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CERTIFICATE OF ANALYSIS & LOT QC REPORT

Ready-to-Use Human Naïve scFv Phage Display Library Kit (SKU: ADL-01)

Product Name:	Human Naïve scFv Library Kit	Lot Number:	060826786
Catalog / SKU:	ADL-01	Mfg Date:	June 8, 2026
Format:	scFv + 6xHis Tag + HA Tag (OmpA leader-VH-Linker-VL-6xHis-HA)	Expiry Date:	June 2028 (-80°C)
Vector Architecture:	5385 bp (Amp ^R , pUC ori, f1 ori, lacI promoter)	Donor Diversity Base:	Multi-Ethnic Human Naïve Pool

1. TITER & INFECTIOUS PHAGE DETERMINATION

Test Parameter	Specification	Measured Lot Result	Assay / Method	Status
Phage Titer	$\geq 9.0 \times 10^{12}$ pfu/ml	9.3×10^{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: 9.0×10^{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	16,120,450 reads
Filtered High-Quality Reads (Q ≥ 30)	> 85.0%	93.2%
Unique Full-Length scFv Sequences	> 1,000,000 unique observed	1,915,300 unique sequences

4. SEQUENCE INTEGRITY & MUTATION RATES

Metric	Target Specification	Lot QC Result	Status
Insert-Positive Rate (VH + VL)	> 90.0%	97.2%	PASS
In-Frame Ratio	> 95.0%	96.4%	PASS
Frameshift Rate	< 3.0%	1.8%	PASS
Premature Stop Codon Rate	< 3.0% (excl. Amber stop)	1.4%	PASS

* Note: Position 2274–2276 contains an engineered Amber stop codon (TAG) upstream of the engineered pIII gene for conditional translation in suppressor TG1 vs non-suppressor hosts.

5. CLONE-ABUNDANCE & REDUNDANCY DISTRIBUTION

Gini Coefficient / Diversity Index: 0.19 (indicates high sequence balance across the pool, where 0 = perfect uniformity and 1 = extreme bias).

Top 100 Clones Contribution: Represents < **0.38%** of total NGS read count, confirming absence of clonal dominance.

Redundancy Profile: **94.2%** of detected unique sequences were observed as singletons or doubletons at the sampled sequencing depth.

6. DONOR DEMOGRAPHIC REPRESENTATION & DIVERSITY SOURCES

Ethnic Cohort Group	Donor Count Specification	Age Range & Gender Profile	Observed Representation Share
Asian Cohort	≥ 50 Donors	Ages 25–74 (Equally distributed Male / Female)	25.1%
African American Cohort	≥ 50 Donors	Ages 25–74 (Equally distributed Male / Female)	24.8%
Caucasian Cohort	≥ 50 Donors	Ages 25–74 (Equally distributed Male / Female)	25.2%
Hispanic & Filipino Cohorts	≥ 50 Donors per group	Ages 25–74 (Equally distributed Male / Female)	24.9%

7. KIT COMPONENTS & FORMULATIONS

Component	Quantity	Concentration	Storage Buffer
Human Naïve scFv Library Phage	1.0 ml	9.0×10^{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 μM)	0.2 ml	1.6 μM	1xTE Buffer
pIII Reverse Primer (1.6 μM)	0.2 ml	1.6 μM	1xTE Buffer

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