

Supplemental Information

Position Weight Matrices from Improbizer

PHA-4 (from Ph-E and Ph-L, respectively):

7.4786 TGTTTGCC
a 0.003 0.003 0.003 0.040 0.003 0.003 0.113 0.259
c 0.003 0.003 0.003 0.113 0.040 0.003 0.442 0.296
g 0.003 0.990 0.003 0.186 0.003 0.990 0.296 0.223
t 0.990 0.003 0.990 0.662 0.954 0.003 0.149 0.223

8.1637 TTGTTTGC
a 0.127 0.003 0.003 0.003 0.003 0.003 0.003 0.065
c 0.250 0.003 0.003 0.003 0.003 0.003 0.003 0.682
g 0.127 0.065 0.990 0.003 0.065 0.127 0.990 0.003
t 0.497 0.928 0.003 0.990 0.928 0.867 0.003 0.250

Early-1:

7.4694 AGAGACGAAG
a 0.435 0.034 0.867 0.003 0.867 0.127 0.003 0.650 0.466 0.249
c 0.096 0.065 0.065 0.065 0.126 0.651 0.003 0.251 0.219 0.157
g 0.281 0.898 0.003 0.929 0.003 0.096 0.990 0.065 0.065 0.343
t 0.188 0.003 0.065 0.003 0.003 0.126 0.003 0.034 0.250 0.250

Early-2:

7.4500 TCTGACCGT
a 0.219 0.003 0.003 0.003 0.960 0.003 0.003 0.034 0.158
c 0.065 0.712 0.158 0.281 0.003 0.959 0.743 0.065 0.003
g 0.126 0.003 0.003 0.713 0.003 0.003 0.250 0.528 0.219
t 0.590 0.281 0.836 0.003 0.034 0.034 0.003 0.373 0.620

Early-3:

7.6078 AAAAAAGTGGGA
a 0.497 0.435 0.528 0.466 0.620 0.713 0.188 0.342 0.003 0.219 0.003 0.497
c 0.096 0.158 0.065 0.281 0.065 0.003 0.003 0.003 0.003 0.003 0.003 0.219
g 0.281 0.342 0.312 0.188 0.188 0.219 0.805 0.003 0.990 0.774 0.990 0.188
t 0.126 0.065 0.096 0.065 0.127 0.065 0.003 0.651 0.003 0.003 0.003 0.096

Late-1:

8.6489 GGGAGGCGGGGA
a 0.378 0.207 0.310 0.582 0.037 0.003 0.037 0.003 0.276 0.139 0.310 0.378
c 0.105 0.037 0.275 0.071 0.071 0.412 0.684 0.003 0.003 0.105 0.037 0.207
g 0.412 0.752 0.310 0.344 0.820 0.582 0.003 0.990 0.718 0.650 0.582 0.310
t 0.105 0.003 0.105 0.003 0.071 0.003 0.275 0.003 0.003 0.105 0.071 0.105

Late-2:

7.61 TTTTTCC
a 0.352 0.003 0.003 0.003 0.032 0.003 0.003
c 0.090 0.032 0.090 0.003 0.003 0.990 0.990
g 0.003 0.003 0.003 0.003 0.119 0.003 0.003
t 0.555 0.961 0.904 0.990 0.845 0.003 0.003

Late-3:

7.6973 TCTCGGAA
a 0.188 0.003 0.065 0.003 0.003 0.003 0.682 0.497
c 0.003 0.867 0.065 0.805 0.003 0.003 0.188 0.003
g 0.127 0.127 0.003 0.188 0.990 0.990 0.003 0.250
t 0.682 0.003 0.867 0.003 0.003 0.003 0.127 0.250

PI:

7.1263 TTTTCACCAG
a 0.185 0.211 0.029 0.003 0.003 0.912 0.029 0.003 0.315 0.341
c 0.133 0.029 0.237 0.029 0.757 0.081 0.964 0.964 0.237 0.159
g 0.211 0.341 0.003 0.029 0.185 0.003 0.003 0.029 0.185 0.393
t 0.471 0.419 0.730 0.938 0.055 0.003 0.003 0.003 0.263 0.107

7.1440 TGGGCTCAC

a	0.250	0.144	0.109	0.003	0.003	0.215	0.038	0.743	0.039
c	0.039	0.144	0.038	0.039	0.955	0.038	0.814	0.039	0.955
g	0.321	0.392	0.462	0.920	0.039	0.003	0.003	0.145	0.003
t	0.391	0.320	0.391	0.038	0.003	0.744	0.144	0.074	0.003

P2:

7.6779 TCTTCCAAA

a	0.180	0.003	0.003	0.109	0.003	0.003	0.779	0.743	0.532
c	0.003	0.497	0.039	0.003	0.955	0.990	0.179	0.003	0.180
g	0.109	0.003	0.003	0.003	0.039	0.003	0.003	0.215	0.003
t	0.708	0.497	0.955	0.885	0.003	0.003	0.039	0.039	0.285

The PWMs are shown with their associated Improbizer score and the 'best match' sequence to the PWM. The score is used as a measure of significance by comparing motif scores to scores generated by control runs of Improbizer against randomized sequence.