method flowchart: motif discovery

1. quantile-rank transformation on RBP binding data
2. randomly split each IP Column into equal sized Train and test sets
3. sequence: either full mRNAs, 5' UTRs, ORFs or 3' UTRs
4. PSAM discovery with MatrixREDUCE software
5. calculate motif scores using AffinityProfile software
6. validation
7. Add at most one nucleotide (N) to flank sides of the discovered PSAMs
8. optimize PSAM with OptimizePSAM software
9. All weights at flanks larger than 0.1?
   - Yes: optimize PSAM on full IP data with OptimizePSAM software
   - No: optimize PSAM with OptimizePSAM software

Figure S2  The flowchart representation of our motif search approach.