

**Antimicrobial Resistance Panel 13: *Pseudomonas aeruginosa* Fluoroquinolone Resistance Pathway Mutants**

**Catalog No. NR-55652**

**Product Description:**

NR-55652 consists of a 2-member panel of *Pseudomonas aeruginosa* (*P. aeruginosa*) PAO1 mutant strains. NB52023 is an efflux deficient mutant lacking *mexXY* operon genes: *mexB* and *mexX* ( $\Delta mexB \Delta mexX$ ). NB52023-CDK0006 is derived from NB52023 by site-directed mutagenesis and contains mutations resulting in amino acid substitutions in DNA gyrase [*gyrA* (T83I)] and topoisomerase IV [*parC* (S87L)].

NR-51969 and NR-51866 were produced by inoculating the deposited material into Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce lots 70046521 and 70048187, respectively.

Quality control testing was completed under propagation conditions unless otherwise noted.

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**Table 1: Kit Components**

COMPONENT NUMBER	STRAIN	DESCRIPTION	LOT NUMBER	MANUFACTURING DATE
NR-51969	<i>P. aeruginosa</i> , strain NB52023	$\Delta mexB \Delta mexXY$	70046521	13AUG2021
NR-51866	<i>P. aeruginosa</i> , strain NB52023-CDK0006	$\Delta mexB \Delta mexX$ <i>gyrA</i> (T83I) <i>parC</i> (S87L)	70048187	21OCT2021

**Table 2: *P. aeruginosa*, Strain NB52023 (NR-51969)**

TEST	SPECIFICATIONS	RESULTS
<b>Phenotypic Analysis</b> Cellular morphology Colony morphology  Motility (wet mount) VITEK® MS (MALDI-TOF)	Gram-negative rods Report results  Report results <i>P. aeruginosa</i>	Gram-negative rods Irregular, convex, undulate, smooth and cream  Motile <i>P. aeruginosa</i> (99.9%)
<b>Antibiotic Susceptibility Profile</b> Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar Chloramphenicol Ofloxacin	Report results Report results	> 1µg/mL 0.125 µg/mL
<b>Genotypic Analysis</b> Digital DNA-DNA hybridization (dDDH) <sup>1</sup> Deletion of <i>mexB</i> and <i>mexX</i>	≥ 70% for species identification Deletions confirmed	<i>P. aeruginosa</i> (95.2%) <b>Pending</b>
<b>Purity (post-freeze)</b> 8 days at 37°C in an aerobic atmosphere with and without 5%CO <sub>2</sub> on Tryptic Soy agar	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
<b>Viability (post-freeze)</b>	Growth	Growth

<sup>1</sup>Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." *Stand. Genomic Sci.* 2 (2010): 117-134. PubMed: 21304684.

**Table 3: *P. aeruginosa*, Strain NB52023-CDK0006 (NR-51866)**

TEST	SPECIFICATIONS	RESULTS
<b>Phenotypic Analysis</b> Cellular morphology Colony morphologies <sup>1</sup>  Motility (wet mount) VITEK® MS (MALDI-TOF)	Gram-negative rods Report results  Report results <i>P. aeruginosa</i>	Gram-negative rods Colony type 1: Irregular, low convex, undulate, rugose and cream Colony type 2: Circular, low convex, entire, smooth and cream  Motile <i>P. aeruginosa</i> (99.9%)
<b>Antibiotic Susceptibility Profile</b> BD BBL™ Sensi-Disc™ Susceptibility Test Discs 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar Gatifloxacin Novobiocin	Report results Report results	11-12 mm 0 mm
<b>Genotypic Analysis</b> Digital DNA-DNA hybridization (dDDH) <sup>2</sup> Deletion of <i>mexB</i> and <i>mexX</i> Confirmation of <i>gyrA</i> (T831) <i>parC</i> (S87L) SNPs	≥ 70% for species identification Deletions confirmed SNPs confirmed	<i>P. aeruginosa</i> (95.2%) Pending Pending
<b>Purity</b> 7 days at 37°C in an aerobic atmosphere with and without 5% CO <sub>2</sub> on Tryptic Soy agar	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
<b>Viability</b>	Growth	Growth

<sup>1</sup>Two colony types were observed. Plating of the individual colony types showed that they reverted to colony type 1. VITEK® MS (MALDI-TOF) analysis identified cells from both colony types as *P. aeruginosa*.

<sup>2</sup>Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." *Stand. Genomic Sci.* 2 (2010): 117-134. PubMed: 21304684.

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