

FINAL REPORT

CUSTOMER ID: CUST01

PROJECT ID: WO-01

Date: January 1, 2015

Prepared for:

Customer

Address

INTRODUCTION

Panoply Bio offers a variety of services related to high-throughput antibody sequencing and high-throughput recombinant antibody expression and screening. Our high-throughput hybridoma sequencing service provides a deep sequencing survey of all of the heavy and light chain IgG transcripts produced by a hybridoma cell line. Panoply Bio also offers a service to convert hybridoma antibody sequences into recombinantly expressed IgG proteins.

REPORT SUMMARY:

The goal of this project was to determine the sequence of the heavy and light chain IgG variable regions of clonal populations of hybridoma cells.

The report contains the follow sections:

1. Description of deliverables
2. Description of sequence data files

Section 1: Description of deliverables

Data files

CUST01_WO-01_SUMMARY.xls

CUST01_WO-01_OTHER_SEQ.tar.gz

Format

read-only disk or flash drive

read-only disk or flash drive

Materials

None

Format

Section 2: Description of sequence data files

File name

CUST01_WO-01_SUMMARY.xls

CUST01_WO-01_OTHER_SEQ.tar.gz

Summary

summary of primary sequences from each hybridoma cell line

gzipped archive of secondary variable region sequences

Note: to decompress and unpack archive files, use unix command: tar -zxvf <FILENAME>

(continued on next page)

Detailed description of files:

CUST01_WO-01_SUMMARY.xls

Summary of the primary nucleotide and protein sequence for the heavy and light variable regions in each hybridoma sample:

COLUMN LABEL	DESCRIPTION
PLATE	Plate name
WELL	Well location
Hybridoma ID	Hybridoma ID provided by customer
# COMMON H Transcripts (>1%)	number of unique heavy chain transcripts that are present at a frequency of greater than 1% in deep sequencing data
# RARE H Transcripts (<1%)	number of unique heavy chain transcripts that are present at a frequency of less than 1% in deep sequencing data
PRIMARY H Transcript %	percent of most frequent heavy chain transcript that is present in deep sequencing data
ABERRANT H %	percent of aberrant heavy chain transcripts present in deep sequencing data
HEAVY V NT SEQ	nucleotide sequence of heavy chain variable region of primary transcript
HEAVY V AA SEQ	amino acid sequence of heavy chain variable region of primary transcript
HEAVY CDR1	amino acid sequence of CDR1
HEAVY CDR2	amino acid sequence of CDR2
HEAVY CDR3	amino acid sequence of CDR3
HEAVY V GENE	germ line V gene of heavy chain transcript
H PRODUCTIVE	indicates whether there is a productive VDJ rearrangement of the heavy chain sequence
H AA MISMATCH	number of amino acid mismatches in the heavy chain amino acid sequence compared to germ line
# COMMON L Transcripts (>1%)	number of unique light chain transcripts that are present at a frequency of greater than 1% in deep sequencing data
# RARE L Transcripts (<1%)	number of unique light chain transcripts that are present at a frequency of less than 1% in deep sequencing data
PRIMARY L Transcript %	percent of most frequent light chain transcript that is present in deep sequencing data
ABERRANT L %	percent of aberrant light chain transcripts present in deep sequencing data
LIGHT V NT SEQ	nucleotide sequence of light chain variable region of primary transcript
LIGHT V AA SEQ	amino acid sequence of light chain variable region of primary transcript
LIGHT CDR1	amino acid sequence of CDR1
LIGHT CDR2	amino acid sequence of CDR2
LIGHT CDR3	amino acid sequence of CDR3
LIGHT V GENE	germ line V gene of light chain transcript
L PRODUCTIVE	indicates whether there is a productive VDJ rearrangement of the light chain sequence
L AA MISMATCH	number of amino acid mismatches in the light chain amino acid sequence compared to germ line

PROJECT01_OTHER_SEQ.tar.gz

Archive of individual sequence files of variable region nucleotide sequence for each hybridoma in fasta file format.