

Supplementary Figure S2. Sequence comparison between the 5' end of the *FH1* and *fh1-CRISPR* alleles. Predicted protein sequence is shown in bold, the single base insertion in *fh1-CRISPR* is highlighted in yellow.

	1	10	20	30	40	50
<i>FH1</i>	1	AAAGAAGAAGATAACACA <u>ATG</u> GCTCTTCTTCTTATTCTTCTTCTACTTACTCTTATCTTCA				
<i>fh1:CRISPR</i>	1				
FH1	1	M L F F L F F F Y L L L S S				
fh1:CRISPR	1				
	61	70	80	90	100	110
<i>FH1</i>	61	TCCTCCGATCTAGTCTTCGCCGACCGTCGTGTACTCCACGAACCATTCTTCCCTATAGAT				
<i>fh1:CRISPR</i>	61				
FH1	21	S S D L V F A D R R V L H E P F F P I D				
fh1:CRISPR	21				
	121	130	140	150	160	170
<i>FH1</i>	121	TCACCACCACCGTCCACCACCATCACCACCACCACTTCCTAAACTACCATTCTCTTCAACC				
<i>fh1:CRISPR</i>	121				
FH1	41	S P P P S P P S P P P L P K L P F S S T				
fh1:CRISPR	41				
	181	190	200	210	220	230
<i>FH1</i>	181	ACTCCTCCATCTTCATCAGACCCAAATGCTTCTCCTTTCTTCCCTTTATACCCTTCATCT				
<i>fh1:CRISPR</i>	181				
FH1	61	T P P S S S D P N A S P F F P L Y P S S				
fh1:CRISPR	61				
	241	250	260	270	280	290
<i>FH1</i>	241	CCACCACCACCTTCTCCAGCCTCCTTCGCTTCTTTTCCGGCGAATATCTCATCTCTAATC				
<i>fh1:CRISPR</i>	241				
FH1	81	P P P P S P A S F A S F P A N I S S L I				
fh1:CRISPR	81				
	301	310	320	330	340	350
<i>FH1</i>	301	GTCCCTCAGCCACTAAATCCCCACCTAACTCCAAAAACTCCTTATCGTCGCTATCTCC				
<i>fh1:CRISPR</i>	301				
FH1	101	V P H A T K S P P N S K K L L I V A I S				
fh1:CRISPR	101				
	361	370	380	390	400	410
<i>FH1</i>	361	GCCGTTTCTCCGCTGCTTTAGTCGCTCTACTTATCGCTTACTCTATTGGCGAAGAAGC				
<i>fh1:CRISPR</i>	361				
FH1	121	A V S S A A L V A L L I A L L Y W R R S				
fh1:CRISPR	121				
	421	430	440	450	460	470
<i>FH1</i>	421	AAACGTAACCAAGATCTTAACTTCTCCGATGATAGCAAACATACACCACCG-ACAGTAG				
<i>fh1:CRISPR</i>	421 T				
FH1	141	K R N Q D L N F S D D S K T Y T T D S S				
fh1:CRISPR	141 V Q *				
	481	490	500	510		
<i>FH1</i>	480	CCGCCGTGTCTACCCTCCTCCTCCGGCAACGGCGCC				
<i>fh1:CRISPR</i>	481				
FH1	161	R R V Y P P P P A T A ...				
fh1:CRISPR	161				

Signal peptide
 Extracytoplasmic
 Transmembrane