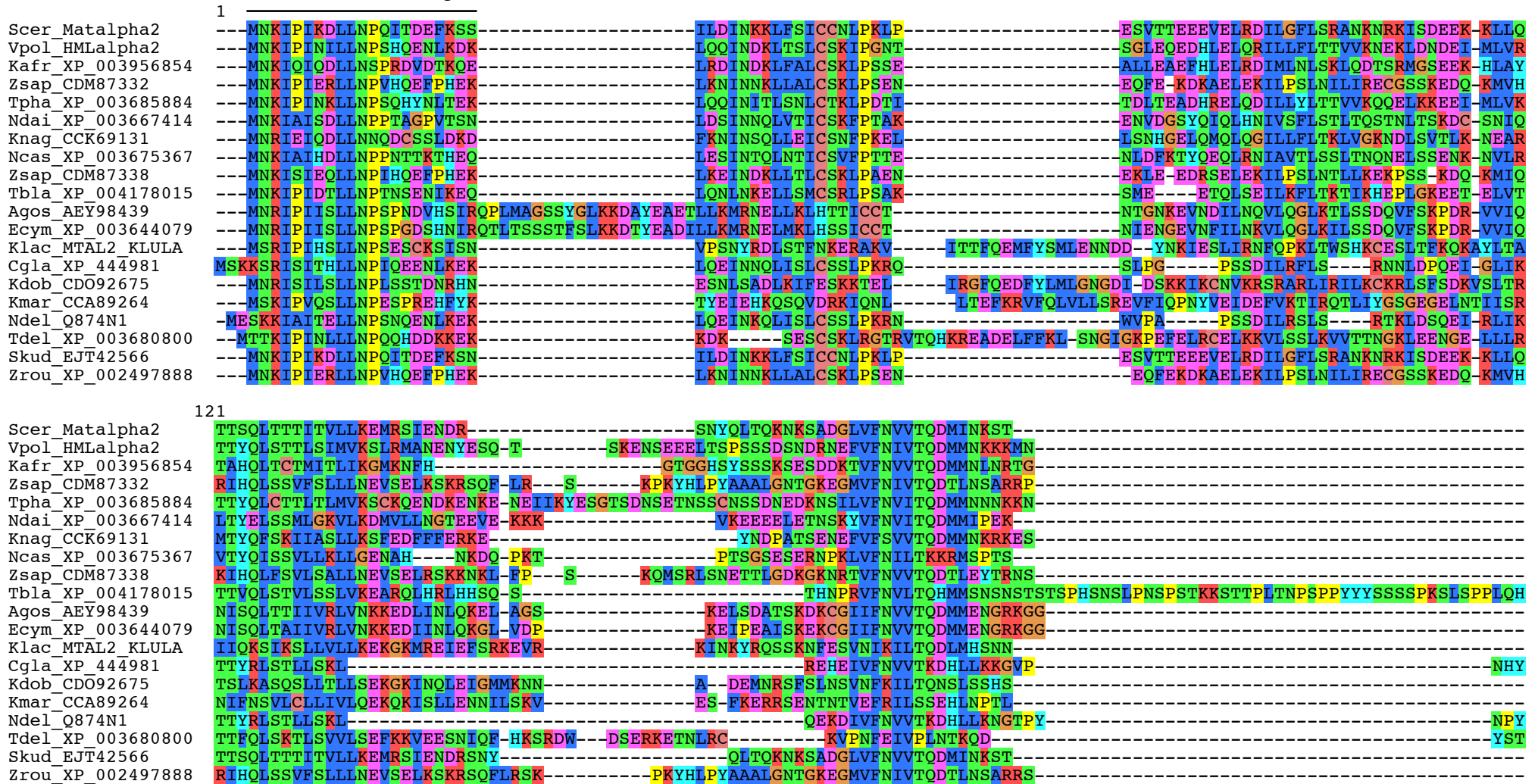


Sup. Fig. S2. Multiple sequence alignment of fungal mating type alpha2 HD proteins.

TUP1 interaction region



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Scer_Matalpha2 -KPYRGHRFTKENVRILESWFAKNIENPYLDTKGLNLMKNTSLSRIOIKNWVSNRRRKEKT-ITIAPELA-DLLSGEPLAKKKE-----
Vpol_HMLalpha2 IKSYRGHRLPKQNVKLLERWYIQNVENPYLDDKSI SELMKITSLSKVQIKNWVSNRRRKEKS-ITISPEVS-RLL-----
Kafr_XP_003956854 -ISYRGHRFSKENVKVLERWYTAHIDRYPYLNROSTEYLISKTGLSRVQIKNWVSNRRRKEKS-VHVSPELI-QLL-----
Zsap_CDM87332 NKTYRGHRLPKHITRLLLESWFNRNIEHPYLQTSMMKELMVETKLSGPOIKNWVSNRRRKEKS-LTISFEVS-ELV-----
Tpha_XP_003685884 NKSYRGHRLPKKNVOYLEDWYMDHRKNPYLNEINIKLLMSKTSLSRIQVKNWISNRRRKEKS-ITISPEVS-ALL-----
Ndai_XP_003667414 NKPHRGHRLPKEKVNRLLEHWYLAHIQKPYLDSKNLKVLMETKLSKVOIKNWI SNRRRKEKL-LSISPDIV-EIINTQ-----
Knag_CCK69131 MRPCRGHRFSSNSTETLEDWYKHHHEKPYLDKRSLHELEFFKTKLSKMQIRNWVSNRRRKEKS-IHVSPVIQ-DLL-----
Ncas_XP_003675367 NEPRRGHRLAKEKVDLLEHWYIQHMDNPYLNKASLOMLMOETSLSKMQIKNWVSNRRRKEKS-LSIAPEIV-DILNKQ-----
Zsap_CDM87338 RKTYRGHRLPKYVTNSLESWFKRNIKHPYLNNSSIKQLITETKLSGPOIKNWVSNRRRKEKS-LTVSFDVS-ELV-----
Tbla_XP_004178015 TPSHRGHRLPKHTLIPLEKWFLLHNKSHPYLHNSDLQALTQOSSLSKTQVKNWISNRRRKEKHSLSKISNNIA-SLLQND-----
Agos_AEY98439 CSSYKGHRLPKQHVQVLEAWYKNNIENPYLNDTDIRYLMRETGFSSQVKNWVANKRRKDKH-STISPELS-DLLA-----
Ecym_XP_003644079 SSSYKGHRLPKKHVQLLESWYKNNIENPYLNDTDIRILMRETGFSSQVKNWVANKRRKDKH-STISPELS-DLLA-----
Klac_MTAL2_KLULA NEFKKGKRFLLKSHIQLLLENWYSMNRNRPYLAENDLAYISKNTTLTKTQIKNWLANRRRKDKI-TEVSSDIR-NIL-----
Cgla_XP_444981 AASYRGHRFTRENVQILETWYRNHIDNPYLDHNSQQYLAQKTNLSKIQIKNWVANRRRKQKS-IYISLFDIHNIESGEYAYIEKVCYIIIIICHLFLVFSLSCLT
Kdob_CDO92675 AECVKKRFPKAQVELLDWYEVNKKNPYITENDINNIRSNSTLSKMQIKNWLANRRRKDKL-TKISEEII-NILN-----
Kmar_CCA89264 NKVGGKRFPKKSIKLLLENWYECNRNSPYLTSNHLDYLCNTGLNKTOIKNWVANRRRKDKN-SRVSLDIK-NIFROQ-----
Ndel_Q874N1 POPYRGHRFTKENVHTLEAWYSNHIDNPYLDPKSLOSQAQKTNLSKIQIKNWVSNRRRQKH-PPFLLI-----
Tdel_XP_003680800 GKRRGHRLPSEKVEKLELWFNQNISKPYLNQRALRLVHETSLSPIQIKNWLSNRRRKKKS-AGIADTIS-DLLFTKKNSTDTKV-----
Skud_EJT42566 -KPYRGHRFTKENVRILESWFAKNIENPYLDTKGLNLMKNTSLSRIOIKNWVSNRRRKEKT-ITIAPELA-DLLSGEPLAKKKE-----
Zrou_XP_002497888 NKTYRGHRLPKHITRLLLESWFNRNIEHPYLQTSMMKELMVETKLSGPOIKNWVSNRRRKEKS-LTISFEVS-ELVKESKQGTEELNE-----

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