

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/23 05:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264617.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_SRR1264617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264617_1.fastq.gz SRR1264617_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 23 05:15:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,172,435,648
Mapped reads	1,167,228,867 / 99.56%
Unmapped reads	5,206,781 / 0.44%
Mapped paired reads	1,167,228,867 / 99.56%
Mapped reads, first in pair	584,893,088 / 49.89%
Mapped reads, second in pair	582,335,779 / 49.67%
Mapped reads, both in pair	1,163,575,540 / 99.24%
Mapped reads, singletons	3,653,327 / 0.31%
Secondary alignments	0
Supplementary alignments	13,421,394 / 1.14%
Read min/max/mean length	30 / 100 / 100.47
Duplicated reads (estimated)	421,797,886 / 35.98%
Duplication rate	35.52%
Clipped reads	80,244,778 / 6.84%

2.2. ACGT Content

Number/percentage of A's	35,748,606,110 / 30.86%
Number/percentage of C's	22,038,223,322 / 19.02%
Number/percentage of T's	35,626,540,986 / 30.76%
Number/percentage of G's	22,360,273,234 / 19.3%
Number/percentage of N's	65,314,603 / 0.06%

GC Percentage	38.33%
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2.3. Coverage

Mean	37.4279
Standard Deviation	39.2738

2.4. Mapping Quality

Mean Mapping Quality	54.35
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2.5. Insert size

Mean	149,867.1
Standard Deviation	3,702,551.21
P25/Median/P75	262 / 298 / 337

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	452,070,983
Insertions	12,280,898
Mapped reads with at least one insertion	1.04%
Deletions	11,774,427
Mapped reads with at least one deletion	0.99%
Homopolymer indels	47.05%

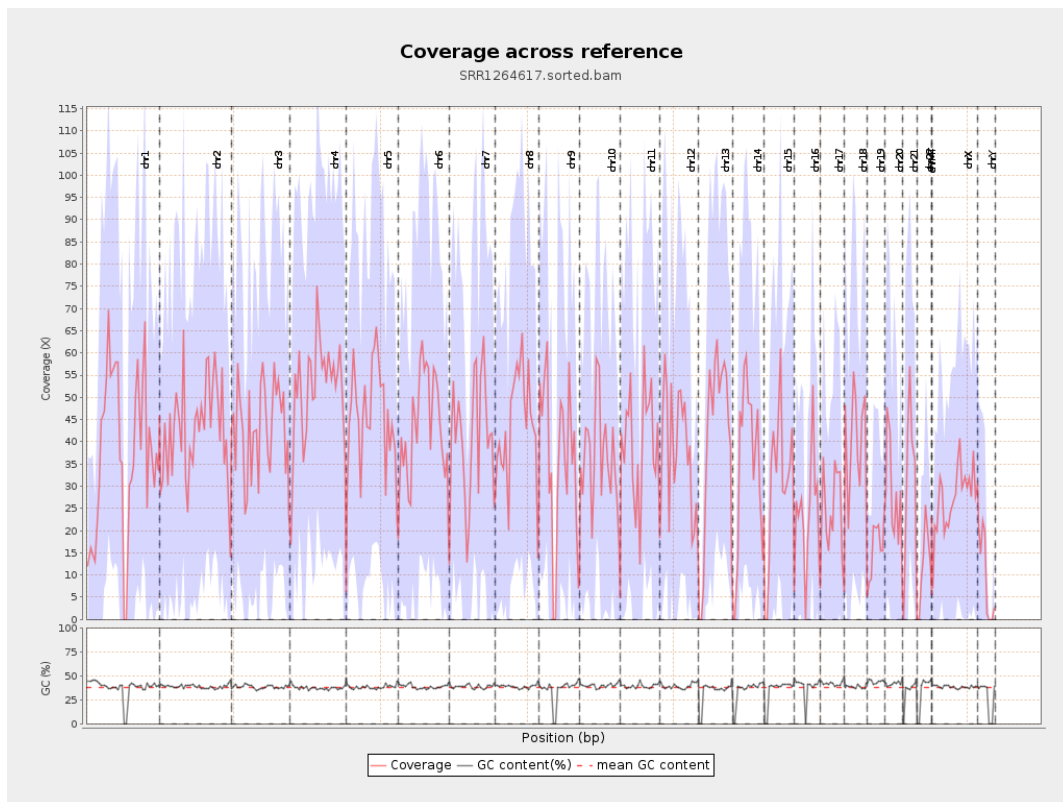
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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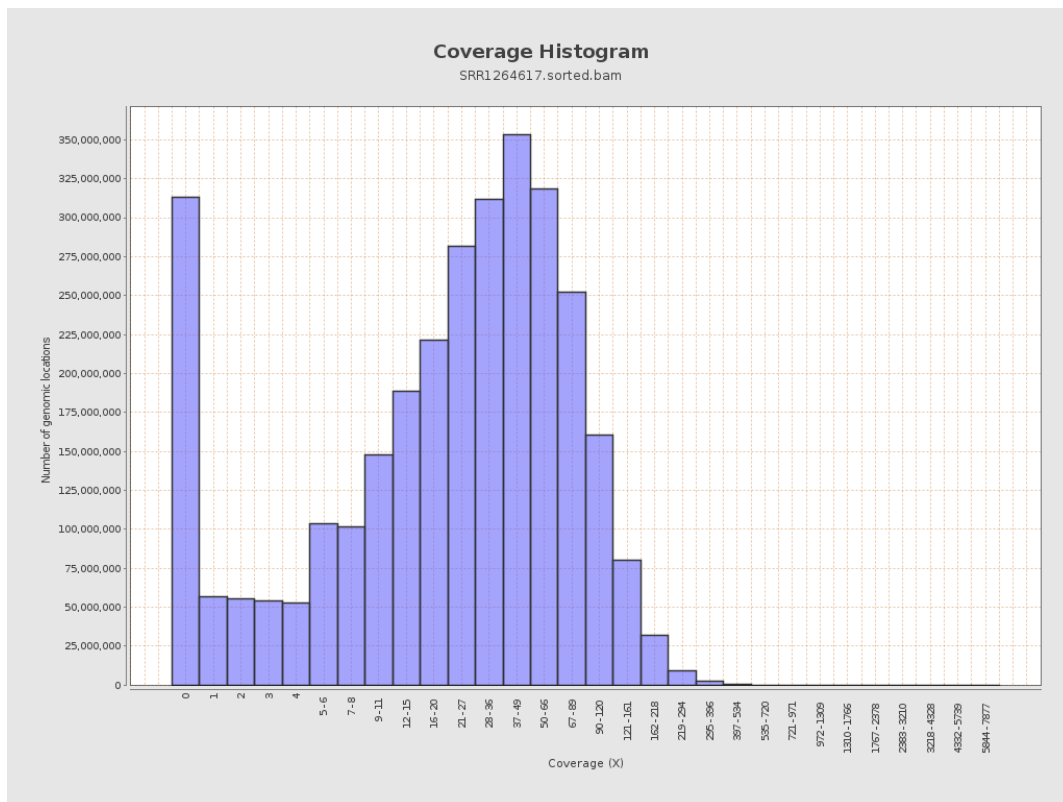
		bases	coverage	deviation
chr1	249250621	9319031825	37.3882	42.3665
chr2	243199373	10349841760	42.557	39.5002
chr3	198022430	8581540877	43.3362	38.7632
chr4	191154276	9995959588	52.2926	42.523
chr5	180915260	8222885953	45.4516	39.7805
chr6	171115067	7573273599	44.2584	40.571
chr7	159138663	6495013184	40.8135	40.353
chr8	146364022	6462509393	44.1537	39.8279
chr9	141213431	4911816447	34.7829	41.7565
chr10	135534747	4961487391	36.6068	35.6201
chr11	135006516	5337833604	39.5376	40.7475
chr12	133851895	5112341782	38.194	38.7451
chr13	115169878	4717639883	40.9624	40.7612
chr14	107349540	3719254018	34.6462	38.8942
chr15	102531392	3180768801	31.0224	38.6599
chr16	90354753	2085489325	23.0811	29.3251
chr17	81195210	1945686007	23.9631	30.0158
chr18	78077248	3171217149	40.6164	37.3583
chr19	59128983	923655375	15.621	22.575
chr20	63025520	1769136332	28.0702	36.4001
chr21	48129895	1565548067	32.5276	41.9331
chr22	51304566	611627461	11.9215	20.751
chrMT	16571	384192	23.1846	9.288
chrX	155270560	4273163749	27.5208	29.1813

chrY	59373566	578307753	9.7402	21.7697
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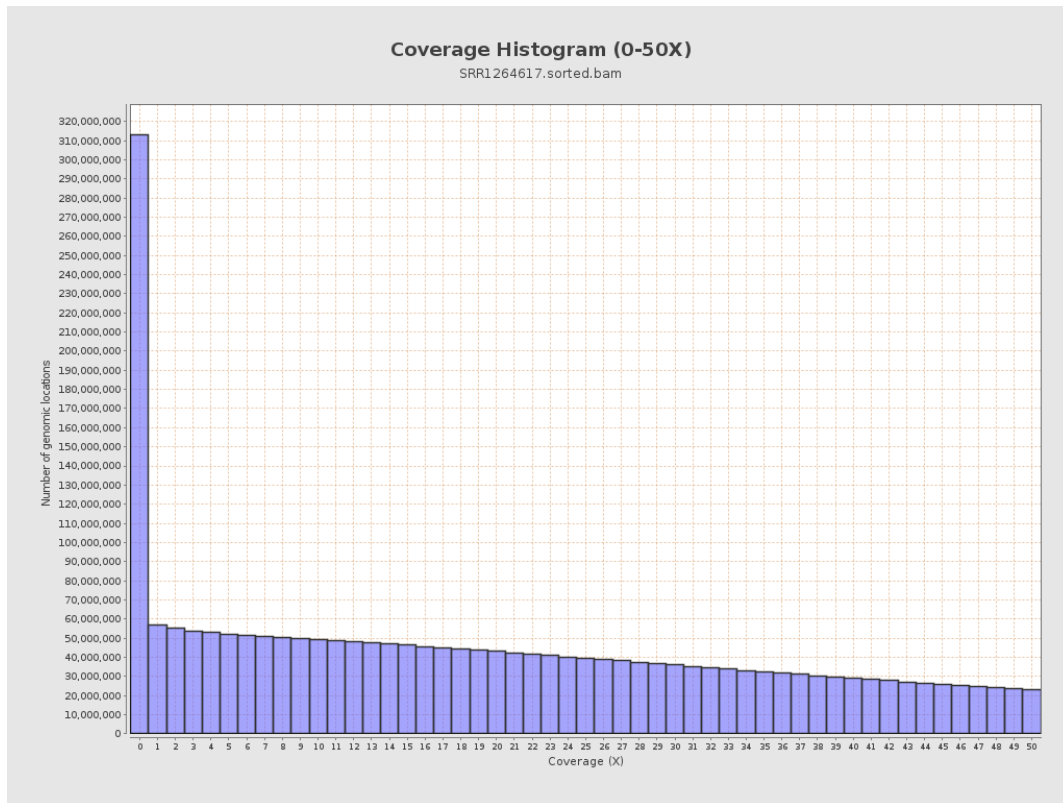
3. Results : Coverage across reference



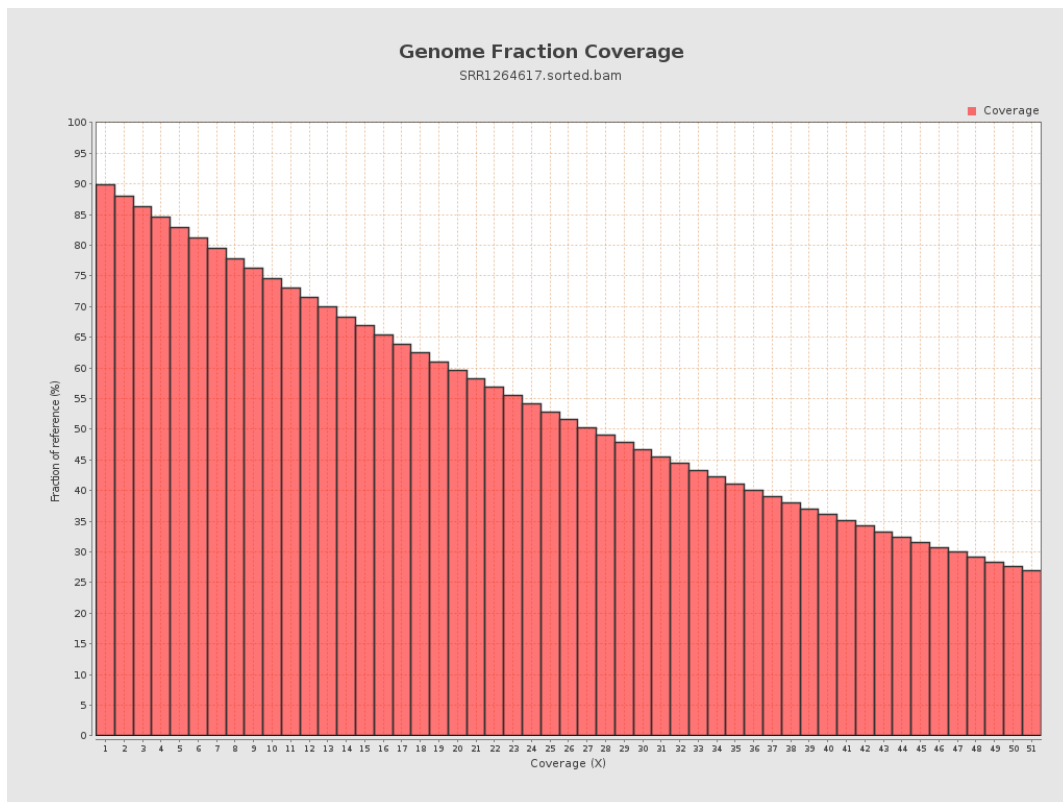
4. Results : Coverage Histogram



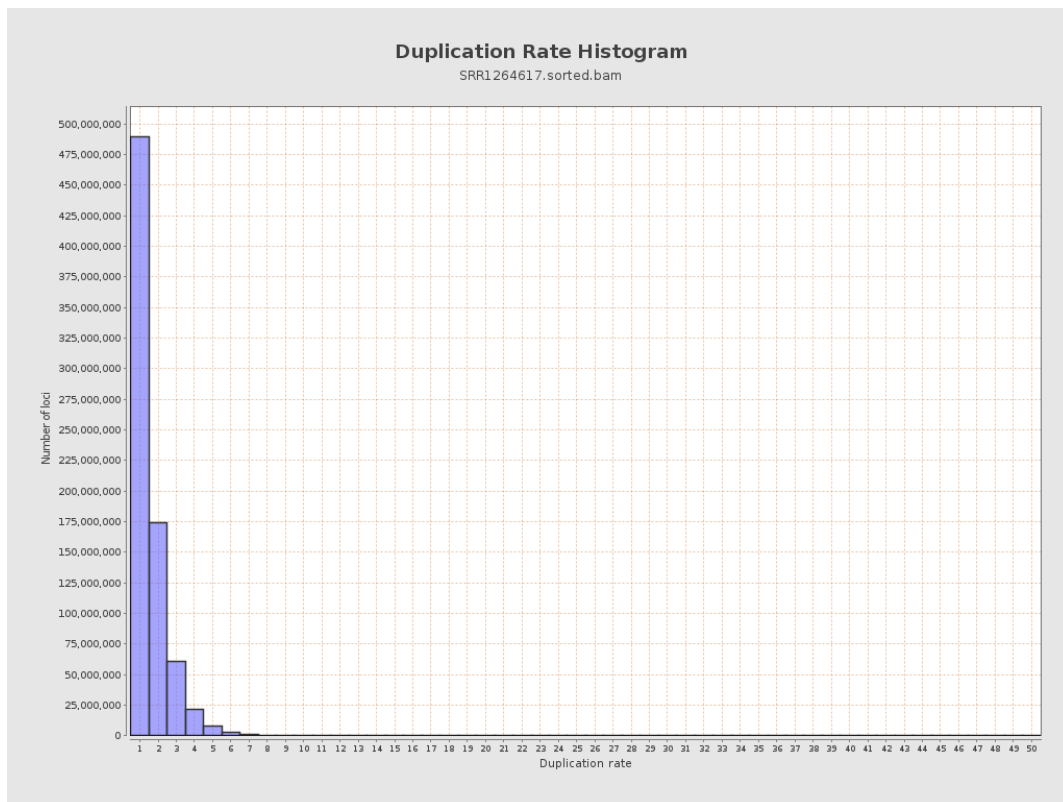
5. Results : Coverage Histogram (0-50X)



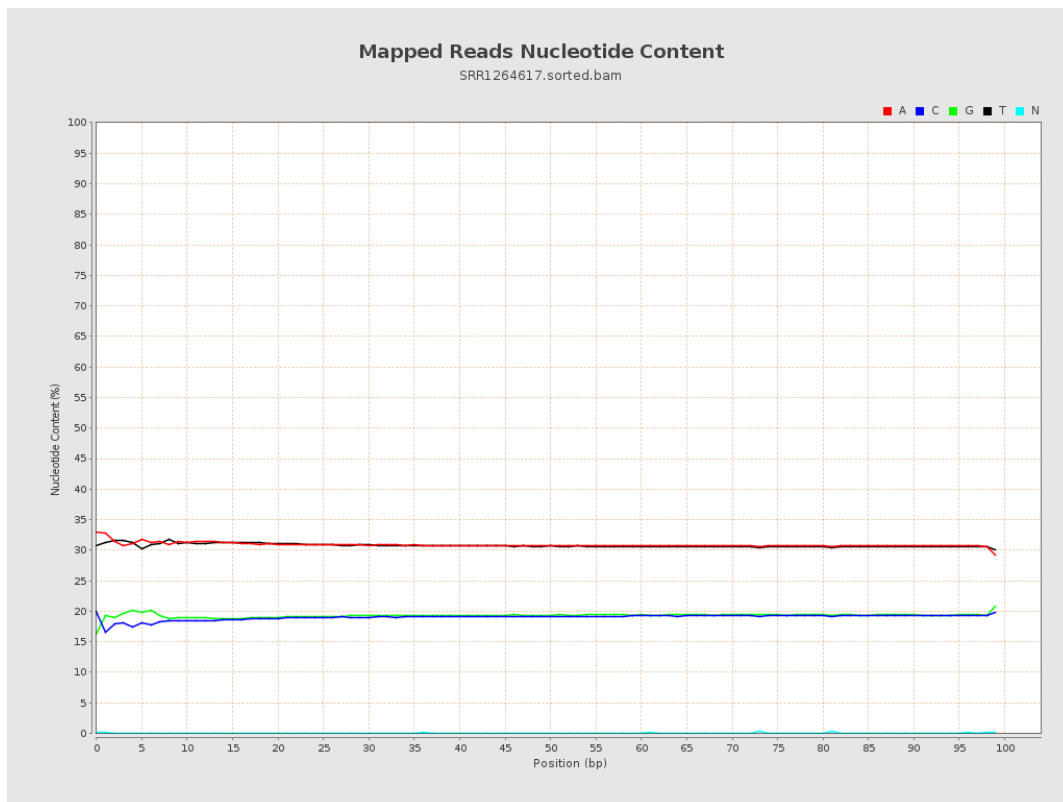
6. Results : Genome Fraction Coverage



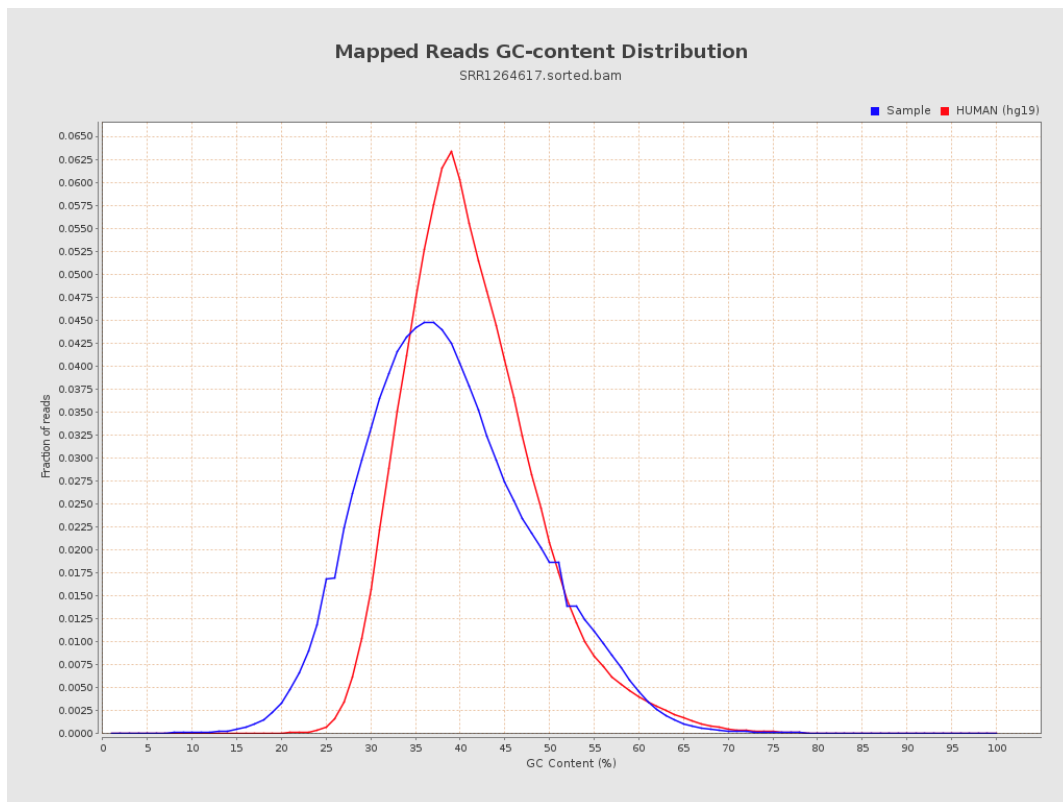
7. Results : Duplication Rate Histogram



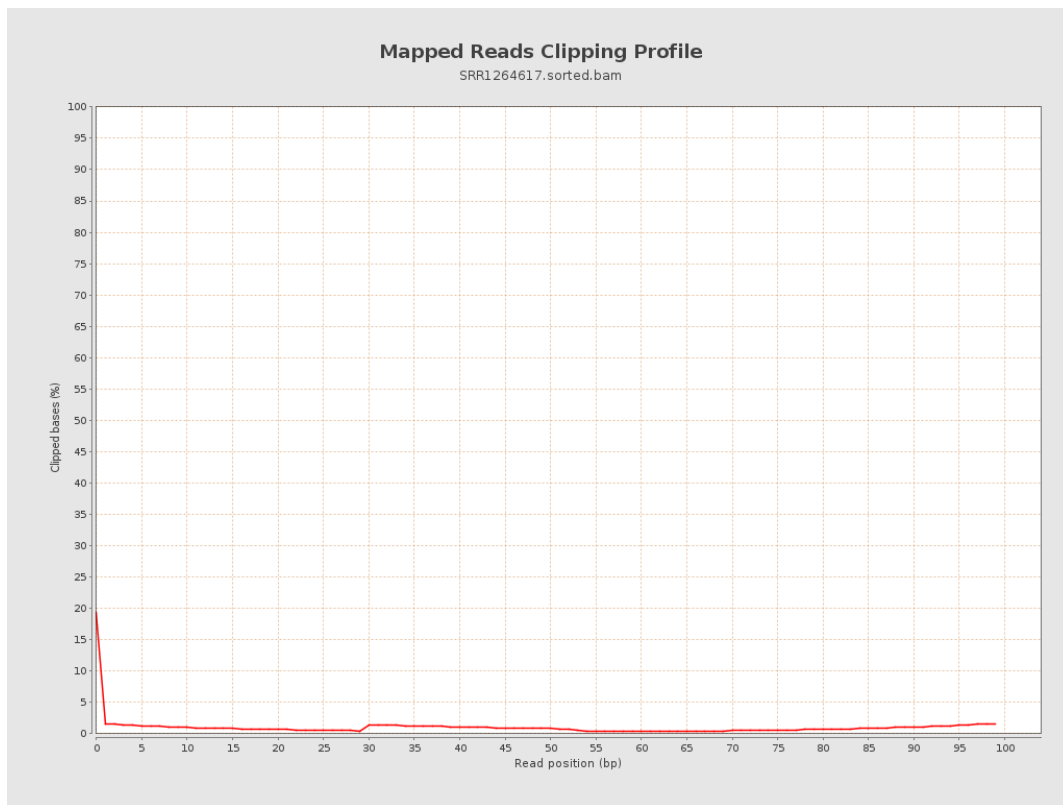
8. Results : Mapped Reads Nucleotide Content



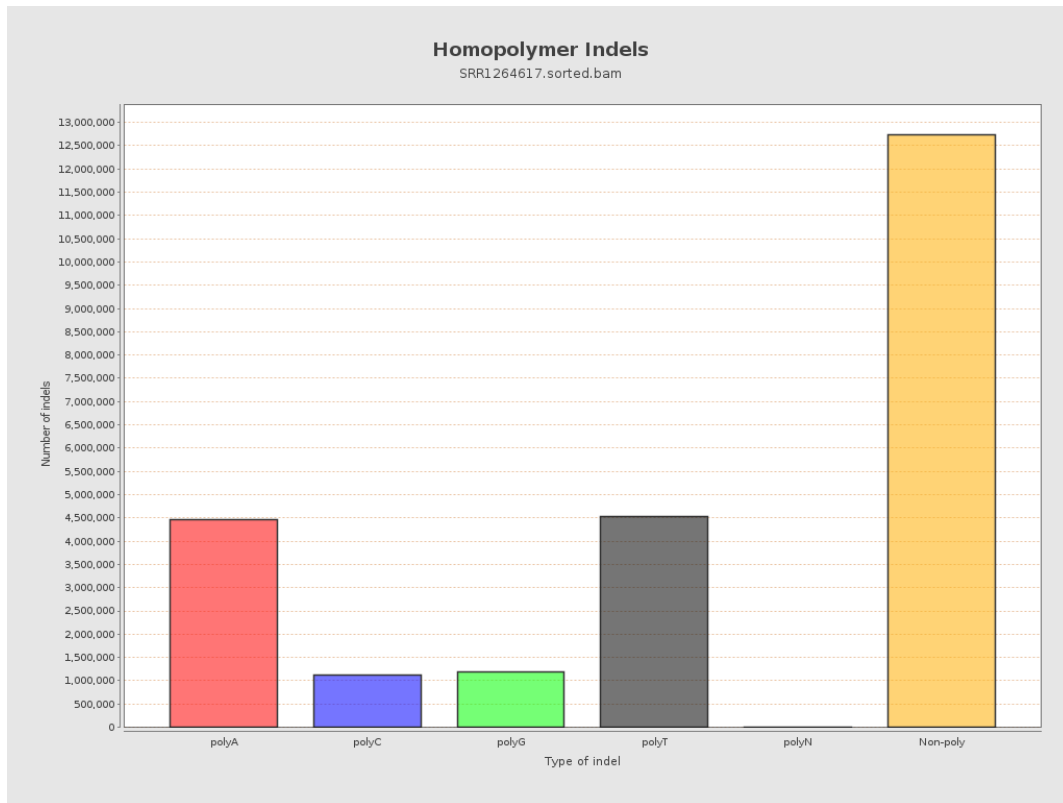
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



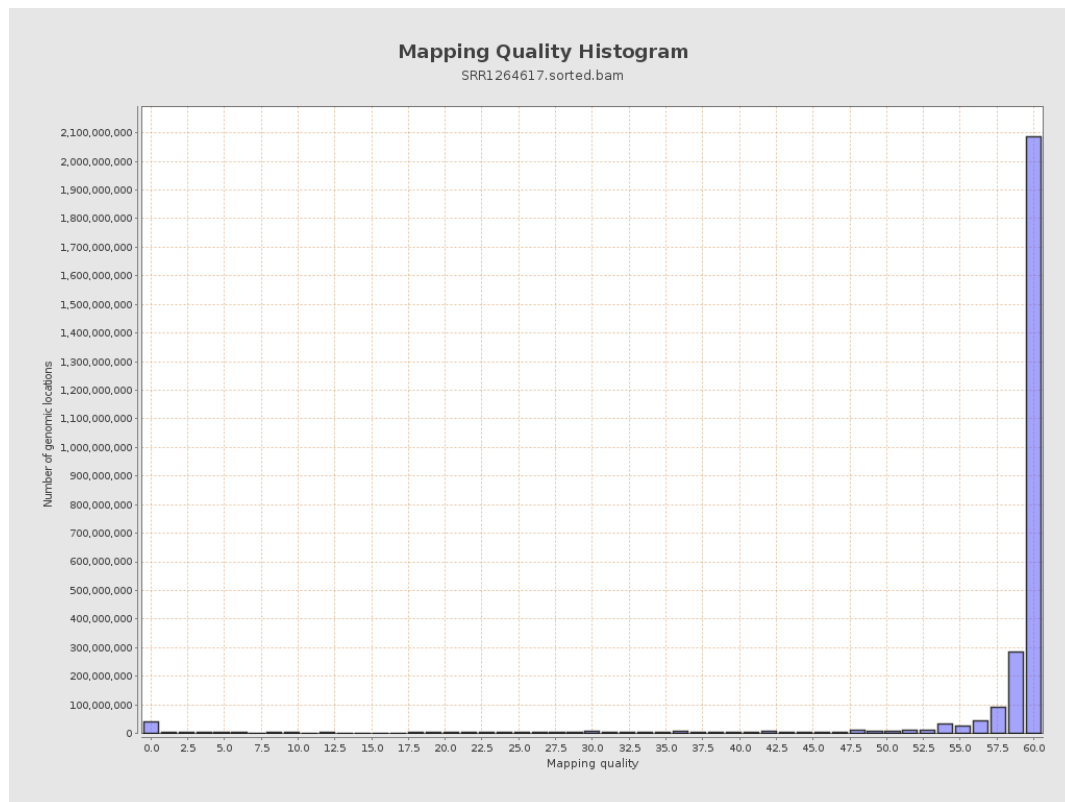
11. Results : Homopolymer Indels



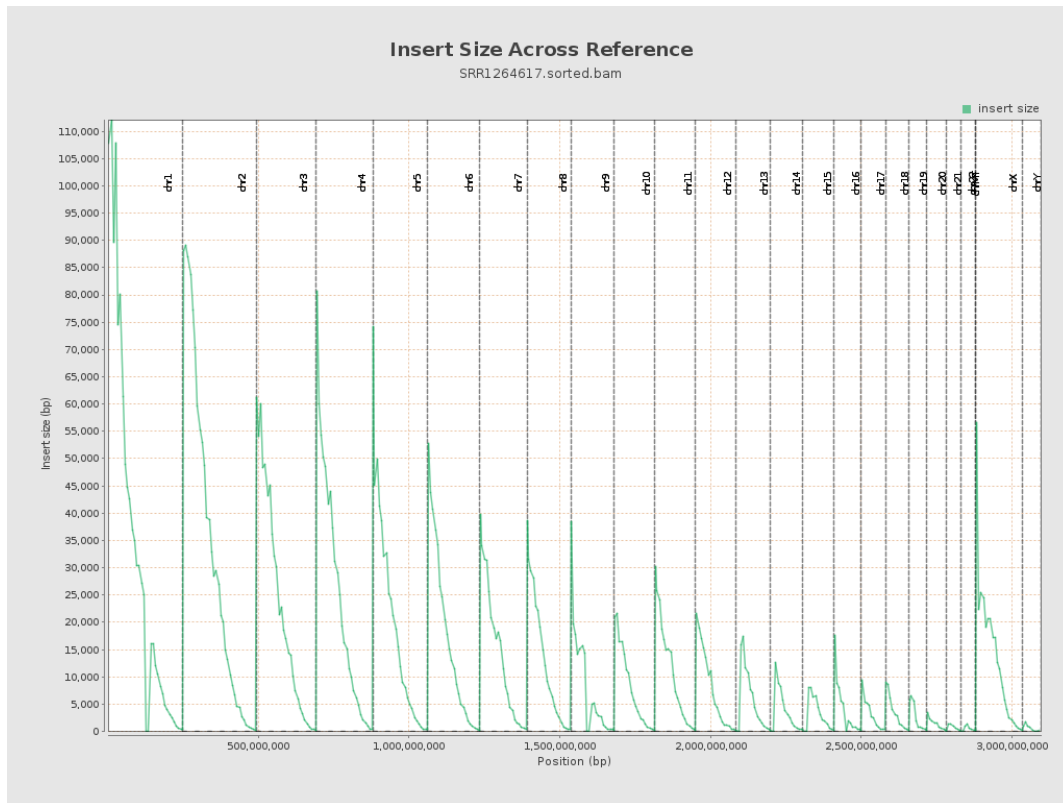
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

