

Supplementary Data 2: Pairwise sequence alignment of full-length and predicted FH isoform based on experimentally verified transcript detected in RT-PCR.

Spliced_FH	1	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR
FH	1	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR
consensus	1	*****
Spliced_FH	61	KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI
FH	61	KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI
consensus	61	*****
Spliced_FH	121	PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
FH	121	PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
consensus	121	*****
Spliced_FH	181	SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
FH	181	SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
consensus	181	*****
Spliced_FH	241	LPSCE-----
FH	241	LPSCEEKSCDNPYPINGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
consensus	241	*****.....
Spliced_FH	246	-----
FH	301	RCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYCDHFETPSGSYWDHIHCTQDG
consensus	301	
Spliced_FH	246	-----
FH	361	WSPAVPCLRKCYFPYLENGYNQNHGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP
consensus	361	
Spliced_FH	246	-----
FH	421	TPRCIRVKTCSSIDIENGFISESQYTYALKEKAKYQCKLGYVTADGETSGSIRCGKDG
consensus	421	
Spliced_FH	246	-----
FH	481	WSAQPTCIKSCDIPVFMNARTKNDFTWFKLNDTLDYEC HDGYESNTGSTTGSIVCGYNGW
consensus	481	
Spliced_FH	246	-----
FH	541	SDLPICYERECLEPKIDVHLVPDRKKDQYKVGEVLKFSCKPGFTIVGPNSVQCYHFGLSF
consensus	541	
Spliced_FH	246	-----
FH	601	DLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCNPRFLMKGPNKIQCVDGEW
consensus	601	
Spliced_FH	246	-----
FH	661	TTLPVCIVEESTCGDIPELEHGWAQLSSPPYYYGDSVEFNCSESFTMIGHRSITCIHGVW
consensus	661	

Spliced_FH 246 -----
FH 721 TQLPQCVAIDKLKKCKSSNLIILEEHLKNKKEFDHNSNIRYRCRGKEGWIHTVCINGRWD
consensus 721

Spliced_FH 246 -----
FH 781 PEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYRDGEKVSVLCQENYLIQEGEEITCKDGRW
consensus 781

Spliced_FH 246 -----
FH 841 QSIPLCVEKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCGGFRRISEENETTCYMG
consensus 841

Spliced_FH 246 -----
FH 901 KWSSPPQCEGLPCKSPPEISHGVVAHMSDSYQYGEEVTKCFEGFGIDGPAIAKCLGEKW
consensus 901

Spliced_FH 246 -----
FH 961 SHPPSICKTDCLSLPSFENAIPMGEKKDVYKAGEQVTTYTCATYYKMDGASNVTICINSRWT
consensus 961

Spliced_FH 246 -----
FH 1021 GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPGGERVRYQCRSPYEMFGDEEVMCLNGNWTE
consensus 1021

Spliced_FH 246 -----DSTGKCGPPPPIDNGDITSFPLSVYAPASSVEYQCQONLYQLEGNKRITCRNGQWS
FH 1081 PPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPASSVEYQCQNL YLEGNKRITCRNGQWS
consensus 1081*****

Spliced_FH 301 EPPKCLHPCVISREIMENYNIALRWTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLR TTC
FH 1141 EPPKCLHPCVISREIMENYNIALRWTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLR TTC
consensus 1141 *****

Spliced_FH 361 WDGKLEYPTCAKRHHHHHH
FH 1201 WDGKLEYPTCAKRHHHHHH
consensus 1201 *****