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CERTIFICATE OF ANALYSIS & LOT QC REPORT

Ready-to-Use Next-Generation Human Synthetic scFv Phage Display Library Kit (SKU: ADL-13)

Product Name:	Next-Generation Human Synthetic scFv Phage Display Library Kit	Lot Number:	081126813
Catalog / SKU:	ADL-13	Mfg Date:	August 11, 2026
Format:	scFv (pelB-VH (VH3-23)-(G4S) ₃ -VL (VK1-39)-HA-6xHis-Amber-cP3)	Expiry Date:	August 2028 (-80°C)
Vector Architecture:	5311 bp (Amp ^R , pUC ori, f1 ori, lacI)	Master Scaffold:	Human Germline IGHV 3-23*01 / IGKV 1-39*01 (O12 allele)

1. TITER & INFECTIOUS PHAGE DETERMINATION

Test Parameter	Specification	Measured Lot Result	Assay / Method	Status
Phage Titer	$\geq 4.8 \times 10^{12}$ pfu/ml	4.8×10^{12} pfu/ml	Plaque Formation Assay (<i> TG1 E. coli</i> overlayer)	PASS
Helper Phage Titer	2.0×10^{12} pfu/ml	2.0×10^{12} pfu/ml	M13KO7 Plaque Assay on K12 Host	PASS
TG1 Competency	$\geq 1.0 \times 10^8$ cfu/ μ g	2.4×10^8 cfu/ μ g	Transformation Efficiency with pUC19 Control	PASS

2. LIBRARY DIVERSITY CALCULATION & METHOD

Reported Functional Diversity: 5.8×10^{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 $\times$ 300 bp)	Illumina NovaSeq 6000
Total Raw Read Depth	> 10,000,000 reads	16,250,000 reads
Filtered High-Quality Reads (Q $\geq$ 30)	> 85.0%	94.2%
Unique Full-Length ScFv Sequences	> 1,000,000 unique observed	1,753,389 unique sequences

4. SEQUENCE INTEGRITY & MUTATION RATES

Metric	Target Specification	Lot QC Result	Status
Insert-Positive Rate (Light & Heavy Chains)	> 90.0%	97.1%	PASS
In-Frame Ratio	> 95.0%	96.2%	PASS
Frameshift Rate	< 5.0%	2.1%	PASS
Premature Stop Codon Rate	< 5.0% (excl. Amber stop)	1.7%	PASS

* Note: Position 2754–2756 contain engineered Amber stop codons (TAG) upstream of cP3 / anchor regions for conditional translation in suppressor TG1 vs non-suppressor host strains.

5. CLONE-ABUNDANCE & REDUNDANCY DISTRIBUTION

Gini Coefficient / Diversity Index: 0.22 (indicates high sequence balance across the pool, where 0 = perfect uniformity and 1 = extreme bias).

Top 100 Clones Contribution: Represents < 0.40% of total NGS read count, confirming absence of clonal dominance.

Redundancy Profile: 93.5% of detected unique sequences were observed as singletons or doubletons at the sampled sequencing depth.

6. CONSTITUENT CDR TRIM PROFILE CONFORMANCE

Region / Domain	CDR Mutagenesis Strategy	Design Target Match	NGS Observed Share
HCDR1 Domain	Soft Randomization (Trimer Phosphoramidite Mix across 4 positions)	Conforms to Specs	PASS
HCDR2 Domain	Soft Randomization (Trimer Phosphoramidite Mix across 4 positions)	Conforms to Specs	PASS
HCDR3 Domain	Varied Length Loops (Trimer Phosphoramidite Mix across 12, 15, 18 AA)	Conforms to Specs	PASS
LCDR1 Domain	Soft Randomization (Trimer Phosphoramidite Mix across 4 positions)	Conforms to Specs	PASS
LCDR2 Domain	100% Fixed Germline (AASSLQS)	100.0% Match	PASS
LCDR3 Domain	Fixed Length Loop (Trimer Phosphoramidite Mix across 9 positions)	Conforms to Specs	PASS

7. KIT COMPONENTS & FORMULATIONS

Component	Quantity	Concentration	Storage Buffer
Next-Generation Human Synthetic scFv library Phage	1.0 ml	4.8×10^{12} pfu/ml	1xPBS with 25% glycerol
M13K07 Helper Phage	0.5 ml	2.0×10^{12} pfu/ml	1xPBS with 25% glycerol
Chemically Competent TG1 <i>E. coli</i>	0.5 ml	2.5×10^8 cfu/ml	2xYT with 25% glycerol
M13 Rev Primer (1.6 μ M)	0.2 ml	1.6 μ M	1xTE Buffer
pIII Rev Primer (1.6 μ M)	0.2 ml	1.6 μ M	1xTE Buffer

Quality Control Analyst
Fusion BioLabs Analytical Services

Director of Quality Assurance
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