

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 21:04:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618664.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_SRR618664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618664_1.fastq.gz SRR618664_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 21:04:12 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	479,430,622
Mapped reads	460,831,302 / 96.12%
Unmapped reads	18,599,320 / 3.88%
Mapped paired reads	460,831,302 / 96.12%
Mapped reads, first in pair	230,748,310 / 48.13%
Mapped reads, second in pair	230,082,992 / 47.99%
Mapped reads, both in pair	453,433,662 / 94.58%
Mapped reads, singletons	7,397,640 / 1.54%
Secondary alignments	0
Supplementary alignments	892,547 / 0.19%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	134,526,566 / 28.06%
Duplication rate	22.65%
Clipped reads	64,414,705 / 13.44%

2.2. ACGT Content

Number/percentage of A's	13,252,624,228 / 29.72%
Number/percentage of C's	9,094,167,280 / 20.39%
Number/percentage of T's	13,197,762,925 / 29.6%
Number/percentage of G's	9,046,283,899 / 20.29%
Number/percentage of N's	3,316,340 / 0.01%

GC Percentage	40.68%
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2.3. Coverage

Mean	14.4095
Standard Deviation	156.2724

2.4. Mapping Quality

Mean Mapping Quality	53.65
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2.5. Insert size

Mean	29,692.9
Standard Deviation	1,633,788.46
P25/Median/P75	210 / 238 / 277

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	507,753,503
Insertions	5,174,636
Mapped reads with at least one insertion	1.09%
Deletions	5,726,247
Mapped reads with at least one deletion	1.21%
Homopolymer indels	40.83%

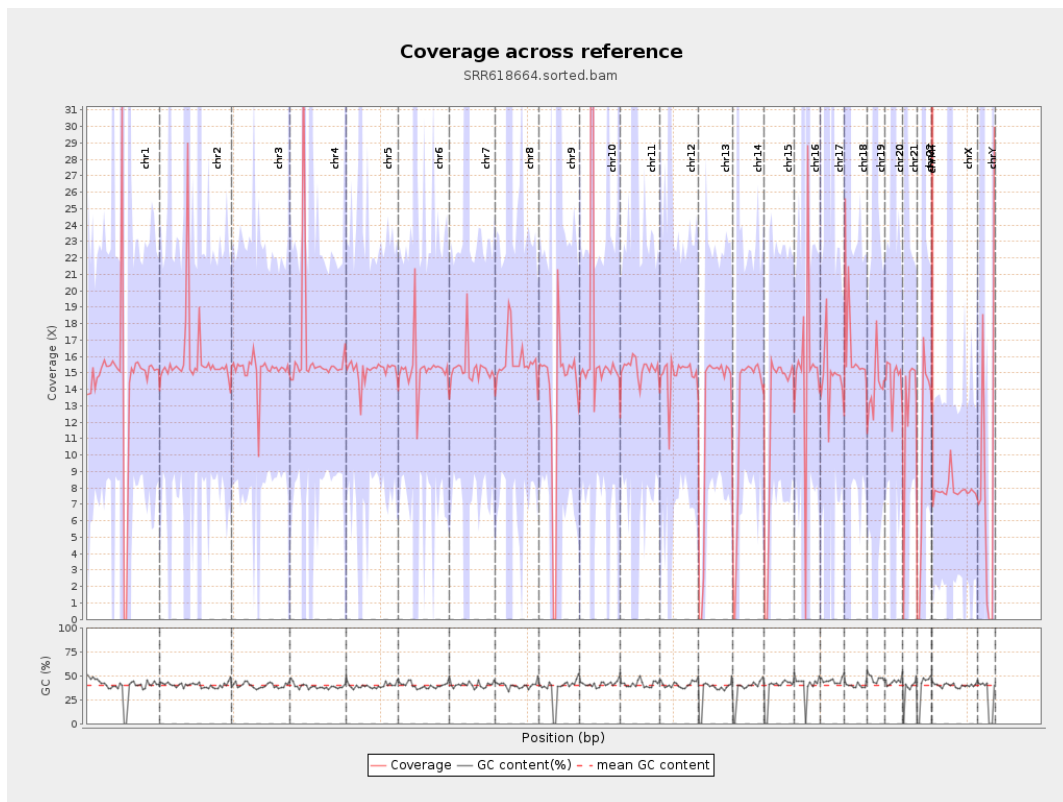
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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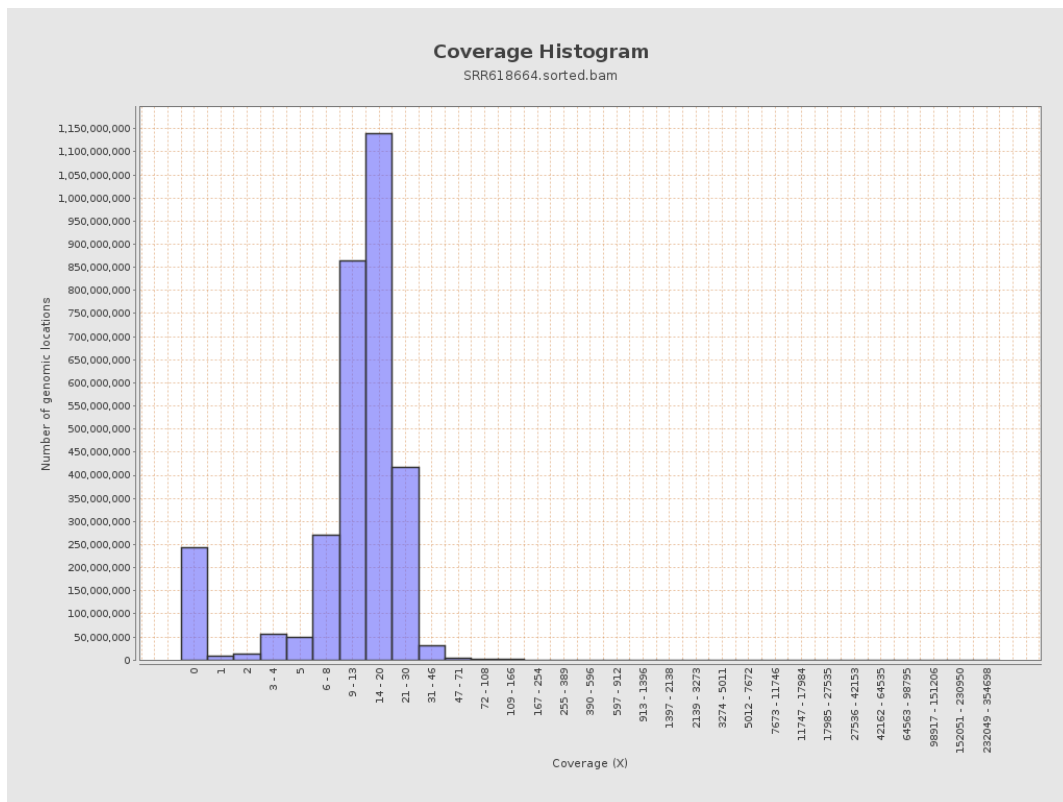
		bases	coverage	deviation
chr1	249250621	3653201242	14.6567	367.2366
chr2	243199373	3859958796	15.8716	88.2948
chr3	198022430	2999566318	15.1476	9.2473
chr4	191154276	3068937597	16.0548	136.1833
chr5	180915260	2734455148	15.1146	11.6618
chr6	171115067	2615212550	15.2834	70.4994
chr7	159138663	2430270440	15.2714	111.3989
chr8	146364022	2301853209	15.7269	221.6254
chr9	141213431	1912130952	13.5407	160.1498
chr10	135534747	2360082310	17.4131	318.536
chr11	135006516	2058688280	15.2488	75.0203
chr12	133851895	1992454104	14.8855	11.938
chr13	115169878	1458797313	12.6665	8.6227
chr14	107349540	1358947356	12.6591	12.9063
chr15	102531392	1270682135	12.3931	8.9509
chr16	90354753	1371710244	15.1814	105.8933
chr17	81195210	1190474039	14.6619	70.5832
chr18	78077248	1277900774	16.3671	207.7464
chr19	59128983	833295661	14.0928	148.873
chr20	63025520	920207145	14.6005	39.4426
chr21	48129895	624550984	12.9764	60.1575
chr22	51304566	534600469	10.4201	59.8335
chrMT	16571	22651748	1,366.9512	176.5756
chrX	155270560	1219624014	7.8548	28.4656

chrY	59373566	537153752	9.047	162.9544
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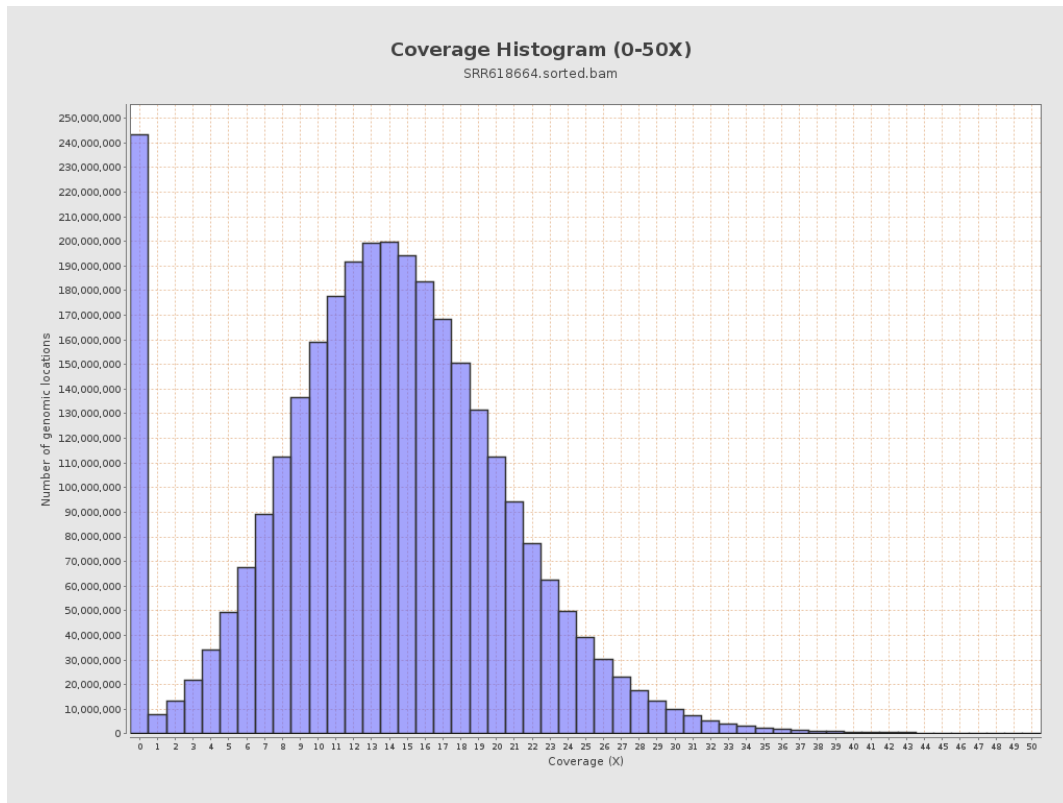
3. Results : Coverage across reference



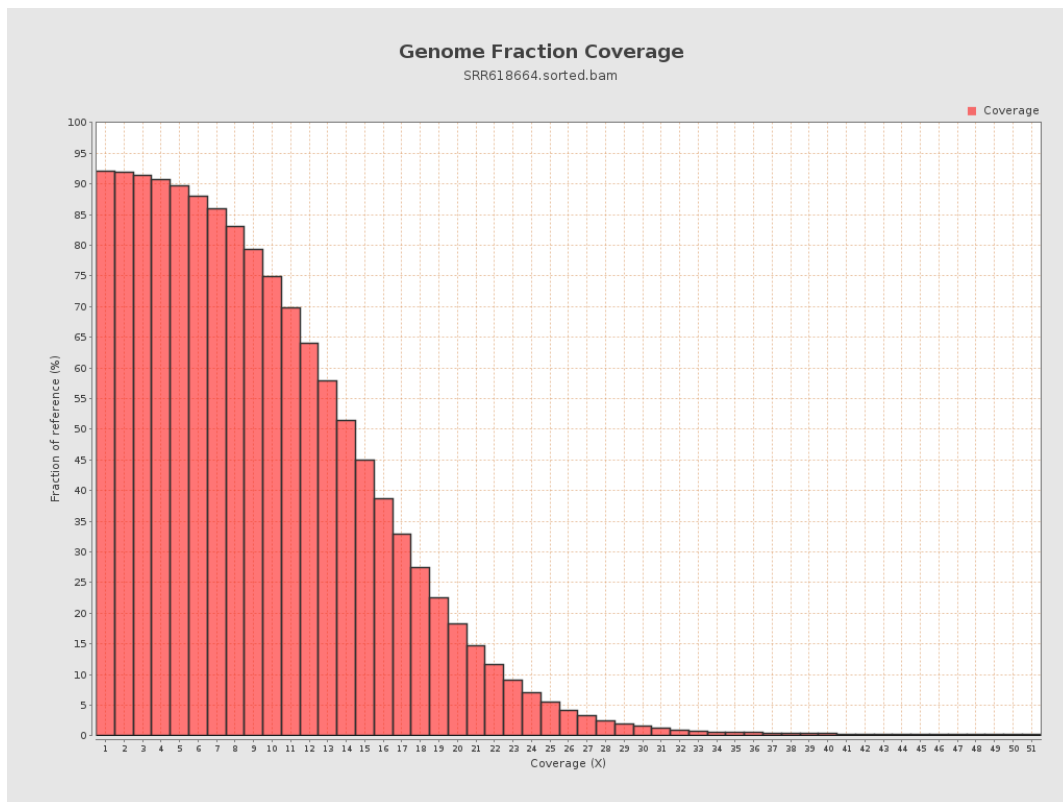
4. Results : Coverage Histogram



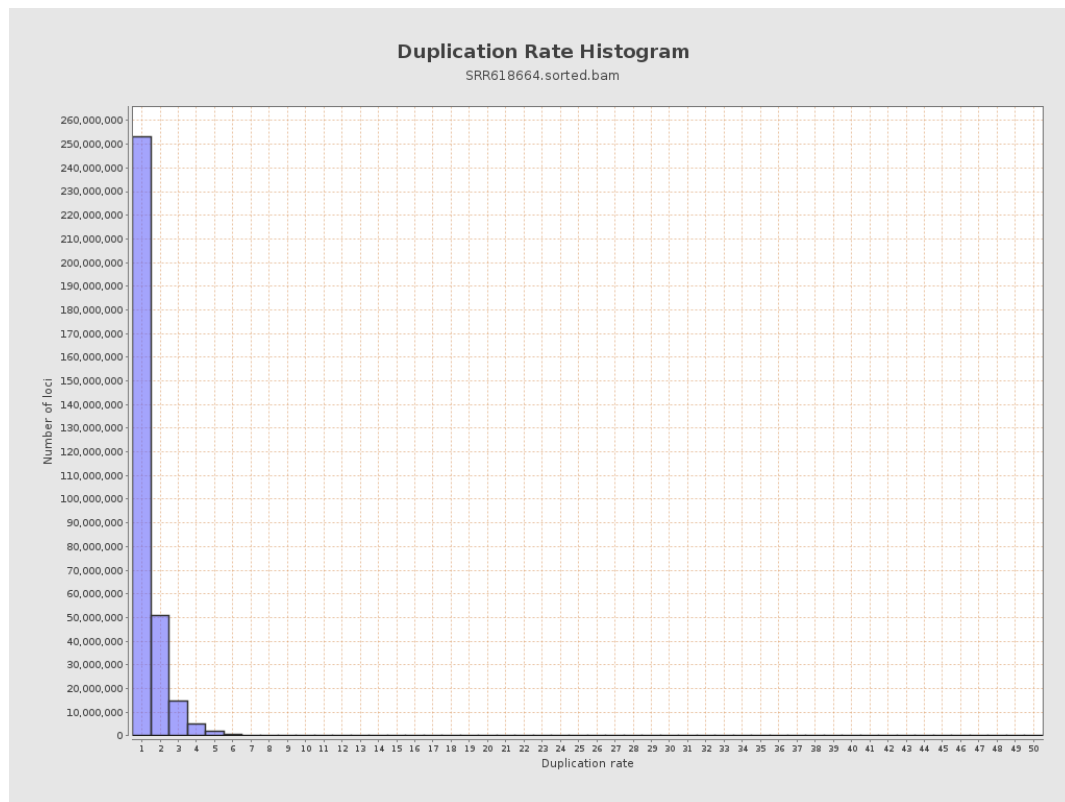
5. Results : Coverage Histogram (0-50X)



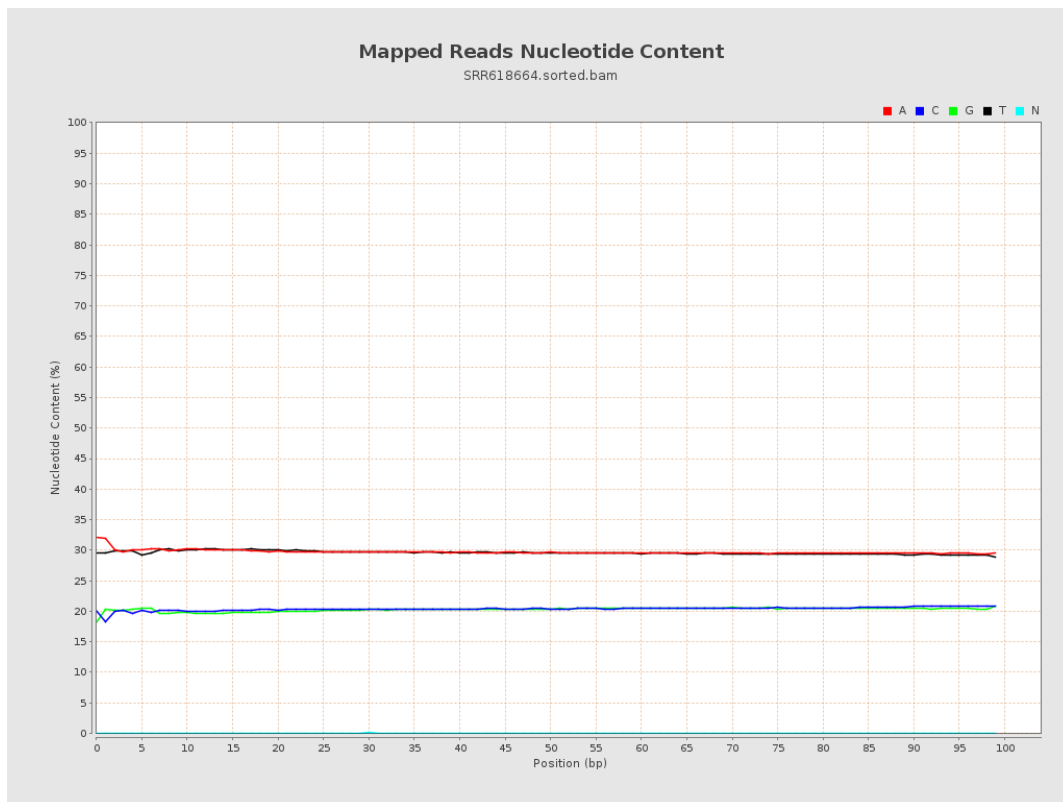
6. Results : Genome Fraction Coverage



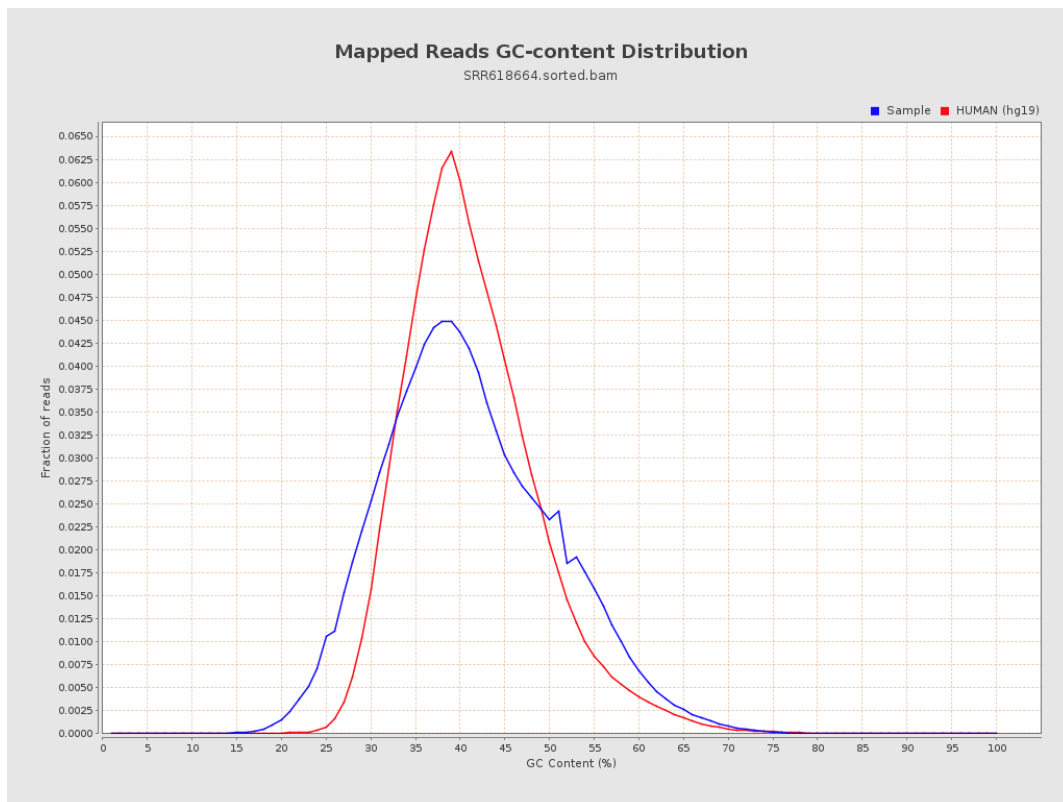
7. Results : Duplication Rate Histogram



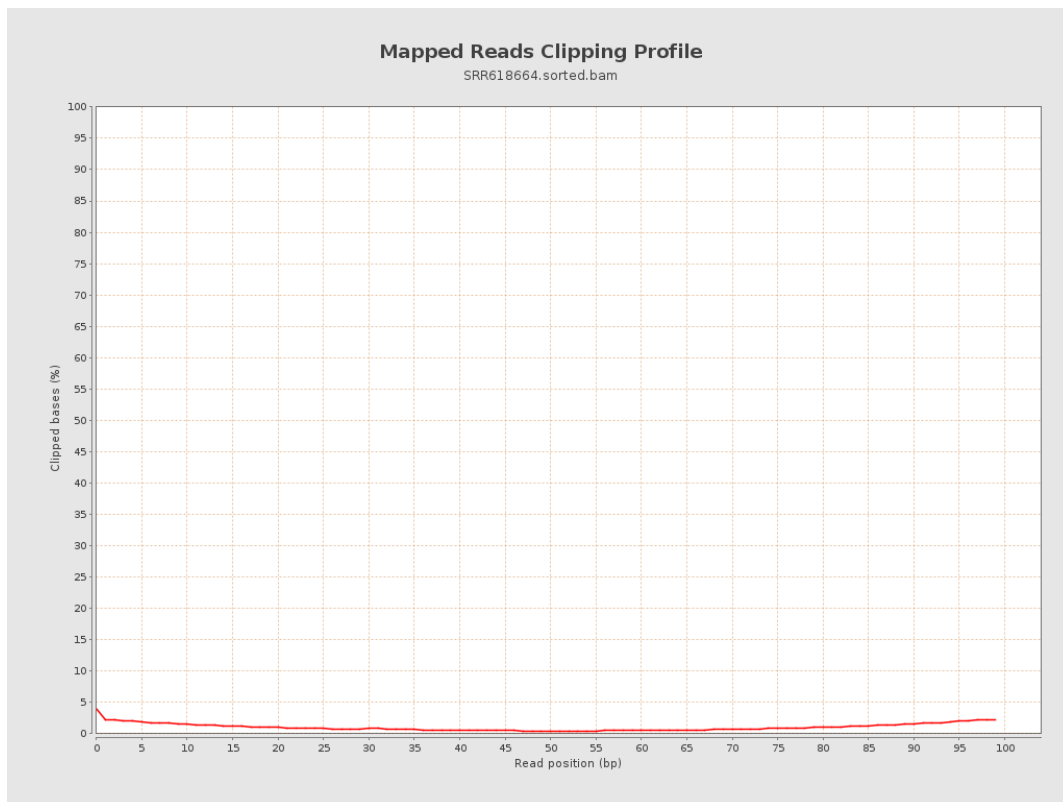
8. Results : Mapped Reads Nucleotide Content



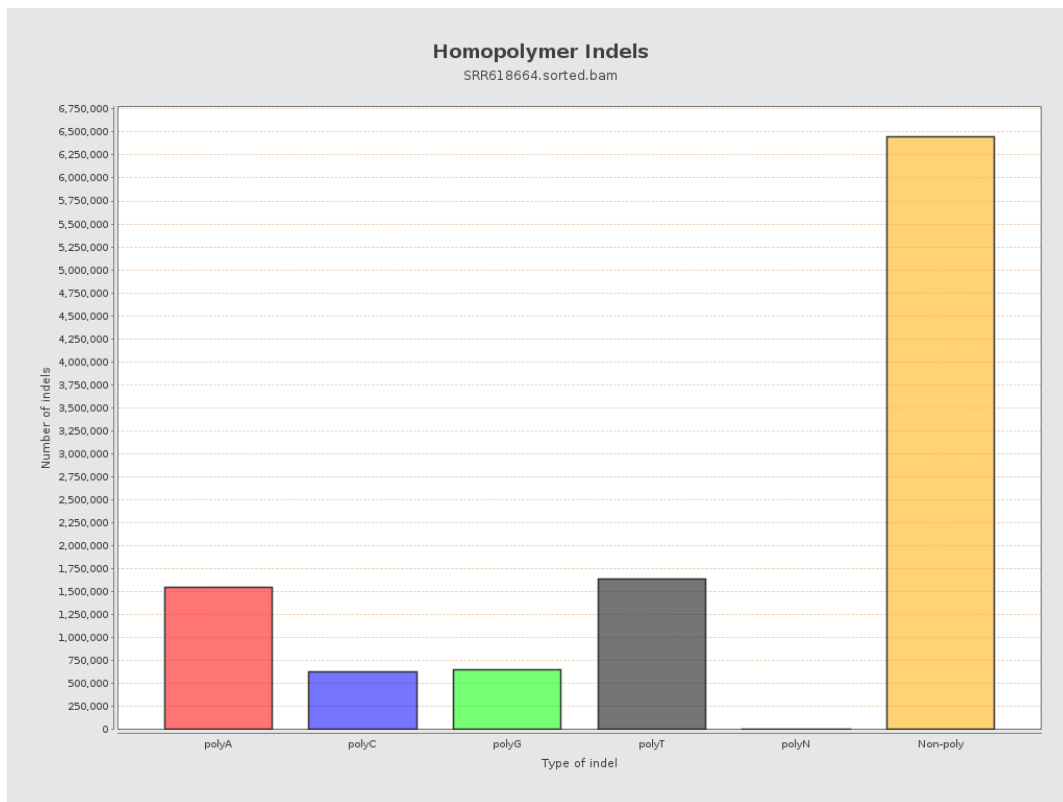
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



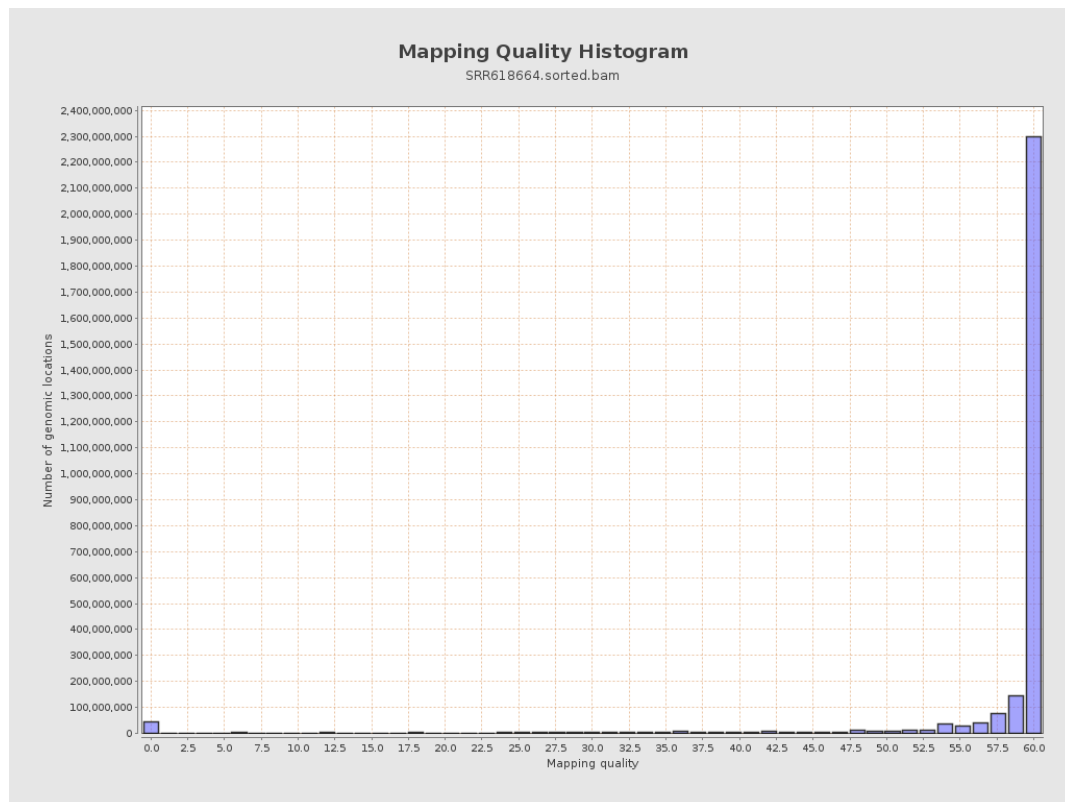
11. Results : Homopolymer Indels



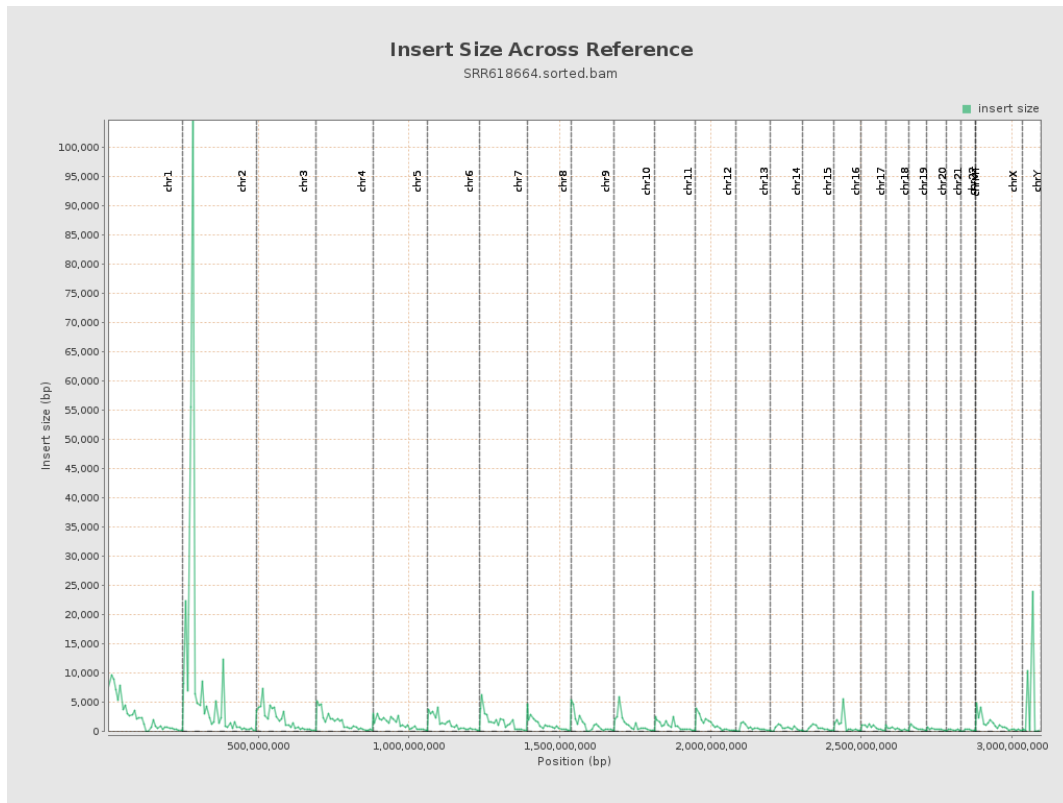
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

