### Transformation Efficiency

100 pg of pUC19 plasmid DNA was used to transform NEB 5-alpha Competent E. coli cells. The transformation efficiency of 1–3 x 10^9 cfu/µg pUC19 DNA was achieved.

### Quality Control Assays

#### Transformation Efficiency

The transformation efficiency was measured by comparing the number of colonies formed on LB-ampicillin plates before and after incubation. The efficiency was calculated using the formula:

\[
\text{Transformation Efficiency} = \frac{\text{Total Transformants (cfu x 10^7)}}{\text{Amount of DNA Transformed (µg)}}
\]

#### Plating

Selection plates were used to count the number of transformants. Colonies were spread onto plates and incubated at 37°C for 1-2 days.

### Reagents Supplied

- NEB 5-alpha Competent E. coli (Lot: 232)
- 25 ml of SOC Outgrowth Medium (Store at room temperature)
- 0.025 ml of 50 pg/µl pUC19 Control DNA (Store at –20°C)

### Transformation Protocol Variables

- **Thawing:** Cells are best thawed on ice and DNA added as soon as the last bit of ice in the tube disappears. Cells can also be thawed by hand, but warming above 0°C will decrease the transformation efficiency.
- **Incubation of DNA with Cells on Ice:** Both the temperature and the timing of the heat shock step are important and specific to the transformation volume and vessel. Using the transformation tube provided, 30 seconds at 42°C is optimal.
- **Heat Shock:** The temperature and the timing of the heat shock step are important and specific to the transformation volume and vessel. Using the transformation tube provided, 30 seconds at 42°C is optimal.
- **Outgrowth:** Outgrowth at 37°C for 1 hour is best for cell recovery and for expression of antibiotic resistance. Expect a 2-fold loss in transformation efficiency for every 10 minutes this step is shortened.

### Transformation Protocol

1. Thaw a tube of NEB 5-alpha Competent E. coli cells on ice until the last ice crystals disappear. Mix gently and carefully pipette 50 µl of cells into a transformation tube on ice.
2. Add 1–5 µl containing 1 pg–100 ng of plasmid DNA to the cell mixture. Carefully flick the tube 4–5 times to mix cells and DNA. Do not vortex.
3. Place the mixture on ice for 2 minutes. Do not mix.
5. Place on ice for 2 minutes. Do not mix.
6. Pipette 950 µl of room temperature SOC into the mixture. Immediately spread 50–100 µl of each dilution onto a selection plate and incubate overnight at 37°C. Alternately, incubate at 30°C for 24–36 hours or 25°C for 48 hours.
7. Place at 37°C for 60 minutes. Shake vigorously (250 rpm) or rotate.
8. Warm selection plates to 37°C.
9. Mix the cells thoroughly by flicking the tube and inverting, then perform several 10-fold serial dilutions in SOC.
10. Spread 50–100 µl of each dilution onto a selection plate and incubate overnight at 37°C. Alternatively, incubate at 30°C for 24–36 hours or 25°C for 48 hours.

### DNA Effects on Transformation Efficiency and Colony Output

The optimal amount of DNA to use in a transformation reaction is lower than commonly recognized. Using clean, supercoiled pUC19, the efficiency of transformation is highest in the 100 pg–1 ng range. However, the total colonies which can be obtained from a single transformation reaction increase up to about 100 ng.
Calculating Transformation Efficiency

Transformation efficiency is a measure of the number of colony forming units (cfu) that can be produced by transforming 1 µg of plasmid DNA into a given volume of competent cells. It is usually calculated by transforming 100 pg of highly purified supercoiled plasmid under ideal conditions. If you plan to calculate efficiency to compare cells or ligations, keep in mind the many variables which affect this metric.

**Transformation efficiency (TE) equation:**

\[
TE = \frac{Colonies}{\mu g \times Dilution}
\]

Where:
- **Colonies** = the number of colonies counted on the plate
- **µg** = the amount of DNA transformed expressed in µg
- **Dilution** = the total dilution of the DNA before plating

**TE calculation example:**

Transform 2 µl (100 pg) of control pUC19 DNA into 50 µl of cells, outgrow by adding 250 µl of SOC and dilute 10 µl up to 1 ml in SOC before plating 30 µl. If you count 150 colonies on the plate, the TE is:

- Colonies = 150
- µg DNA = 0.0001
- Dilution = 10/300 x 30/1000 = 0.001
- TE = 150/0.0001/0.001 = 1.5 x 10^9 cfu/µg

**Solutions/Recipes**

- **SOB:**
  - 2% Vegetable peptone (or Tryptone)
  - 0.5% Yeast Extract
  - 10 mM NaCl
  - 2.5 mM KCl
  - 10 mM MgCl₂
  - 10 mM MgSO₄

- **SOC:**
  - SOB + 20 mM Glucose

- **LB agar:**
  - 1% Tryptone
  - 0.5% Yeast Extract
  - 0.17 M NaCl
  - 1.5% Agar

- **Blue/White Screening:**
  - X-gal 80 µg/ml
  - IPTG* 0.3 mM

*Omit IPTG for potentially toxic genes

**Antibiotics for Plasmid Selection**

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>Working Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ampicillin</td>
<td>100 µg/ml</td>
</tr>
<tr>
<td>Carbenicillin</td>
<td>100 µg/ml</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>33 µg/ml</td>
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<tr>
<td>Kanamycin</td>
<td>30 µg/ml</td>
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<tr>
<td>Streptomycin</td>
<td>25 µg/ml</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>15 µg/ml</td>
</tr>
</tbody>
</table>

**Strain Properties**

The properties of this strain that contribute to its usefulness as a cloning strain are described below. The genotypes underlying these properties appear in parentheses.

**Blue/White Screening** (80s/laclM15): makes the α-fragment of β-galactosidase (β-gal); αf-lacZ) deletes the β-gal gene on the chromosome. pUC19 and similar plasmids code for the α-peptide of β-gal (lacZ). The α-peptide can combine with the α-peptide of β-gal that is carried on β80 (α-complementation). When β-gal is reconstituted in this manner it can cleave 5-bromo-4-chloro-3-indolyl-β-D-galactosidase (X-gal) and results in blue colonies on an X-gal plate. Inserts cloned into the plasmid polylinker disrupt the α-peptide gene and the colonies are white.

**Recombination Deficient (recA):** E. coli has a repair system that will recombine homologous sequences. Genomic clones often have duplicated regions, and RecA mediated rearrangements can be problematic, particularly when regions of homology are longer than 50 bp. Strains which have the RecA function deleted tend to grow more slowly than recA- strains.

**Endonuclease I Deficient (endA):** The periplasmic space of wild type E. coli cells contains a nonspecific endonuclease. Extreme care must be taken to avoid degradation of plasmids prepared from these cells. The endA mutation deletes this endonuclease and can significantly improve the quality of plasmid preparations.

**Restriction Deficient (hsdR):** Wild type E. coli K12 strains carry a restriction endonuclease which cleaves DNA with sites (AAC(N6)GTGC and GCAC(N6)GTT. While E. coli DNA is protected from degradation by a cognate methyl-transferase, foreign DNA will be cut at these sites. The hsdR mutation eliminates this endonuclease activity. However, this strain has functional methyl restriction systems and may not be suitable for direct cloning of eukaryotic DNA.

**T1 Phage Resistant (thuA2):** T1, an extremely virulent phage requires the E. coli ferric hydroxamate uptake receptor for infectivity. Deletion of this gene confers resistance to this type of phage, but does not significantly affect the transformation or growth characteristics of the cell.

**Genotype:** thuA2 Δ(argF-lacZ)U169 phoA glnV44 β80s(lacZ)M15 gyrA96 recA1 relA1 endA1 thi-1 hsdR17

**Companion Products Sold Separately:**

- **SOP Outgrowth Medium #B9020S** 4 x 25 ml medium