

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 00:29:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618566.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_SRR618566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618566_1.fastq.gz SRR618566_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 00:29:35 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	267,348,940
Mapped reads	256,145,362 / 95.81%
Unmapped reads	11,203,578 / 4.19%
Mapped paired reads	256,145,362 / 95.81%
Mapped reads, first in pair	128,961,928 / 48.24%
Mapped reads, second in pair	127,183,434 / 47.57%
Mapped reads, both in pair	252,122,158 / 94.3%
Mapped reads, singletons	4,023,204 / 1.5%
Secondary alignments	0
Supplementary alignments	2,903,577 / 1.09%
Read min/max/mean length	30 / 100 / 100.45
Duplicated reads (estimated)	101,459,595 / 37.95%
Duplication rate	32%
Clipped reads	66,998,150 / 25.06%

2.2. ACGT Content

Number/percentage of A's	6,497,739,941 / 27.09%
Number/percentage of C's	5,233,565,728 / 21.82%
Number/percentage of T's	6,551,468,865 / 27.31%
Number/percentage of G's	5,705,306,066 / 23.78%
Number/percentage of N's	1,580,540 / 0.01%

GC Percentage	45.6%
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2.3. Coverage

Mean	7.7546
Standard Deviation	26.3968

2.4. Mapping Quality

Mean Mapping Quality	53.44
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2.5. Insert size

Mean	155,967.45
Standard Deviation	3,900,614.23
P25/Median/P75	187 / 208 / 236

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	326,299,746
Insertions	4,050,260
Mapped reads with at least one insertion	1.56%
Deletions	11,929,585
Mapped reads with at least one deletion	4.54%
Homopolymer indels	52.15%

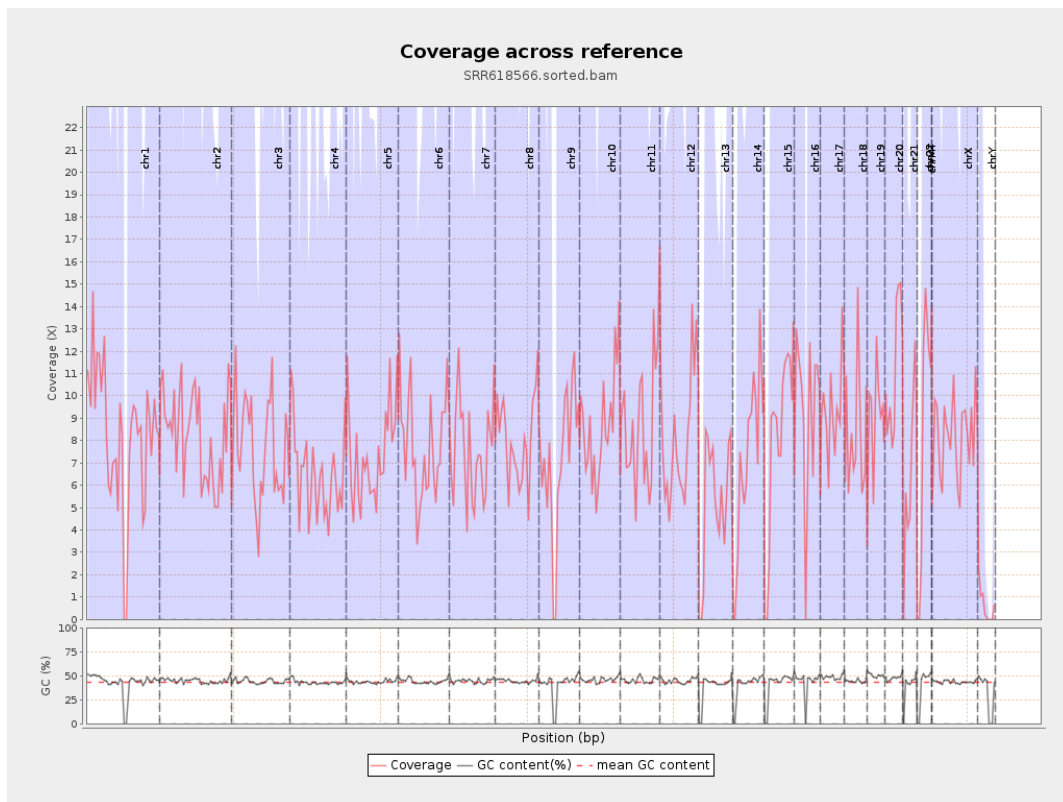
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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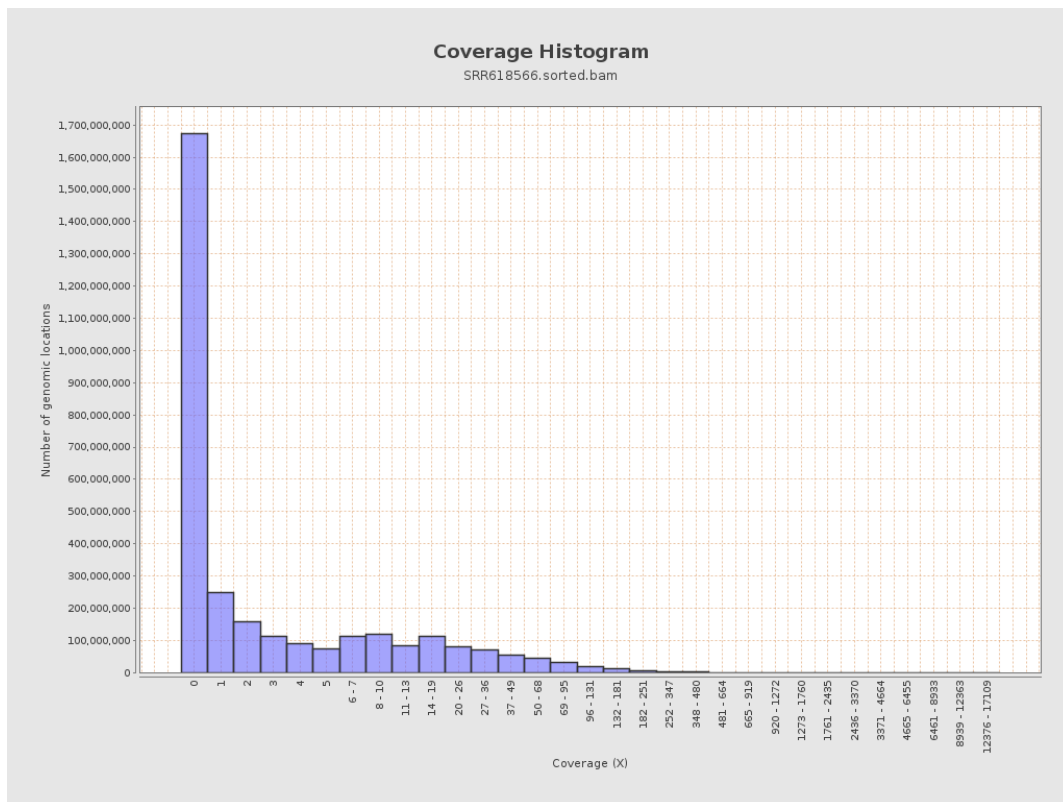
		bases	coverage	deviation
chr1	249250621	2043224972	8.1975	30.9469
chr2	243199373	2014370233	8.2828	28.8643
chr3	198022430	1520619193	7.679	22.6963
chr4	191154276	1228313501	6.4258	23.0916
chr5	180915260	1348405032	7.4532	22.0782
chr6	171115067	1327701466	7.7591	23.8217
chr7	159138663	1197806939	7.5268	22.7631
chr8	146364022	1172060118	8.0078	23.1891
chr9	141213431	1007243237	7.1328	29.3525
chr10	135534747	1173402861	8.6576	25.9415
chr11	135006516	1151508281	8.5293	27.8567
chr12	133851895	1080935627	8.0756	24.0031
chr13	115169878	608042705	5.2795	16.9565
chr14	107349540	761099444	7.0899	23.103
chr15	102531392	812699481	7.9263	25.0338
chr16	90354753	830041017	9.1865	37.3079
chr17	81195210	762508112	9.391	29.5716
chr18	78077248	658052976	8.4282	32.9257
chr19	59128983	541137899	9.1518	30.4591
chr20	63025520	703213809	11.1576	31.8776
chr21	48129895	322119154	6.6927	38.1816
chr22	51304566	438113753	8.5395	29.716
chrMT	16571	84307	5.0876	12.0204
chrX	155270560	1267042958	8.1602	22.9639

chrY	59373566	36271329	0.6109	14.4043
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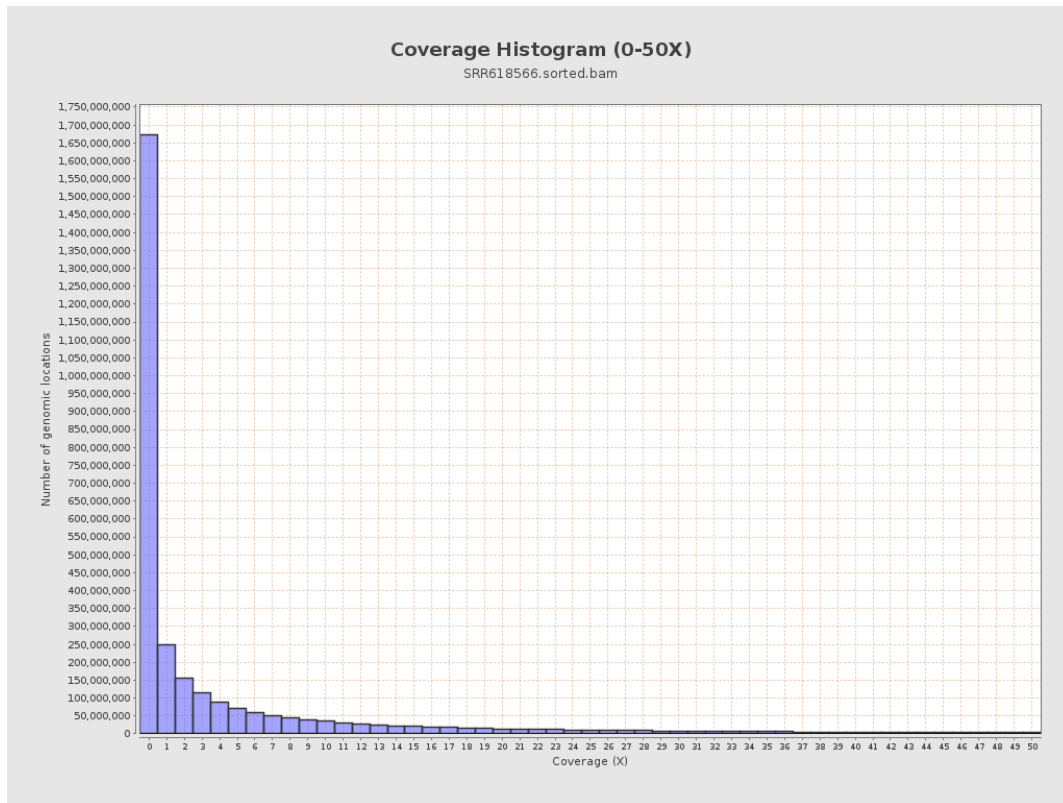
3. Results : Coverage across reference



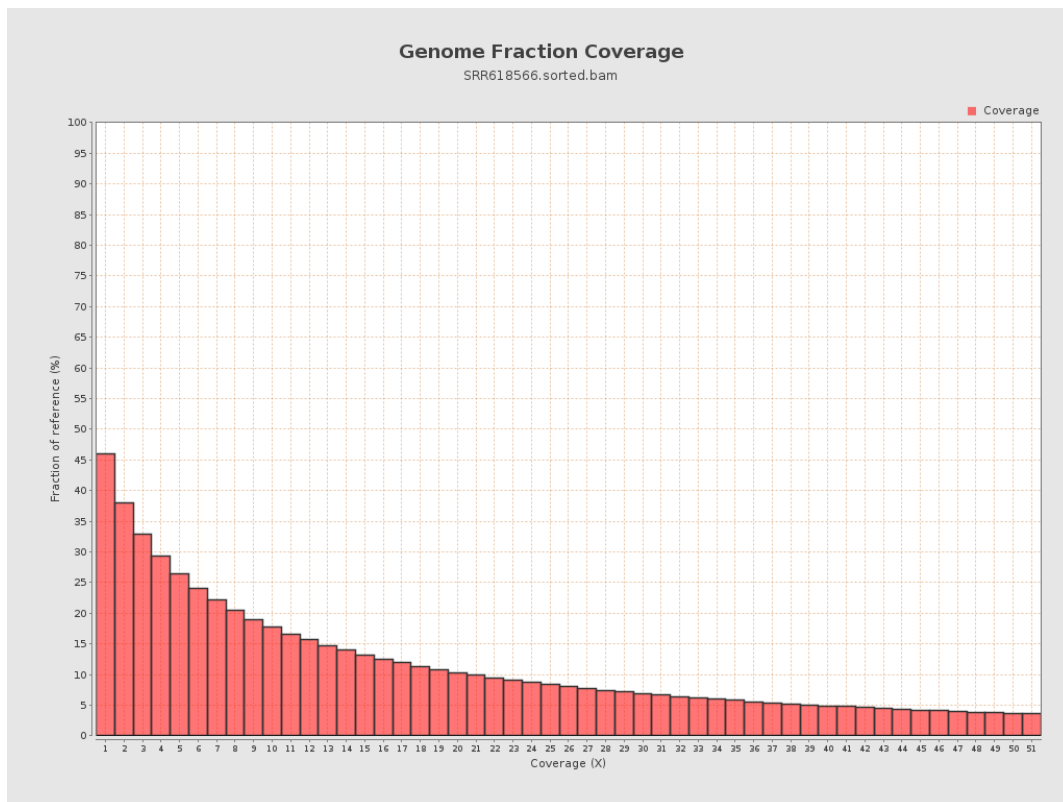
4. Results : Coverage Histogram



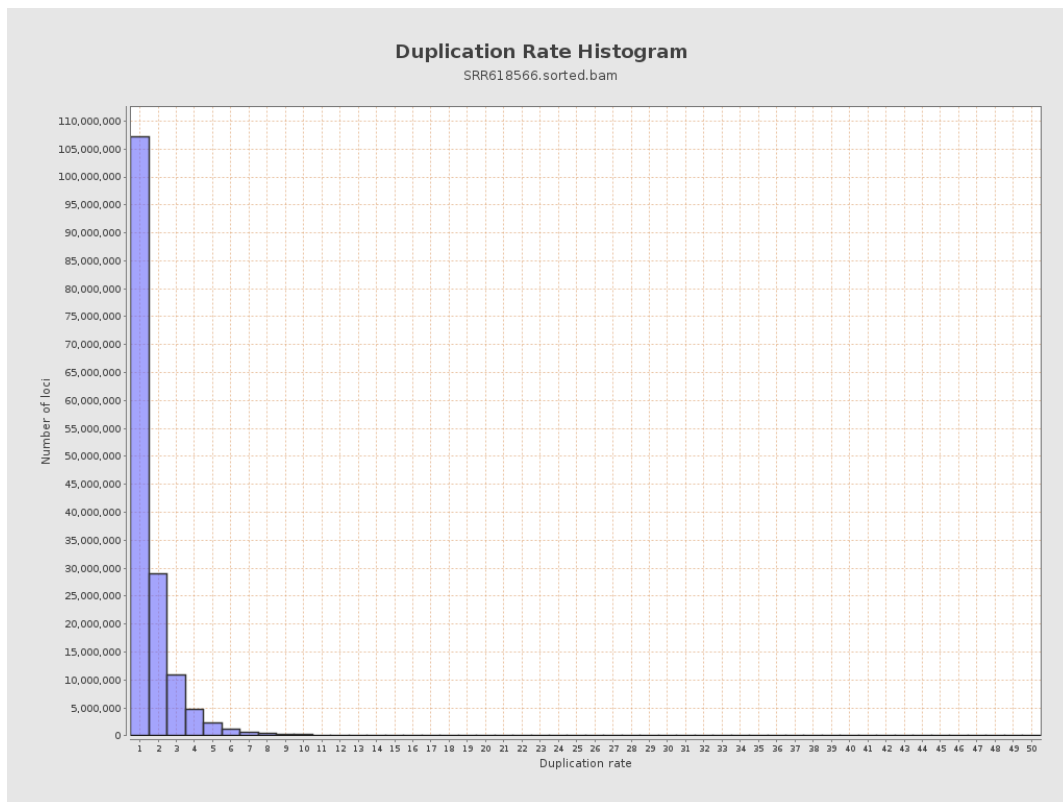
5. Results : Coverage Histogram (0-50X)



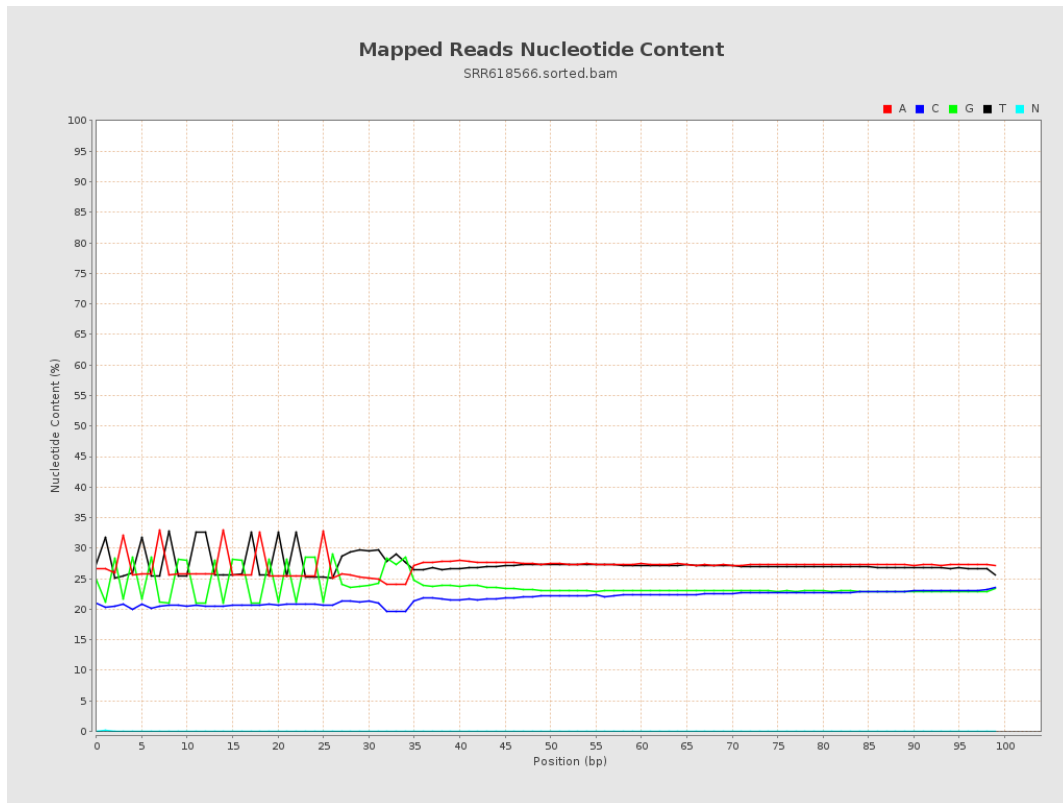
6. Results : Genome Fraction Coverage



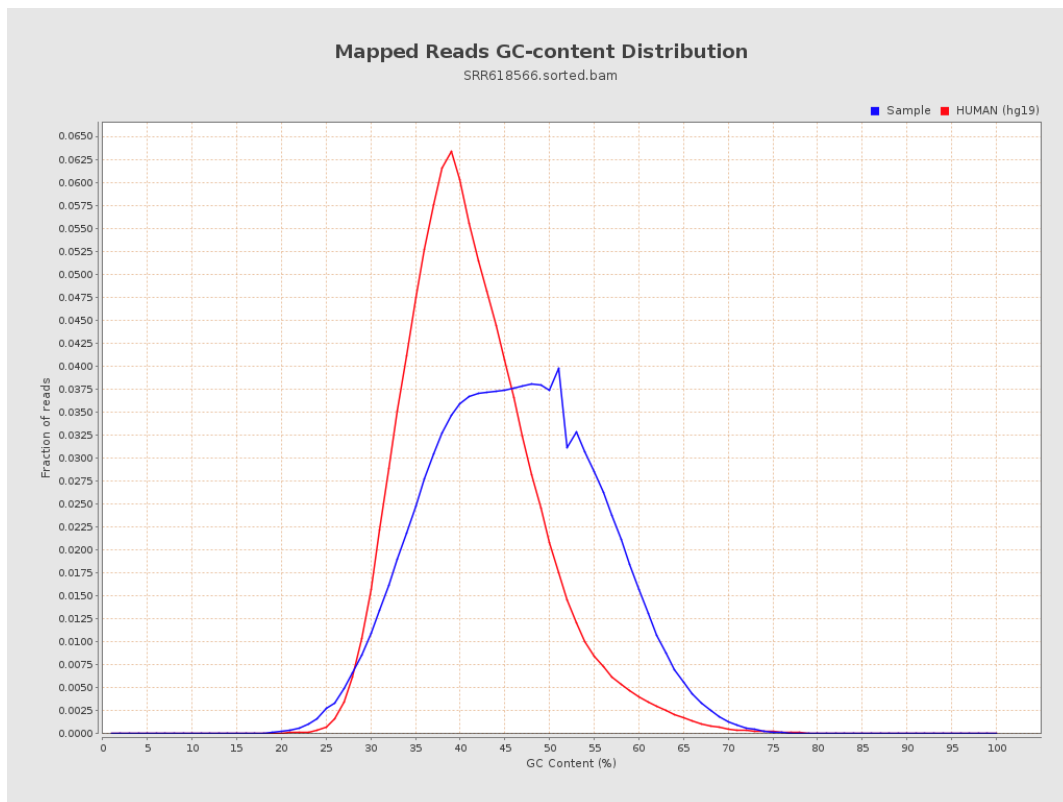
7. Results : Duplication Rate Histogram



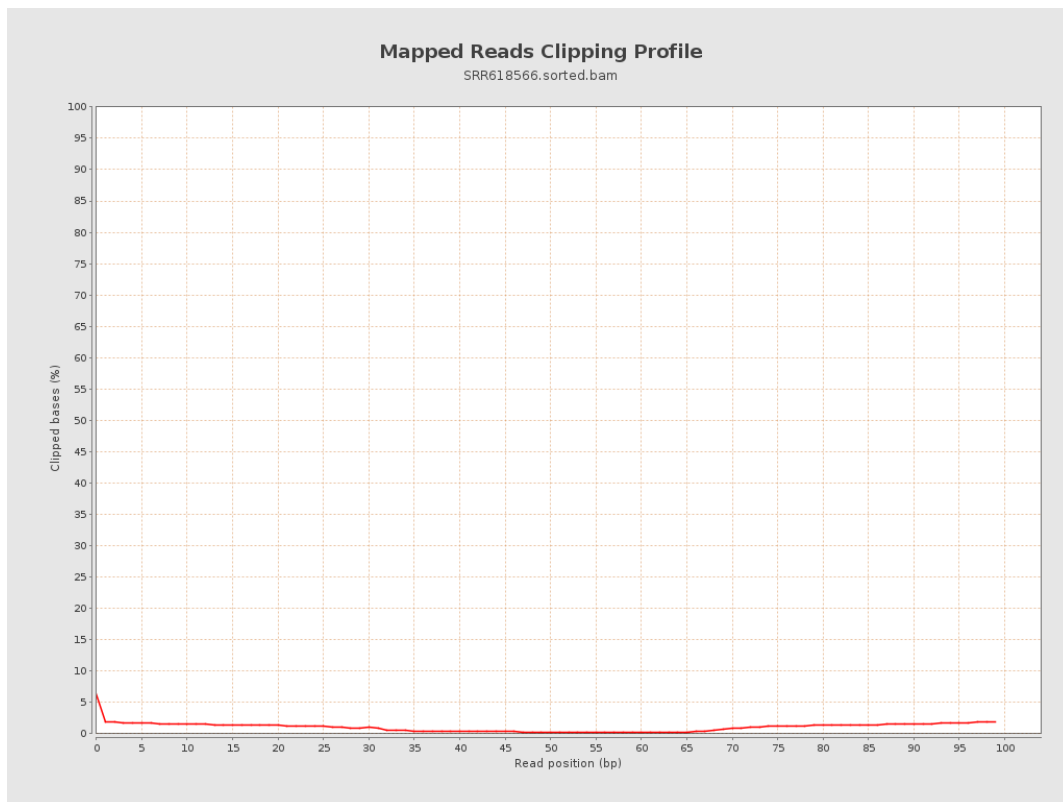
8. Results : Mapped Reads Nucleotide Content



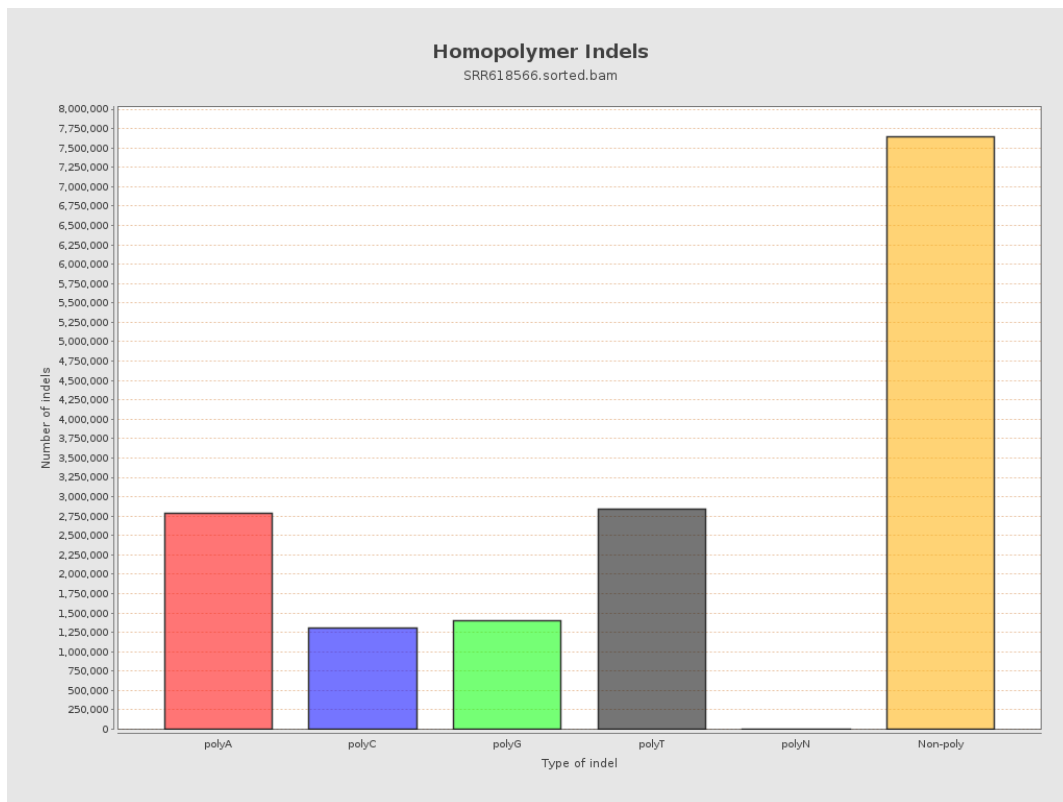
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



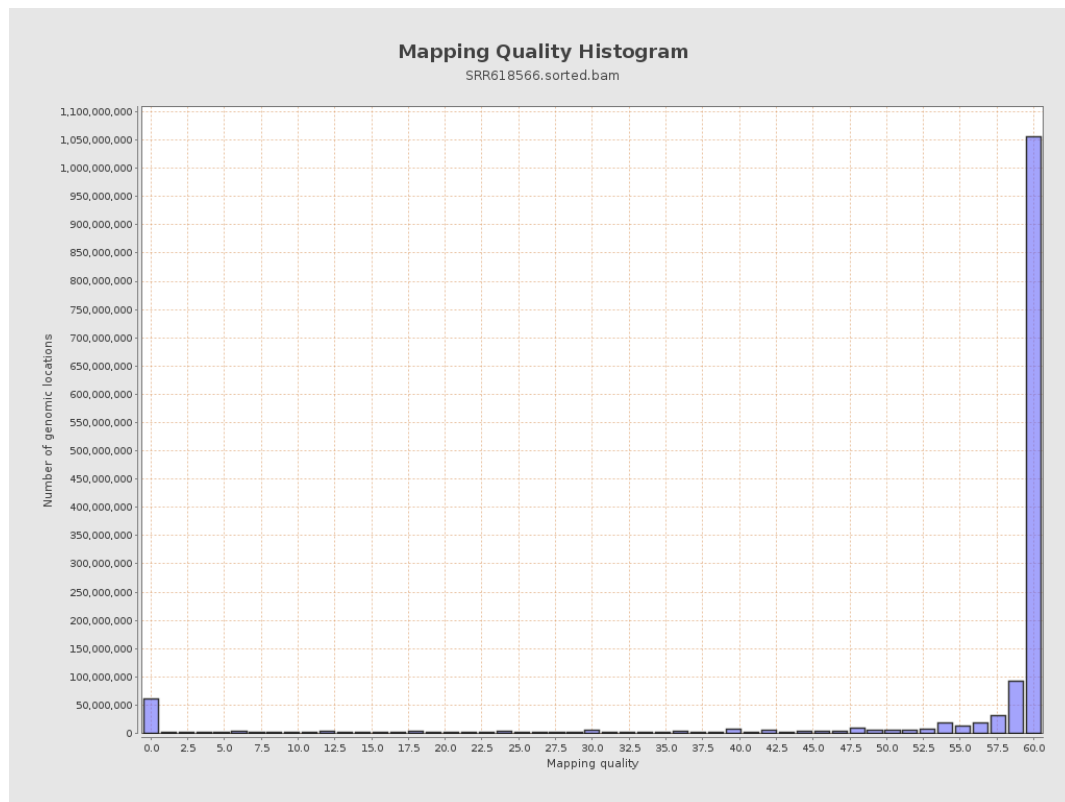
11. Results : Homopolymer Indels



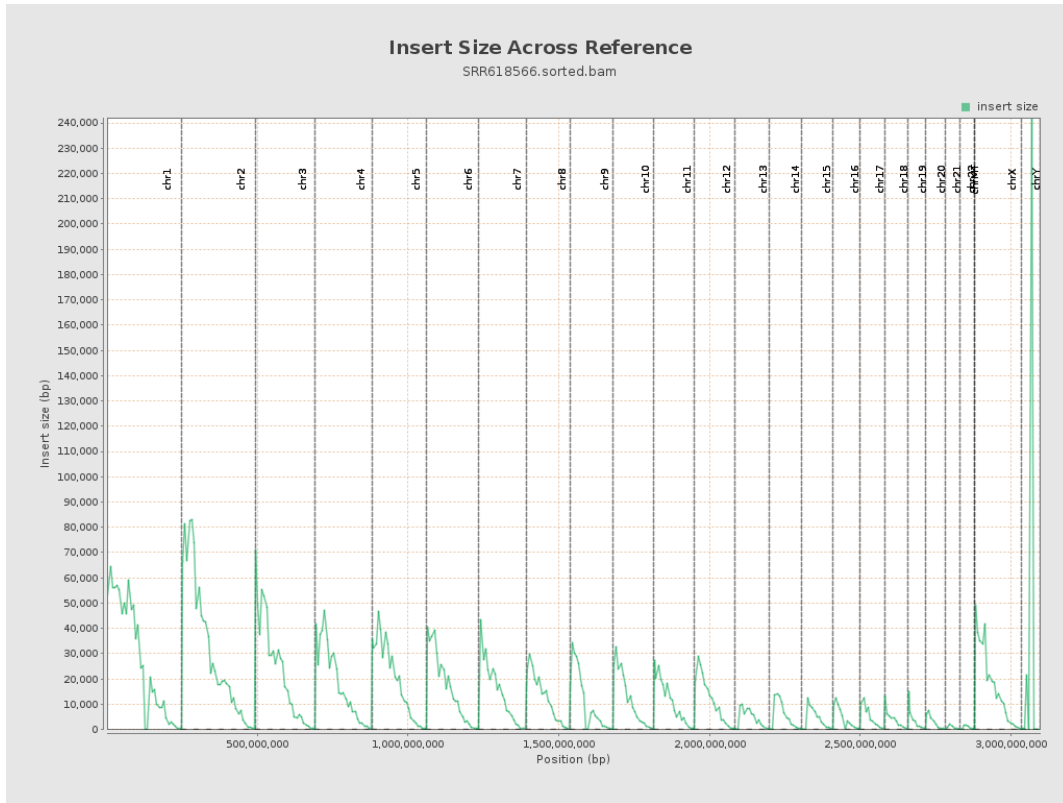
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

