

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 20:56:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618597.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_SRR618597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618597_1.fastq.gz SRR618597_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 20:56:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,977,736
Mapped reads	46,164,498 / 92.37%
Unmapped reads	3,813,238 / 7.63%
Mapped paired reads	46,164,498 / 92.37%
Mapped reads, first in pair	23,337,418 / 46.7%
Mapped reads, second in pair	22,827,080 / 45.67%
Mapped reads, both in pair	45,178,386 / 90.4%
Mapped reads, singletons	986,112 / 1.97%
Secondary alignments	0
Supplementary alignments	78,133 / 0.16%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	11,613,900 / 23.24%
Duplication rate	22.06%
Clipped reads	9,012,282 / 18.03%

2.2. ACGT Content

Number/percentage of A's	1,157,350,812 / 26.41%
Number/percentage of C's	1,000,559,714 / 22.84%
Number/percentage of T's	1,164,200,059 / 26.57%
Number/percentage of G's	1,059,402,690 / 24.18%
Number/percentage of N's	153,201 / 0%

GC Percentage	47.01%
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2.3. Coverage

Mean	1.4163
Standard Deviation	6.7212

2.4. Mapping Quality

Mean Mapping Quality	54.01
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2.5. Insert size

Mean	35,666.27
Standard Deviation	1,866,419.73
P25/Median/P75	162 / 193 / 237

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	52,926,134
Insertions	754,309
Mapped reads with at least one insertion	1.6%
Deletions	1,974,069
Mapped reads with at least one deletion	4.18%
Homopolymer indels	52.6%

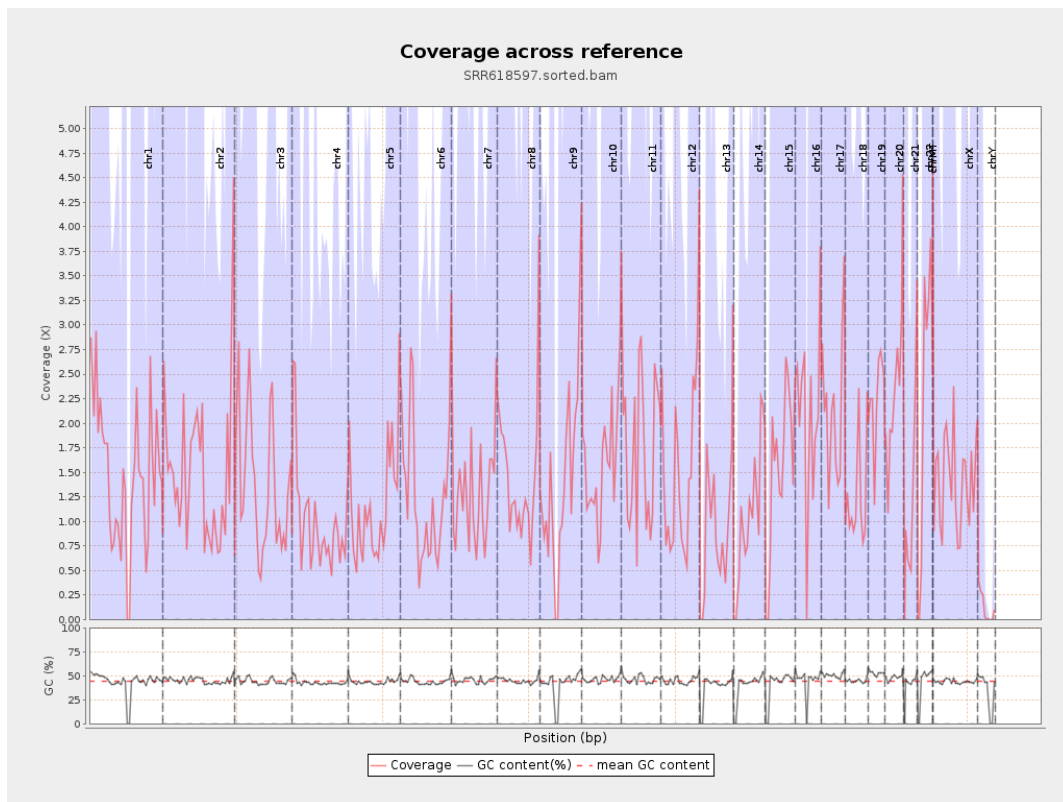
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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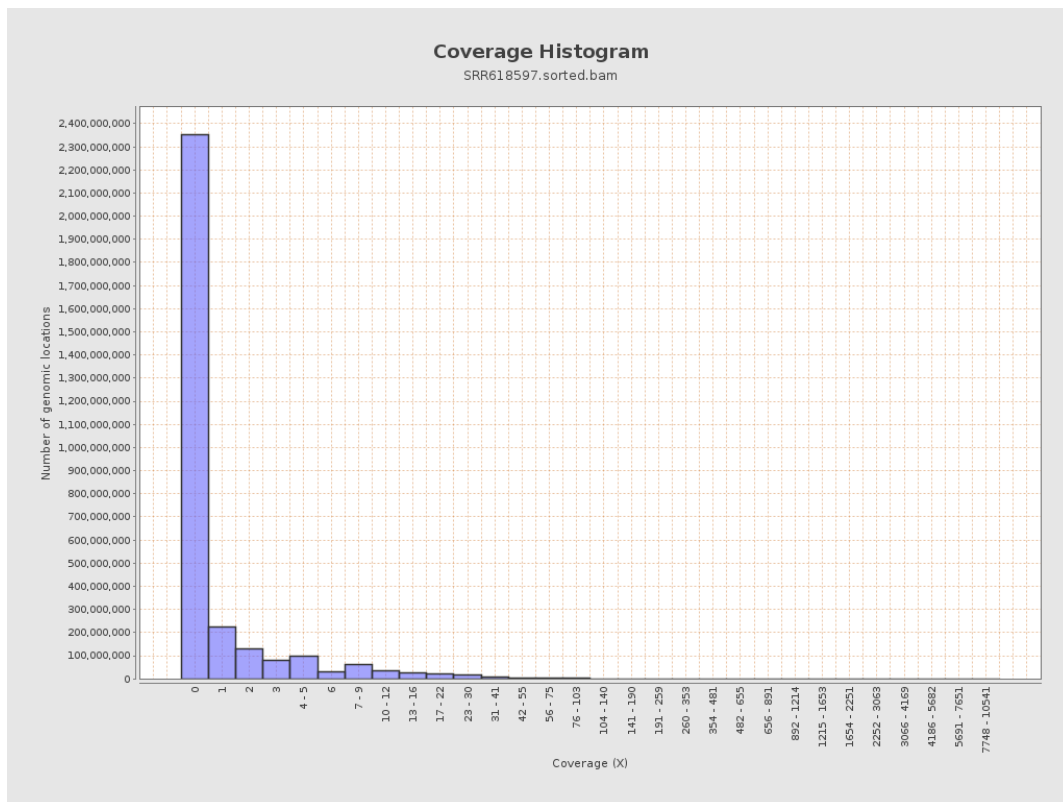
		bases	coverage	deviation
chr1	249250621	364147175	1.461	6.2389
chr2	243199373	365125990	1.5013	8.4869
chr3	198022430	267673213	1.3517	5.2306
chr4	191154276	189964867	0.9938	6.0465
chr5	180915260	214447630	1.1853	4.5983
chr6	171115067	210448089	1.2299	4.6745
chr7	159138663	210944797	1.3255	5.2842
chr8	146364022	210293945	1.4368	5.482
chr9	141213431	196024543	1.3881	6.6978
chr10	135534747	210535769	1.5534	5.9332
chr11	135006516	238841518	1.7691	6.6135
chr12	133851895	204095630	1.5248	5.9164
chr13	115169878	105179536	0.9133	3.8408
chr14	107349540	113186841	1.0544	4.5858
chr15	102531392	154204589	1.504	5.7947
chr16	90354753	188317495	2.0842	17.12
chr17	81195210	170854537	2.1042	7.5247
chr18	78077248	94416181	1.2093	5.0336
chr19	59128983	131056759	2.2165	8.5157
chr20	63025520	144333609	2.2901	7.6152
chr21	48129895	61078295	1.269	8.992
chr22	51304566	114205049	2.226	8.3801
chrMT	16571	77639	4.6852	7.1593
chrX	155270560	217872040	1.4032	4.9228

chrY	59373566	7087198	0.1194	5.8616
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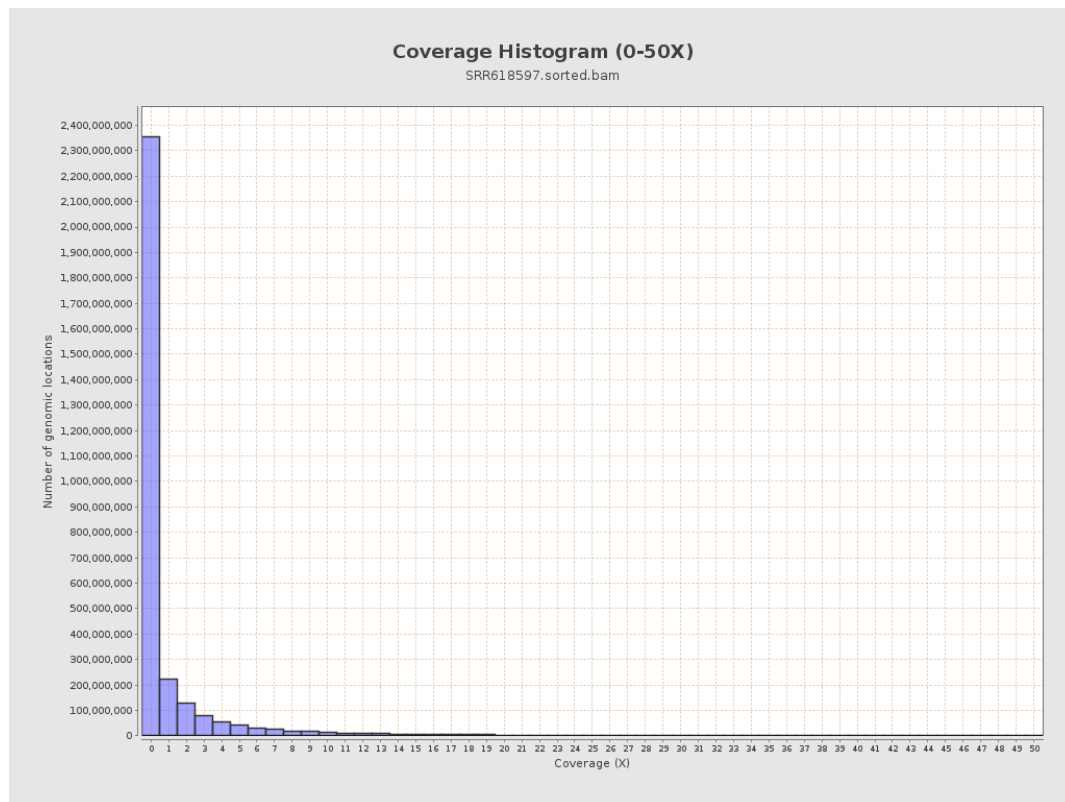
3. Results : Coverage across reference



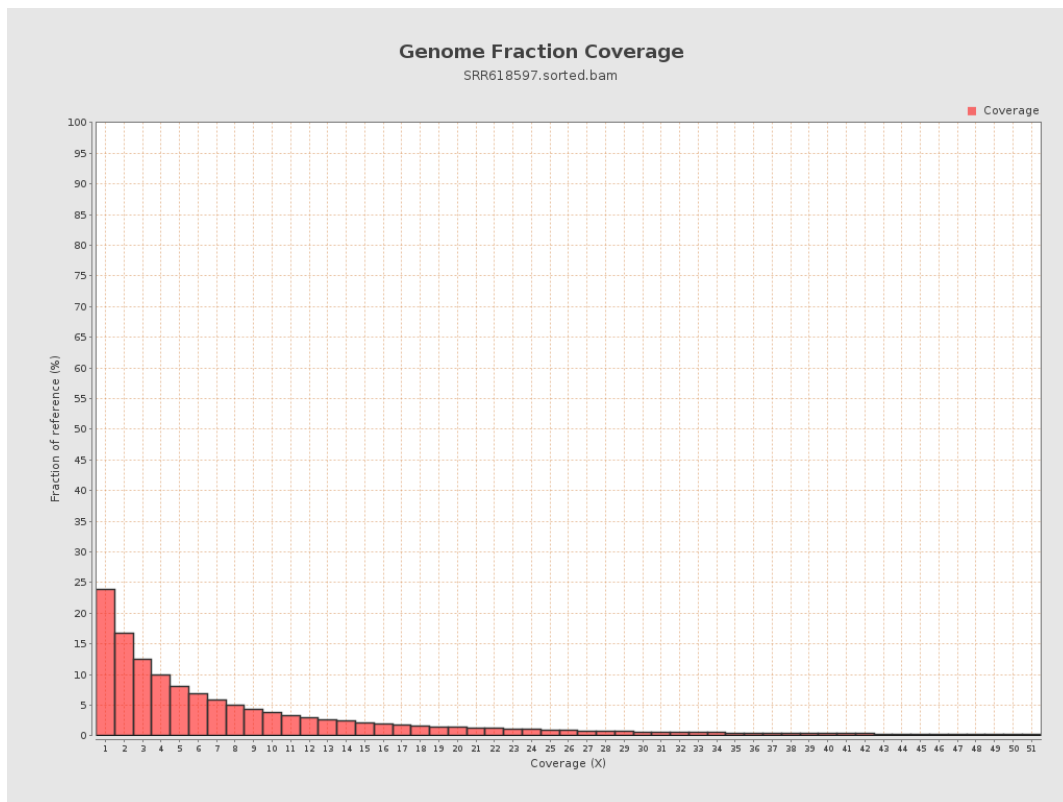
4. Results : Coverage Histogram



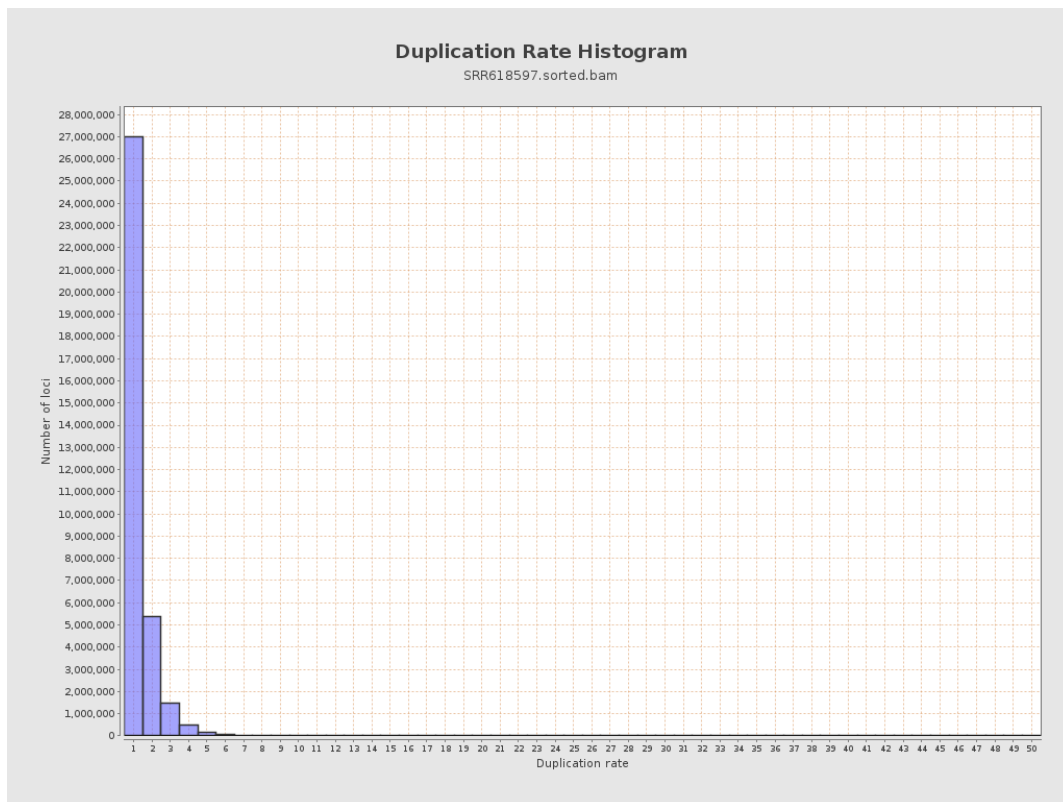
5. Results : Coverage Histogram (0-50X)



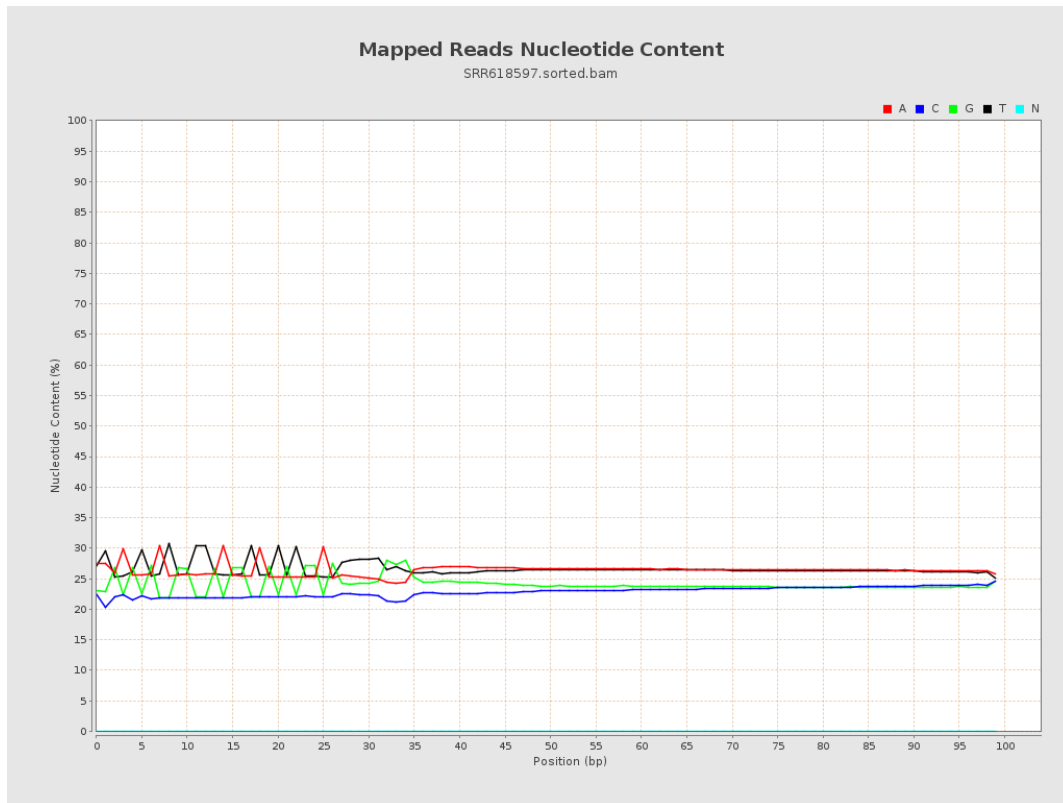
6. Results : Genome Fraction Coverage



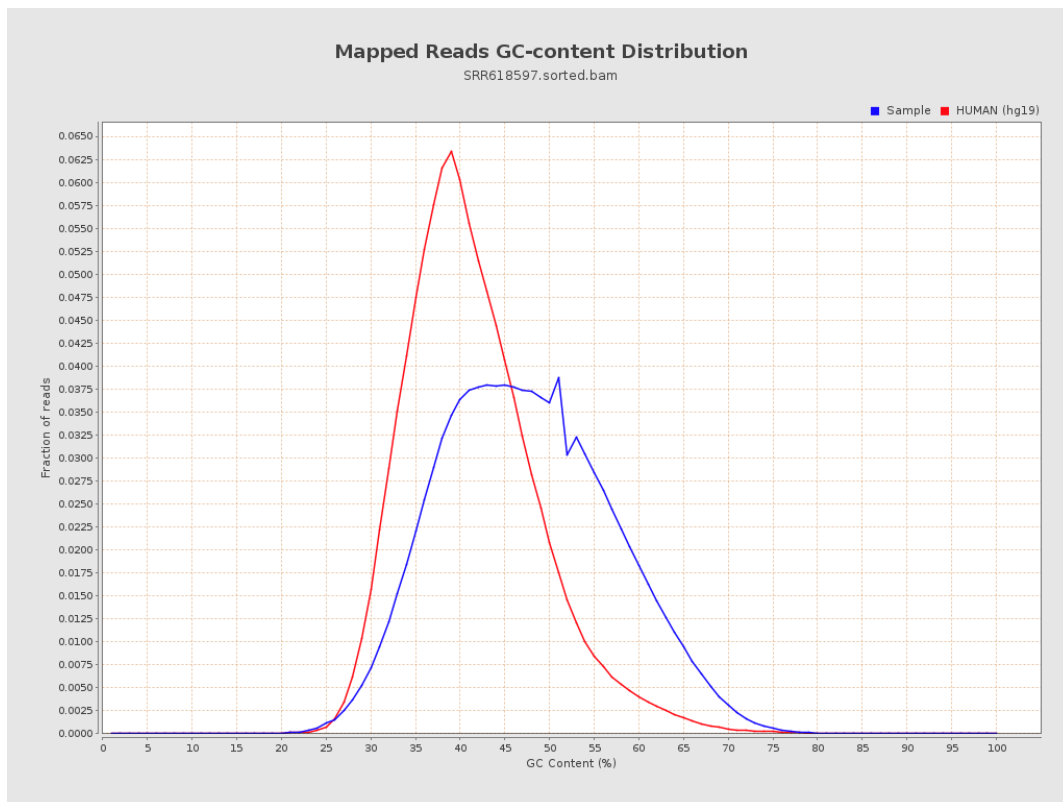
7. Results : Duplication Rate Histogram



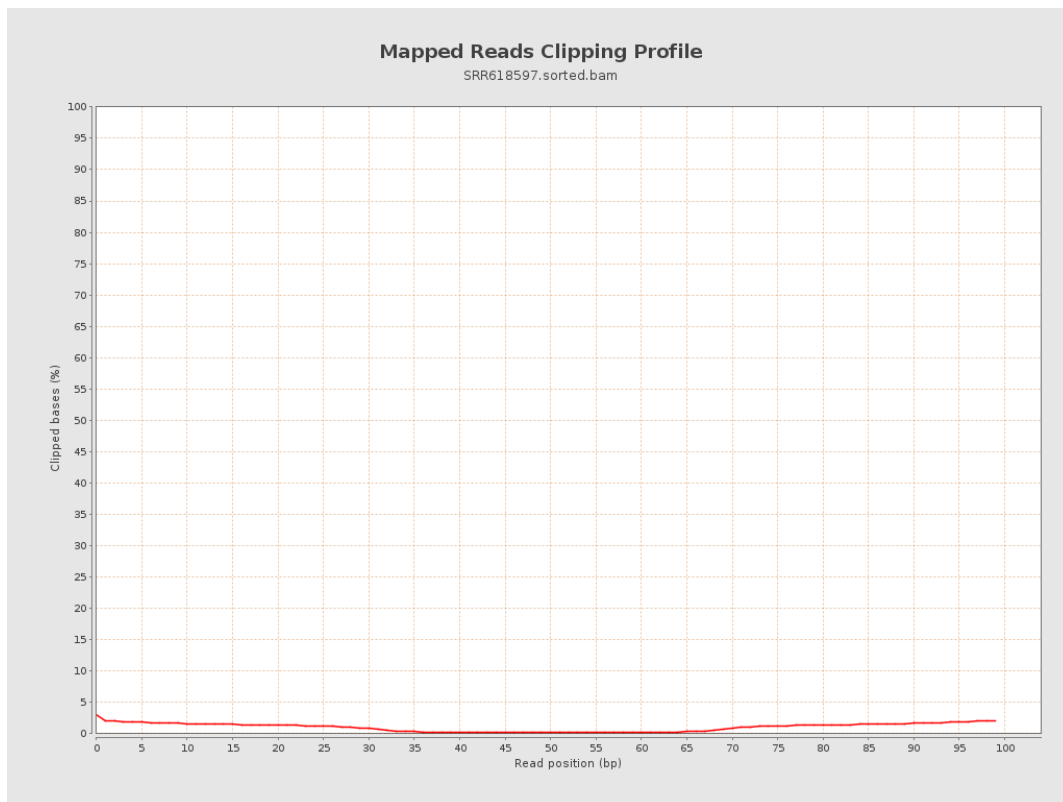
8. Results : Mapped Reads Nucleotide Content



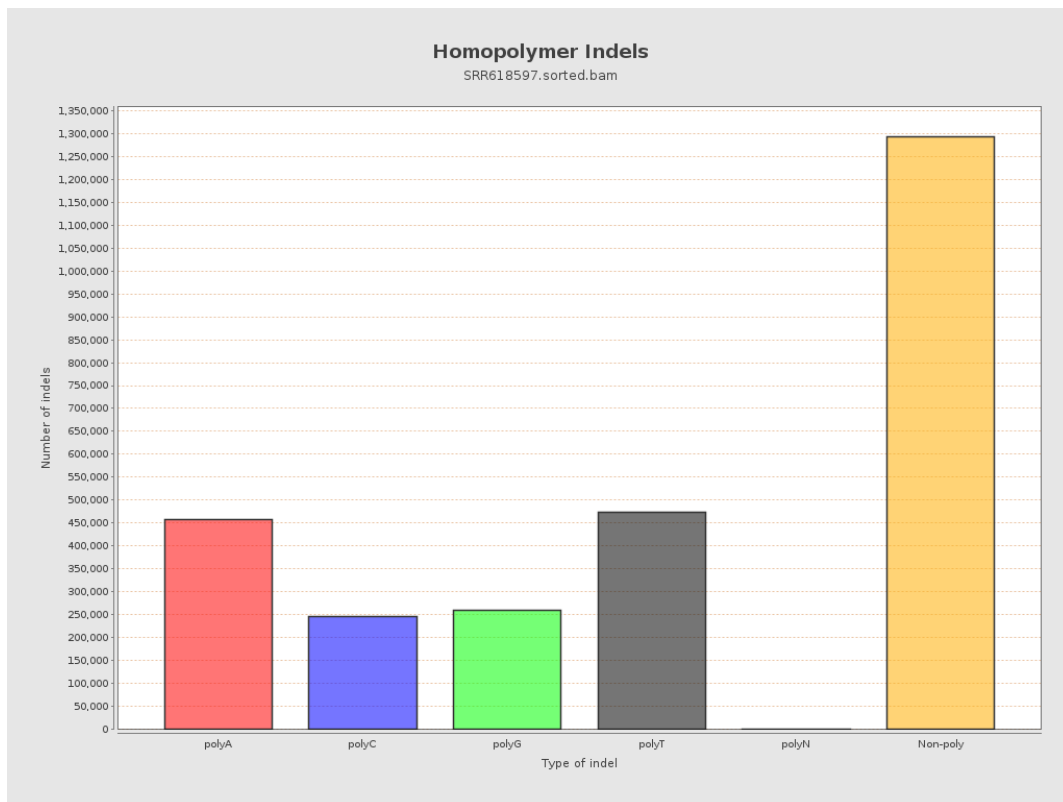
9. Results : Mapped Reads GC-content Distribution



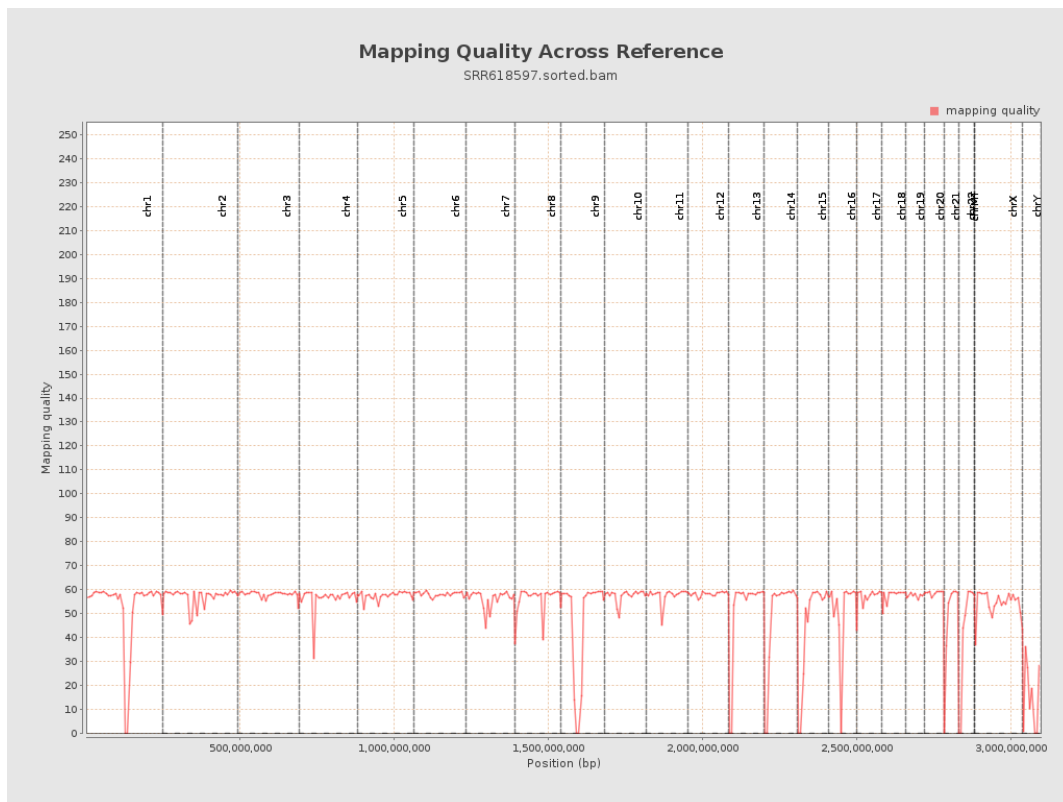
10. Results : Mapped Reads Clipping Profile



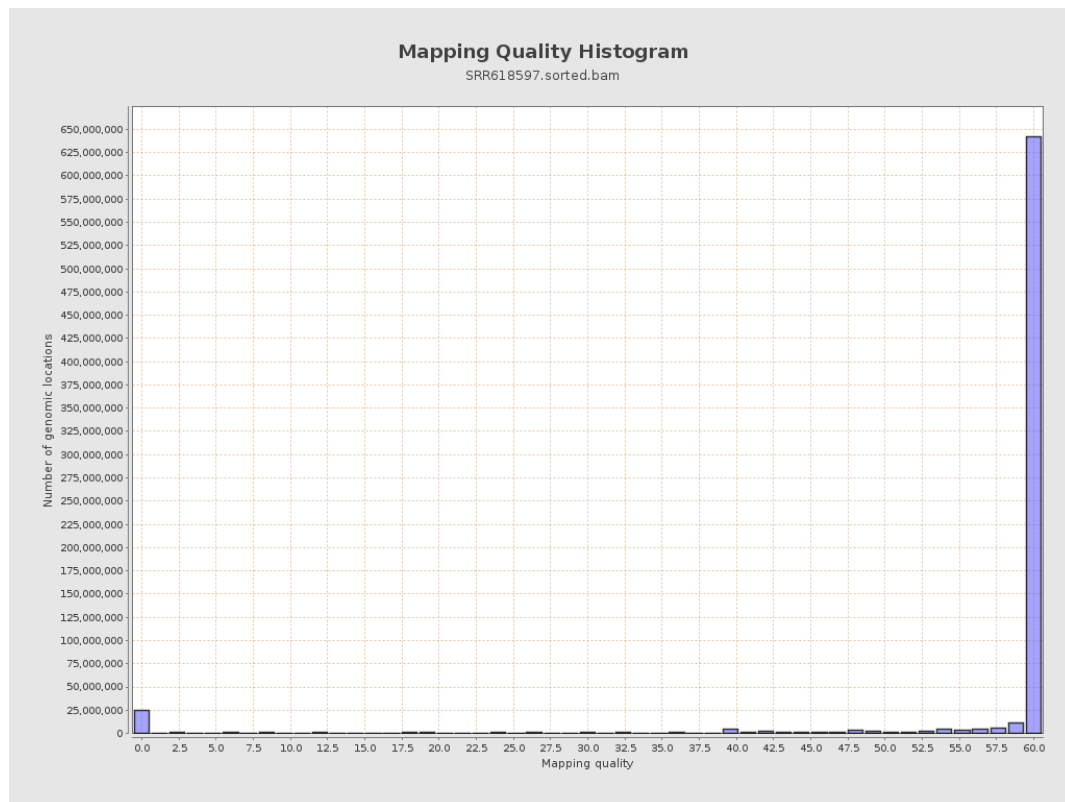
11. Results : Homopolymer Indels



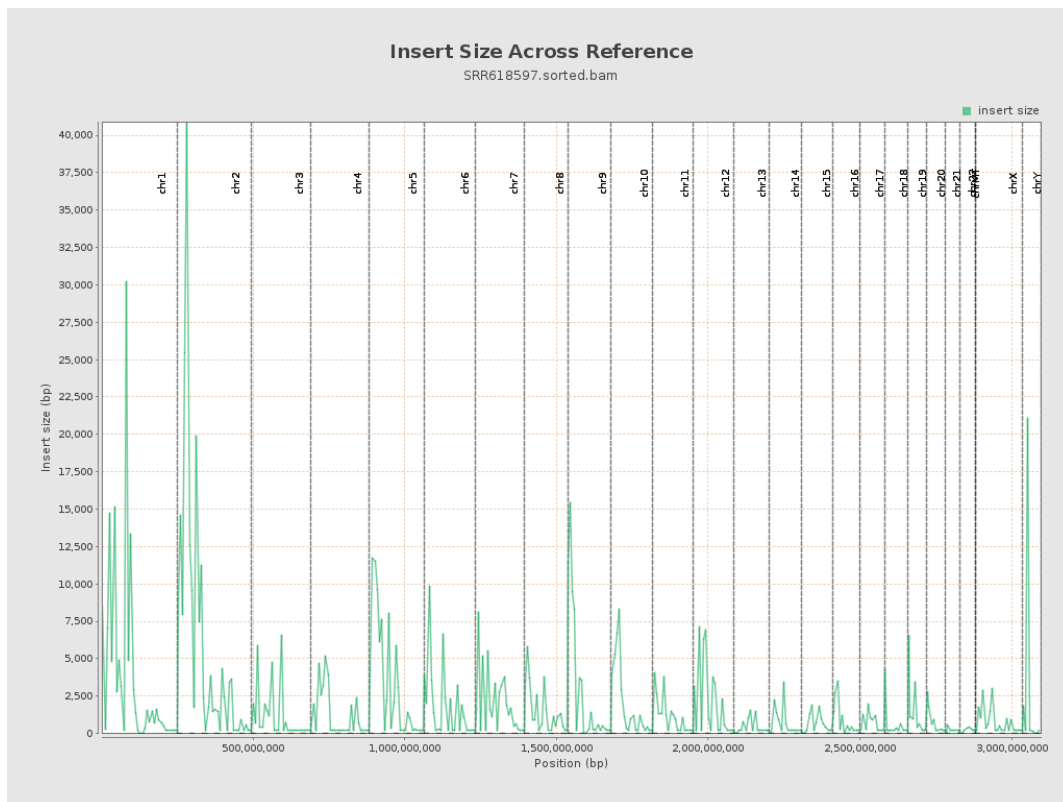
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

