

VIALAB Operating Instructions

Document Change History

| Vers. | Status: | Name: | Date: | Change: |
|--------------|----------------|----------------|--------------|---|
| V00 | Draft | ULe, SSt | 07-12-2017 | Document issued |
| V01 | Released | SSt | 15-03-2018 | Document released |
| V02 | Released | SSt | 10-10-2018 | download information added, troubleshooting "Program Transfer To Pipette" added |
| V03 | Released | ULe, SSt | 09-01-2019 | New Software V 2.0 |
| V04 | Released | SSt | 13-02-2019 | System Requirements for VIALAB 2.0 changed |
| V05 | Released | SSt | 04-03-2020 | New Software V 2.1 – new features |
| V06 | Released | MFr | 21-04-2020 | Update Pipette Communication Module |
| V07 | Released | JBa2 | 13-08-2020 | Typos removed |
| V08 | Released | ULe, JBa2, SSt | 08-04-2022 | New Software V 3.0 |
| V09 | Released | SSt | 05-12-2022 | System Requirements updated |
| V10 | Released | CBa | 21-02-2024 | New Software V 3.2 – new features |
| V11 | Released | CBa | 31-05-2024 | New Software V 3.3 – new features |
| V12 | Released | CBa | 17-01-2025 | New Software V 3.4 – new features |

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1 Introduction

1.1 Purpose

VIALAB enables creating programs and transfers programs to INTEGRA multichannel VIAFLO/VOYAGER electronic pipettes and D-ONE single channel pipetting modules. VIALAB programs for use with ASSIST PLUS only.

Programming in VIALAB can be created without a connected pipette.

1.2 Scope

These operating instructions describe the installation and operation of VIALAB V 3.3 or higher.

1.3 Third party licenses

VIALAB contains copyrighted open source software components. Please refer to the list in the [Download center](#) of our website under "Open Source Licenses".

For other requests concerning open source and instrument software or if you encounter problems accessing above, please contact INTEGRA BIOSCIENCES via support@integra-biosciences.com or call us on +41 81 286 95 11. This service is free of charge. If you request physical copies, you will be charged a fee covering the cost of reproduction and shipment.

2 System requirements

2.1 Personal computer / laptop

| | |
|-------------------|---|
| CPU: | INTEL or AMD (not older than 5 years) |
| USB port: | 2.0 / 3.0 |
| Bluetooth: | optional |
| Memory: | > 4 GB |
| Internet access: | recommended during installation, required for updates |
| Operating system: | MS Windows 8.1, MS Windows 10.x, MS Windows 11.x, |
| Framework: | Microsoft .NET 4.7.2 (or later) |
| Resolution: | 1920 x 1080, Scaling/Zoom factor 100 % |

2.2 Compatibility

| Pipette: | Serial No.: | Pipette Firmware connectable to | | | | | |
|---|--------------------|---------------------------------|-----------------|-----------------|-----------------|----------------------------|-----------------|
| | | VIALAB V 1.0.x | VIALAB V 2.0.x | VIALAB V 2.1.x | VIALAB V 3.0.x | VIALAB V 3.2.x and V 3.3.X | VIALAB V 3.4.x |
| VIAFLO electronic multichannel pipette | 7000000 and higher | 4.12 and higher | 4.20 and higher | 4.21 and higher | 5.04 and higher | 5.12 and higher | 5.13 and higher |
| VOYAGER electronic adjustable tip spacing pipette | 7000000 and higher | 4.12 and higher | 4.20 and higher | 4.21 and higher | 5.04 and higher | 5.12 and higher | 5.13 and higher |
| D-ONE single channel pipetting module | 7000000 and higher | - | - | - | 5.04 and higher | 5.12 and higher | 5.13 and higher |

2.3 Useful accessories

| Part No. | Name | Description |
|----------|---|--|
| 4211 | Charging/communication stand for 1 pipette, incl. mains adapter | Connect the stand to the USB port of your PC and place the pipette/D-ONE on the stand. The stand can be used to charge the battery and enables the communication between the PC and the pipette/D-ONE. |
| 4221 | Pipette communication module | For wireless communication between pipette/D-ONE and PC or ASSIST PLUS. |
| 4549 | Charging cable for pipette on ASSIST PLUS | For charging of pipette/D-ONE on ASSIST PLUS. |

3 Installation of VIALAB

3.1 Preparation

Download VIALAB from www.integra-biosciences.com/download-vialab. Register, download the ZIP file and unzip the file.

3.2 First time installation

Log in to your computer with administrator log in.

- Run the setup routine and choose a directory where VIALAB should be installed (e.g. C:\Programs\Integra Biosciences AG\VIALAB). If you are not logged in as administrator, you may be prompted for the administrator login.
- VIALAB can also be installed on a network drive. Choose your network drive during installation.

3.3 Running VIALAB without installation

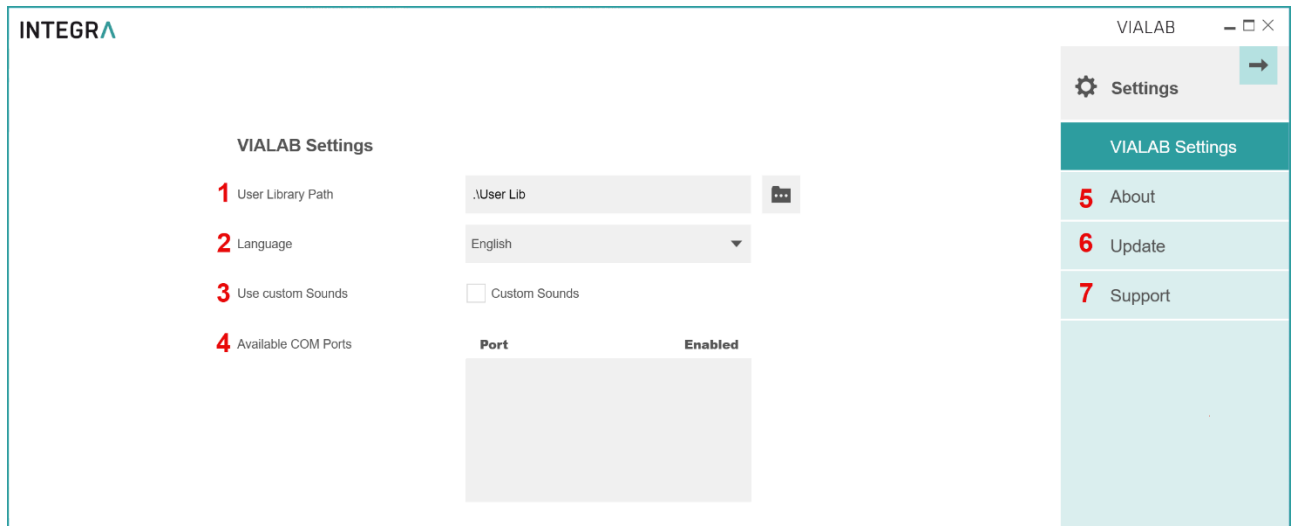
VIALAB can be run from a USB drive or any other program folder. Simply copy the installed directory (e.g. C:\Programs\Integra Biosciences AG\VIALAB) to your specific drive.

4 Settings

4.1 VIALAB settings and information



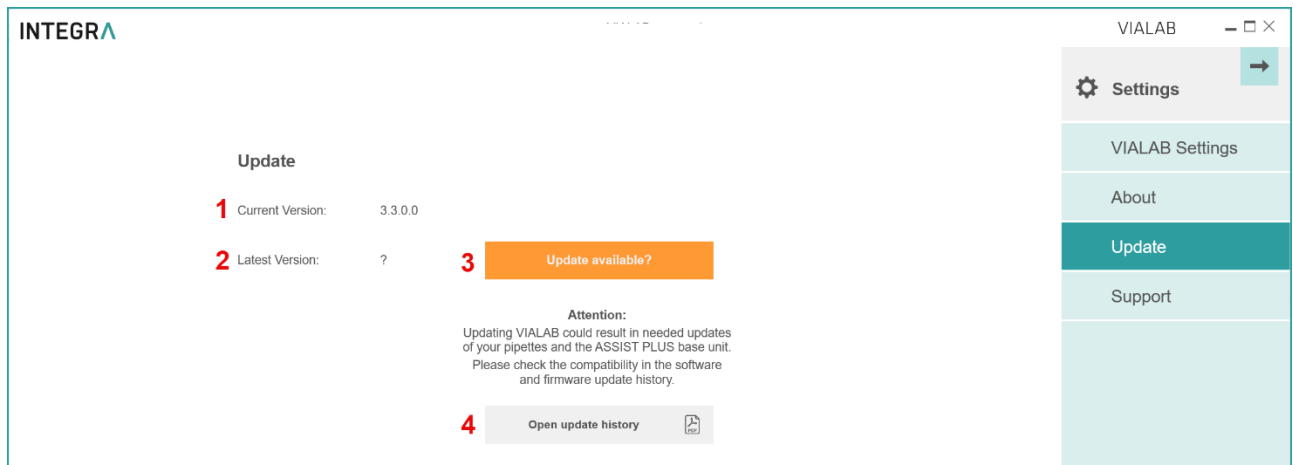
Click on the Settings button in the top right corner. Use the VIALAB Settings to define your preferences and get additional information.



- 1 User Library Path:** define the storage path of your labware library.
- 2 Language:** choose your preferred language.
- 3 Use Custom Sounds:** upload .wav sound files for Error or Information messages. Sounds played from computer in PC Control mode
- 4 Available COM Ports:** shows all available communication ports.
- 5 About:** information about the VIALAB software version and the INTEGRA contact data
- 6 Update:** check for new updates, see 4.2.
- 7 Support:** download the latest VIALAB operating instructions and generate a support report.

4.2 Update VIALAB

If an update for VIALAB is available and you are connected to the internet you can check for new updates.



- 1 Current Version:** displays the currently installed VIALAB version.
- 2 Latest Version:** displays the latest VIALAB version.
- 3 Update available?:** check for new updates. Note: Internet connection needed.
- 4 Available COM Ports:** shows all available communication ports.
- 5 Open update history:** history of VIALAB and VIALINK software versions, as well as, VIAFLO/VOYAGER pipettes, D-ONE / MAG / HEATMAG module and ASSIST / ASSIST PLUS pipetting robots' firmware versions.

4.3 Support

1 Open help

2 **Generate support report**

VIALAB version Pipette firmware version

ASSIST PLUS firmware version Pipette - Serial Number

IAA file name

Exact error time

3 Logfile date range (automatically attached)

Start End

4 Attach additional files (optional)

Add Description

5

6 Send the email with attached Support Report to: customersupport@integra-biosciences.com

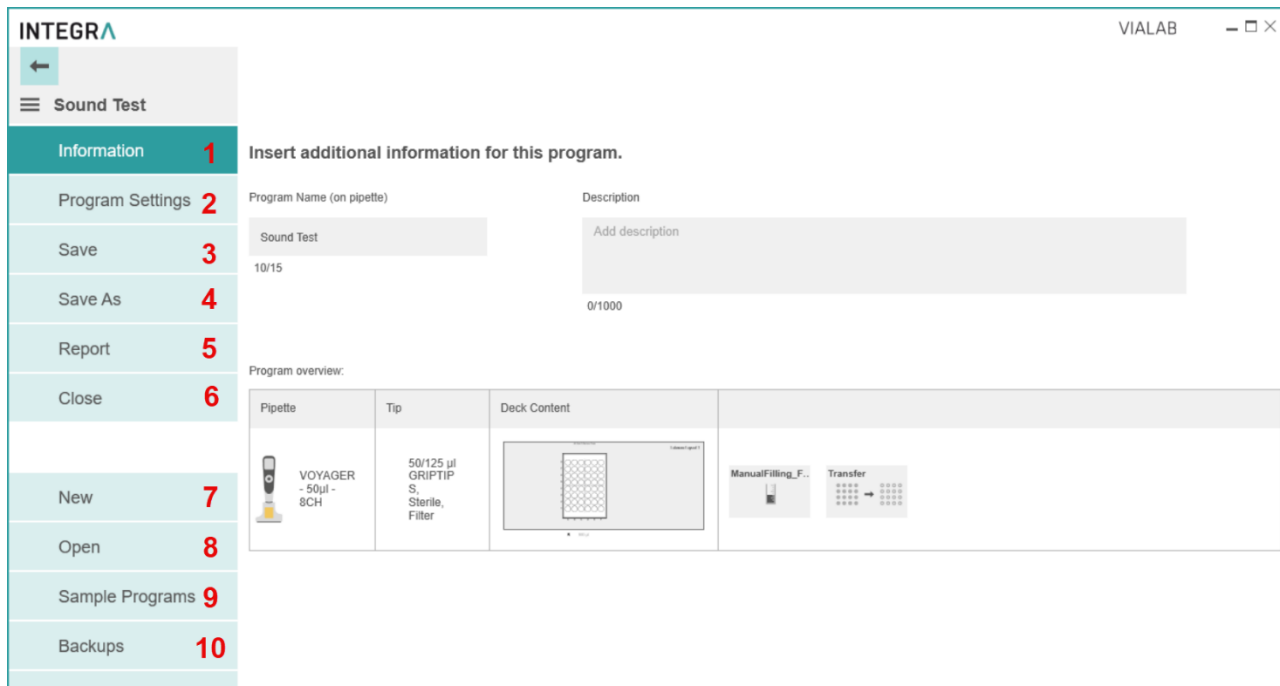
- 1 Open help:** download the latest VIALAB operating instruction.
- 2 Generate support report:** of an encountered misbehavior.
- 3 Logfile date range:** select the time span of observed misbehavior.
Note: Logfiles are automatically collected and attached to the support report.
- 4 Attach additional files:** optionally attach protocols, photos, videos that facilitate the understanding of the support request.
- 5 Generate support report:** create compressed support report. Only available when all mandatory fields are filled out.
- 6 Send Email:** with attached support report to customersupport@integra-biosciences.com.

5 Main menu

5.1 Information and saving options



Within a program, click on the Menu button in the top left corner to open the main menu. Here information about the program is displayed and saving options are listed.



1 Information: change the Program name and add a description, if desired.

2 Program Settings: define the clearance height and offsets of each deck position for your program.

3 Save: save your program.

4 Save As: save you program under a new name.

5 Report: generate a printable PDF-report of your program, e. g. for standard operating procedures.

6 Close: close your program.

7 New: create a new program.

8 Open: open an existing program, recently used programs are listed.

9 Sample Programs: select and open a sample program.

10 Backups: Program backups of the last ten minutes working with VIALAB



Note: You should save your current VIALAB program on your computer to have a backup or if you need to transfer the program to more than one pipette.

5.1.1 Program Settings



The following settings apply to each VIALAB program individually.

- 1 **Clearance Height:** distance over the highest point of the labware at which the pipette moves over the labware.
- 2 **Safety Bottom Offset:** defines the minimum distance of tips to the bottom of the labware.
- 3 **Collision Offset:** defines a relative distance to increase or decrease the predefined collision safety distance.
- 4 **Deck Position Offsets:** deck positions A, B or C can be shifted in X, Y and Z axis for max. 2 mm.
- 5 **Tip Ejection Type:** choose whether to display or hide an additional option for the tip ejection. If activated in the tab "Tip Change" the tips can be ejected either at the ejector ledge (**Ledge**) or directly in the waste bin without touching the ejector ledge (**Waste**).
- 6 **Waste as target:** choose whether to display or hide the option to dispense directly into the waste bin. If activated the waste bin can be selected as target position in a Multi Aspirate step or in Serial Dilution step as a waste position for the last aspiration.
- 7 **Copy Step – Height Adjustments:** when copying steps, the liquid level changes for the copied step. If tip travel is activated in a step, the heights are automatically adjusted relative to the new liquid level (Automatic). Alternatively, the heights of a copied step aren't changed and identical to the original step (Manual).
- 8 **Re-use Labware Dialog:** it is helpful to enable this function when working with more than one labware layout (see section 6.2). If you (accidentally) delete a labware in one of the following layouts, clicking on its position opens a dialog from which the recently used labware can be re-used.
- 9 **Collision Detection:** Enables or disables all collision detection calculations.

6 Programming

6.1 Overview

The screenshot shows the VIALAB software interface. At the top, the title bar reads 'INTEGRA VIALABprogram1 VIALAB'. A sidebar on the left contains a menu with options: Information, Program Settings, Save, Save As, Report, Close, New (highlighted), Open, Sample Programs, and Exit. The main area displays the prompt 'Select a deck to create a new program:' above a table with the following data:

| Deck Name | Deck | Description |
|---------------------------|---|-------------|
| 3 Position Universal Deck |  | PN 4520 |
| 4 Position Portrait Deck |  | PN 4521 |

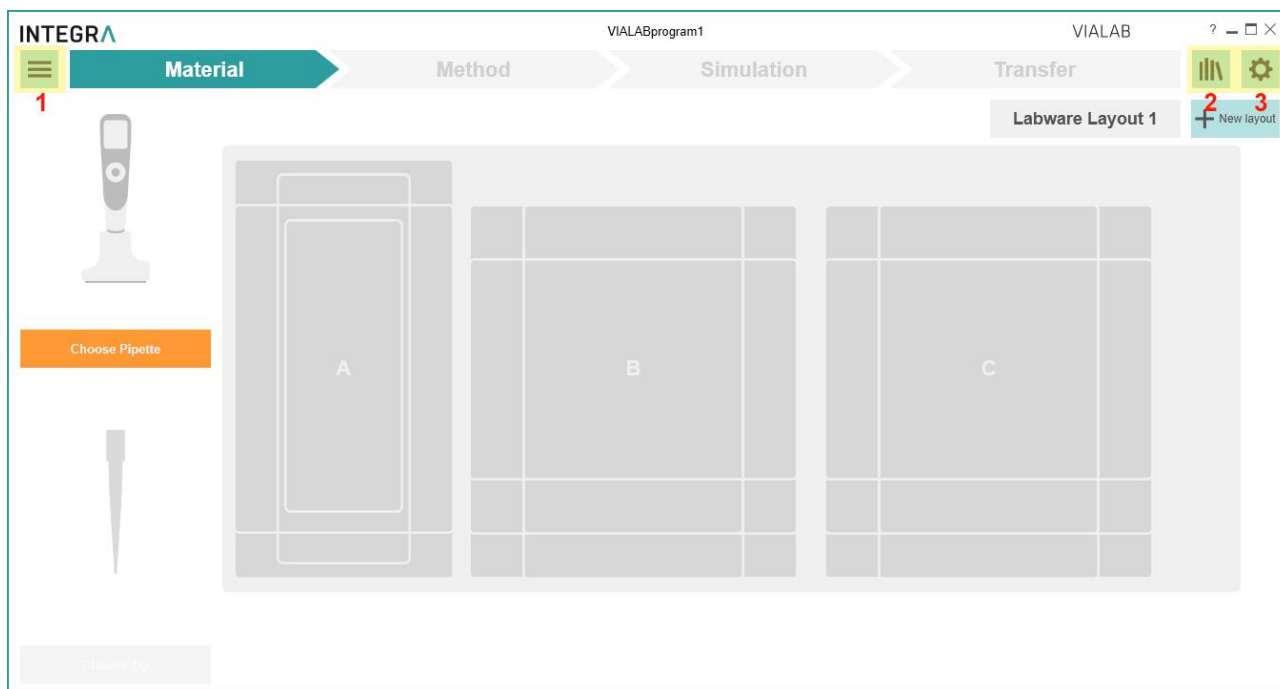
After starting VIALAB, you can create a new pipetting program, open an existing or recently used program or get started with a sample program.

To create a new program, select first the deck you want to use, e.g. the 3 Position Universal Deck with one reservoir position and two spring loaded plate positions.



Note: The D-ONE pipetting module requires its own tip deck (PN 4535) which need to be installed on the ASSIST PLUS.

The program menu will be displayed:



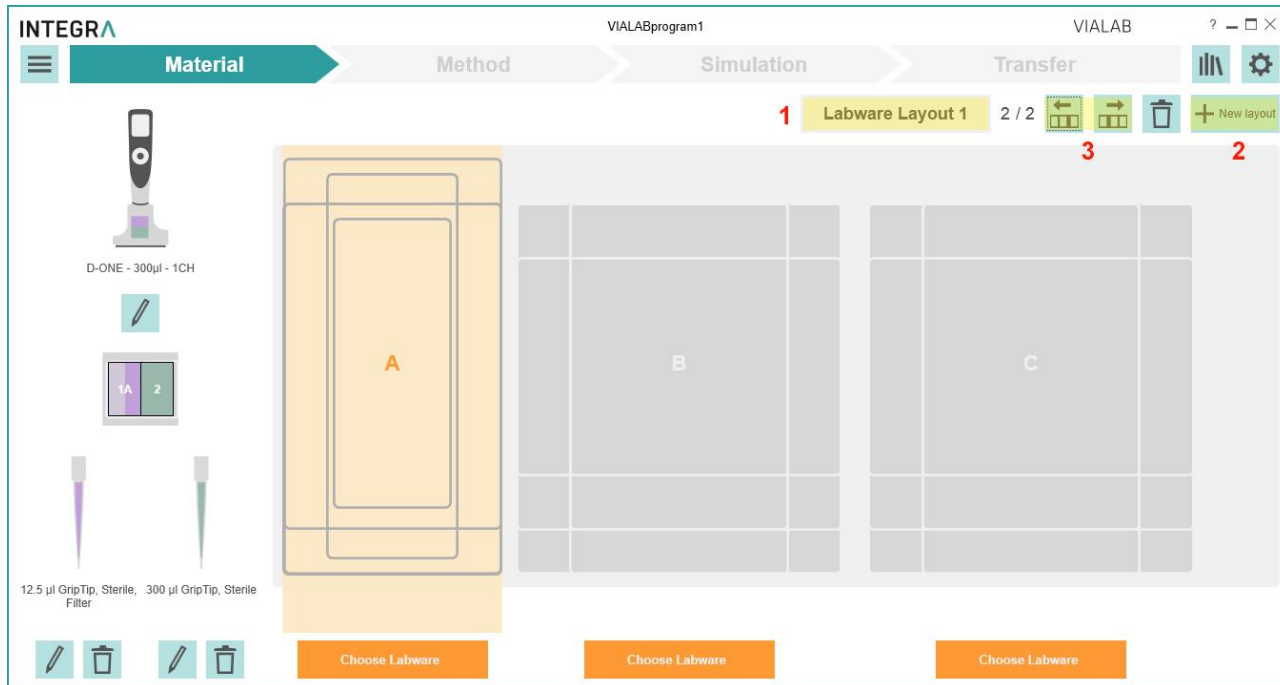
- 1 Main Menu:** information and saving options of the defined program (see chapter 5).
- 2 Library:** labware library listing available decks, pipettes, tips, reservoirs, plates, tube racks, and COMBI systems with COMBI bases which can be used for a program. You can also define new reservoirs, plates, tube racks and COMBI systems. Alternatively, import already defined labware files to the labware library.
- 3 Gear Wheel:** settings and updates of VIALAB.

The table below shows the different sections for creating a program. After one section is completed, the next can be defined.

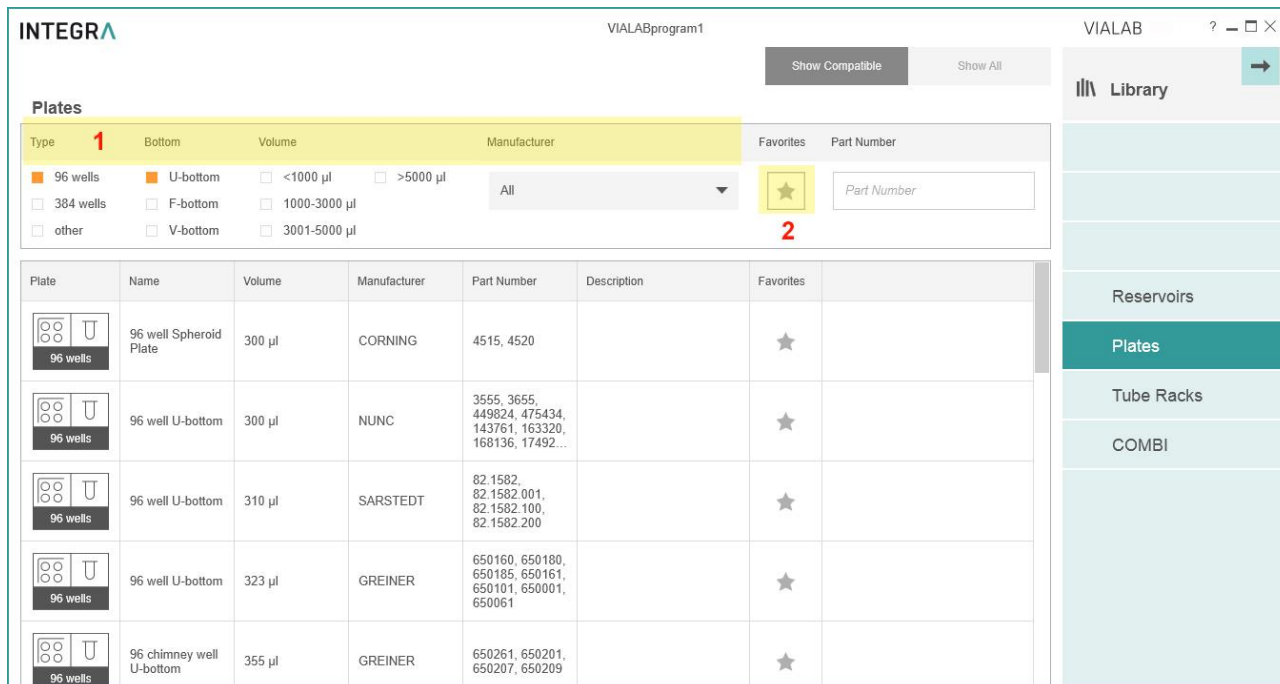
| Section | Description |
|------------|---|
| Material | Choose the pipette with tips and the labware on the deck, e.g. the reservoir used as source container and the kind of well plates with orientation. |
| Method | Create your individual pipetting program |
| Simulation | Review a simulation of all steps in your pipetting program. |
| Transfer | Transfer your VIALAB program to your pipette and run it from your pipette. Alternatively connect the ASSIST PLUS via USB to the PC, connect the Pipette and start a program from VIALAB directly. |

6.2 Material

First click on the orange square to choose any multichannel VIAFLO/VOYAGER pipette or D-ONE module and afterwards select the GripTips. This enables the selection of the other labware used in the program.



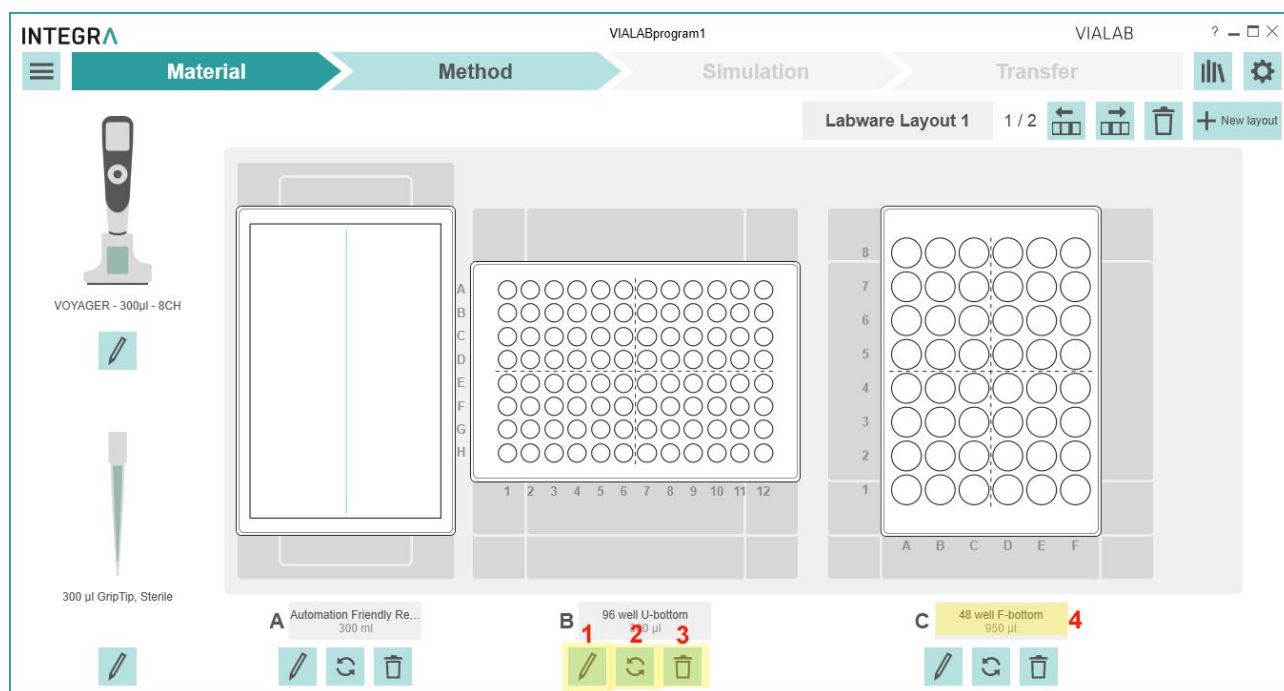
Click on an orange button or directly on the deck position to choose the predefined labware on all required positions. Click on the Labware Layout button (1) to name the deck. To create an additional labware layout, click on New layout (2). Use the arrow keys to switch between all available labware layouts (3).



Select the desired properties or manufacturer (1) to quickly show reservoirs/plates/tube racks/COMBI Systems which are compatible with the selected pipette and deck position. Click on the star (2) to show favorites only (to be defined in the labware library).

Scroll to one reservoir, plate, tube rack or COMBI System and select it by clicking on it.

| Labware | Description |
|--------------|---|
| Reservoirs | Select an INTEGRA reservoir or define a new reservoir, see Library icon. |
| Plates | Select one of predefined, commercially available plates. Search for any plate or enter the part number directly, if known. Alternatively, define the dimensions of a new plate, see Library icon. |
| Tube Racks | Select a tube rack or define a new one, see Library icon. |
| COMBI System | To add a COMBI System, select a COMBI BASE and fill each selected column with modules, e.g. plates, tube racks or reservoirs and click on Apply COMBI System, see also section 7.5. |



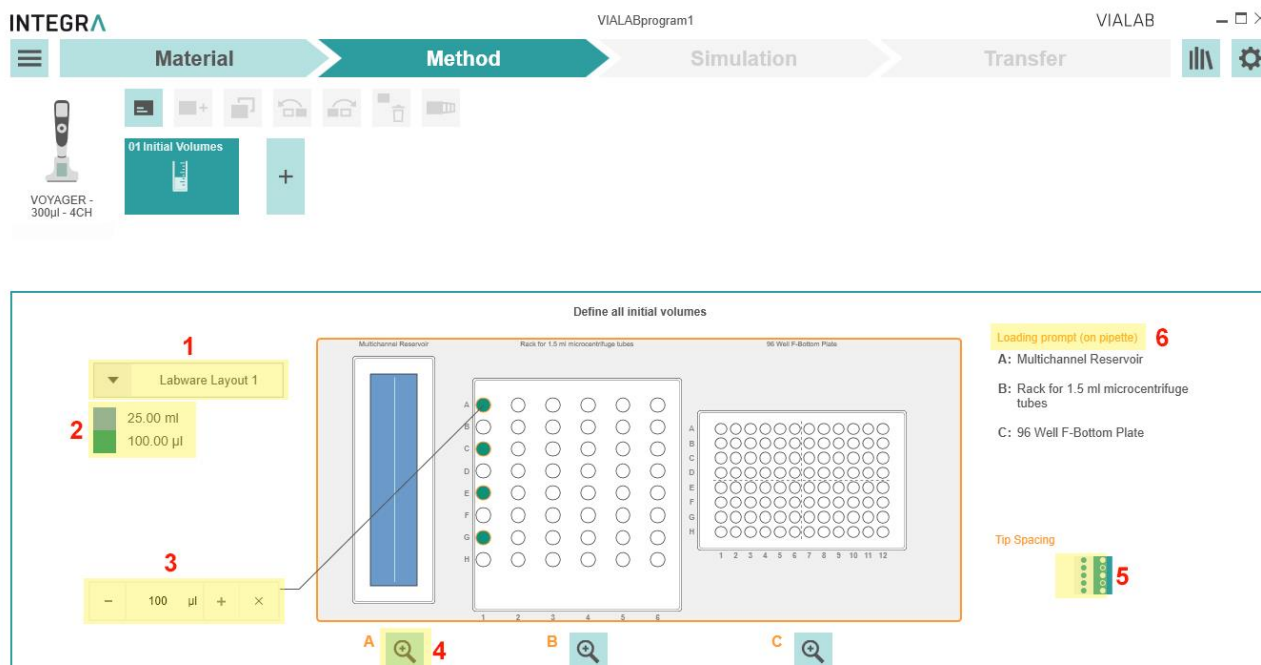
- 1 **Edit:** change the chosen labware.
- 2 **Change orientation:** rotate counterclockwise by 90° (all 4 possible orientations).
- 3 **Delete:** delete the selected labware on this position.
- 4 **Rename:** name the chosen labware.

Note: changing the material of an already defined program, e.g. pipette or plate orientation, will delete all subsequent program steps in the “Method” section, if they are not compatible with the previous settings.

6.3 Method

Your pipetting program is composed of several steps.

When you open the section Method the first time, the first step “Initial Volumes” is already preset, and you are prompted to set the volumes of the labware which are already filled.



- 1 Choose labware layout:** if more than one is available, choose the corresponding layout.
- 2 Color legend:** shows the pre-fill (initial) volume of the labware on position A, B or C. Each color represents one pre-fill volume.
- 3 Pre-fill volume:** click on the vessel which is already filled at the start of your program and enter the pre-fill volume.
- 4 Zoom:** displays a close-up view of one deck position.
- 5 Tip spacing:** choose a different tip spacing to change the filling pattern of your plate e.g. as shown with plate on position C (only for VOYAGER tip spacing pipettes).
- 6 Loading prompt (on pipette):** shows the used labware inclusive deck position of every available labware layout within the current VIALAB program.

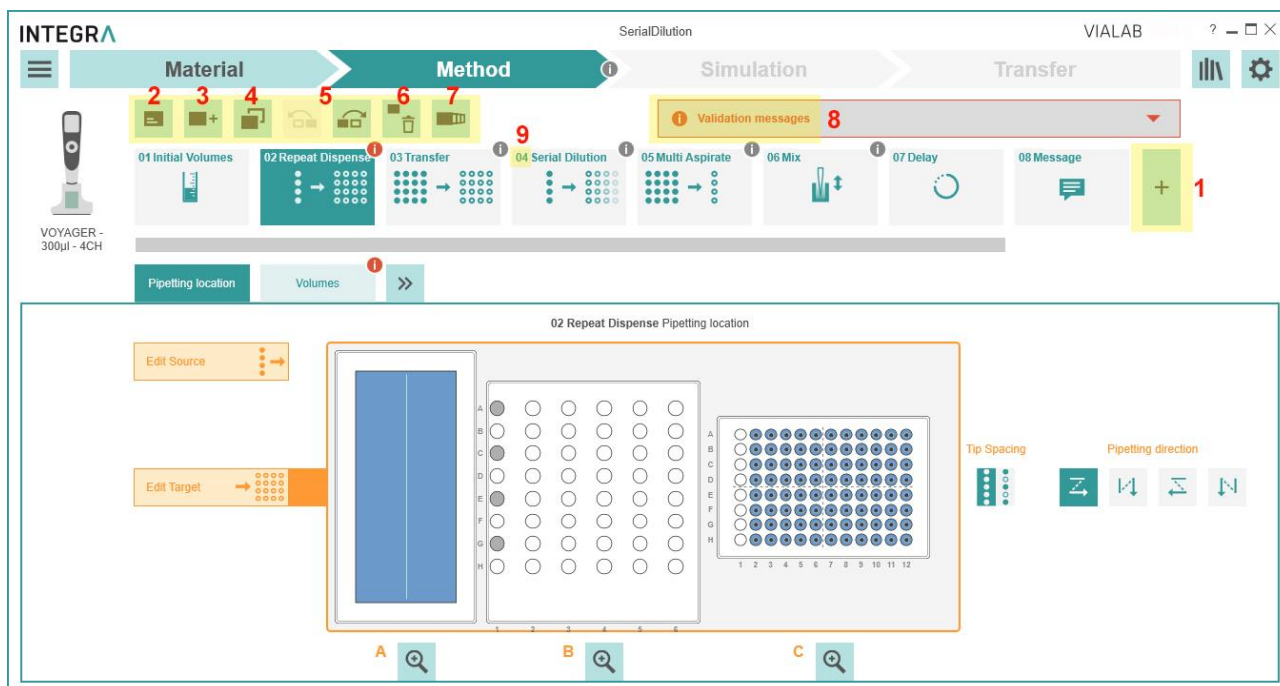
Select the wells which are prefilled at the start of your program via click or drag and drop. In the pop-up window you type in the dedicated volume in the given unit to assign a volume.

To view or edit the assigned volume select wells and the current volume is displayed. If needed, edit the volume, or delete it.



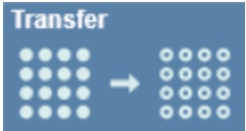

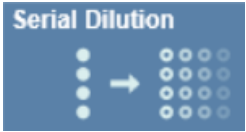



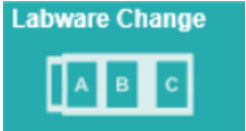
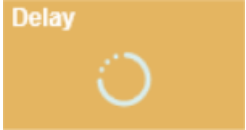



Note: If you're using D-One pipetting modules, this step can be skipped as D-One features liquid level detection.



To add further steps, click on a plus square (1, 3). To move, copy or delete steps click on the corresponding icon (4, 5, 6). The steps are processed sequentially according to the step number (9).



- 1 **Plus square:** add a new step to the end of the method.
- 2 **Add Description:** add a description for the current step. The first 15 characters are displayed at the bottom of the step icon.
- 3 **Add Step:** add a new step after a selected step to the method.
- 4 **Copy Step:** copy selected step to the end.
- 5 **Move left/right:** move the selected step forwards or backwards.
- 6 **Delete Step:** delete selected step.
- 7 **Multi-Selection:** click on this button to select multiple steps in parallel to copy or delete them.
- 8 **Validation messages:** click on this field for programming error details.
- 9 **Step number:** the step number indicates the step sequence in the program.

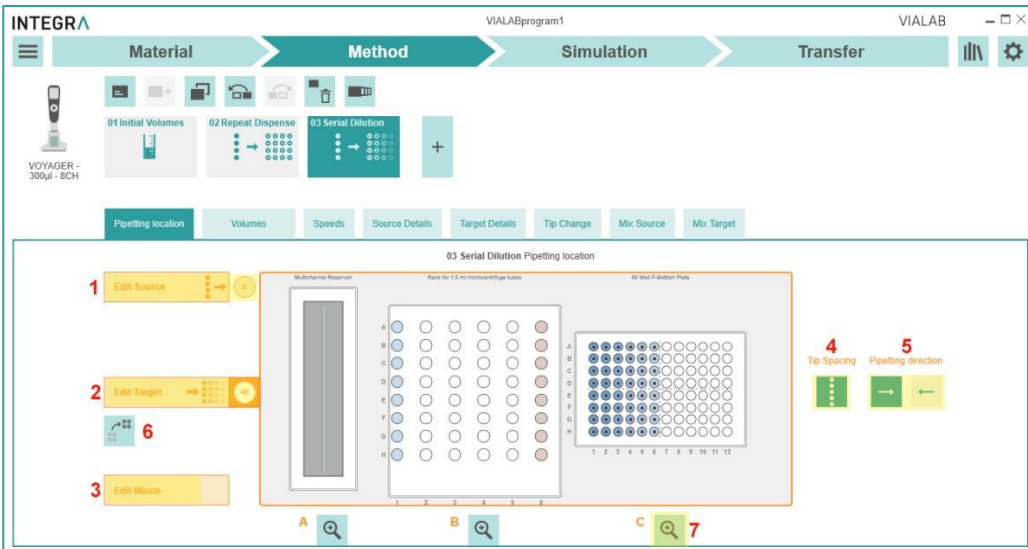
Following steps are available for VIAFLO/VOYAGER pipettes and D-ONE modules:

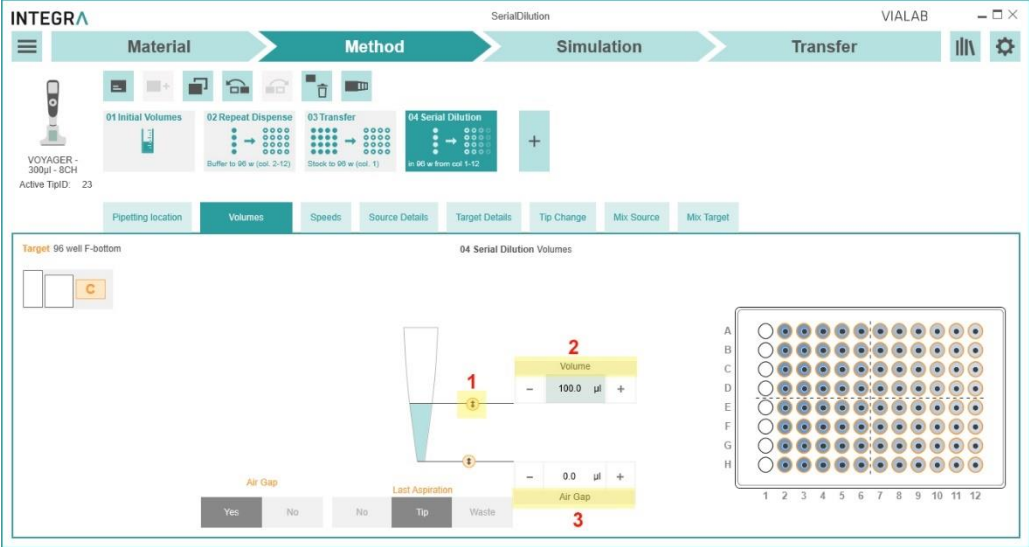
| Symbol | Step | Description |
|---|-----------------|--|
|  | Transfer | Transfers an equal number of samples from a source to target (N:N), e.g. plate copy. |
|  | Repeat Dispense | Dispenses from one source into multiple targets (1:N), e.g. reagent addition |
|  | Serial Dilution | Aspirates sample from a source and performs a serial dilution in the defined number of wells. |
|  | Multi Aspirate | Collects several samples from one source and transfers into one target (N:1). |
|  | Mix | Mixes a sample by pipetting up and down in the selected vessel. |
|  | Volume Change | Enter the filling volume of the vessels e.g. after manual filling steps within a method. The volume defined in this step is an absolute volume. It does not consider previous liquid handling steps. |
|  | Labware Change | Change labware items on the deck within the same program. Switch between the labware layouts defined under Materials. |
|  | Delay | Defines a pause between the last and the next step in seconds. |
|  | AUX Port | Turning devices on and off which are connected to the auxiliary port of the ASSIST PLUS. |
|  | Message | Pauses the program and displays a message. Three lines with 12 characters each are available. |
|  | Temperature | Heats samples for a specified time at a specified temperature (°C). |

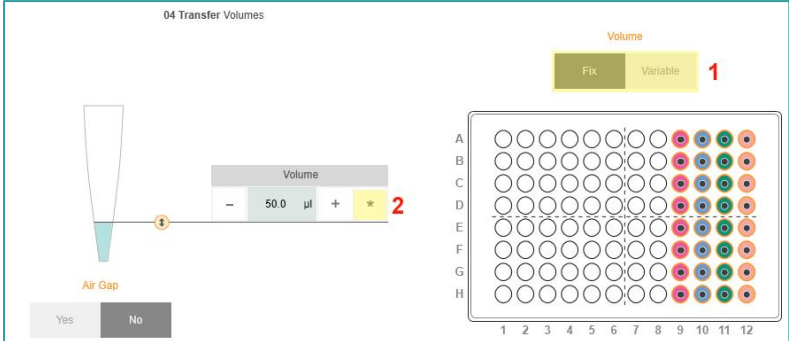
| Symbol | Step | Description |
|---|--------|---|
|  | Magnet | Brings a movable magnet to a specified height to capture or release magnetic beads. |
|  | Shaker | Shakes a sample at a specified speed (rpm) for a specified time. |

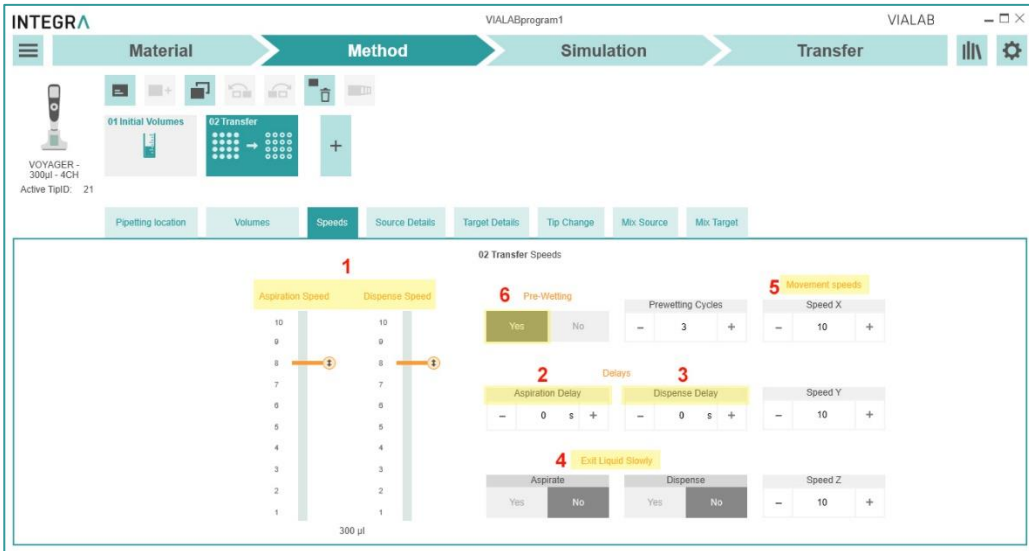
For D-ONE pipetting module additional steps are available, see 6.4.

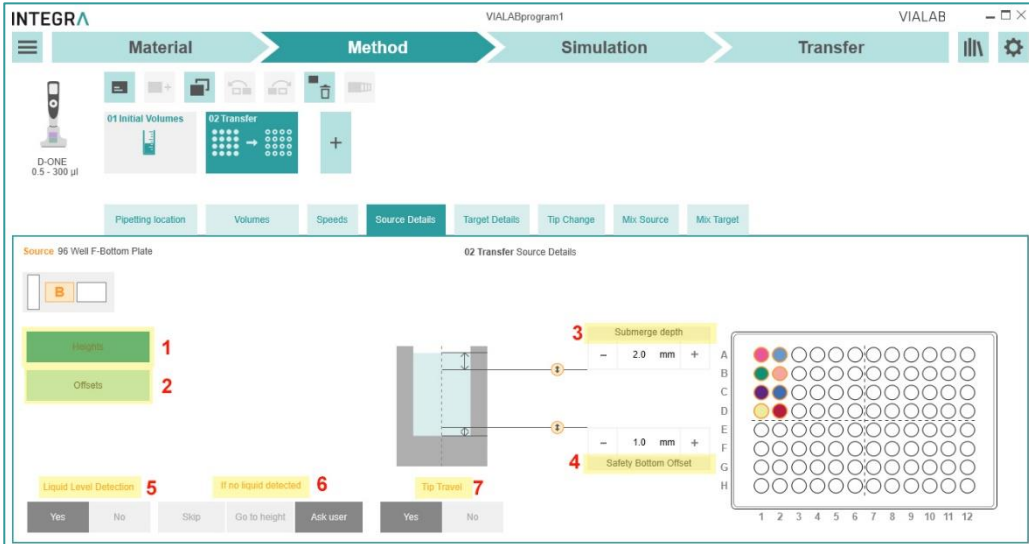
- Within one step, adjust the following parameters:

| Parameter | Description |
|--------------------|---|
| Pipetting location | <ul style="list-style-type: none"> • Edit Source (1): click on the button and then select the wells (for plates on upmost well of column) where the liquid should be aspirated from. It will be colored. The number of source wells is displayed next to it, e.g. 8. • Edit Target (2): click on the button and then select the wells (for plates on upmost well of column) where the liquid should be dispensed in. It will be marked with a black dot in the middle of the well. The number of target wells is displayed next to it, e.g. 48. • Edit Waste (3): only for step “Serial Dilution” and if under Volumes “Last aspiration back to “Waste” was selected. Click on the button to select waste vessel location.  <p>If needed, adapt the tip spacing (4) or the pipetting direction (5). For changing the selected wells deselect the chosen ones or move all selected wells together within one plate (6). For a detailed view of the plates, use the zoom-in function (7).</p> |

| Parameter | Description |
|----------------|--|
| <p>Volumes</p> |  <p>Move the slider up or down (1), type in the volume (2) or use the “+” and “-” buttons to set the desired Volume(s) for the current step. An Air Gap (3) can be set to aspirate a defined air volume after an aspiration of liquid.</p> |

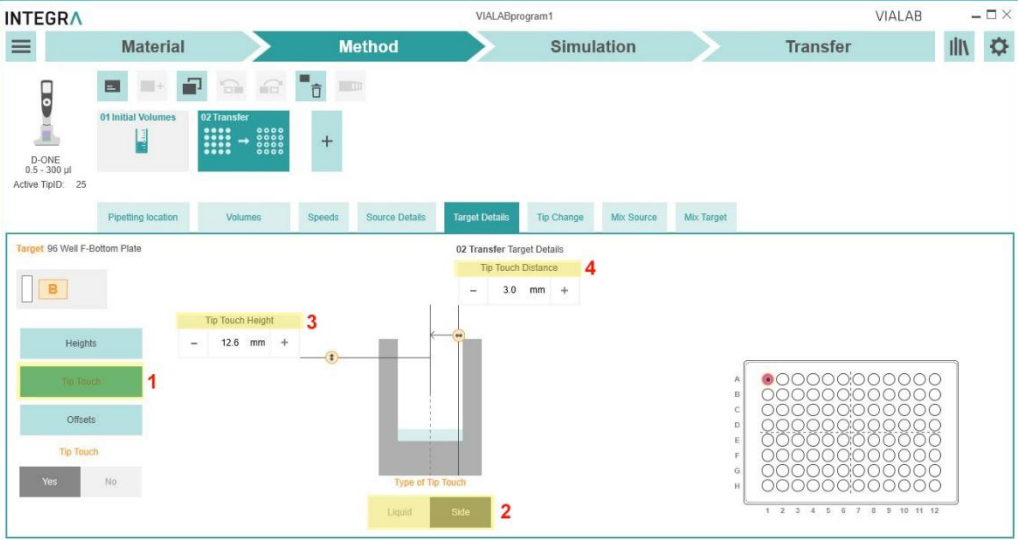
| Volumes | Step Type | Volume description |
|---------|-----------------|---|
| | Transfer | <p>Volume: define whether the volume is variable or fix for all transfers (1). If variable, select each individual column and assign a volume. If the calculated volume exceeds the tip volume, the volume is dispensed multiple times with the same tip, indicated by a multiplier (*,2).</p>  |
| | Repeat Dispense | <p>Post-Dispense Location: select if the post-dispense should be purged in the source vessel of aspiration or should remain in the tips.</p> <p>Reuse Post-Dispense: click on “Yes” if the post-dispense should remain in the tip and be used for the next aspiration.</p> <p>Dispense Type: click on “Single” to aspirate and dispense the selected volume or on “Multi” to aspirate a multiple of the selected volume and perform several dispenses.</p> <p>Volume: define whether the volume(s) to be dispensed (for every dispense step) is fix or variable. If variable, select each individual column and assign a volume. Set the pipetting direction. Additionally, to the dispense volume set also the Pre-Dispense and the Post-Dispense volume.</p> <p>Note: we recommend a pre- and post-dispense volume of 3-5 % of the nominal volume of the pipette.</p> |
| | Serial Dilution | <p>Last Aspiration:</p> <ul style="list-style-type: none"> - “No”: the last aspiration is not performed; the liquid remains in the last row. - “Tip”: the last aspiration remains in the tips that are ejected into the Waste bin. - “Waste”: the last aspiration is purged in a dedicated liquid waste vessel. The location must be defined in “Pipetting location”. <p>Volume: the sample volume that will be transferred from well to well.</p> |
| | Multi Aspirate | <p>Aspirate Type: click on “Single” to aspirate only one volume or on “Multi” to perform several aspirations consecutively.</p> <p>Volume: define whether the volume to be aspirated (for every aspirate step) is fix or variable. If variable, select each individual column and assign a volume.</p> <p>Set the aspiration volume.</p> |


| Parameter | Description |
|-----------|---|
| Speeds | <ul style="list-style-type: none"> • Aspiration and Dispense Speed (1): set the aspiration and dispense speeds for this step. Set the slider to the appropriate speed from 1 (slow) to 10 (fast). • If necessary, adapt parameters for viscous and volatile liquids: <ul style="list-style-type: none"> Aspiration Delay (2): a delay in seconds after aspiration before moving out of the liquid. Dispense Delay (3): a delay in seconds after dispensing before moving out of the liquid. Exit Liquid Slowly (4): the tips move slowly out of the liquid (for aspiration and for dispense).  |
| | <ul style="list-style-type: none"> • Movement Speeds (5): changes the speeds of the Tower in X-direction, of the Pipette arm in Z-direction or the Pipette holder in Y-direction [1 (slow) to 10 (fast)]. • Pre-Wetting (6): if pre-wetting of the tips is desired activate it and set the number of cycles. All fresh tips are pre-wetted with the maximal tip volume and specified speeds. |

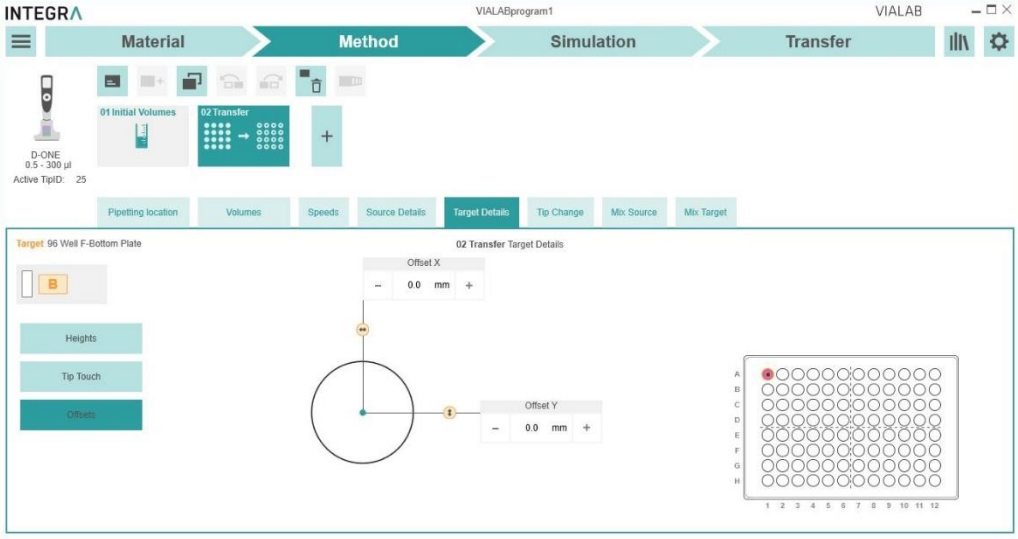
| Parameter | Description |
|----------------|--|
| Source Details | The calculated liquid level in the well is displayed to ease height definition graphically. |
| Target Details | <p>Click on Heights (1) and move the line up or down to enter the heights for aspiration/dispense referring to the deck (deck height is 0 mm). The Safety Bottom Offset (4) defines the minimum distance of the tips to the bottom of the labware and is calculated automatically according to the labware dimensions and pipetting volume.</p> <p>If the Heights are variable, define the pipetting heights for every column.</p> <p>Tip Travel (7) is the movement of tip during one aspiration/dispense to compensate the decrease/increase of the liquid level. It is recommended for high pipetting volumes in vessels with small diameter. If activated, aspiration/dispense starts at the Start Height / Submerge Depth (3) and ends at the End Height / Safety Bottom Offset (4), which is calculated automatically according to the labware dimensions and pipetting volume. If Tip Travel is deactivated the aspiration/dispense is performed at a constant Height (1).</p> |
| |  |
| | <p>D-ONE only:</p> <p>Liquid Level Detection (5) is on per default and the Submerge depth (3) is displayed on top of the well. The liquid level is detected by the D-ONE automatically. If "No" is selected, the pipetting start height must be set manually.</p> <p>Define the error handling, If no liquid detected (6). "Skip" automatically continues with the next source well. "Go to height" continues by aspirating from a pre-defined pipetting height. "Ask user" stops and asks the user to select one of these options: Skip, Repeat and Go to height.</p> <p>Note: it is possible to fine-tune the Pipetting Height / Start Height directly on the pipette to optimize the heights according to the used liquid (see ASSIST PLUS Operating Instructions chapter 5.4 "Adjust heights and positions").</p> |

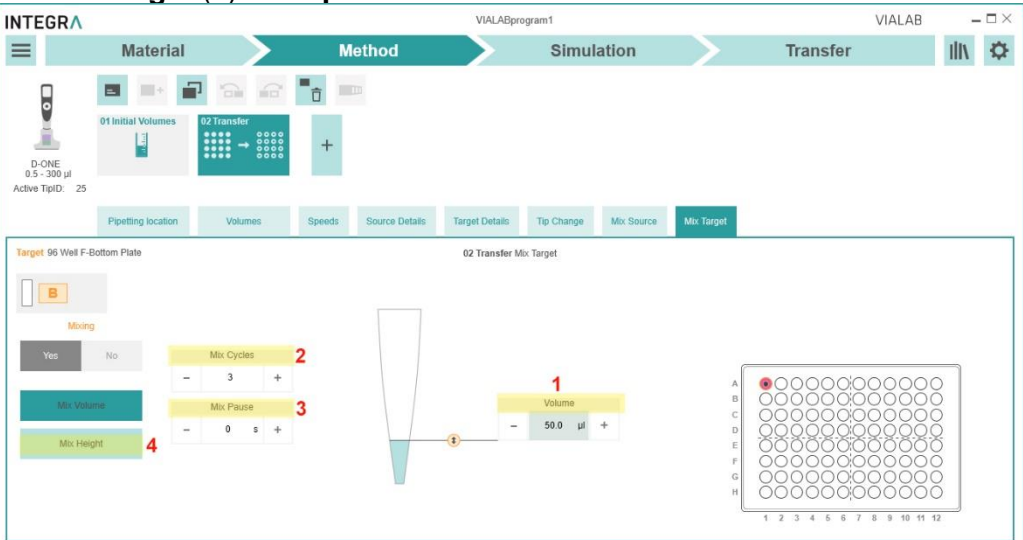
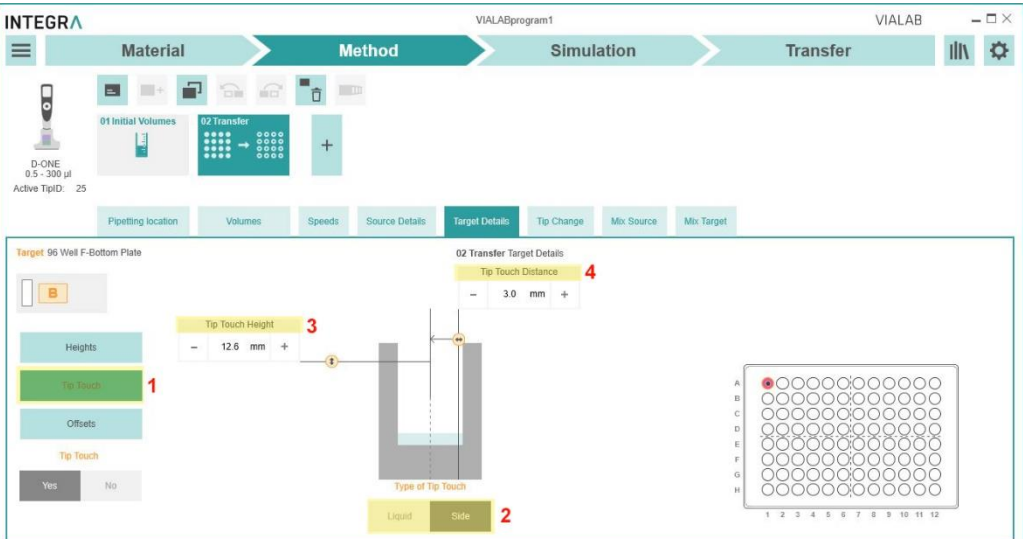


Note: LLD feature exclusive for the D-ONE modules and not for VIAFLO/OYAGER pipettes.

| Parameter | Description |
|-----------|---|
| Tip Touch | <p>Set a tip touch (1) after dispensing to remove drops that may cling on the pipette tips. Set whether the tip touch should be performed into the Liquid or on the Side (2) of the wells. Enter the Tip Touch Height (3) and the Distance (4) to the vessel wall.</p>  |



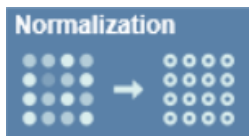


 **Note:** If red exclamation marks appear, the program contains errors. Click on “Validation messages” for further details.

| Parameter | Description |
|-----------|--|
| Offset |  <p>Define a well Offset, if you want to pipette off the well center or even out of wells, this is helpful for processing e. g. for transwell plates.</p> |

| Parameter | Description |
|-------------------|---|
| <p>Tip Change</p> | <p>Set when tips should be changed. The Tip change options can vary from step to step in VIALAB. Here some examples:</p> <p>Continue next step without change: same tips will be used for next step. After step complete: change tips after completing the current step After each transfer/dispense/dilution: change tips after each dispense Before each new aspiration: change tips before each new aspiration</p> <p>If the “Tip Ejection Type” is activated in the Program Settings (see chapter 0), the tips can be either positioned on the ejector ledge before ejection (Ledge) or are directly ejected into the middle of the waste bin (Waste). Tips may stack up and the waste bin needs to be emptied more often.</p> |
| <p>Mix</p> | <p>Define, if the sample should be mixed in the source well before aspiration and in the target well after dispensing. Define the mix Volume (1), the number of Cycles (2), if a Pause (3) should be performed in between mixing cycles. Define the Mix Height (4) and Speed.</p>  |
| <p>Tip Touch</p> | <p>Set a tip touch (1) after dispensing to remove drops that may cling on the pipette tips. Set whether the tip touch should be performed into the Liquid or on the Side (2) of the wells. Enter the Tip Touch Height (3) and the Distance (4) to the vessel wall.</p>  |

6.4 Method steps only for D-ONE pipetting module

These additional steps are only available for D-ONE pipetting module (PN 4531, 4532):

| Symbol | Step | Description |
|---|------------------------|--|
|  | Master Mix | Add multiple master mix reagent components from individual tubes to one target tube or well. A Master Mix reaction calculator generates reagent volumes required. |
|  | Hit Picking | Individual wells from multiple source plates are transferred to one target plate (condense the hits). Create and import a worklist containing the source plate and sample location. |
|  | Normalization | Sample of different concentrations are diluted to a final concentration. Pipetting location, sample identifier and concentration data are entered manually by the user. |
|  | Normalization Worklist | Sample of different concentrations are diluted to a final concentration. Pipetting location, sample identifier and concentration data is imported from a worklist file. |
|  | Worklist | Pipetting steps are created based on an imported worklist. Allows higher pipetting flexibility useful for e.g., NGS Library Pooling and any sample transfers imported in a table format. |

6.4.1 Importing worklists

D-ONE module allows importing worklists that either follow a specific worklist format or have been created using the worklist templates provided by INTEGRA. The pipetting steps Hit Picking, Normalization Worklist and Worklist allow import of worklists with max. 384 lines.

6.4.1.1 Worklist format

Hit Picking worklist:

| | |
|-------------------|--|
| File format: | .csv |
| Column separator: | Semicolon or comma |
| Number of columns | 6 |
| Column header | SampleID, SourcePlateID, SourceWell, TargetPlateID, TargetWell, TransferVolume |

Find below an example of a Hit Picking worklist:

```
SampleID;SourcePlateID;SourceWell;TargetPlateID;TargetWell;TransferVolume
Sample 01;Source 1;C5;TARGET;A1;25
Sample 02;Source 1;H11;TARGET;B1;25
Sample 03;Source 1;D3;TARGET;C1;25
Sample 04;Source 1;C8;TARGET;D1;25
Sample 05;Source 1;A7;TARGET;E1;25
```

Normalization worklist:

| | |
|-------------------|--|
| File format: | .csv |
| Column separator: | Semicolon or comma |
| Number of columns | 6 |
| Column header | SampleID, SourcePlateID, SourceWell, TargetPlateID, TargetWell, InitialConcentration |

Find below an example of a Normalization worklist:

```
SampleID;SourcePlateID;SourceWell;TargetPlateID;TargetWell;InitialConcentration;
01 DNA sample;Sample Plate;A1;Destination Plate;A1;39;
02 DNA sample;Sample Plate;B1;Destination Plate;B1;38;
03 DNA sample;Sample Plate;C1;Destination Plate;C1;37;
04 DNA sample;Sample Plate;D1;Destination Plate;D1;77;
05 DNA sample;Sample Plate;E1;Destination Plate;E1;89;
```

Worklist:

| | |
|-------------------|---|
| File format: | .csv |
| Column separator: | Semicolon or comma |
| Number of columns | 6 |
| Column header | SampleID, SourceDeckPosition, SourceWell, TargetDeckPosition, TargetWell, TransferVolume [µl] |

Find below an example of a Worklist:

```
SampleID;SourceDeckPosition;SourceWell;TargetDeckPosition;TargetWell;TransferVolume [µl]
Sample 1;B;A1;C;A1;50
Sample 2;B;B1;C;B1;100
Sample 3;B;C1;C;C1;125
Sample 4;B;D1;C;D1;25
Sample 5;B;E1;C;E1;100
Sample 6;B;F1;C;F1;50
Sample 7;B;G1;C;G1;75
```

6.4.1.2 Create a worklist with INTEGRA's template

- If the worklist is already defined, click on **Import (1)** to import the worklist into VIALAB.
- To create a new worklist, click on **Templates (2)** and you are automatically directed to the VIALAB folder "MyWorklists" containing templates and sample work lists for Hitpicking and Normalization.

The screenshot shows the INTEGRA VIALAB software interface. The top navigation bar includes 'Material', 'Method', 'Simulation', and 'Transfer'. Below this, there are icons for '01 Initial Volumes', 'Normalization', '02.01 Repeat Diluent', and '02.02 Transfer samples'. A 'Validation messages' dropdown is visible. The main workspace displays a table titled '02 Normalization Worklist & Volumes' with columns for Index, Use, Sample ID, Source, Target, Initial conc., Vol. Sample, Vol. Diluent, Vol. target, Target conc., Validation, and Comment. A red '1' is placed above the table, and a red '2' is placed below it with the text 'You can create your worklist by the supplied Templates'.



Note: Always use the templates provided by INTEGRA to generate a worklist.

- Open the corresponding template, e.g. the normalization template:

The screenshot shows an Excel spreadsheet template for normalization. The columns are labeled 1 through 6: SampleID, SourcePlateID, SourceWell, TargetPlateID, TargetWell, and InitialConcentration. An 'INTEGRA' logo is centered in the background. A box labeled '7 Instructions' contains the following steps: Step 1: Enter your data; Step 2: Press the button below to generate a Normalization Worklist; Step 3: Save the Worklist file on your PC; Step 4: Import the file into VIALAB. Below the instructions is a button labeled 'Generate a Normalization Worklist for import into VIALAB'. A red '8' is placed above the 'Copying_Aid_Wells' tab at the bottom.

- 1 SampleID:** name of sample, e.g. barcode.
- 2 SourcePlateID:** name of source plate, e.g. barcode or source plate 1, source plate 2, etc.
- 3 SourceWell:** position of source well, e.g. A1, B3, etc.
- 4 TargetPlateID:** name of target plate, e.g. target plate.
- 5 TargetWell:** position of target well.
- 6 TransferVolume [µl]:** transfer volume.
- 7 Instructions:** follow the instructions to generate the Normalization template.
- 8 Copying_Aid_Wells:** list of well numbers which can be used to copy source and target wells into the template.

- Copy data from e.g. another excel file column by column into the template file, or use Copying_Aid_Wells (8):

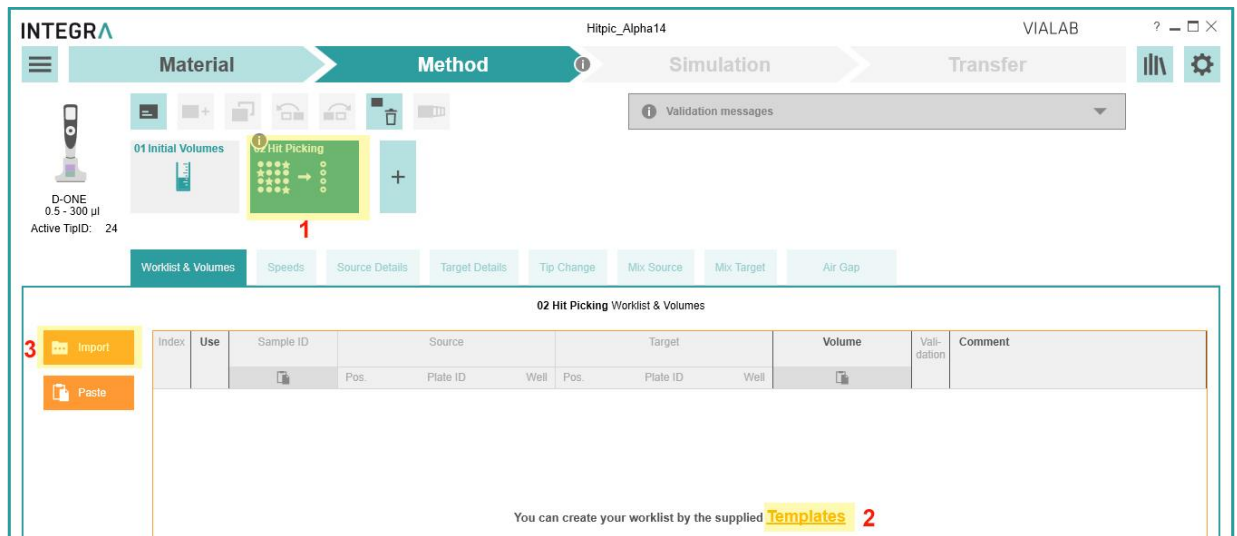
The screenshot shows an Excel spreadsheet with a grid of well indices. The columns are labeled with letters A through T, and the rows are numbered 1 through 32. A 'Copying_Aid_Wells' tab is active at the bottom. The grid contains a list of well numbers for copying, such as A1, A2, B1, B2, etc., up to T32. The 'Index' column on the right lists the corresponding well numbers.

INTEGRA

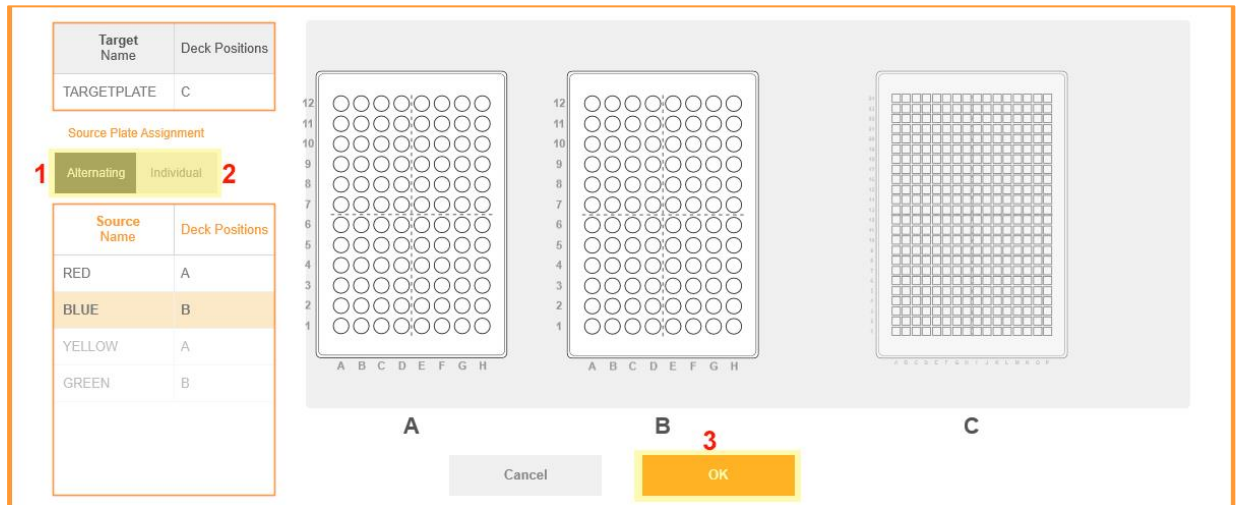
- After the template is filled out press on the orange button "Generate a Normalization Worklist", and a worklist.csv file is automatically generated. Name the file and save on e.g. your local drive.
- Go back to VIALAB and import the previous defined worklist.csv file.

6.4.2 Hit Picking

- Start your method by adding a **Hit Picking (1)** step.



- Click on **Templates (2)** to open an EXCEL file and define a worklist with source and target wells, see 6.4.1. After pressing the orange button in the template, a worklist in a csv file format necessary for import into VIALAB is generated. Click on **Import (3)** to load the worklist.
- You are requested to assign the deck position where the target plate is placed.




If the source plates should be processed in a fix pattern, select **Alternating (1)** and just assign plates and corresponding deck positions of the first layout. Click on **Individual (2)** if the source plates should be assigned individually to each deck position. Press **OK (3)**.

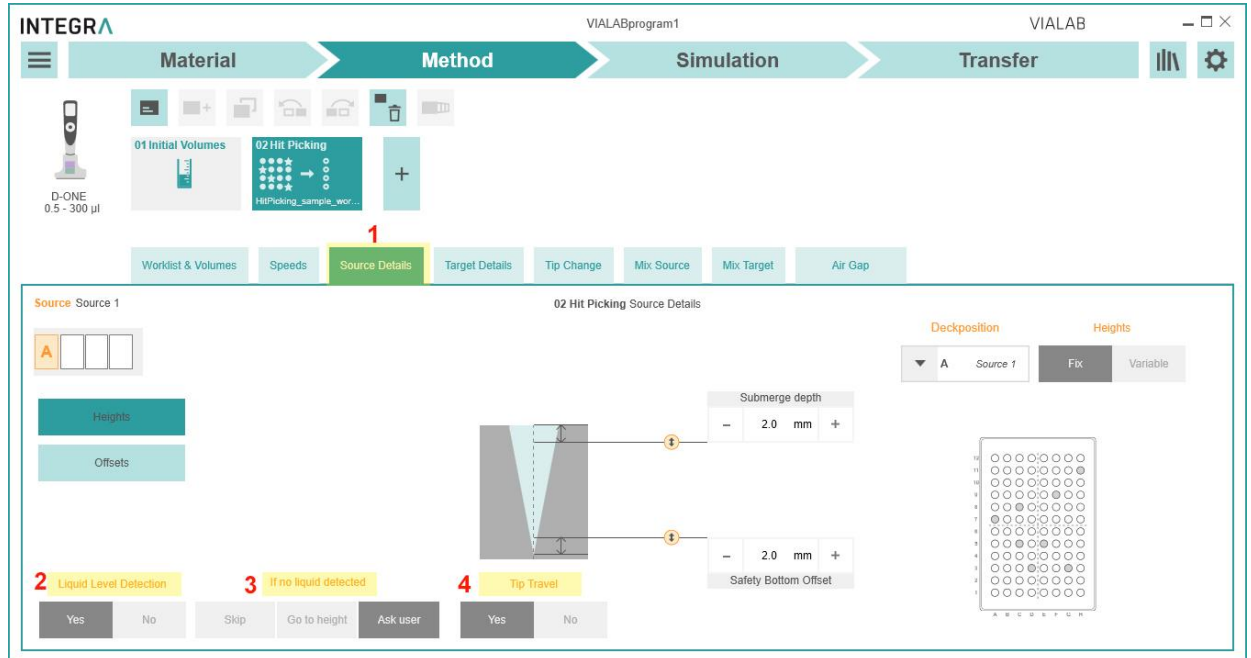
- The worklist is displayed:



By removing the checkmark under **Use (1)**, you can exclude samples from processing. You can also change the sample ID **(2)**, the volume **(3)** and the tip type **(4)** and. The number of hits and source plates are shown at the side **(5)**.

- Adjust the other parameters like Speeds, Source and Target Details, Tip Change.
- Under **Source Details** (1) **Liquid Level Detection** (2), **Tip Travel** (4) are default switched on. Consequently, the aspiration height and the initial volume must not be defined.

 **Note:** LLD is only possible with new and dry tips.

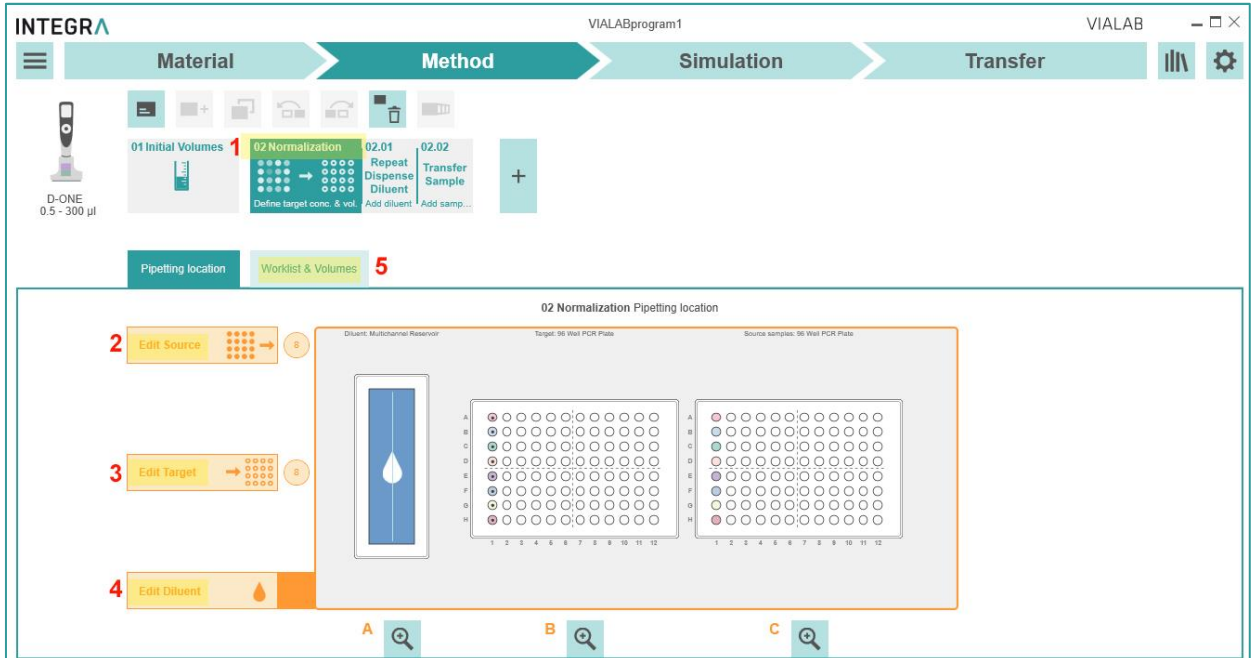


Define the error handling, **If no liquid detected** (3), as described under Method, see 6.3.

6.4.3 Normalization

With this step the samples which need to be normalized must be chosen in the graphics.

- Add a **Normalization (1)** step to your method. Define the source (2), target (3) wells and then the diluent (4).



- Under **Worklist & Volumes (5)** the worklist is displayed:

| Index | Use | Sample ID | Source | | Target | | Initial conc. ng/µl | Vol. Sample [µl] | Vol. Diluent [µl] | Vol. target [µl] | Target conc. | Validation | Comment |
|-------|-------------------------------------|---------------|--------|------|--------|------|---------------------|------------------|-------------------|------------------|--------------|------------|---------|
| | | | Pos. | Well | Pos. | Well | | | | | | | |
| 1 | <input checked="" type="checkbox"/> | 01 DNA sample | C | A1 | B | A1 | 39 | 20.5 | 59.5 | 80 | 10 | ✓ | |
| 2 | <input checked="" type="checkbox"/> | 02 DNA sample | C | B1 | B | B1 | 38 | 21 | 59 | 80 | 10 | ✓ | |
| 3 | <input checked="" type="checkbox"/> | 03 DNA sample | C | C1 | B | C1 | 37 | 21.5 | 58.5 | 80 | 10 | ✓ | |
| 4 | <input checked="" type="checkbox"/> | 04 DNA sample | C | D1 | B | D1 | 77 | 10.39 | 69.5 | 79.89 | 10 | ✓ | |
| 5 | <input checked="" type="checkbox"/> | 05 DNA sample | C | E1 | B | E1 | 89 | 8.99 | 71 | 79.99 | 10 | ✓ | |
| 6 | <input checked="" type="checkbox"/> | 06 DNA sample | C | F1 | B | F1 | 48 | 16.67 | 63.5 | 80.17 | 10 | ✓ | |

- By removing the checkmark under Use (1), you can exclude samples from processing. Copy or type sample details, i.e. the name/barcode (Sample ID, 2) and the initial concentration (3).
- If you switch on the **Dilution calculator (4)**, you can adjust the target volume and concentration. Click on **Calculate all samples (5)** to automatically calculate all parameters (volumes, pipette tips) automatically.

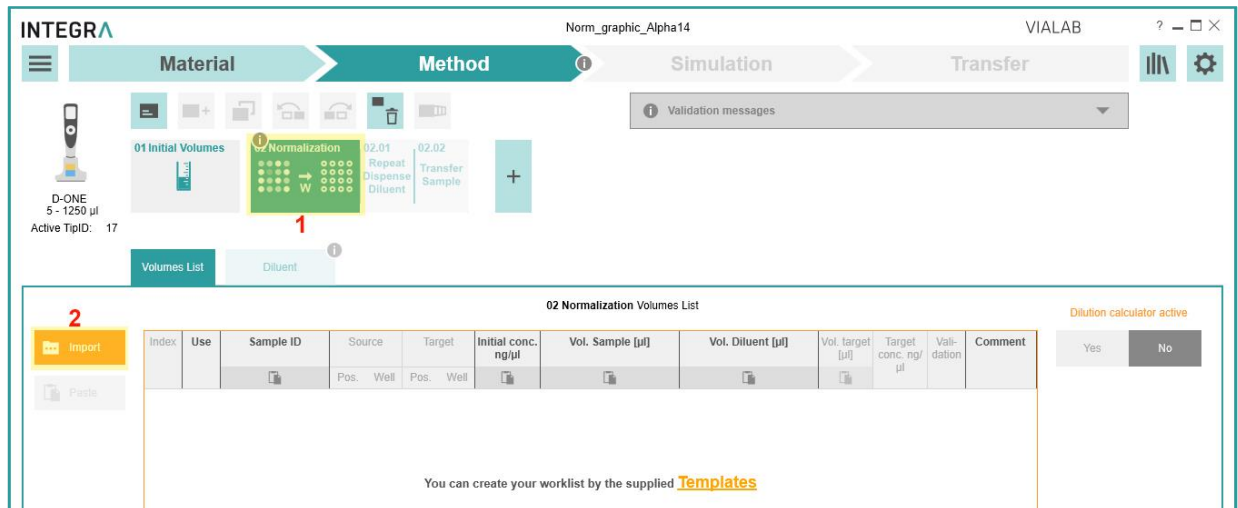
- The step **Repeat Dispense Diluent (1)** first transfers the diluent, followed by **Transfer Sample (2)**. Both steps allow to set pipetting parameters such as Speeds.

The screenshot displays the INTEGRA VIALAB software interface. At the top, the title bar shows 'INTEGRA', 'VIALABprogram1', and 'VIALAB'. Below the title bar, a navigation bar contains four main sections: 'Material', 'Method', 'Simulation', and 'Transfer'. The 'Method' section is active, showing a sequence of steps: '01 Initial Volumes', '02 Normalization', '02.01 Repeat Dispense Diluent', and '02.02 Transfer Sample'. The '02.01 Repeat Dispense Diluent' step is highlighted in yellow and labeled with a red '1', while '02.02 Transfer Sample' is labeled with a red '2'. Below the step sequence, there are tabs for 'Speeds', 'Volumes', 'Source Details', 'Target Details', 'Tip Change', and 'Mix Source'. The 'Speeds' tab is selected, showing the configuration for '02.01 Repeat Dispense Diluent Speeds'. This configuration includes two vertical sliders for 'Aspiration Speed' and 'Dispense Speed', both set to 6. To the right, there are several control panels: 'Pre-Wetting' (Yes/No), 'Delays' (Aspiration Delay: 0 s, Dispense Delay: 0 s), 'Exit Liquid Slowly' (Aspirate: Yes/No, Dispense: Yes/No), and 'Movement speeds' (Speed X: 10, Speed Y: 10, Speed Z: 10). The volume '300 µl' is indicated at the bottom of the sliders.

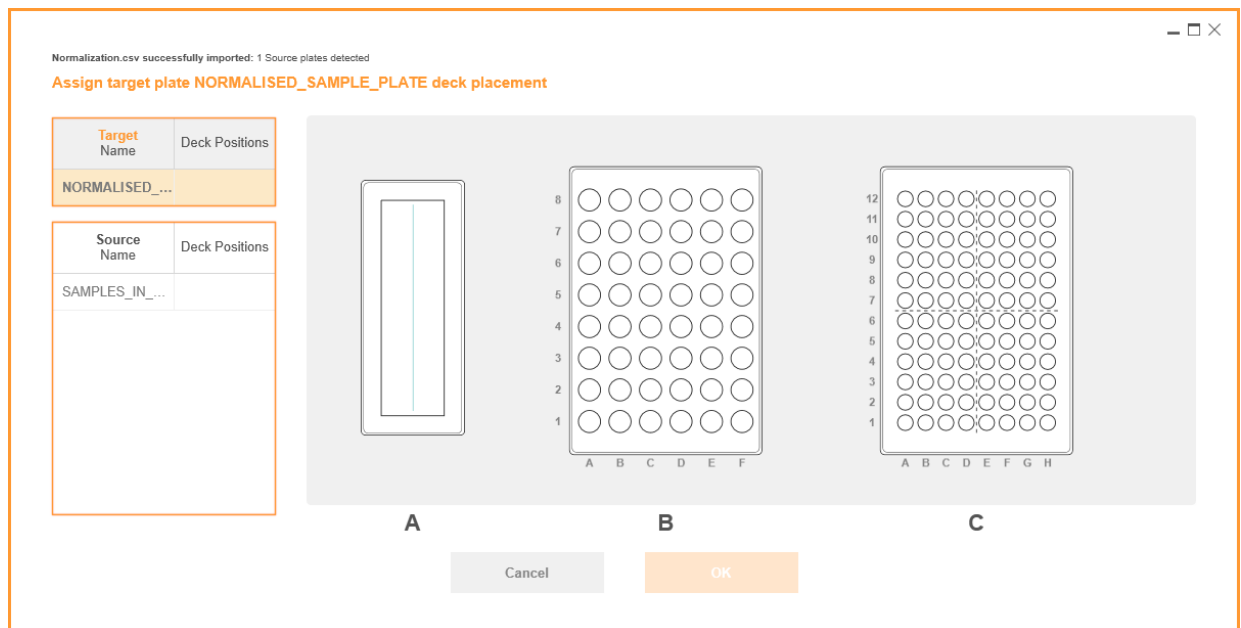
6.4.4 Normalization Worklist

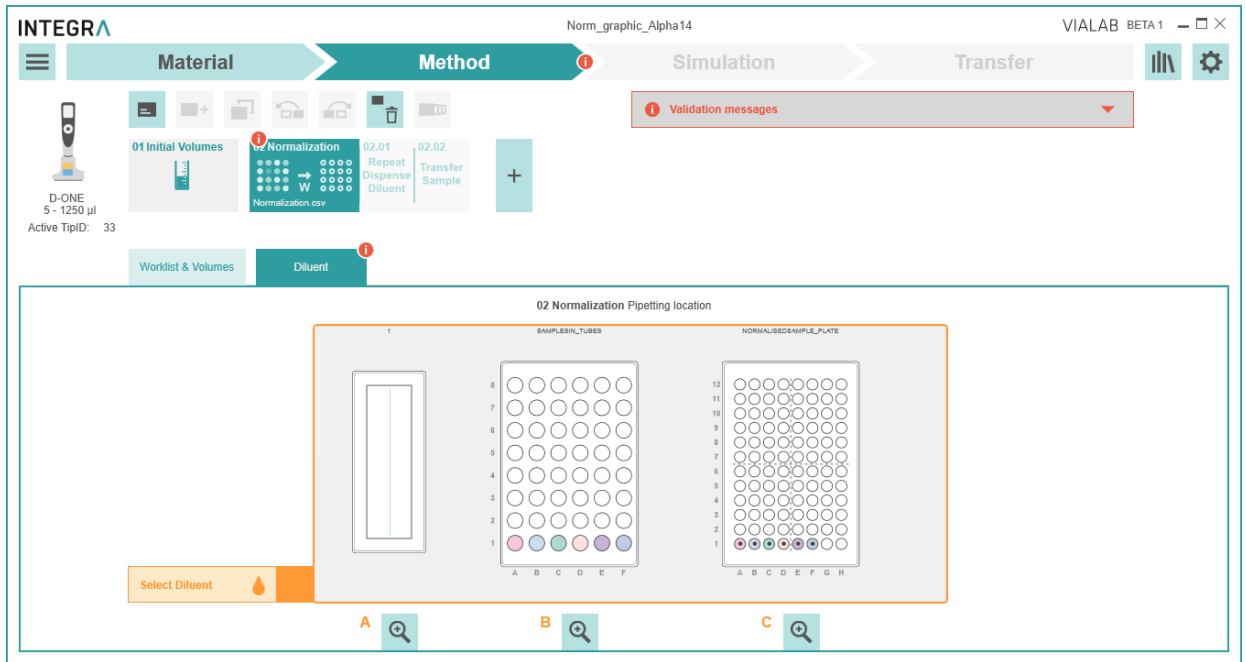
With this step the samples which need to be normalized must be previously defined in a worklist and imported.

- Add a **Normalization Worklist (1)** step to your method. Click on **Import (2)** to load the worklist file, see 6.4.1.



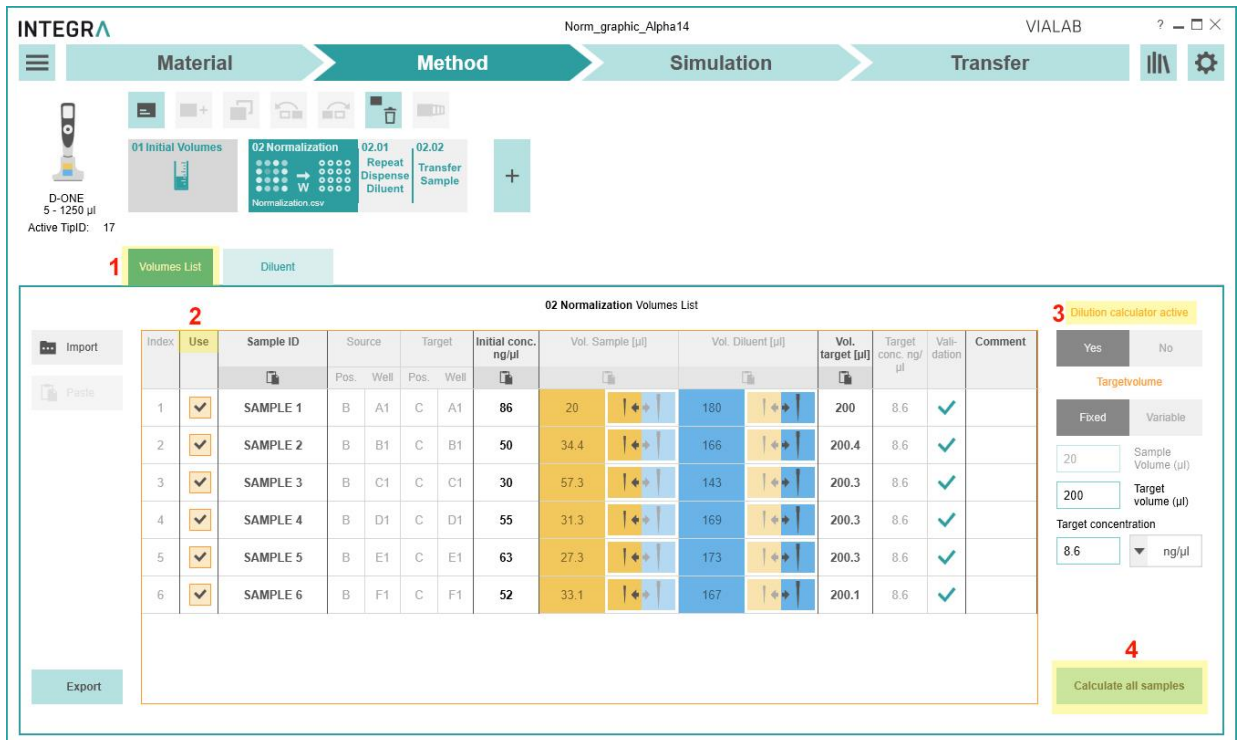
- Assign where the target and source plates are placed on deck. Then assign the position of the diluent.





Click on the diluent, i.e. the reservoir in the example above.

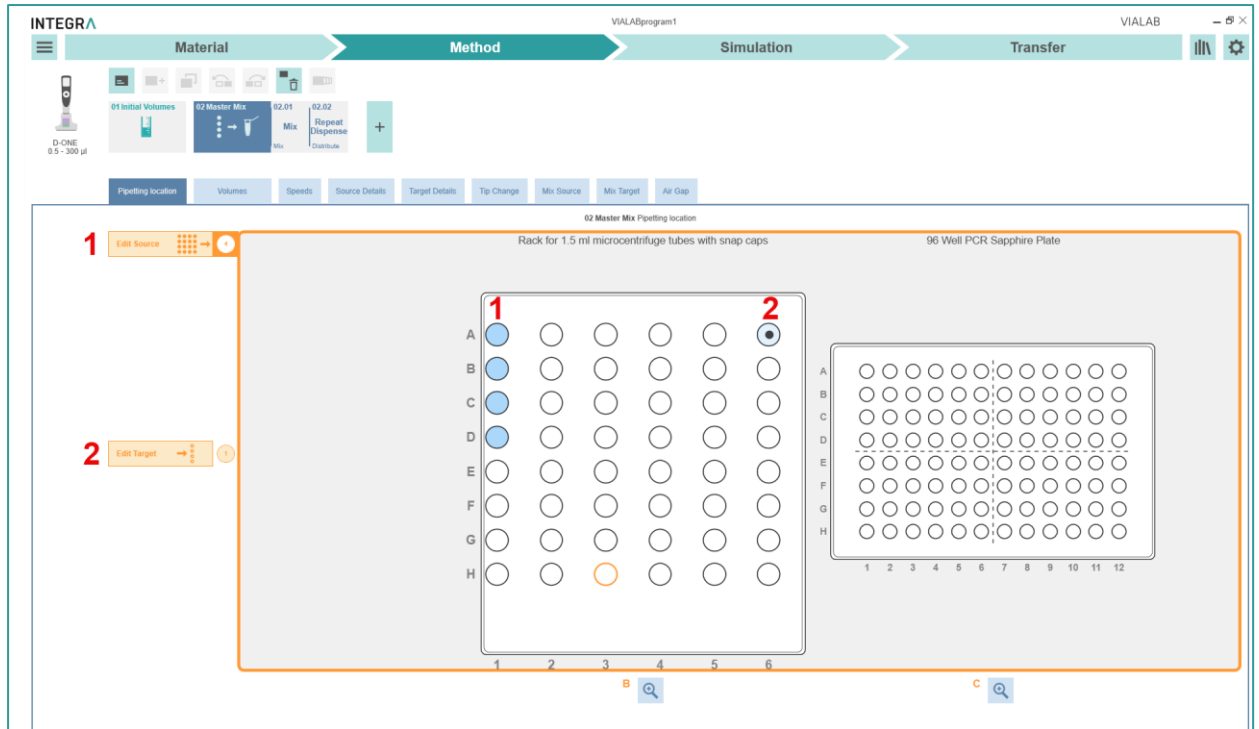
- Under **Volumes List** (1) the worklist is displayed. By removing the checkmark under Use (2), you can exclude samples from processing.



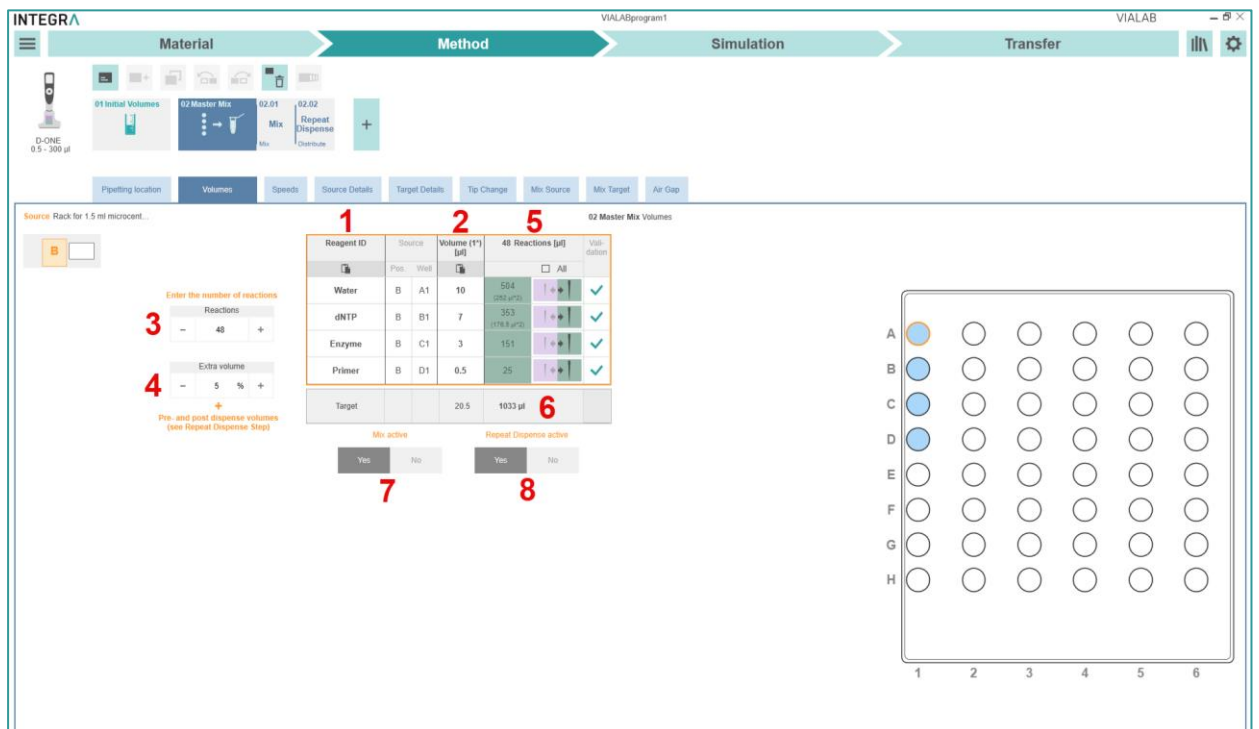
If you switch on the **Dilution calculator** (3), you can adjust the target volume and concentration. Click on **Calculate all samples** (4) to automatically calculate all parameters (volumes, pipette tips) automatically.

6.4.5 Master Mix

- Define the location of the source (1) containing the reagents and the target (2) vessel for the master mix.



- Under **Volumes**, name the reagents (1), e.g. water, dNTP, enzyme, primer, and enter the Volume (2) for a single reaction.

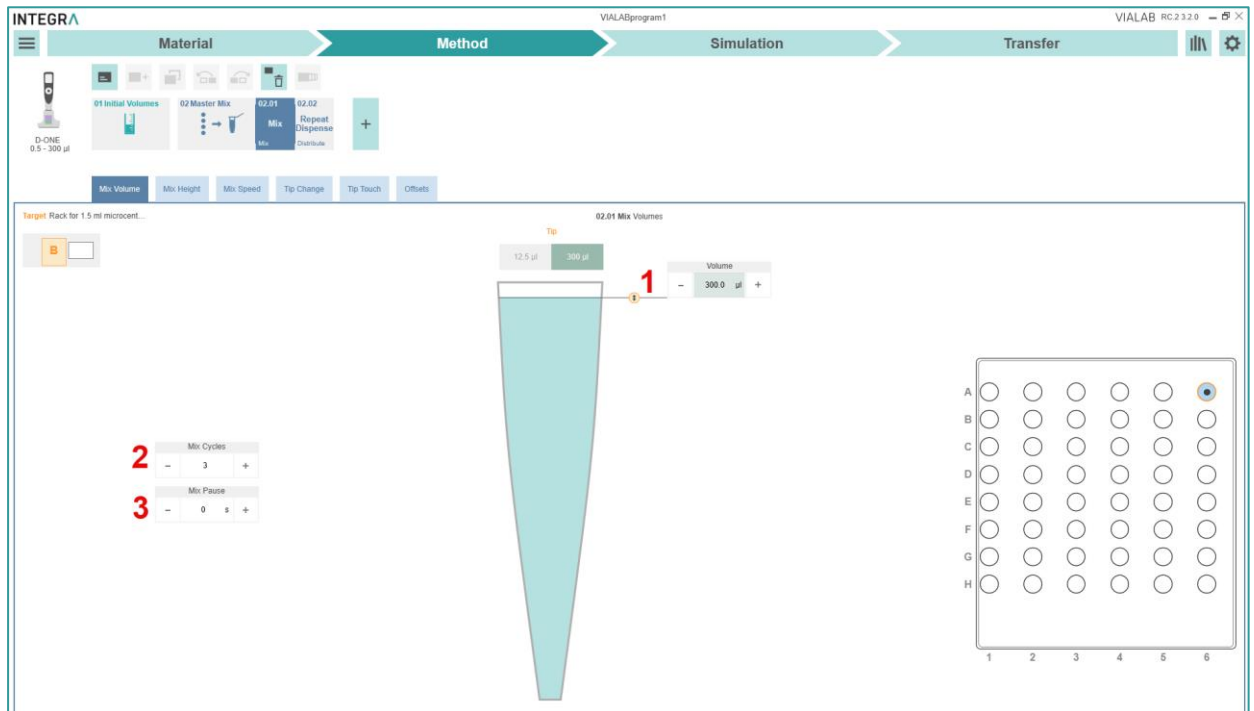


Enter the total number of reactions (3). Define extra volume (4) to account for dead volume in labware. The total reagent volumes and the target (5) volume are calculated automatically. If the calculated volume exceeds the tip volume, the volume is dispensed multiple times with the same tip, indicated by a multiplier (*). The correct tip size is selected automatically by VIALAB. If desired, the tip type can be manually changed by the user (6). Mix active (7) to activate or

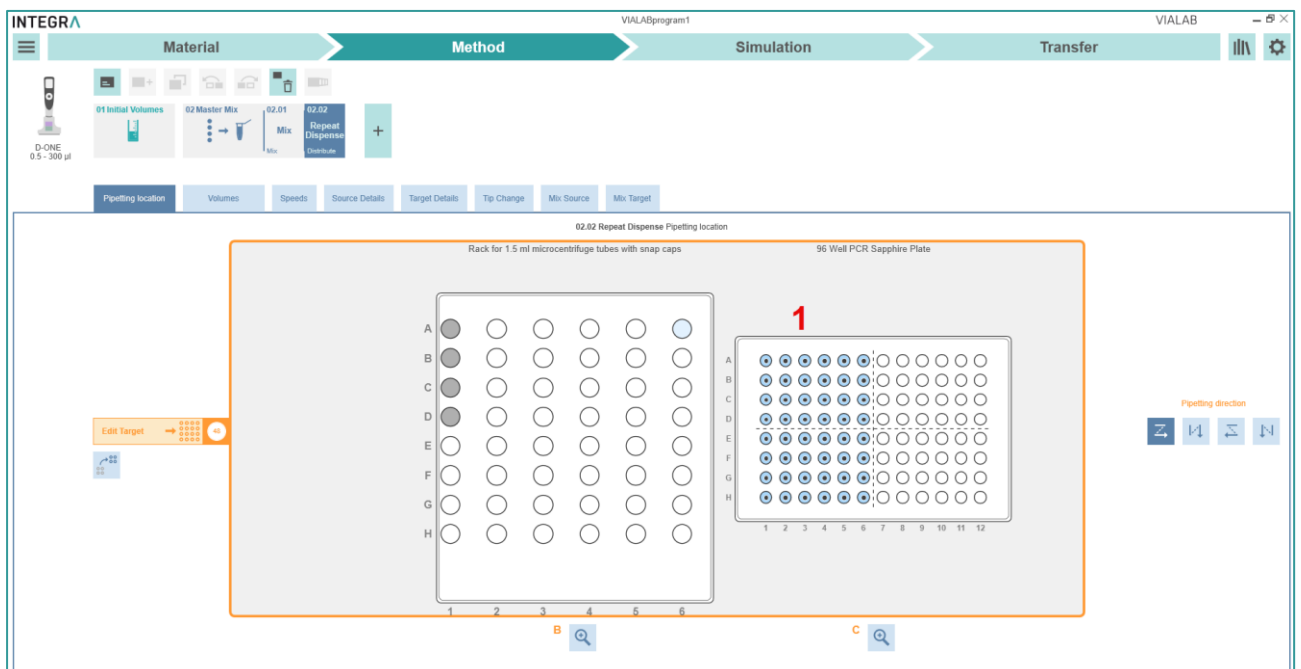
deactivate the subsequent mixing step. Repeat Dispense active (8) to include or exclude the continuous Repeat Dispense step.

Note: By changing the total number of reactions (3) the subsequent Mix and Repeat dispense step regarding volume and target wells are automatically adjusted.

- In the Mix step mix select the (1) volume, (2) mixing cycles and (3) mix pause for the master mix.



- In the Repeat Dispense step, select the target wells (1) to distribute the master mix.



6.4.6 Worklist

- Use the Worklist step to set up a program based on an imported worklist, see 6.4.1. Use the "Worklist Template" to specify the most common pipetting parameters or the "Worklist Template Extended" for extensive option of pipetting parameters.

The screenshot displays the '02 Worklist Worklist & Volumes' configuration screen in the INTEGRA software. The interface features a top navigation bar with tabs for 'Material', 'Method', 'Simulation', and 'Transfer'. Below the navigation bar is a toolbar with various icons and a 'Validation messages' dropdown menu. The main workspace contains a table for defining worklist entries. The table has the following structure:

| Index | Use | Sample ID | Source | | Target | | Volume [µl] | Validation | Comment |
|--|-----|-----------|--------|------|--------|------|-------------|------------|---------|
| | | | Pos. | Well | Pos. | Well | | | |
| You can create your worklist by the supplied Templates | | | | | | | | | |

Additional elements include an 'Import' button, a 'Paste' button, and an 'Overview' button in the bottom left corner. The interface also shows a 'D-ONE 0.5 - 300 µl' pipette icon and a 'Worklist & Volumes' tab selected in the bottom navigation bar.

6.4.6.1 Worklist with a COMBI system

- To use a worklist with a COMBI system e.g Slider Adapter, create and import the worklist as explained in 6.4.1 Importing worklists.
- To identify the well and deck positions, click on Show Deck (1).

The screenshot shows the '02 Worklist Worklist & Volumes' configuration window. It features a table with the following data:

| Index | Use | Sample ID | Source | | Target | | Volume [µl] | Validation | Comment |
|-------|-------------------------------------|-----------|--------|------|--------|------|-------------|-------------------------------------|---------|
| | | | Pos. | Well | Pos. | Well | | All | |
| 1 | <input checked="" type="checkbox"/> | Sample 1 | A1 | A1 | B1 | A1 | 100 | <input checked="" type="checkbox"/> | |

On the left sidebar, the 'Show Deck' button is highlighted with a red '1'.

- In the opened pop-up window, when you hover over the wells (1), the well is displayed first, followed by the deck position in brackets (e.g., well C1 on deck position A1).

The '3 Position Universal Deck' window displays three diagrams labeled A, B, and C:

- A:** Labware Pedestal (+24mm) portrait. Shows a 3x3 grid of wells. The top-left well is labeled 'C1 (A1)'. The bottom row is labeled 'A1'.
- B:** Dual Reservoir Adapter. Shows two columns of wells labeled 'B2' and 'B4'.
- C:** Slider base plate for 6 sliders. Shows six columns of wells labeled 'C1' through 'C6'.

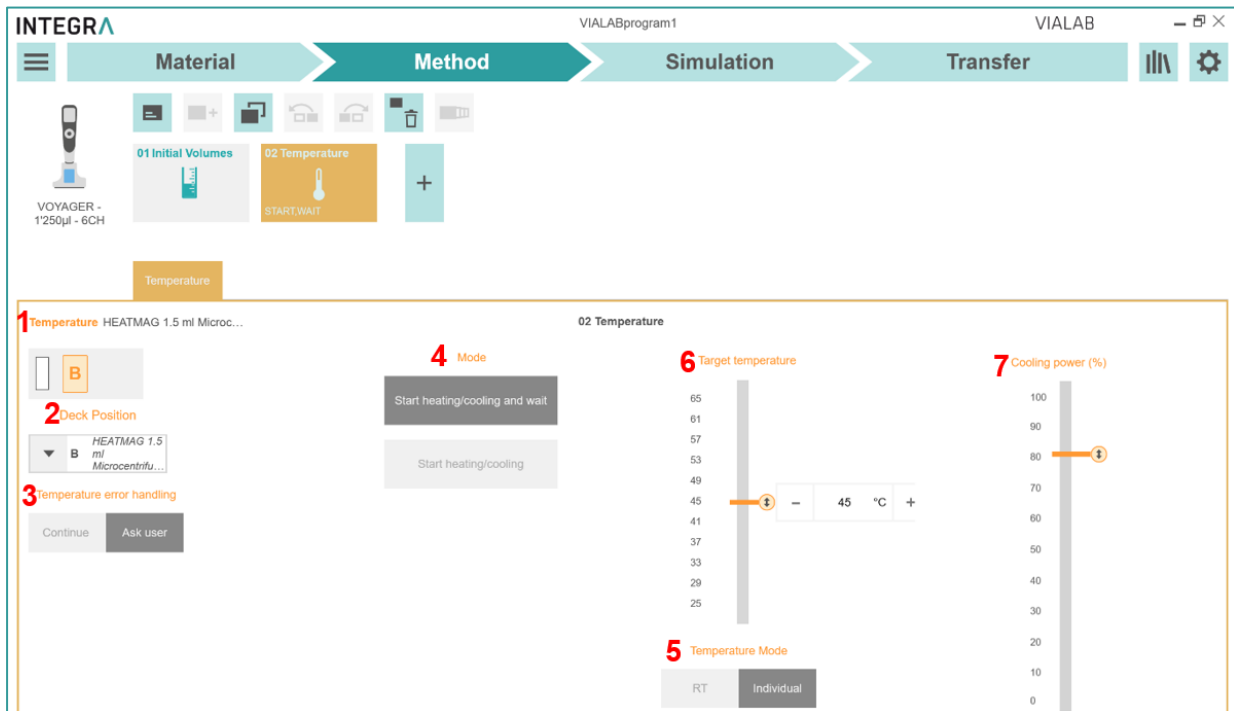
A red '1' and a hand cursor are shown hovering over the 'C1 (A1)' well in diagram A.

6.5 Methods for Modules

The method steps in this section are only compatible with the MAG, HEATMAG, BIOSHAKE 3000, BIOSHAKE 3000-T, and COLDPLATE modules.

6.5.1 Temperature

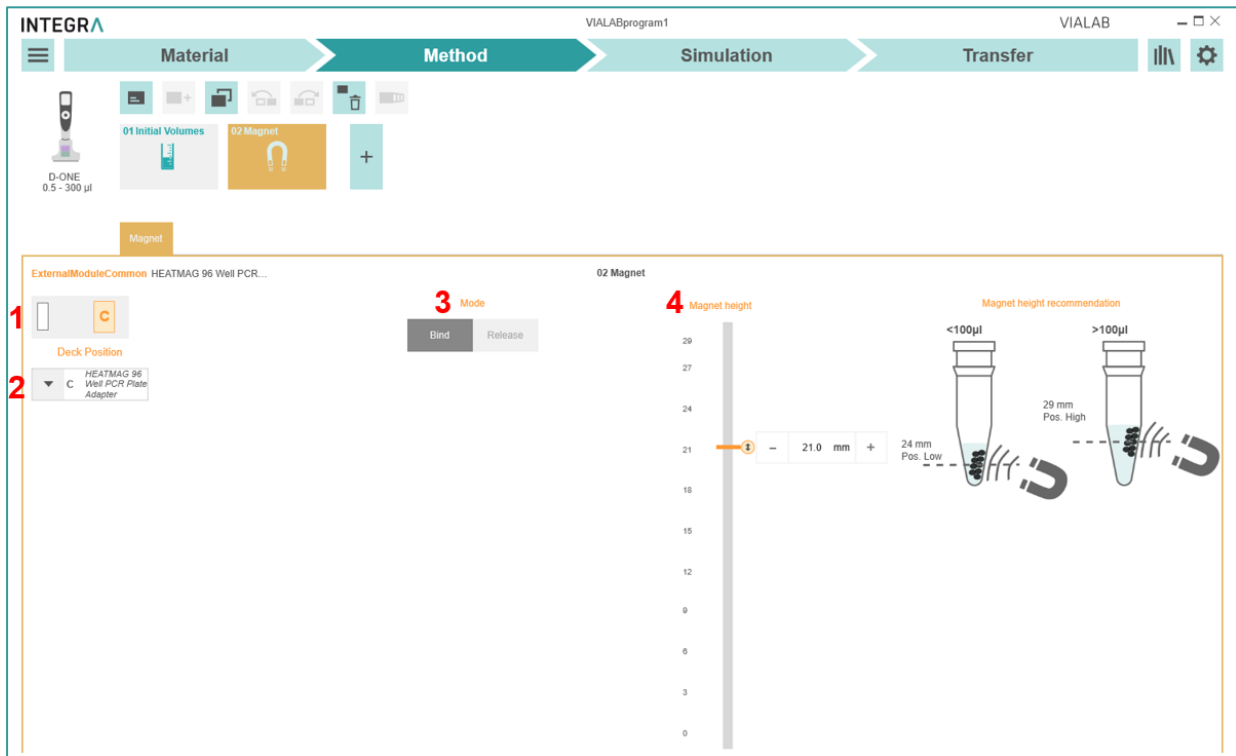
With this step you can heat and cool samples for a certain time at a specific temperature (°C).



- 1 Temperature:** To verify which external module is connected
- 2 Deck Position:** Select the deck position where the controlled module is located. Note: Only one module can be connected to and controlled by the ASSIST PLUS at any time.
- 3 Temperature error handling:** In case a target temperature cannot be reached in a certain time you can either continue the program or ask user how to handle the error.
- 4 Mode:** Select Start heating/cooling and wait in order to wait until the target temperature is reached before continuing in the protocol or select Start heating/cooling to continue the protocol allowing for other pipetting steps in parallel to save time
- 5 Temperature Mode:** Select individual to set a specific target temperature or RT to bring a module back to ambient temperature. **Note:** Only for INTEGRA HEATMAG
- 6 Target temperature:** Specify the temperature to which your sample should be heated/cooled.
- 7 Cooling power:** Specify the cooling power percentage of the external module. **Note:** Only for INTEGRA HEATMAG.

6.5.2 Magnet

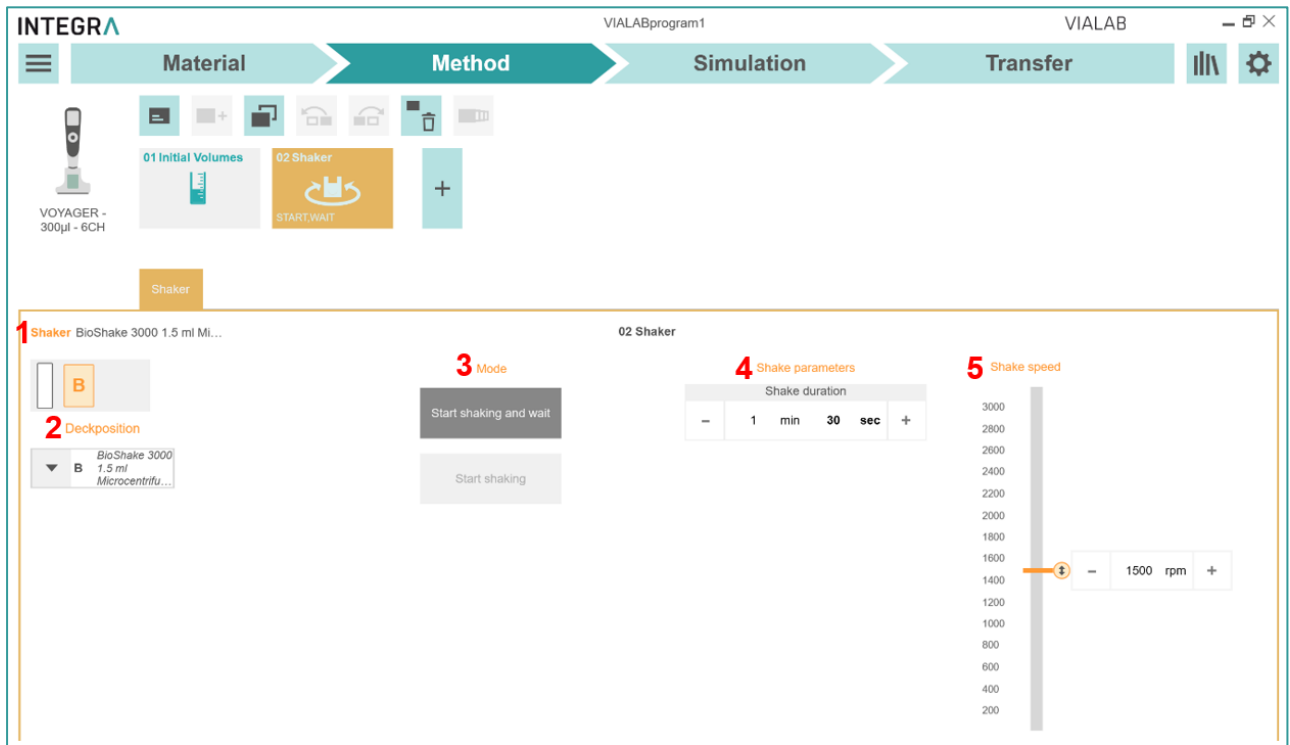
This step moves the magnetic array of MAG / HEATMAG up (Bind Mode) and down (Release Mode).



- 1 **Magnet:** To verify which module is connected
- 2 **Deck Position:** Select the deck position where the controlled module is located. Note: Only one module can be connected to and controlled by the ASSIST PLUS at any time.
- 3 **Mode:** Select bind to move magnet to specified height or release to move magnet down. **Note:** your beads will be bound throughout the next steps until you release them with a Release step
- 4 **Magnet height:** Specify the optimal magnet height according to your protocol.

6.5.3 Shaker

With this step you can shake your samples for a specific duration at a specific speed.



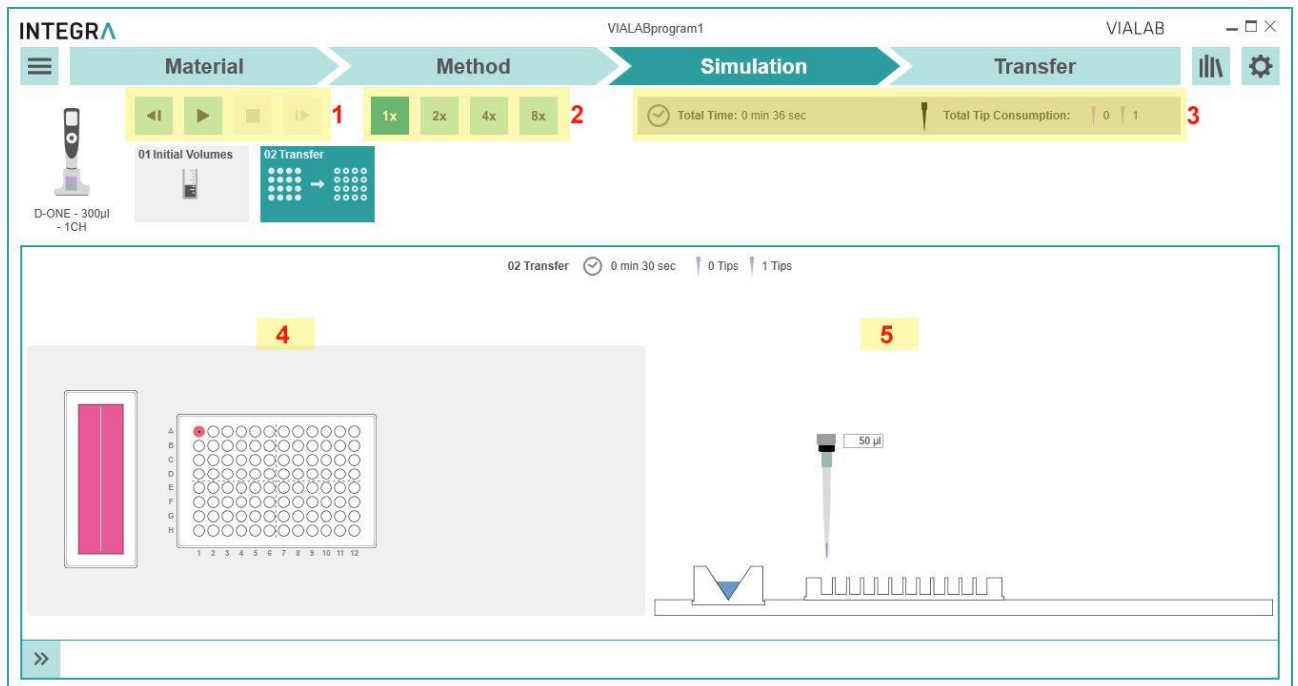
- 1 Shaker:** verify which module is connected
- 2 Deck Position:** Select the deck position where the controlled module is located. Note: Only one module can be connected to and controlled by the ASSIST PLUS at any time.
- 3 Mode:** Select either start shaking and wait in order to shake for a specific duration or start shaking while continuing in the protocol in parallel.
- 4 Shake parameters:** Specify the duration of shaking according to your protocol.
- 5 Shake speed:** Specify the revolutions per minute (rpm) according to your protocol.

6.6 Simulation

In the simulation window the deck with the defined labware is displayed. On the top all steps are listed. Click on the play button to start the simulation of your program. Watch the whole simulation or navigate between steps or stop the simulation (1).

To speed up the simulation to 2-, 4- or 8-fold speed, select the appropriate button (2). An estimation of the Total Time and the Total Tip Consumption is listed (3).

The simulation is displayed as top (4) and side (5) view of the deck.



For all error-free programs a report is generated by clicking on the Main Menu and selecting "Report". A report in pdf format with all settings of the program is generated.

6.7 Transfer

Transfer your VIALAB program to your pipette and run it from your pipette. Alternatively connect the ASSIST PLUS via USB to the PC, connect the Pipette and start a program from VIALAB directly.

6.7.1 Connect pipette or pipetting module to the PC

Connection via charging/communication stand (#4211)

Connect the USB cable to the stand and a free USB port on your computer. It is recommended to connect the stand to the mains power supply. Then hang the pipette or the D-ONE module onto the stand.

Go to the “Toolbox” of the pipette/D-ONE. In the menu “Communications” select “USB”. Stay in this menu for transfer.

Connection via communication module for pipette (#4221)

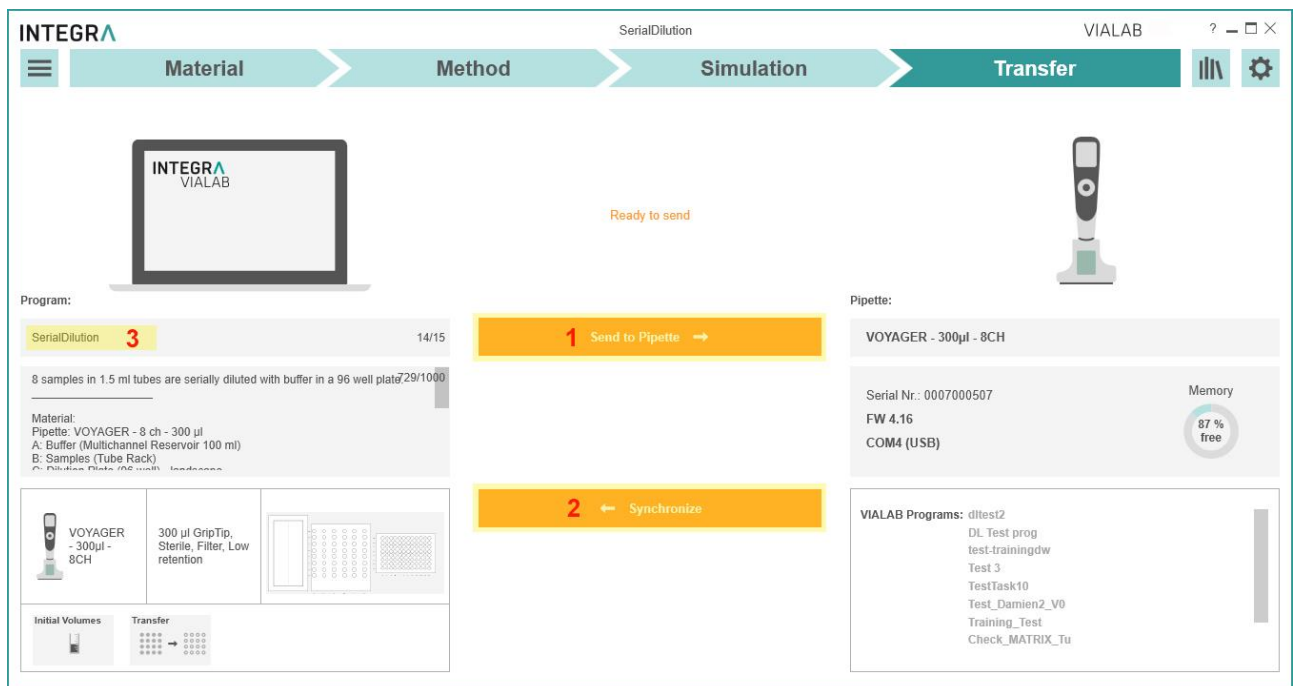
Pipette or D-ONE and PC need to be paired for the first connection. Please refer to MS Windows Help to learn how to pair Bluetooth devices. The following pairing code may be required: 12345.

Go to the “Toolbox” of the pipette. In the menu “Communications” select “via ASSIST PLUS”.

6.7.2 Transfer

In VIALAB switch to the section “Transfer” for saving the program to the pipette.

Upon establishing the connection successfully, the pipette details, such as pipette model, serial number, and firmware version, are displayed on the right side. All VIALAB programs already saved on the pipette are also listed.



Send to Pipette (1) starts the transfer of the current program to the pipette. If certain parameters of the program are directly modified on the pipette (offsets, pipetting heights), synchronization of the program to VIALAB is possible (2).

To change the program display name on the pipette type in an alternative program name with max. 15 characters (3).

Successful saving or synchronization of the program to the pipette / to VIALAB is indicated by a temporary message at the bottom of the window.

6.8 Run a program directly from VIALAB

To run a program directly from VIALAB, connect your ASSIST PLUS to your PC via USB. Then connect your pipette via ComModule to the ASSIST PLUS.


Enable a connection on the pipette under Toolbox – Communication, select PC Control A+.



As soon as the connection is successfully established the Transfer tab changes to Run Program (1) and the connected device is displayed with serial number (2).

Press Run Protocol (3). The VIALAB program is transferred automatically to the pipette. Under Live Log (4) the actual steps are displayed.

After the Run is done, the run report is generated automatically, showing all information such as serial numbers of ASSIST PLUS, pipette, user information, deck layout, method.

| VIALABprogram1 Report | | INTEGRA VIALAB |
|---|--|-------------------|
| Program Name | VIALABprogram1.iaa | |
| Program Name (on pipette) | Test | |
| Last Saved Date: | 24. Mar 2022 | |
| Last Save Operator: | | |
| Instrument - Serial Number | 0020081124 | |
| Pipette - Serial Number | 0007031096 | |
| Tip Type (PN 6434) Lot Nr.: | | |
| Run Operator: | jan-peter.baldin | |
| Run Date: | 24.Mar.2022 | |
| Run Start Time: | 11:30 | |
| Run End Time: | 11:31 | |
| Notes: | 11:30:57 : Run started 11:31:00 : Transfer (Step 02) 11:31:26 : Run finished | |
| Signature: | | |
| Overview Method  D-ONE - 300µl - 1CH Total Time: 0 min 29 sec Total Tip Consumption: Tip 300µl: 1 | | |
| Deck Layout | | |

7 Labware library

You can access the labware library by clicking on the Library icon in the top right corner.

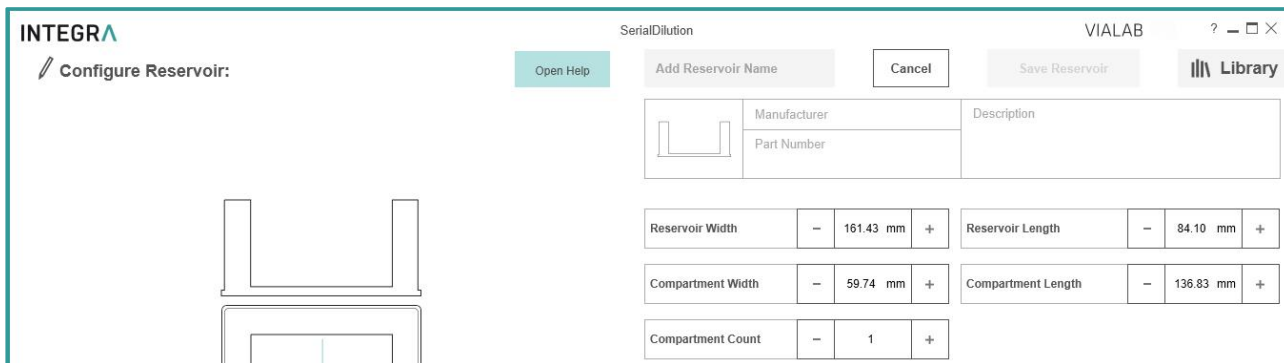
Within the labware library, you can define the dimensions of decks, reservoirs, plates, tube racks and COMBI Bases/Systems. Pipettes, GripTips and reservoirs from INTEGRA are already defined and cannot be modified.

7.1 Reservoirs

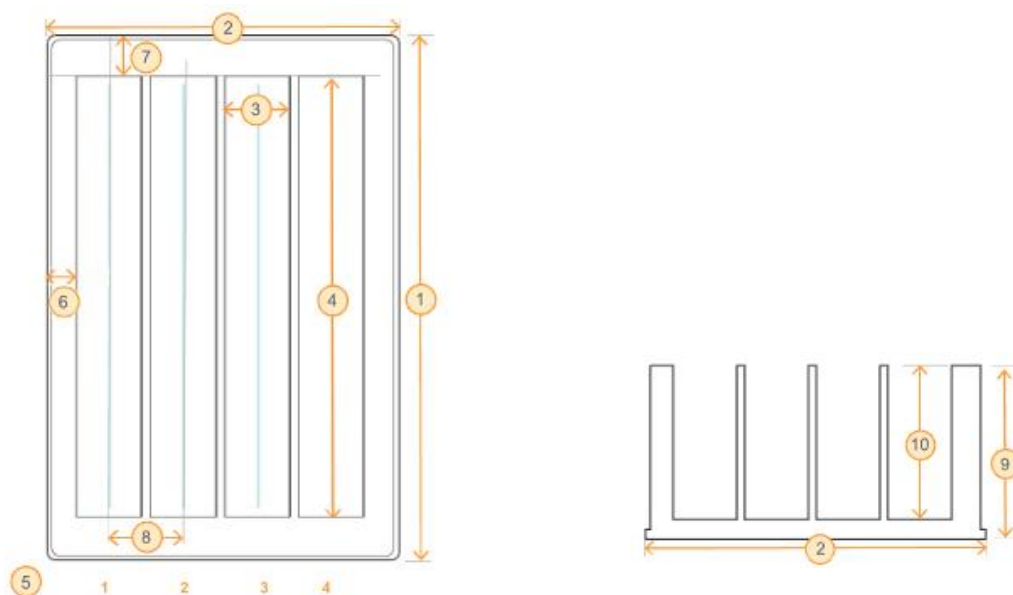
In the reservoir menu all predefined plates are listed. Select a desired property, e.g. Type, to quickly show already defined reservoirs of this property.

- 1 Reservoir:** the icon shows the number and shape of the wells and well bottom.
- 2 Name:** indicates the number and shape of the wells and well bottom, as well as other properties such as half-area.
- 3 Volume:** shows the maximal well volume of the reservoir or compartment as defined by the manufacturer.
- 4 Manufacturer:** name of the reservoir manufacturer
- 5 Part Number:** part number in accordance to the reservoir manufacturer
- 6 Description:** optional
- 7 Favorites:** select to mark as favorite. The material section in the program set-up has a filter to show only favorites.
- 8 Tools:** Edit/View details, Copy, Export or Delete the selected labware. It is not possible to edit or delete INTEGRA items. To modify other predefined labware, create a copy first and then edit the copy.

To add new reservoirs to the library, click on “Define new item”. In the Configure Reservoir menu enter a unique name, the manufacturer, the part number of the reservoir and a description, if applicable. The description can also be used for lab personal to identify the reservoir.



Enter the reservoir dimensions. You will be supported by live drawing of the defined reservoir.



Note: Reservoirs are always set up with their compartment(s) in vertical direction.

| Dimension | Description |
|--|---|
| Reservoir Width | The outside Width (1) of the reservoir including the bottom outside flanges, i.e. the displayed dimension from back to front. |
| Reservoir Length | The outside Length (2) of the reservoir including the bottom outside flanges, i.e. the displayed sideward dimension. |
| Compartment Width | The width of the compartments, i. e. the inner sideward dimensions (3). |
| Compartment Length | The length of the compartments, i. e. the inner distance from back to front (4) |
| Compartment Count | The number of the compartments (5), e. g. 4. |
| Left edge offset of First Compartment | The distance between the left outside edge of the reservoir and the left edge of the first compartment, including the bottom outside flange (6). |
| Top edge offset of First Compartment | The distance between the top outside edge of the reservoir and the top edge of the first compartment including the bottom outside flange (7). |
| Distance between Compartment Positions | The distance between the compartments, from the middle of one compartment to the middle of the next (8), e. g. 9 mm. This is the compartment width plus the spacing wall. |
| Type | Block. Rectangular flat bottom reservoirs can be defined. |
| Reservoir Height | The outside height (9) of the reservoir. |
| Compartment Depth | The inner depth (10) of the reservoir. |
| max. Volume | The maximal filling volume of one compartment. |

7.2 Plates

In the plate menu all predefined plates are listed.

The screenshot shows the VIALAB software interface. At the top, there's a header with 'INTEGRA', 'VIALABprogram1', and 'VIALAB'. A 'Define new item' button is visible. Below this is the 'Plates' section, which includes a filter and search area and a table of predefined plates.

| Type | Bottom | Volume | Manufacturer | Favorites | Part Number |
|------------------------------------|-----------------------------------|---------------------------------------|-----------------------------------|-----------|-------------|
| <input type="checkbox"/> 96 wells | <input type="checkbox"/> U-bottom | <input type="checkbox"/> <1000 µl | <input type="checkbox"/> >5000 µl | All | Part Number |
| <input type="checkbox"/> 384 wells | <input type="checkbox"/> F-bottom | <input type="checkbox"/> 1000-3000 µl | | ★ | |
| <input type="checkbox"/> Other | <input type="checkbox"/> V-bottom | <input type="checkbox"/> 3001-5000 µl | | | |

| Plate | Name | Volume | Manufacturer | Part Number | Description | Favorites |
|-------|--|---------|--------------------|----------------|-------------|-----------|
| | 48 well F-bottom | 1700 µl | GREINER | 677102, 677180 | | ★ |
| | 48 Deepwell V-Bottom Plate | 7000 µl | AXYGEN CORNING | P-5ML-48-C | | ★ |
| | 96 well PCR Low Profile Semi Skirt | 100 µl | CORNING | PCR-96-LP-AB | | ★ |
| | 96 Well PCR Low Profile Semi Skirt Plate | 100 µl | CORNING | PCR-96-LP-AB | | ★ |
| | 96 Well Fast Reaction Plate | 100 µl | APPLIED BIOSYSTEMS | 4346907 | | ★ |

To add new plates to the library, click on “Define new item”.

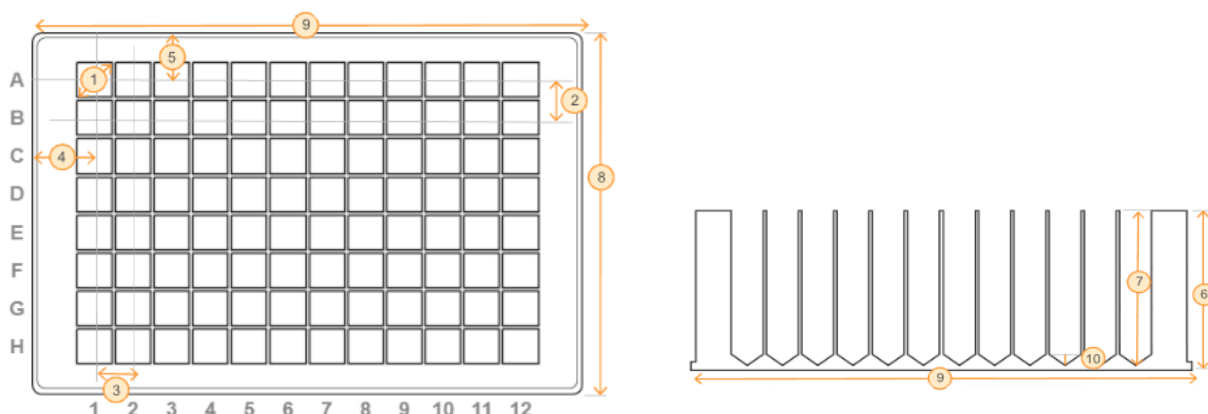
In the Configure Plate menu enter a unique name (e.g. well number and shape), the manufacturer and the part number of the plate.





The screenshot shows the 'Configure Plate' dialog box. It features a 96-well plate layout with row labels A-H and column labels 1-12. To the right of the layout are various configuration parameters:

- Row Count: 8
- Column Count: 12
- Well Shape - Top View: Round
- Well Bottom: V-bottom
- Well Inner Diameter: 8.00 mm
- Center to Center Spacing - Rows: 9.00 mm
- Center to Center Spacing - Columns: 9.00 mm
- Offset Row 1: 11.24 mm
- Offset Column 1: 14.38 mm
- Plate Height: 14.35 mm
- Well Depth: 10.00 mm
- Plate Width: 85.48 mm
- Plate Length: 127.76 mm
- max. Well Volume: 0 µl
- Well V-shape Depth: 0.00 mm

Note: For plates in adapters, e. g. in PCR 96 or 384 well cooling plates, define the dimensions of the inserted plate in combination with the adapter as one plate.

Enter all plate dimensions. You will be supported by live drawing of the defined plate.



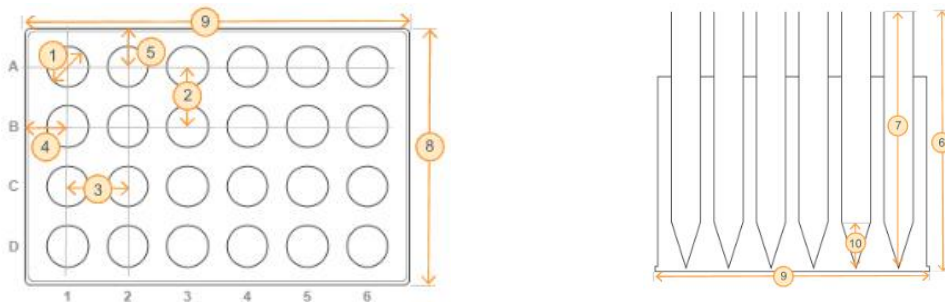
| Dimension | Description |
|------------------------------------|---|
| Row Count | A 96 well microplate is arranged as 8 rows by 12 columns. |
| Column Count | A 384 well microplate is arranged as 16 rows by 24 columns. |
| Well Shape - Top View | Shape on the top of the well, is usually round. |
| Well Bottom |  U-bottom = round |
| |  F-bottom = flat |
| |  C-bottom = curved edges of flat bottom, e. g. for easy wash |
| |  V-bottom = conical |
| Well Inner Diameter | Well diameter (1) on the top of the well |
| Center to Center Spacing - Rows | The distance between the rows (2) /columns (3) from the middle of one well to the middle of the next well. |
| Center to Center Spacing - Columns | 96 well: ANSI/SLAS-standard ¹ : 9 mm 384 well: ANSI/SLAS-standard: 4.5 mm |
| Offset Row 1 | The distance between the top outside edge of the plate and the center of the first row of wells (4). |
| | 96 well ANSI/SLAS-standard: 11.24 mm |
| | 384 well ANSI/SLAS-standard: 8.99 mm |
| Offset Column 1 | The distance between the left outside edge of the plate and the center of the first column of wells (5). |
| | 96 well ANSI/SLAS-standard: 14.38 mm |
| | 384 well ANSI/SLAS-standard: 12.13 mm |
| Plate Height | Plate height (6). ANSI/SLAS-standard: 14.35 mm ± 0.76 mm |
| Well Depth | Depth in the center of the well (7). |
| Plate Width | The shorter side (8), ANSI/SLAS-standard: 85.48 mm ± 0.5 mm |
| Plate Length | The longer side (9), ANSI/SLAS-standard: 127.76 mm ± 0.5 mm |
| max. Well Volume | The total, calculated well volume, not the working volume |
| Well V-shape Depth | Depth from start of conical narrowing to well bottom only for V-bottom wells (10). |





¹ ANSI: American National Standards Institute, SLAS: Society for Laboratory Automation and Screening.

7.3 Tube Rack

To create new tube racks, select Tube Racks and click on “Define new item”. In the Configure Tube Rack menu enter a unique name, the manufacturer, the part number and a description, if applicable.

Enter all tube rack dimensions and the tube type. You will be supported by live drawing of the defined rack.



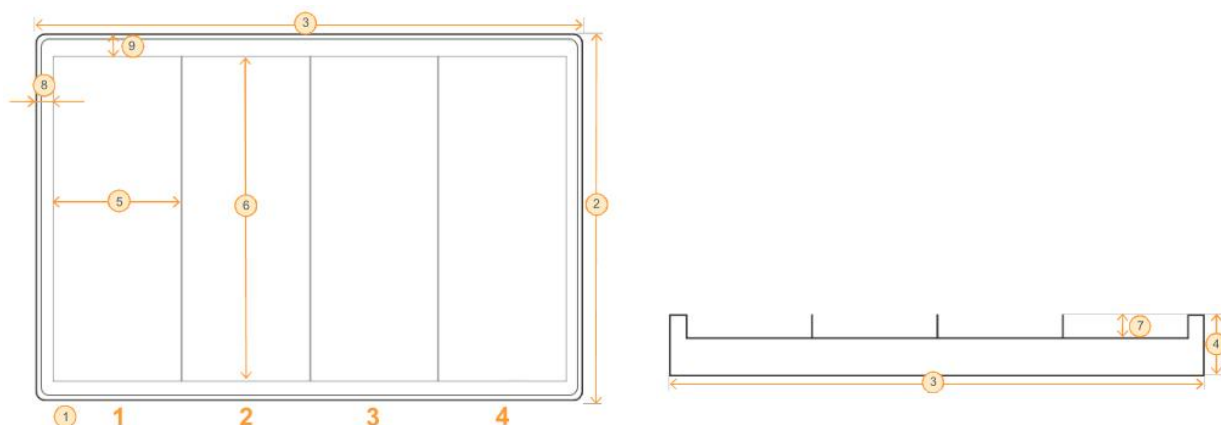
| Dimension | Description |
|------------------------------------|---|
| Row Count | Number of rows. |
| Column Count | Number of columns. |
| Tube Shape - Topview | Shape on the top of the tubes, is usually round. |
| Tube Shape - Bottom |  U-bottom = round |
| |  F-bottom = flat |
| |  C-bottom = curved edges of flat bottom |
| |  V-bottom = conical, including typical conical tube form with round bottom |
| Tube Inner Diameter | Tube inner diameter at the broadest position of the tube (1). |
| Center to Center Spacing - Rows | The distance between the rows, from the middle of one tube to the middle of the next tube (2). |
| Center to Center Spacing - Columns | The distance between the columns, from the middle of one tube to the middle of the next tube (3). |
| Offset Column 1 | The distance between the left outside edge of the rack and the center of the first column of tubes (4). |
| Offset Row 1 | The distance between the top outside edge of the rack and the center of the first row of tubes (5). |
| Tube Rack Height | Total height of tube rack and tubes (6). |
| Tube Depth | Depth in the center of the tube (7). |
| Tube Rack Width | Width of the rack(8). ANSI/SLAS-standard: 85.48 mm ± 0.5 mm. |
| Tube Rack Length | Length of the rack (9). ANSI/SLAS-standard: 127.76 mm ± 0.5 mm. |
| Max. Tube Volume | The total, calculated tube volume, not the working volume. |
| Tube V-shape Depth | Depth from start of conical narrowing to tube bottom, e. g. 3.1, only for V-bottom wells (10). |

7.4 COMBI Base

A COMBI Base is a platform where a module, i.e. a reservoir, plate or tube rack, can be placed on. It only acts as an adapter and you cannot choose a COMBI Base alone as a pipetting location (only a COMBI System see chapter 7.5)

To create a new COMBI Base, select COMBI Base and click on “Define new item”. In the Configure COMBI Base menu enter a unique name, the manufacturer, the part number of the COMBI Base and a description, if applicable.

Enter all COMBI base dimensions. You will be supported by live drawing of the defined COMBI base.



| Dimension | Description |
|-----------------------------|--|
| Division | Regular: a repeated number of identical sections are lined up. Irregular: sections are positioned freely within the outer dimensions of the base. |
| Sections | Number of sections (1). |
| Base Width | Width of the base (2). ANSI/SLAS-standard: 85.48 mm ± 0.5 mm. |
| Base Length | Length of the base (3). ANSI/SLAS-standard: 127.76 mm ± 0.5 mm. |
| Base Height | Total height of the base (4). |
| Sections Width | The width of a section (5). |
| Section Length | The length of a section (6). |
| Section Height | The height of a section (7). Negative values indicate that the bottom of the section is deeper than the whole COMBI base. |
| Left edge offset of section | The distance between the left outside edge of the base and the left edge of the first section, including the bottom outside flange (8). |
| Top edge offset of section | The distance between the top outside edge of the base and the top edge of the first section including the bottom outside flange (9). |

Offset Row 1 The distance between the top outside edge of the rack and the center of the first row of tubes (5).

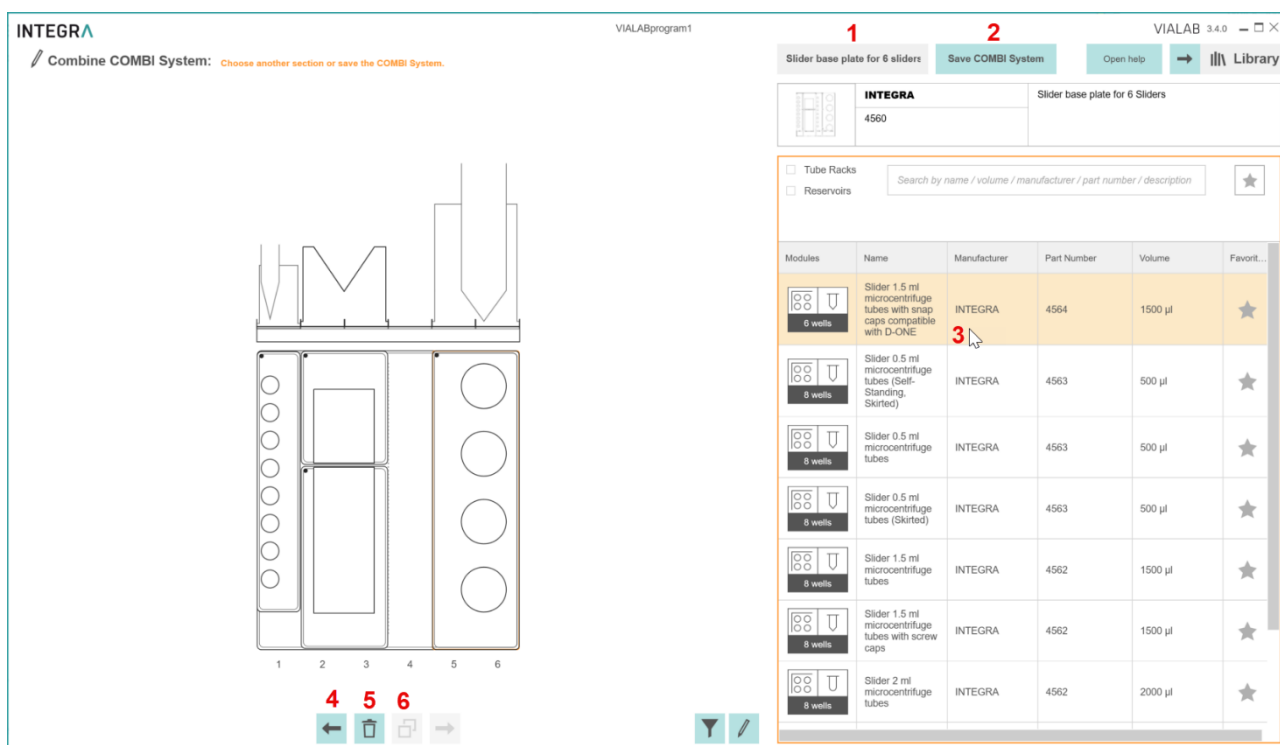
7.5 COMBI System

A COMBI System consists of a COMBI Base and individual modules, i.e. a reservoir, plate or tube rack, which are placed on the COMBI Base.

To create a new COMBI System, click on “Define new item”. In the Combine COMBI System menu select a COMBI Base.

Enter a unique name (1), the manufacturer, the part number and a description of the COMBI System, if applicable.

Select a labware (3) and move (4) it to the desired location, delete (5), or copy (6) it. Click on Save COMBI System (2) to transfer it to the labware library.



1 Name: unique name under which the COMBI system is stored.

2 Save COMBI system: save button.

3 Select: labware to be placed on the COMBI Base.

4 Move: the placed labware to the left and right with the arrow.

5 Delete: placed labware from the COMBI Base.

6 Copy: to place multiple times the same labware.

7.5.1 Slanted Plate Holder

The Slanted Plate Holder (PN 4510) can accommodate plates in three different angles: 10°, 20° and 30°.

To assemble a Slanted Plate Holder with a plate select in “Material” deck position **B** or **C** on the 3 Position Universal deck. Choose the menu option “COMBI” on the right menu bar and select the COMBI Base “Slanted Plate Holder” at the desired angle.

Select either the landscape or portrait deck section on the Slanted Plate Holder and choose a compatible plate from the list on the right side.

Choose “Apply COMBI System” and use it for your program.

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If you want to reuse a COMBI System, you can also create a new COMBI System in the labware library and save it with an appropriate name. Then the already assembled COMBI System (adapter and plate) can be used in your method.

Note: A change of the angle needs a change of the COMBI system used in the Material section. All steps in the Method section will be deleted then. We advise to define the appropriate angle in a test program first, before programming a lot of steps, which might be lost.

The screenshot shows the VIALAB software interface. On the left, there is a 3D model of a slanted plate holder and a 2D grid of a 24-well plate. The main window displays the 'Apply COMBI System' dialog for a 'Slanted Plate Holder 20°'. The dialog includes a 'Manufacturer' field with the value '4510' and a note: '- Slanted Plate Holder tilted at 20° - microplates in ANSI/SLAS format can be accommodated in landscape or portrait orientation'. Below the dialog is a list of modules with the following data:

| Modules | Name | Manufacturer | Part Number | Description | Favorit... |
|---------|------------------|--------------|------------------------------|-------------|------------|
| | 8 PCR tubes | | | | ★ |
| | 24 well F-bottom | CORNING | 3337, 3524, 3526, 3527, 3473 | | ★ |
| | 24 well F-bottom | GREINER | 662102, 662160 | | ★ |
| | 24 well F-bottom | TPP | 92024, 92424, 92124 | | ★ |
| | Pack for Schott | | | | |

In the labware library, the Slanted Plate Holder (20°) is assembled e.g. with a 24 well plate.

8 Troubleshooting

| Topic | Issue | Remedy |
|---|--|---|
| Labware Library | I cannot place my labware item on the deck, although it is defined correctly in the labware library. | <ul style="list-style-type: none"> • Make sure the selected labware item is compatible with your pipette. |
| | | <ul style="list-style-type: none"> • Make sure your labware item fits to the selected deck position e.g. a tube rack cannot be placed on deck position A. |
| Labware Library / Method | I created my labware item and placed it on the deck, but I cannot fill it with volume. | <ul style="list-style-type: none"> • Make sure the Max. Well Volume is > 0 µl. |
| Connection between pipette and computer | I cannot get a connection between pipette and VIALAB. | <ul style="list-style-type: none"> • Make sure the pipette is in communication mode (see chapter 6.7.1.) • Make sure the Charging/communication stand or device is connected to the computer. • ComModule: The Communication module for pipette and PC need to be paired if connected for the first time. Refer to Windows Help to learn how to pair Bluetooth devices. The passcode 12345 may be required. • Make sure the drivers for the Charging/communication stand are installed. While the stand is connected, go to your System Settings -> Device Manager. Check under Ports (COM & LPT) if there is an entry "USB Serial Port (COM X)". If there is not, install the drivers manually. |
| Synchronization of programs from pipette to VIALAB. | The "Synchronize" button is not activated. | <ul style="list-style-type: none"> • Make sure that no changes were made in VIALAB after saving the program to the pipette. |
| Pipette status in section Transfer. | I connected the pipette and its status is "Pipette is incompatible". | <ul style="list-style-type: none"> • Make sure that the correct pipette model matching the current program is connected. You can only transfer programs to the pipette model used in the program. |
| Program Transfer To Pipette | The pipette is connected, after "Send To Pipette" the program is not saved on the pipette. | <ul style="list-style-type: none"> • Make sure, that you do not use any special characters in your program name on the pipette (Transfer Screen). |