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An atom-by-atom assembler of defect-free arbitrary 2D atomic arrays

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Large arrays of individually controlled atoms trapped in optical tweezers are a very promising platform for quantum engineering applications. However, deterministic loading of the traps is experimentally challenging. Here, we demonstrate the preparation of fully loaded, two-dimensional arrays of up to ~50 microtraps each containing a single atom, and arranged in arbitrary geometries. Starting from initially larger, half-filled matrices of randomly loaded traps, we obtain user-defined target arrays at unit filling. This is achieved with a real-time control system and a moving optical tweezer that performs a sequence of rapid atom moves depending on the initial distribution of the atoms in the arrays. These results open exciting prospects for quantum engineering with neutral atoms in tunable two-dimensional (2D) geometries.

The last decade has seen tremendous progress over the control of individual quantum objects (*1*, *2*). Many experimental platforms, from trapped ions (*3*) to superconducting qubits (*4*), are actively explored. The current challenge is now to extend these results toward large assemblies of such objects, while keeping the same degree of control, in view of applications in quantum information processing (*5*), quantum metrology (*6*), or quantum simulation (*7*). Neutral atoms offer some advantages over other systems for these tasks. Besides being well isolated from the environment and having tunable interactions, systems of cold atoms hold the promise of being scalable to hundreds of individually controlled qubits. Control of the atomic positions at the single-particle level can been achieved with optical potentials. In a 'top-down' approach using optical lattices and quantum gas microscopes, hundreds of traps can now be created and addressed individually (*8*). By making use of the superfluid to Mott-insulator transition, single atom filling fractions exceeding 90% are achieved (*9*), albeit at the expense of relatively long experimental duty cycles and constraints in the lattice geometries.

Single atoms can also be trapped in 2d arrays of microscopic optical tweezers with single-site resolution using holographic methods (*10*–*12*). This bottom-up approach offers faster preparation and a higher degree of tunability of the underlying geometry. However, achieving unit filling of the arrays is hampered by the stochastic nature of the loading and has remained elusive. Although proof-of-principle demonstrations of quantum gates (*13*) and quantum simulations (*14*) using this latter platform have been reported (*15*), this non-deterministic loading poses a serious limitation for applications where large-scale ordered arrays are required. To solve this problem, several approaches have been considered, such as exploiting the Rydberg blockade mechanism (*16*), or using tailored light-assisted collisions (*17*). To date, despite those efforts, loading efficiencies of around 90% at best for a single atom in a single tweezers could be achieved (*18*, *19*), making the probabilities to fully load large arrays still exponentially small.

A different approach toward this goal, pioneered in (*20*) for a few atoms, and revisited recently in (*21*, *22*), consists in sorting disordered arrays of atoms using moving optical potentials (*23*). Here we demonstrate the deterministic preparation of arrays as large as $N \sim 50$ individual atoms in arbitrary 2d geometries with filling fractions η up to 98%, which enables us to engineer defect-free arrays with a fast repetition rate. This is accomplished through the sequential assembly of the atoms in the arrays using a fast programmable control system. Starting from stochastically loaded half-filled arrays with $\sim 2N$ traps, we analyze in real-time the initial atom distribution, and use a fast, moving optical tweezer to rearrange the atoms into a user-defined target spatial configuration, thus implementing an atom-sorting device reminiscent of Maxwell's demon (*24*) (only the entropy associated with the atomic positions in the arrays is removed; the -much higher- entropy associated to the motion of each atom in each trap remains unaffected). We anticipate that this approach could be scaled up to a few hun-

dreds of atoms, still maintaining filling fractions close to unity, as the size of the arrays we can prepare is at present mostly limited by the available laser power. These results may lead to an alternative procedure for initializing two-dimensional arrays of single atoms for quantum simulation using e.g., strong interactions between Rydberg states (*14*).

Our experimental setup (*25*, *26*) is shown schematically in Fig. 1A. We use a Spatial Light Modulator (SLM) to create arbitrary two-dimensional arrays of up to 100 traps, separated by distances $a > 3$ μm in the focal plane of a high-numerical aperture (NA = 0.5) aspheric lens. Each trap has a $1/e^2$ radius of ~1 μm and a depth of $U_0/k_B \approx 1$ mK (for a power of about 5 mW), yielding radial (longitudinal) trapping frequencies around 100 kHz (20 kHz). In the single-atom regime, the traps are stochastically loaded from a magneto-optical trap with cold single ^{87}Rb atoms with a probability p ~ 0.5. We monitor the occupancy of the traps observing the fluorescence of the atoms at 780 nm with a CCD camera, with a time resolution of 50 ms. For deterministic atom transport we superimpose a second moving 850-nm laser beam on the trapping beam. This moving optical tweezer (with $1/e^2$ radius ~1.3 μm) is controlled using a 2d acousto-optic deflector (AOD).

Figure 1B shows how we extract an atom from a filled trap using the moving optical tweezer. We first set the horizontal and vertical AOD frequencies to position the beam at the source trap, and ramp up linearly the optical power diffracted by the AODs to reach a tweezers depth $U \sim 10U_0$ in a time τ (inset). The applied optical potential effectively captures the atom from the trap. Then, we steer the beam toward the target trap, at velocity v, by sweeping the vertical and horizontal AOD frequencies. Finally, we release the atom from the tweezers in the target trap. For $\tau \sim 0.3$ ms and $v \sim 10$ nm/μs, the probability to succeed in transferring the atoms from the source to the target traps reaches 99.3% (*27*). Our method to synthesize fully loaded arrays of N atoms is sketched in Fig. 1C and works as follows. We use an array of ~2N traps which contains the target array as a subset and load it from the MOT. The loading of the array is stopped as soon as at least N traps are filled with single atoms, and a fluorescence image is acquired to record the initial position of the atoms. Following the analysis of the image, an algorithm (see below) computes on the fly a list of individual atom moves which can rearrange the configuration into the desired two-dimensional pattern. This list is then sent to micro-controllers via serial port communication. The micro-controller program converts this list into a series of voltage sweeps to control the RF drivers driving the AODs. Finally, after the rearrangement operation is completed (in about 50 ms for $N \sim 50$) a final image is acquired to reveal the new positions of the atoms in the array.

To implement the atom-sorting shown schematically in Fig. 1C, we have used, depending on the nearest-neighbor distance a in the target arrays, two types of elementary moves to transfer an atom from a source trap to a target trap (Fig. 1, D and E). "Type-1" moves transfer an atom by moving it in between other traps, which allows us to minimize the number of moves needed to assemble an array. However, type-1 moves were found to lead to atom loss in the traps close to the moving tweezers trajectory when $a < 5$ μm, and thus, for such arrays, we used "type-2" moves where atoms are moved along the links of the arrays.

Choosing the best algorithm to calculate the atom moves would ideally require finding the optimal list that minimizes the number of moves and total distance (thus minimizing the time it takes to reorder the array): in our arrays trapped atoms have a vacuum-limited lifetime $\tau_{vac} \sim 10$ s, and thus, the estimated lifetime of a configuration with N atoms is τ_{vac}/N. The total sequence should remain shorter than this to achieve high fidelities. However, finding the optimum set of paths is a difficult computational task, reminiscent of the traveling salesman problem. We have developed a heuristic path-finding algorithm, which first computes a list of all possible individual moves, and then orders it according to their length; we then select moves from source to target traps, starting from the shortest ones, until all target traps are filled. This results in ~N/2 moves (however, this does not necessarily minimize the total travel distance). We finally discard the unused extra atoms (if any) by moving them to positions far away from any trap. Additionally, for "type-2" moves, we have to avoid moving the tweezer over filled traps (to prevent the tweezer from dragging along other atoms during its motion). We enforce this constraint in the following way. If the source atom S needs to be moved to the target trap T (we denote this move by $S \rightarrow T$) and an "obstacle" O is on the way, we replace the move $S \rightarrow T$ by the two moves $O \rightarrow T$ and $S \rightarrow O$. This increases slightly the number of needed moves, as sometimes some filled traps are "in the way", but the overhead is moderate (*27*).

For our largest arrays, the total arrangement process is typically performed within less than 50 ms after the initial image is acquired, a timescale still shorter than the lifetime of the initial configuration. Despite being quite simple and non-optimal, our algorithm is efficient and versatile. Finding better algorithms might however be important for scaling up our approach to hundreds of atoms.

Figure 2 shows a gallery of two-dimensional trap arrays with arbitrary, user-defined geometries relevant for quantum simulation, e.g., one-dimensional chains, ladders, lattices with square, triangular, honeycomb or kagome structures. Neighboring traps are separated by distances $3 < a < 6$ μm, for which interactions in the MHz range can be achieved by exciting the atoms to Rydberg states (*14*). In (A), type-1 moves were used, whereas in (B), type-2 moves were

used. For each array, we show on the top panel a fluorescence image of single atoms obtained with the CCD camera at the beginning of the sequence. Because the probability for each trap to be filled is $p \sim 0.5$, the arrays are initially half-filled. In the accompanying bottom image we show the final fluorescence image after the sorting is completed. Analyzing 100 repetitions of the experiment for a 5×5 square target array (Fig. 3A), we achieve a filling fraction $\eta > 96\%$, mainly limited by background gas collisions during the rearrangement (*27*). This corresponds to a probability of getting a defect-free array of about 40%. The filling fraction decreases only marginally when the number of atoms increases, showing the scalability of our approach (Fig. 3B). In order to achieve even higher filling fractions, one could iterate the procedure presented here, i.e., skip the disposal of unused atoms, analyze the "final" image and fill in defects (if any) with remaining atoms.

Analyzing the technical limitations of the current implementation suggests that preparing hundreds of individual atoms in arrays of arbitrary geometries very close to unit filling is realistic with state-of-the-art technology (*27*). These results, possibly combined with Raman sideband cooling of atoms in optical microtraps (*28*, *29*), open promising paths to studying many-body physics in two-dimensions and constitute an important resource for quantum information processing with cold neutral atoms. In the future, using the same technique, it should be possible to insert atoms one at a time into a microtrap (*30*), thus preparing small samples with an exact atom number, e.g., for applications in cold chemistry.

Note added: During completion of the work, we became aware of related work in one dimension (*31*).

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SUPPLEMENTARY MATERIALS

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Supplementary Text
Figs. S1 to S3
Movie S1

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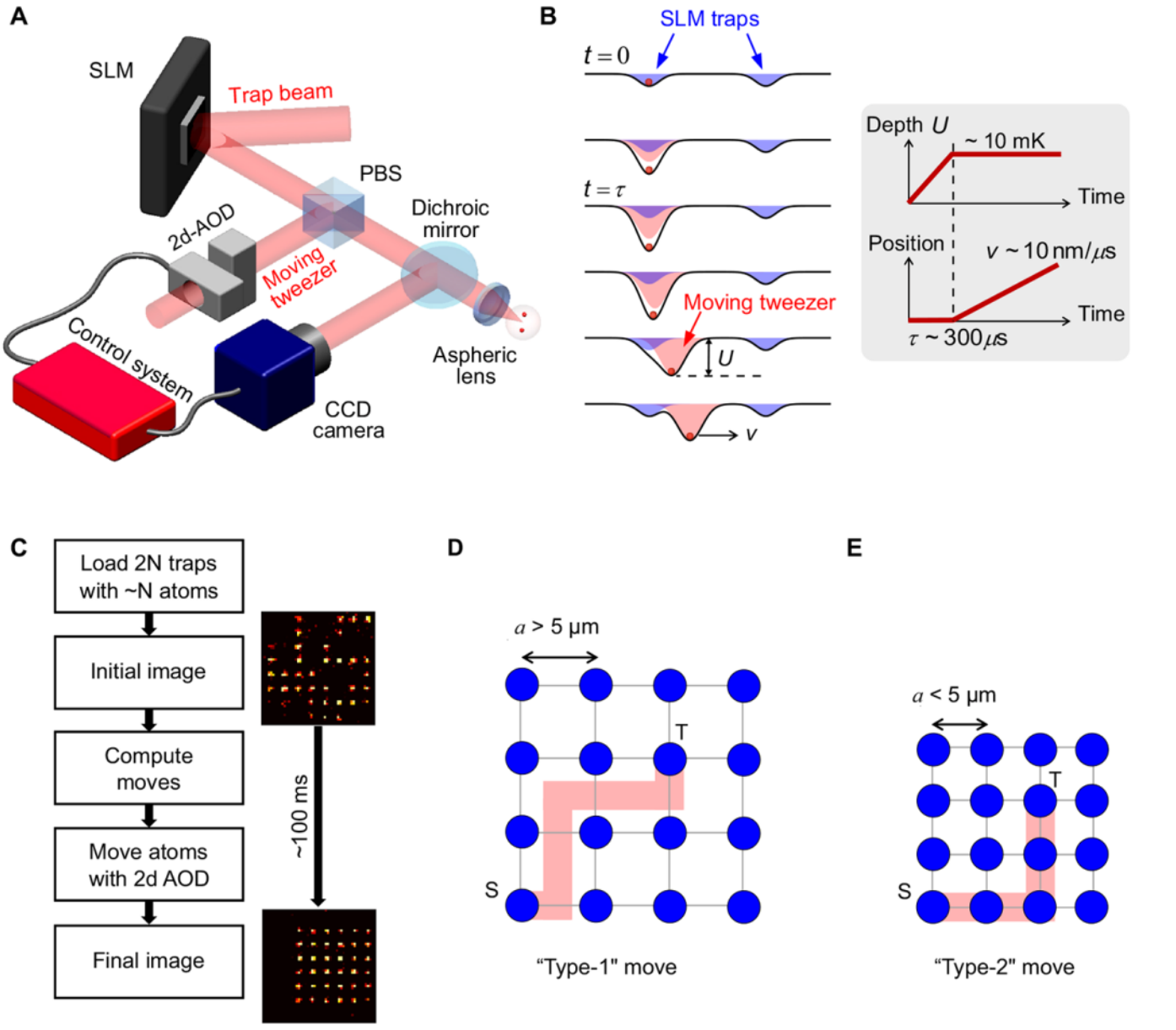

Fig. 1. Principle of the atom assembler. (**A**) Schematics of the experimental setup. Arbitrary 2d arrays of microtraps are created by imprinting an appropriate phase onto the dipole trap beam using a SLM, and focusing it with a high-NA aspheric lens. The moving beam is generated with a 2d AOD and superimposed on the trap beam with a polarizing beam-splitter (PBS). The CCD camera collects the fluorescence of the atoms in each trap. A control system made of a computer, two microcontrollers, and two AOD drivers allows us to implement a series of rapid moves to reshuffle the atomic array. (**B**) Extracting a single atom (red disk) from a fixed trap (blue Gaussian) with the moving optical tweezers (red Gaussian). The grey inset shows the time evolution of the moving tweezer's depth and position. (**C**) Block diagram of the control system. Depending on the initial configuration where on average half of the traps are filled, the control system steers each atom toward its target final position. (**D** and **E**) Basic moves implemented in the atom-sorting algorithms. (D) If the nearest-neighbor distance in the array is large enough (typically $a > 5$ μm), we move directly the tweezers from the source to the target, passing in between adjacent atom rows ("Type-1" moves). (E) Otherwise the atoms are moved along the lattice links ("Type-2" moves).

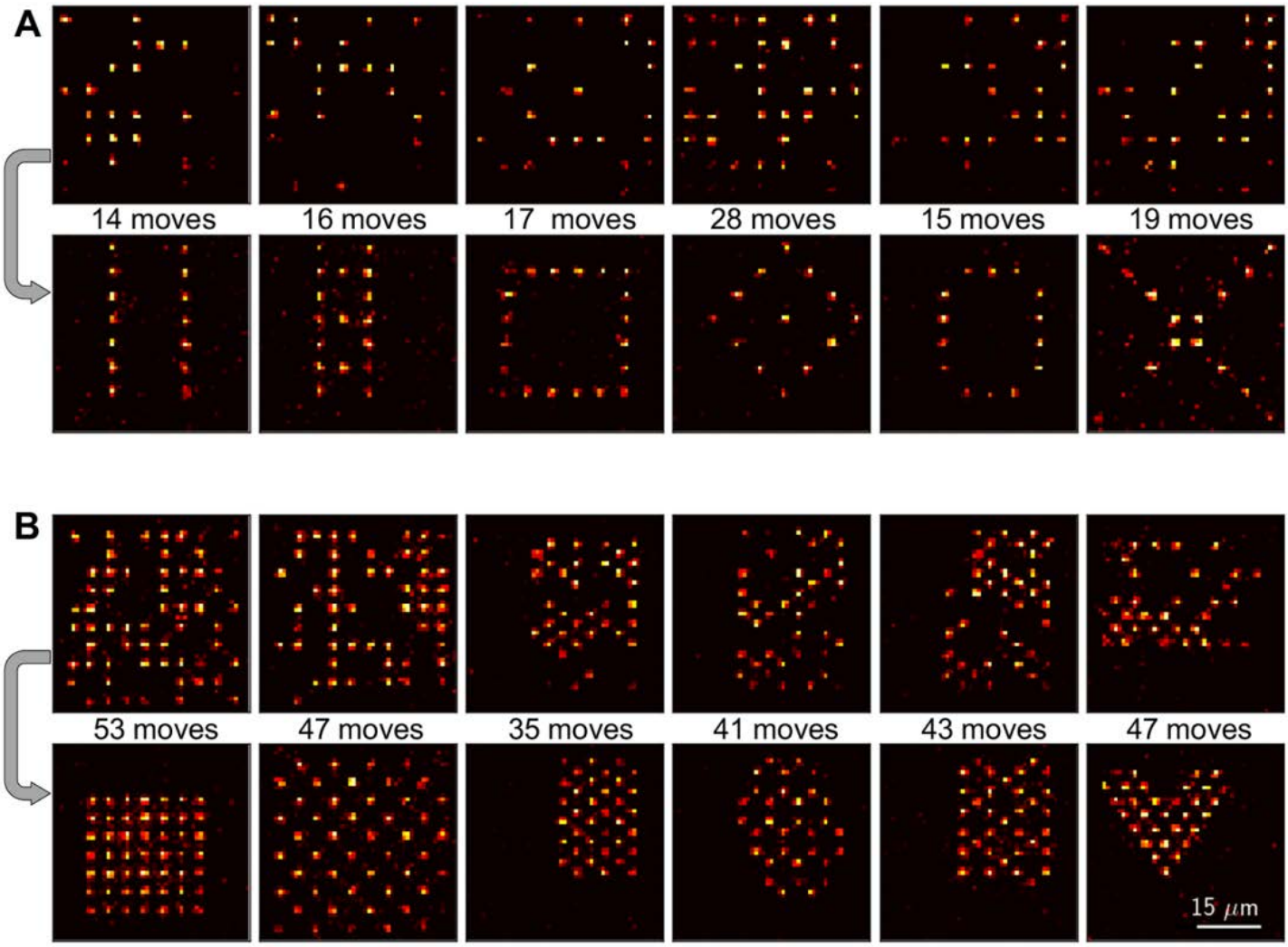

Fig. 2. Gallery of fully loaded arrays. Arbitrary, user-defined two-dimensional arrays (bottom images) are obtained from the initial, random configurations (top images). All images are single shots. (**A**) "Type-1" moves were used; (**B**) "Type-2" moves were used. The numbers of elementary moves needed to achieve the sorting are indicated.

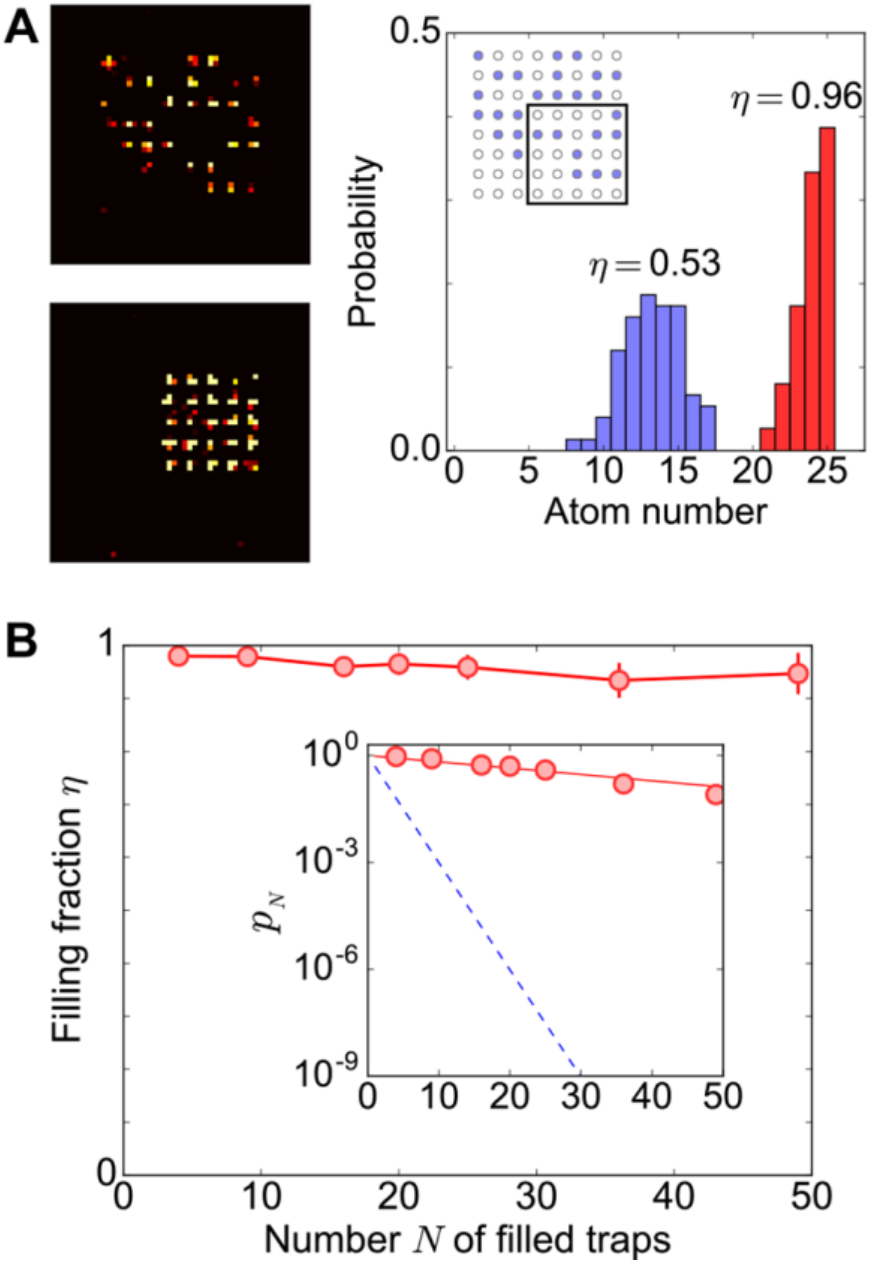

Fig. 3. Loading statistics of reordered arrays. (**A**) Images of the initial and final configurations for a square array of 25 atoms. Distribution of the number of atoms in the target 5 × 5 square array (black square in the inset to the graph) before (blue) and after sorting (red), in 100 repetitions of the experiment. The sorted array has η = 96% filling fraction (with a standard deviation of 4%), and defect-free arrays are obtained in ~40% of the cases. (**B**) Evolution of the filling fraction η as a function of the number of traps in the sorted array. The error bars are the standard error on the mean. Inset: circles show the observed probability p_N to obtain a defect-free array of N atoms; the dashed line shows the result $p_N = 2^{-N}$ corresponding to random loading.

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