Supplementary Figures and Table Legends:

Figure S1. Clustered distribution of POU5F1 (Oct4) binding (related to Figure 3) Example of Wide Binding in POU5F1. We computed an average log ratio of binding for every position in the genome within 100bp upstream or 100bp downstream of the center of POU5F1 enriched oligos (top 1% enrichment). We plotted this curve and computed the area under the curve (and above a background rate of enrichment) for the oligo ligand and the adjacent regions. See Table S2 for data in all of the transcription factor enrichments.

Figure S2, Architecture of NANOG octaomer composite motif (related to Figure 6) NANOG-to-octamer Distance in top 5% NANOG enrichment relative to bottom 25% enrichment. The blue bars represent the position of the center of NANOG recognition elements (CATT) in the top 5% enrichment for NANOG binding. The red line plots the analogous distribution in the bottom 25% enrichment. We find that there did not exist substrates with NANOG 7-12 nucleotides upstream of the center of the octamer in the bottom enrichment, whereas there are 7 such substrates in the top enrichment. Refer to Table S3 for the calculation of test statistic.

Figure S3. Gibbs Sampling Motifs for Top Enrichments (related to Figure 4). Gibbs Sampling Motifs for Top Enrichments. Refer to Supplementary Experimental Procedures: Gibbs Sampling for information on the presentation of motif logos.

Table S1. Phastcons Scoring for Top 1% Enrichment

Table S2, related to Figure 3: Binding Width Ratio Calculation

Table S3, related to Figure 6: χ^2 Table for NANOG recognition element

Table S4: Log Ratio Scores for All Oligonucleotides

Table S5, related to Figure 2: MORE and PORE Oligonucleotide Scores

Table S6, related to Figure 4: TRANSFAC/JASPAR Centroids

Table S7, related to Figure 7: Enriched 5-mer Words in POU2F1 (Oct1) Top 1% Enrichment (Dr. Octamer)