

Figure 1 – figure supplement 1

A. Protein sequence alignment of *Hs* NHE1 (uniprot P19634-1) and *Dm* Nhe2 (B7YZY1)

Hs_NHE1	LVDLLAVKKKQETKRSINEEIHQTFLDHLITGIEDICGHYGHWWKDKLNRFNKKYVKKC	561	KRA motif
Dm_Nhe2	LVKILNVKRAANKRKPTMNERIHERFMDHLMAGIEDIVGKTGNYNVRDKFKRFDNRFIRPL	659	CHP2 interaction domain
Hs_NHE1	LIAGERSKEPQLIAFYHKMEMKQAIELVESGG--MGKIPSAVSTVSMQNIHPKSLPSE-	618	
Dm_Nhe2	LIRDLKGAEPKIIETYSKLTMRDAMEVMRRNPSTIGQMTGTESMSALFRNYTNNYIGGRW	719	
Hs_NHE1	-----ILPALSKDKEEEIRKILRNNLQKT-RQRLRS	648	
Dm_Nhe2	APPTIYTTCPSLTNLDNTCSRNLDMAELDYNPSKKDLTDARIHLLAEELKPYRRHRRLS	779	Akt phos.
Hs_NHE1	YNRHTLVADPYEEAWNQMLLR-----	670	
Dm_Nhe2	YSRHAVDDRDLSTQVNYKMQMNFRRMFNDRKHHKRSKRGASNKEAKENVKQNHVSFHDFO	839	
Hs_NHE1	-----		
Dm_Nhe2	QNGTTKQLTNAEECQQNPNEINVVGPSDDWDDGLTFTAKSS-----LAEHPIP	887	
Hs_NHE1	QKARQLEQKINNYLTPAHKLDSPMTSRARIGSDPLAYEPKEDLPVITIDP-----	721	
Dm_Nhe2	EEDRNLSRESDGERRVATPTATESQLPWKRQGDECTDAVQQNEFPWASNKEYLAYNSPS	947	
Hs_NHE1	-----ASPQSPESVDLVNEELKGKVLGLSRDPAKVAEEDE-DDDGGIMMRSKETSSPG	773	
Dm_Nhe2	ATFLGGINKPKQPKSVIGLFRRESSSSKAGSVGVGSTGAMDSAASGSETMVVSMSSQPPN	1007	
Hs_NHE1	TDDVFTPAPSDSPSQRIRCLSDPGHPPEPGESEP-----	809	
Dm_Nhe2	APSTSIHNPRLDKRSQSISSSSSLGAGAHQLGPEGHSGFFPVTASHRRNVRRGSMLELSGD	1127	ATM/ATR phos.
Hs_NHE1	-----FFPKGQ-----	815	
Dm_Nhe2	TIPEESSYQHGHSKSLCEPADSDEWEGAPLSAAGGANSELLMRMSGREPLLPRPSNTPRA	1189	
Dm_Nhe2	QIRRMNAGAVGGAGVSQAGRKNQVTKALLDYEDSETDSDENDDDEDEDFDSYDDENIVVT	1187	
Dm_Nhe2	FTTPATGRRPGSSPGSGSEANTATTTTTSIRLTRNNDESII	1229	