

**Table S4. PeakSeq program parameters**

| PeakSeq                |                      |               |   |
|------------------------|----------------------|---------------|---|
| Script                 | Name                 | Value         | Description   |
| compile.py             | merlen               | 36            | tag length  |
| create_signal_map      | dna_fragment_length  | 200           | length of sheared fragments                                   |
| score_hits             | dna_fragment_length  | 200           | length of sheared fragments                                   |
|                        | window_size          | 1.0E6         | window size for scoring                                       |
|                        | max_threshold        | 100           | maximum allowed threshold for mapped reads                    |
|                        | max_gap              | 200, 350, 589 | allowable distance to merge peaks                             |
|                        | FDR_required         | 0.05          | required FDR from simulations                                 |
|                        | number_of_sims       | 10            | number of simulations to run per window                       |
| filter_hits            | dna_fragment_length  | 200           | length of sheared fragments                                   |
|                        | bin_size             | 1000          | bin size for linear regression                                |
|                        | max_count            | 3             | maximum number of tags allowed to start at the same position  |
|                        | extended_region_size | 2000          | distance to count control tags                                |
|                        | Pf                   | 1             | portion of peaks to consider for adjusting control tag counts |
| adjust_and_select_hits | pval_threshold       | 0.05          | p-value to determine significant peaks                        |

This table shows the parameters that were used when running PeakSeq. Default parameters were used for all other values. PeakSeq was run three times using a different max\_gap parameter each time. All other parameters were the same for each run.