| Factor | Consensus | Description | Source | Subtraction BH p-value | Microarray DRG BH p-value | Microarray Cerebellum BH p-value |
|---|---|---|---|---|---|---|
| CDP | RATCRATA | Cut-like homeobox 1 | Xie | 1.61E-01 | 8.54E-04 | 1.34E-01 |
| CHX10 | CTAATTW | Ceh-10 homeo domain containing | Xie | 1.41E-02 | 5.20E-01 | 1.57E-01 |
| DM_102 | ATGGYGGA | Discovered motif 102 | Xie | 6.96E-02 | 1.75E-03 | 1.25E+00 |
| DM_109 | YGTCCTTGR | Discovered motif 109 | Xie | 3.06E-02 | 1.01E+00 | 7.18E-02 |
| DM_114 | YTCCCRNNAGGY | Discovered motif 114 | Xie | 9.80E-04 | 1.01E-02 | 6.30E-01 |
| DM_115 | YRTCANNRCGC | Discovered motif 115 | Xie | 1.57E-05 | 2.07E-08 | 3.31E-01 |
| DM_118 | GGCNRNWCTTYS | Discovered motif 118 | Xie | 5.70E-02 | 1.14E-04 | 2.85E-01 |
| DM_123 | GGCNNMSMYNTTG | Discovered motif 123 | Xie | 8.12E-02 | 6.18E-04 | 4.49E-01 |
| DM_138 | MYAATNNNNNNNGGC | Discovered motif 138 | Xie | 1.34E-02 | 3.33E-06 | 1.10E+00 |
| DM_152 | WCAANNNYCAG | Discovered motif 152 | Xie | 5.59E-03 | 1.65E-04 | 4.40E-01 |
| DM_158 | CCCNNNNNNAAGWT | Discovered motif 158 | Xie | 1.48E-02 | 5.59E-02 | 6.95E-01 |
| DM_162 | TAANNYSGCG | Discovered motif 162 | Xie | 4.78E-07 | 3.11E-03 | 4.39E-01 |
| DM_165 | CCAWNWWNNNGGC | Discovered motif 165 | Xie | 4.30E-01 | 4.07E-02 | 6.89E-01 |
| DM_174 | WTGAAAT | Discovered motif 174 | Xie | 1.50E-04 | 5.29E-04 | 4.23E-01 |
| DM_19 | GKCGCNNNNNNNTGAYG | Discovered motif 19 | Xie | 4.32E-01 | 5.14E-03 | 8.64E-01 |
| DM_27 | TGGNNNNNNKCCAR | Discovered motif 27 | Xie | 1.80E-02 | 7.45E-01 | 5.92E-02 |
| DM_29 | CTTTAAR | Discovered motif 29 | Xie | 3.49E-02 | 2.21E-02 | 1.16E+00 |
| DM_34 | CYTAGCAAY | Discovered motif 34 | Xie | 3.82E-01 | 4.27E-02 | 3.60E-01 |
| DM_63 | AAGWWRNYGGC | Discovered motif 63 | Xie | 7.66E-04 | 6.84E-04 | 5.23E-01 |
| DM_66 | RACTNNRTTTNC | Discovered motif 66 | Xie | 9.12E-03 | 4.53E-01 | 1.56E-01 |
| DM_74 | GGAMTNNNNNTCCY | Discovered motif 74 | Xie | 7.61E-03 | 8.08E-03 | 9.89E-01 |
| DM_80 | SNACANNNYSYAGA | Discovered motif 80 | Xie | 1.01E-02 | 6.19E-01 | 5.46E-02 |
| DM_81 | CGGAARNGGCNG | Discovered motif 81 | Xie | 6.98E-04 | 8.05E-04 | 2.04E-01 |
| DM_91 | GTGGGTGK | Meningioma (disrupted in balance | Xie | 1.43E-03 | 7.38E-03 | 7.84E-01 |
| DM_99 | ATCMNTCCGY | Discovered motif 99 | Xie | 1.08E-02 | 1.96E-01 | 1.97E-01 |
| ER | TGACCT | Estrogen receptor | Xie | 1.40E-01 | 8.94E-03 | 1.21E+00 |
| ERRALPHA | TGACCTTG | Estrogen related receptor, alpha | Xie | 4.56E-02 | 1.60E-01 | 8.43E-01 |
| ESRRA | TGACCTY | Estrogen related receptor, alpha | Xie | 5.33E-01 | 2.05E-02 | 1.15E+00 |
| F$ABAA_01 | YNNBYYNCATTCCNNNNNN | AbaA (Aspergillus nidulans) | Transfac | 1.91E-02 | 8.01E-01 | 2.68E-01 |
| F$CBF1_B | NRTCACRTGA | Cbf1 (Saccharomyces cerevisiae) | Transfac | 5.81E-01 | 3.35E-05 | 1.73E-01 |
| F$DDE1_B | CGCTCAGCC | Dde box (Neurospora crassa) | Transfac | 1.34E-02 | 1.49E-03 | 3.96E-01 |
| F$FACBALL_Q2 | NNNNNKCCNNTCNNBCNNGGMNNNWN | Facb (Aspergillus nidulans) | Transfac | 3.38E-02 | 7.32E-02 | 1.01E+00 |
| F$GBF_Q6 | TTGGGGGTG | Gbf (Dictyostelium discoideum) | Transfac | 1.24E-02 | 1.64E-01 | 2.29E-01 |
| F$GCR1_01 | GGCTTCCWC | Gcr1 (Saccharomyces cerevisiae) | Transfac | 5.98E-01 | 4.28E-02 | 4.09E-01 |
| F$HAC1_Q2 | KGMCAGCGTGTC | Hac1 (Saccharomyces cerevisiae) | Transfac | 3.13E-02 | 1.27E+00 | 1.02E+00 |
| F$HAP234_01 | AYCVDCCAATNANMNN | HAP2/3/5, yeast homolog to verte | Transfac | 2.34E-02 | 1.27E+00 | 2.22E-01 |
| F$MAT1MC_02 | YCNATTGTTW | M-box interacting with Mat1-Mc ( | Transfac | 4.37E-02 | 9.63E-01 | 9.82E-01 |
| F$MATALPHA2_( | NCATGTNAWN | mating factor alpha2 (Schizosaccha | Transfac | 1.74E-03 | 2.28E-02 | 1.21E+00 |
| F$STE12_Q4 | ATGAAAC | Ste12 ((Saccharomyces cerevisiae) | Transfac | 2.36E-03 | 3.81E-02 | 3.22E-01 |
| F$STRE_01 | TMAGGGGN | Stress response element | Transfac | 1.16E-05 | 2.16E-04 | 9.52E-01 |
| F$XBP1_Q2 | CTTCGAG | Xbp1 (Saccharomyces cerevisiae) | Transfac | 3.37E-02 | 7.22E-06 | 1.25E-01 |

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|---|---|---|---|---|---|---|
| GFI-1 | TGATTTRY | Growth factor independent 1 tran | Xie | 2.27E-02 | 9.42E-01 | 6.44E-01 |
| I$ABDB_Q6 | CATAAAA | Abd-B (Drosophila melanogaster) | Transfac | 8.27E-03 | 4.01E-01 | 2.01E-01 |
| I$BRCZ4_01 | WWWRTAAASAWAA | Broad-Complex Z4 (Drosophila me | Transfac | 3.02E-02 | 3.25E-01 | 4.70E-01 |
| I$CF1_01 | GGGGTCAYS | Chorion factor 1 (Drosophila mela | Transfac | 1.20E-01 | 2.20E-03 | 6.73E-01 |
| I$CF1_02 | GGGGTCACG | Chorion factor 1 (Drosophila mela | Transfac | 2.63E-02 | 1.14E-04 | 6.10E-01 |
| I$CF2II_01 | RTATATRTA | Chorion factor 2 (Drosophila mela | Transfac | 1.38E-02 | 8.21E-01 | 1.04E+00 |
| I$PRD_Q6 | AAATTRY | Paired (Drosophila melanogaster) | Transfac | 1.42E-02 | 8.55E-02 | 1.31E+00 |
| I$SD_Q6 | CATTYCN | Scalloped (Drosophila melanogast | Transfac | 1.72E-02 | 4.43E-03 | 2.11E-01 |
| I$SGF3_Q6 | TTRTKCA | SGF-3 (Bombyx mori) | Transfac | 2.07E-02 | 8.71E-01 | 4.26E-01 |
| IPF1 | TCATTAnY | Pancreatic and duodenal homeob | Xie | 7.41E-02 | 3.40E-02 | 2.92E-01 |
| LEF1 | CTTTGT | Lymphoid enhancer-binding factor | Xie | 3.70E-02 | 8.15E-01 | 2.62E-01 |
| MEIS1 | TGACAGNY | Meis homeobox 1 | Xie | 5.98E-03 | 6.70E-01 | 4.48E-01 |
| N$TRA1_01 | TGGGWGGT | TRAnsformer (Caenorhabditis eleg | Transfac | 8.12E-03 | 1.30E-01 | 5.01E-01 |
| N$TRA1_02 | TGGGWGGT | TRAnsformer (Caenorhabditis eleg | Transfac | 8.08E-03 | 1.30E-01 | 5.02E-01 |
| NF-E2 | TGASTMAGC | v-maf musculoaponeurotic fibrosa | Xie | 1.99E-01 | 4.14E-02 | 1.14E+00 |
| NF-MUE1 | CGGCCATYK | YY1 transcription factor | Xie | 2.15E-01 | 3.08E-02 | 3.95E-01 |
| NKX6-2 | TAATTA | NK6 homeobox 2 | Xie | 1.40E-02 | 5.19E-01 | 1.57E-01 |
| OCTAMER | YATGYAAAT | Octamer Motif | Xie | 5.06E-01 | 2.74E-03 | 1.00E+00 |
| OCT-X | YATGnWAAT | Octamer binding transcription fact | Xie | 1.73E-03 | 1.30E-03 | 1.19E-01 |
| P$ABI4_01 | NNGCACCGCCC | Abi4 (Zea mays) | Transfac | 5.57E-08 | 1.54E-03 | 7.21E-01 |
| P$ABZ1_01 | KKNTKACGTGGNNN | Abz (Lycopersicon esculentum) | Transfac | 1.26E+00 | 2.79E-02 | 4.22E-01 |
| P$DOF2_01 | NNNWAAAGCNN | Dof2 zing finger (Zea mays) | Transfac | 7.59E-03 | 3.00E-03 | 6.60E-02 |
| P$EMBP1_Q2 | GCCACGTGDN | EmBP-1b (Triticum aestivum) | Transfac | 8.89E-02 | 3.23E-02 | 1.46E-01 |
| P$HBP1A_Q2 | GNCACGTGGC | Hbp1a (Triticum aestivum) | Transfac | 8.70E-01 | 1.34E-02 | 4.57E-01 |
| P$HBP1B_Q6 | NKCNGHYACGTCAC | Hbp1b (Triticum aestivum) | Transfac | 1.22E+00 | 3.95E-02 | 1.07E+00 |
| P$LIM1_01 | CCACCANMNNCN | Lim1 (Tabacco, Nicotiana tabacum | Transfac | 1.47E-04 | 2.09E-02 | 4.62E-01 |
| P$PIF3_02 | NNNVCCACGTGGNMVNN | Pif3 (Arabidopsis thaliana) | Transfac | 7.58E-03 | 5.17E-03 | 1.27E-01 |
| P$RAV1_02 | NNCACCTGRNNN | Rav1 (Arabidopsis thaliana) | Transfac | 8.06E-03 | 2.64E-01 | 3.96E-01 |
| P$ROM_Q2 | GCCACSTCA | Rom2 (Phaseolus vulgaris) | Transfac | 3.95E-01 | 1.87E-02 | 5.23E-02 |
| SF-1 | TGACCTTG | Steroidogenic Factor 1 (NR5A1) | Xie | 4.54E-02 | 1.60E-01 | 8.42E-01 |
| STAT | TCCCRGAAR | Signal transducer and activator of | Xie | 2.31E-03 | 1.56E-06 | 5.38E-02 |
| STAT1 | TNCATNTCCYR | Signal transducer and activator of | Xie | 3.35E-03 | 9.81E-01 | 2.76E-01 |
| T3R | TGACCTY | Thyroid hormone receptor | Xie | 5.32E-01 | 2.04E-02 | 1.15E+00 |
| TATA | TATAAA | TATA Motif | Xie | 9.84E-03 | 2.46E-05 | 3.60E-01 |
| TBP | TATAAA | TATA Box binding protein | Xie | 9.80E-03 | 2.45E-05 | 3.59E-01 |
| V$AP2_Q6 | MKCCCSCNGGCG | Activator protein 2 | Transfac | 5.95E-01 | 4.75E-02 | 9.81E-02 |
| V$AP2REP_01 | CAGTGGG | Transcription factor Ap2 gamma | Transfac | 2.02E-03 | 1.93E-03 | 4.85E-01 |
| V$AP3_Q6 | TCYMMATT | AP-3 / Unknown | Transfac | 2.27E-02 | 1.05E+00 | 2.62E-01 |
| V$AP4_Q6_01 | RNCAGCTGC | Transcription factor Ap4 | Transfac | 3.63E-04 | 6.22E-02 | 1.05E-01 |
| V$AR_Q6 | WGAGCANRN | Androgen receptor half site matrix | Transfac | 7.71E-04 | 3.77E-02 | 3.90E-01 |
| V$ATF_01 | CNSTGACGTNNNYC | Activating transcription factor | Transfac | 1.21E-01 | 4.17E-02 | 1.03E+00 |
| V$ATF_B | NTGACGTCANYS | Activating transcription factor | Transfac | 2.17E-02 | 1.20E-03 | 4.41E-01 |
| V$ATF1_Q6 | CYYTGACGTCA | Activating transcription factor 1 | Transfac | 1.18E+00 | 7.92E-03 | 2.80E-01 |

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|---|---|---|---|---|---|---|
| V$BRCA_01 | KTNNGTTG | BRCA1 containing protein complex | Transfac | 1.93E-02 | 2.19E-02 | 6.77E-01 |
| V$CBF_02 | NNNNNTGYGGTYNNNN | Core binding factor (Bos Taurus) | Transfac | 1.71E-03 | 1.95E-04 | 6.07E-02 |
| V$CEBPB_01 | RNRTKDNGMAAKNN | CCAAT/enhancer binding protein b | Transfac | 4.13E-01 | 4.95E-02 | 5.61E-01 |
| V$CRX_Q4 | YNNNTAATCYSMN | Retina and anterior neural fold ho | Transfac | 3.02E-02 | 3.77E-01 | 1.23E+00 |
| V$E12_Q6 | RRCAGGTGNCV | E12 (Xenopus laevis) | Transfac | 1.84E-02 | 7.76E-04 | 4.06E-01 |
| V$E2A_Q2 | NCACCTGYYNCNKN | Myogenin (myogenic factor 4) | Transfac | 8.85E-05 | 1.33E-02 | 2.67E-01 |
| V$E2F_Q6_01 | NKCGCGCSAAAN | E2F transcription factor 7 | Transfac | 1.52E-01 | 2.14E-02 | 1.24E-01 |
| V$EGR_Q6 | GTGGGSGCRRS | Early growth response 3 | Transfac | 9.83E-04 | 9.36E-04 | 4.82E-01 |
| V$ER_Q6_02 | NAGGTCANNNY | Estrogen receptor | Transfac | 8.80E-01 | 4.52E-03 | 1.21E+00 |
| V$GATA3_03 | ANAGATMWWA | GATA-binding factor 3 (Gallus gall | Transfac | 2.70E-02 | 1.84E-01 | 1.12E-01 |
| V$GATA6_01 | NNNGATWANN | Gata6 (Xenopus laevis) | Transfac | 1.58E-02 | 3.10E-03 | 6.42E-02 |
| V$GR_Q6_01 | NNTGTYCT | Glucocorticoid receptor (NR3C1) | Transfac | 1.82E-01 | 2.24E-02 | 2.20E-01 |
| V$HEB_Q6 | RCCWGCTG | Transcription factor 12 | Transfac | 1.10E-02 | 1.56E-02 | 4.63E-01 |
| V$HIC1_03 | NNNGGKTGCCCSNNNNNN | Hypermethylated in cancer 1 | Transfac | 3.65E-03 | 4.59E-03 | 1.24E-01 |
| V$IK2_01 | NNNTGGGAWNNC | IKAROS family zinc finger 1 (Ikaros | Transfac | 2.34E-01 | 4.78E-02 | 2.74E-01 |
| V$IRF_Q6_01 | RAAANTGAAAN | Interferon regulatory factor | Transfac | 4.59E-02 | 1.70E-01 | 3.53E-01 |
| V$KAISO_01 | NTCCTGCNAN | Zinc finger and BTB domain contai | Transfac | 1.85E-02 | 6.43E-01 | 7.70E-01 |
| V$KROX_Q6 | CCCGCCCCCRCCCC | Early growth response 4 | Transfac | 1.43E-02 | 6.35E-05 | 4.62E-01 |
| V$LMO2COM_0 | NMGATANSG | LIM domain only 2 (rhombotin-like | Transfac | 4.40E-02 | 8.47E-02 | 7.00E-02 |
| V$MEF2_02 | NNNNNNKCTAWAAATAGMNNNN | Myocyte enhancer factor 2A | Transfac | 4.61E-01 | 2.75E-02 | 4.24E-01 |
| V$MYB_Q3 | NNNGNCAGTTN | c-Myb (Gallus gallus) | Transfac | 5.15E-01 | 2.71E-03 | 8.02E-01 |
| V$MYB_Q6 | NNNAACTGNC | c-Myb (Gallus gallus) | Transfac | 1.37E-02 | 1.76E-01 | 1.30E-01 |
| V$MYCMAX_01 | NNACCACGTGGTNN | c-Myc:Max heterodimer | Transfac | 3.64E-02 | 1.98E-01 | 1.23E+00 |
| V$MYCMAX_B | GCCAYGYGSN | c-Myc:Max heterodimer | Transfac | 6.35E-02 | 4.68E-03 | 5.72E-01 |
| V$MYOD_Q6_01 | CNGNRNCAGGTGNNGNAN | Myogenin (myogenic factor 4) | Transfac | 1.08E+00 | 1.05E-02 | 1.23E+00 |
| V$MZF1_02 | KNNNKAGGGGNAA | Myeloid zinc finger 1 | Transfac | 9.00E-03 | 4.96E-01 | 5.23E-01 |
| V$NFY_Q6 | TRRCCAATSRN | Nuclear transcription factor Y, gam | Transfac | 1.22E-02 | 6.85E-05 | 6.88E-02 |
| V$NKX62_Q2 | NWADTAAWTANN | NK related homeobox factor 6-2 | Transfac | 4.55E-02 | 6.52E-01 | 4.01E-01 |
| V$OCT1_03 | NNNRTAATNANNN | Octamer factor 1 | Transfac | 2.08E-02 | 1.21E-01 | 2.73E-01 |
| V$OCT1_B | TATGCAAATN | Octamer binding factor 1 | Transfac | 1.55E-01 | 4.50E-02 | 9.36E-01 |
| V$OCT1_Q6 | NNNNATGCAAATNAN | Octamer factor 1 | Transfac | 4.55E-02 | 4.68E-02 | 1.25E+00 |
| V$OSF2_Q6 | ACCACANM | Runt related transcription factor 2 | Transfac | 5.34E-01 | 4.13E-02 | 7.37E-02 |
| V$P53_02 | NGRCWTGYCY | Tumor suppressor p53 | Transfac | 1.05E-02 | 2.53E-01 | 3.51E-01 |
| V$P53_DECAME | RGRCAWGNCY | Tumor suppressor p53 | Transfac | 6.82E-02 | 3.81E-02 | 4.38E-01 |
| V$PAX3_B | NNNNNNCGTCACGSTYNNNNN | Paired box gene 3 | Transfac | 3.21E-03 | 8.25E-01 | 1.26E+00 |
| V$PITX2_Q2 | WNTAATCCCAR | Paired-like homeodomain transcri | Transfac | 2.62E-03 | 6.41E-01 | 1.28E+00 |
| V$RFX1_02 | NNGTNRCNATRGYAACNN | Regulatory factor X, 1 (influences | Transfac | 2.55E-01 | 1.08E-02 | 4.39E-01 |
| V$SOX5_01 | NNAACAATNN | SRY (sex determining region Y)-bo | Transfac | 3.18E-01 | 9.65E-03 | 4.07E-01 |
| V$SP1_01 | GGGGCGGGGT | Stimulating protein 1 | Transfac | 1.22E-02 | 5.88E-11 | 3.40E-01 |
| V$STRA13_01 | NYSTCACGTGABNN | Basic helix-loop-helix family, mem | Transfac | 1.02E+00 | 4.12E-04 | 8.89E-01 |
| V$T3R_01 | SNNTRAGGTCACGSNN | Thyroid hormone receptor, alpha ( | Transfac | 1.02E+00 | 2.07E-02 | 1.34E+00 |
| V$T3R_Q6 | MNTGWCCTN | Thyroid hormone receptor, beta ( | Transfac | 3.43E-02 | 1.95E-01 | 2.05E-01 |
| V$TBP_01 | TATAAATW | TATA binding protein | Transfac | 1.67E-02 | 9.42E-03 | 1.17E-01 |

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|---|---|---|---|---|---|---|
| V$TBP_Q6 | TTTATAN | TATA binding protein (Saccharomy | Transfac | 2.96E-03 | 4.72E-03 | 6.79E-02 |
| V$TBX5_02 | YNRGGTGTKV | T-box 5 | Transfac | 1.19E-04 | 1.97E-01 | 1.15E+00 |
| V$TFE_Q6 | TCATGTGN | Transcription factor EC | Transfac | 1.69E-01 | 5.69E-03 | 4.56E-01 |
| V$UF1H3BETA_ | GGYGGGGGAGGGGC | UF1-H3beta | Transfac | 2.35E-02 | 8.69E-01 | 8.26E-02 |
| V$USF_Q6_01 | NRCCACGTGASN | Upstream transcription factor | Transfac | 6.80E-01 | 4.59E-02 | 6.98E-01 |