

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|----------------------|------------------------|-----------------|
| | DME_ACAGRWKYYR | 5.83111442999999e-26 | L3D6_L3D9 |
| | gimme_119_MEME_6_w14 | 3.12119309057e-18 | L3D6_L3D9 |
| | gimme_149_MEME_6_w14 | 8.6337720765e-18 | L3D6_L3D9 |
| | gimme_159_MEME_6_w14 | 1.5834470691100003e-16 | L3D6_L3D9 |
| | DME_GTKMYWAYMB | 7.16401268048e-16 | L3_L3D6 |
| | gimme_139_MEME_6_w14 | 2.46612936627e-15 | L3D6_L3D9 |
| | gimme_137_MEME_8_w10 | 5.56252185659e-14 | L3D6_L3 |
| | DME_KSMBGCAMTH | 6.975558231269999e-14 | L3_L3D6 |
| | DME_AAGTGMKKVM | 8.93847419528e-14 | L3_L3D6 |
| | DME_SMSTSATYHR | 1.1572735682200002e-12 | L3_L3D9 |
| | DME_WWCCTGTY | 1.0015232355e-11 | L3D6_L3D9 |
| | DME_SGKTKAAC | 1.86836603585e-11 | L4_L3 |
| | DME_KARCMKTHAT | 2.5396492126599998e-11 | L3_L3D9 |
| | DME_CADCARAC | 4.96769378776e-11 | L3_L4 |
| | gimme_153_MEME_4_w14 | 6.43673007752e-11 | L3D6_L3 |
| | DME_TRCHBBAGRA | 1.1240885187899999e-10 | L3_L3D6 |
| | DME_RARGYGGAA | 1.48493790136e-10 | L3D6_L4 |
| | DME_TWTCAGABWR | 1.6603833145299998e-10 | L3D6_L4 |
| | DECOD_Motif5_10 | 2.7986438423900004e-10 | L3D6_L3 |
| | DECOD_Motif6_8 | 4.13776690814e-10 | L3_L4 |

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|------------|------------------------------|------------------------|-----------------|
| | DME_SWTKMACKMY | 6.07087310923e-10 | L3_L3D6 |
| | DME_AAGCAAAA | 6.9000364243e-10 | L3D9_L3D6 |
| | DME_DAWCCTGT | 6.96763364108e-10 | L3D6_L3D9 |
| | gimme_26_BioProspector_w10_5 | 8.974579180639999e-10 | L3D9_L3 |
| | DME_HATMCATC | 1.04207011616e-09 | L3D6_L4 |
| | DME_HVMATMCAKC | 1.19117831479e-09 | L3D6_L4 |
| | DME_KRVAAMGGD | 1.5480824967e-09 | L3D6_L3 |
| | DME_GAAVRKGC | 1.5971044169099999e-09 | L3D9_L3D6 |
| | DME_AAGCGCAATTCAATTG | 1.6843114291499999e-09 | L3D9_L3 |
| | DME_TGCWATGR | 1.86268835835e-09 | L3D9_L3D6 |
| | DME_MYMGCTSWRW | 2.77881147796e-09 | L3_L3D6 |
| | DME_MAAYAAYADC | 2.95831650732e-09 | L3D6_L4 |
| | DME_ATCASABWRK | 3.65156250279e-09 | L3D6_L4 |
| | DME_WRMAATGAYM | 1.40407109058e-08 | L3D9_L3D6 |
| | DECOD_Motif4_10.2 | 1.43366681789e-08 | L4_L3 |
| | DME_CDKYWBCAA | 2.2976758483599998e-08 | L3D9_L3D6 |
| | DME_AGCGCAATTCAATTCT | 3.01796745719e-08 | L3D9_L3 |
| | DME_YYAGATGA | 3.18648013269e-08 | L4_L3 |
| | DME_TYGWMACMWB | 3.73688409945e-08 | L3_L3D6 |
| | DME_AAAAGTTATT | 3.74020186852e-08 | L3D6_L3 |

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|------------|------------------------------|------------------------|-----------------|
| | gimme_94_MDmodule_Motif.14.9 | 3.85329584809e-08 | L3_L3D9 |
| | DME_MAVCMSGT | 3.9960560497300007e-08 | L4_L3D6 |
| | gimme_65_MDmodule_Motif.10.3 | 4.65965767697e-08 | L3_L4 |
| | DME_AAAAWGSG | 4.7876649673e-08 | L3D6_L3D9 |
| | DME_TSARAYWRGW | 5.04088887714e-08 | L3D6_L4 |
| | DME_AAGCTAAA | 5.70125250699e-08 | L3D9_L3 |
| | DME_TKCYGVAWHC | 5.70672365112e-08 | L3_L3D6 |
| | DME_AGTGAAAACCTCTAAA | 5.80952481507e-08 | L3D9_L3D6 |
| | DME_GAARCTAM | 6.62449184479e-08 | L3_L3D6 |
| | DME_WKAGKAAG | 7.66659295855e-08 | L4_L3D6 |
| | DME_ATTAATTAAWTAAT | 9.55618444018e-08 | L3D9_L3D6 |
| | DME_AATTAMTRATTMC | 1.13106397213e-07 | L4_L3 |
| | DME_AATRATAATAGTGR | 1.20025043938e-07 | L3D6_L4 |
| | DME_GVVTGCAA | 1.33101491575e-07 | L4_L3 |
| | DECOD_Motif3_8 | 1.40949594405e-07 | L4_L3 |
| | DME_MAGMAACT | 1.67219532874e-07 | L4_L3D6 |
| | DME_TCATTCSY | 1.68817414144e-07 | L4_L3D6 |
| | DME_AMARCAGM | 1.80897230282e-07 | L4_L3D6 |
| | DME_AAAATCAC | 1.87610233721e-07 | L3_L3D6 |
| | DME_AATAATARTRRYRA | 1.9582137158e-07 | L3D6_L3 |

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|------------|----------------------|------------------------|-----------------|
| | DME_AAAMVGGA | 1.9886226040899998e-07 | L3D6_L3 |
| | DME_SRRAAGTYWR | 2.03262016393e-07 | L3_L3D9 |
| | gimme_169_Weeder_5 | 2.08484378324e-07 | L4_L3 |
| | DME_ATAATAGTAA | 2.15029540656e-07 | L3D9_L3D6 |
| | DME_ACDGCAMT | 2.63117179009e-07 | L4_L3 |
| | DME_AGTRRTAACATAAY | 2.66656159452e-07 | L3D6_L4 |
| | DME_AWTAATARYMCT | 2.95335718791e-07 | L3D6_L4 |
| | DME_CAKTRRCA | 2.96847983901e-07 | L3_L3D9 |
| | DME_WTKRATRGDA | 3.4776418837800003e-07 | L3D6_L3D9 |
| | DME_TSAWCAGA | 3.64701135108e-07 | L3_L3D9 |
| | DME_ATTAAGGTAAAGTT | 4.29214570271e-07 | L4_L3 |
| | DME_AAKAASMAWG | 4.4286917854700004e-07 | L3D6_L3 |
| | DME_TTYRMRVMC | 4.54677789588e-07 | L3_L3D6 |
| | DECOD_Motif4_10.1 | 4.94381063021e-07 | L3D9_L3 |
| | DME_TWAGCWAAAT | 5.20922042222e-07 | L3D9_L3 |
| | DME_AARGGGMV | 5.39806974798e-07 | L4_L3D6 |
| | gimme_44_Homer_12_1 | 7.61154688034e-07 | L3D6_L3 |
| | gimme_160_MEME_8_w14 | 7.685647789609999e-07 | L3_L4 |
| | gimme_120_MEME_8_w14 | 7.86979778034e-07 | L3_L4 |
| | DME_CAACKAYT | 8.51267215048e-07 | L3D6_L3 |

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|------------|--------------------------------------|------------------------|-----------------|
| | DME_VRGAAGHRBA | 8.6540623658e-07 | L3_L3D6 |
| | gimme_32_Homer_12_1 | 8.69824250586e-07 | L3D6_L3 |
| | DME_CAMWSMYMARHK | 8.92806907447e-07 | L3D9_L3D6 |
| | gimme_140_MEME_8_w14 | 9.07296118952e-07 | L3_L4 |
| | DME_AATAATAGTA | 9.644639282280001e-07 | L3D6_L4 |
| | DME_AWYAAACG | 9.8677658018e-07 | L3_L4 |
| | gimme_103_Improbizer_AAGTGATAATAATAA | 9.91527522721e-07 | L3D6_L3 |
| | DECOD_Motif10_10.1 | 1.02622529372e-06 | L3D9_L3D6 |
| | DME_TACAGAAA | 1.05902635165e-06 | L4_L3D6 |
| | gimme_171_Weeder_9 | 1.06001796433e-06 | L3D9_L3D6 |
| | DME_TGAAASYG | 1.0914315344e-06 | L3D9_L3D6 |
| | DME_CTGATRAR | 1.0967685337399999e-06 | L3D6_L3D9 |
| | DME_AGATTAAAAT | 1.11980949803e-06 | L3D6_L3 |
| | DME_MATHCAWYMA | 1.16050933631e-06 | L3D6_L3D9 |
| | gimme_20_BioProspector_w12_2 | 1.17823204884e-06 | L3_L3D9 |
| | gimme_60_Improbizer_TTACTTCT | 1.19284017542e-06 | L3D9_L3D6 |
| | DME_MAMKTGADYR | 1.24992665786e-06 | L3_L3D6 |
| | DME_SAKKCARWRK | 1.28104816497e-06 | L3_L3D6 |
| | DME_MGCTRWAT | 1.36081388155e-06 | L3_L3D6 |
| | DME_MAUGWVVKCAM | 1.427906603e-06 | L3D6_L4 |

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|------------|-----------------------------|------------------------|-----------------|
| | DME_TGAAKSAC | 1.44174054236e-06 | L3_L3D6 |
| | DME_AYAATVATAGTR | 1.4609276697100001e-06 | L3D6_L4 |
| | DECOD_Motif10_10.2 | 1.60310800143e-06 | L3D9_L3 |
| | DME_GAAAMCHG | 1.6335434548799999e-06 | L3_L3D6 |
| | DME_GSTGDRTYMM | 1.6984206600899999e-06 | L3_L3D6 |
| | DME_CATTAATTAA | 1.72624619369e-06 | L4_L3 |
| | DME_GKYDMAAATM | 1.80046045643e-06 | L3D6_L3D9 |
| | DME_SAAACKTK | 1.8358152387099998e-06 | L3_L4 |
| | DME_TTCRMKAYVR | 1.91600465685e-06 | L3_L3D6 |
| | DME_CAAATACT | 1.91833228891e-06 | L3_L4 |
| | DME_WWTRCAATGR | 1.99268244051e-06 | L3D9_L3D6 |
| | DME_AAAWCAATAGMTTT | 1.99829659399e-06 | L3D6_L3 |
| | DME_DKAAARSKRG | 2.17666092173e-06 | L4_L3 |
| | DME_WYGAGAAWWK | 2.2588532652e-06 | L3_L4 |
| | DME_TTAAGATTCAGAGAA | 2.3591911497599997e-06 | L3D6_L3D9 |
| | gimme_12_BioProspector_w8_1 | 2.42541418687e-06 | L3D6_L3D9 |
| | DME_GCAAKYA | 2.43554262418e-06 | L3D9_L3D6 |
| | gimme_159_MEME_10_w14 | 2.52739900366e-06 | L3D6_L3 |
| | DECOD_Motif8_10.1 | 2.84629606825e-06 | L3D6_L3D9 |
| | DME_AAACRAGW | 3.04612211977e-06 | L3_L4 |

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|------------|---|------------------------|-----------------|
| | DME_TCRTYTSMAW | 3.05759965386e-06 | L3D6_L3 |
| | DME_KSAVKTAWMAA | 3.22946444838e-06 | L3D9_L3D6 |
| | DME_GCAAAAMA | 3.5202735692800004e-06 | L3_L4 |
| | DECOD_Motif8_10.2 | 3.6297350967199996e-06 | L3D9_L3 |
| | DME_AATWWGARCR | 3.6942894741199997e-06 | L3_L3D9 |
| | DME_AAKAGGRA | 4.0304027306e-06 | L4_L3D6 |
| | DME_CAAATAATT | 4.26950522889e-06 | L3D9_L3D6 |
| | DME_WTSAAACG | 4.3979149927800005e-06 | L3_L4 |
| | DME_CTCTSAWA | 4.431665893969999e-06 | L3D6_L4 |
| | DME_THMRTHYAWCMA | 4.634799109019999e-06 | L3D6_L3 |
| | DME_SAGAGMAA | 4.74961970082e-06 | L3D6_L3D9 |
| | DME_TYACAACYTA | 4.76522837332e-06 | L3D6_L3D9 |
| | DME_HTRCAATGRM | 4.8278965698099995e-06 | L3D9_L3D6 |
| | gimme_53_Improbizer_TTATTAACAGTAGAAATAAAA | 5.52344012738e-06 | L3_L4 |
| | DME_AYMAACWRAS | 5.94815586555e-06 | L3_L3D9 |
| | DME_ATATCAAATT | 6.46544854454e-06 | L3D9_L3 |
| | DME_TGCWAAMS | 6.512614932919999e-06 | L3_L3D9 |
| | DME_YCATYCAW | 6.67699365386e-06 | L3_L3D9 |
| | DME_GTAAACAA | 6.7100041988e-06 | L3_L3D6 |
| | DME_TRCTRACA | 6.75511015243e-06 | L4_L3D6 |

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|------------|-----------------------------|------------------------|-----------------|
| | DME_MMAMATYGAB | 6.77347216876e-06 | L3_L4 |
| | DME_GCAAWGAW | 7.30174695665e-06 | L3D9_L3D6 |
| | gimme_163_MEME_8_w14 | 7.3244757406100005e-06 | L3_L3D6 |
| | gimme_20_BioProspector_w8_4 | 7.44606355435e-06 | L3D9_L3 |
| | DME_TYHAKMCAYS | 7.572639860569999e-06 | L3D6_L4 |
| | DME_AAATTAATTAAT | 7.5750464225899995e-06 | L3D6_L3 |
| | DME_CAGWAAWC | 7.5879986156699994e-06 | L4_L3D6 |
| | DME_MAYAAMAMYAAY | 7.66733243802e-06 | L3D6_L4 |
| | DME_MAACACMA | 7.7171117801e-06 | L3_L3D6 |
| | DME_AATTAAAATC | 7.840741723339999e-06 | L3_L3D6 |
| | DME_AARTAAKAATAA | 8.15832688557e-06 | L3D6_L3 |
| | DME_AGATCATT | 8.4457216956e-06 | L3_L4 |
| | DME_YTCAAAATAA | 8.67921885925e-06 | L3_L4 |
| | DME_RAWYCTGT | 8.768305401510001e-06 | L3D6_L4 |
| | DME_KASAKTYVAS | 8.87028116263e-06 | L3_L4 |
| | DECOD_Motif7_8 | 9.071014351639999e-06 | L4_L3 |
| | DME_AWTGASCA | 9.33467797719e-06 | L3D6_L3 |
| | DME_AGTATAAAAA | 9.4539813538e-06 | L3D6_L4 |
| | DECOD_Motif1_8 | 9.46131657748e-06 | L3D9_L3D6 |
| | DME_AGNAAGYAAR | 9.46662233715e-06 | L3D9_L3D6 |

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|------------|------------------------|-------------------|-----------------|
| | DME_AAGAAAGA | 9.50949508507e-06 | L4_L3 |
| | DME_TGTAAACA | 9.91399266496e-06 | L3_L3D6 |
| | DME_GTCWCWA | 1.01360338332e-05 | L4_L3D6 |
| | DME_CAAATACR | 1.035146166e-05 | L3_L4 |
| | DME_CTGGTCAAAGAGAAAA.1 | 1.03765116072e-05 | L3D9_L3D6 |
| | DME_TAAKAMTAVTAAMA | 1.06078625783e-05 | L3D6_L4 |
| | DME_AAAGAAATT | 1.06997840874e-05 | L3D6_L4 |
| | gimme_135_MEME_10_w14 | 1.0947374842e-05 | L3D6_L4 |
| | DME_TAATAAACAA | 1.09768654109e-05 | L3D6_L4 |
| | DME_AGCAAAAR | 1.14218233151e-05 | L3_L4 |
| | DME_CTTCAAAA | 1.14922540139e-05 | L3D6_L3 |
| | DME_TAACAAATT | 1.16823533679e-05 | L3D6_L3 |
| | DME_GRYCWAAA | 1.26323723722e-05 | L3_L4 |
| | gimme_39_Homer_12_1 | 1.28156608892e-05 | L3_L3D9 |
| | DME AAAAGGAA | 1.30466762562e-05 | L3D6_L3 |
| | DME_ATGAATGA | 1.3217653183e-05 | L3D6_L4 |
| | DME TRGYAATAAYDATA | 1.43087825516e-05 | L3D6_L3 |
| | DME CTTKTSAAAA | 1.43114205827e-05 | L3D9_L3 |
| | DME AGCTAAAA | 1.46519125294e-05 | L3D6_L3D9 |
| | DME TTAATTGAAA | 1.51067257809e-05 | L3D9_L3D6 |

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|------------|--------------------------------|-------------------|-----------------|
| | DME_TCTGAAAACCAAAT | 1.63073355833e-05 | L3_L3D9 |
| | DME_TTAAAATTAAA | 1.72069416958e-05 | L3D6_L4 |
| | gimme_72_MDmodule_Motif.14.10 | 1.75931352978e-05 | L3D9_L3D6 |
| | DME_AYACAGYT | 1.79123708379e-05 | L3_L4 |
| | gimme_96_MDmodule_Motif.14.1 | 1.81645366732e-05 | L3_L3D9 |
| | DME_TAATGAATTAATTA | 1.8253673932e-05 | L3D9_L3D6 |
| | DME_ATHTCAGASD | 1.85721164702e-05 | L3D6_L4 |
| | DME_TRATRGAAAT | 1.89295428756e-05 | L3D6_L4 |
| | gimme_114_MDmodule_Motif.14.10 | 1.93938262087e-05 | L4_L3 |
| | DME_YCAWYCATT | 2.02047276557e-05 | L3D6_L4 |
| | DME_AATBARTTAAAA | 2.13405549081e-05 | L3D9_L3 |
| | DME_KHYMRCAART | 2.23230616206e-05 | L3D9_L3D6 |
| | gimme_84_MDmodule_Motif.14.10 | 2.27010792543e-05 | L4_L3 |
| | DME_AVAKKGATDG | 2.45277509003e-05 | L3D6_L3D9 |
| | DME_HTTCYRCYW | 2.50244260277e-05 | L3D9_L3D6 |
| | gimme_165_Weeder_3 | 2.54378767942e-05 | L3_L4 |
| | DME_AATAATCAAATGG | 2.5452601427e-05 | L3_L3D9 |
| | DME_RCAAAMGT | 2.60946805351e-05 | L3D9_L3D6 |
| | DECOD_Motif3_10 | 2.69733540405e-05 | L3_L4 |
| | DME_GSAAAAGD | 2.89049592067e-05 | L4_L3 |

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|------------|-----------------------------------|------------------------|-----------------|
| | gimme_60_Improbizer_AAATAAAAGCAA | 2.89127013717e-05 | L3_L4 |
| | DME_AAKTKAWTAATKAA | 2.91453302648e-05 | L3D6_L4 |
| | DME_AARGRTCA | 3.04486586204e-05 | L3_L3D6 |
| | DME_TATCGAAA | 3.09757125866e-05 | L3D9_L3 |
| | DECOD_Motif1_10 | 3.50719247451e-05 | L3_L3D9 |
| | gimme_103_MDmodule_Motif.12.1 | 3.51406396661e-05 | L3_L4 |
| | DME_AAAAACATTT | 3.54210929232e-05 | L3_L4 |
| | DME_AATGAATTAT | 3.87268778359e-05 | L3_L3D9 |
| | DME_AMAGYWATSK | 3.88591644016e-05 | L3_L4 |
| | DME_WAWRAAKKAWTGAA | 3.9546180953000004e-05 | L3D9_L3D6 |
| | gimme_60_Improbizer_ATAGTAGCATT | 4.02718199385e-05 | L3_L3D9 |
| | DME_AAAAKRCG | 4.07539642481e-05 | L3D6_L3 |
| | gimme_56_Improbizer_AATGGAAGGAAAA | 4.32357625183e-05 | L3D9_L3D6 |
| | DME_AVGAAAGK | 4.54997610946e-05 | L3D9_L3D6 |
| | DME_CAATGATA | 4.55329209565e-05 | L3D9_L3D6 |
| | DME_MCAAAYGT | 4.63388349339e-05 | L3D9_L3 |
| | DME_KAAAMGGA | 4.73511993832e-05 | L3D6_L3D9 |
| | DME_CTTTGAAAGTATAAAA | 4.82544089504e-05 | L3D6_L4 |
| | DME_CTTMARAATA | 5.13546155713e-05 | L3_L3D9 |
| | DME_AGCAADKC | 5.17259900467e-05 | L4_L3 |

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|------------|------------------------------|-------------------|-----------------|
| | DME_AAAASGGW | 5.39083405716e-05 | L3D6_L3D9 |
| | DME_TGAAWTGC | 5.42807234366e-05 | L4_L3 |
| | DME_GMTMAGAT | 5.51626991405e-05 | L3D6_L3D9 |
| | DME_VATKBATAKC | 5.65030467141e-05 | L3D6_L3D9 |
| | DME_HACTACTR | 5.67692973331e-05 | L3D9_L3 |
| | DME_ACTMMWAC | 5.77533662081e-05 | L3_L4 |
| | gimme_79_MDmodule_Motif.12.7 | 6.02931479968e-05 | L3_L4 |
| | DME_GAAGKGWM | 6.19061809506e-05 | L4_L3D6 |
| | DME_TYMTTCKWGM | 6.19672547831e-05 | L4_L3 |
| | gimme_154_MEME_5_w14 | 6.45610230461e-05 | L3D6_L3 |
| | DME_ARVAATWGTAMT | 6.73285482778e-05 | L3D6_L3 |
| | DME_GCAATAAT | 6.90537336294e-05 | L3D9_L3D6 |
| | DME_AAAATTCAA | 7.0660988088e-05 | L3D6_L4 |
| | DME_KAATTAATTAAWTA | 7.11981297025e-05 | L3D9_L3 |
| | DME_AAATBACMTTKT | 7.14889843067e-05 | L3D9_L3 |
| | DME_GAATGAAA | 7.58181190799e-05 | L3D9_L3D6 |
| | DME_ARBAAMAAYAAC | 7.60126857983e-05 | L3D6_L3D9 |
| | gimme_82_MDmodule_Motif.14.9 | 7.61077103555e-05 | L3D6_L3D9 |
| | gimme_73_MDmodule_Motif.12.1 | 7.61257822887e-05 | L3_L4 |
| | DME_ACAAATGT | 7.65426622181e-05 | L3D9_L3 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|---------------------------------------|------------------------|-----------------|
| | DME_RMGGAMAA | 7.71830394285e-05 | L3D9_L3D6 |
| | DME_AAAACAATTAA | 7.84238524812e-05 | L3_L3D6 |
| | DME_AATAATTGAA | 7.95983498607e-05 | L3D9_L3D6 |
| | DME_MRTWTTKAMGVAAA | 8.02671955403e-05 | L3D6_L3 |
| | DME_AGAAAATTAT | 8.26645470963e-05 | L3_L3D9 |
| | DME_AATGATAAAAT | 8.28080095377e-05 | L3D9_L3 |
| | DME_GATAGAAA | 8.318769962000001e-05 | L3D6_L3 |
| | DME_TGAAAATCAATAGATT | 8.8035551985e-05 | L3D6_L3 |
| | DME_AAAGGATT | 8.80988825294e-05 | L3D6_L3 |
| | DME_TCAAAAATTT | 8.90769775936e-05 | L4_L3 |
| | gimme_53_m1_c1_mATCCATCCATCCATCCATymA | 9.3487191091e-05 | L3D6_L4 |
| | DME_MMAAATAATYRK | 9.42146583852e-05 | L3_L3D9 |
| | DME_TKAMARCAAATWT | 9.95981861603e-05 | L3D9_L3 |
| | DME_TAGTACTAATAATAAT | 0.000101436291051 | L3D6_L3D9 |
| | DME_TAATAATCAAAATG | 0.00010237940257200002 | L3_L3D9 |
| | DME_TCAAATTAAA | 0.000103638499697 | L3D6_L4 |
| | DME_ATATGAAC | 0.00010489068121799999 | L3_L4 |
| | DME_TYMATTYAWC | 0.00010508933514799999 | L3D6_L3 |
| | gimme_151_MEME_6_w14 | 0.000106366464111 | L3D6_L4 |
| | gimme_59_Improbizer_TAAATATGTGATAC | 0.00010732160567700001 | L4_L3 |
| | DME_TCHAWYCAWM | 0.00011031799537899999 | L3D6_L3 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|-----------------------------|------------------------|-----------------|
| | DME_AGTBAGAA | 0.00016748046691299998 | L3D9_L3 |
| | DME_TTGAACAA.2 | 0.00016755315342200004 | L3D6_L4 |
| | DME_TCAAATTAAAAA | 0.000168591042223 | L3D6_L4 |
| | gimme_15_BioProspector_w8_4 | 0.00016966944642399999 | L3D6_L3D9 |
| | DME_AGTAAGAA | 0.000171420088751 | L3D9_L3 |
| | DME_CCAATMRT | 0.000171654433562 | L3D9_L3 |
| | DME_AATRATAAKTKT | 0.000172944861713 | L3_L4 |
| | DME_VKAAAGTHWG | 0.00017366121925200002 | L3_L4 |
| | DME_WAYTKGMTSA | 0.000181129745979 | L3D9_L3D6 |
| | gimme_41_Homer_12_3 | 0.000186091700337 | L3_L3D9 |
| | DME_AAAGTAATMAWT | 0.00018836292934099999 | L3_L3D9 |
| | gimme_124_MEME_2_w14 | 0.00018974002193700002 | L3D9_L3D6 |
| | DME_TAAGAACAC | 0.00019895804342 | L4_L3D6 |
| | DME_CAAAAATT | 0.00020069470216699999 | L4_L3 |
| | DME_TAAAATTAAAG | 0.000204718284603 | L3_L4 |
| | DME_ATKCAATG | 0.00021333554916400002 | L3D9_L3D6 |
| | DME_DGAAARGG | 0.00021756409716799997 | L3D9_L3D6 |
| | DME_AAAGARGCACTTTGT | 0.00021890870058099998 | L3D6_L3 |
| | DME_TCAAGAAT | 0.00022394931435900002 | L4_L3 |
| | DME_AAGTTAACAAAGATTGA | 0.000224773373561 | L3D9_L3D6 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|----------------------|------------------------|-----------------|
| | DME_GCAAAGAACCGCAAAT | 0.000226399142527 | L4_L3D6 |
| | DME_CCTAAAAA | 0.00023279631708400005 | L3D6_L3D9 |
| | DME_AAGCAAAGAACGCAA | 0.00023352982428 | L3D9_L3D6 |
| | DME_CAAAKAATAA | 0.00024033599483599998 | L3D9_L3 |
| | DME_TGAAAAATTAA | 0.00026858472736900003 | L3_L4 |
| | DME_YGAMTTGMMWAA | 0.00027151046287500003 | L3D9_L3 |
| | DME_TRKCAATAATAA | 0.000272033141482 | L3D6_L3D9 |
| | DME_AAAAGTTTC | 0.000282356709675 | L3D9_L3D6 |
| | DME_ATGGAAAA | 0.00028557699786 | L4_L3D6 |
| | DME_MTGAGTTAAW | 0.000292837647726 | L4_L3 |
| | gimme_176_Weeder_11 | 0.00029435282346499997 | L3_L3D6 |
| | DME_TGAAGTAA | 0.000295645091908 | L3_L3D9 |
| | DME_TTGATAAAAA | 0.00029999778176 | L3D9_L3D6 |
| | DME_ATTMAAAKAC | 0.00030257690138400003 | L3D9_L3 |
| | DME_TTAAAAATTYYTAAAA | 0.000305347711065 | L3D9_L3 |
| | DME_CAATATCA | 0.000316631904271 | L3_L4 |
| | DME_AACTCAAA | 0.00031838638476999997 | L3_L3D9 |
| | DME_GMWATRATRAWT | 0.00031989629665499995 | L3D9_L3 |
| | DME_AAATTGAAAT | 0.000319942273639 | L3D6_L3D9 |
| | DME_RAKGAARARK | 0.000319950594566 | L4_L3D6 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|-------------------------------------|------------------------|-----------------|
| | DME_ATCAATTAAAT | 0.00032041066024699995 | L3D9_L3 |
| | DME_TAASAAAARA | 0.000321199545493 | L3D6_L3D9 |
| | DME ACAATAATTATTGT | 0.00033013890285200003 | L4_L3 |
| | DME_TAATTYGAAAYA | 0.000338204310415 | L3_L4 |
| | DME_TTAATGAAAA | 0.00034036294140499994 | L3_L4 |
| | DME_AAAGGAAA | 0.000346530476632 | L3D9_L3D6 |
| | DME_CWTGCATD | 0.00034773773663599995 | L3D6_L4 |
| | gimme_19_BioProspector_w12_1 | 0.00034847462109 | L3_L3D9 |
| | DME_GCRGNAAR | 0.000350591128691 | L3D9_L3D6 |
| | DME_AGATCAAA | 0.00035128942736099996 | L3D6_L4 |
| | DME_SHKVAATGKT | 0.000353769782956 | L3_L3D9 |
| | DME_CAAAYKAG | 0.00037540554241800004 | L3_L4 |
| | DME_AATTTATGAA | 0.00038663627955000005 | L3_L4 |
| | gimme_55_Improbizer_TTTCTGTCCTTTTTT | 0.0003909985116590001 | L3D9_L3D6 |
| | DME_GRACAARA | 0.000395790020866 | L3D9_L3 |
| | DME_GATCAAAA | 0.00039672255315099995 | L3D9_L3 |
| | DME_AATAGCAT | 0.00040347895149800005 | L3_L3D6 |
| | DME_TTGAACAA.1 | 0.000403952910634 | L3D6_L3D9 |
| | DME_AATGACAA | 0.00040550549523400004 | L3D6_L3 |
| | DME_CTTTTAAAAA | 0.00041848444494000005 | L4_L3 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|---|------------------------|-----------------|
| | DME_GWVWMARCATTT | 0.00042112654305600004 | L3_L4 |
| | DME_AGAATTAATT | 0.000421333291366 | L3D6_L3D9 |
| | DME_MARATTSADWSAW | 0.00042566285069800004 | L3D6_L4 |
| | DME_CTTAATGA | 0.00043405158960500005 | L3D6_L4 |
| | DME_AYTYSAGARA | 0.00044048379736199997 | L3D6_L4 |
| | DME_TCAAWAAYAA | 0.000450486965633 | L3_L4 |
| | DME_GAAGTAAA | 0.00046889304740800006 | L3_L4 |
| | DME_CTTATGAAGAGTTCAA | 0.00047411271060600004 | L3D6_L3 |
| | DME_CTGGTCAAAGAGAAAA.2 | 0.00048759543433800004 | L4_L3D6 |
| | DME ACAACAACAACACAC | 0.0004963393942480001 | L3D6_L3D9 |
| | DME_TKYGYTWCAR | 0.0004964201737530001 | L3_L4 |
| | DME_TAACATTG | 0.000509945715741 | L3D6_L4 |
| | gimme_59_Improbizer_TAGCAAAA | 0.000514698756807 | L3_L4 |
| | DME_TCAAATTTC | 0.000528576080245 | L3D9_L3 |
| | DME_AAATAACTTAAATCA | 0.000532873214189 | L3D6_L3D9 |
| | gimme_57_Improbizer_AAATTTCAGATGAAAAAAA | 0.00056127854991 | L3D6_L3D9 |
| | DME_ATGATAATAA | 0.0005734986566880001 | L3D9_L3 |
| | gimme_36_Homer_10_3 | 0.000580610925786 | L4_L3 |
| | DME_AYYMATKCHT | 0.000588212595625 | L3D9_L3D6 |
| | DME_AATTKCHAST | 0.000588705875872 | L3D9_L3 |
| | gimme_177_Weeder_12 | 0.000593392203398 | L3_L3D9 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|------------------------------|-----------------------|-----------------|
| | DME_AAAGCATT | 0.000596133421853 | L3_L4 |
| | DME_GAATBAMTSA | 0.0006012421701189999 | L3_L3D6 |
| | DME_ATCACAAA | 0.000616213498713 | L3D9_L3D6 |
| | gimme_67_MDmodule_Motif.10.5 | 0.0006178264770519999 | L3_L4 |
| | DME_TAAGCTAA | 0.000623534479887 | L3D9_L3 |
| | DME_CAARAACA | 0.000627757162596 | L3_L4 |
| | DME_AAAARACC | 0.000629370044424 | L3_L4 |
| | DME_TAAATTGAAT | 0.0006306896544219999 | L4_L3D6 |
| | DME_AMAAARCATT | 0.000652662511765 | L3_L3D9 |
| | DME_AGAARCRA | 0.0006528939641790001 | L4_L3D6 |
| | DME_VAAACGAA | 0.0006849996227740001 | L3D6_L3 |
| | DME_TTTCAATAAA | 0.0006996838564219999 | L3D9_L3 |
| | DME_AATAATAATAAT | 0.000704355742573 | L3D6_L3D9 |
| | DME_ATAAAAGTTA | 0.0007463824203 | L4_L3D6 |
| | gimme_10_BioProspector_w14_3 | 0.0007514551164189999 | L3D6_L4 |
| | DME_GTTAGAAA | 0.000751745121082 | L3_L3D9 |
| | DME_ARGAHWGG | 0.0007534203841 | L3D9_L3 |
| | DME_GAATTATTAA | 0.00077570939227 | L3_L3D6 |
| | DME_CAAWRRDCAARA | 0.0007977032032789998 | L3D6_L3 |
| | DME_AGAGTAAA | 0.0007981521398510001 | L3D6_L3 |

| Motif logo | Motif Name | Motif p_value | Discovery stage |
|------------|-------------------------------|-----------------------|-----------------|
| | DME_AAGARAAAAW | 0.000814302974685 | L3D9_L3D6 |
| | DECOD_Motif9_8 | 0.000819129791192 | L4_L3D6 |
| | DECOD_Motif10_10.3 | 0.000826572859519 | L4_L3 |
| | DME_GTTGAAAA | 0.000837993893335 | L4_L3D6 |
| | gimme_108_MDmodule_Motif.12.6 | 0.000859063054049 | L3_L4 |
| | DME_GAAATGAT | 0.000865909354209 | L4_L3D6 |
| | DME_TCYWTCYAWH | 0.000881773133256 | L3_L3D6 |
| | DME_GATGSAAM | 0.000943119057269 | L4_L3D6 |
| | DECOD_Motif6_10 | 0.000943790303451 | L3_L3D6 |
| | DME_MTTAAGAAAATAGA | 0.00094517326613 | L3D6_L3 |
| | DME_ACAGCAGAAGTAAATA | 0.0009850030937939998 | L4_L3D6 |
| | DME_GACAATT | 0.000989002098618 | L3_L3D9 |
| | DME_CAAAAGTTAACRAA | 0.0009914273911699998 | L3D6_L3 |