Süss MA6Gen3 – Assisted Alignment

Version of 2024-11-22.

1. Introduction

This document illustrates "assisted alignment" on the Süss MA6Gen3.

Users should already be trained on the Ma6Gen3 for standard manual alignment before reading further.

The alignment marks:

a) enable to align in x-axis, y-axis, and if used as a pair, also for theta,
b) their vernier structures covering four ranges (50, 100, 200, 500nm) allow to align independently of process linewidth bias, and indicate alignment at contact & after development,
c) fit within the field of vision of the microscope objective 10x (x=800um y=1100um).

The recognition software detects alignment mark patterns on the mask and on the substrate. Both patterns must before handedly and separately be trained. Once this is done, upon aligning, the software simultaneously recognizes the marks, and shows in real-time the offsets between centers of the two markers in x-axis, y-axis, theta-rotation, for both the left and the right microscope. While aligning by moving the substrate via the joystick relative to the mask, the offset or misalignment reading is continuously updated, and thanks to this real-time feedback, allows to reach a highly accurate alignment, i.e. **"assisted alignment".**

2. Alignment marker templates

For optimal image recognition/processing, CMi recommends to use simple geometrical shapes such as **square/square**, **circle/circle** and **cross/cross** structures. Adding verniers/nonius scales give additional sub-resolution alignment feedback.

If you design yourself alignment markers, consider that the recognition software works on contrast gradients, therefore put a gap between the two markers so that contrast curves don't overlap.

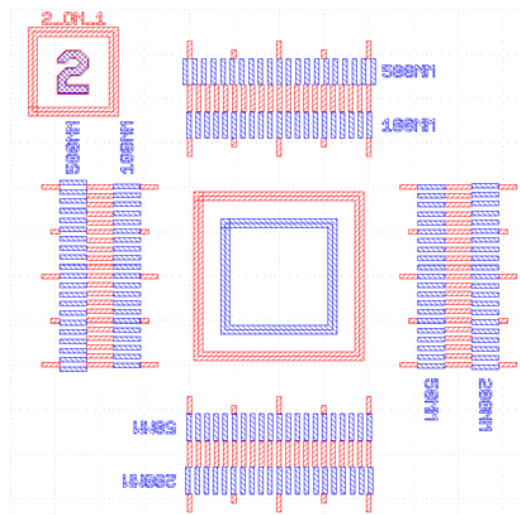The following guide shows an example of square inside square layout, with a gap maker:

Figure 1: inner square mark 2 aligned to outer square mark 1.

The two layers shown separated in Figure 2 & fig Figure 3. The bigger square is patterned on the substrate during "first exposure", the smaller square is on the mask during allowing for "alignment exposure.
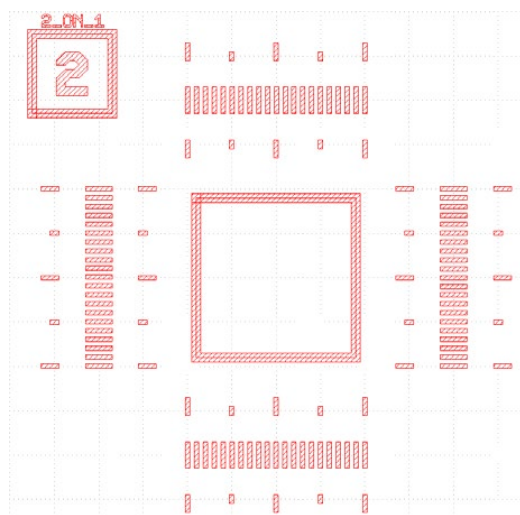

Figure 2: red outer square mark 1, patterned on substrate.

There are 8 Verniers, 4 for each axis, spanning four ranges, Vernier 50nm reaches up to 500nm in either direction, same 10x for 100, 200, 500nm.
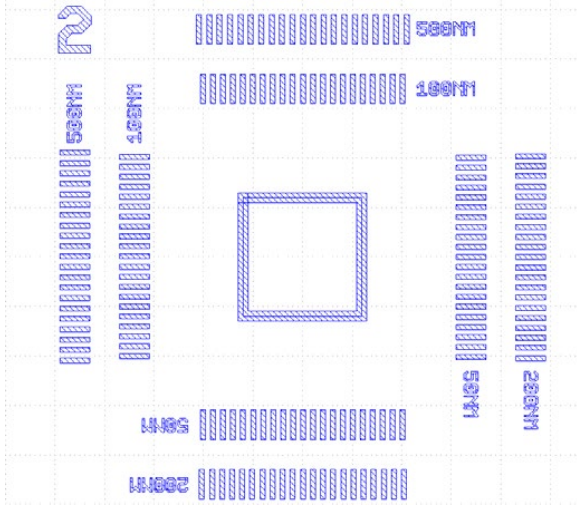

Figure 3: blue inner square mark 2, mask to be aligned

NB: The "inner square mark 2" of Figure 3, must be inverted, as shown in Figure 4, so that the substrate is visible through the mask during alignment. Blue is the digitized data. When exposed in positive photoresist it develops away, and in Cr etch is removed from the mask and allows to peek through the glass onto the substrate.
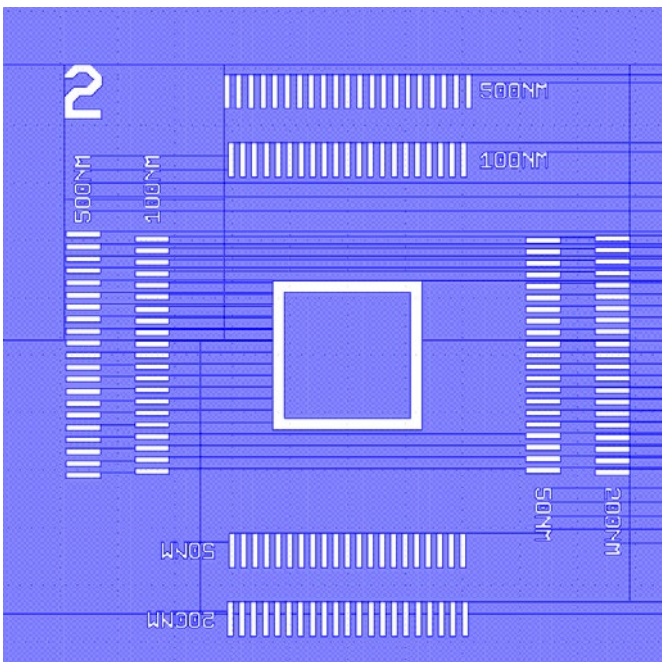

Figure 4: blue square mark 2 inverted, so that substrate is visible during alignment, blue = exposed = Cr etched away from mask.

On the mask aligner, the user interface

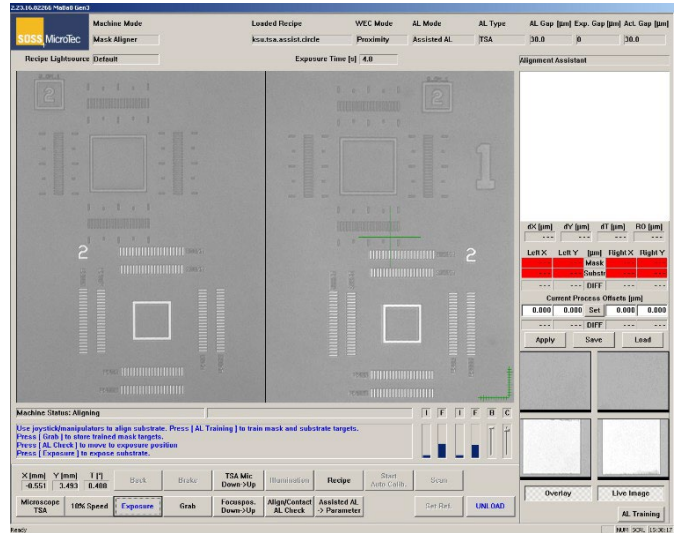presents itself as follows in Figure 5 MA6Gen3 full screen for square marks.

Figure 5: MA6Gen3 full screen for square marks.

A typical detail of what the microscope shows is in Figure 6, where the structured substrate appears as a dark big square, such as after pattern transfer into SiO2, and the mask appears as a bright small square, with its Chrome reflecting a lot of light.
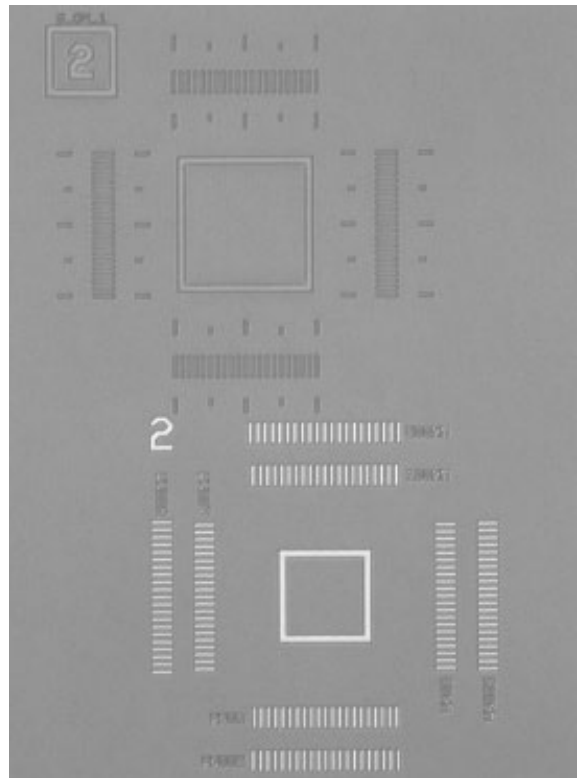

Figure 6: White zones with small square and dual verniers (bottom half) are the markers of the mask of the 2nd layer lithography. They are to be superimposed / overlaid with the less bright marks of the pattern on mask 1, with a bigger square and a single vernier (top half).

Note that the classical cross & squares layout design found in some of CMi templates (see Figure 7) may cause problems for pattern recognition, as it is designed for "by eye" alignment, and in a machine environment. The touching cross features create overlapping contrast gradients, which are difficult to handle by the recognition algorithm.
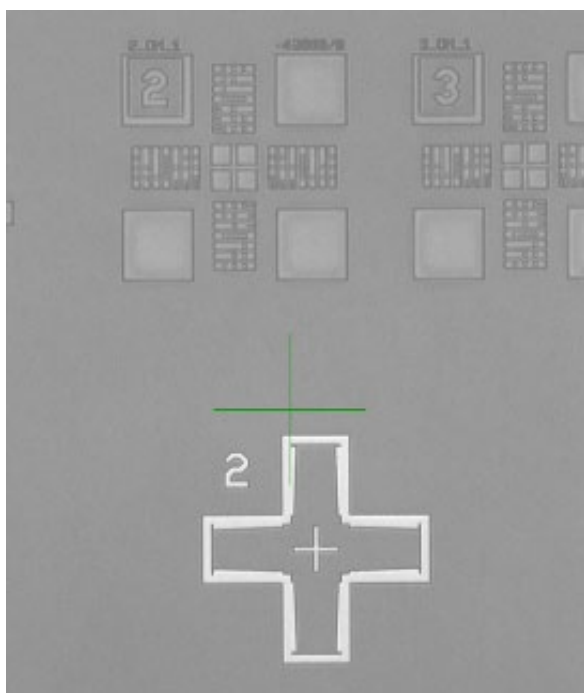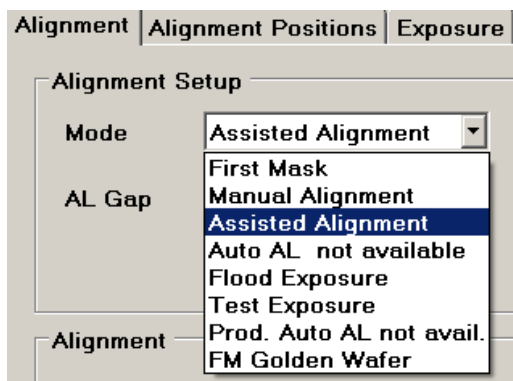

Figure 7: Classical cross and square not compatible with pattern recognition

3. Target training

You will first train your exposure recipe to use the alignment marks, then use them.

In the recipe editor, tab Alignment, field Alignment Setup, select: Mode "Assisted alignment".

Load your mask, then start by positioning your mask features (e.g. small squares) near center of both microscopes (ocular/screen) as Figure 8.
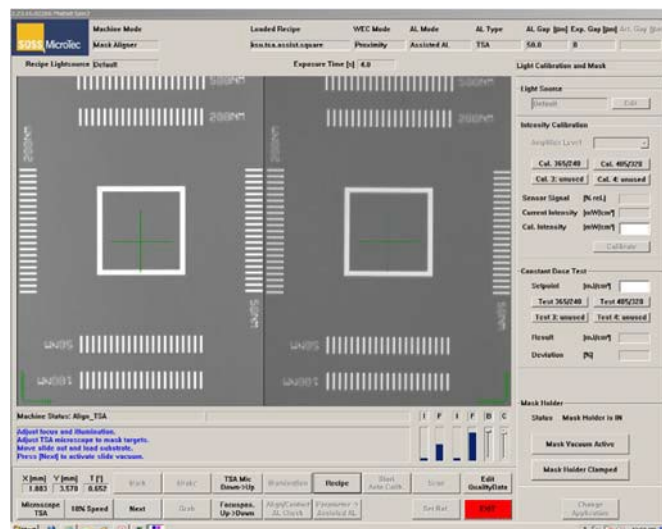

Figure 8: Start by finding marks on mask.

Then insert the substrate, and move it also into the field of vision. This is not an alignment, this is getting them to be at arm's length, see Figure 9.
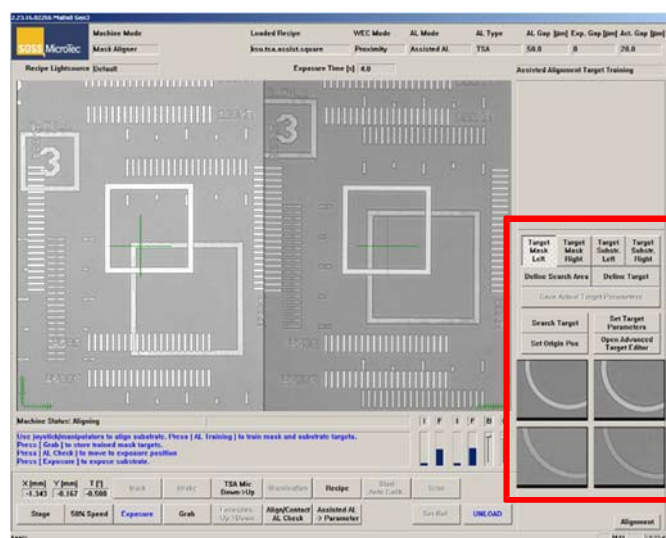

Figure 9: After loading substrate, trained targets are from recipe "circles", therefore inadequate and to be retrained.

As you train mask/substrate targets separately, move the substrate back out of the field of view with the joystick set to mode "Stage" as in Figure 8.

Concentrate on alignment markers of layer 2 (mask), and put them in the centers, choose good focus and illumination.

Switch to "assisted alignment training mode" by clicking "AL Training" (bottom right corner Figure 9:
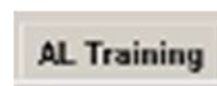
This switches to training buttons (in red square), and the current wrong targets (circles) Figure 10.

Figure 10: Target Training mode (AL Training)

The teaching task is to cycle through the four targets, and for each teach them to be squares, and define the "search area" and "define target" as given in these buttons.

Start with one of them:

Target Mask Left ->Define Search Area:

Make the search area (pink rectangle) as big as possible. For this kind of structure this works best. One reason to make it smaller is if you have multiple identical markers in the field of vision, and you want to restrict the algorithm, alike a blinker for a horse.
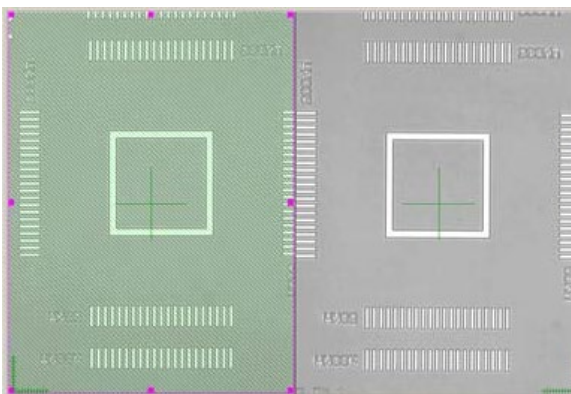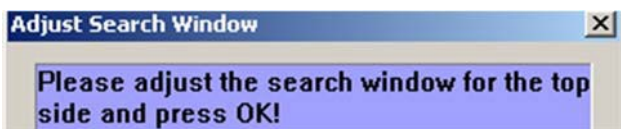

Figure 11: Target Mask Left ->Define Search Area

Adjust Search Window

Please adjust the search window for the top side and press OK!

Then specify what the target itself looks alike in this search area

Target Mask Left ->Define Target:

Make the recognition area for the target snug but not touching with the target. Shapes (contrast gradients) outside of the target rectangle do not disturb the recognition, such as neighboring features, dust, defocus, or the substrate related distractions. The recognition is done on contrast/illumination gradients, make those transitions be fully in the target defined area.
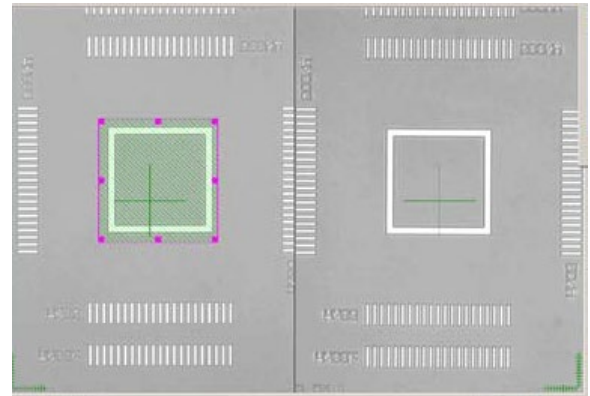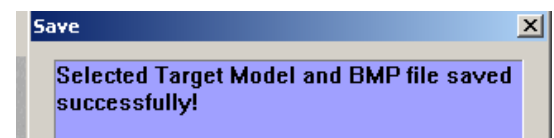

Figure 12: Target Mask Left ->Define Target

Adjust Target Window

Please adjust the target window for the top side and press OK!

Then you get your training result:

Training Result

0°:
Target position: 254.227, 286.967
Accuracy: 100.00
[Angle: -0.00°, UniformScale: 100.00]

180°:
Target position: 258.958, 285.359
Accuracy: 100.00
[Angle: -180.00°, UniformScale: 100.00]

Save your work!!! Otherwise, you have to redo it over and over and over and over.
The interface comes back and happily reports:

Save

Selected Target Model and BMP file saved successfully!

Note that the "target" image has been updated for the square (one square corner, and still three circles form the previous example.).
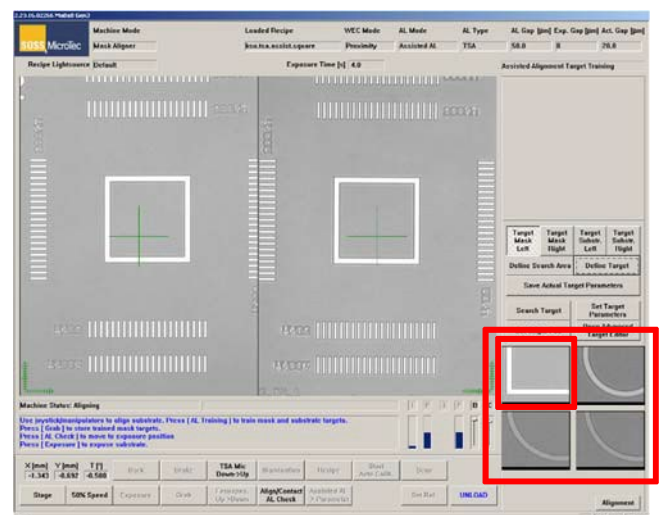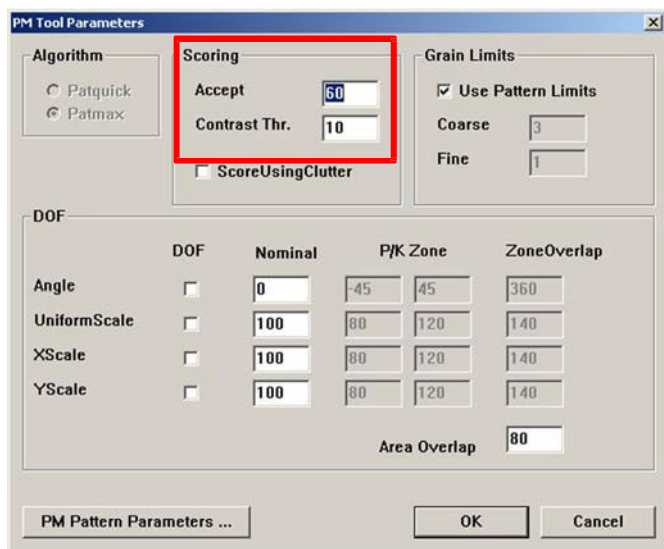

Figure 13: Target Mask Left: trained

Advanced users may go and tweak the recognition algorithm, modify the scoring algorithm by changing contrast thresholds, and acceptance, but for this simple example here, this is sufficient.

Do another time for right mask.

Then move the microscope to the substrate markers, and train left and right substrate.

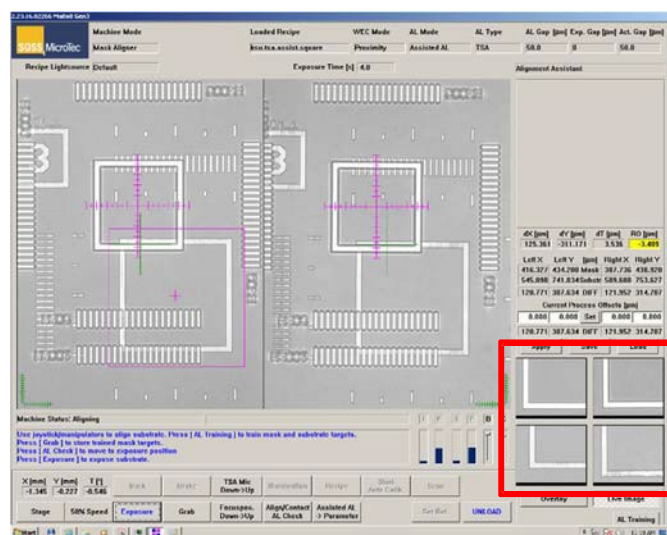Then move both targets one on top of each other. You see four targets trained (Figure 16):

Figure 14: Four targets trained, back in alignment mode.

4. Alignment

Once training of all targets is done, return to "alignment" mode by click on:

The recognition algorithm is live and working and giving feedback about the alignment. Since we did not align yet, there are hundreds of micrometers of distance of misalignment, both dX & dY, (see Figure 15)

dX [µm]	dY [µm]	dT [µm]	RO [µm]
125.361	-311.171	3.536	-3.409

Left X	Left Y	[µm]	Right X	Right Y
416.327	434.200	Mask	387.736	438.920
545.090	741.034	Substr	509.688	753.627
128.771	307.634	DIFF	121.952	314.707

Figure 15: Assist align feedback, detail of previous figure

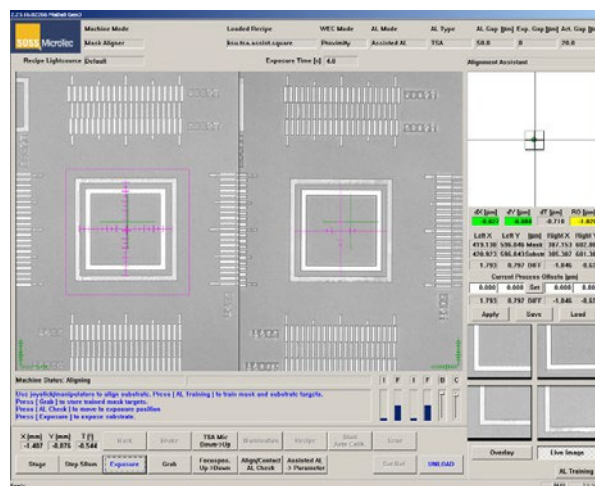Use the joystick (Stage) to align the substrate as best as possiblr:

Figure 16: Alignment with the joystick

In Figure 17 the misalignment has shrunk to sub-micrometer distances. The green fields are in very good agreement, dX and dY, the rotation theta, dT was not improved for this case.

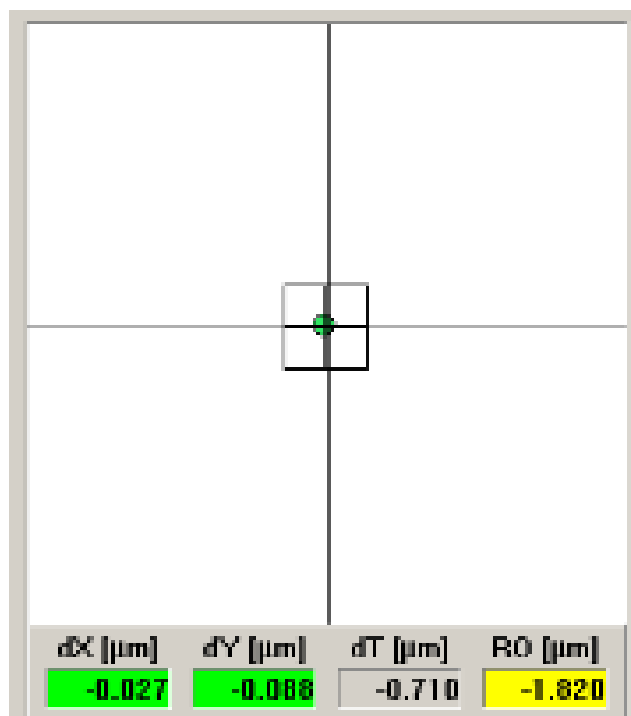| dX [µm]	dY [µm]	dT [µm]	RO [µm]
-0.027	-0.088	-0.710	-1.820

Figure 17: Assisted alignment dX dY dT RO numbers

The RO, the "thermal run-out", meaning the difference between the distance of the markers on the mask and distance of the markers on the substrate, is RO=1.8um. This is due to different

thermal expansion coefficients of the two materials, combined with different temperatures and different exposure tools used for the patterning steps, resulting in differing dimensions.

See in Figure 19 the square indicative for displacement in X and Y, and the colored circle for displacement in Theta, green-CW, orange-CCW.

Another example using the traditional cross, right cross is too high, results in a rotation or theta misalignment:

Figure 18: assisted alignment with traditional cross

The detail of the feedback is:

dX [μm]	dY [μm]	dT [μm]	RO [μm]
6.149	-20.797	37.058	-2.043

Left X	Left Y	[μm]	Right X	Right Y
415.608	535.966	Mask	414.942	529.707
423.800	519.706	Substr	419.047	587.562
8.192	-16.260	DIFF	4.105	57.855

After correcting with substrate movement, the three dX, dY and dT go into happy green. Thermal Runoff RO cannot be fixed but is premonitory of increasing misalignment towards edges of wafer.
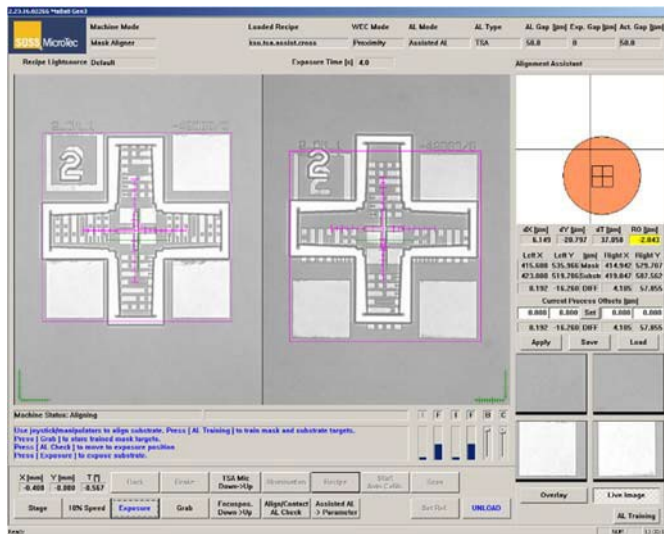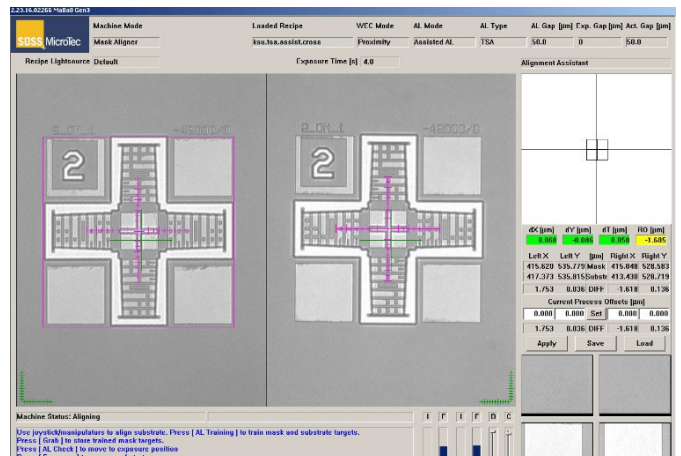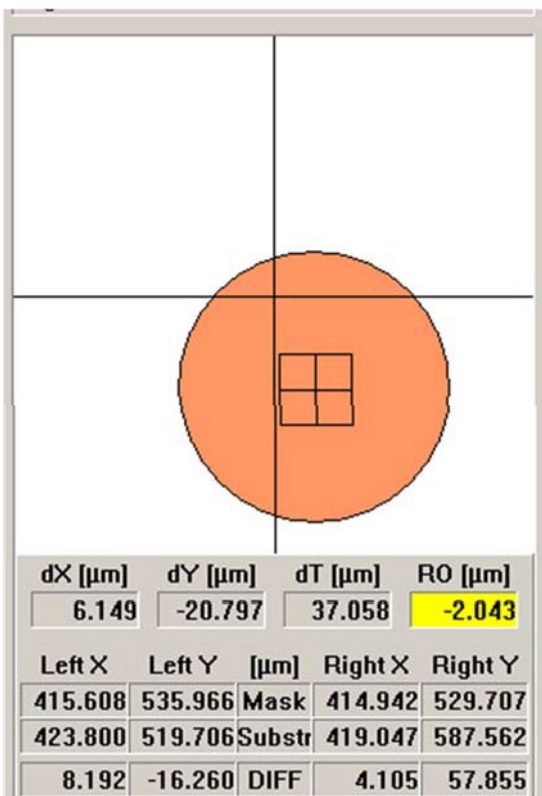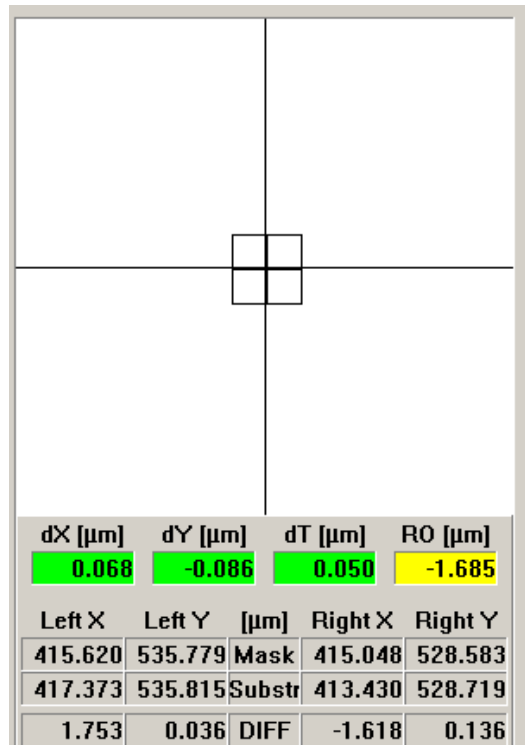

Details:

dX [μm]	dY [μm]	dT [μm]	RO [μm]
0.068	-0.086	0.050	-1.685

Left X	Left Y	[μm]	Right X	Right Y
415.620	535.779	Mask	415.048	528.583
417.373	535.815	Substr	413.430	528.719
1.753	0.036	DIFF	-1.618	0.136

It is up to the user to decide what precision is enough for an application.

Then the usual "Contact", then "AL Check" and "exposure" sequences ensues.