Supporting Information

Alme et al. 10.1073/pnas.1421056111

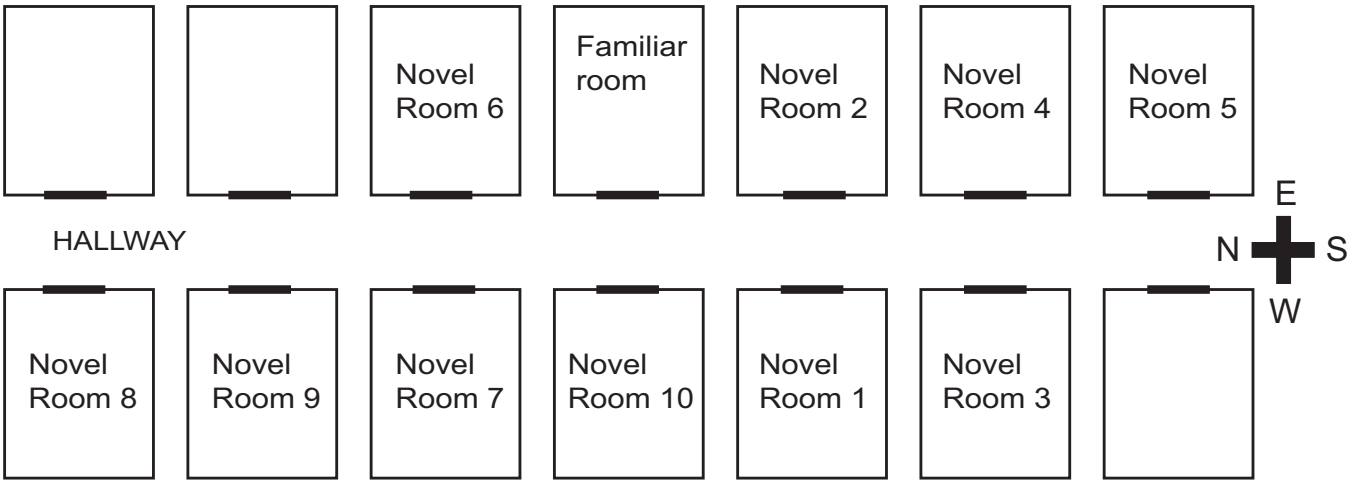

Fig. S1. Schematic of the location of rooms in relation to each other. Thick black lines indicate the position of the door in each room.

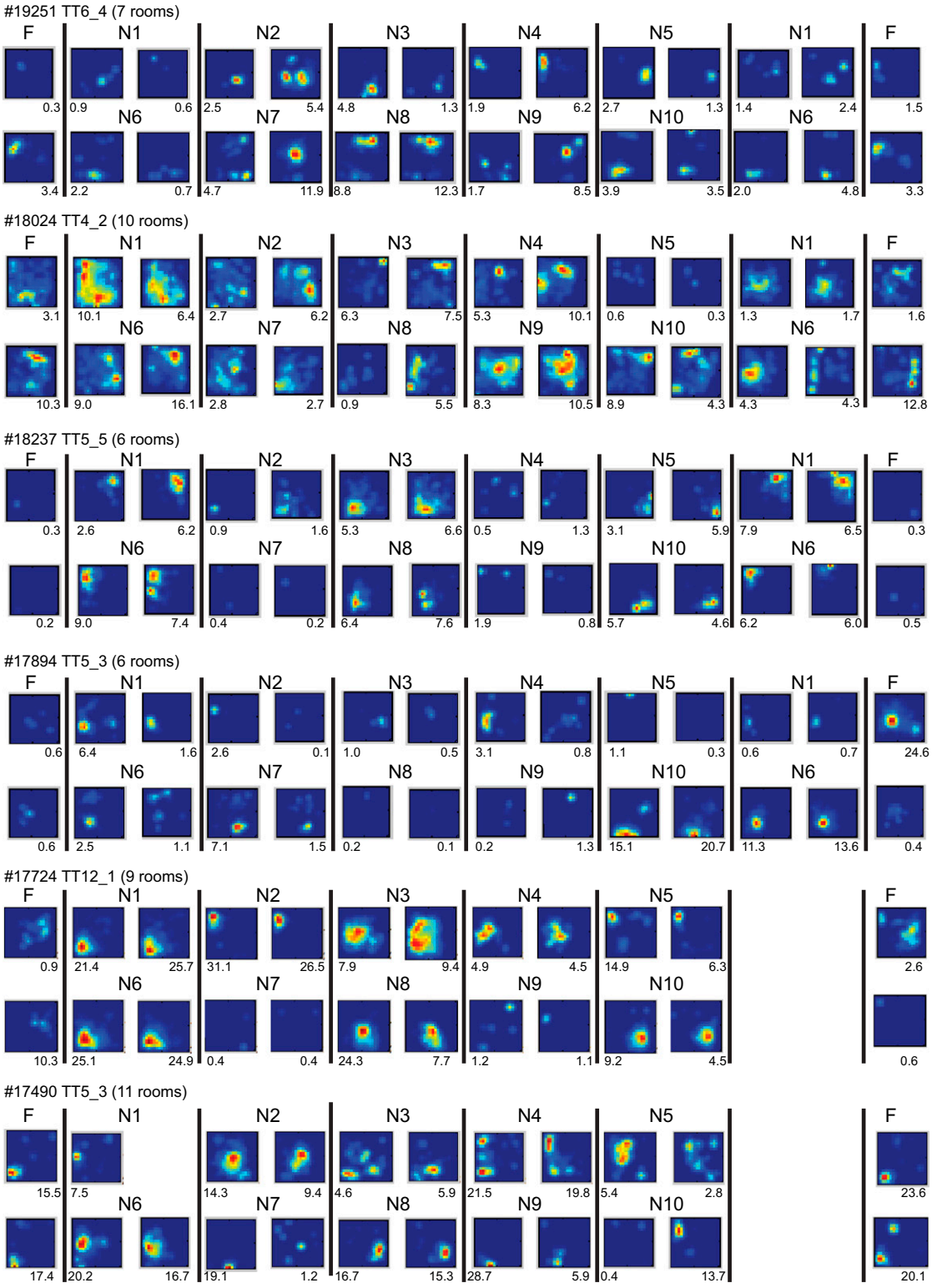

Fig. S2. Rate maps from six different rats showing examples of cells that were active in six or more rooms. Cells that were active in many rooms were similar to cells with few active rooms in that they did express global remapping, that is, maps changed place field locations across rooms, and that their spatial maps were not spatially correlated across rooms ($r = 0.15 \pm 0.01$, average $\pm$ SEM) although the cells expressed the same map across trials in the same room ($r = 0.73 \pm 0.04$). Animal number in five digits and tetrode (TT) are indicated above each rate map. Rate maps are scaled to their individual peak rate in Hz indicated below each rate map. (Rats 17724 and 17490 did not experience repeated tests to N1 and N6.)

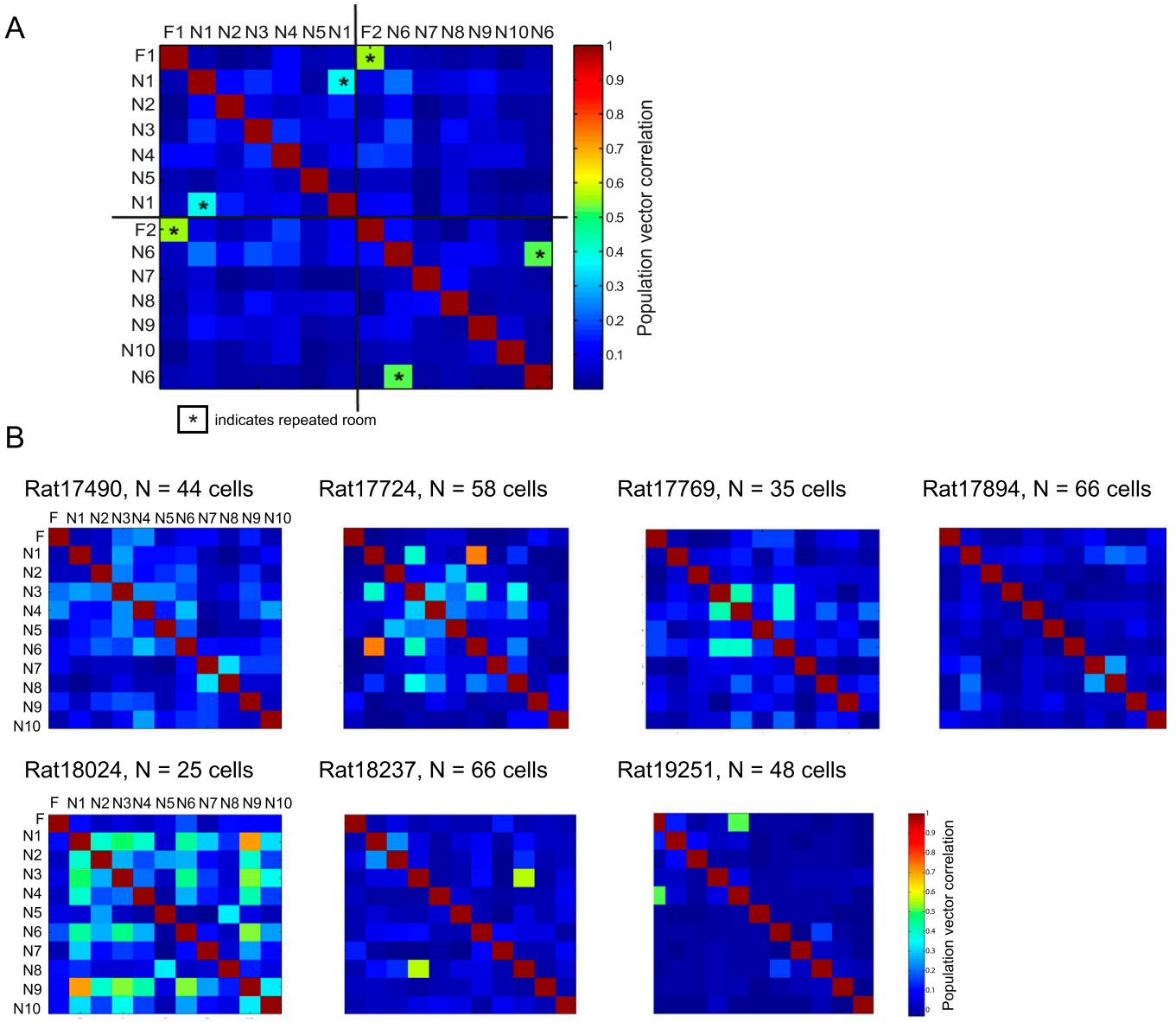

Fig. S3. Color-coded matrix showing Pearson correlation between population vectors across all combinations of test rooms. (*A*) Average correlation values for population vectors between rooms, including repeated exposures to the familiar room (F) and rooms N1 and N6, which were presented twice. Repeated trials are indicated by asterisks. Note the near absence of correlation between all different pairs of rooms but clear correlation between repeated rooms. (*B*) Population vector correlation for individual animals where the total number of cells for each rat including silent cells is indicated above each matrix. Each matrix is scaled to 1 (maximal correlation value).

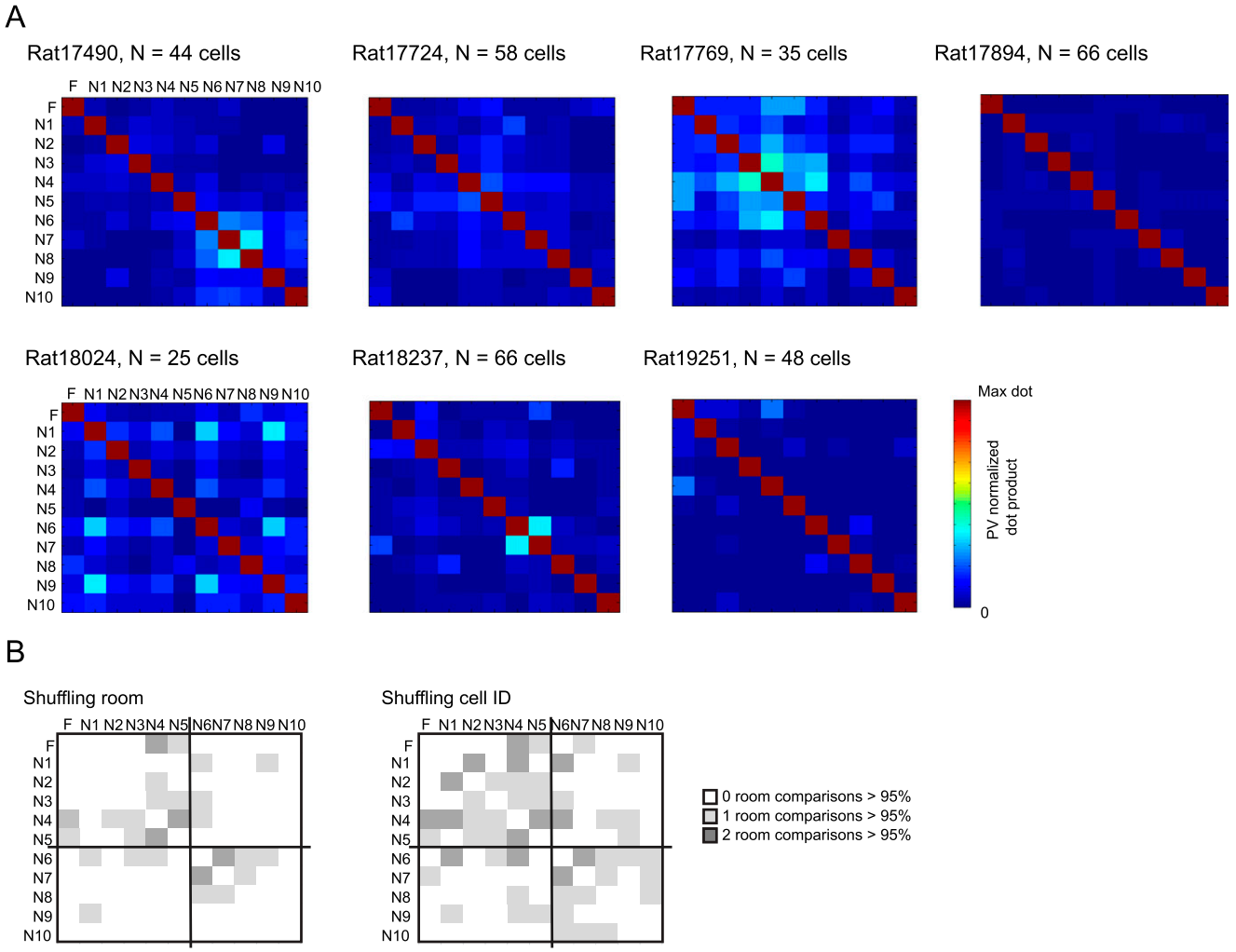

Fig. S4. Population vector analyses for individual animals. (*A*) Normalized dot product for individual rats, with each matrix scaled to the maximum dot product across all rats. Rat numbers and numbers of cells recorded are indicated. (*B*) Matrices indicating which room pairs have a dot product >95% of the shuffled distribution of room (*Left*) and cell ID (*Right*).

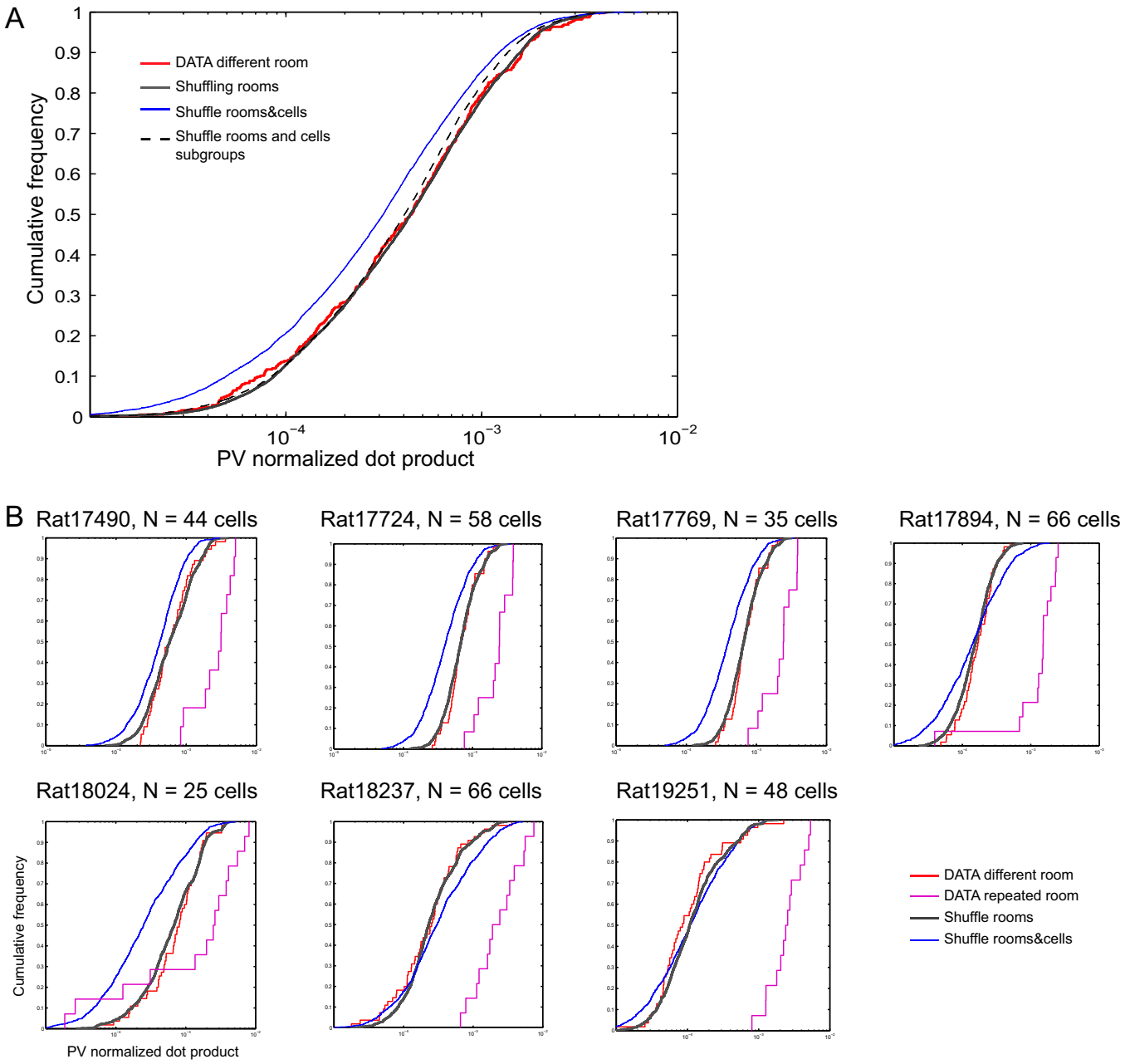

Fig. S5. (*A*) Additional shuffling procedure where, besides shuffling across rooms, cells with activity in three rooms or more and cells with activity in one or two rooms were shuffled only within their respective subgroups. Note that this restriction on the shuffling removes much of the left-shift compared with data or room shuffling that is observed when shuffling is performed across all cells. This indicates that the difference between the cell-shuffled CDF and the data were primarily caused by the nonuniform activation of the cell sample. The observed data across different rooms were not significantly different from the restricted shuffling procedure with two subpopulations (Mann–Whitney *u* test, Z = 0.95, df = 7,383, *P* = 0.30). (*B*) Cumulative frequency distributions showing normalized dot products for each of the seven animals.