

SELECTED EXPERIMENTAL EVIDENCE / REVIEWER GUIDE

Experimental work, with its context.

Five selected gel photographs and their associated lane annotations support laboratory development of preparation-to-PCR and preparation-to-LAMP workflows. The existing GAPDH example remains available on the application website.

01 Acinetobacter preparation-variable study

Documented exploration of preparation variables and downstream PCR compatibility for *A. baumannii*.

02 Bacterial preparation in a blood matrix

A qualitative feasibility example for sample preparation followed by bacterial 16S PCR in this experiment.

03 Swift preparation beside a spin-column comparator

A side-by-side qualitative PCR compatibility example, with a named extraction comparator in the same record.

04 Leptospira sample-preparation-to-LAMP work

An internal record linking preparation-route development with downstream LAMP experimentation.

05 Swift-prepared Candida enters LAMP

A qualitative preparation-to-amplification development example using the Swift workflow.

HOW TO READ THESE FIGURES

Photographs are rectangular extracts of team-supplied screenshots. Gel pixels are unchanged: no bands were added, removed, sharpened or contrast-adjusted. Lane maps follow source notes; uncertain labels remain explicit. Personal chat content and reagent recipes are excluded.

Evidence level: qualitative internal development records. These are selected images, not five independent validation studies or a clinical cohort. Band sizes, detection limits, diagnostic accuracy and AMR detection are not established by this annex.

The practical C-CAMP objective: turn existing experimental records into a focused intended use, controlled design requirements, a traceable verification plan and quality documentation.

FIGURE 01 / 16S PCR / INTERNAL DEVELOPMENT

Acinetobacter preparation-variable study

Acinetobacter baumannii



EXPERIMENTAL QUESTION

How does preparation condition affect downstream bacterial PCR?

DESIGN RECORDED

The source compares a higher cell input with three preparation-time conditions at another annotated input. SC and NC positions are recorded.

Experiment date: Not supplied. Source: 1000314387.png.

LANE MAP / TRANSCRIBED SOURCE ANNOTATIONS

Lane	Source assignment
1	1 kb DNA ladder
2	9 × 10 ⁸ cells, as annotated
3	1 × 10 ⁷ cells; 10-minute preparation condition
4	1 × 10 ⁷ cells; 20-minute preparation condition
5	1 × 10 ⁷ cells; 30-minute preparation condition
6	SC, as annotated; definition pending
7	NC, as annotated; definition pending

OBSERVED IN THE PHOTOGRAPH

Band visibility differs across the sample lanes in this photographed gel. That variation is a development finding to investigate.

WHAT THIS SUPPORTS

Documented exploration of preparation variables and downstream PCR compatibility for A. baumannii.

INTERPRETATION LIMIT

The source-annotated cell counts are not independently verified and their input basis is unspecified. One photographed run cannot establish an optimum, detection limit or reproducibility. Expected product size and the SC/NC definitions require confirmation.

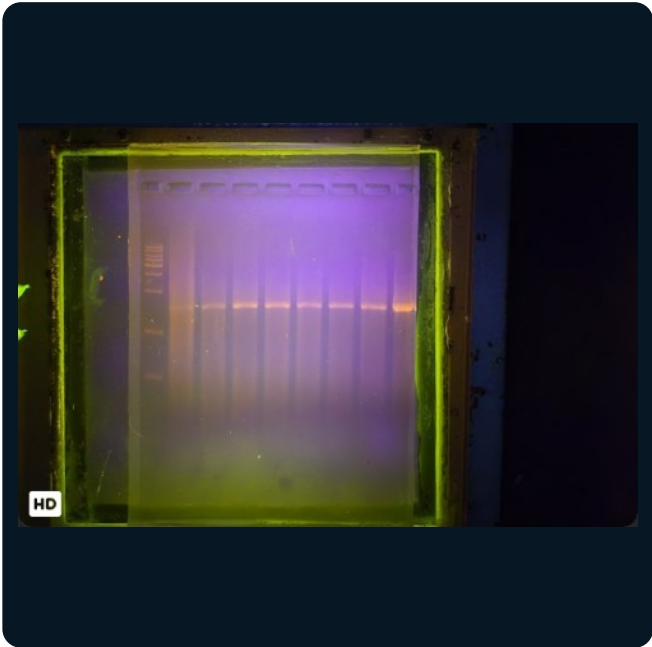
NEXT EVIDENCE STEP

Repeat the controlled comparison with fixed input, confirmed control identities and pre-defined interpretation criteria.

FIGURE 02 / 16S PCR / INTERNAL DEVELOPMENT

Bacterial preparation in a blood matrix

Klebsiella; a second organism labelled “S. Auris”



EXPERIMENTAL QUESTION

Can prepared bacterial material from a blood matrix enter a conventional PCR workflow?

DESIGN RECORDED

The source describes cultured-cell pellets suspended in whole blood, with three sampled input volumes for each organism and a PBS comparison lane.

Experiment date: Not supplied. Source: 1000314385.png.

LANE MAP / TRANSCRIBED SOURCE ANNOTATIONS

Lane	Source assignment
1	1 kb DNA ladder
2-4	“S. Auris”: 5, 10 and 50 µL sampled from the suspension; organism identity to confirm
5-7	Klebsiella: 5, 10 and 50 µL sampled from the suspension
8	Swift preparation / Klebsiella in PBS, as annotated
9	SC, as annotated; abbreviation not defined

OBSERVED IN THE PHOTOGRAPH

Several sample lanes show bands at a similar migration position. The source-labelled PBS comparison and SC lanes also show signal.

WHAT THIS SUPPORTS

A qualitative feasibility example for sample preparation followed by bacterial 16S PCR in this experiment.

INTERPRETATION LIMIT

The source label “S. Auris” needs identity confirmation. The blood matrix is experimentally prepared, not a clinical diagnostic cohort. No NC lane is identified in this record; band identity, expected amplicon size and specificity remain unverified.

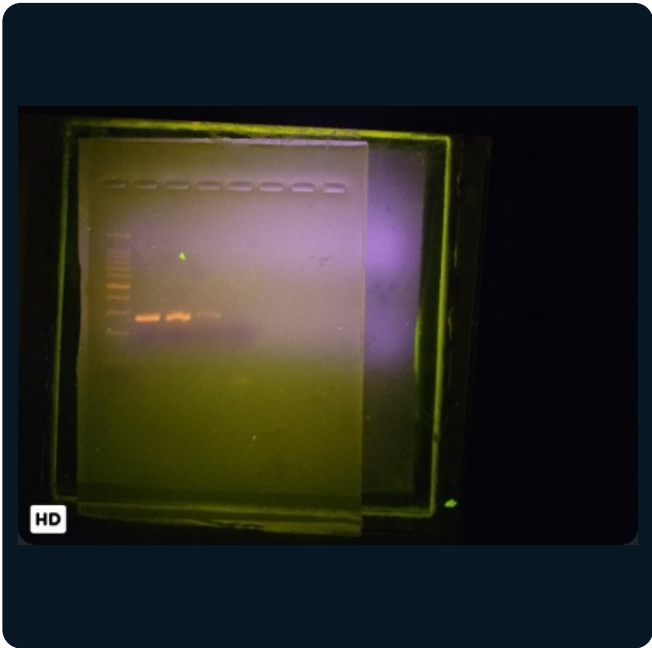
NEXT EVIDENCE STEP

Confirm the organism label, define the controls and amplicon size, and repeat matched blood-matrix and reference-method comparisons.

FIGURE 03 / CONVENTIONAL PCR / INTERNAL DEVELOPMENT

Swift preparation beside a spin-column comparator

Candida albicans / Candida glabrata



EXPERIMENTAL QUESTION

Can Swift-prepared material support PCR alongside a conventional extraction comparator?

DESIGN RECORDED

The source identifies C. albicans-specific primers, Swift and spin-column C. albicans preparations, a spin-column C. glabrata lane and an NC lane.

Experiment date: Not supplied. Source: 1000314393.png.

LANE MAP / TRANSCRIBED SOURCE ANNOTATIONS

Lane	Source assignment
1	100 bp DNA ladder
2	Swift-prepared C. albicans
3	Spin-column-prepared C. albicans
4	Spin-column-prepared C. glabrata
5	NC, as annotated; definition pending

OBSERVED IN THE PHOTOGRAPH

Bands are visible in the lanes annotated as Swift-prepared and spin-column-prepared C. albicans. The non-target and NC lanes require review at the expected product size.

WHAT THIS SUPPORTS

A side-by-side qualitative PCR compatibility example, with a named extraction comparator in the same record.

INTERPRETATION LIMIT

This is not a quantitative equivalence, extraction-yield or assay-specificity study. A faint signal cannot be assigned to a target without its expected size and run interpretation. Matched inputs, independent samples, repeats and NC definition are unconfirmed.

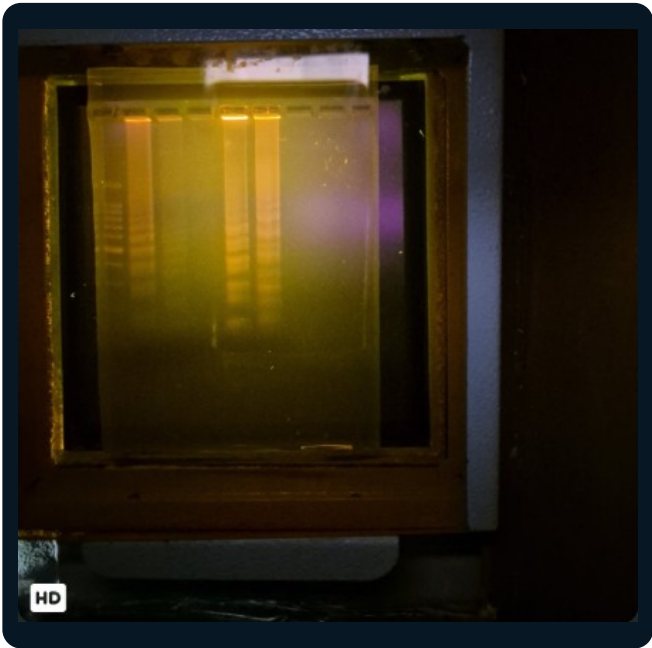
NEXT EVIDENCE STEP

Document matched inputs and control identities, then compare repeat runs using a defined amplicon size and acceptance criteria.

FIGURE 04 / LAMP / GEL READOUT / INTERNAL DEVELOPMENT

Leptospira sample-preparation-to-LAMP work

Leptospira, species not specified



EXPERIMENTAL QUESTION

Can different preparation routes feed the developing LAMP workflow?

DESIGN RECORDED

The source labels culture preparations in a centrifuge tube and Swift device, using two lysis approaches, plus a blood sample labelled positive. The gel is annotated as 2%.

Experiment date: Not supplied. Source: 1000314390.png.

LANE MAP / TRANSCRIBED SOURCE ANNOTATIONS

Lane	Source assignment
1	100 bp DNA ladder
2	Centrifuge-tube culture preparation, approach A
3	Centrifuge-tube culture preparation, approach B
4	Swift-device culture preparation, approach A
5	Swift-device culture preparation, approach B
6	Swift-device blood sample labelled positive

OBSERVED IN THE PHOTOGRAPH

The photographed gel shows multi-band/smeared amplification patterns in several lanes. Such patterns alone do not establish target-specific amplification.

WHAT THIS SUPPORTS

An internal record linking preparation-route development with downstream LAMP experimentation.

INTERPRETATION LIMIT

No negative-control lane is listed. The label “positive blood sample” does not establish a clinical reference result or patient cohort. Species, target, control evidence and specificity are unconfirmed. This does not verify the SensoAid hardware.

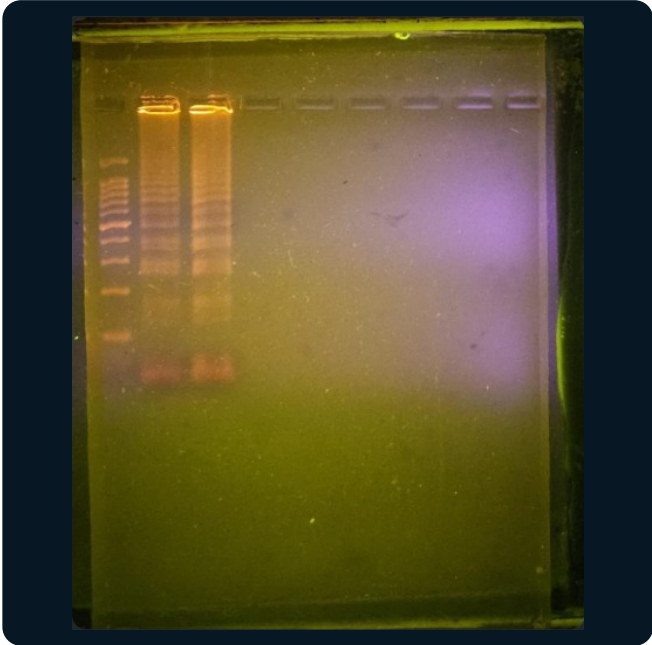
NEXT EVIDENCE STEP

Add and define negative/extraction controls, verify target identity and test the complete workflow against a suitable reference.

FIGURE 05 / LAMP / GEL READOUT / INTERNAL DEVELOPMENT

Swift-prepared Candida enters LAMP

Candida albicans



EXPERIMENTAL QUESTION

Can Swift-prepared *C. albicans* material enter the experimental LAMP pathway?

DESIGN RECORDED

The source identifies *C. albicans*-specific LAMP primers and compares Swift-prepared material with an SC-labelled sample.

Experiment date: Not supplied. Source: 1000314401.png.

LANE MAP / TRANSCRIBED SOURCE ANNOTATIONS

Lane	Source assignment
1	100 bp DNA ladder
2	SwiftDNA-prepared <i>C. albicans</i> ; 1.3×10^8 cells, as annotated
3	SC <i>C. albicans</i> , as annotated; SC definition pending

OBSERVED IN THE PHOTOGRAPH

Both annotated sample lanes show prominent multi-band/smeared amplification patterns.

WHAT THIS SUPPORTS

A qualitative preparation-to-amplification development example using the Swift workflow.

INTERPRETATION LIMIT

No negative-control lane is listed. The cell input is source-annotated, not independently quantified. A LAMP-like pattern does not establish target specificity, clinical accuracy or final-device performance; SC is not defined.

NEXT EVIDENCE STEP

Confirm the SC identity and input basis; add defined negative controls and verify target-specific amplification across repeat runs.