Transcription Factor	Excess Conservation	Bayesian Branch Length (BBL)	Improvement Over BBL
AP2ALPHA	0.039	0.029	35.2%
AP2GAMMA	0.050	0.038	31.6%
ATF3	9.9×10^{-5}	7.3×10^{-5}	35.2%
BATF	0.022	0.018	21.0%
BCL3	0.006	0.005	20.3%
BHLHE40	0.035	0.012	193.0%
CEBPB	0.004	0.005	-20.8%
CTCF	0.440	0.340	29.3%
E2F1	0.306	0.292	4.9%
E2F4	0.352	0.319	10.0%
E2F6	0.318	0.278	14.6%
EBF	0.025	0.021	18.2%
EGR1	0.014	0.008	71.9%
ESRRA	0.004	0.002	171.7%
FOS	0.019	0.010	85.1%
FOSL2	0.035	0.020	77.7%
FOXP2	1.8×10^{-4}	7.8×10^{-5}	40.9%
GABP	0.198	0.073	170.5%
GATA1	0.005	0.003	67.0%
GR	0.015	0.013	17.9%
HNF4A	0.012	0.009	33.6%
HSF1	0.002	0.001	28.5%
IRF4	0.012	0.010	12.2%
JUN	0.038	0.035	10.6%
JUND	0.073	0.052	40.1%
MAX	0.048	0.022	121.7%
MYC	0.057	0.025	127.7%
NFE2	0.020	0.008	133.6%
NFKB	0.042	0.041	2.3%
NFYA	0.082	0.013	526.8%
NFYB	0.079	0.013	514.1%
NRSF	0.052	0.047	10.3%
PAX5	0.035	0.023	53.2%
PBX3	0.0011	0.0012	-5.5%
POU2F2	0.005	0.002	131.2%
PU1	0.027	0.019	38.4%
RXRA	0.011	0.011	7.6%
SIX5	2.7×10^{-4}	2.5×10^{-4}	4.4%
SP1	0.044	0.036	22.6%
SREBP1	0.001	0.0006	56.0%
SREBP2	0.001	0.0005	67.2%
SRF	0.025	0.010	144.6%
STAT1	0.023	0.020	11.2%
STAT2	0.004	0.003	57.6%
TCF4	0.008	0.009	-8.9%
USF1	0.035	0.014	153.1%
YY1	0.019	0.005	250.1%
Better performing:	44	3	