Home Page

Ready to submit samples? Use these links

To submit a new project or get detailed pricing information, use these links. You'll be given a 6-digit request ID to refer to your request later. Your requests stay here until you're ready to submit samples. You return to this link when you're ready to submit your samples.

1. Create a UT EID

- In order to access your job home page you will need a UT EID, Create a UT EID first.

2. Select this link to enter a new project (a.k.a. "job request")

- See this web page for sample input guidelines.
- Metagenomics, GBS and TagSeq, note that DNA concentrations should be normalized before submission.

Announcements:

8Feb21: Due to the overwhelming number of COVID sequencing projects, the GSAF is experiencing longer than usual turn around times, we ask for your patience during this period, in addition we are having to limit the number of external projects we can accept. UPDATE(things have returned to normal, thanks for the patience!)

9Sept19: GSAF will officially launch the NovaSeq 6000, please join us at 1pm for an introduction to the new system. Contact the GSAF for details!

18Jan19: The GSAF is happy to officially announce our new 10X Single Cell 3' (v3) Gene Expression Service, scRNA-Seq. We will begin accepting customer samples the week of January 28th. Important notes regarding 10X below.

- The 10X single cell RNA-Seq service is by appointment only, we must have advance notice due to the nature of these preparations, since we will need to have someone on standby to receive the cells please meet with me prior to planning your experiment to discuss the timing.
    - Signup here using google calendar or email me at gsaf@utgsaf.org to discuss project details
    - Pricing can be found here on our website

4April18: GSAF introduces a new library prep service, TagSeq based on the published methods below. TagSeq is a 3' RNA library prep method, please visit our pricing page for more details.

- **Evaluation of TagSeq, a reliable lowcost alternative for RNAseq**
- **Profiling gene expression responses of coral larvae (*Acropora millepora*) to elevated temperature and settlement inducers using a novel RNASeq procedure**

19April17 Index Switching Preprint Concerns Sequencing Community *Update-19Apr17 See Below for Notes from Illumina

What is Index Switching?

A preprint released April 9, 2017 by Sinha, *et. al.*, describes a "spreading-of-signal" phenomenon that is attributed with causing 5-10% of sequencing reads to be incorrectly assigned in situations where multiplexed libraries are run on Illumina's HiSeq 3000/4000 systems. The observed errors are restricted to the HiSeq 3000/4000 and X Ten systems that use the exclusion amplification method for generating clusters in the nanowells of patterned flow cells.   According to the pre-print titled: "Index switching causes 'spreading-of-signal' among multiplexed samples in Illumina HiSeq 4000 DNA sequencing," low levels of free index primers in the pool get extended by DNA polymerase to create a new library molecules in the *Cbot* during the initial stage of cluster generation but prior to binding to the patterned flow cell.

What is the extent of the problem?

According to the authors, the RNA-seq experiments in this study revealed a 5-10% error rate associated with "signal spreading." In a commentary in the Molecular Ecologist, Ethan Linck, proposed that the problem is most likely to be troublesome for multiplexed RNA-seq studies or "studies attempting extremely low frequency variant detection, where a handful of erroneously indexed reads could have a big impact on inferences." Studies not affected by the phenomenon include non-multiplexed studies, and dual-indexed samples where each end is unique. Clearly, more data is needed under different situations and study designs to gain a better understanding of the extent of this potential problem.

What is being done?

Soon after the pre-print was released on April 9th, Illumina responded by tweeting, "we're aware & working on it. Data indicates it occurs at low rates,and impact may be mitigated w/other index approaches. Correcting this is a high priority and we are evaluating fixes. Pls keep feedback coming via DM, your Illumina team or email (2/2)."   The GSAF wants to reassure our customers that we are actively looking into this issue and will be working on alternatives to our current indexing system with the continual goal of delivering highly accurate sequencing data.

White Paper and Best Practices Release from Illumina

Best Practices from Illumina

Effects of Index Misassignment on Multiplexing and Downstream Analysis

Browse the wiki: