Synaptically targeting the ligand of the synthetic system TRACT, for tracing neuronal connections
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The synapse is a specialized type of cell-cell interaction that neuronal cells form which transmits information through brain circuits. We are focusing on the olfactory systems in the *Drosophila* brain which have Olfactory Sensory Neurons (OSNs) expressing the same olfactory receptor gene projecting their axons to a specific glomerulus in each antennal lobe, where the OSN axons form synapses with projection neuros (PNs) and local interneurons (LNs). A synthetic and genetically-encoded system, TRanscellular ACtivation of Transcription (TRACT) uses the Notch signalling pathway to monitor cell-cell contact. The interaction of ligand and receptor results in the proteolysis of the intracellular domain, which activates the expression of a marker in the receptor-cell. Here, the ligand and receptor are targeted to the pre-synaptic and post-synaptic sites of the contacting neurons respectively by fusing with different pre-synaptic and post synaptic markers. Here, we characterized three different pre-synaptic markers for the ligand (CD19), namely Syndecan (Sdc), Defective proboscis extension response-10 (Dpr 10) and Dpr-interacting protein γ (Dip γ). *Drosophila* adult brains were immunostained and confocal microscopy was performed to analyse the results.

The role of microRNAs in modulating HIV infection
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Cellular microRNAs (miRNAs) are a class of small, noncoding RNAs that regulate gene expression by binding to mRNA, resulting in the inhibition of the translation or the degradation of these mRNA. Recently, miRNAs have been found to play a vital role in antiviral defense, including defense against HIV infection. The miRNAs that influence HIV infection have not been studied comprehensively. In this project, we used a genetic approach to identify potential roles of miRNAs in modulating HIV infection. To study HIV infection, we engineered a replication competent HIV strain with two reporter genes: an extracellular myc tag driven by the HIV promoter and an extracellular V5 tag driven by a constitutive promoter. This reporter allows us to differentiate uninfected, productively infected, and latently infected cells. We also used a CRISPR/Cas9 library that is designed to target only miRNA genes to generate a library of miRNA-knockout cells. Using these two reagents, we identified several individual miRNAs that modulate HIV infection. These results are encouraging as they have the potential to uncover novel roles for miRNAs in HIV infection.

Investigating the distribution of anaerobic methanotrophic archaea in sediment from Monterey Canyon, CA using hybridization chain reaction-fluorescence in situ hybridization
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Methane, an abundant hydrocarbon, plays a significant role in both post-industrial global warming as well as many of the earth's biogeochemical processes. The microorganisms such as anaerobic methanotrophic archaea (ANME) and its associated sulfate-reducing bacterial partner (SRB) contribute to the anaerobic oxidation of methane in environments like cold seeps and serve as a methane sink in oceans. Due to the difficulty of working with organisms in sediment, these organisms have yet to be fully understood. Studying the distribution and localization of ANME, as well as the spatial association of ANME and SRB in environmental samples can provide insight into their niche differentiation and broaden our understanding of seep ecosystem structure and function. In this work, we use sediment samples from Monterey Canyon, California to visualize ANME and SRB by Hybridization Chain Reaction- Fluorescence In Situ Hybridization (HCR-FISH). Using the results produced from HCR-FISH, I am able to both characterize and identify free living cells and aggregates found in the environmental samples as well as identify possible correlations between the spatial associations and localizations of ANME and SRB, and geochemistry data from the environmental samples.