Tool owner: David Barth, dsbarth@seas.upenn.edu, x 3-5871
Backup: Ana Cohen, coana@seas.upenn.edu

EBPG 5200+ Standard Operating Procedure

Version 1.0.1, Updated 5/7/2024

QUICK GUIDE

PROCEDURE OVERVIEW

1. Design
2. Conversion
3. Sample Loading
4. Prealignment
5. Job Creation
6. Job Scheduling
7. Unloading
8. Developing

CRITICAL PRECAUTIONS AND COMMON MISTAKES

- The load lock door is a pinch point. Be cautious of your fingers when loading and unloading
- To keep pumpdown times low, keep the load lock door closed at all times
- Check that your sample is oriented correctly when you load it. Remember that the EBPG coordinate system is rotated from what you might expect.
- If you try to pattern within ~1mm of the edge of your sample, you will likely get a height sensor error. Height mapping (Appendix A) or sample redesign can resolve this.
- This SOP is written to ONLY provide some key operational procedures in a step-by-step

Tool condition for the next user

- Pump the load lock with sample holders inside
- Close all software windows except for cEBPG and cSYS
- Make sure the illumination on the prealignment microscope is off and remote control is unselected in Calign
- Log out on NEMO

MATERIALS RESTRICTIONS

Needs to be vacuum compatible. Approved materials:

Only these Materials are Allowed	Restricted Materials (Staff permission req'd for each use)	Known Forbidden Materials
• Standard semiconductor and dielectric materials • E-beam resists • Low vapor pressure metals	All other polymers	⃠ Unbaked resist ⃠ Outgassing materials ⃠ Tape ⃠ Silver Paste

HANDLING REMINDERS

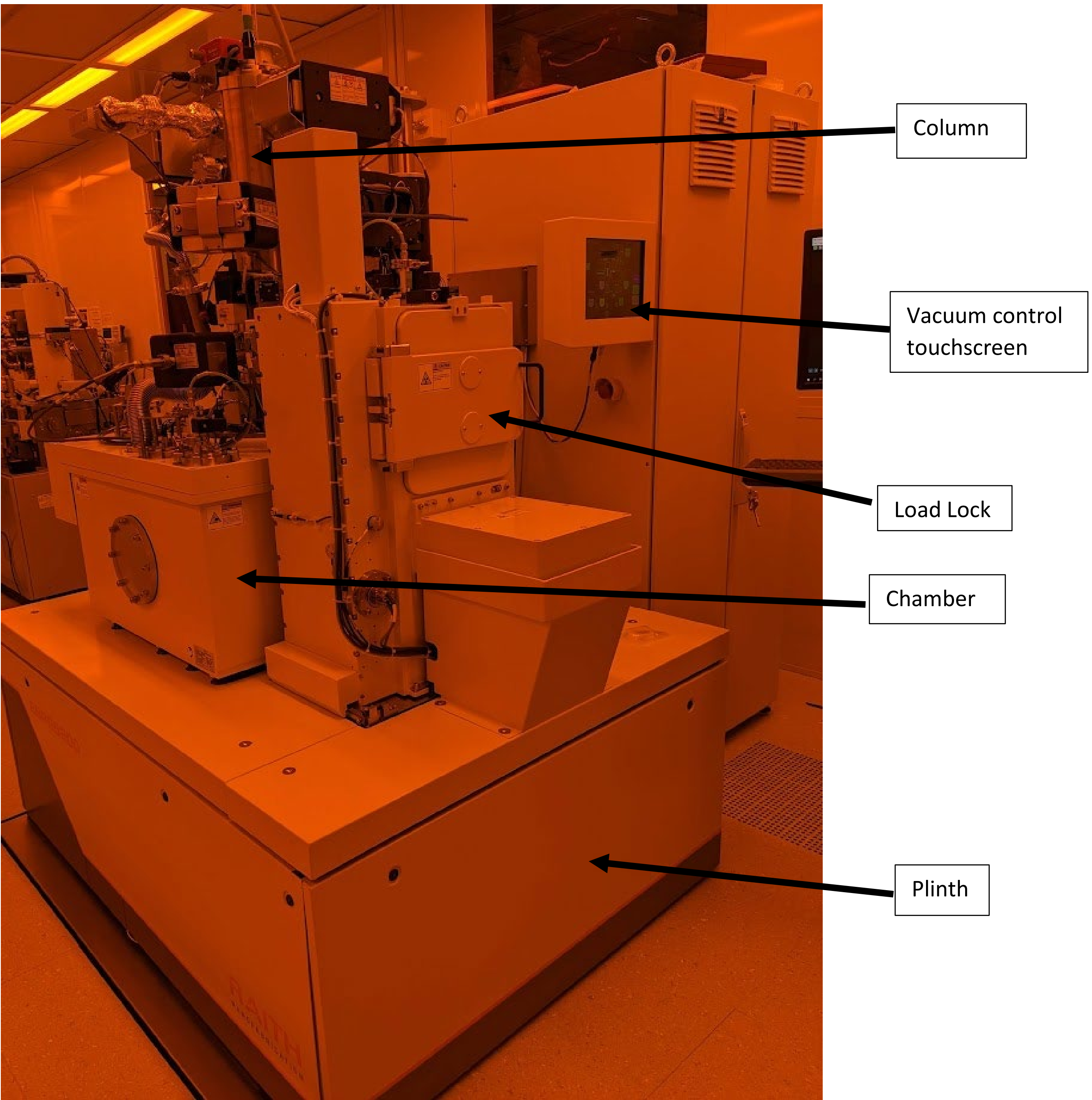
- Double glove when touching anything that enters the chamber
- Never touch or bump the reference samples affixed to the sample holders
- Soft tweezers are recommended
- Make sure back side of sample is clean
- Bake sample thoroughly to get rid of any solvents before writing
- Use the nitrogen gun to blow any particles off of the sample holder before loading

Tool Overview

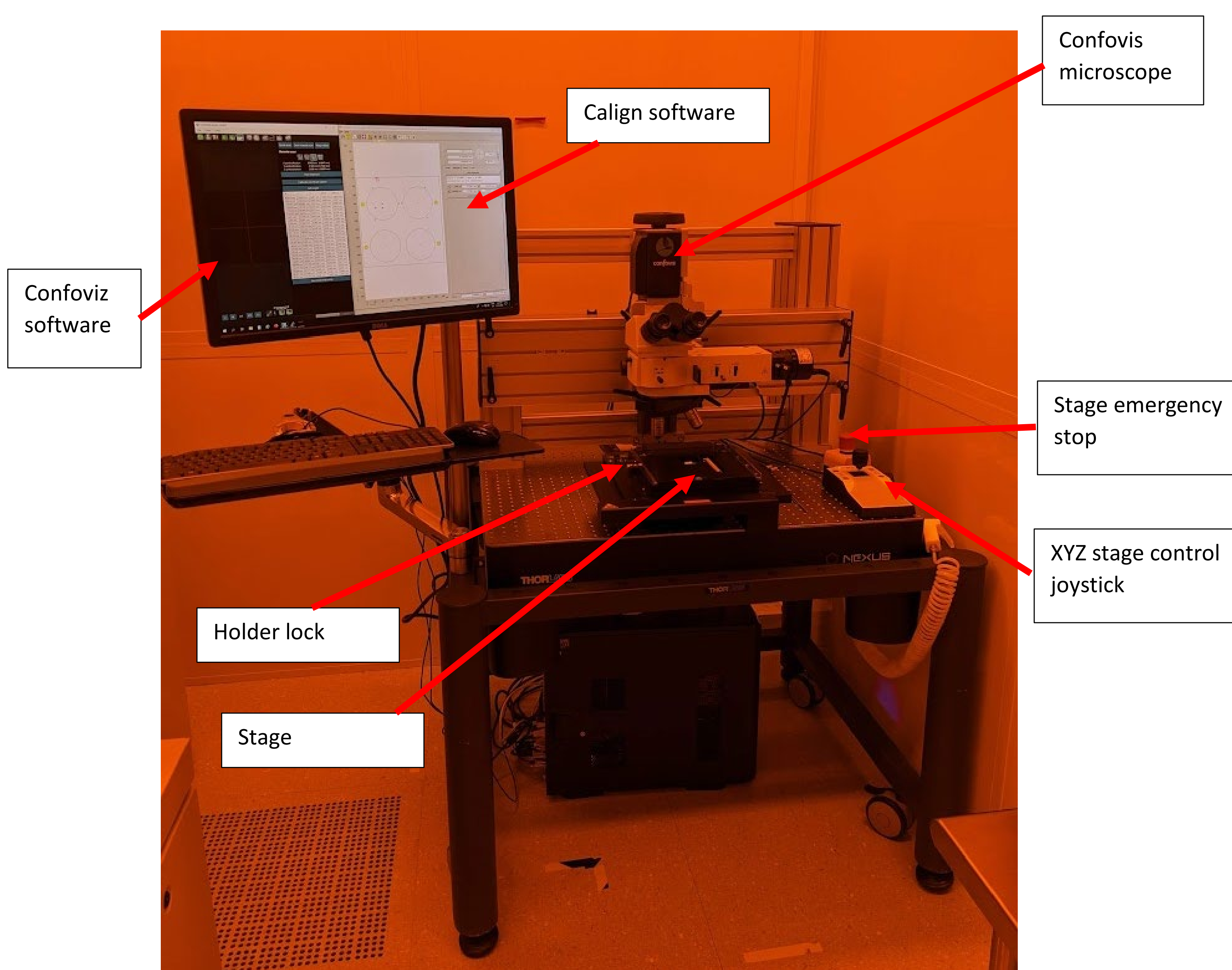
The EBPG 5200+ can be used for writing features with critical dimension down to ~8 nm over chips and wafers up to 200 mm in diameter. The accelerating voltage is 100 kV, and the beam current can be up to 350 nA. Overlay and stitching alignment accuracy of less than 10 nm can easily be achieved. The tool has automatic focus, stigmation, alignment, and beam and aperture switching. It has a 125 MHz pattern generator and 1.04 mm main field size.

Hardware Overview

EBPG 5200+ System

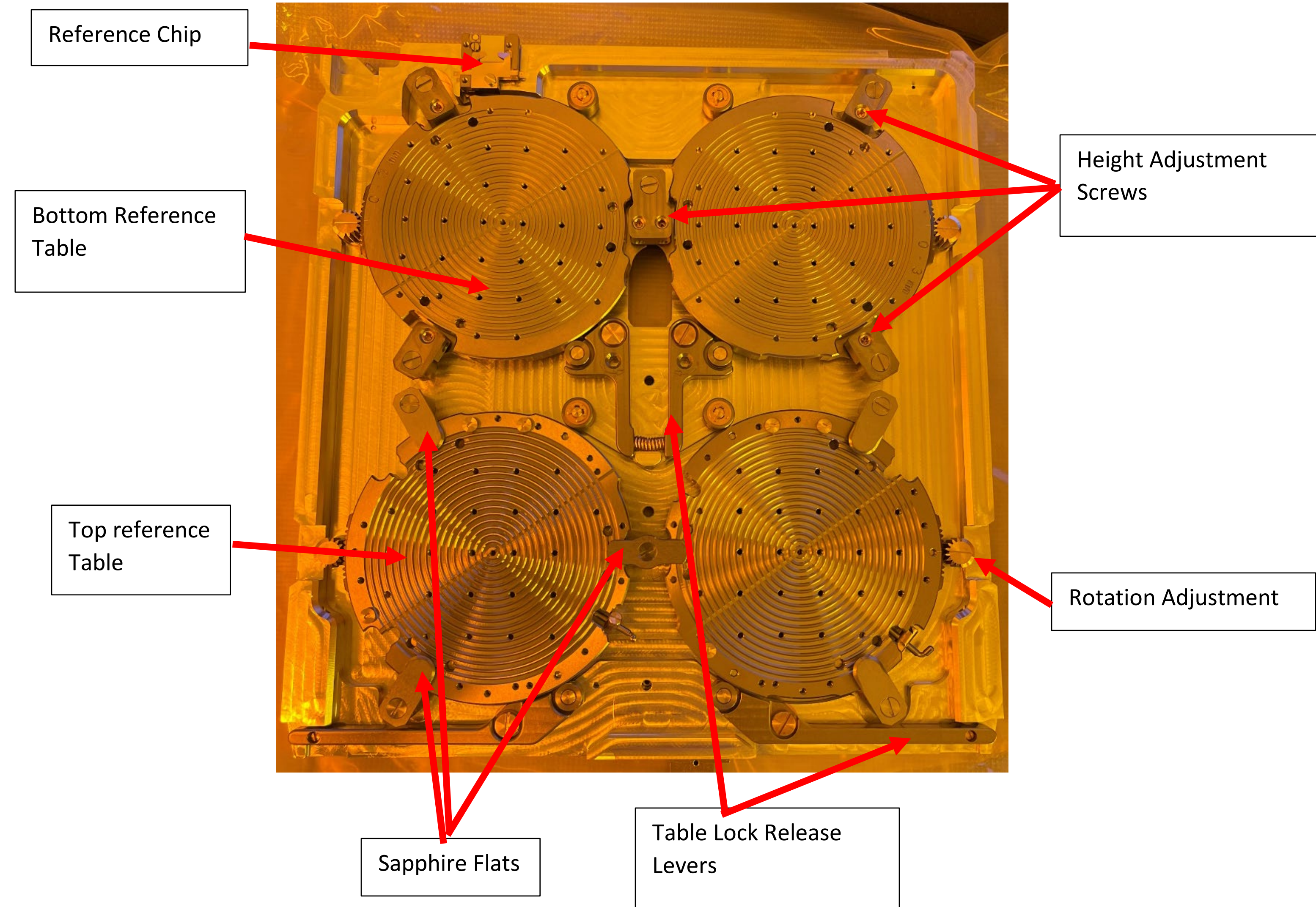


Prealignment Microscope

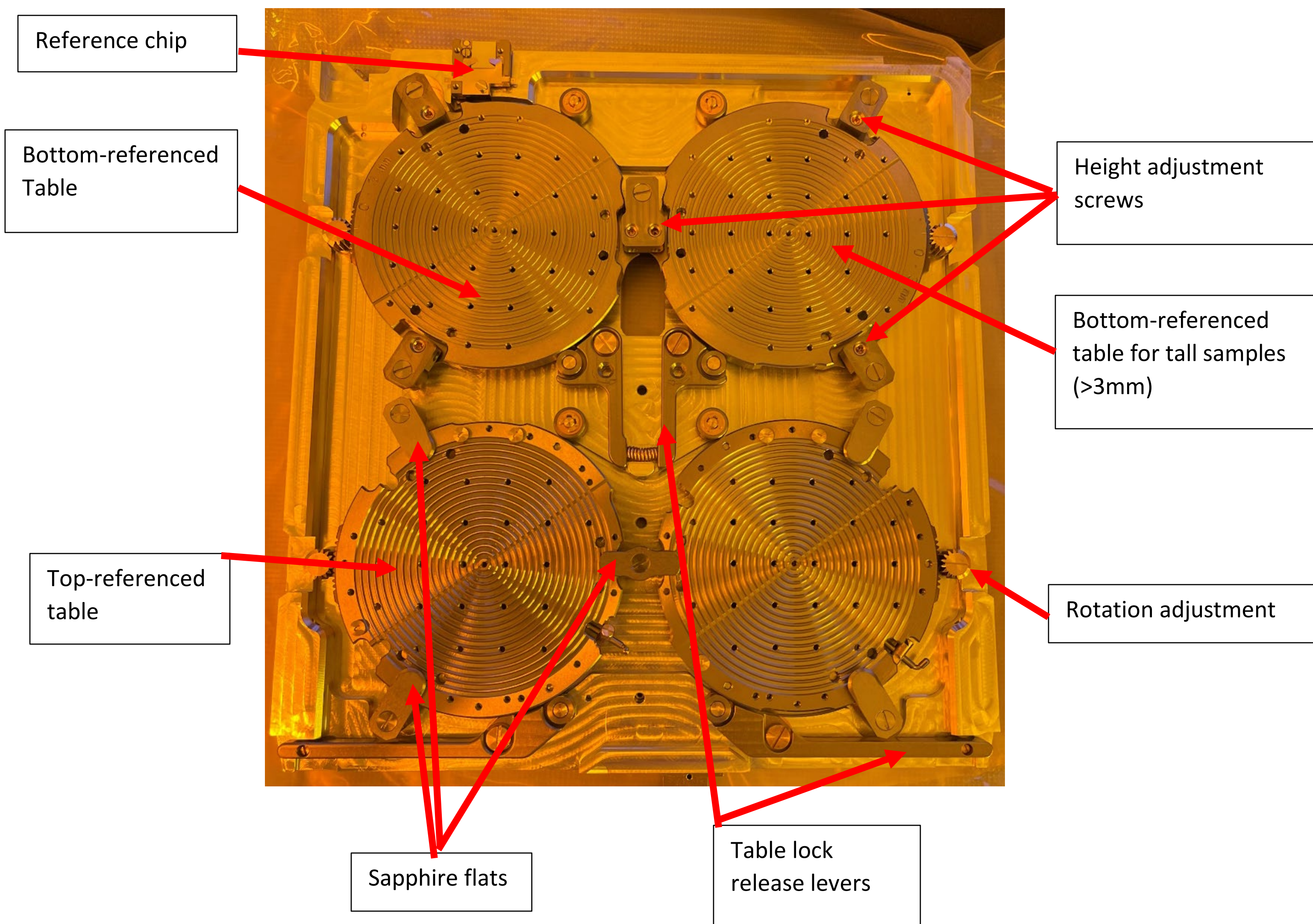


Sample Holders

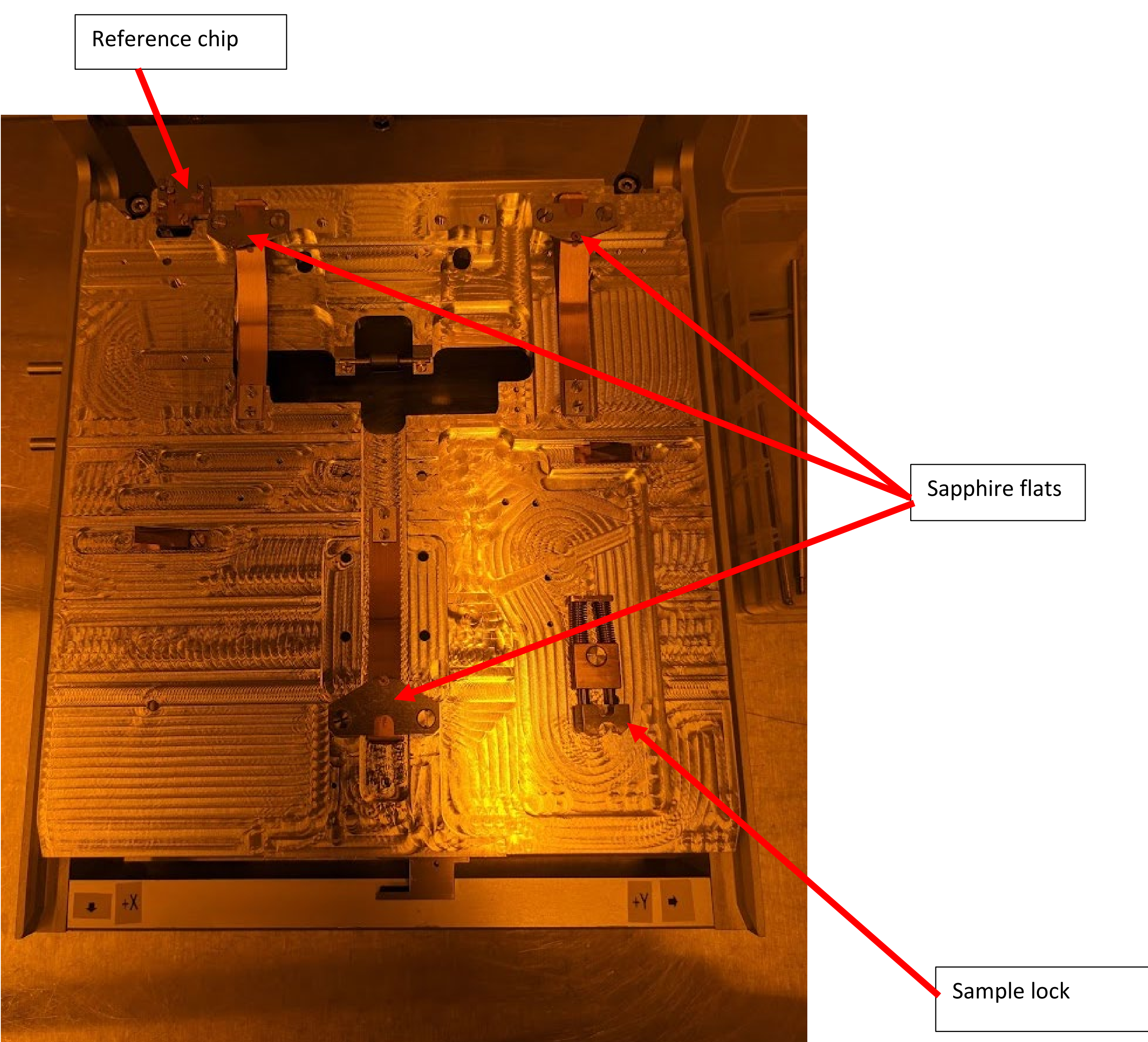
0216 – 4x3" for piece parts – Slot 3



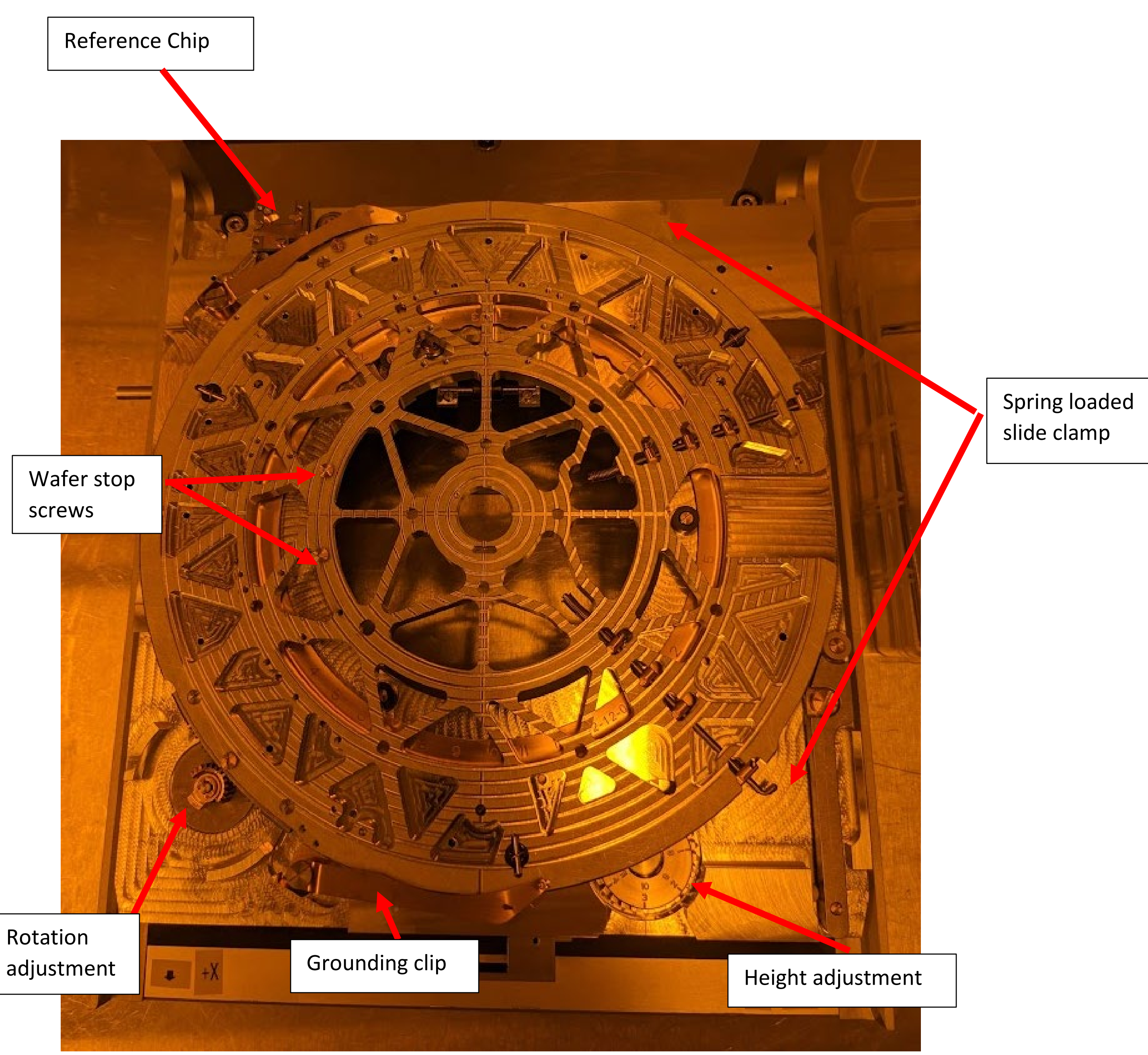
0218 – 4x3" for piece parts and tall samples – Slot 4



0088 – 6” mask holder – Slot 6



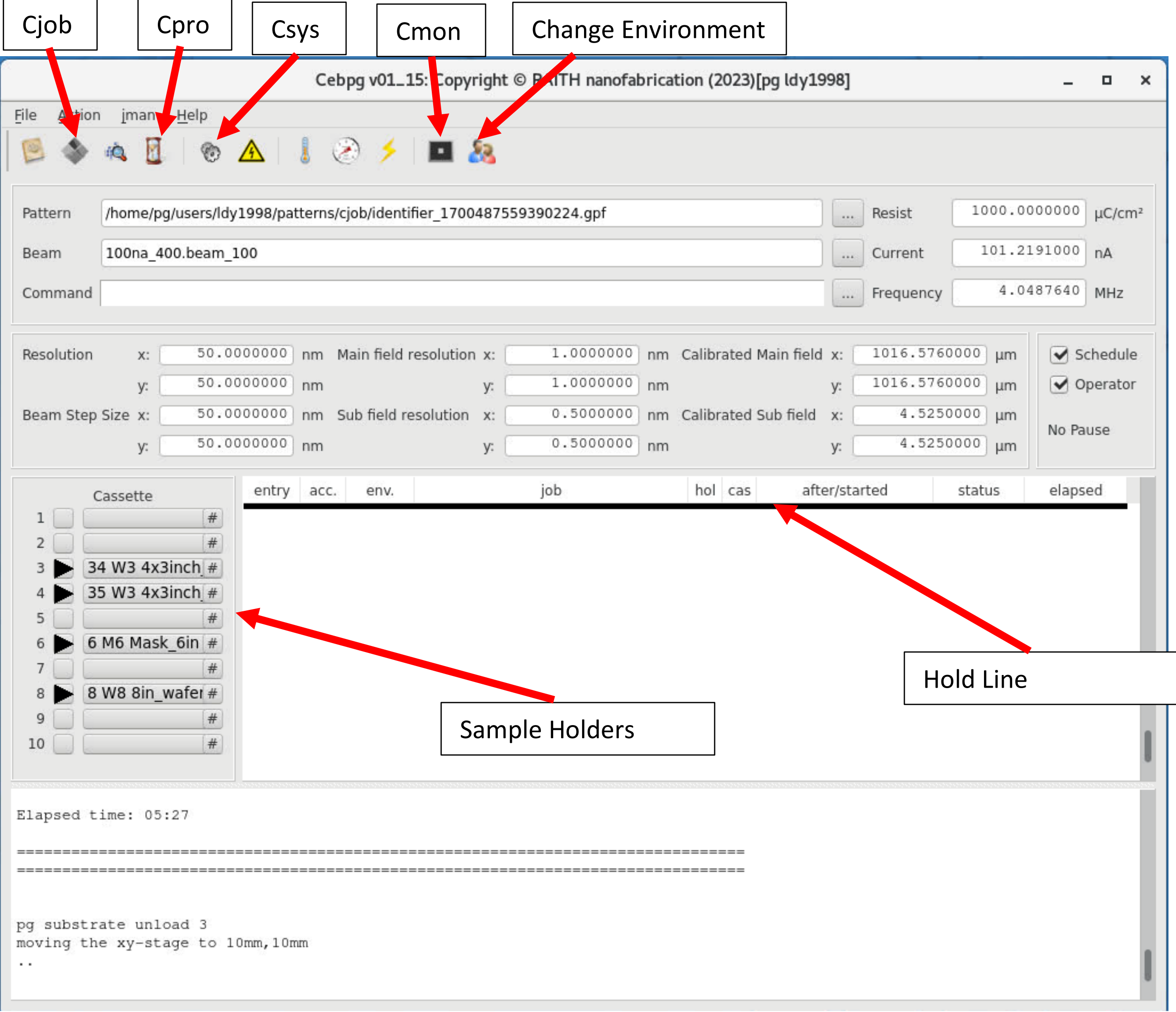
0087 – Universal wafer holder, for 4”,5”,6”,8” wafers – Slot 8



Software Overview

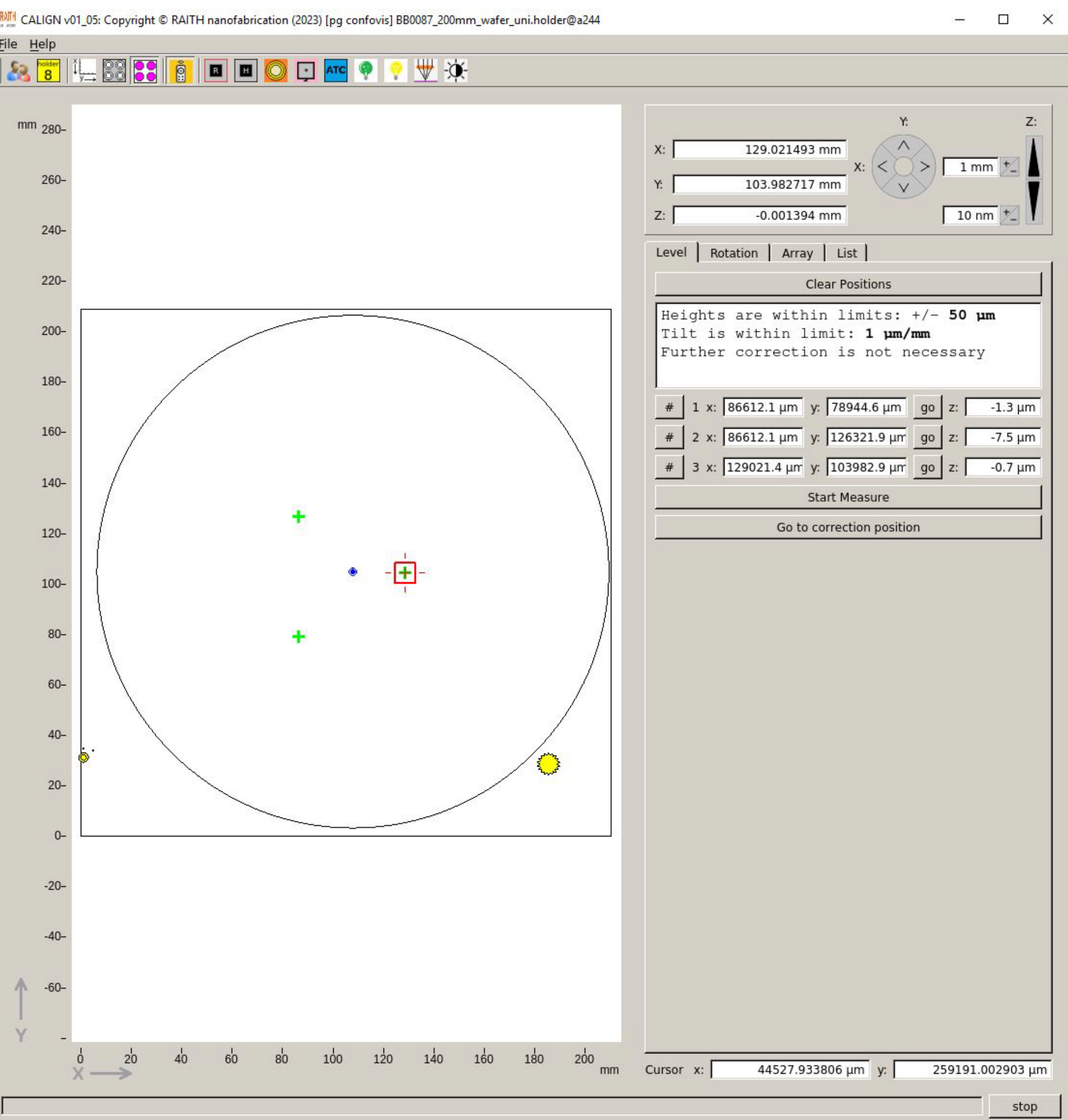
Cebpg

Cebpg is the main software to control the tool. It should always be open.



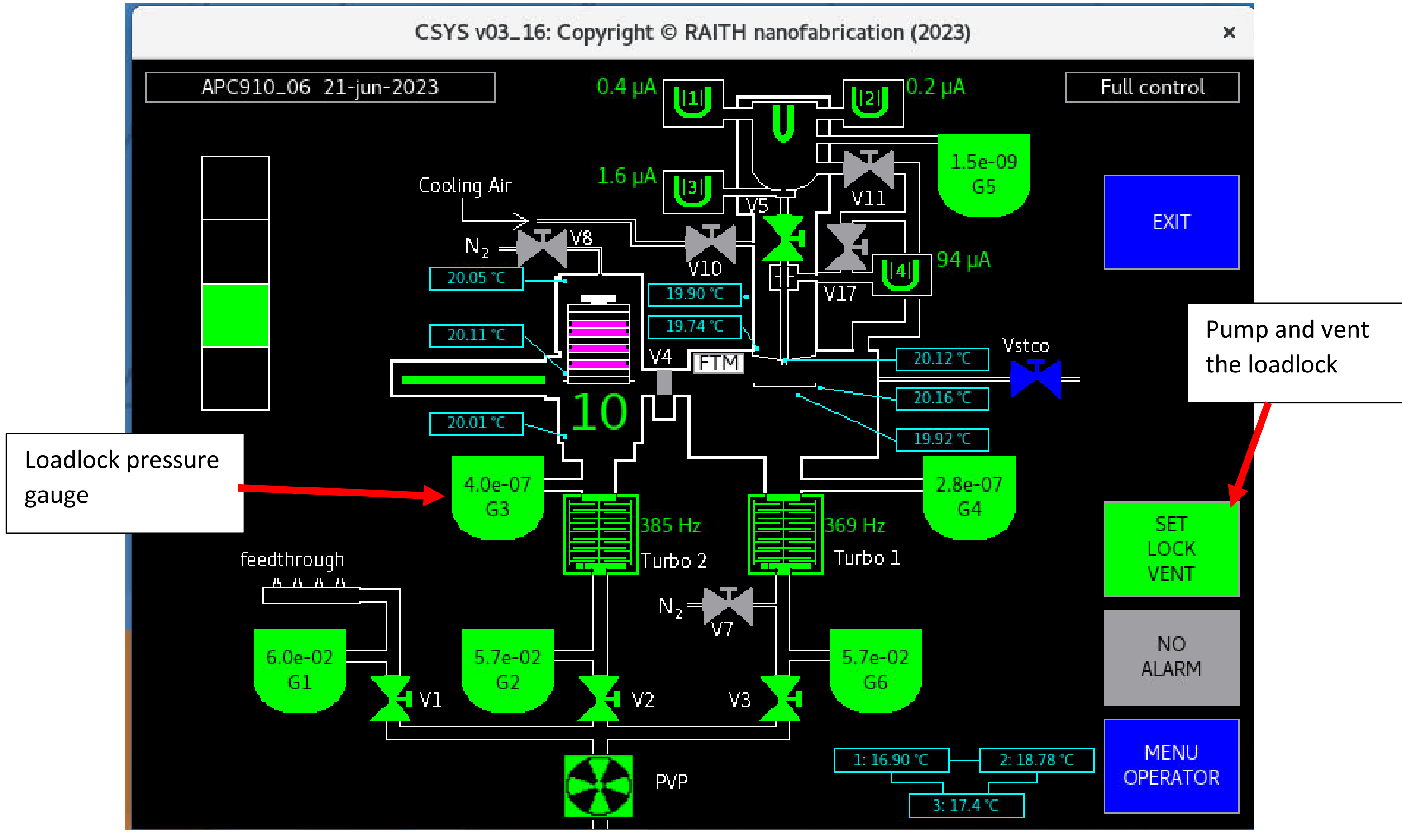
Calign

Calign is used on the prealignment microscope PC to measure and correct sample height, rotational alignment, and position



Csys

Csys should always be open. It shows an overview of the system, the vacuum status, and is where errors will appear. This is also displayed on the touchscreen, where the loadlock vacuum is controlled.



Full Procedure

Design

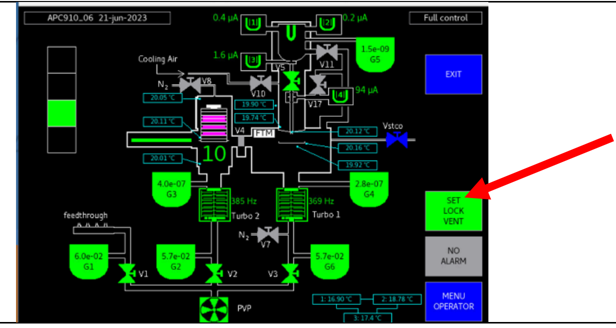
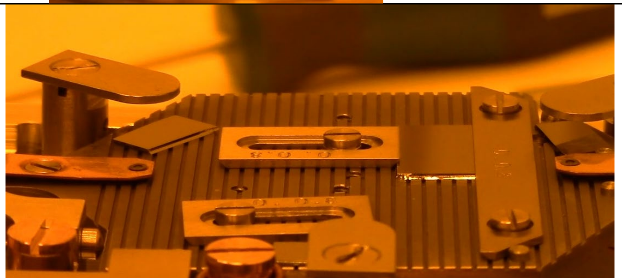
Layout files can be designed in your preferred software. LayoutEditor is provided and recommended. Designing your layout in GDS format is strongly recommended, though DXF and other formats are possible. In the EBPG, the origin will be in the center of your CAD, so designing it this way from the beginning can make things easier.

Conversion

1. GDS files must be fractured and converted to the tool readable format [GPF]. This is done in beamer. A complete Beamer tutorial is beyond the scope of this SOP, but many resources are available.
2. Decisions made at this step in the lithography process are critical to the outcome. Proper pattern prep is among the most important parts of achieving the best possible results from your lithography. Take the time to do it right. The most important steps usually happen in the Beamer export module. A few important points about the export module are mentioned below.
    a. The Beam Step Size (BSS, or shot pitch) must be chosen here. Generally, you should pick something 1/4 to 1/10 of your critical feature. Smaller BSS does not necessarily mean better writing.
    b. Even though Beamer makes the resolution the same as the BSS by default, there is no reason for this. The resolution is effectively the pattern's design grid in the tool. Your BSS should always be a multiple of your resolution. There is generally no downside to setting the resolution to 1 nm. It can be set smaller, but this limits the maximum writing field size, so it should only be done if necessary.
    c. The EBPG has a few unique fracturing and shot filling modes available in Beamer that drastically improve the fidelity of curves and circles, even with larger BSS

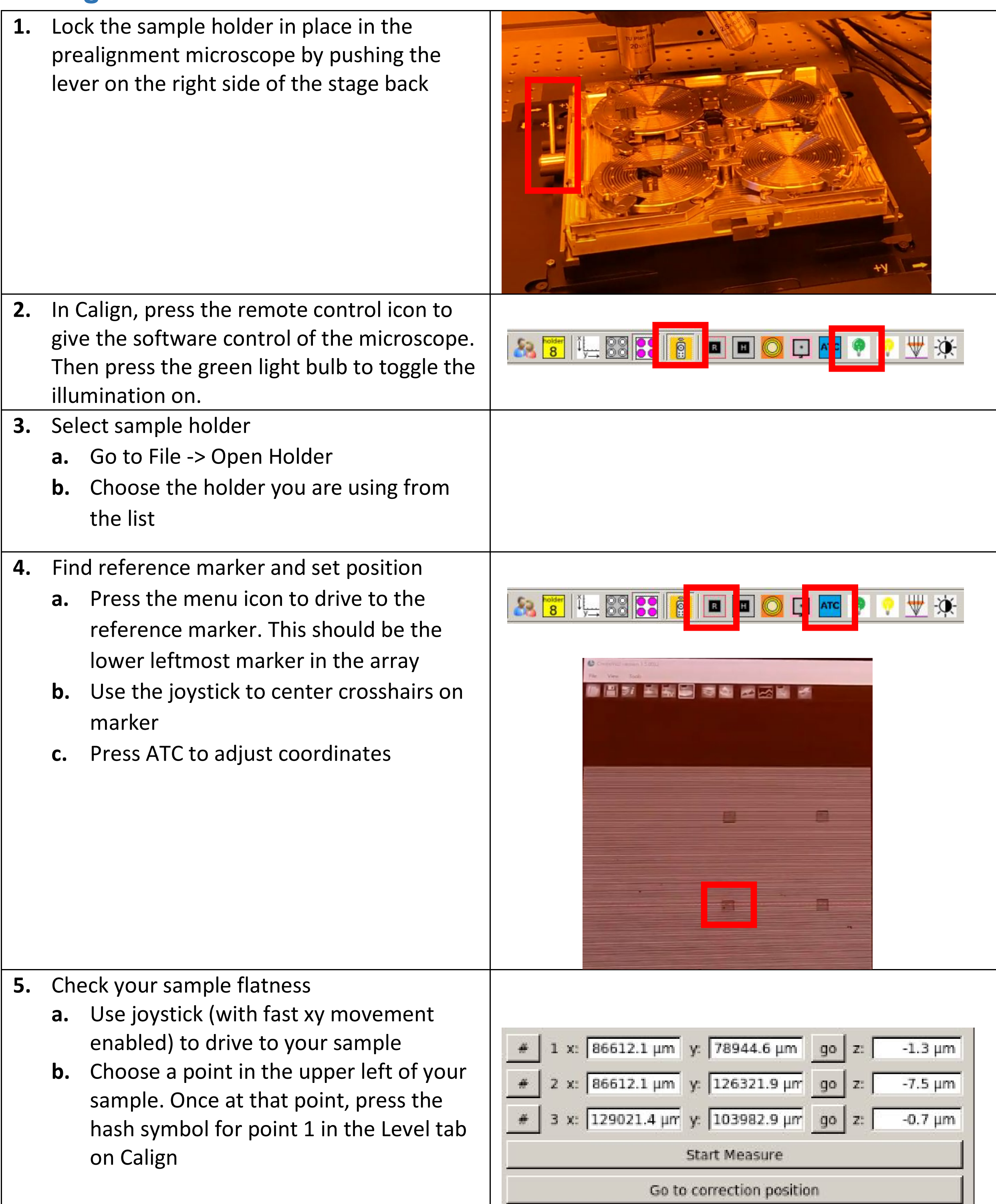
Loading a Sample

Note: There is a training video about sample loading. Please watch it.

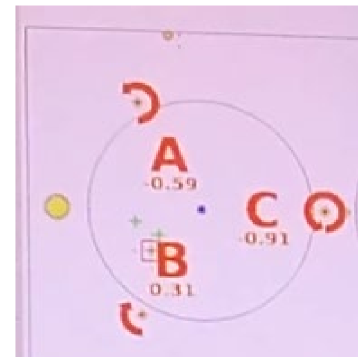
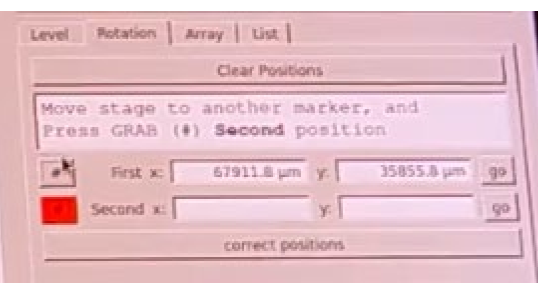
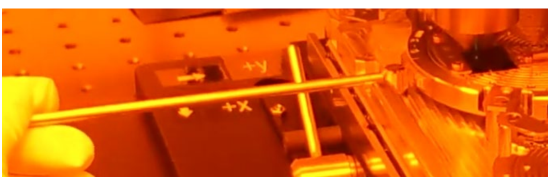
1. Enable the tool on NEMO.	
2. Make sure there is no sample holder in the main chamber, then vent the load lock by pressing “Set Lock Vent” in on the touchscreen and pressing yes on the popup prompt. Venting takes about 2 minutes, and you can hear when the load lock is ready.	
3. Open the load lock door. Carefully slide sample holder out and place it directly in loading jig. Close the load lock door. If you expect to take a long time loading your samples, pump down the load lock. **Note:** The sample holders should always be in the same slots: **#3 –** 0216 (4x3” for piece parts) **#4 –** 0218 (4x3” for piece parts) **#6 –** 0088 (6” mask holder) **#8 –** 0087 (Universal wafer holder) The following instructions are only for loading piece parts. For masks, wafers, or any other samples, additional sample specific training is required.	
4. Affix your samples using the provided clips. The clips press against the edge of your sample, they do not go on top. **a.** Pay attention to the orientation of your sample. The coordinate system is rotated 90° from what you might expect. This is labeled on the loading jig.	
5. If using piece parts in a top-referenced sample holder, place shims of the same height as your sample under the three sapphire flats	

6. Slide the sample holder out of the loading jig and into the prealignment microscope	

Prealignment

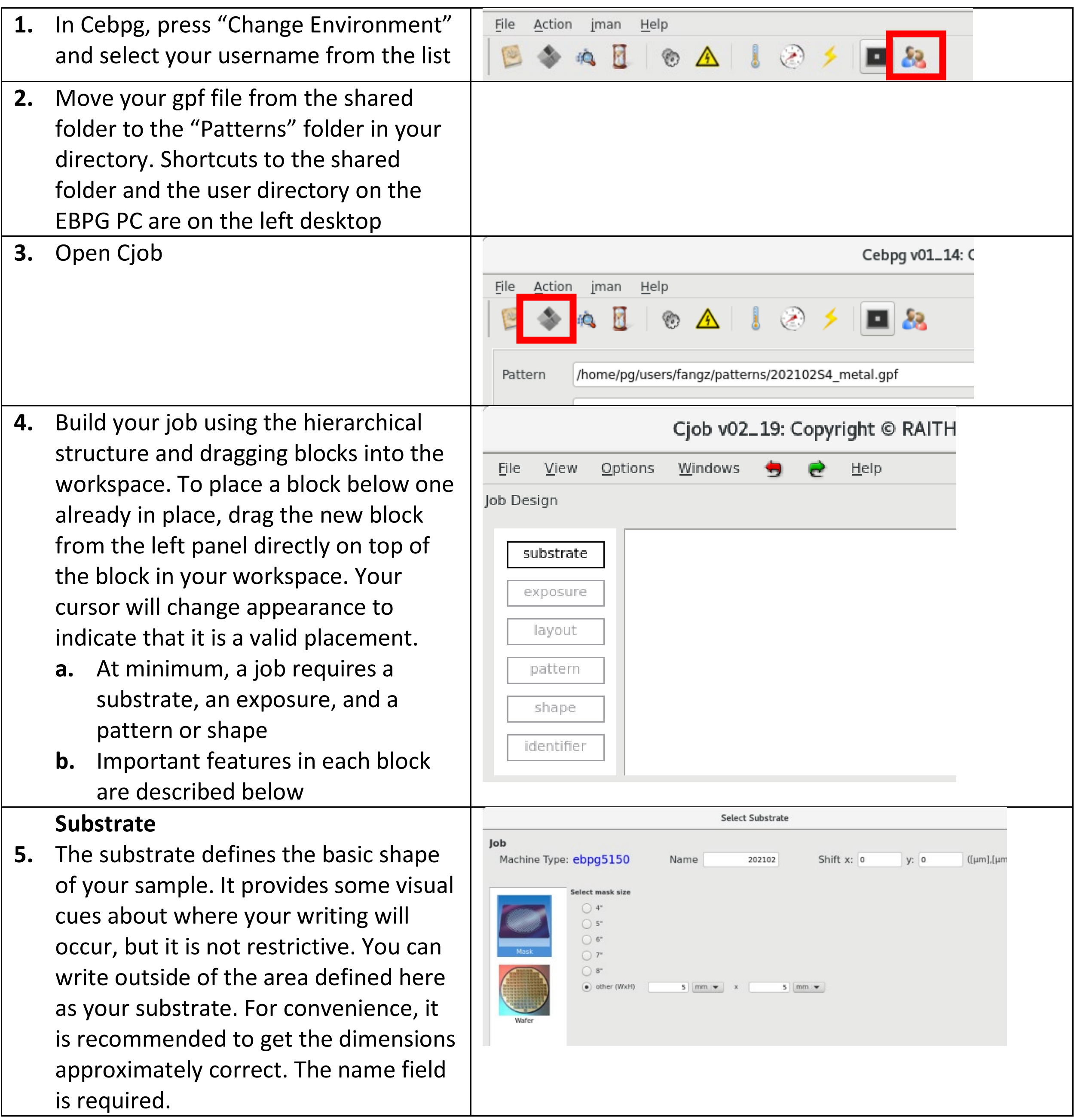


Step	
1. Lock the sample holder in place in the prealignment microscope by pushing the lever on the right side of the stage back	
2. In Calign, press the remote control icon to give the software control of the microscope. Then press the green light bulb to toggle the illumination on.	
3. Select sample holder **a.** Go to File -> Open Holder **b.** Choose the holder you are using from the list	
4. Find reference marker and set position **a.** Press the menu icon to drive to the reference marker. This should be the lower leftmost marker in the array **b.** Use the joystick to center crosshairs on marker **c.** Press ATC to adjust coordinates	
5. Check your sample flatness **a.** Use joystick (with fast xy movement enabled) to drive to your sample **b.** Choose a point in the upper left of your sample. Once at that point, press the hash symbol for point 1 in the Level tab on Calign	

c. Repeat for point 2 and 3 in the top right and bottom center of sample respectively **d.** Once all points are defined, press 'Start Measure'	
6. On a bottom-referenced table, the height and flatness can be corrected by following the on-screen instructions **a.** Go to the correction position **b.** Adjust each set screw by the amount shown on the display. **c.** Press the locking lever **d.** Remeasure flatness by pressing 'Start Measure' again. **7.** If using a top-referenced table, usually height will be in spec. If not: **a.** Make sure shims are in place (and the right size) **b.** Make sure sample is sitting flat and correctly clipped in place **c.** Make sure back side of sample is clean **d.** Remove shims and make sure they are clean on front and back **e.** If none of these work, try a bottom-referenced table	
8. If overlay alignment is required, perform rotation prealignment **a.** The rotational alignment spec is 0.2^o (= 3.5 µm/mm). Aligned writing cannot proceed if rotation is out of spec. **b.** Select the 'Rotation' tab in Calign **c.** Center microscope on first alignment mark and press the hash symbol next to 'First'. **d.** Drive to second mark (the two marks must be at the same x or y position in your design). Press the hash symbol **e.** Press 'Correct Positions' **f.** The software will instruct you to drive to one of the mark positions. Use the 'go' button next to the position **g.** The software will instruct you on turning the rotation bolt. Follow the instructions to use the rotation correction tool to	 

turn the bolt until the marker moves back to the center of the crosshairs	
9. Measure a reference position on your sample. For aligned writes, this is typically one known alignment mark. For unaligned writes, it is generally where you want the center of your pattern to be. **a.** Drive to desired position. Record X and Y coordinate from Calign software.	X: 129.021493 mm Y: 103.982717 mm Z: -0.001394 mm
10. Load your sample into the tool **a.** Open the load lock door **b.** Unlock holder from microscope stage **c.** Slide holder into the correct spot in the load lock and close door **d.** Press "Set lock vacuum" on touchscreen **e.** Pumpdown usually takes ~5 minutes, depending on how long the loadlock was at atmospheric pressure	
11. Turn off the microscope illumination in Calign, and press the remote icon to turn off remote control	

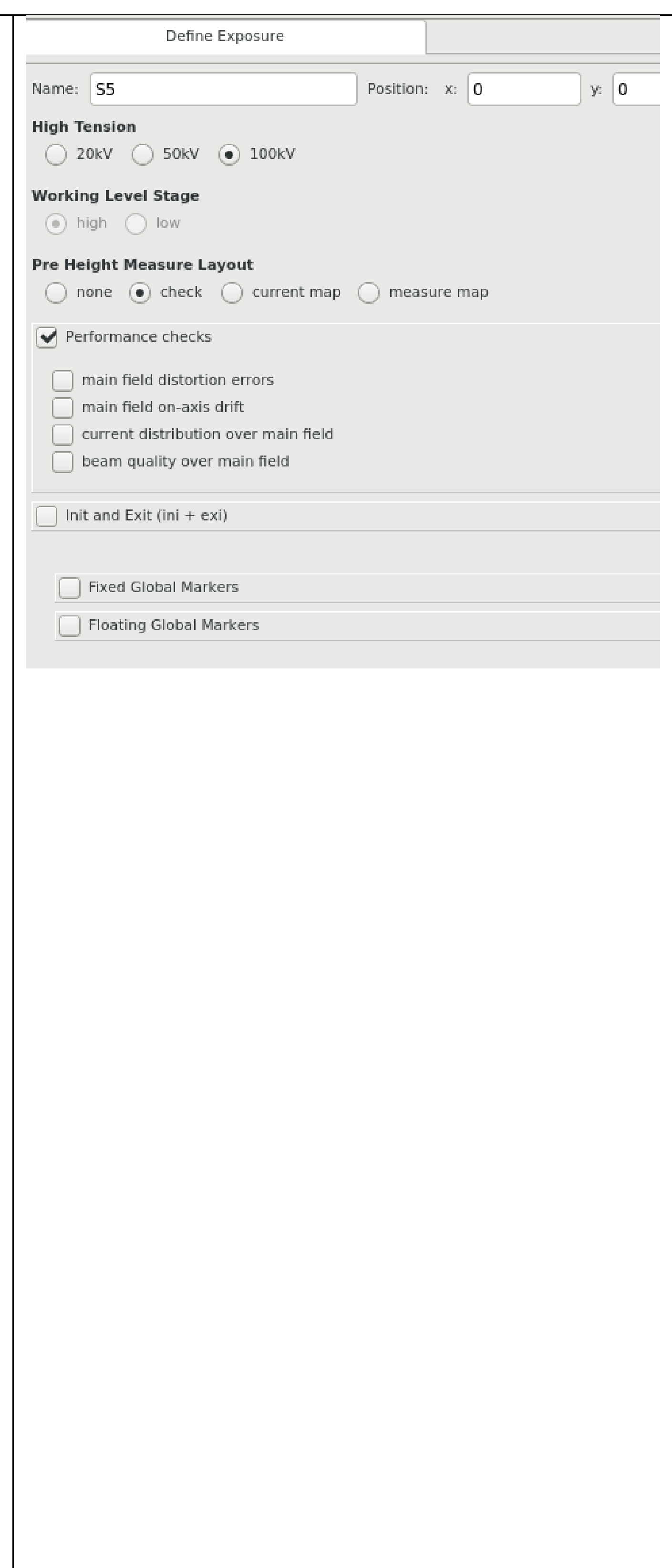
Job Creation



Step	
1. In Cebpg, press "Change Environment" and select your username from the list	
2. Move your gpf file from the shared folder to the "Patterns" folder in your directory. Shortcuts to the shared folder and the user directory on the EBPG PC are on the left desktop	
3. Open Cjob	
4. Build your job using the hierarchical structure and dragging blocks into the workspace. To place a block below one already in place, drag the new block from the left panel directly on top of the block in your workspace. Your cursor will change appearance to indicate that it is a valid placement. **a.** At minimum, a job requires a substrate, an exposure, and a pattern or shape **b.** Important features in each block are described below	
Substrate **5.** The substrate defines the basic shape of your sample. It provides some visual cues about where your writing will occur, but it is not restrictive. You can write outside of the area defined here as your substrate. For convenience, it is recommended to get the dimensions approximately correct. The name field is required.	

Exposure

6. An exposure is a single file sent to the tool containing instructions on what and how to write. A single exposure can contain multiple patterns with different writing conditions (BSS, current, etc) as long as they are to be written at the same time. A job must have at least one exposure, and it can have multiple exposures (e.g. for the different steps of a multistep pattern).
   a. The Pre Height Measure Layout selection is critical. It defines how the tool will manage the sample height during the exposure.
      i. The default 'check' means that the tool will do a quick precheck of the expected write area. If any point in the precheck is either out of range or unmeasurable, the write will immediately fail. After the precheck, it will also check the height and adjust at every field in your pattern. If your sample is reflective and you are not writing within 1-2 mm of the edge of your chip, this is recommended.
      ii. 'None' skips the precheck, but still checks the height at every field. By default, even if it cannot get a good measurement at a field, it will continue to write. This works when you are confident that the height is measurable in all critical areas, but the precheck might fail, for instance because the extents of your gpf file go off of your chip. If your height is out of spec, using this mode will result in very poor patterning.



iii. 'Current map' uses a predefined height map, which is created manually, and does not measure the height at all. This is used when the height is not measurable everywhere you need to write, but there are measurable areas. The height at the unmeasurable areas is calculated by fitting the measurable points to an equation. This mode is commonly used when patterns (or markers) are very close to the edge of the chip, where the laser cannot measure. The procedure for manually defining a height map is in Appendix A. iv. 'Measure map' is generally not recommended. It will not fail even when there are obvious problems that ruin your patterning. **b.** 'Fixed global markers' are used to define markers for aligned writes. The procedure is covered in Appendix B.	

Layout

7. A layout is used to create an array of patterns, and can be used to perform dose testing by varying the dose in each element of the array. Layouts are not required unless arraying of patterns is desired.
    - **a.** Count sets the number of repetitions in each direction
    - **b.** It is preferred to set the center to center spacing of the patterns with dx and dy, not x and y
    - **c.** Dose update can be done with an additive absolute dose, or with a multiplicative factor. Subtracting or dividing is not recommended.

Pattern

8. Each pattern has a single gpf file and associated writing parameters. Multiple patterns with different writing parameters can exist within a single exposure or layout. The position field can be used to apply an offset to the location of the pattern. This is useful, but be cautious with it.

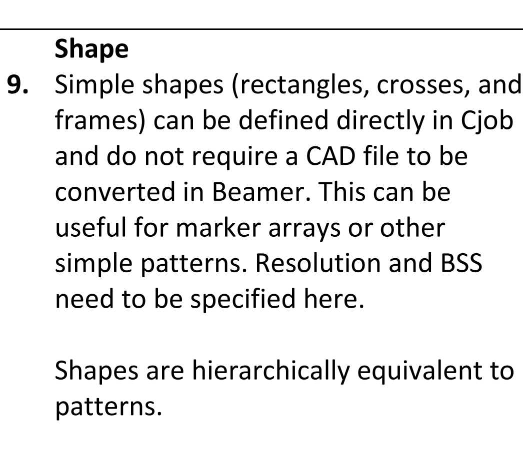
    Beam current and aperture are selected here. Keep in mind that beam parameters and BSS (chosen in Beamer) are closely interrelated, so these should already have been decided upon during the design phase.

    Patterns can be placed directly under exposures or within layouts in the job design.

Shape

9. Simple shapes (rectangles, crosses, and frames) can be defined directly in Cjob and do not require a CAD file to be converted in Beamer. This can be useful for marker arrays or other simple patterns. Resolution and BSS need to be specified here.

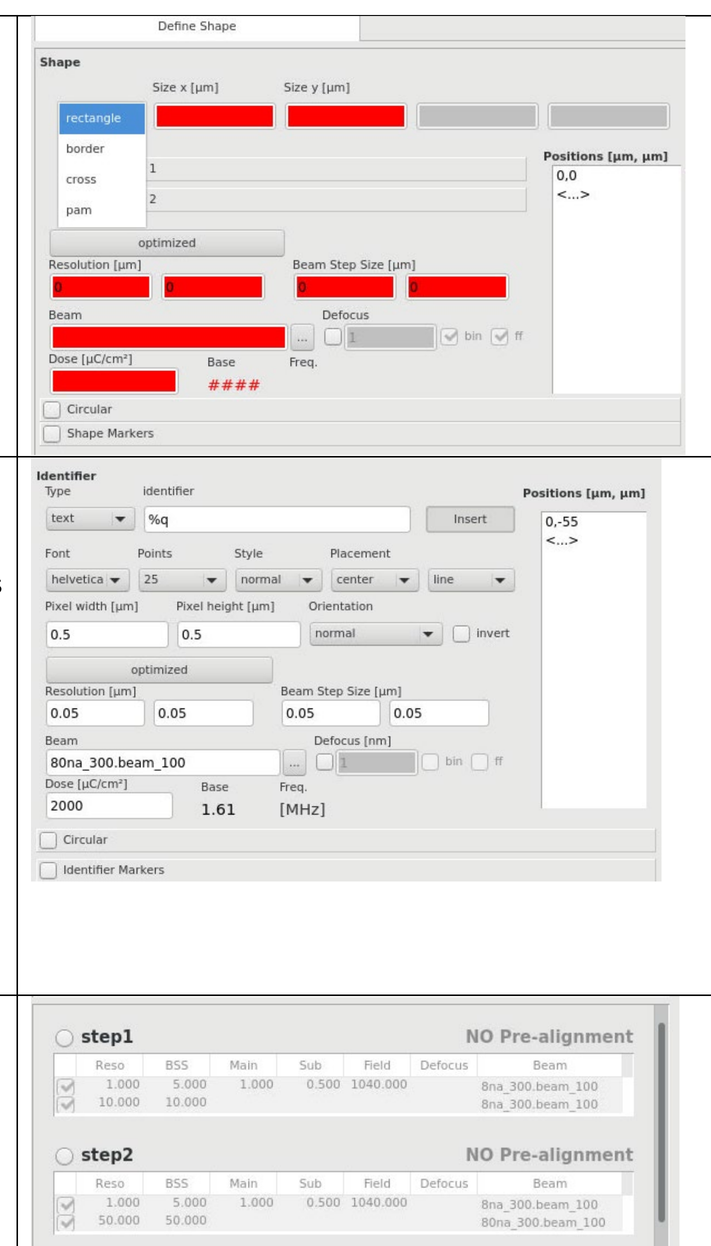
Shapes are hierarchically equivalent to patterns.



Identifier

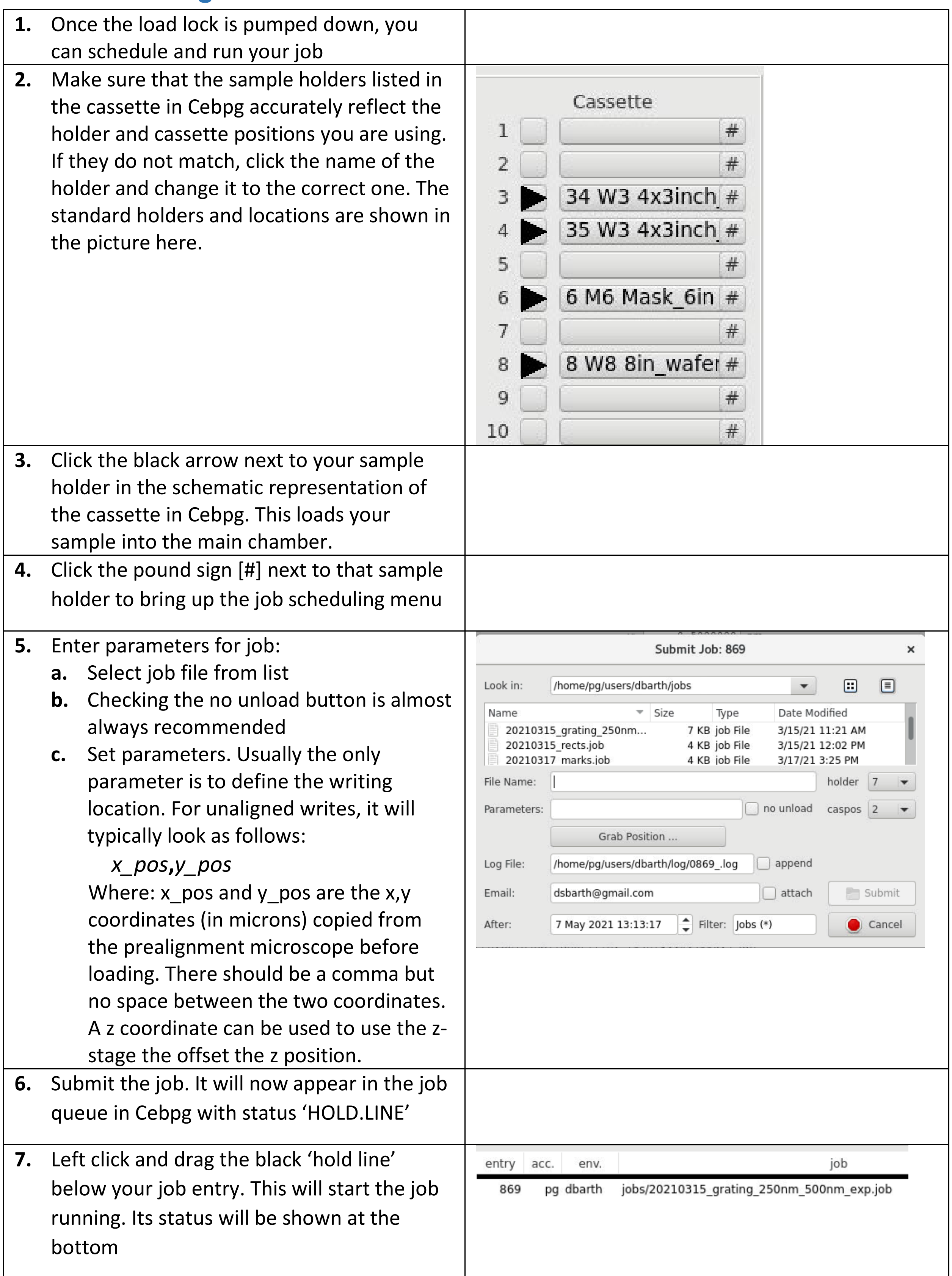
10. cJob can dynamically generate patterns with text and numbers to label your data. Most commonly, this is used to label a dose array with the dose of each element. It can also be use to add numbers to marker arrays or text labels. The insert button contains a list of commonly used identifiers.

Identifiers fall below patterns hierarchically, so they should be placed under patterns in the job design.



11. Once job creation is finished and the preview accurately reflects the desired writing, the job should be exported. At this time, the software can also estimate the writing time for the job. Each exposure in the design is exported separately. A preview of the contents of each exposure can be seen on clicking the associated radio button.

Job Scheduling



Step	
1. Once the load lock is pumped down, you can schedule and run your job	
2. Make sure that the sample holders listed in the cassette in Cebpg accurately reflect the holder and cassette positions you are using. If they do not match, click the name of the holder and change it to the correct one. The standard holders and locations are shown in the picture here.	
3. Click the black arrow next to your sample holder in the schematic representation of the cassette in Cebpg. This loads your sample into the main chamber.	
4. Click the pound sign [#] next to that sample holder to bring up the job scheduling menu	
5. Enter parameters for job: **a.** Select job file from list **b.** Checking the no unload button is almost always recommended **c.** Set parameters. Usually the only parameter is to define the writing location. For unaligned writes, it will typically look as follows: *x_pos,y_pos* Where: x_pos and y_pos are the x,y coordinates (in microns) copied from the prealignment microscope before loading. There should be a comma but no space between the two coordinates. A z coordinate can be used to use the z-stage the offset the z position.	
6. Submit the job. It will now appear in the job queue in Cebpg with status 'HOLD.LINE'	
7. Left click and drag the black 'hold line' below your job entry. This will start the job running. Its status will be shown at the bottom	

Unloading your Sample

1. When the job finishes, unload the sample holder from the chamber, vent the load lock, and unload your sample.	
2. Refasten all clips, make sure all shims are removed and tables are fully raised, load sample holder back into load lock, and pump down load lock.	
3. Close all software except for Cebpg and Csys	
4. Disable the tool in NEMO	

Appendices

Appendix A: Manual Height Mapping

When automatic height mapping and measurement cannot be used because of the specifics of a sample, manual mapping is required. This is usually done by using the laser height sensor to map height of the writing area and then using that to interpolate the height at each field. If, for example because of a transparent sample, the laser height sensor cannot be used at all, the tool can measure height by finding alignment marks at various offsets and make the height map by measuring multiple marks this way. Both procedures will be explained.

Successful application of either of these techniques require a good knowledge of the location and features of the sample when it is loaded into the tool. Make sure you understand your sample before it is in the tool, or you will likely have to take it out and try again.

Note: For terminal commands below, **Bold** text should be entered exactly as is, and *italicized* text indicates that a specific value needs to be substituted

1. During job creation, in the exposure settings, select 'current map' as the Pre Height Measure Layout	Name: exp Position: x: 0 High Tension 20kV 50kV 100kV Working Level Stage high low Pre Height Measure Layout none check current map measure map
2. Load the sample holder into the chamber once load lock is pumped down	
3. Open a terminal by right clicking on the desktop and selecting 'open terminal'	
4. Open the SEM control software, Cmon	
5. Switch to your environment in the terminal	**ce** *username*
6. Do initial stage calibration: **a.** Find the sample holder marker **b.** Perform transform to adjust for offset in marker location **c.** Drive to faraday cup and measure current	 **mvm** **atc** **mcur**
7. Drive to reference position on your sample. A known location such as an alignment marker in the bottom left corner of your sample is preferred. The coordinates should have been obtained from the prealignment microscope, and they should be entered in microns	**pg move pos** *x_pos,y_pos*
8. If using the laser height sensor, attempt a height measurement.	**mpgm height**

a. If the height cannot be measured at that position, usually this means that the position is too close to the edge of the sample. Use the step buttons in Cmon to move in towards the center of your sample, ~500 µm at a time, each time measuring the height as above. When you get a successful measurement, this is a good place to start your height map.	
9. If using marker based height measurement, turn on the SEM image and find your first marker manually. When you are centered on the marker, turn off the SEM and have the tool do a marker search at the current location	**mvm --rel 0,0** *markertype*
10. When you have found a suitable location for the start of your height map using one of the two methods above, get the current stage position	**mpg tab**
11. Choose the size and spacing of points to measure in your height map. This depends entirely on your sample, but should encompass as much of the writing area as possible. For the marker method, each point must be at a marker on the sample	
12. Run the height mapping command **a.** For laser mapping: Where: i. start_x and start_y are the absolute stage coordinates in µm of the position to start the height map (determined in step 10) ii. step_x and step_y are the distance between measured points in µm iii. num_x and num_y are the number of points in the array in each direction iv. An order of 1 means that a linear fit is used on the measurements to interpolate the height. Other	**pg measure height arraymap** *start_x,start_y step_x,step_y num_x,num_y* **--order=1**

orders can be used, but for small chips, a linear fit is usually best. Note: It is possible, and often more convenient to enter these values in mm instead of µm. This can be done by specifying the units in the command (e.g. 3mm,3mm instead of 3000,3000) **b.** For marker mapping:	**pg measure height arraymap** *start_x,start_y step_x,step_y num_x,num_y* **--order=1 --marker=***markertype*
13. Check the height map. Make sure there are no bad points and the numbers seem reasonable.	**pg info measure height map**

Appendix B: Overlay Alignment

Overlay alignment can be performed at all levels of the job hierarchy. If any overlay alignment is to be done, exposure level (global) alignment is required. All others are optional. Pattern level alignment is often used. Layout, shape, and identifier alignment is rare, but works the same way.

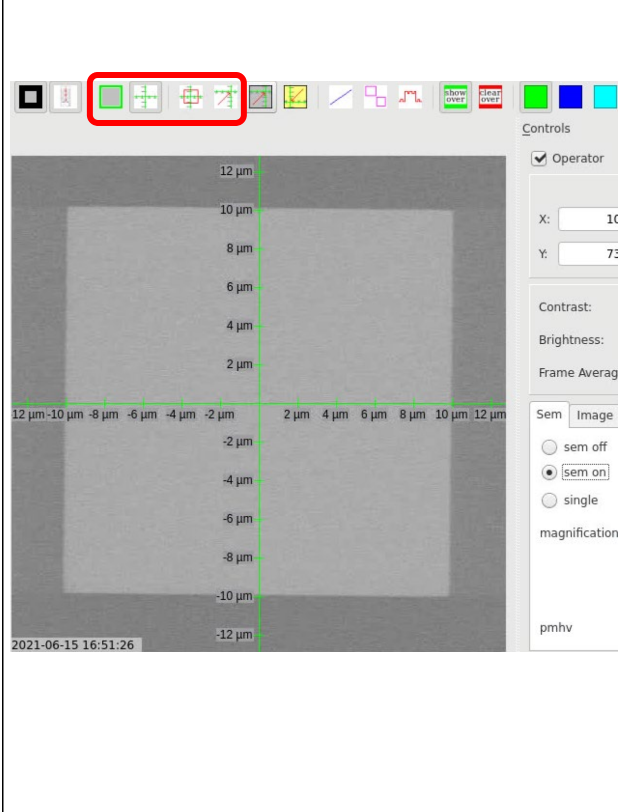
Note: For terminal commands below, **bold** text should be entered exactly as is, and *italicized* text indicates that a specific value needs to be substituted

1. Define alignment marks in Cjob. Mark positions are in relative coordinates, so a thorough understanding of the coordinate system is necessary. The Cjob preview window is very helpful for this. If pattern level marks are being used, it is easier to define them first. Otherwise, skip to step 2 for exposure level marks.	
2. Define exposure level marks	
3. Define prealignment mark (optional but highly recommended)	
4. Open a terminal window by right clicking on the desktop and selecting "open terminal"	
5. Switch to your environment in the terminal	
6. Do initial stage calibration: **a.** Find the sample holder marker **b.** Perform transform to adjust for offset in marker location **7.** Drive to faraday cup and measure current	 **mvm** **atc** **mcur**
8. Drive to your first global marker (or your prealignment marker) using the coordinates recorded from the prealignment microscope.	**pg move pos** *x_pos,y_pos*

9. Turn on SEM in Cmon and find your marker. Double click on the SEM image to position your beam directly over the marker	
10. If using automatic marker search, find the marker using the automatic search. If the markers cannot be found automatically by the tool, it can sometimes be possible to change the marker search settings to enable automatic mark finding. If you encounter this, discuss with staff. More often, the size is not correct or the sharpness at the edges is insufficient. In this case, manual mark finding must be used. The marker type in Cjob should be changed to 'manual'.	**mvm --rel 0,0** *markertype*
11. Get the marker position	**mpg tab**
12. If prealignment marker is not used, repeat steps 8-11 for each global marker	
13. Schedule the job. The position of the prealignment mark (or all global marks in order) should go in the parameters section.	
14. Run the job. For automatic mark finding, no further input is necessary	

15. For manual mark finding, a prompt will appear in the info area at the bottom of Cebpg. Follow the prompt:

- **a.** Turn on the SEM. The marker should be in or near the field of view.
- **b.** Use SEM crosshairs and the 'move to crosshairs' button in Cmon to center the marker.
  - i. Instead of the crosshairs, the 'mark' overlay can also be used. Right clicking allows different defined marks to be selected
- **c.** Turn off the SEM
- **d.** Click on the bottom line in Cebpg, where the prompt is, and press enter.
- **e.** Repeat for each mark. If any mark cannot be seen, the job should be cancelled. Depending on the mark material, it can be necessary to adjust the brightness, contrast, and PMHV



Appendix C: Cold Development

Cold development can improve resolution, contrast, and line edge roughness of positive resists (especially PMMA and ZEP) at the expense of sensitivity. A cold development tank is set up in the Nano-Process hood for this purpose. This consists of a thermoelectric cold plate with an aluminum bead bath on top of it. The cold plate is set at -10° C. To develop using the cold tank, the development solution should be prepared in a beaker about 10 minutes in advance of development. The beaker should then be placed into the bead bath, making sure the beads cover the solution, and left to cool.

Note: do not leave the bead bath uncovered for more than a few minutes, as condensation can contaminate your development solution and make the bead bath difficult to use.

Once the developer solution is cool, place your sample in the solution for the desired amount of time (usually 30 to 120 seconds) remove the sample and rinse into a second beaker (usually with IPA). All liquid waste from this process should be poured into the solvent carboy cupsink in the Nano-Process hood.

Note: MIBK-IPA is no longer considered the standard recommended developer for PMMA. IPA:Water (3:1) gives superior contrast, resolution, and line edge roughness and is now considered the standard.

Version history

Draft	*Date*	*Author*	*Notes on changes*
v.1.0.0	11/22/2023	David Barth	First Draft
v.1.0.1	5/7/2024	David Barth	Minor Corrections