

Figure S4. Blind prediction of 3D contacts of disordered proteins with known structures captured by evolutionary couplings (30 proteins, Table S2B).

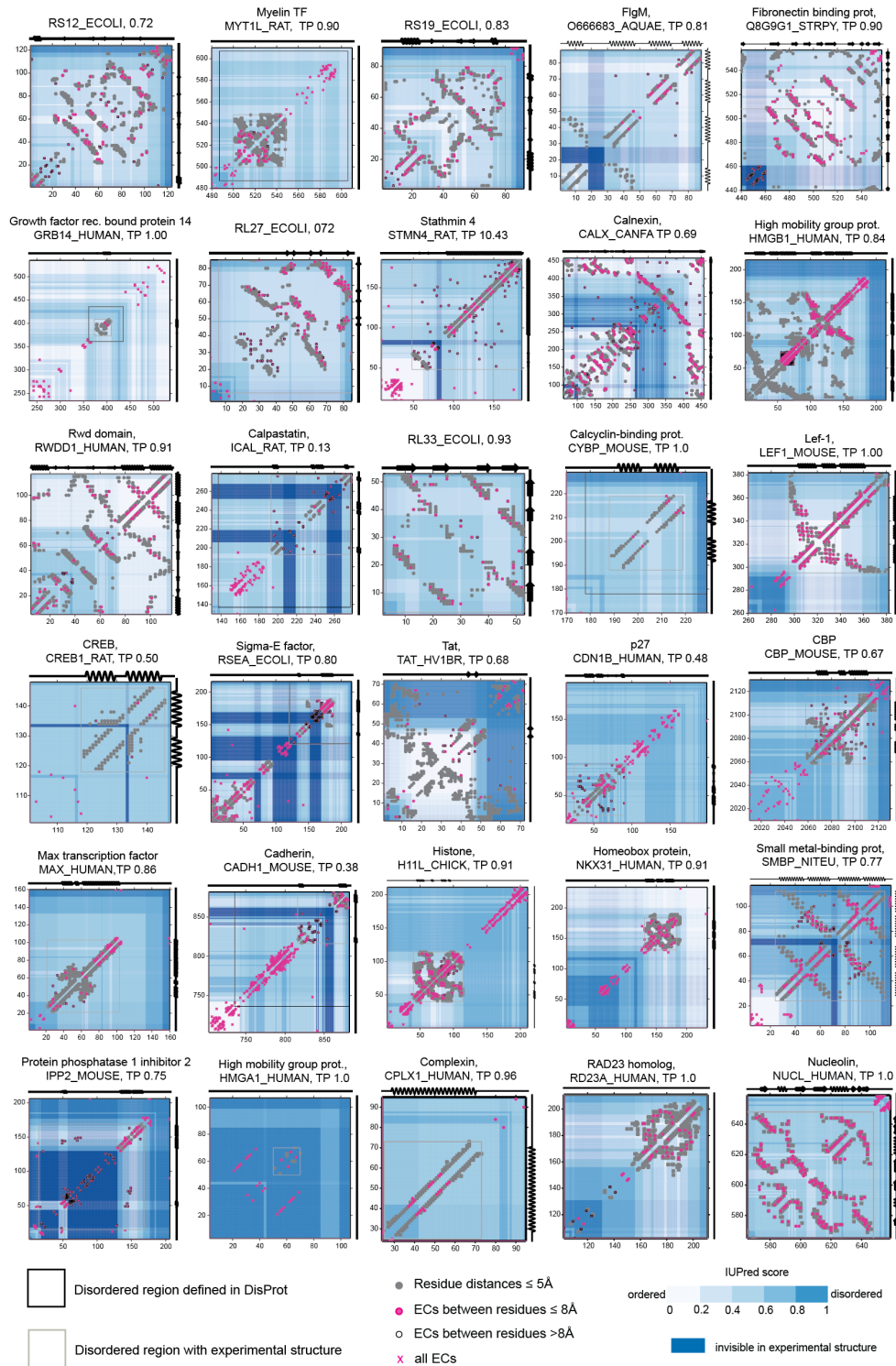


Figure S4. Blind prediction of 3D contacts of disordered proteins with known structures captured by evolutionary couplings (30 proteins, Table S2B).

Contact maps of all disordered proteins in our dataset that were captured in a 3D conformation (28 proteins, **Table S2B**). Contacts in experimental structures are shown as grey spheres, predicted contact are shown as pink spheres. False positive ECs are shown as empty circles. True positive rates (TP) are indicated above each contact map plot (Supplementary Table 1). Predicted disorder scores (by IUPred) are shown as blue color gradient in the background. Uniprot ids and PDB codes and chains are as follows: RS12_ECOLI (3j0e_F), MYT1L_RAT (1pxe_A), RS19_ECOLI (2ykr_S), O66683_AQUAE (1rp3_B), Q8G9G1_STRPY (2x5p_A), GRB14_HUMAN (2auh_B), RL27_ECOLI (3j5l_W), STMN4_RAT (3ryc_E), CALX_CANFA (1jhn_A), HMGB1_HUMAN (2yrq_A), RWDD1_HUMAN (2ebm_A), ICAL_RAT (3df0_C), RL33_ECOLI (3j5l_1), CYBP_MOUSE (2jtt_C), LEF1_MOUSE (2lef_A), CREB1_RAT (1kdx_B), RSEA_ECOLI (3m4w_E), TAT_HV1BR (1jfw_A), CDN1B_HUMAN (1jsu_C), CBP_MOUSE (1kbh_B), MAX_HUMAN (1nkp_B), CADH1_MOUSE (1i7w_B), H11L_CHICK (1ghc_A), NKX31_HUMAN (219r_A), SMBP_NITEU (3u8v_A), IPP2_MOUSE (2o8a_I), HMGA1_HUMAN (2ezf_A), CPLX1_HUMAN (3rl0_g), RD23A_HUMAN (1qze_A), NUCL_HUMAN (2fc8_A).