

Table S1. Oligonucleotides used to obtain FISH probes from bands predicted by the four chromatin state model

Probe	Forward primer	Reverse primer	Probe coordinates (dm3)
PlexB	5'-ACAACCTTCGCTGATATT-3'	5'-TGTTCGCTTGCTTAGAG-3'	chr4:59994-60799
ci	5'-CATCCAGGTGCTTCTATAC-3'	5'-GTTCTCGGTAGTGGTTGA-3'	chr4:69435-70241
pan	5'-CCAAGTCGCAGCTCTATT-3'	5'-GCCTAAGAGTATCCACATCC-3'	chr4:121380-122168
CG32006	5'-TCCACCACACGCATTATT-3'	5'-GAGTTGGTTCTGTGTTCT-3'	chr4:171797-172593
Nfi	5'-TCTCACACACCGACATTAG-3'	5'-CCCAAGCCGAAGAGTTTA-3'	chr4:291032-291853
Lin29	5'-CATACGGACGGAAAGACTAA-3'	5'-CCACACATAGGAGGAACAA-3'	chr4:409421-410217
zfh2	5'-GCGCATCTCCGAAATA-3'	5'-GGTTGAGAGTAAGCGTAGAG-3'	chr4:546526-547326
CG1909	5'-GAGCCGAGACGTACTTAAA-3'	5'-TCCCTCCGACTATCCTATC-3'	chr4:605956-606771
bt	5'-TGTAAGGGCGTCGTAAAG-3'	5'-CCTGGTCTATCTGGTTCATC-3'	chr4:774728-775516
Sox102F	5'-GAGGTGAACACCTGATAAA-3'	5'-GACCTGGCAACGATAAT-3'	chr4:826731-827536
toy	5'-GTCAGAAACGCTTCTACT-3'	5'-CTTCCCGTTAGTCCAGATAC-3'	chr4:1025961-1026761
Rfabg	5'-CATCGACGGCAGTATCAA-3'	5'-TACTTCTCGGTCATAAC-3'	chr4:1091079-1091901
CG11155	5'-CGCAGTTCCCGAGATATT-3'	5'-AGAGCGACGGAATAAA-3'	chr4:1154175-1154991
CG33521	5'-GCTTTGTGGCGATAGTTTAC-3'	5'-CTAGACCTCGGCGTTTATAG-3'	chr4:1207907-1208708
Cadps*	5'-TAGCTTATGTGGTGTACACG-3'	5'-AGATGCAACTTGAGCATAGTG-3'	chr4:1268218-1269117

*This probe from the end of the fourth chromosome was obtained by lowering the PCR elongation temperature to 60°C

Table S2. Oligonucleotides used to obtain FISH probes from open chromatin predicted by the four chromatin state model

Probe	Forward primer	Reverse primer	Probe coordinates (dm3)
Zip102B	5' - GGAGTCCACAATTAAGTCA - 3'	5' - GGGTATGCCCATGTTTATA - 3'	chr4:331263-331983
Hcf	5' - TATAGGGAAGCGTCTAGTT - 3'	5' - AAGACGACCATTAGCTCTT - 3'	chr4:380790-381582
Asator	5' - AGTTTCGTTGAACTTCTAT - 3'	5' - CAACTGGTGTCTCTATG - 3'	chr4:502957-503631
Eph	5' - CGTCCCTTAACAAGAATAC - 3'	5' - GCTTCTCGAGTTGTATCC - 3'	chr4:631665-632380
mav	5' - CCATTAGGGTTCCTTTGC - 3'	5' - CCGAATCCGATCTGGTTA - 3'	chr4:646226-646906
Ekar	5' - CCAATCTGACCAAGGGT - 3'	5' - CCCTGCAGTTACATTAC - 3'	chr4:667070-667779
Slip1	5' - CTACCAAGTCTGTAGTAA - 3'	5' - TTGGAAGAGCAGAGACCA - 3'	chr4:686812-687535
myo	5' - CAAATAGACCCGAAGAAAC - 3'	5' - GCTTACAATCCATCCAATAA - 3'	chr4:717011-717731
l_Sox102F	5' - TGTTACCATCCCTATTATAC - 3'	5' - TCAACTCGGCTATTTATCC - 3'	chr4:856150-856850
CG11148	5' - CTTTCGTAACGAGACCTAAA - 3'	5' - TGTGAAGGAGACAGTAATC - 3'	chr4:888766-889498
unc-13	5' - CAAGGGAGAAAGAAGAAGA - 3'	5' - ATTGCCCATGCAGTAATAAA - 3'	chr4:899961-900686
l_unc-13	5' - CAAGGGAGGGTTAAGTATA - 3'	5' - CTAAGCAACAGTAGCGAAA - 3'	chr4:925604-926283
eIF4G	5' - CTGGAGCCTTACTTATTTG - 3'	5' - CGGAAAGGGCTCATTATC - 3'	chr4:950896-951616
mGluR	5' - GCCTATATCCTAACCAATAA - 3'	5' - GTAGAATTTGAATCTCGAAG - 3'	chr4:968580-969277
4E-T	5' - TCTACGCATACAGTGATAG - 3'	5' - GTCCGATTCGTAGCAATA - 3'	chr4:980957-981641
CG11076	5' - CTTCGTCCAGGTCATTAG - 3'	5' - GATCCACATCTGCTAGTC - 3'	chr4:1050543-1051253
CaMKII	5' - GGCATGGGATAAAGCATG - 3'	5' - CGCATGTAACCTGCAAAG - 3'	chr4:1072731-1073408
Zyx	5' - CTGTATGACCTCCCTGT - 3'	5' - GTCGAGTGAGCGAATTTAT - 3'	chr4:1082117-1082864
Cals	5' - CGGCTTTGAGCTAATAAA - 3'	5' - GGGCAGAATGACTAAAAG - 3'	chr4:1138891-1139561
CG32017	5' - AGAGCATTCCCATACATTC - 3'	5' - CAATAAGTCTTTCCCAACC - 3'	chr4:1167296-1167995
pho	5' - GATACGGTCCACAATACA - 3'	5' - GGATTAGCAAAGGAGAAGT - 3'	chr4:1202556-1203255
PIP4K	5' - GAAATTCTTGCCATATTAG - 3'	5' - TCGTACATATGACCTTTG - 3'	chr4:1217808-1218513
l_Cadps	5' - CCACCATCGAAGTTATCG - 3'	5' - CGTGGAAACATGAGTATGA - 3'	chr4:1235568-1236287