

Genome-Wide Identification and Characterization of the *Salvia miltiorrhiza* Histone Deacetylase (HDAC) Family in Response to Multiple Abiotic Stresses

Junyu Chen ^{1,†}, Yuxin Ying ^{2,†}, Lingtiao Yao ¹, Zhangting Xu ¹, Zhenming Yu ^{1,*} and Guoyin Kai ^{1,*}

¹ School of Pharmaceutical Sciences, Academy of Chinese Medical Sciences, Zhejiang Chinese Medical University, Hangzhou 310053, China

² College of Food and Health, Zhejiang A & F University, Hangzhou 311300, China

* Correspondence: yuzhenming@zcmu.edu.cn (Z.Y.) ; kaiguoyin@163.com (G.K.)

† These authors contributed equally to this work.

Table S1 Protein sequence of all SmHDACs.

Table S2 Protein sequences used to construct the phylogenetic tree.

Table S3 Gene ID used to construct a co-expression network.

Figure S1 Seventeen motif logos in SmHDAC protein.

Table S1 Protein sequence of all SmHDACs.

Gene name	Gene ID	Protein sequence
SmHDA1	SMILT033186.1	MSRNNDSVSGRDGRVGLIFDERMCKHYAPAEEDHPECNRI IRVIWNLLDSSGLAKRCIILKAKDAEYNHLALVHTKKHISLI KNISSRNTQSKRERIAVKFDSIYFNEGSTEAACLAAGSVIEA AEKVASGEIDSAFAIVRPPGHHAKEGEPMGFCLYNNVAIAA SYLLNERQELGINKILIVDWDVHHGNGTQNMFYKDPRVLV FSVHRHDFGTFYPSGNGGSYIMTGEGEGAGHNINVPWEHG QCGDADYLAVWDHILIPVAKEFKPDIIISAGFDAAGKGPLG GCCVSPNGYSVMLHKLMEFAGGKIVMALEGGYNLNSTAS SALACVQALLHNEPPNVVSQARPFASWVRVIQQVCGVLRP YWPVLARIDNNHPTESDPVTSFHVPEKGLLRPCNMSSIKKS TGQSSGEADSLQTLAGDIGSGAGADKPANFPRPLRNLTGA ECQAQMEAQIASSGLKEMDDMDPEKFADALCYAAKVERA RARKLA AVRRLCSVTAALKAKAAELMAALEEDPLAAQET AAQLKAERDYLNTELERANA AKAEELEAAKKALTQAFNT RFQKAKTRWLA EKENAYILGMKECRSQFFLTARGHQFLRI MLNDTLEAF CRTPESLDVLGPGMGHLINDVCTLLMDQIGA TPEQRALYDFDQIVDSVDAEGLDRVLGIDSQAPRTPAWWA PVVDKALKQFVEGTCADPLPTSPLLRTPYLDRLQAAAATR LNAEAAAGEPLFYPRPPAAAMTGAAAMELQASATHDHDQ LRDAMLC
SmHDA2	SMILT020074.1	MSRSSNDSVSTRNQRVGLIFDERMYKHHAPHEKDHVECP DRIRVIWDLNSSGLAKRCIILKAKAAEDNHLALVHTKNHI TLIKNISSKNTKSKRKRIAEKFDSIYFNEGSTEAACLAAGSV IEAAEKVAKGEIDSAFAIVRPPGHHAEEGEPMGFCLYNNVA IAASYLLNERQELGINKILIVDWDVHHGNGTQKMFYKDPR VLVFSVHRHDFGTFYPTGDDGSYIMTGEGAGAGHNINVP WEHGKCGDADYLAVWDHILIPITKEFEPDMIIISAGFDAAG GDPLGGCCVSPNGYSIMLHKLMKFAGGKIVMSLEGGYNL NSTACSVRACVEVLLHEKSPNVVLAANPFDSTWSVILDVG RVLRPYWACDLLDLKLWTFMGSSDDQDLIDFNEFSTVLG SEQNLPALAEKKTTLTLEQLGSLMPEPSIAKKTSTLSLAEPS DTEPLSKRLKSKASTTKRVLTY SPEISSPTNQPTSSPFKQISA PHSSDNPLSVVPIQQTLPETVVQSPTPNDQIMPTLPPRQPSP PQQTPAHISALISPEPPISQEKQSDNIEQPVLHSDQATSPHVS KKSSGKKKCRDAQGPSSEPGAKKSWPSVSPVPQKGSQTKI QLPGSLLKLNPA GSWAFVRSLTSSHDLAKLTSAECWAVLD ALTSSKDVAMLRELSTEQLVDMICFNLVEQIILVSEVGSRL SCEEKDAALKELKSEVKEKDVKLVKTRNLNAKLEAKNRE LQQRLANAEKENEALTMKARAEGKEDGIKLCRERILMAL DRPF
SmHDA3	SMILT020076.1	MESNGEIESPLSRSNDGVSGKDRRVGLIFDERMCKHYAPAE EDHPESPDRIRVIWDLNSSGLAKRCILLKAKDAEDNHLAL

		VHTKNHISLIKSISSGNSGSKRKRIAAKFNSIYFNEGSTEAA CLAAGSVIEAAENVAIGEIDSAFAIVRPPGHHAEEGEPMGF CLYNNVAIATSYLLNERRDLGIKKILIVDWDVHHGNGTQK MFYKDPRLVFFSVHRYDFGTFYPSGHDGSYIMTGEPPGAG HNINVPWEHGRCGDADYLAVWDHILIPVAKEFNPDMIISA GFDAAGDPLGGCRISPYGYSIMLDKLMFAGGKIVMALE GGYNLNSIASSARACVEVLLHDKPPNVLSEAYPFASTWRVI QEVRELSTYWPVLAGDLPEKMISKTSQIEILSSDSEAETEE ITLAVPEEVQTIEDIIQPLSNLKIDLDSRDQEATVKPSWRSEL SKVDIWIYATYGSNMKMSRFCCYIEGGQIEGMMRPCVGS DKSKPKEIWKTFPHRLFFARERTATWGPGGVAFHLPTSNV QEKTYMCLYKITLEQFNDVLLQENISNQEMSRPLFDSTALQ TIQTEKCISVELVQRGWYHNVVYLGKEGDIPILMTCSLSD VDNFLAGVFPINPPCKEYANTLIKGLVEGKQLSEEEASAYIQ EASSKHL
SmHDA4	SMILT031105.1	MNHFSPEIELLNGKVIYSVAAAAMGHNKESHPECNSRVP DALEKMKLTSEFRGMDIIELEKFRPAKVEDIARVHERAYVS GLEKAMDQASEQGLILIEGSGPTYATSTTFQESLLAAGAGIS LVDVVAASKIRKDPVGFALVRPPGHHAVPTGPMGFCVF GNVAIAARYAQRAHGLKRIFIIDFDVHHGNGTNDAFYDDP DIFFLSTHQDGSYPGTGRINQIGRGDGEGATLNLPLPGSG DRAIRDVFEEVIAPCAQRFKPDILVSAGYDAHVLDPANL QFTTSTYYMLASSIQQIARDLCGGRCVFFLEGGYNLTSLSH SIADSFRAFLGEPSLAAEFDNPAFLYEESKRVKEAIQRVKH IHSL
SmHDA5	SMILT012722.1	MDTGNSLPSGADGSKRKVCYFYDPEVGNYYYGQGHM KPHRMRMTHALLAHYGLLQNMHVLPKNPARDKDLCRFH ADDYVSFLRRITPETQQDQLRQLKRFNVGEDCPVFDGLYS FCQTYAGGSIGGAVKLNHGHCDIAINWAGGLHHAKKCEAS GFCYVNDIVLAILELLKTHEVLYVDIDIHHDGVEEAFYIT DRVMTVSFHKFGDYFPGTGDIRDIGFGKGKYYALNVPLDD GIDDESYSQSLFKPIISKVMEVYRPGAVVLQCGADSLSGDRL GCFNLSVKGHAECVRFMRSFDVPLLLGGGGYTIRNVARC WCYETGVALGIEIDDKMPQHEYIEYFGPDYTLHVAPS NME NKNCRDMLEEIRAELLKNLSRLQHAPSVQFQERPPDIELPE VDEDEENKDERKRPDSNVNIDYERNSTPSRVKMEFVEPMA NDKNDEAVDELARKIDSTLAPTSSKGSMAAA EVDGMQYV KLEKENTKTLLDELAPMDQH
SmHDA6	SMILT011069.1	MDTGNSLASGADGVKRKVSYFYDPEVGNYYYGQGHM KPHRIRMTHFLAHYGLLQMHVLPKNPARDKDLCRFHA DDYVSFLRSITPETQQEQLRQLKRFNVGEDCPVFDGLYSFC QTYAGGSVGGAVKLNHGHCDIAVNWAGGLHHAKKCEAS GFCYVNDIVLAILELLKVHERVLYVDIDIHHDGVEEAFYT TDRVMTVSFHKFGDYFPGTG DVRDIGYKGKYYSLNVPL

		DDGIDDESYSQSLFKPIMGKVMEIFKPGAVVLQCGADSLSG DRLGCFNLSIKGHAECVKFMRSFNVPLLLGGGGYTIRNV ARCWCYETGVALGIELDDKMPQHEYYEYFGPDYTLHVAP SNMENKNSRHLLEEIRSKLLDNLSRLQHAPSVQFQERPPDS ELPQMEEDHDGEDERYDPDSDMDIDDERKPLPGRVKSEFP EPEPKDMDDAKEDEPNREVDLKCSEPLA
SmHDA7	SMILT025982 .1	MKGTAGDVGNVYFGPNHPMKPHRLCMTHHLVLAYELHN KMEIYRPHKAYPVELAQFHSPDYVEFLQRITPDKQVLFANE MAKYNLGEDCPVFENLFEFCQIYAGGTLDAAARLNNRLCD IAINWAGGLHHAKKCEASGFCYINDLVLGILELLKYHARVL YIDIDVHHGDGVEEAFYFTDRVMTVSFHKYGDLFFPGTGD VKDVGEKEGKNYAINVPLRDGIDDGSFLRLFKTIILKVVEC YAPGAIVLQCGADSLAGDRLGCFNLSIDGHAACVKFVKQL NLPLLVTGGGGYTKENVARCWTVETGALLGVELASEIPEN EYFKYFAPDYSCLKCASGHMENLNSKSYLNNIRQQVCENLS AIQHAPGVQMQUEVPPDFYIPDFEDEQNPDERVNRHLQDK QVQRDDEYYEGDNDNDQNNDDS
SmHDA8	SMILT016201 .1	MSRFKEEEIGTRLRNGDSAPLAEAASSNSFKPHLAEQLMK QKNGKRKSDMSLEEMYNSQYDFGDDDDSDWEPSALP AHSVVEIPKWFCLNCTMLNIGDDSHCDVCGEHRESGILKR GFVSSASSREVVTQNGAHAADGLQDPHPLMQSIASDNPTA IGFDERMLLHEEVVMKSHPPPERPDLRAIAASLATTGIFP GRCHPISAREITQEELLKVHSLNIEAVEITSRVFSSYFTPDT YANQYSATAARLAAGLCFDLAAAIWSGRAKNGFALVRPPG HHAGVKHAMGFCLHNNAALAASAAQIAGAKKVLIIDWD VHHGNGTQEIFEKNKSVLYISLHRHEGGKFYPGTGSAYETR NIILVPVTFICEGKWYSFQLVDVANLFHMTGSMGAEGHCV NIPWSRGGVGDNDYIFAFQHVVLPATEFDPDFTIISAGFDA ARGDPLGGCDVTPAGYAQMTQMCRALSGGKVLVILEGGY NLRSSSSATAVIEVLLGESPKQNVGQVMPSKAGVRVAVLEV LKIHLNYWSSLESKFTKLQSEWGWTLEDKS
SmHDA9	SMILT029344 .1	MDSDGGASLPSSCPDARKRRVSYFYEPTIGDYYYGQGHPM KPHRIRMAHNLIVHYSLHRRMEISRPFAAFGDIRRFHSPEY VEFLSSVSPDTLHDHTHARHLRRFNVGEDCPVFDGLFNFC QASAGGSIGAAVKLNRQDADIAINWAGGLHHAKKSEASGF CYVNDIVLGILELLKVHRRVLYVDIDIHHGDGVEEAFYVTD RVMTVSFHKFGDFPPTGTHIKDIGVASGKYALNVPLNDG LSDDNFRSLFRPILEKVMGVYQPDVAVLQCGADSLSGDRL GCFNLSVKGHADCLRFLRSFNVPLMTAVAVDVEPDNKLPY NEYEYFGPDYTLHVEPSNMENLNTLRDLEKIRNMLLDQL SKLQHAPSTQFQTMPPTTEVPEEREEDMEVRPKPRIWNGD LGYYESDEDEIDKPTVRRSLNNE DAYGENTDLRSRTLSNN QLKLPHPPRK

SmHDA10	SMILT005242 .1	MADEVIHVFWEEGMLRHDAGRGVFDSGLDPGFLDVLEAH PENAGRVKNMVSILKRGPIAPFLSWHQRRALISELLSFHT QEYIDELVEADRS GGKDFGGGTFLNPGSWDSALLAAGTTL SAMKHILDGNGKVS YALVRPPGHHAQPTRADGYCFLNNA GLAVELALSSGVSKVAVIDIDVHYGNGTAEGFYRSNRVLTIS LHMNHGSWGPSHPQNGTVDELGE GEGYGYNLNIPLNGS GNRGYAHAVTEL VVPAIERFDPEMMVLVVGQDSSAFDANG RQCLTMEGYRKIGQIVGEMAEKHSAGRV LIVQEGGYHLTY SAYCLHATLEGVLGFPAPLLSDPLGCYPEDEAFTVAVVQSI NKFHRESVVPFLK
SmHDA11	SMILT020075 .1	MKKMSRSSKDCVSGRDRRVGLIFDERMYKHYAPHEKDHV ECPDRIRVIWDL LNSSGLAKRCIILNAKAAEDNHLALVHTK NHITLIKNIKKVAKGEIDS AFAIVRPPGHHAEEAEPMGFCLY NNVAIAASYLLNDRQELGINKILIVDWDVHHGNGTQNMFY KDPRVLVSVHRHDFGTFYPTGGDGSYFMTGEGAGAGHN INVPWEHGQCGDADYLAVWDHILIPVAEEFKPDMIISAGF DAEALQSRVNEMDAELKKTRNLNAKLEAEKLELQQLGN AEKGKEIVRMKARAEGKEEGIKLCRERILMPF
SmHDA12	SMILT030323 .1	MSSVPTRRHVAPIHGTSPPIKSSATLLHLYNFRHSIKIAFSGD MAATSSSRGESSDTAASVSHGGESVRRNRILASKLYFDVPA SKIPLIYSSSYDIAFLGMEKLHPFDSSKWGRICRFLIAEGLL DKKHIVEPLEAKRDDLLV VHPESYLDLSSSLNVATIVEVP PVALLPNC LVDKNVLHPFRKQVGGTILAAKLAKERGWAIN VGGGFHHCSAQKGGGFCAYADISLCIQFAFTRLDISRVMIID LDAHQGN GHEKDFSDRRVYILDMYNPAIYPLDYEARRYI TQKVEVACGTNTDEYLSKLDGALKVAGGA FDELIINYAG TDILDGDPLGKLKISPEGIATRDEKVFTFARGYMKSSARVIA DSIINLSKKS LITIGDDQNDTIT
SmSRT1	SMILT012742 .1	MYETSLNELELTEPKRARVRLRFNNRAGPSRARAHRICNR VELELKNLKLDRVELELELD TYRPSSSSKTVRSISMNKETF WRPRMISFQGSLKFVHTYRITPTGATMENKELPSNYLKDK MMVPNADPPRDEDVNLLSQFFKRSSLVILT GAGISTESGIP DYRSPNGAYSTGFRPITHQEFMRSSRARRRYWARSYAGWR KFTTAQPGPAHIALASLEKAGRVKFM MTQNVDR LHHRAG SNPLELHGTVYIVACTNCGFSLSRSSFQDQVKAINPKWAEA IESLDYDSRSDKSFGMKQRPDGDIEIDEKFWE EEFHIPNCE KCDGILKPDVVFVFGDNVPKGRSDRAVEAAKECDAFLVLGS SLMTMSAFRLIRAAHEAGAATAIVNIGVTRADDFVPLKINS RLGEILPRLLSVGSLGVPVV
SmSRT2	SMILT009140 .1	MSLGYAEKLSFIEDVGNVGM AEFFDPPHVFQEKVERLAG MIQKSKHLVVFTGAGISTSCGIPDFRGPKGIWTLQRQGKAL PEASLPFHRATPSTTHMALVEFEKAGILKFLISQNV DGLHL RSGIPREKLSELHGNSFMEQCPSCGAEYVRDFE IETIGLKET TRRCSKAGCGAKLRD TVLDWEDALPPKEMDPAEKHCKM

		ADLVLC LGTRFCSWPKISPGKITPACNLPLKCLKGGGKIVIV NLQKTPKDKKASLVIHGRVDKVM TGVM DMLSMRIPPFI RI DLFQIITQALSLDKKYVNWTLRIASVHGKQAPLPFIKSVEV SFSESLSMKAAVLYDQPLHLKRRTAKSTKPFDFVLNLFSA GCKCTYADLKIPVD FEIPTDCLKEDKDSIIEKLKERAVREPC CGQTAVVERRGILVPKSEVIVHAIVTNII EYGGSLGASSLSN GSLKRRNEGLIDSGVCWKRTKARKRTSRHRR
SmHDT1	SMILT015039 .1	MEFWGVEVKVGEKLVQPKPGKLIHISQAAMGEVKDVK AAKNVHLRMKIDDKDFIIGSLAAEIRPQLMFDLVFEKDFEL SHDLKNGSVHFMGYIADDPED EVEFSDFGSESAD EEEPIEA KEEAKENGKAKARSVDAKPA AAGKAHKEEKVAPKVEE DSDDDEDDSDDEMAFDTS DLSGDS DDEEDEDSSSSEEELP VAKQQQQSKKRPAASAEKSPA AKKAKSATPDKSGKKGQN ATPFPKASAGKTPNKPKEQSPKTGGHATGKPFNKNFSGKG KGKHGGK
SmHDT2	SMILT013286 .1	MAFWGIEVKPGKPYILSDEEKGR LHVTQATLGSGSSTK KSI LQCEVGDKKPIYLC SLLPDRLETCPLNLEFEED EKVTFSIIG PQSVHLSGFFYGD ESDDEDEDGYGCGLYEDDAMGIGSE DEEDADYDSEDEEDEDLSEDDLCCGYPHSPV PNSGVKIE EIVDDGKPTNENGMSKRAKKKKTDGNDNSNSQIVPKAGT SVPVLESEDEDGFPVPAHDKKSEANLEKTKQESSGKKSQN KSEKTDAAASGRNLKRKSGAVNQDEQPASDIEPHSSSAQPD TTTNEVKQKKKKKKV VQKLDSSLENEKPDSDGMKESPV AEAGNDLKPSSEKKKDKKKKKQNK LQENTPTPSAEKKVA DKNESNLEKQEKGDASKSLQVR TFPNGLVIEELVMGRPDG KRASPGKKVGVHYIGKLKNGKIFDSNVGTAPFKFRLGIG QVIKGWDVGVNGMRVGDKRRLTIPPAMGYGAKGCPPAIPP NSWL VFDVELVDAN

Table S2 Protein sequences used to construct the phylogenetic tree

Gene name	Gene ID
<i>Salvia miltiorrhiza</i>	
SmHDA1	SMILT033186.1
SmHDA2	SMILT020074.1
SmHDA3	SMILT020076.1
SmHDA4	SMILT031105.1
SmHDA5	SMILT012722.1
SmHDA6	SMILT011069.1
SmHDA7	SMILT025982.1
SmHDA8	SMILT016201.1
SmHDA9	SMILT029344.1
SmHDA10	SMILT005242.1
SmHDA11	SMILT020075.1
SmHDA12	SMILT030323.1
SmSRT1	SMILT012742.1
SmSRT2	SMILT009140.1
SmHDT1	SMILT015039.1
SmHDT2	SMILT013286.1
<i>Arabidopsis thaliana</i>	
AtHDA2	At5G26040
AtHDA5	At5G61060
AtHDA6	At5G63110
AtHDA7	At5G35600
AtHDA8	At1G08460
AtHDA9	At3G44680
AtHDA10	At3G44660
AtHDA14	At4G33470
AtHDA15	At3G18520
AtHDA17	At3G44490
AtHDA18	At5G61070
AtHDA19	At4G38130
AtHDT1	At3G44750
AtHDT2	At5G22650
AtHDT3	At5G03740
AtHDT4	At2G27840
AtSRT1	At5G55760
AtSRT2	At5G09230
<i>Oryza sativa</i>	
OsHDA713	LOC_Os07g41090.3
OsHDA704	LOC_Os07g06980.2
OsHDA709	LOC_Os11g09370.1
OsHDA714	LOC_Os12g08220.1
OsHDA702	LOC_Os06g38470.3

OsHDA705	LOC_Os08g25570.1
OsHDA710	LOC_Os02g12380.3
OsHDA703	LOC_Os02g12350.1
OsHDA701	LOC_Os01g40400.1
OsHDA712	LOC_Os05g36920.1
OsHDA716	LOC_Os05g36930.2
OsHDA711	LOC_Os04g33480.1
OsHDA706	LOC_Os06g37420.1
OsHDA707	LOC_Os01g12310.1
OsSRT702	LOC_Os12g07950.2
OsSRT701	LOC_Os04g20270.1
OsHDT701	LOC_Os05g51830.1
OsHDT702	LOC_Os01g68104.1

Solanum lycopersicum

SIHDA1	Solyc09g091440
SIHDA3	Solyc06g071680
SIHDA2	Solyc03g112410
SIHDA4	Solyc11g067020
SIHDA5	Solyc08g065350
SIHDA9	Solyc03g115150
SIHDA8	Solyc03g119730
SIHDA7	Solyc01g009110
SIHDA6	Solyc06g074080
SIHDA10	Solyc01g009120
SISRT1	Solyc07g065550
SISRT2	Solyc04g009430
SIHDT2	Solyc10g085560
SIHDT3	Solyc11g066840
SIHDT1	Solyc09g009030

Zea mays

ZmHDA101	Zm00001d053595
ZmHDA102	Zm00001d003813
ZmHDA103	Zm00001d018346
ZmHDA104	Zm00001d016381
ZmHDA105	Zm00001d014076
ZmHDA106	Zm00001d050139
ZmHDA107	Zm00001d024221
ZmHDA108	Zm00001d039202
ZmHDA116	Zm00001d046388
ZmHDT101	Zm00001d042433
ZmHDT102	Zm00001d011139
ZmHDT103	Zm00001d032210
ZmSRT101	Zm00001d019276
ZmSRT102	Zm00001d023585

ZmSRT103	Zm00001d025705
ZmSRT104	Zm00001d046205
ZmSRT105	Zm00001d047121

Table S3 Gene ID used to construct a co-expression network.

Gene name	Gene ID in PRJNA393563	Gene ID in PRJNA703309
SmPAL1	SMil_00019885	TRINITY_DN23917_c0_g2
SmTAT1	SMil_00024924	TRINITY_DN15459_c0_g1
SmC4H1	SMil_00000716	TRINITY_DN18900_c0_g1
SmHPPR1	SMil_00002680	TRINITY_DN14918_c0_g1
Sm4CL1	SMil_00008129	TRINITY_DN20844_c0_g1
SmRAS1	SMil_00025190	TRINITY_DN23540_c0_g1
SmHDA6	SMil_00014906	TRINITY_DN23308_c1_g1
SmMYC2	SMil_00026019	?
SmJAZ9	SMil_00002123	?
SnRK2	?	TRINITY_DN7280_c0_g1
PP2C	?	TRINITY_DN23712_c2_g1

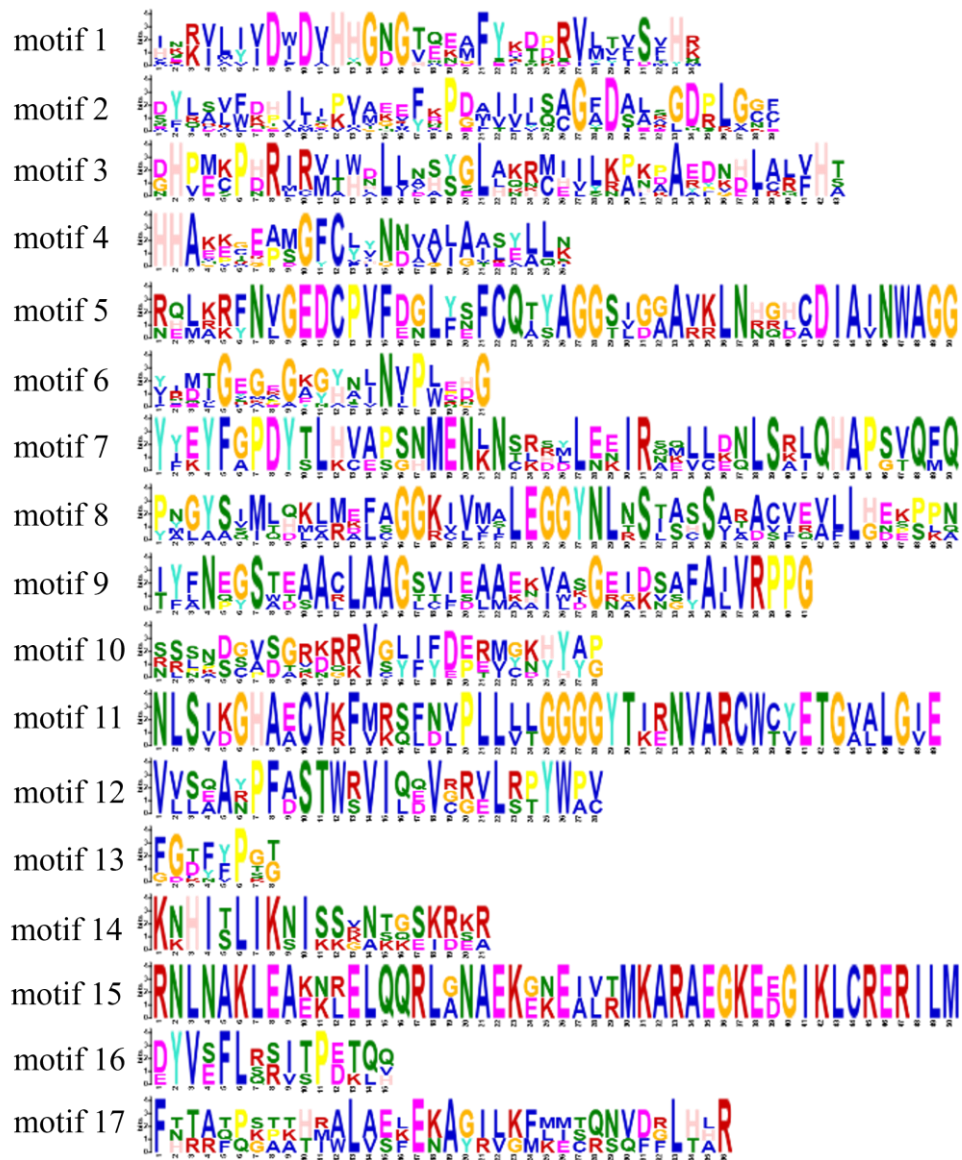


Figure S1 Seventeen motif logos in SmHDAC protein