

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 09:12:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354882.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_SRR22354882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354882_1.fastq.gz SRR22354882_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 09:12:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,407,702
Mapped reads	16,283,025 / 99.24%
Unmapped reads	124,677 / 0.76%
Mapped paired reads	16,283,025 / 99.24%
Mapped reads, first in pair	8,148,311 / 49.66%
Mapped reads, second in pair	8,134,714 / 49.58%
Mapped reads, both in pair	16,252,252 / 99.05%
Mapped reads, singletons	30,773 / 0.19%
Secondary alignments	0
Supplementary alignments	437,310 / 2.67%
Read min/max/mean length	30 / 150 / 151.02
Duplicated reads (estimated)	6,678,094 / 40.7%
Duplication rate	40.16%
Clipped reads	7,651,739 / 46.64%

2.2. ACGT Content

Number/percentage of A's	604,444,800 / 28.82%
Number/percentage of C's	433,489,131 / 20.67%
Number/percentage of T's	610,397,271 / 29.11%
Number/percentage of G's	448,784,999 / 21.4%
Number/percentage of N's	25,346 / 0%

GC Percentage	42.07%
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2.3. Coverage

Mean	0.6778
Standard Deviation	19.3353

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	239,661.46
Standard Deviation	5,608,378.33
P25/Median/P75	113 / 168 / 236

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	15,665,783
Insertions	421,063
Mapped reads with at least one insertion	2.42%
Deletions	440,443
Mapped reads with at least one deletion	2.58%
Homopolymer indels	44.38%

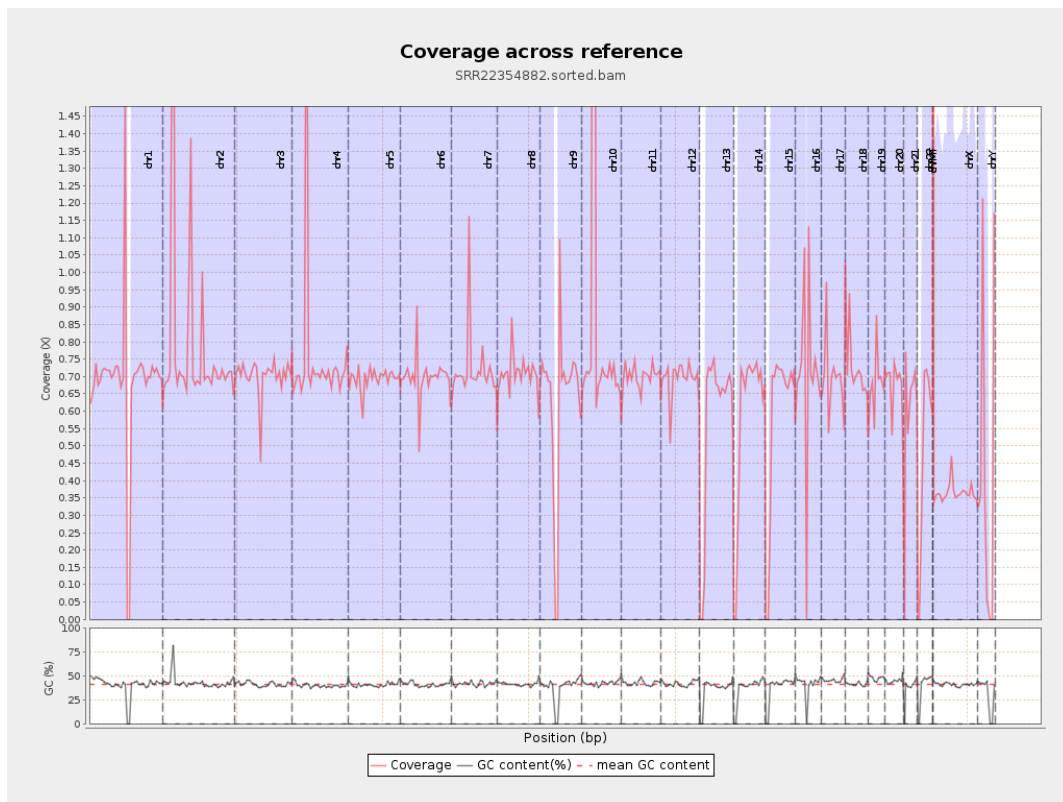
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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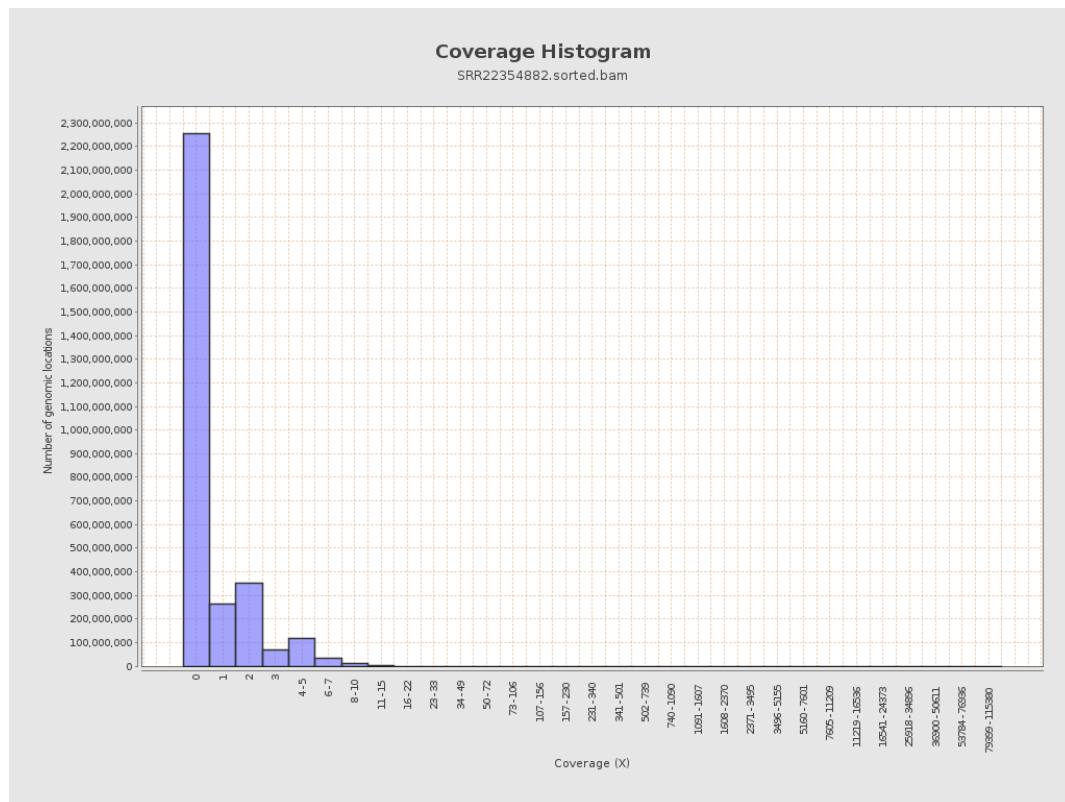
		bases	coverage	deviation
chr1	249250621	170643050	0.6846	18.7556
chr2	243199373	191622847	0.7879	60.4629
chr3	198022430	138841060	0.7011	1.7429
chr4	191154276	145342373	0.7603	10.3244
chr5	180915260	125243597	0.6923	1.4517
chr6	171115067	119569094	0.6988	2.7687
chr7	159138663	114638103	0.7204	11.3191
chr8	146364022	103503303	0.7072	2.9009
chr9	141213431	89396641	0.6331	9.6461
chr10	135534747	117357086	0.8659	25.3333
chr11	135006516	94516794	0.7001	3.517
chr12	133851895	93195186	0.6963	1.5266
chr13	115169878	65850038	0.5718	1.2646
chr14	107349540	63775711	0.5941	2.9035
chr15	102531392	58539145	0.5709	1.2705
chr16	90354753	63319413	0.7008	4.6764
chr17	81195210	56790093	0.6994	4.0698
chr18	78077248	57091141	0.7312	8.5819
chr19	59128983	40291690	0.6814	9.2849
chr20	63025520	42752299	0.6783	3.5126
chr21	48129895	29108909	0.6048	5.38
chr22	51304566	24439552	0.4764	1.9862
chrMT	16571	9791692	590.8932	132.7694
chrX	155270560	56709464	0.3652	1.5496

chrY	59373566	26054024	0.4388	12.9207
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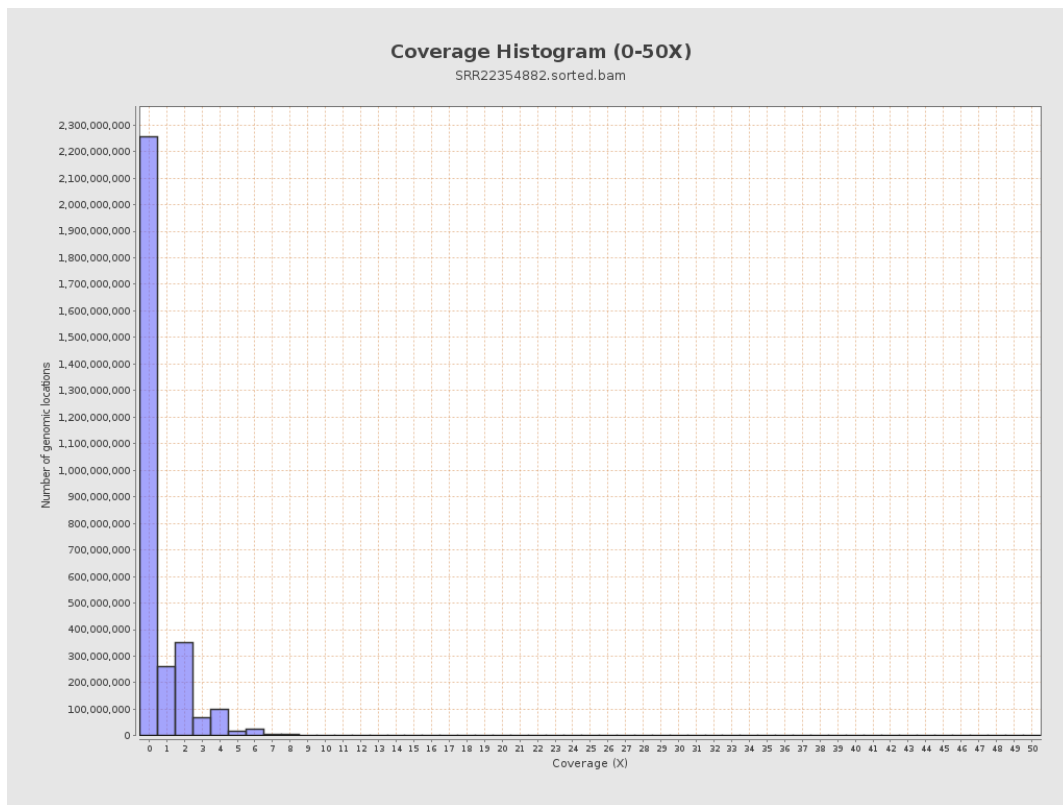
3. Results : Coverage across reference



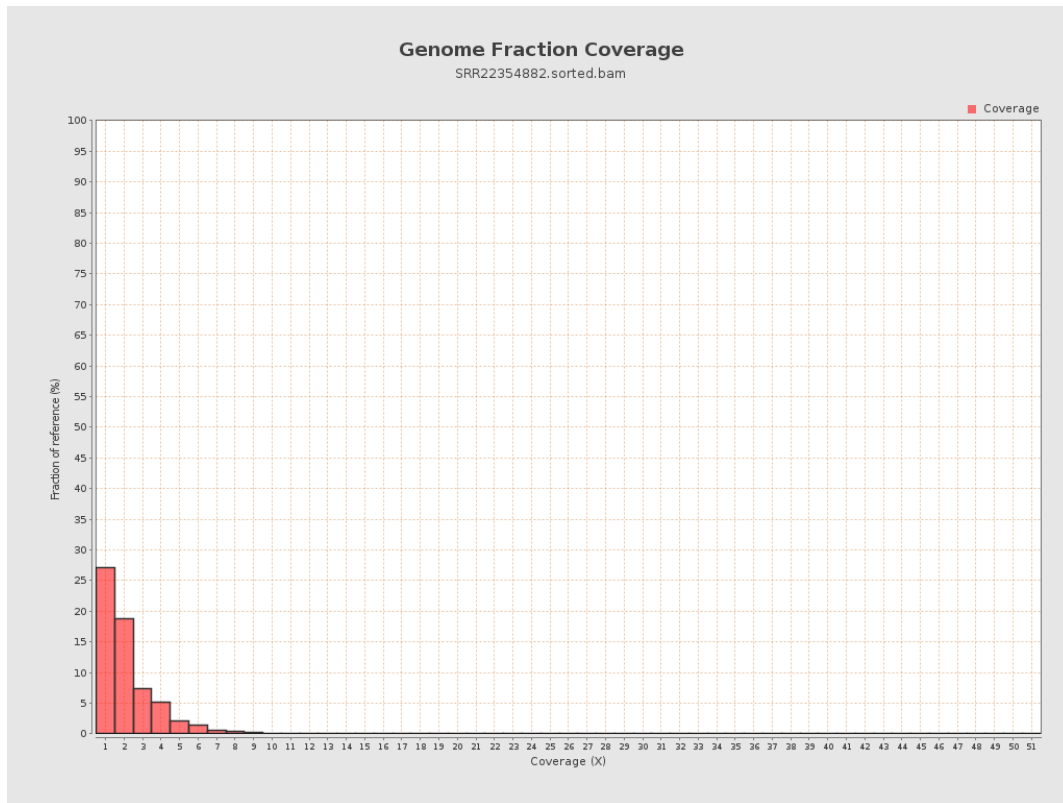
4. Results : Coverage Histogram



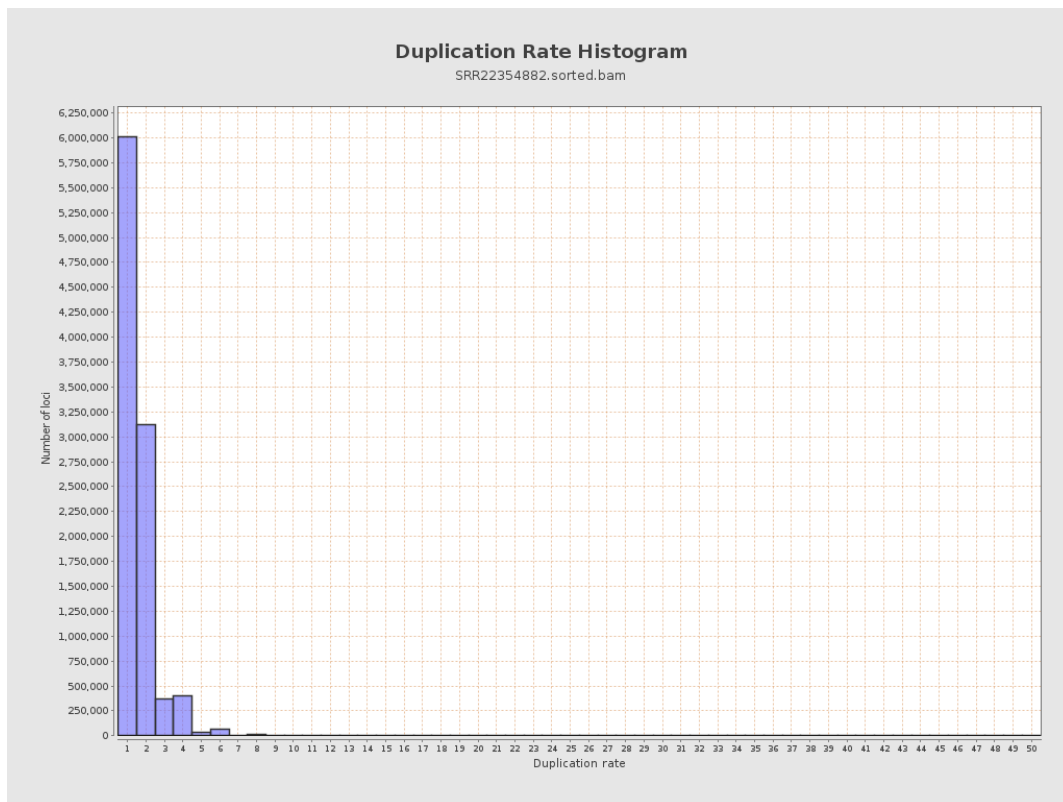
5. Results : Coverage Histogram (0-50X)



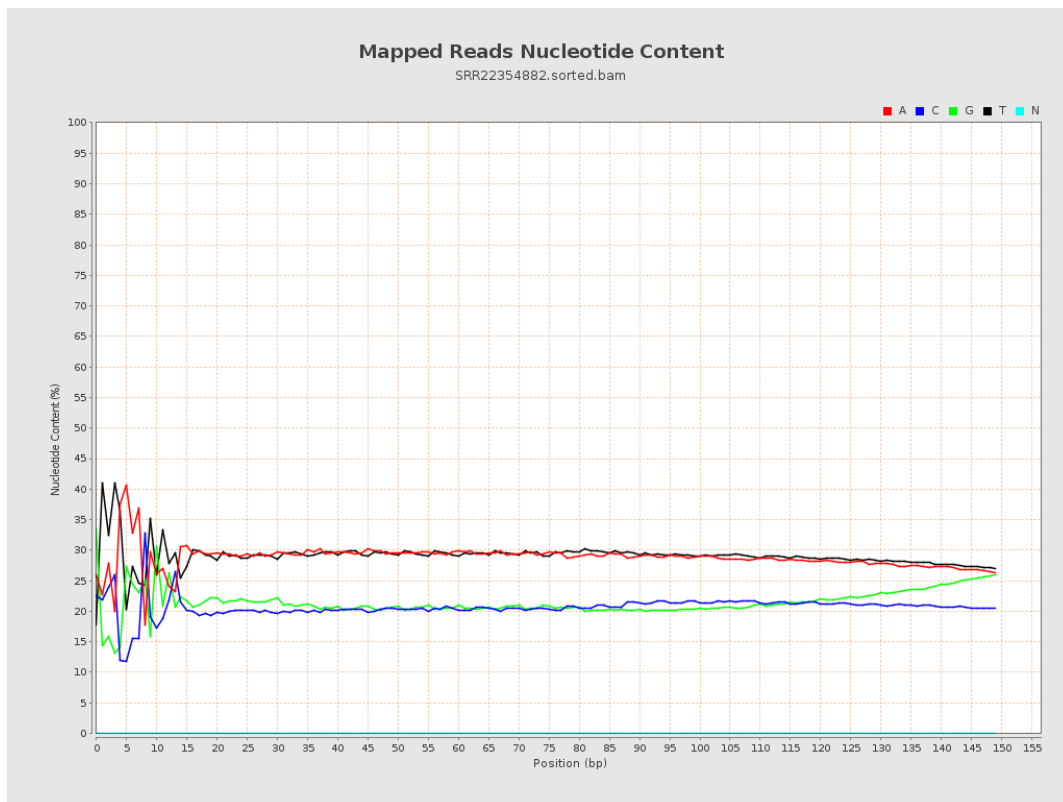
6. Results : Genome Fraction Coverage



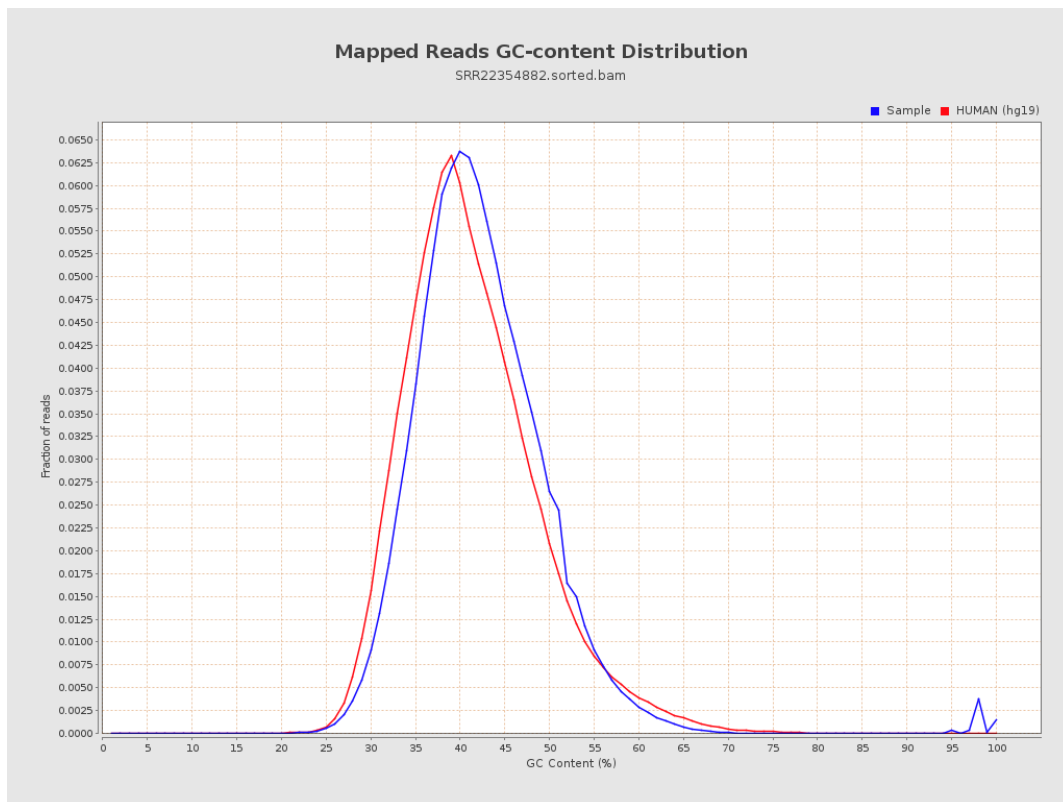
7. Results : Duplication Rate Histogram



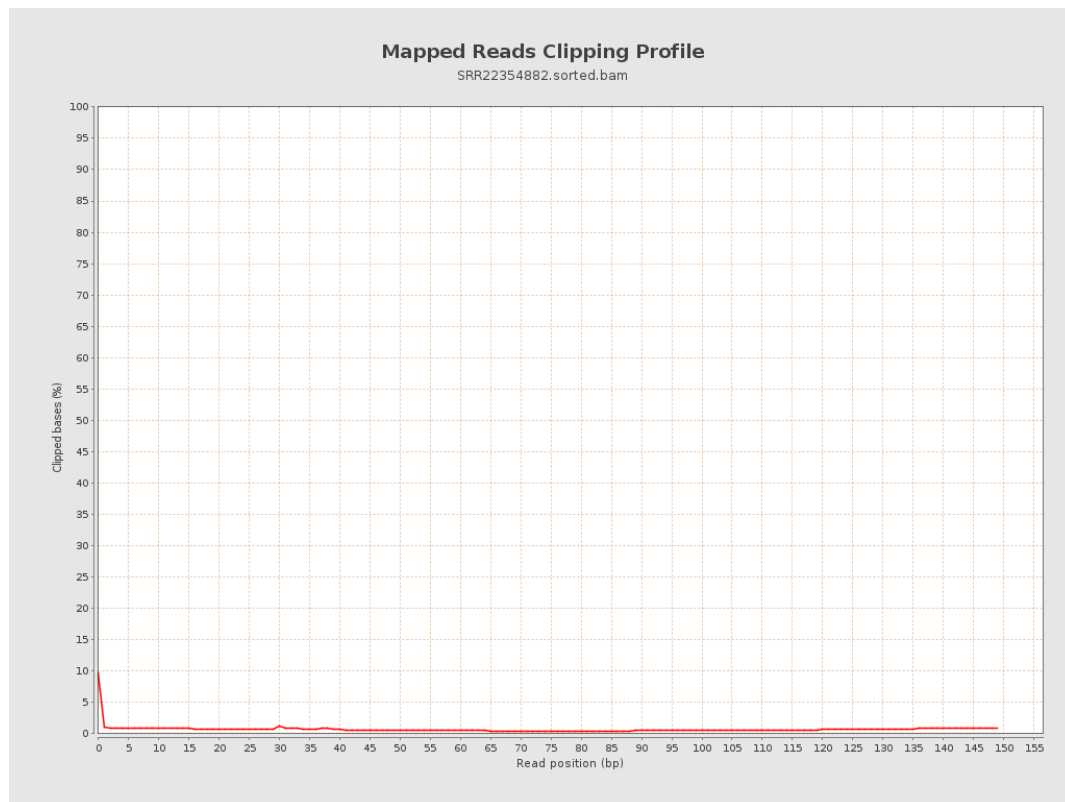
8. Results : Mapped Reads Nucleotide Content



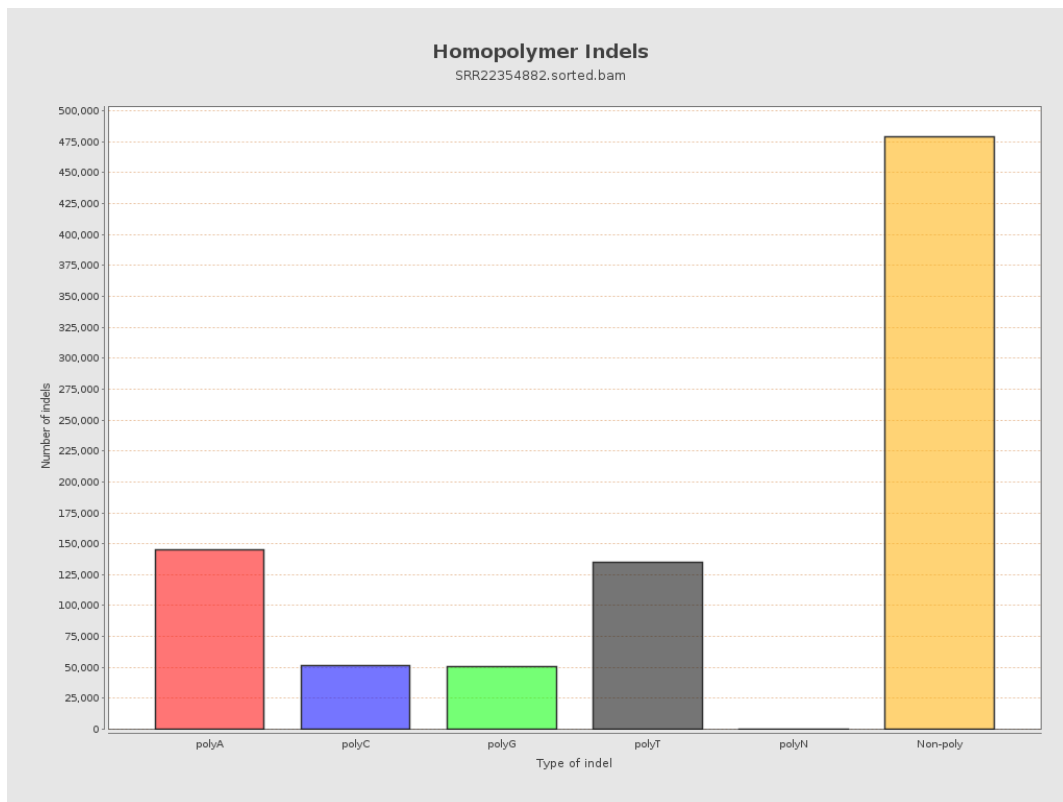
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



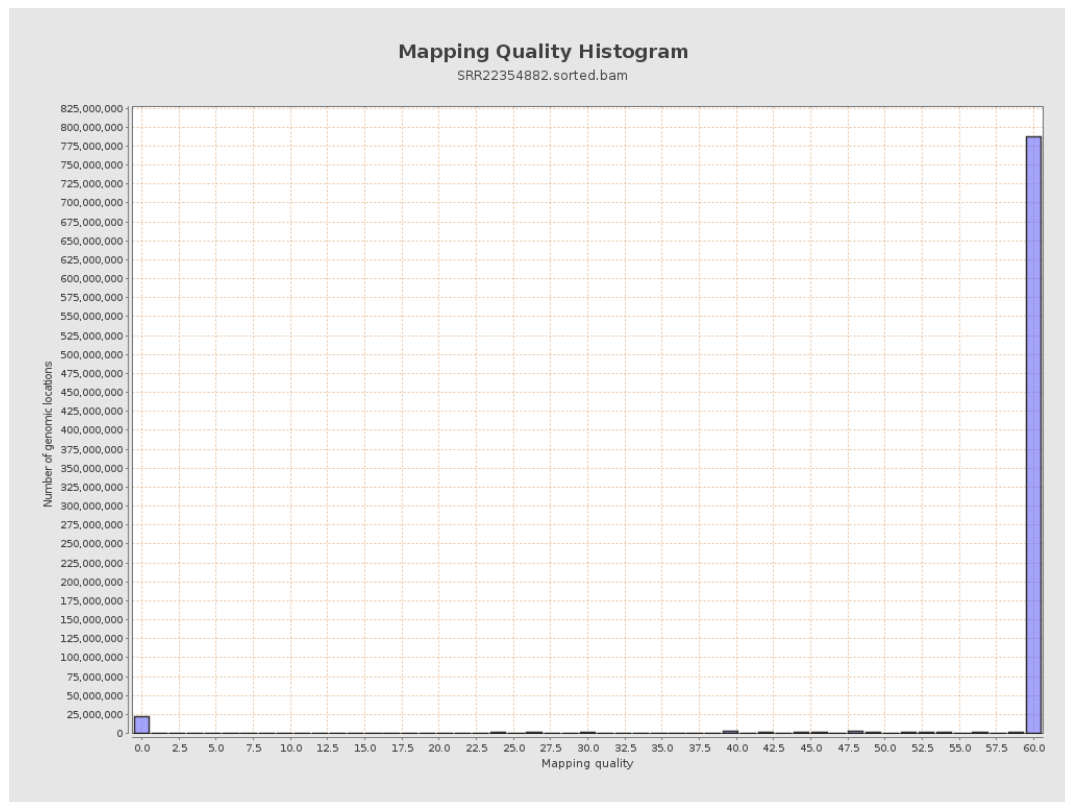
11. Results : Homopolymer Indels



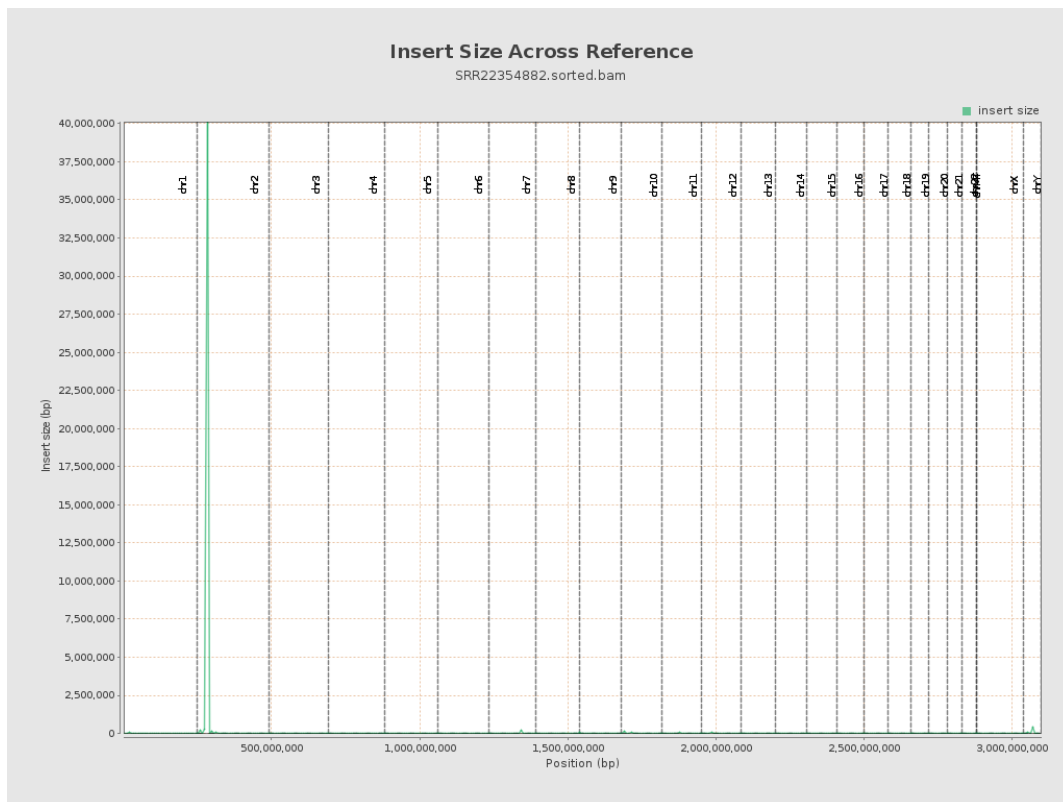
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

