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CERTIFICATE OF ANALYSIS & LOT QC REPORT

Ready-to-Use Synthetic VHH Phage Display Library Kit (SKU: ADL-11)

Product Name:	Synthetic VHH Library Kit	Lot Number:	060726924
Catalog / SKU:	ADL-11	Mfg Date:	June 7, 2026
Format:	VHH + HA Tag + 6xHis Tag	Expiry Date:	June 2028 (-80°C)
Vector Architecture:	5703 bp (Amp ^R , pUC ori, f1 ori)	Master Scaffold:	ADE99145

1. TITER & INFECTIOUS PHAGE DETERMINATION

Test Parameter	Specification	Measured Lot Result	Assay / Method	Status
Phage Titer	$\geq 8.0 \times 10^{12}$ pfu/ml	8.4×10^{12} pfu/ml	Plaque Formation Assay (<i>TG1 E. coli</i> overlayer)	PASS
Helper Phage Titer	2.0×10^{12} pfu/ml	2.1×10^{12} pfu/ml	M13KO7 Plaque Assay on K12 Host	PASS
TG1 Competency	$\geq 1.0 \times 10^8$ cfu/ μ g	2.5×10^8 cfu/ μ g	Transformation Efficiency with pUC19 Control	PASS

2. LIBRARY DIVERSITY CALCULATION & METHOD

Reported Functional Diversity: 9.6×10^{10} total unique transformants.

Calculation Methodology: Determined via extrapolation of total colony-forming units (cfu) across all transformation electroporations during library synthesis, scaled by the full-length in-frame clone ratio established by Next-Generation Sequencing (NGS).

3. LOT-SPECIFIC NGS SEQUENCING & READ DEPTH SUMMARY

NGS Quality Metric	Target Specification	Measured Lot Value
Sequencing Platform	Illumina Paired-End (2 × 300 bp)	Illumina NovaSeq 6000
Total Raw Read Depth	> 10,000,000 reads	15,240,890 reads
Filtered High-Quality Reads (Q ≥ 30)	> 85.0%	91.4%
Unique Full-Length VHH Sequences	> 1,000,000 unique observed	1,842,105 unique sequences

4. SEQUENCE INTEGRITY & MUTATION RATES

Metric	Target Specification	Lot QC Result	Status
Insert-Positive Rate	> 90.0%	96.5%	PASS
In-Frame Ratio	> 85.0%	88.2%	PASS
Frameshift Rate	< 5.0%	2.3%	PASS
Premature Stop Codon Rate	< 5.0% (excl. Amber stop)	1.8%	PASS

* Note: Position 1905–1907 contains an engineered Amber stop codon (TAG) upstream of the pIII gene for conditional translation in suppressor TG1 vs non-suppressor hosts.

5. CLONE-ABUNDANCE & REDUNDANCY DISTRIBUTION

Gini Coefficient / Diversity Index: 0.21 (indicates high sequence balance across the pool, where 0 = perfect uniformity and 1 = extreme bias).

Top 100 Clones Contribution: Represents < **0.42%** of total NGS read count, confirming absence of clonal dominance.

Redundancy Profile: **93.1%** of detected unique sequences were observed as singletons or doubletons at the sampled sequencing depth.

6. CONSTITUENT SUB-LIBRARY REPRESENTATION

Sub-Library ID	CDR Mutagenesis Profile	Expected Share	NGS Observed Share
Sub-library 1	Saturation Mutagenesis: CDR1 (7 aa), CDR2 (6 aa), CDR3 (M17)	~ 20%	19.8%
Sub-library 2	Saturation Mutagenesis: CDR1 (7 aa), CDR2 (6 aa), CDR3 (M23)	~ 20%	20.4%
Sub-library 3	Wildtype CDR1/CDR2; Saturation Mutagenesis: CDR3 (M17)	~ 20%	19.5%
Sub-library 4	Wildtype CDR1/CDR2; Saturation Mutagenesis: CDR3 (M23)	~ 20%	20.1%
Sub-library 5	Wildtype CDR1; Saturation Mutagenesis: CDR2 (6 aa), CDR3 (M23)	~ 20%	20.2%

7. KIT COMPONENTS & FORMULATIONS

Component	Quantity	Concentration	Storage Buffer
VHH Synthetic Library Phage	1.0 ml	8.0×10^{12} pfu/ml	1xPBS with 50% glycerol
M13KO7 Helper Phage	0.5 ml	2.0×10^{12} pfu/ml	1xPBS with 50% glycerol
Chemically Competent TG1 <i>E. coli</i>	0.5 ml	Host Strain	2xYT with 25% glycerol
M13 Reverse Primer (1.6 μ M)	0.2 ml	1.6 μ M	1xTE Buffer
pIII Reverse Primer (1.6 μ M)	0.2 ml	1.6 μ M	1xTE Buffer

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