WHAT IS CLAIMED IS:

1. A chip for assays comprising:

a substrate comprising at least one field region and at least one track region;

experiment sites disposed in a first patterned array in the at least one field region, the first patterned array being defined by a first pitch; and

alignment sites disposed in a second patterned array in the at least one track region, the second patterned array being defined by a second pitch along a single dimension;

wherein the first pitch differs from the second pitch by a non-integer multiple in order to permit Moiré averaging-based alignment.

2. The chip of Claim 1, wherein the at least one field region has a density of one object space pixel per one experiment site.

3. The chip of Claim 1, wherein the at least one field region has a density of two object space pixels per one experiment site, and wherein the experiment sites in the at least one field region are arranged in a checkerboard pattern.

4. The chip of Claim 1, wherein the at least one field region has a density of four object space pixels per one experiment site.

5. The chip of Claim 1, wherein said alignment sites are operative to support biochemical experiments.

6. The chip of Claim 1, wherein selected ones of the alignment sites are deleted in accordance with a preselected pattern.

7. The chip of Claim 1, wherein selected ones of the alignment sites are deleted in accordance with a pseudo-random pattern.

8. The chip of Claim 1, wherein said experiment sites and said alignment sites are configured to support biochemical experiments.

9. The chip of Claim 1, wherein areas of the substrate, other than said experiment sites and said alignment sites, are configured to inhibit binding of target nucleic acids.

10. The chip of Claim 1, wherein said experiment sites and said alignment sites are configured to support attachment of DNA nanoballs.

11. The chip of Claim 1, wherein said single dimension is a horizontal dimension.

12. The chip of Claim 1, wherein said single dimension is a vertical dimension.

13. The chip of Claim 1, wherein the at least one track region is separated from the at least one field region by a site-free band.

14. The chip of Claim 1, wherein said single dimension is a vertical dimension and the width of said at least one track region is one of: three times the size of an object space pixel; and five times the size of an object space pixel.

15. The chip of Claim 1, wherein:

the substrate further comprises a horizontal track region that is disposed substantially perpendicular to said at least one track region; and

said horizontal track region comprises track sites disposed according to the second patterned array along a second dimension that is substantially perpendicular to said single dimension.

16. A method comprising:

capturing with an imaging instrument an image of a chip on which target nucleic acids have been disposed, the chip comprising:

a substrate comprising at least one field region and at least one track region;

experiment sites disposed in a first patterned array in the at least one field region, the first patterned array being defined by a first pitch; and

alignment sites disposed in a second patterned array in the at least one track region, the second patterned array being defined by a second pitch along a single dimension;

wherein the first pitch differs from the second pitch by a non-integer multiple; and

wherein the target nucleic acids are attached to the experiment sites and to the alignment sites;

determining according to correlation logic a first correction alignment term for the single dimension by using, at least in part, Moiré averaging based on signals recorded in the image that are emitted from the target nucleic acids attached to the alignment sites in the at least one track region; and

automatically aligning the chip with the imaging instrument along the single dimension based on the correction alignment term.

17. The method of Claim 16, wherein:

the substrate of the chip further comprises a horizontal track region that is disposed substantially perpendicular to said at least one track region, wherein said horizontal track region comprises track sites disposed according to the second patterned array along a second dimension that is substantially perpendicular to said single dimension;

the method further comprising:

determining according to the correlation logic a second correction alignment term for the second dimension by using, at least in part, Moiré averaging based on signals recorded in the image that are emitted from the target nucleic acids attached to the track sites in the second track region; and

automatically aligning the chip with the imaging instrument along the second dimension based on the second correction alignment term.

18. The method Claim 16, wherein the correlation logic determining the correction alignment term for the single dimension further comprises:

as part of the correction alignment term, determining a track pitch misalignment error based at least in part on:

the signals recorded in the image that are emitted from the target nucleic acids attached to the alignment sites in the at least one track region; and

information representing a pattern of deletion sites in the at least one track region.

19. The method Claim 16, wherein the target nucleic acids comprise DNA nanoballs.

20. The method of Claim 16, wherein a subset of said alignment sites are selectively deleted to form a pattern of deletions, and the correlation logic

3 determining the correction alignment term further comprises computing the correction
4 alignment term based at least in part on an ordered data set that represents the pattern
5 of deletions.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An assay chip for performance of biochemical assays on macromolecules, the assay chip comprising:

a solid-phase support comprising a substantially planar surface, the surface comprising at least one field region and at least one track region;

experiment sites comprising discrete, spatially defined areas on the surface separated from one another, the areas being configured for biochemical experiments on the macromolecules attached to the experiment sites, wherein the experiment sites are disposed in a first patterned array in the at least one field region, the first patterned array being defined by a first pitch specifying a first separation among said experiment sites; and

alignment sites disposed in a second patterned array in the at least one track region, the second patterned array being defined by a second pitch along a single dimension specifying a second separation between said alignment sites;

wherein the second patterned array differs from the first patterned array in that the first pitch differs from the second pitch by a non-integer multiple of the second pitch in order to permit Moiré averaging-based alignment.

2. An assay chip for performance of biochemical assays on DNA nanoballs, the assay chip comprising:

a solid-phase support comprising a substantially planar surface, the surface comprising at least one field region and at least one track region;

experiment sites comprising discrete, spatially defined areas on the surface separated from one another, the areas being configured for biochemical experiments on the DNA nanoballs attached to the experiment sites, wherein the experiment sites are disposed in a first patterned array in the at least one field region, the first patterned array being defined by a first pitch specifying a first separation among said experiment sites; and

alignment sites disposed in a second patterned array in the at least one track region, the second patterned array being defined by a second pitch along a single dimension specifying a second separation between said alignment sites;

wherein the second patterned array differs from the first patterned array in that the first pitch differs from the second pitch by a non-integer multiple of the second pitch in order to permit Moiré averaging-based alignment.

3. The chip of either Claim 1 or Claim 2, wherein the chip is disposed to be observed through optics with a pixel-based sensor, the sensor and the optical configuration defining size of an object-based pixel, and wherein the at least one field region has a density of one object space pixel per one experiment site.

4. The chip of either Claim 1 or Claim 2, wherein the chip is observed through optics with a pixel-based sensor, the sensor and the optical configuration defining size of an object based pixel, and wherein the at least one field region has a density of two object space pixels per one experiment site, and wherein the experiment sites in the at least one field region are arranged in a checkerboard pattern.

5. The chip of either Claim 1 or Claim 2, wherein the chip is disposed to be observed through optics with a pixel-based sensor, the sensor and the optical configuration defining size of an object based pixel, and wherein the at least one field region has a density of four object space pixels per one experiment site.

6. The chip of either Claim 1 or Claim 2, wherein the areas forming the alignment sites are configured for biochemical experiments on the macromolecules or DNA nanoballs attached to the alignment sites.

7. The chip of either Claim 1 or Claim 2, wherein selected ones of the alignment sites are deleted in accordance with a preselected pattern of remaining alignment sites.

8. The chip of either Claim 1 or Claim 2, wherein selected ones of the alignment sites are deleted in accordance with a pseudo-random pattern of remaining alignment sites.

9. The chip of either Claim 1 or Claim 2, wherein areas of the surface, other than said experiment sites and said alignment sites, are configured to inhibit binding of target nucleic acids.

10. The chip of Claim 1, wherein the macromolecules are DNA nanoballs.

11. The chip of either Claim 1 or Claim 2, wherein said single dimension is a horizontal dimension.

12. The chip of either Claim 1 or Claim 2, wherein said single dimension is a vertical dimension.

13. The chip of Claim 1 or Claim 2, wherein the at least one track region is separated from the at least one field region by a site-free band.

14. The chip of Claim 1 or Claim 2, wherein the chip is disposed to be observed through optics with a pixel-based sensor, the sensor and the optical configuration defining size of an object based pixel, and wherein said single dimension is a vertical dimension and the width of said at least one track region is one of: three times the size of an object space pixel; and five times the size of an object space pixel.

15. The chip of either Claim 1 or Claim 2, wherein:

the surface further comprises a horizontal track region that is disposed substantially perpendicular to said at least one alignment region; and

said horizontal track region comprises track sites disposed according to the second patterned array along a second dimension that is substantially perpendicular to said single dimension.

16. A method comprising:

capturing with an imaging instrument an image of a chip on which target nucleic acids have been disposed, the chip comprising:

a solid-phase support comprising a substantially planar surface, the surface comprising at least one field region and at least one track region;

experiment sites comprising discrete, spatially defined areas on the surface separated from one another, the areas being configured for biochemical experiments on the macromolecules attached to the experiment sites, wherein the experiment sites are disposed in a first patterned array in the at least one field region, the first patterned array being defined by a first pitch specifying a first separation among said experiment sites; and

alignment sites disposed in a second patterned array in the at least one track region, the second patterned array being defined by a second pitch along a single dimension specifying a second separation between said alignment sites;

wherein the second patterned array differs from the first patterned array in that the second pitch differs from the first pitch by an integer multiple of the first pitch; and

wherein the target nucleic acids are attached to the experiment sites and to the alignment sites;

determining according to correlation logic a first correction alignment term for the single dimension by using, at least in part, Moiré averaging based on signals recorded in the image that are emitted from the target nucleic acids attached to the alignment sites in the at least one track region; and

automatically aligning the chip with the imaging instrument along the single dimension based on the correction alignment term.

17. The method of Claim 16, wherein:

the surface of the chip further comprises a horizontal track region that is disposed substantially perpendicular to said at least one track region, wherein said horizontal track region comprises track sites disposed according to the second patterned array along a second dimension that is substantially perpendicular to said single dimension;

the method further comprising:

determining according to the correlation logic a second correction alignment term for the second dimension by using, at least in part, Moiré averaging based on signals recorded in the image that are emitted from the target nucleic acids attached to

the track sites in the second track region; and

automatically aligning the chip with the imaging instrument along the second dimension based on the second correction alignment term.

18. The method of Claim 16, wherein the correlation logic determining the correction alignment term for the single dimension further comprises:

as part of the correction alignment term, determining a track pitch misalignment error based at least in part on:

the signals recorded in the image that are emitted from the target nucleic acids attached to the alignment sites in the at least one track region; and

information representing a pattern of deletion sites in the at least one track region.

19. The method of Claim 16, wherein the target nucleic acids comprise DNA nanoballs.

20. The method of Claim 16, wherein a subset of said alignment sites are selectively deleted to form a pattern of deletions, and the correlation logic determining the correction alignment term further comprises computing the correction alignment term based at least in part on an ordered data set that represents the pattern of deletions.

21. The chip according to Claim 1 or Claim 2 or the method according to Claim 16, substantially as hereinbefore described.