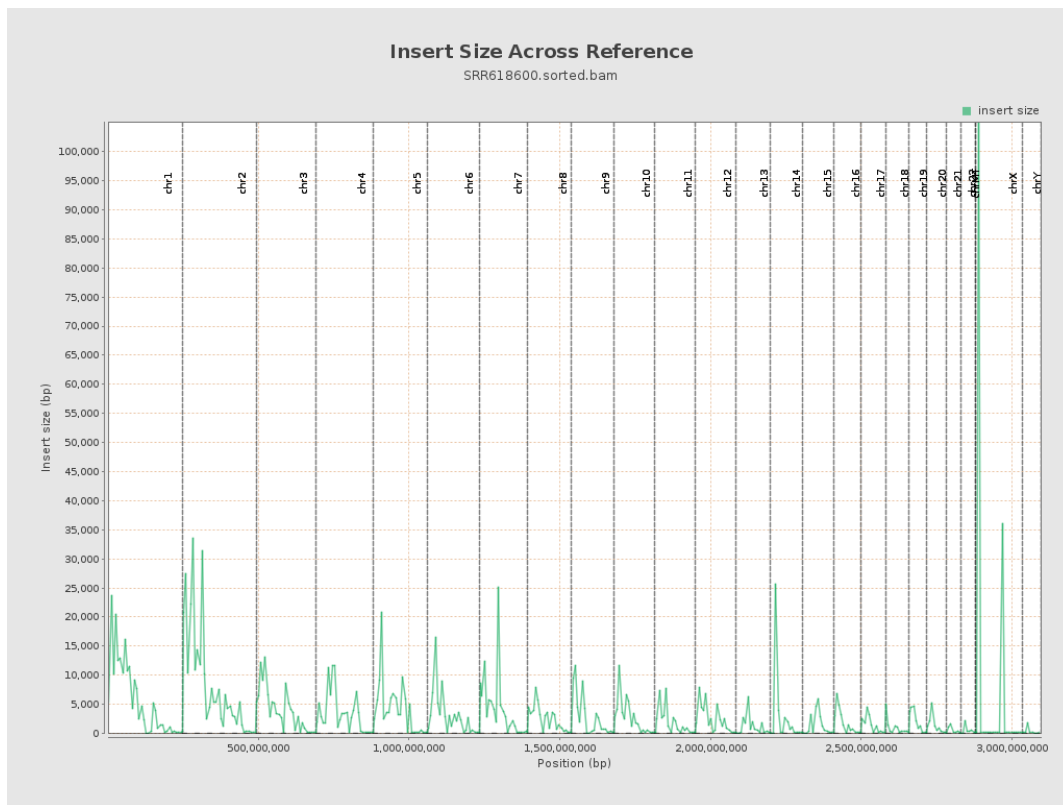
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

