

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 09:37:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618615.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_SRR618615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618615_1.fastq.gz SRR618615_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 09:37:37 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,830,542
Mapped reads	36,551,903 / 96.62%
Unmapped reads	1,278,639 / 3.38%
Mapped paired reads	36,551,903 / 96.62%
Mapped reads, first in pair	18,452,477 / 48.78%
Mapped reads, second in pair	18,099,426 / 47.84%
Mapped reads, both in pair	35,934,686 / 94.99%
Mapped reads, singletons	617,217 / 1.63%
Secondary alignments	0
Supplementary alignments	103,202 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	9,784,068 / 25.86%
Duplication rate	23.01%
Clipped reads	8,428,949 / 22.28%

2.2. ACGT Content

Number/percentage of A's	934,872,015 / 27.26%
Number/percentage of C's	739,961,186 / 21.58%
Number/percentage of T's	949,270,825 / 27.68%
Number/percentage of G's	805,075,056 / 23.48%
Number/percentage of N's	121,343 / 0%

GC Percentage	45.05%
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2.3. Coverage

Mean	1.1085
Standard Deviation	4.0727

2.4. Mapping Quality

Mean Mapping Quality	52.1
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2.5. Insert size

Mean	65,334.24
Standard Deviation	2,562,615.89
P25/Median/P75	175 / 204 / 242

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	40,814,072
Insertions	612,959
Mapped reads with at least one insertion	1.65%
Deletions	1,758,389
Mapped reads with at least one deletion	4.69%
Homopolymer indels	53.16%

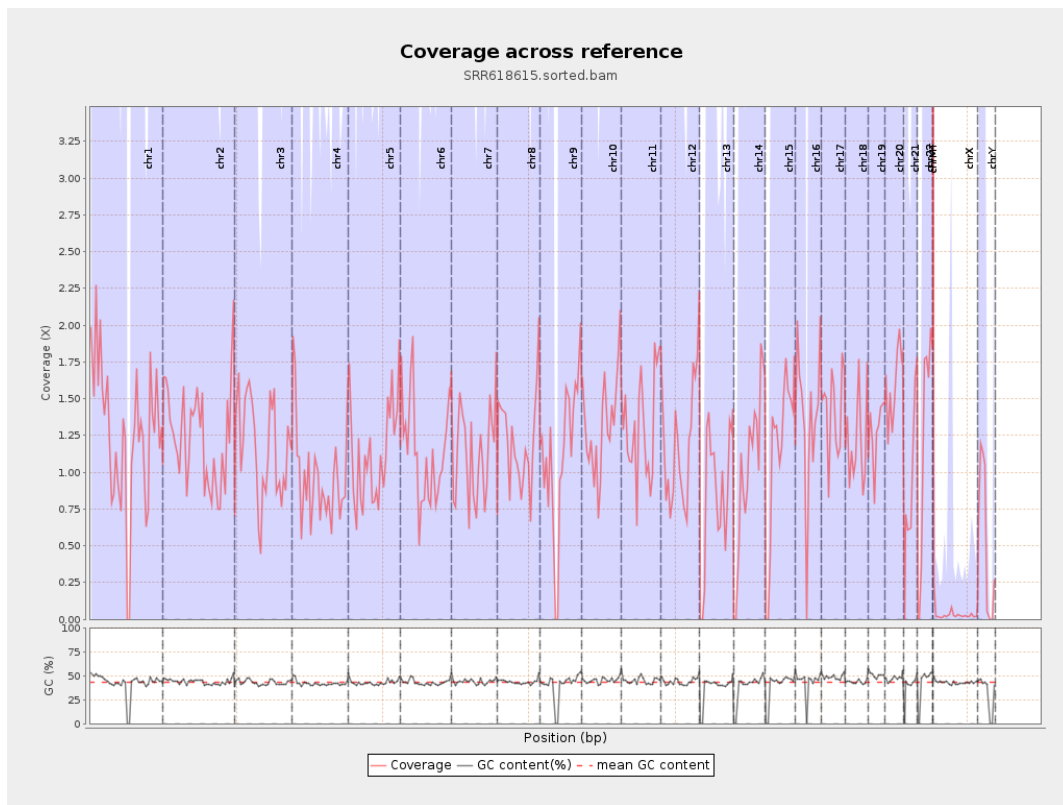
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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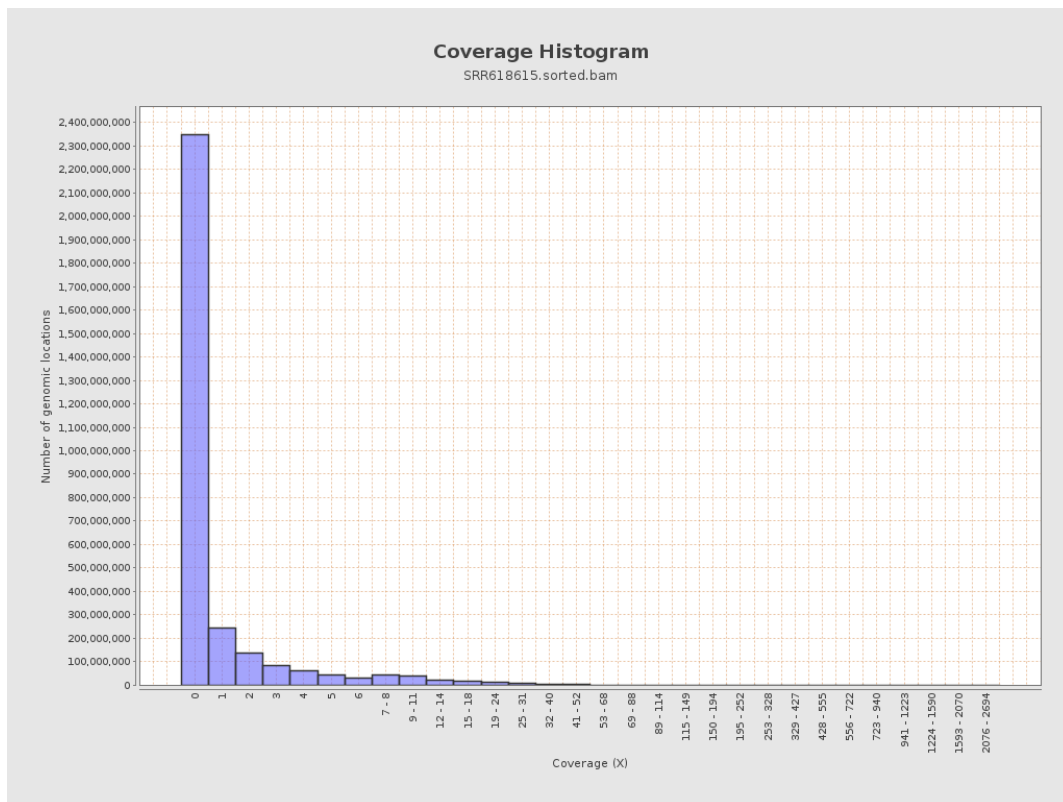
		bases	coverage	deviation
chr1	249250621	312331474	1.2531	4.7978
chr2	243199373	300488331	1.2356	4.4523
chr3	198022430	229693838	1.1599	3.5238
chr4	191154276	183930376	0.9622	3.4521
chr5	180915260	205852047	1.1378	3.5189
chr6	171115067	193817992	1.1327	3.7057
chr7	159138663	180614689	1.135	3.6919
chr8	146364022	176781480	1.2078	3.7558
chr9	141213431	157664500	1.1165	5.2888
chr10	135534747	177844363	1.3122	4.0672
chr11	135006516	176592032	1.308	4.5628
chr12	133851895	159340350	1.1904	3.8601
chr13	115169878	97454168	0.8462	2.9295
chr14	107349540	110237096	1.0269	3.5978
chr15	102531392	117000617	1.1411	3.7868
chr16	90354753	123048849	1.3618	5.4288
chr17	81195210	114598041	1.4114	4.5211
chr18	78077248	92554234	1.1854	5.2211
chr19	59128983	75164634	1.2712	4.4758
chr20	63025520	100791295	1.5992	4.6681
chr21	48129895	45539991	0.9462	5.5105
chr22	51304566	62156602	1.2115	4.3395
chrMT	16571	170108	10.2654	22.9183
chrX	155270560	5548176	0.0357	0.9093

chrY	59373566	32467444	0.5468	3.0224
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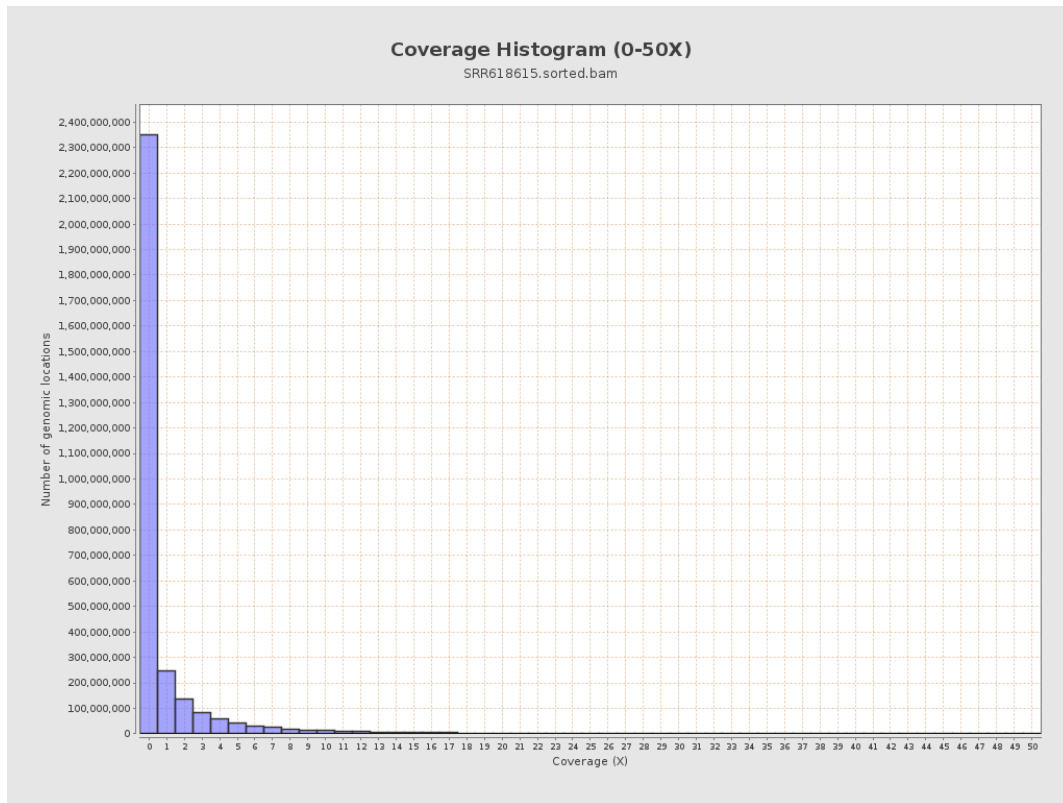
3. Results : Coverage across reference



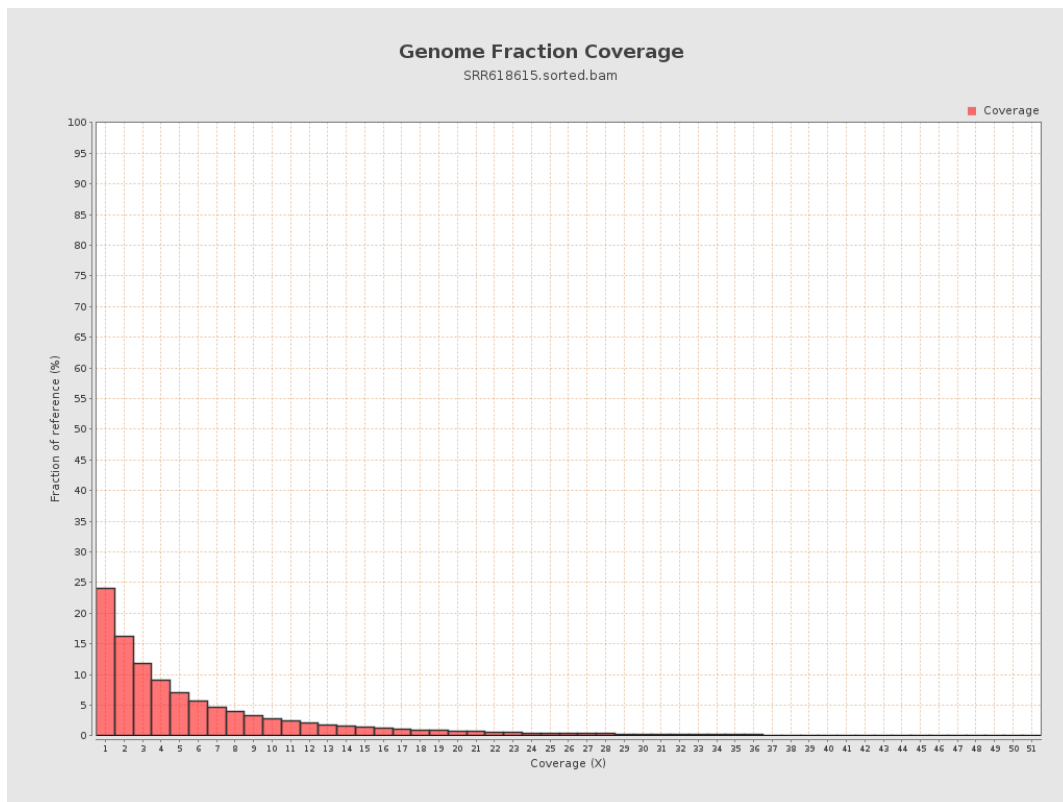
4. Results : Coverage Histogram



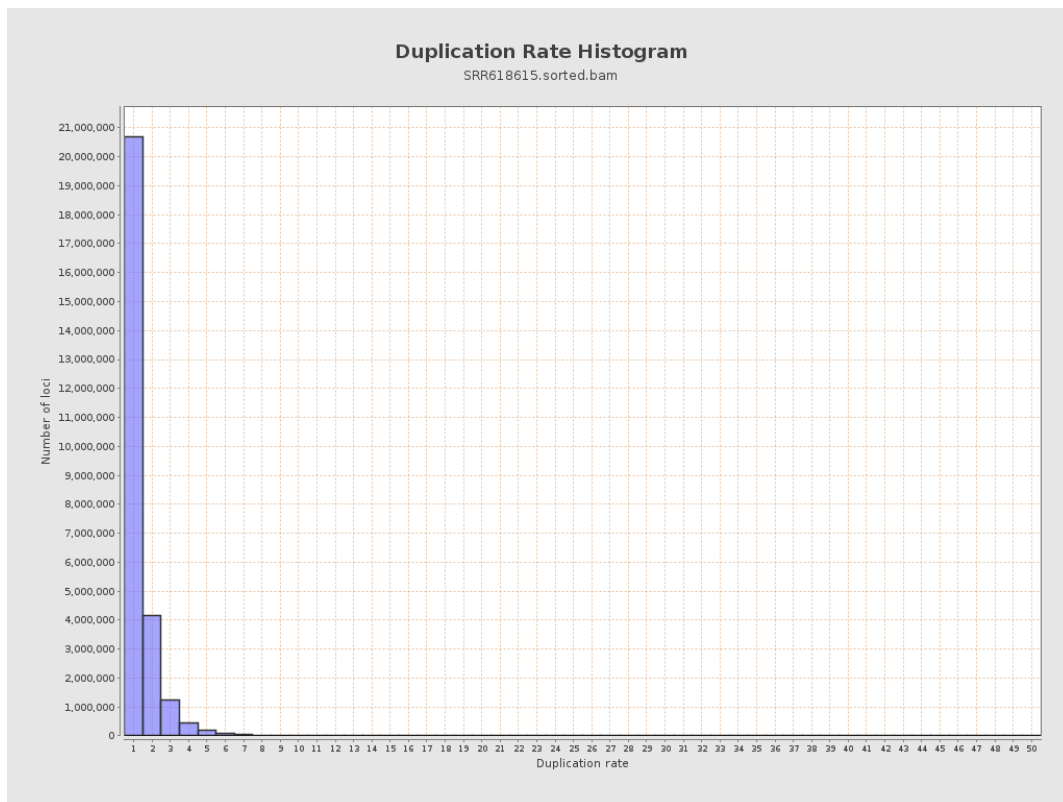
5. Results : Coverage Histogram (0-50X)



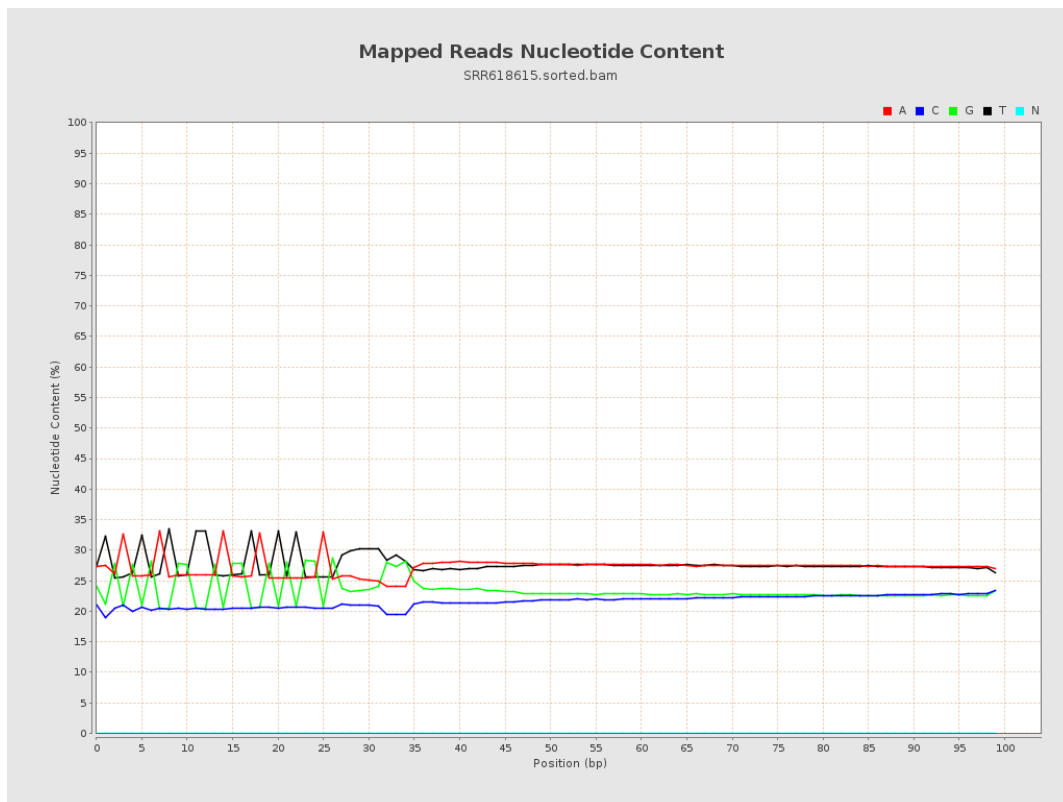
6. Results : Genome Fraction Coverage



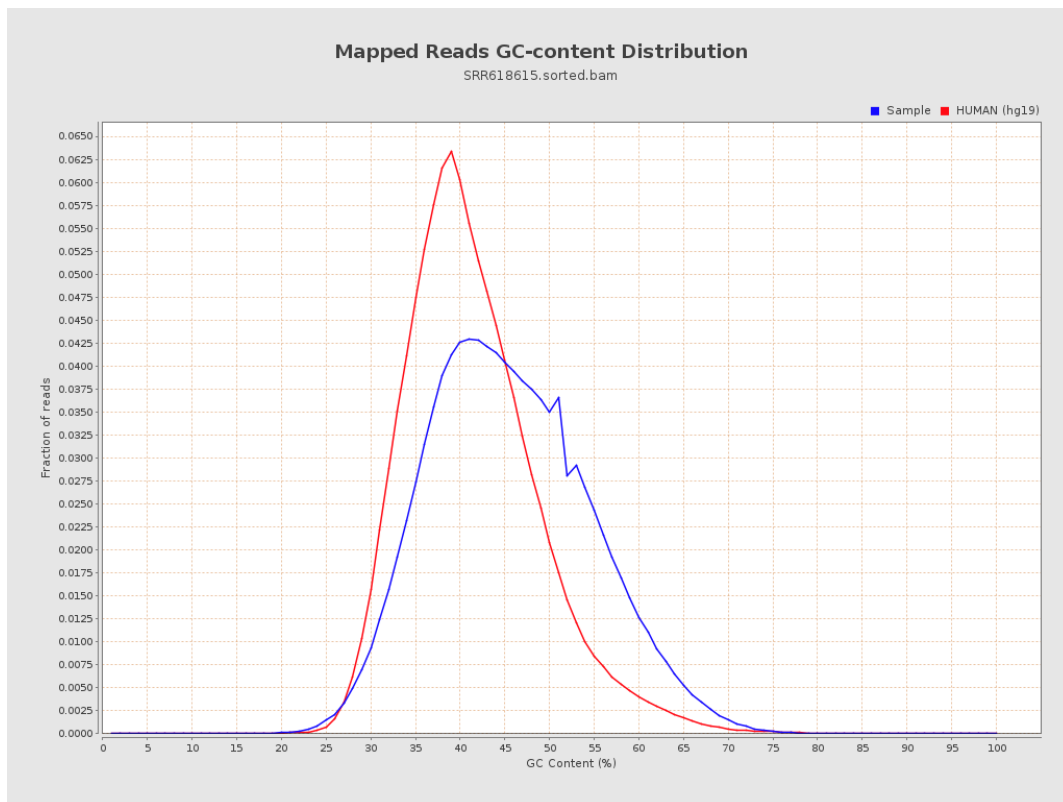
7. Results : Duplication Rate Histogram



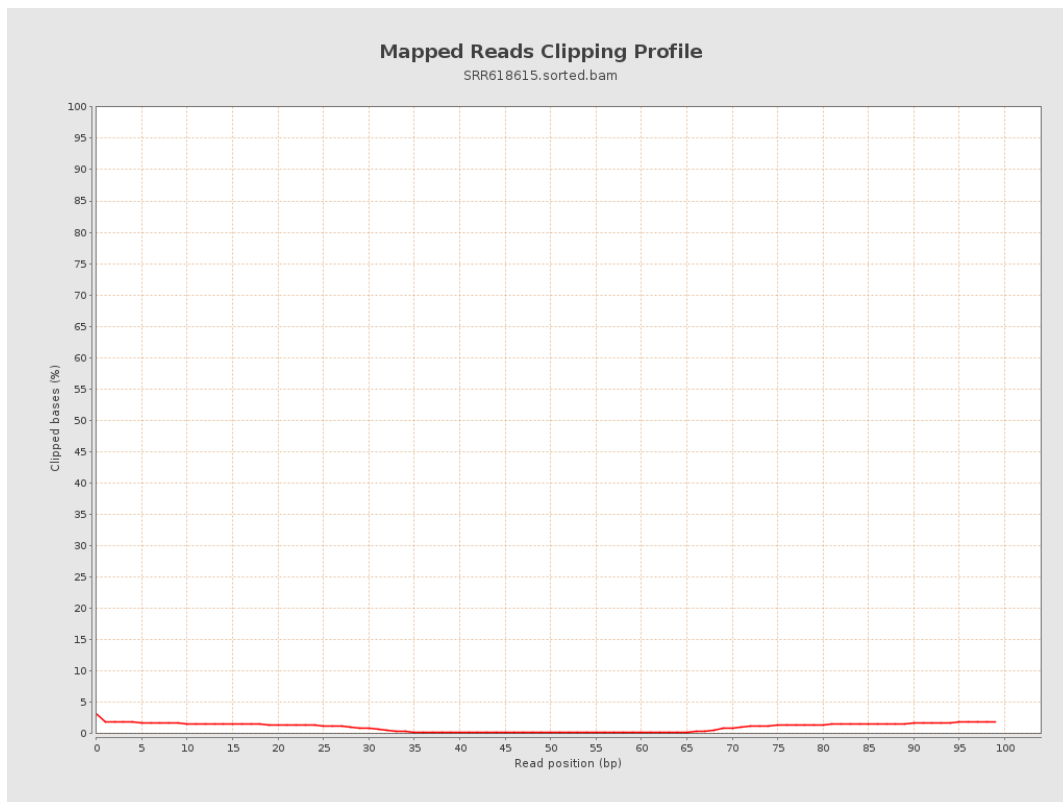
8. Results : Mapped Reads Nucleotide Content



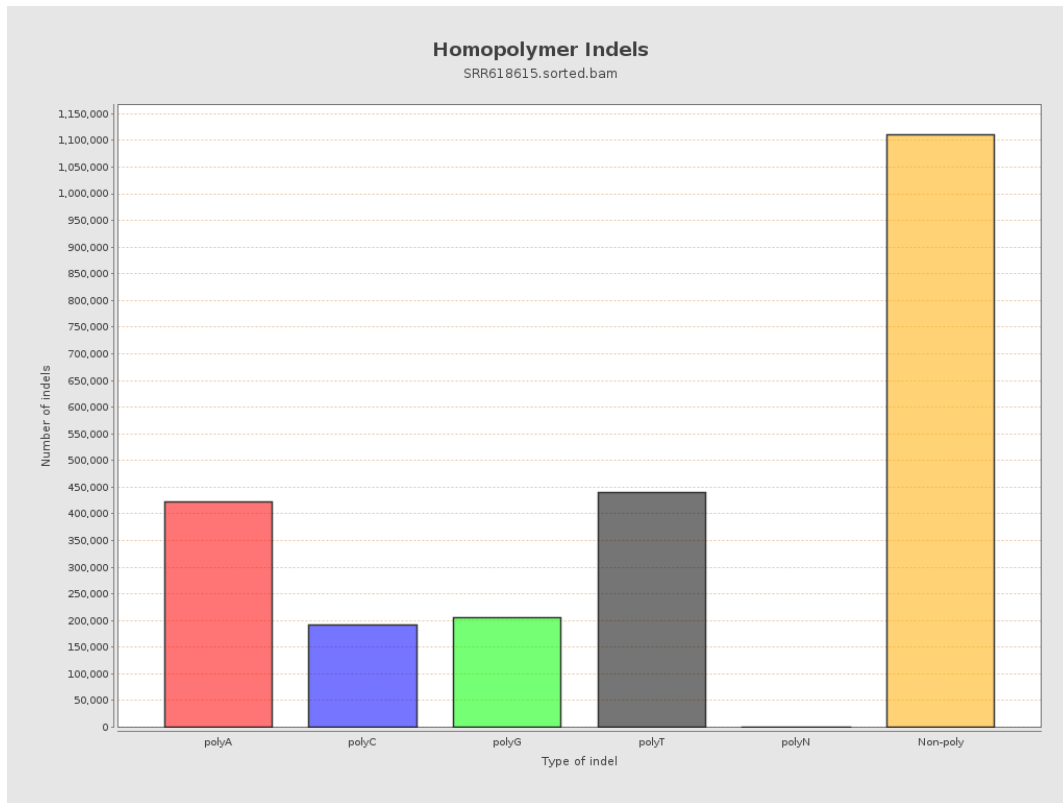
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



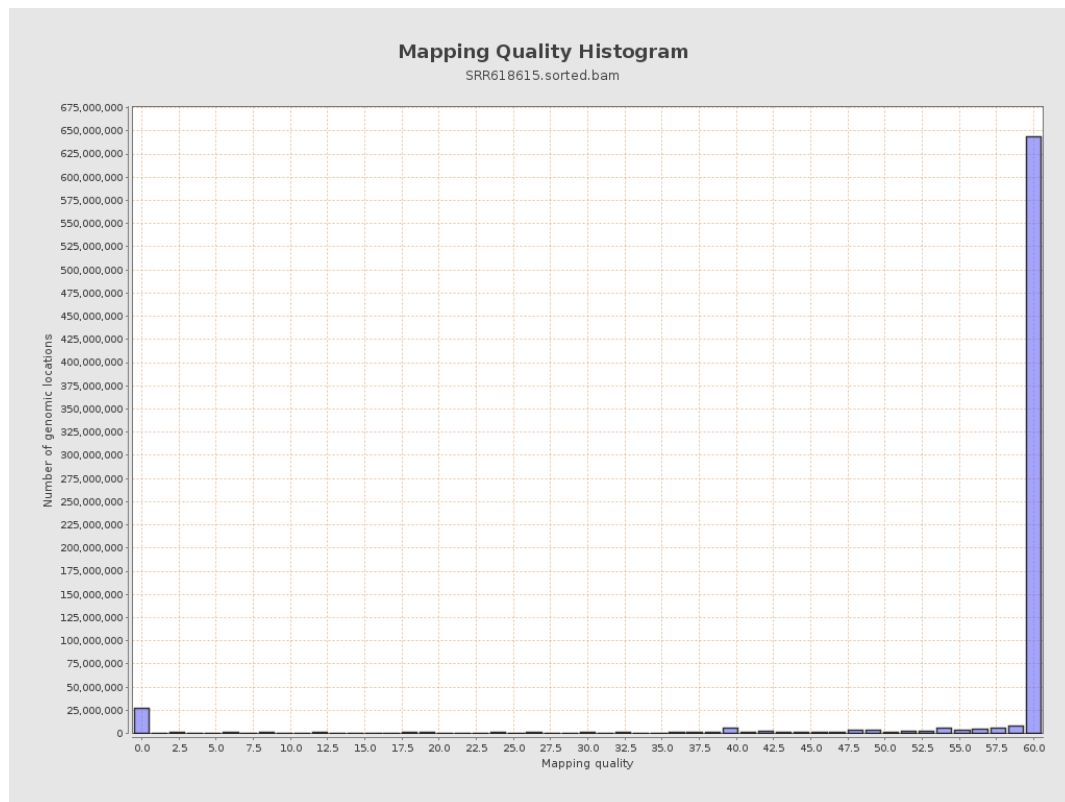
11. Results : Homopolymer Indels



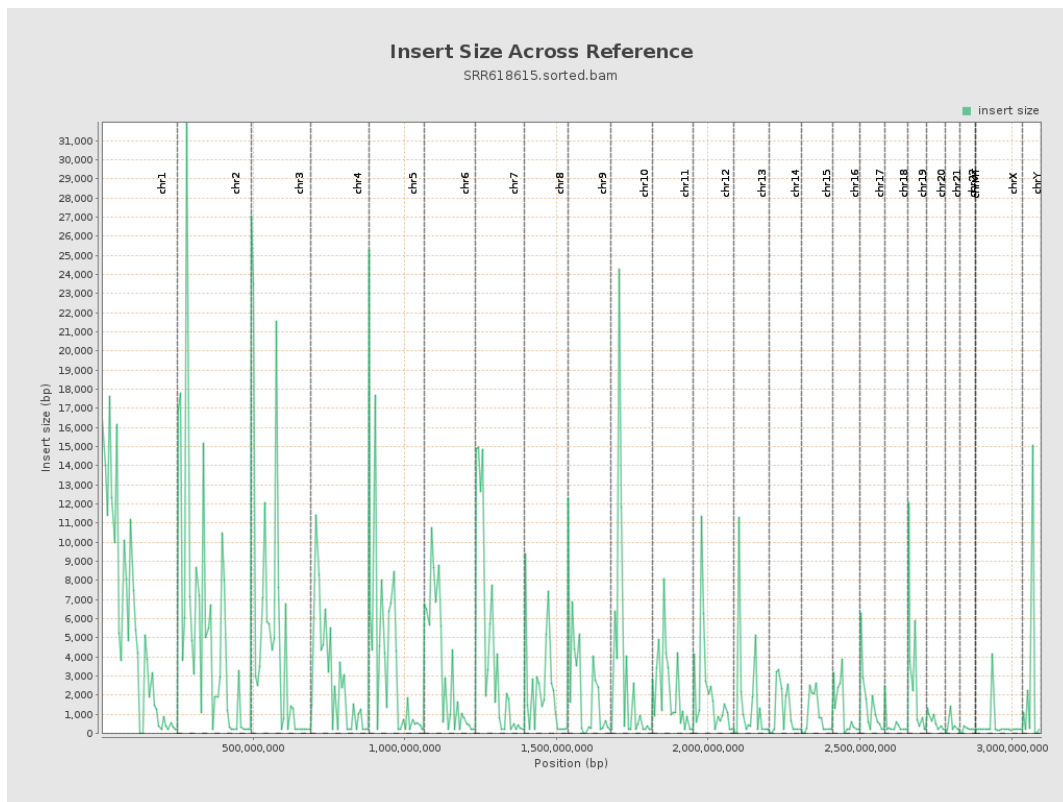
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

