



TITLE: CERTIFICATE OF ANALYSIS – ADAPTOR PLATE C (i193-288)

REF: N3

DOCUMENT No. COA-01-N3

ISSUED: 2018-07-06

STATUS: CURRENT

VERSION: 1

## Certificate of Analysis of Adaptor Plate C (i193-288)

Product name	Adaptor Plate C (i193-288)
Reference number	N3
LOT number	N3/007
Date of Manufacture	2017-12-20
Expiration date	2019-05-14

### 1 96 well Indexed Adaptor Plate

The 96 well indexed adaptor plate component contains ready to use indexed NGS adaptors (double stranded DNA oligonucleotides) in 5 µL solution for generating individual NGS libraries. The 96 well indexed adaptor plate contains sufficient kind of indexed adaptors for 24 individual NGS library generation and for downstream sample identification.

Product type	Associated Reagent	REF #	Rxns	Vol/well	# Plates
Holotype	Adaptor Plate C (i193-288)	N3	96	5 µL	1

### 2 Summary of Quality Control testing

Evaluation/Assessment	Pass/Fail
Physical inspection	Pass
Assessment of adaptors for index sequence and location	Pass
Assessment of adaptors for cross-contamination	Pass
Assessment of adapter variability	Pass

#### 2.1 Physical inspection

All contents of the kit are inspected for proper components, volumes and labeling. The condition of all plates were inspected after packaging and shipping.

## 2.1.1 Results of physical inspection

Criteria for acceptability	Pass/Fail
Expected volumes in all wells	Pass
Proper labeling	Pass
Proper shipping condition ( on dry ice)	Pass
Reagents clear and not discolored	Pass
Proper plate sealing	Pass

## 2.2 Indexed Adapter Plate quality control testing

### 2.2.1 Assessment of adapters for index sequence and location

The test is performed on a specific sample panel developed for this purpose. 24 different libraries are prepared where no library possesses the same allele(s). Each sample has a unique HLA allele and the placement of the sample on the plate is known, the location of the indexed adapter can be confirmed with genotyping each of the samples.

Criteria for acceptability	Pass/Fail
<b>Index sequence and location:</b> <b>Pass: All allele calls match the expected reference genotyping.</b> <b>Fail: At least one allele call does not match the expected genotyping.</b>	Pass

### 2.2.2 Assessment of indexed adapters for cross-contamination

The test is performed on a specific sample panel developed for this purpose. 24 different libraries are prepared where no library possesses the same allele(s). Index cross- contamination is assessed by looking for unexpected allele calls. Cross contamination would be evident through the detection of unexpected alleles and the contaminating adaptors identified.

#### 2.2.2.1 Results of indexed adapters cross-contamination

Criteria for acceptability	Pass/Fail
<b>A sufficient amount of reads is available:</b> <b>Pass: For every tested index, at least 4000 read pairs were mappable to the expected allele.</b> <b>Fail: For at least one tested index, less than 4000 read pairs were mappable to the expected allele.</b>	Pass
<b>A sufficient amount of reads is only available for the tested indices:</b> <b>Pass: More than 1000 read pairs is only available for the tested indices.</b> <b>Fail: More than 1000 read pairs is available for at least on not tested index.</b>	Pass
<b>Contamination with a single index is not observed:</b> <b>Pass: No index was identified with more than 1% contamination from another single index. The criterion must be true for all different contamination % estimates.</b> <b>Fail: At least one index was found with more than 1% contamination from another index.</b>	Pass



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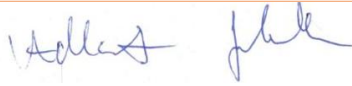
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### Authorization for release

Name	Zoltán Simon - Omixon	Function	COO
Signature		Sign date	2018.07.06
Name	Gabriella Adlovits - Omixon	Function	RAQS Manager
Signature		Sign date	2018.07.06