

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/21 03:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618666.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_SRR618666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618666_1.fastq.gz SRR618666_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 21 03:35:30 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	462,571,116
Mapped reads	420,200,474 / 90.84%
Unmapped reads	42,370,642 / 9.16%
Mapped paired reads	420,200,474 / 90.84%
Mapped reads, first in pair	211,682,859 / 45.76%
Mapped reads, second in pair	208,517,615 / 45.08%
Mapped reads, both in pair	410,651,478 / 88.78%
Mapped reads, singletons	9,548,996 / 2.06%
Secondary alignments	0
Supplementary alignments	1,341,366 / 0.29%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	133,377,058 / 28.83%
Duplication rate	25.29%
Clipped reads	31,043,972 / 6.71%

2.2. ACGT Content

Number/percentage of A's	12,446,520,561 / 30.14%
Number/percentage of C's	8,215,682,071 / 19.9%
Number/percentage of T's	12,339,365,392 / 29.88%
Number/percentage of G's	8,275,013,656 / 20.04%
Number/percentage of N's	15,979,722 / 0.04%

GC Percentage	39.94%
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2.3. Coverage

Mean	13.3427
Standard Deviation	145.1437

2.4. Mapping Quality

Mean Mapping Quality	53.62
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2.5. Insert size

Mean	42,079.96
Standard Deviation	1,950,333.22
P25/Median/P75	163 / 170 / 177

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	446,183,351
Insertions	4,166,801
Mapped reads with at least one insertion	0.96%
Deletions	4,969,922
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.93%

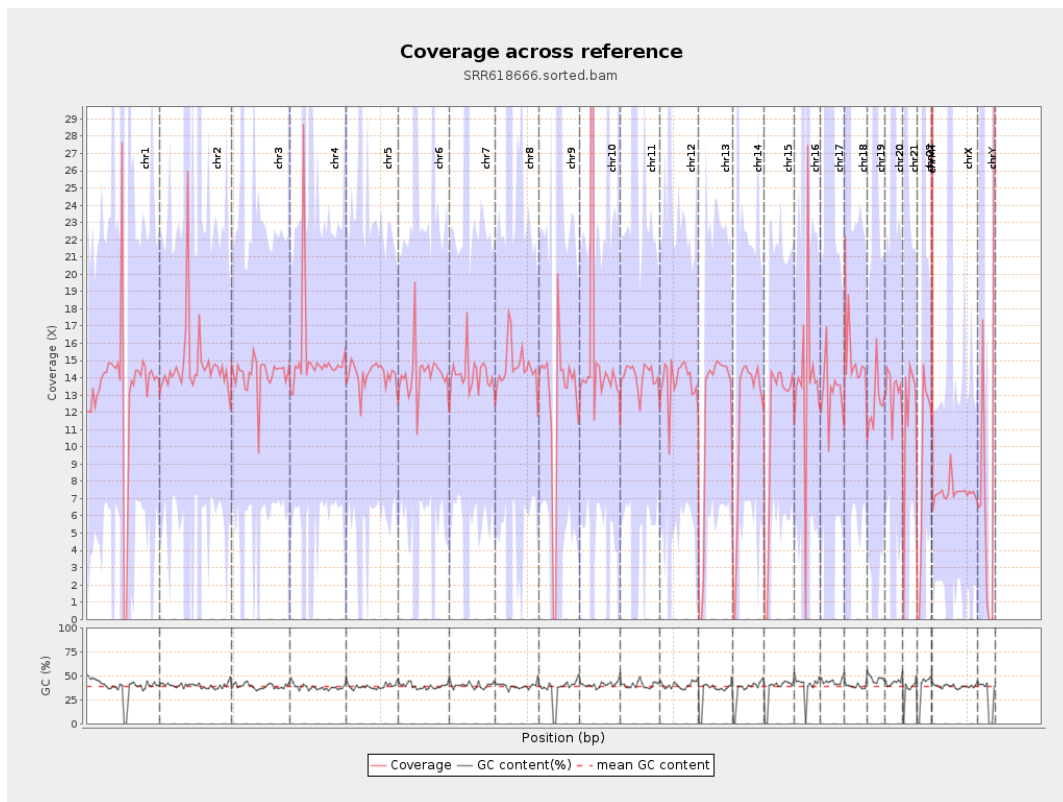
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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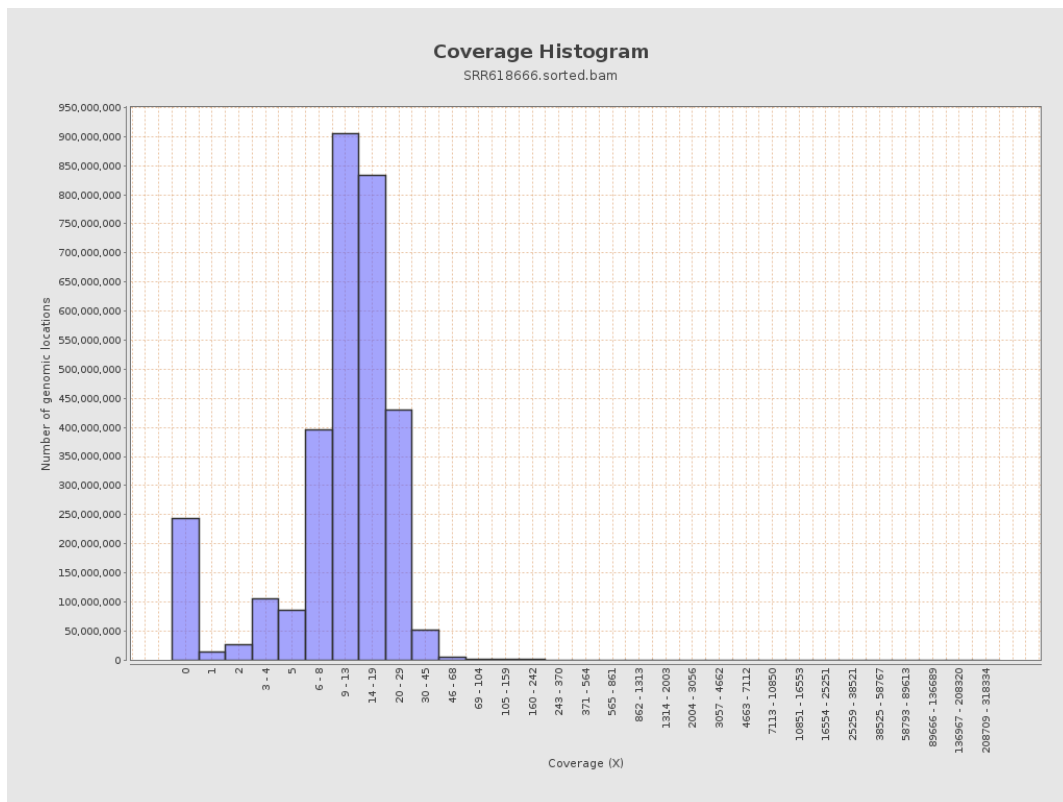
		bases	coverage	deviation
chr1	249250621	3352613398	13.4508	323.2155
chr2	243199373	3586905413	14.7488	91.3146
chr3	198022430	2801796476	14.1489	17.7862
chr4	191154276	2887744523	15.1069	81.5649
chr5	180915260	2557414668	14.136	12.5311
chr6	171115067	2440994742	14.2652	60.4324
chr7	159138663	2252933438	14.157	100.0746
chr8	146364022	2140182840	14.6223	191.7762
chr9	141213431	1769036271	12.5274	150.7288
chr10	135534747	2177625888	16.0669	350.6121
chr11	135006516	1893165687	14.0228	71.9278
chr12	133851895	1844864147	13.7829	11.3473
chr13	115169878	1380432873	11.9861	8.975
chr14	107349540	1261117106	11.7478	13.4963
chr15	102531392	1161521974	11.3285	9.2954
chr16	90354753	1249401240	13.8277	111.8154
chr17	81195210	1065138898	13.1182	60.5576
chr18	78077248	1180147536	15.1151	178.6797
chr19	59128983	739997760	12.515	141.8033
chr20	63025520	831356649	13.1908	45.2502
chr21	48129895	583559564	12.1247	67.0715
chr22	51304566	469314816	9.1476	63.7091
chrMT	16571	19246691	1,161.4683	204.8103
chrX	155270560	1142153081	7.3559	31.2666

chrY	59373566	516226913	8.6946	169.8482
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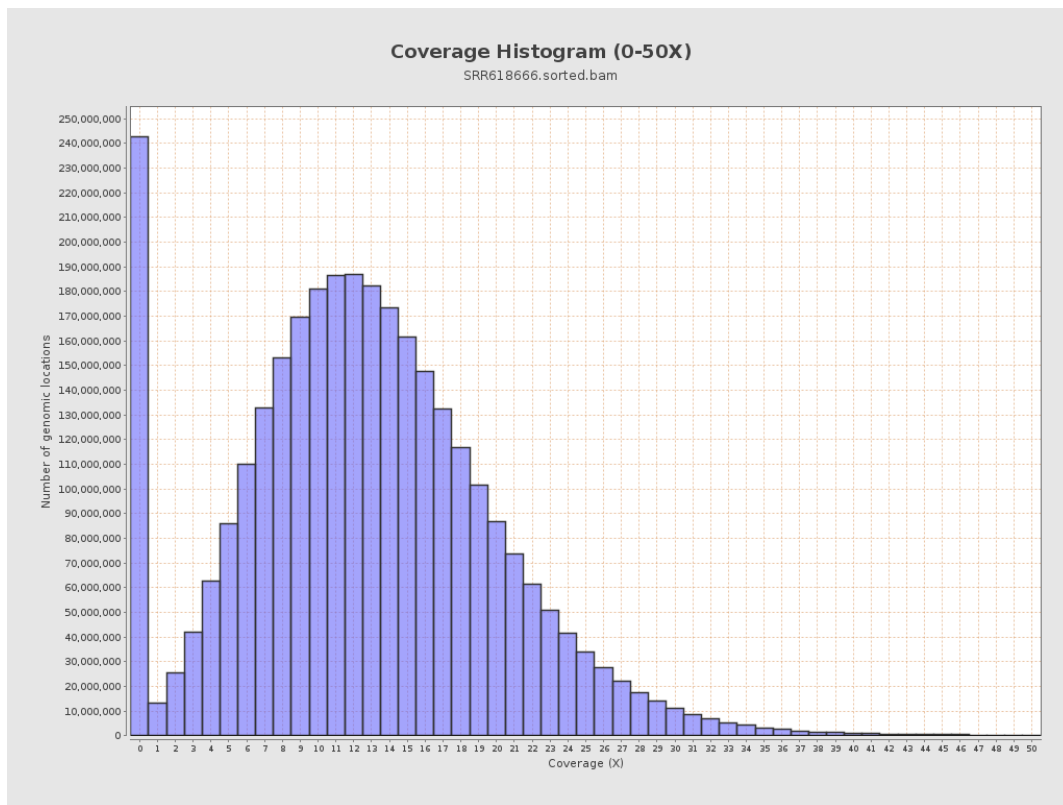
3. Results : Coverage across reference



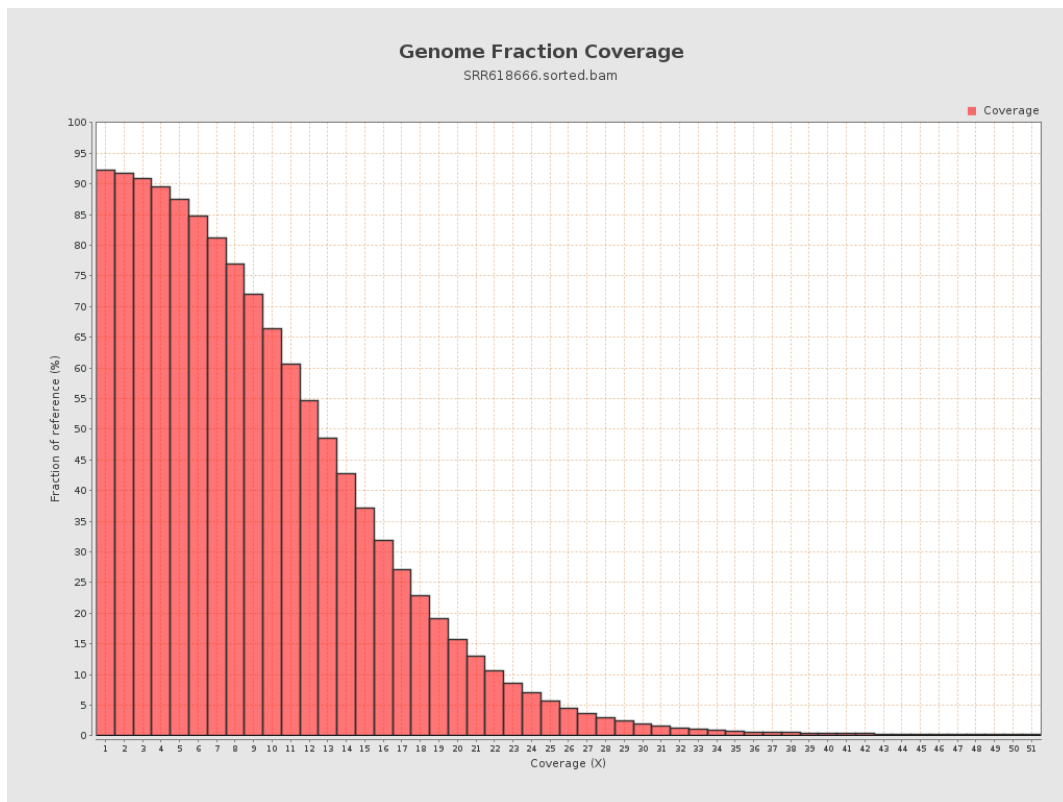
4. Results : Coverage Histogram



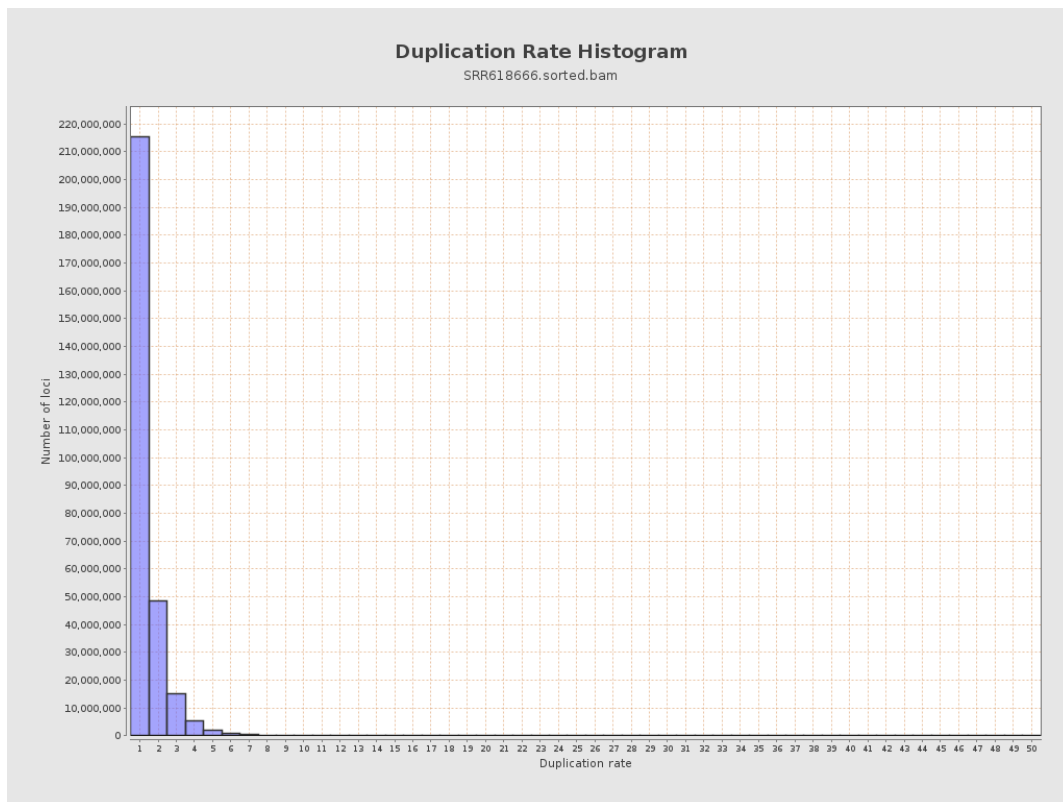
5. Results : Coverage Histogram (0-50X)



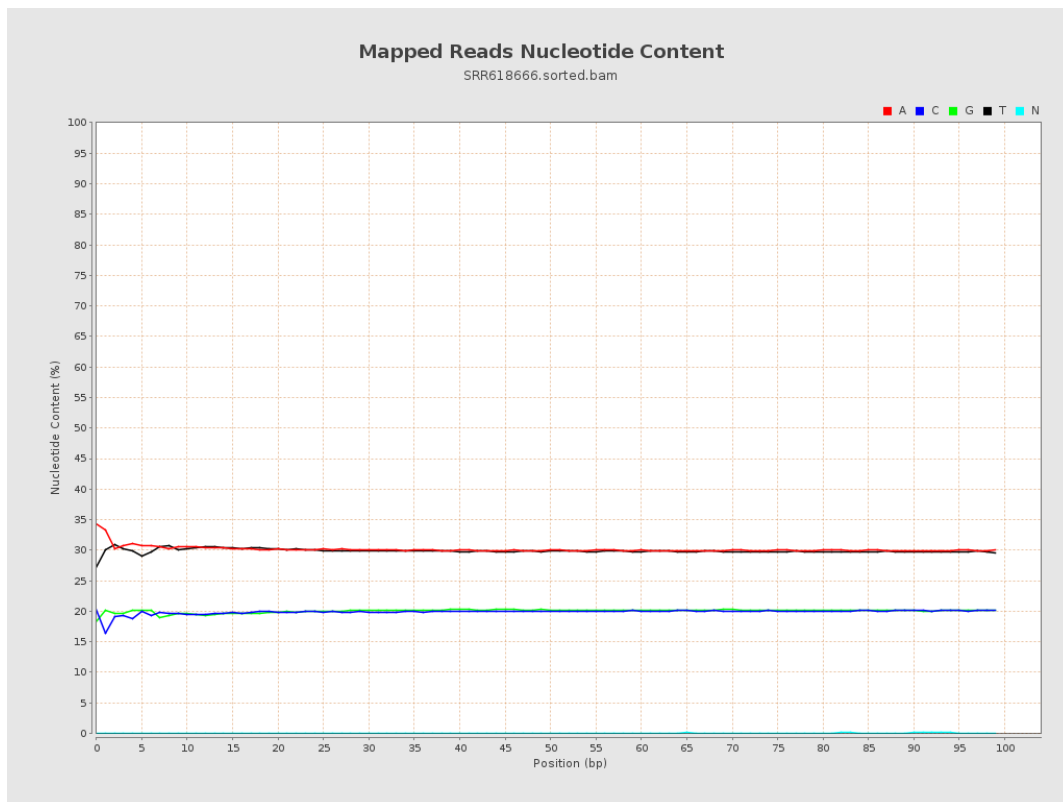
6. Results : Genome Fraction Coverage



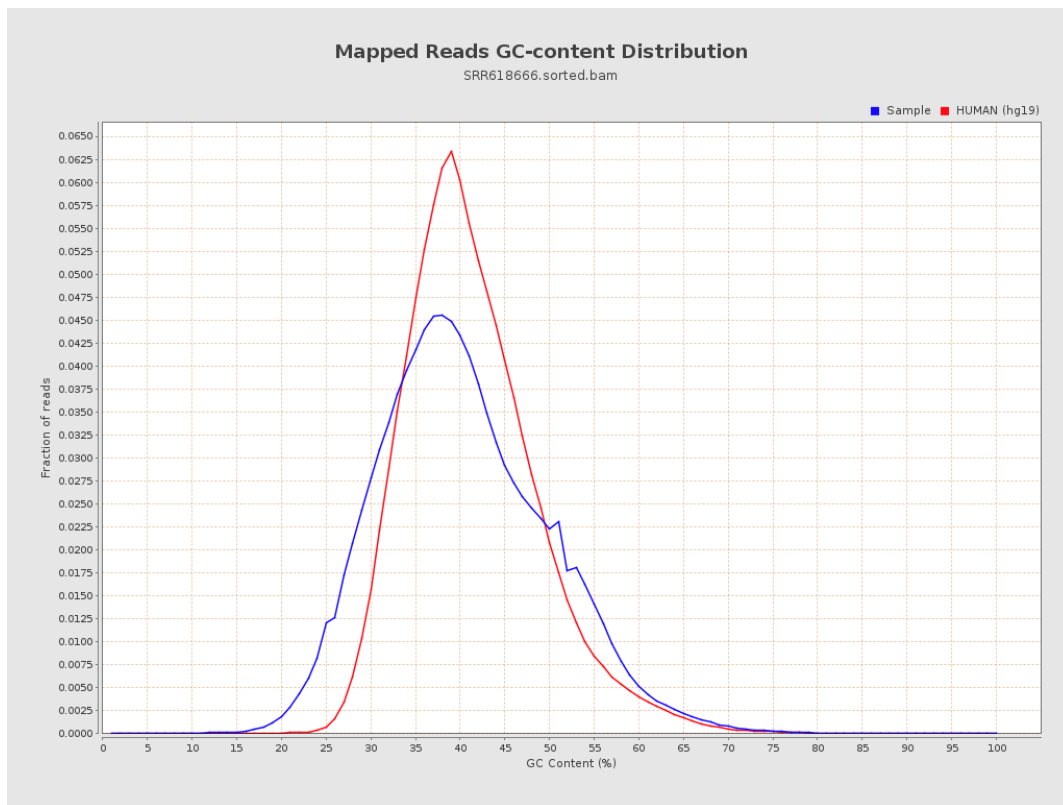
7. Results : Duplication Rate Histogram



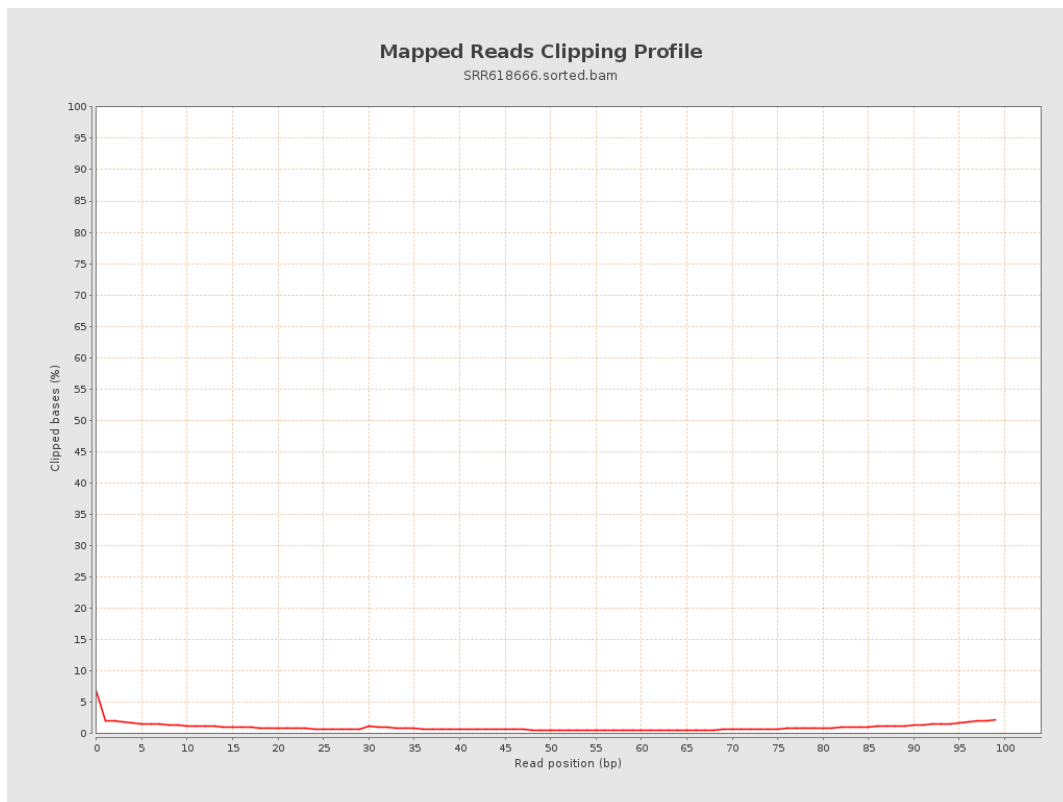
8. Results : Mapped Reads Nucleotide Content



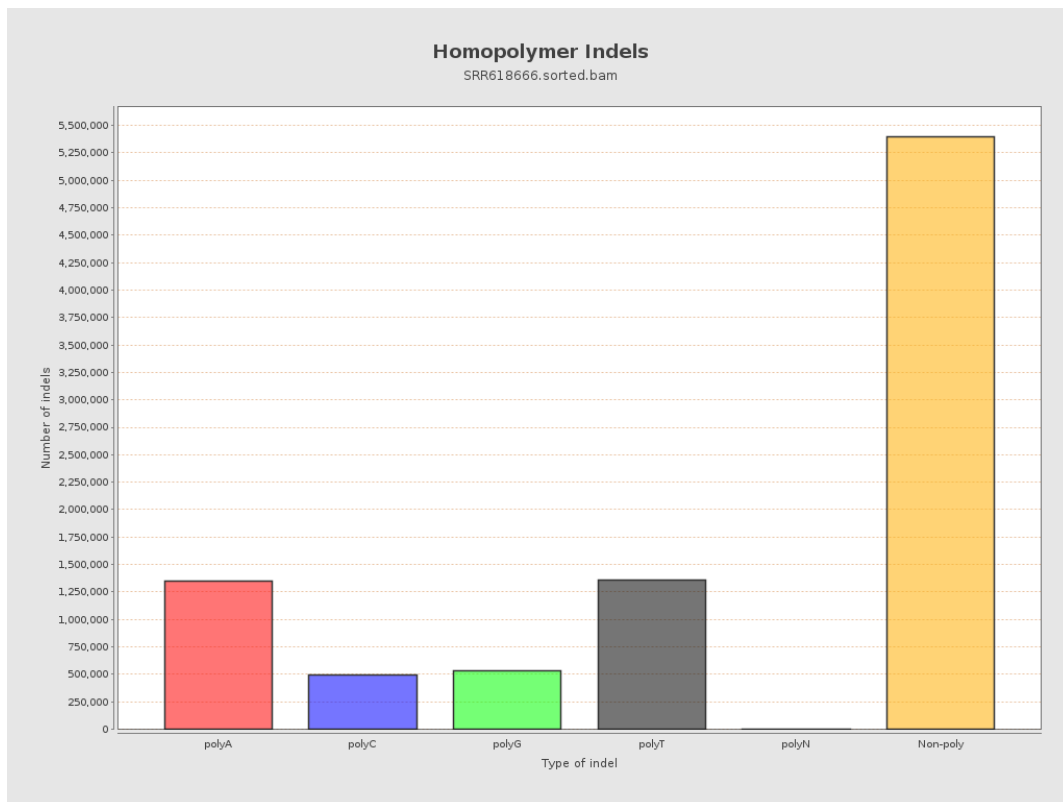
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



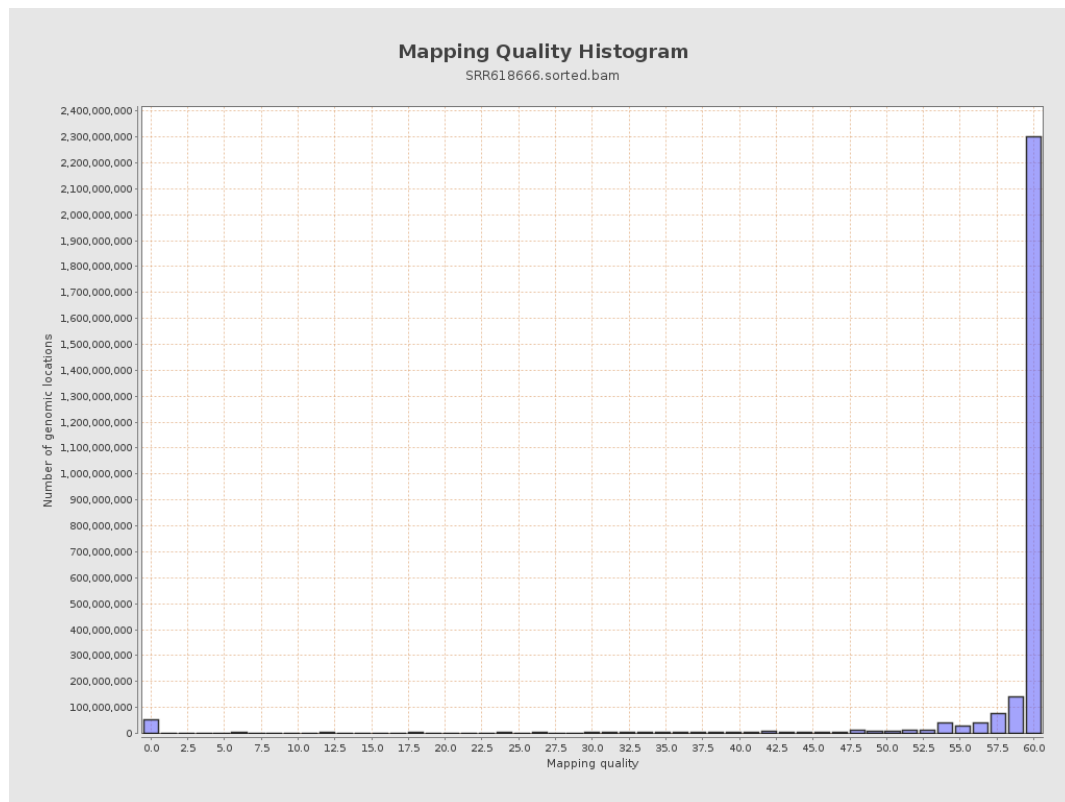
11. Results : Homopolymer Indels



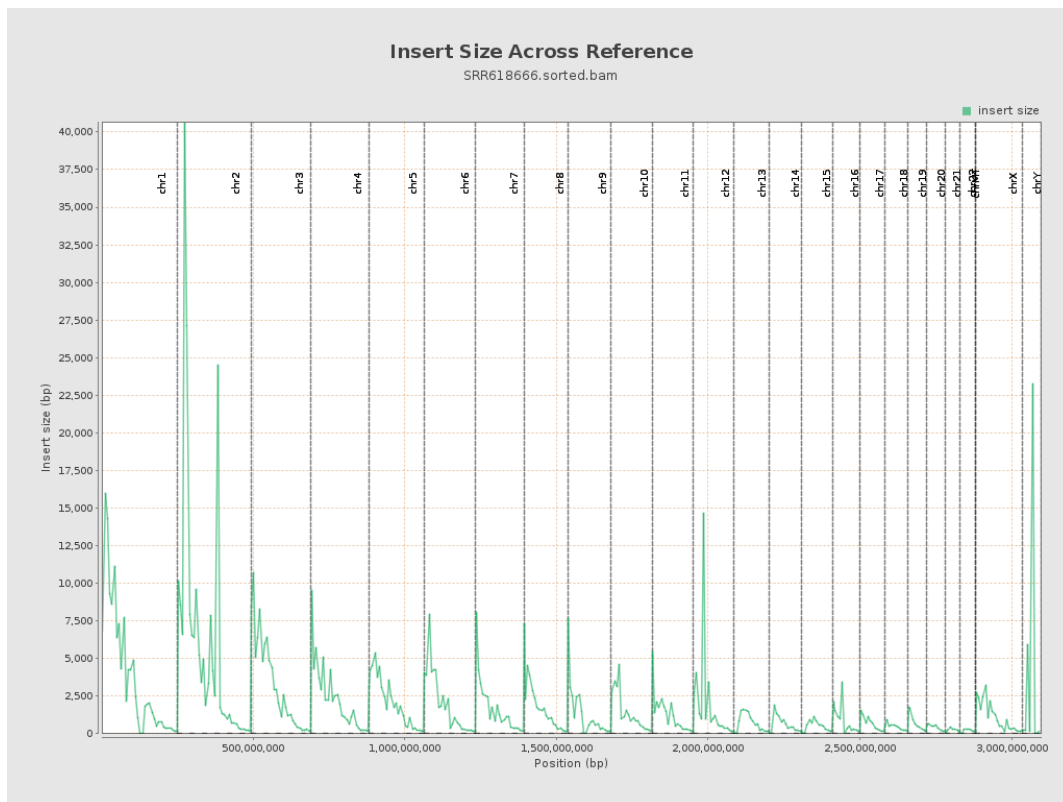
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

