

Product Analysis Certificate

Human Genome-Wide (hGW) Lentiviral shRNA Library (Packaged)



Human Genome-Wide (hGW) Lentiviral shRNA Library (165K)

Shipment Contents: Human Genome-Wide (hGW) Lentiviral shRNA Library (Packaged)
— Store at -80°C

Description:

Cellecta's shRNA libraries are pooled barcoded lentiviral shRNA libraries constructed in third-generation lentiviral vectors and optimized for RNAi genetic screens in pooled format. The use of our proprietary shRNA design algorithm and database of validated shRNAs results in a high percentage of functional sequences, typically at least 70% knockdown efficiency for more than 95% of the target genes represented and 65% of the shRNAs (depending on the cell type). The vast majority of shRNA constructs in the library are represented equally, with the difference in concentrations usually not exceeding two orders of magnitude. Typically, virtually 100% of the population of shRNA constructs is present within a 10 to 100-fold range. We guarantee that at least 90% are present within a 100-fold range and 70% are present within a 10-fold range.

Specially-designed, optimized barcodes facilitate HT sequencing data analysis and identification of functional shRNAs. Using the Illumina GAIIx, HiSeq, or NextSeq HT Sequencing platform, barcodes are identified and converted to lists of genes/shRNA with enumerated barcode data. Amplification of shRNA hairpins is not required, as only the barcode sequence is required for identification. This enables unbiased amplification and unambiguous identification of each shRNA species.

The Human Genome-Wide shRNA library consists of 3 modules and targets all protein-encoding genes:

- Each module covers approximately 6,500 genes
- Each gene is targeted by 7-8 hairpins for a total of 55,000 hairpins per module
- Modules are made with non-overlapping barcodes so that they can be combined to form a complete genome-wide shRNA library
- Library targets all (19,276) protein encoding genes

The libraries are constructed in Cellecta's pRSI16cb-U6-sh-13kCB18-HTS6-UbiC-TagRFP-2A-Puro lentiviral vector that expresses shRNA under a wild-type U6 promoter and TagRFP (Evrogen) and Puro resistance gene under a human ubiquitin C promoter. For more information on the 13k Clonal Barcodes (13kCB18), please contact Cellecta at tech@cellecta.com.

The lentiviral shRNA libraries were packaged into VSV-G pseudotyped viral particles using Cellecta's second-generation psPAX2/pMD2.G packaging plasmid mix (Ready-to-use Packaging Plasmid Mix, Cat.# CPCP-K2A, 250 µg).

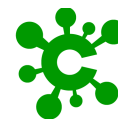
The titer of packaged libraries provided by Cellecta can be functionally determined by transduction of target cells and FACS of RFP-positive transduced cells.

Biosafety Level: BSL-2

Storage: -80°C

Shelf Life: 1 year from date of receipt

Shipping Conditions: Dry Ice



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Product Information (Cellecta Website):

User Manual: <http://www.cellecta.com/resources/protocols/>
 Target Gene List: <http://www.cellecta.com/products-and-services/...>
 Vector Info (Sequence, cassette, etc): <http://www.cellecta.com/resources/vectors/>
 shRNA sequences/barcodes: Please contact Cellecta at orders@cellecta.com.

Contents:

Catalog #	Description
HGW-V8	Human Genome-Wide Pooled Lentiviral shRNA Library (165K) hGW-pRSI16cb In pRSI16cb-U6-sh-13kCB18-HTS6-UbiC-TagRFP-2A-Puro Packaged, $>2 \times 10^8$ TU: 2.52×10^8 TU , 1.23×10^9 TU/ml (205 μ l total: 50 μ l x 4 vials, 5 μ l x 1 vials) Lot# 18010454; Store at -80°C <i>NOTE: Exact number of tubes and volume may vary. Total TU is always $>2 \times 10^8$.</i>

Quality Control

Library Representation

Please see attached Excel file, **hGW-pRSI16cb-shRNA-Lib-HTSeq-QC-130723.xlsx**.

Individual Clone Sequencing Data

The sequencing data shown is that of the Human Genome-Wide Library (hGW) which is comprised of equal amounts of hGWM1, hGWM2, and hGWM3.

	Library:	hGW in pRSI16cb
Plasmid Lot #:		12121403
Library Complexity (number of clones):		100×10^6
Number of random clones picked:		72
Correct Structure (with clonal barcode):		$>95\%$
Number of clones with at least one mutation, deletion, or insertion:		12
Mutation / Deletion / Insertion Rate:		0.1%
Estimated % of Inserts without any mutations, deletions, or insertions in <u>antisense</u> portion and considered to be functional:		$>95\%$

Cellecta now offers sample prep, HT sequencing, and data analysis services. Please contact us at sales@cellecta.com or visit our website at <http://www.cellecta.com/products-and-services/HT-sequencing-and-analysis/> for more information.

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