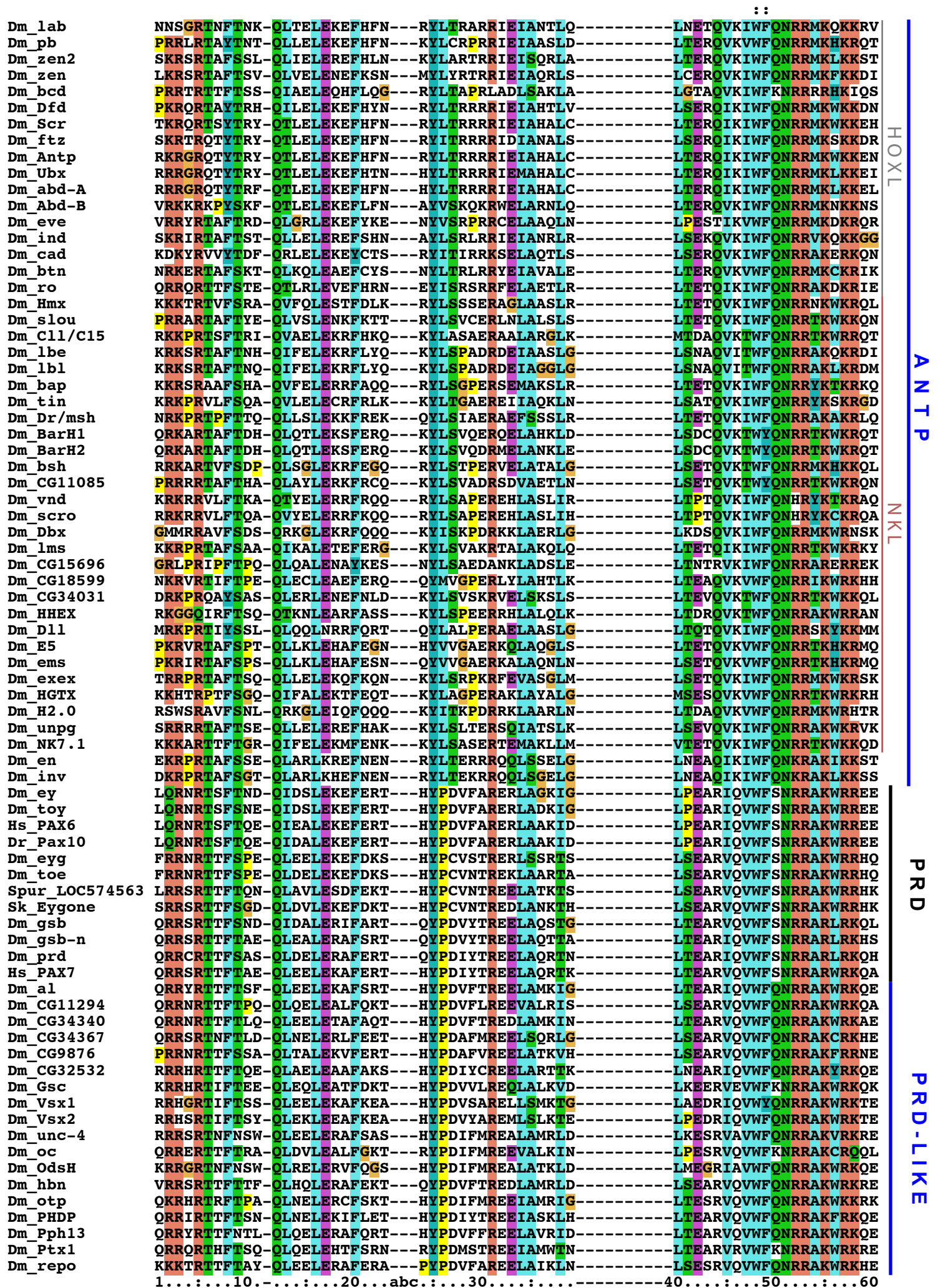


Sup. Fig. S1 Multiple sequence alignment of HDs



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                                                                    ::
Dm_Rx      HRRNRTTFTTY-OLHELERAFEKS---HYPDVYSREELAMKVN-----LPEVRVQVWFONRRAKWRRQE
Dm_tup     PTRVRTVLNEK-OLHLTRTCYNAN---PRPDALMKEOLVEMTS-----LSPRVIRVWFONKRCKDKKKT
Dm_ap      TKRMRTSFKHH-OLRTMKSYFAIN---HNPDAKDLKOLSQKTG-----LPKRVLQVWFONARAKWRRMM
Dm_Awh     TKRVRTTFTEE-OLQVLOANFQID---SNPDGQDLERIASVTG-----LSKRVIQVWFONSRARQKKHI
Dm_Lim1    RRGPRTTIKAK-OLEVLKTAFNQT---PKPTRHIREOLAKETG-----LPMRVIQVWFONKRSKERRMK
Dm_Lim3    NKRPRTTITAK-OLETLKTAYNNS---PKPARHVREQLSQDTG-----LDMRVVQVWFONRRAKEKRLK
Dm_CG32105 PKRPRTILTSQ-ORQFKASFDQS---PKPCRKVVREALAKDTG-----LSRVVQVWFONQRAKMKKIQ
Dm_CG4328  PKRPRTILNTE-ORRAFKAQFEVS---PKPCRKVVRENLAQDTG-----LSLRIVQVWFONRAKVKKIQ
Dm_zfh1    KVRVRTAINEE-QQQOLKQHYSLN---ARPSRDEFRMIARLQ-----LDPRVVQVWFONNRSRERKMQ
Dm_zfh2_HD1 QKRARTRITDD-OLKILRAHFDIN---NSPSEESIMEMSOKAN-----LPMKVVKHWFRTLFKERQRN
Dm_zfh2_HD2 KRANRTRFTDY-OKVLOEFFENN---SYPKSDSLEYLSKLL-----LSPRVIVVWFONARQKQKRIY
Dm_zfh2_HD3 NKRLRTTILPE-OLNFLYECYQSE---SNPSRKMLEEISKKVN-----LKKRVVQVWFONSRADKKSR
Dm_cut     SKKQRVLFSEE-OKEALRLAFALD---PYPNVGTIEFLANELG-----LATRTITNWFHNRMRLLKQV
Dm_onecut  PKKPRLVFTDL-ORRTLOAIFKET---KRPSKEMQVTIARQLG-----LEPTTVGNFFMNARRRSMDKW
Hs_SATB1   KTRPRTKISVE-ALGILOSFIQDV---GLYPDEEAIQTLQAQLD-----LPKYTIKFFONQRYLKHGG
Dm_dve_HD1 KTRMRTSFDPEMELPKLQKWFADN---PHPSRQOIQTYVVLNALSRRGRKPLDVNNVVWFKNARAAQKRAE
Dm_dve_HD2 RKRNRFTIDPVTEVPKLEQWFAMN---THPSHNLILKYTEDLNTMPYRQKFPRLSKNVQVWFKNRRAKCKRLK
Dm_nub     RRRKRRTSIETT-IRGALEKAFLAN---QKPTSEEITOLADRLS-----MEKEVVRVWFONRRQKEKRIN
Dm_nub2    RRRKRRTSIETT-VRTTLEKAFLMN---CKPTSEEISOLSERLN-----MDKEVIRVWFONRRQKEKRIN
Dm_vv1     KRKRRTSIEVS-VKGALQHFHKQ---PKPSAQEITSLADSLQ-----LEKEVVRVWFONRRQKEKRMT
Dm_acj6    GEKKRTSIAAP-EKRSLEAYFAVQ---PRPSGEKIAAIAEKLD-----LKKNVVRVWFONRQKQKRIV
Dm_pdm3    KRKRRTSFTTPO-ALELLNAHFERN---THPSGTEITGLAHQLG-----YEREVIRIWFONKRQALKNTV
Hs_HNF1A   GRRNRFKWGPA-SQQILFOAYERQ---KNPSKEERETLVEECNRAE xGLGSNLVTEVRVYNWFANRRKEEAFRH
Dm_schlang GIRSSRPKKA-NVPILEKTYAKS---TRLDKKKLVPLSKQTD-----MSEREIERWRLRRAQDKPST
Dm_pros    TPLHSSTLTPM-HLRKAKLMFFWV---RYPSSAVLKMYPDIK-----FNKNNTAQLVKWFSNFRFYIYIQM
Dm_so      GEETSYCFKEK-SRSVLRDWYSHN---PYPSPREKRDLAETG-----LTTTOVSNWFKNRRQRDRAAE
Dm_Optix   GEOKTHCFKER-TRSLLEWYLQD---PYPNPTKKRELAKATG-----LNPTQVGNWFKNRRQRDRAAA
Dm_Six4    GEETVYCFKEK-SRNALKDCYLTN---RYPTPDEKKTAKKTG-----LTLTOVSNWFKNRRQRDRTPQ
Ce_UNC-39  GEEIVYSFKDS-SRKFLKQFFRNVS---EYPTQEQKREISRATG-----LKIVQISNWFKNRRQRDKSNN
Dm_CG11617 SRATKRLFTPD-IKRMLKDWLIRRRENYPSPREEKKQLAETG-----LTYTOICNWFANWRRKLNSE
Dm_ara     LAARRKNATRE-STATLKAWLNEHKKNPYPTKGEKIMLAIITK-----MTLTOVSTWTFANARRRLKKN
Dm_caup    LAARRKNATRE-STATLKAWLSEHKKNPYPTKGEKIMLAIITK-----MTLTOVSTWTFANARRRLKKN
Dm_mirr    NGARRKNATRE-TTSTLKAWLNEHKKNPYPTKGEKIMLAIITK-----MTLTOVSTWTFANARRRLKKN
Dm_vis     LRKRGNLPKS-SVKILKRWLYEHRYNAYPSDAEKFTLSQEAN-----LTVLQVCNWFINARRRILPEM
Dm_achi    LRKRGNLPKT-SVKILKRWLYEHRYNAYPSDAEKFTLSQEAN-----LTVLQVCNWFINARRRILPEM
Dm_hth     NOKKRGIFPKV-ATNILRAWLFQHLTHPYPSEDQKKQLAODTG-----LTILOVNNWFINARRRIVQPM
Dm_exd     ARRKRNFNSKQ-ASEILNEYFYSHLSNPYPSEEAKEELARKCG-----ITVSOVSNWFGNKRIRYKKNI
Hs_PBX1    ARRKRNFNFKQ-ATEILNEYFYSHLSNPYPSEEAKEELARKCG-----ITVSOVSNWFGNKRIRYKKNI
Pt_TALE    KNSNKNKFQKR-SIDILKKWFLDHLDNYPYDNTKQRLSKITG-----MHVROIQNWFTNSRKRYLEPL
1.....10.....20...abc.....30.....40.....50.....60

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Helix 1



Helix 2



Helix 3