Integrative OMICS approach to characterize Sf21 an Hi5 cell lines

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Multiple library type approach

Datasets (Sf21)

Library Input Mode Fragment size (bp) Coverage seq. / spanning
1. DNA Paired-End (PE) ~290 94.9 / 227.3
2. DNA Paired-End (PE) ~590 1.4 / 12.7
3. DNA Mate Pair (MP) ~4500 4.9 / 120.9
4. DNA Mate Pair (MP) ~4500 13.9 / 320.1
5. DNA Synthetic long reads (SLR) ~4900 (max 19 Kbp) 1.9 / NA
6. DNA Oxford Nanopore (ONT) ~8000 (max 34 kbp) 0.2 / NA
7. RNA Paired-End (PE) ~280 10.1 / 37.8

Motivation:

Insect derived cell-lines, from Spodoptera frugiperda (Sf21) and from Trichoplusia ni (Hi5), are widely used systems for recombinant protein expression. Genomic sequences and annotations are still incomplete for Sf21 or absent for Hi5.

Conclusion:

This integrative approach results in assemblies at an unprecedented resolution. With these information available, Sf21 and Hi5 cells-lines will become an even better tools for protein expression and could be used in a wide range of applications, from promoter identifications to genome engineering and editing. We could in theory apply to any genomes and results to valuable resources.