

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 02:07:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264616.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_SRR1264616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264616_1.fastq.gz SRR1264616_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 02:07:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,195,630,648
Mapped reads	1,189,184,192 / 99.46%
Unmapped reads	6,446,456 / 0.54%
Mapped paired reads	1,189,184,192 / 99.46%
Mapped reads, first in pair	595,902,050 / 49.84%
Mapped reads, second in pair	593,282,142 / 49.62%
Mapped reads, both in pair	1,185,322,156 / 99.14%
Mapped reads, singletons	3,862,036 / 0.32%
Secondary alignments	0
Supplementary alignments	11,192,320 / 0.94%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	445,683,344 / 37.28%
Duplication rate	37.12%
Clipped reads	74,085,679 / 6.2%

2.2. ACGT Content

Number/percentage of A's	36,395,159,251 / 30.84%
Number/percentage of C's	22,472,617,939 / 19.04%
Number/percentage of T's	36,304,127,852 / 30.76%
Number/percentage of G's	22,788,546,333 / 19.31%
Number/percentage of N's	66,053,354 / 0.06%

GC Percentage	38.35%
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2.3. Coverage

Mean	38.1348
Standard Deviation	38.3681

2.4. Mapping Quality

Mean Mapping Quality	54.34
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2.5. Insert size

Mean	113,324.75
Standard Deviation	3,222,760.15
P25/Median/P75	259 / 302 / 340

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	458,633,750
Insertions	12,527,101
Mapped reads with at least one insertion	1.04%
Deletions	12,032,916
Mapped reads with at least one deletion	0.99%
Homopolymer indels	47.05%

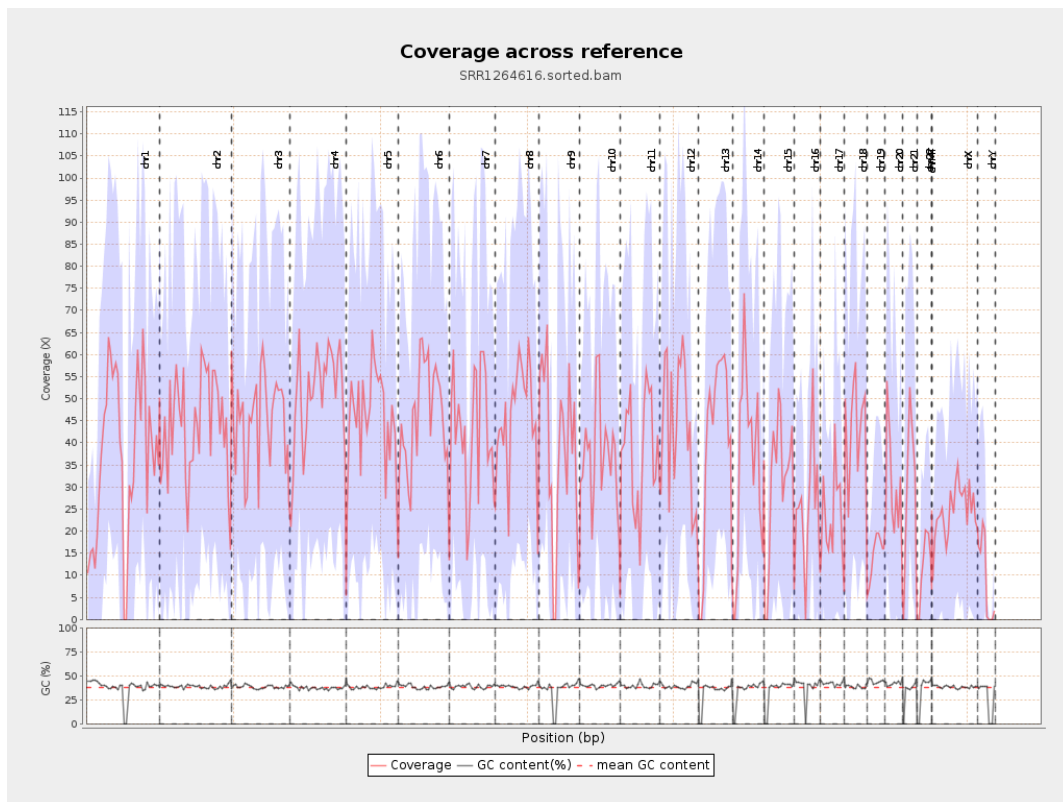
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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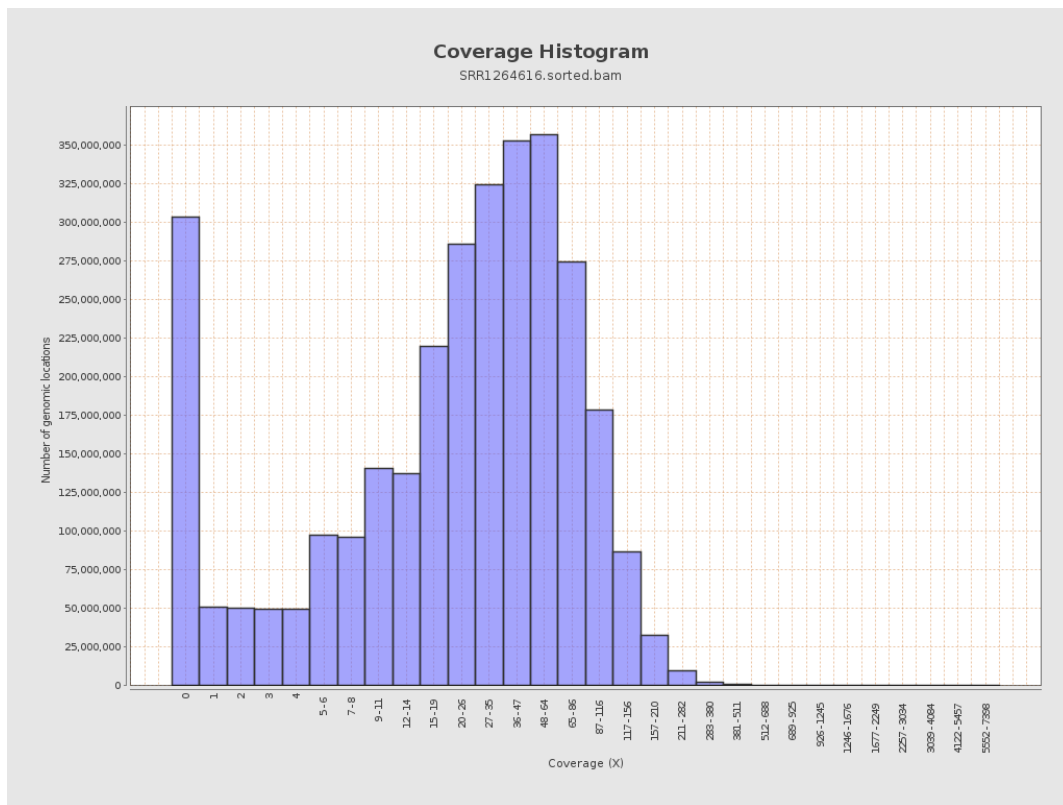
		bases	coverage	deviation
chr1	249250621	9293893492	37.2873	39.7404
chr2	243199373	10695836520	43.9797	39.0034
chr3	198022430	8950839247	45.2011	37.761
chr4	191154276	9841867976	51.4865	40.532
chr5	180915260	8216366410	45.4156	37.8182
chr6	171115067	7990651946	46.6975	39.9993
chr7	159138663	6687752752	42.0247	39.766
chr8	146364022	6815165736	46.5631	38.6723
chr9	141213431	5189468414	36.7491	41.1578
chr10	135534747	5045016271	37.223	35.3242
chr11	135006516	5138883113	38.064	37.5768
chr12	133851895	5732994840	42.8309	40.0649
chr13	115169878	4735833654	41.1204	39.2341
chr14	107349540	3871175847	36.0614	39.3791
chr15	102531392	3174908483	30.9652	37.7215
chr16	90354753	2200603330	24.3551	30.1287
chr17	81195210	1865041562	22.9698	28.4227
chr18	78077248	3399500389	43.5402	38.0022
chr19	59128983	868517355	14.6885	21.4112
chr20	63025520	1857820689	29.4773	37.7308
chr21	48129895	1497025508	31.1039	40.1757
chr22	51304566	605122358	11.7947	20.0044
chrMT	16571	409806	24.7303	6.8037
chrX	155270560	3826347557	24.6431	25.7143

chrY	59373566	552614896	9.3074	20.2329
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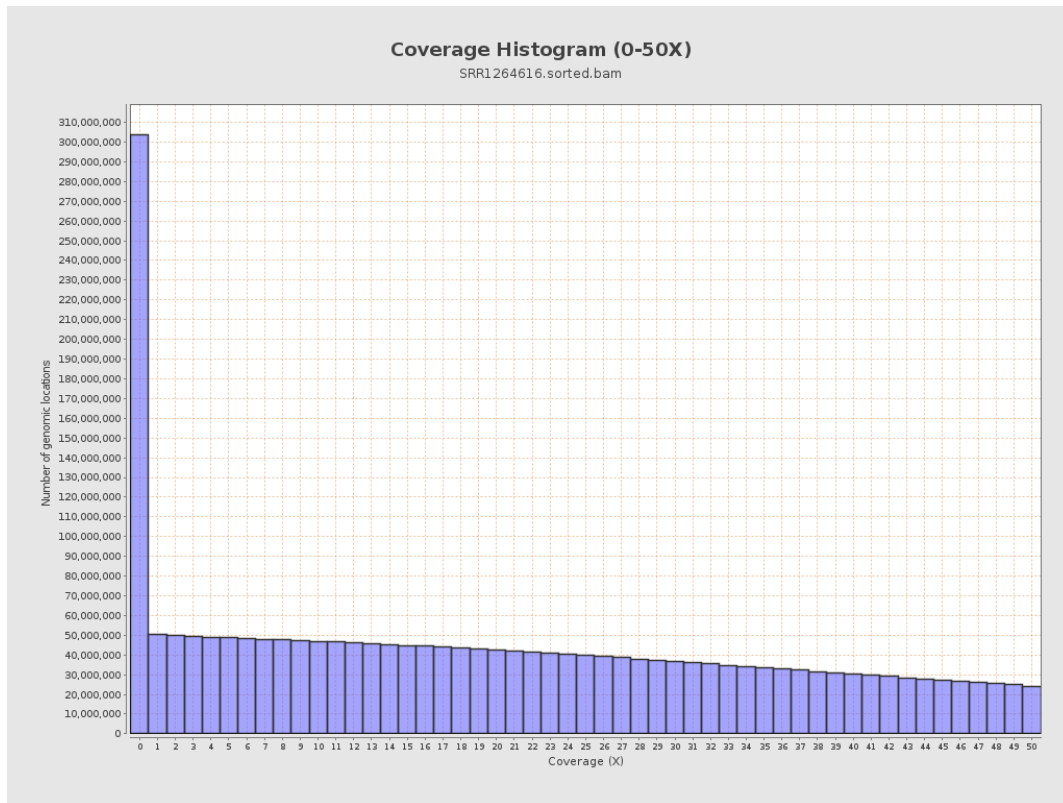
3. Results : Coverage across reference



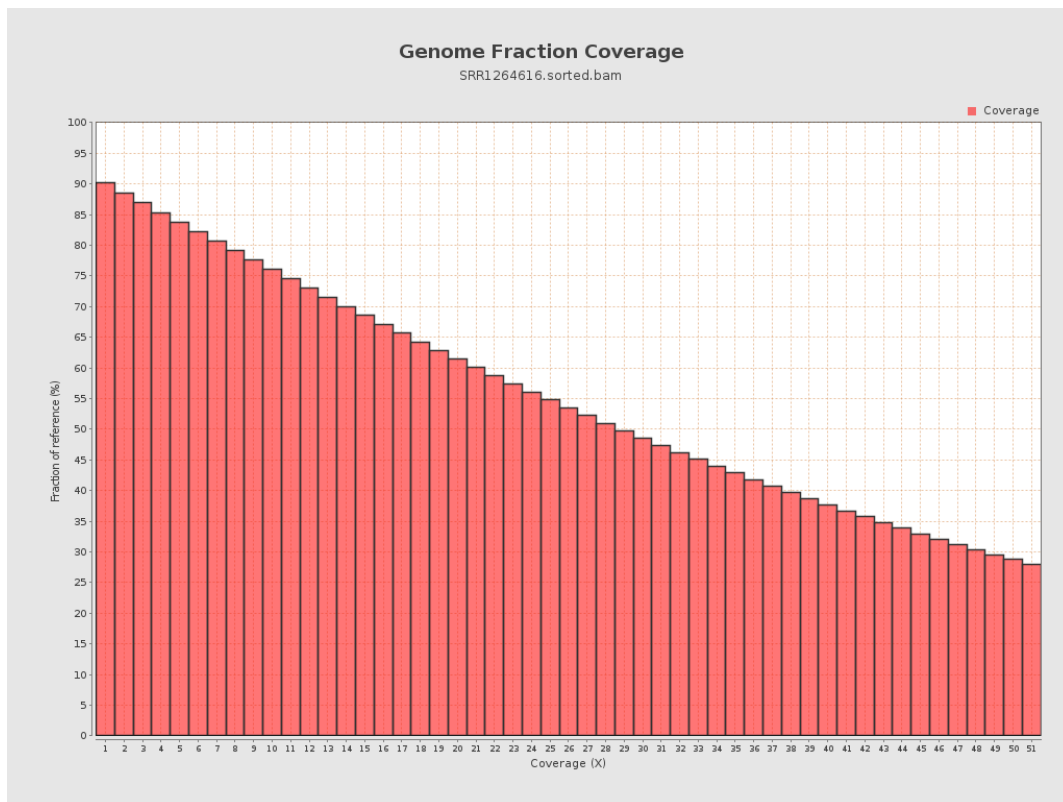
4. Results : Coverage Histogram



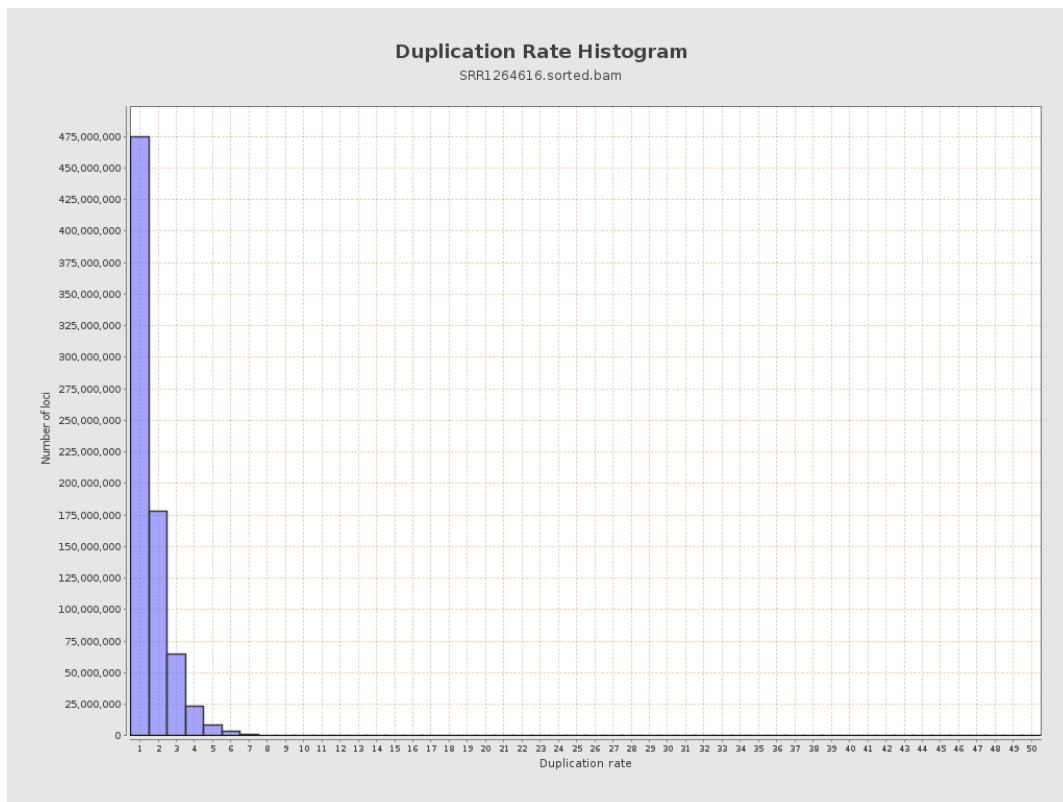
5. Results : Coverage Histogram (0-50X)



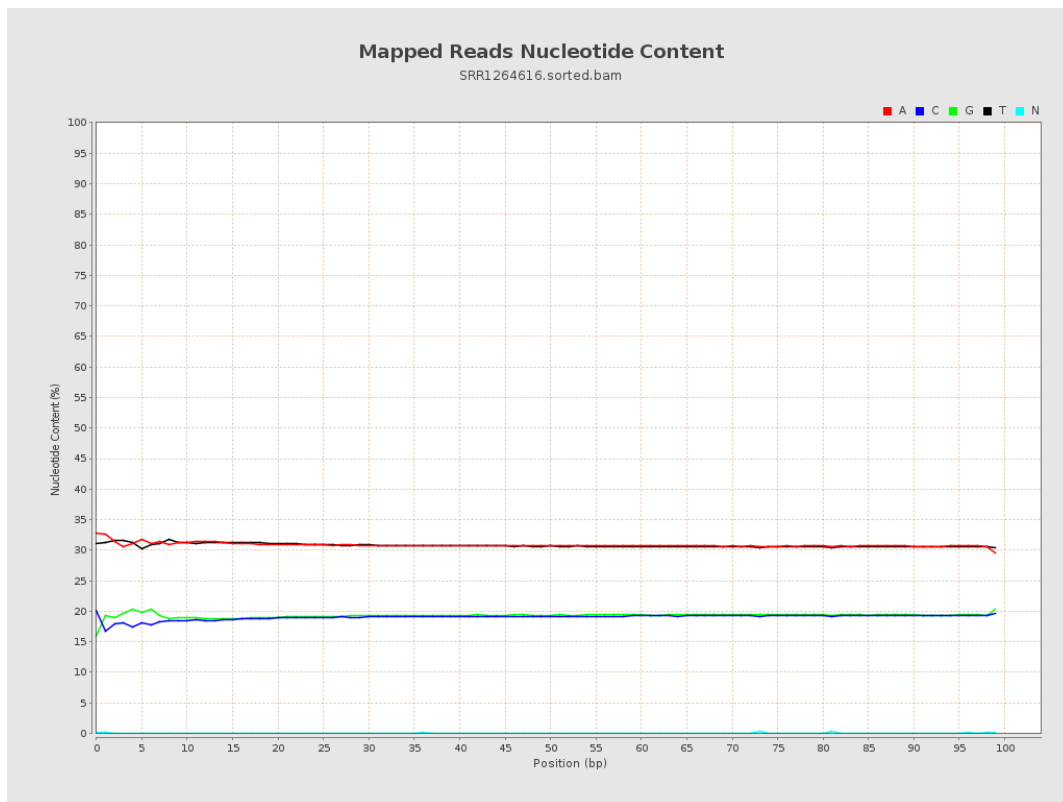
6. Results : Genome Fraction Coverage



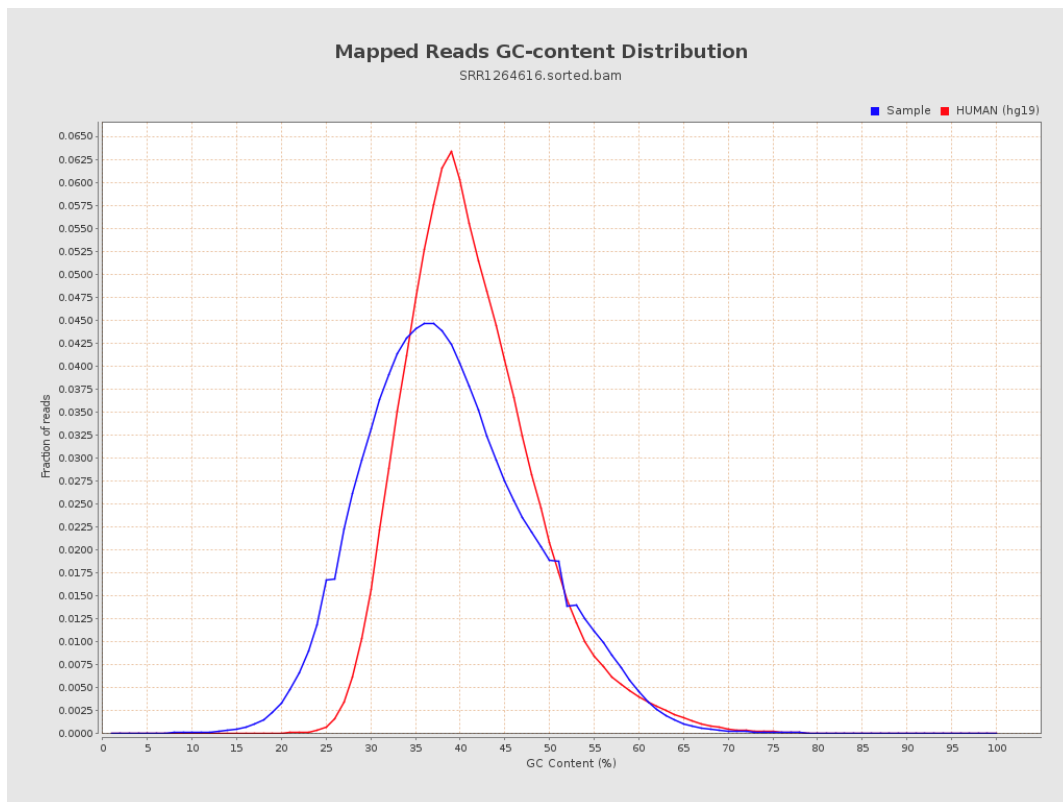
7. Results : Duplication Rate Histogram



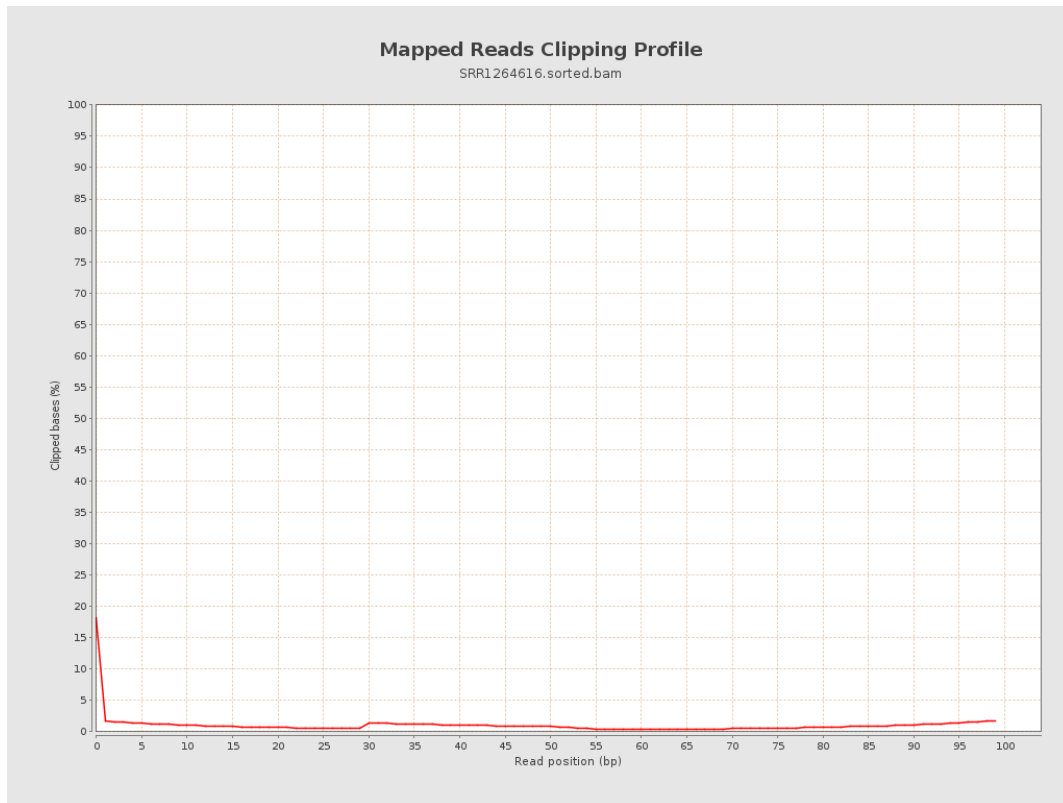
8. Results : Mapped Reads Nucleotide Content



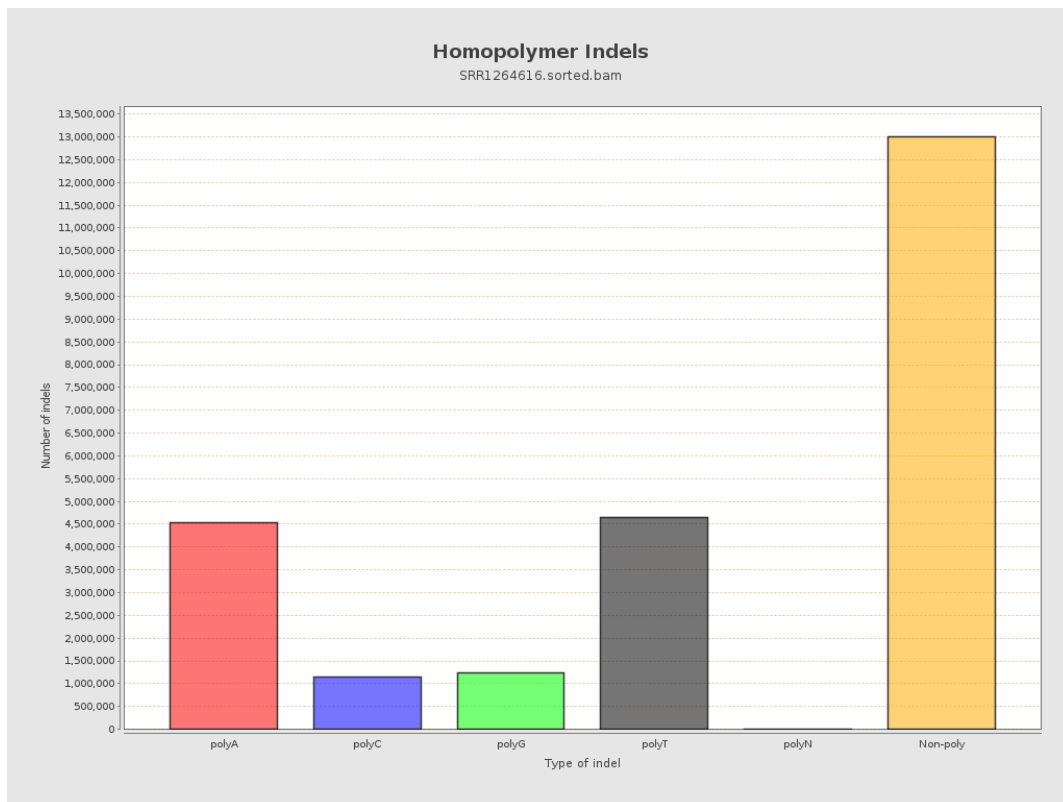
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



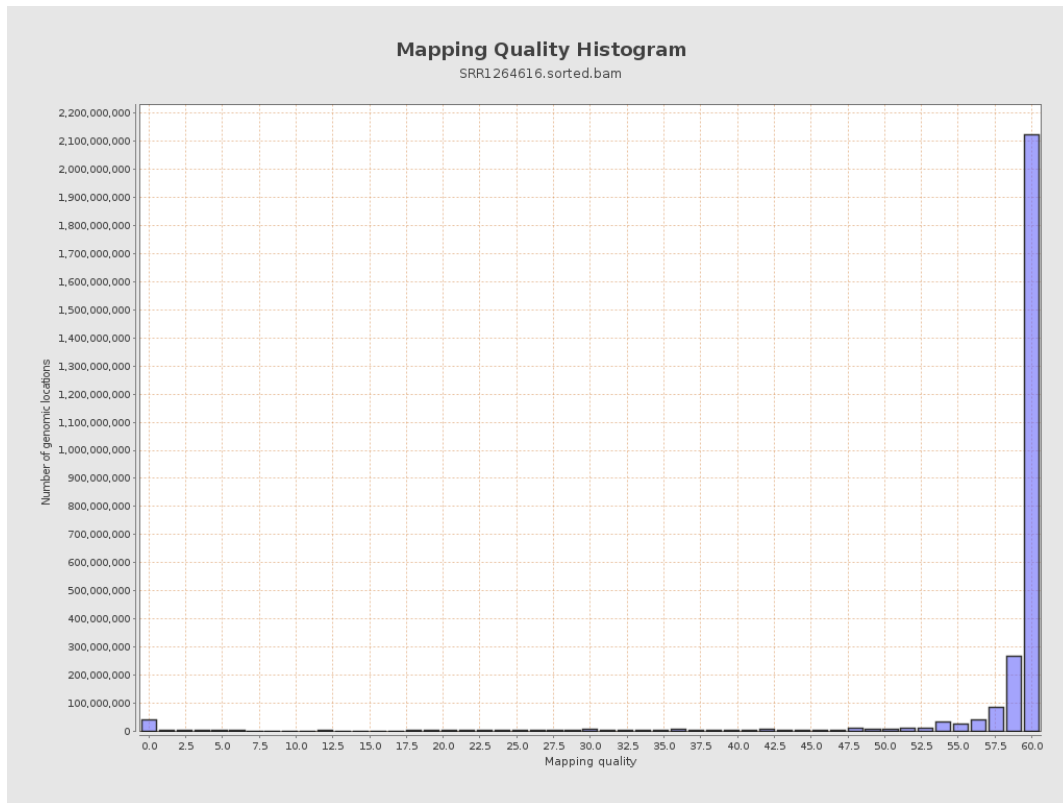
11. Results : Homopolymer Indels



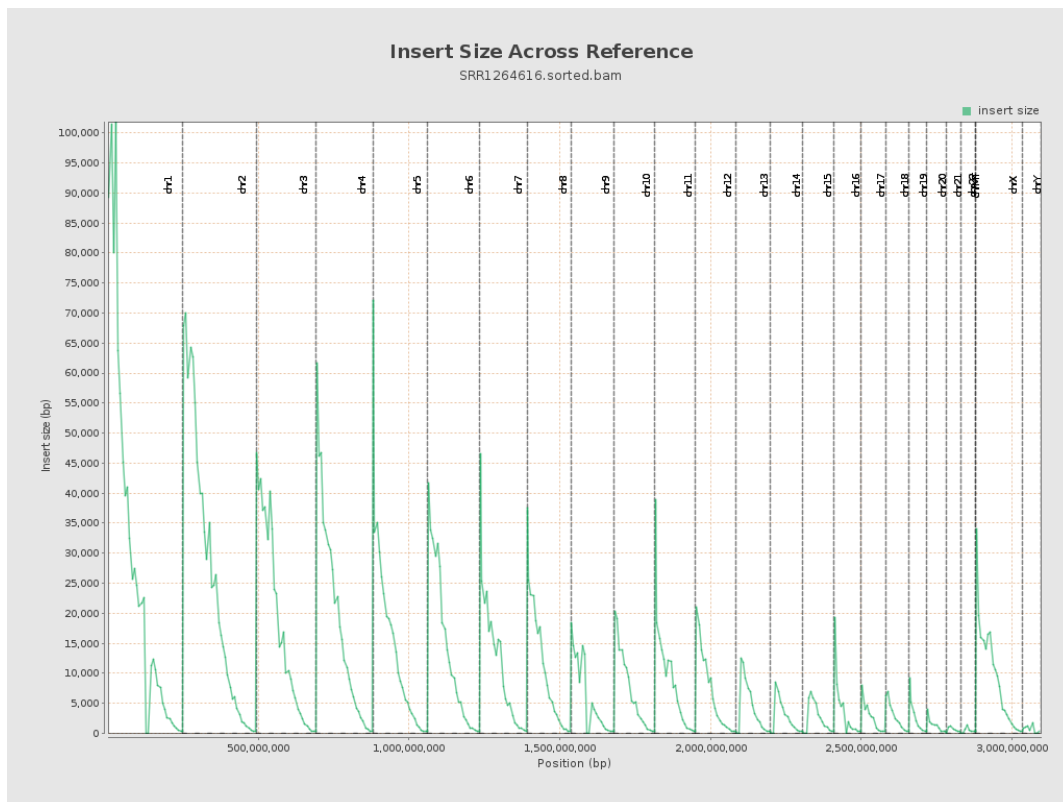
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

