Here we provide some details about our spike sorting procedures and the quality of spike sorting achieved with the arrays. The data acquisition system saves a small segment of the waveform, sampled at 30 kHz, every time the signal crosses a threshold. We set this threshold to a low level for each channel (~2 to 3 standard deviations of the background) to ensure that in the absence of any large spikes background signals had a reasonable chance of crossing the threshold. Scatter-plots between the coefficients of the three principal components were plotted to perform spike sorting. The presence of a spike in any one channel was signaled by the presence of two clusters: one corresponding to the spike, the other to threshold crossings caused by the background signal.

Supplemental Figures 1 and 2 illustrate the results of spike sorting in one monkey (Monkey #2) and one cat (Cat #1, Right hemisphere), respectively. (Figures appear on pages 4 and 5). The examples were selected to span the range of orientation tuning bandwidths observed. The left column shows the scatter plot of the first and second principal components for sorted spikes (red dots) and background noise (blue dots). The black circle within the blue cloud indicates the origin of the graph. The second column depicts the mean waveforms for each cluster, with one standard deviation of the waveforms above and below the mean shown by the shaded areas (the time interval shown is 1.6ms in length). The non-overlap of the shaded regions at times within the duration of the signals is an indication of their separability. We computed a measure of the segregation between the background signal and the spikes by projecting the waveforms onto the vector joining the mean of the
two clusters (third column). For each waveform this results in a single number. The distribution of the projections for background noise (blue) and sorted spikes (red) are shown in the third column. Given that the distributions are approximately Gaussian we calculated a measure of their discriminability by 

\[ d' = \left| \mu_s - \mu_n \right| \sqrt{\left( \sigma_s^2 + \sigma_n^2 \right) / 2} \]  

The estimate of \( d' \) appears at the inset to the distributions. The maximum value of \( d' \) across all our population of cells was 9.3 and the minimum 2.8. The mean value of \( d' \) was 5.7 with a standard deviation of 1.17. For the mean value of \( d' = 5.7 \) one expects a hit rate of 99.7% and a false positive error rate of 0.18%. The small false positive rate represents the degree of contamination by unwanted sources. We note that the value of \( d' \) estimated represents a lower bound on the degree of separation in our data, as decision boundaries were sometimes curved and not simply a hyper-plane. This degree of segregation is comparable or better than those achieved with tetrodes in previous studies (compare to Fig 1 in Hetherington and Swindale (1999) and Fig 1 in Gray et al (1995)). The examples in the figures are ordered from top to bottom in order of increasing bandwidth. The orientation tuning curves of the sorted spikes and estimated bandwidths are shown in the fifth column. Good isolation of spikes was obtained for cells that were sharply or broadly tuned. Finally, the inter-spike interval (ISI) distribution of the sorted spikes is shown on the rightmost column in each case. Following the work of Nirenberg et al (2001), a measure of spike contamination was defined as the relative number of spikes that appeared within 1 ms right after the end of a spike, which is indicated at the inset of the ISI distributions.
Table 1. Data Yield and Selection

<table>
<thead>
<tr>
<th></th>
<th># Tuned MU Sites</th>
<th>#SU Isolated</th>
<th>#SU Selected</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cat #1 (R/L)</td>
<td>64/64</td>
<td>21/28</td>
<td>14/7</td>
</tr>
<tr>
<td>Cat #2</td>
<td>81</td>
<td>29</td>
<td>25</td>
</tr>
<tr>
<td>Monkey #1</td>
<td>67</td>
<td>45</td>
<td>40</td>
</tr>
<tr>
<td>Monkey #2</td>
<td>69</td>
<td>25</td>
<td>16</td>
</tr>
</tbody>
</table>

The table shows, for each animal, the total number of sites where multiunit activity (MUA) was tuned; the total number of individual neurons that could be isolated (middle column); and the number of these cells that were used in the analyses. These were restricted to well-isolated spikes that yielded tuning curves for which a Gaussian fit explained more than 60% of the variance. Furthermore, the location of the electrode had to be within the region of interest defined by good signal-to-noise in the orientation maps. In Cat #1 we performed two implants, one in the right (R) and one in the left (L) hemispheres. The total number of active electrodes in the 10 × 10 array is 96 (the electrodes at the corners of the array are not wired).
\( d' = 3.8 \)  
\( 22.4^\circ \)  
\( 0.6\% \)  
\( 10 \)  
\( 0 \)  
\( 20 \)  
\( 1.7\% \)

\( d' = 9.3 \)  
\( 0.6\% \)  
\( 18.2^\circ \)

\( d' = 5.6 \)  
\( 0.5\% \)  
\( 13.9^\circ \)

\( d' = 7.9 \)  
\( 0.03\% \)  
\( 13.3^\circ \)

\( d' = 8.3 \)  
\( 1.7\% \)  
\( 9.2^\circ \)

\( d' = 5.6 \)  
\( 0.5\% \)  
\( 13.9^\circ \)

\( d' = 9.3 \)  
\( 0.6\% \)  
\( 18.2^\circ \)

\( d' = 3.8 \)  
\( 22.4^\circ \)  
\( 0.6\% \)
References for Supplemental Data

