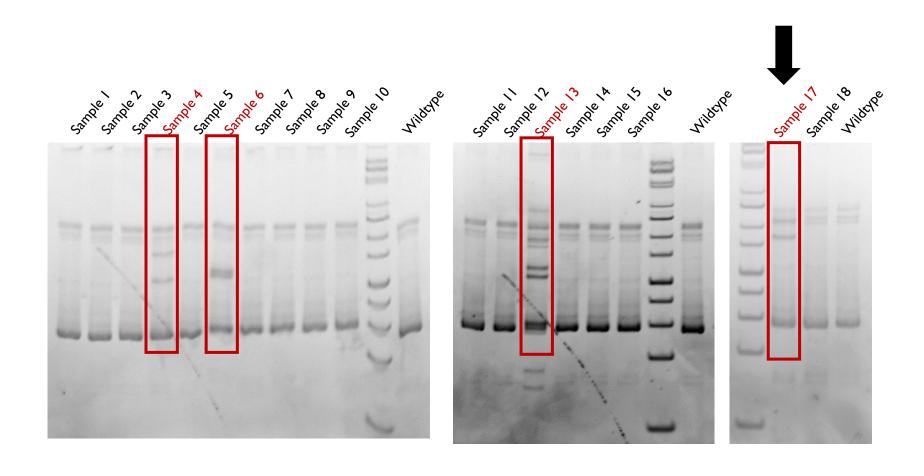
Zfhx4 Seq Results and Genotyping Issues

08/01/2018

Zfhx4 founder PCR products on 10% TBE page gel



Zfhx4 Founder 17 in pGEM-Teasy: clone #1

51	 ATGGT	 TGTGTTAGTG	ATGGGAAGAG ATGGGAAGAG ATGGGAAGAG	. GAAACCTGTC	 TTAATGTGTT	TCTTGTGCAA TCTTGTGCAA TCTTGTGCAA	2189 105 105	No definition line found major minor
2190	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	2249	No definition line found
106	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	165	major
106	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	165	minor
2250	TCTCAATGAT	GAGGAGCAGA	GGCTCCTCAG	TAATAAATGC	GTCTCCGCCA	TAATACAGGG	2309	No definition line found
	11111111111	11111111111	11111111111	11111111111	11111111111			
166	TCTCAATGAT	GAGGAGCAGA	GGCTCCTCAG	TAATAAATGC	GTCTCCGCCA	TAATACAGGG	225	major
166	TCTCAATGAT	GAGGAGCAGA	GGCTCCTCAG	TAATAAATGC	GTCTCCGCCA	GGG	218	minor
2310	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	2369	No definition line found
	11111111111	11111111111	11111111111	11111111111	11111111111	11111111111		
226	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	285	major
219	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	278	minor
2370	TTATCCCAAT	TTTTCTACTA	CAAACCTCAT	AGGACCTGAT	CCAA 2413	No def:	inition lin	e found
	11111111111	11111111111	11111111111	11111111111	HH			
286	TTATCCCAAT	TTTTCTACTA	CAAACCTCAT	AGGACCTGAT	CCAA 329	major		
279	TTATCCCAAT	TTTTCTACTA	CAAACCTCAT	AGGACCTGAT	CCAA 322	minor		

PREDICTED: Mus musculus zinc finger homeodomain 4 (Zfhx4), transcript variant X3, mRNA Sequence ID: XM 017319816.1 Length: 14533 Number of Matches: 1

Score 508 bi	its(562	Expect) 4e-141	Identities 283/284(99%)	Gaps 0/284(0%)	Strand Plus/Plus
Query	46	ATTCGATGGTTGTGTTAG	TGATGGGAAGAGGAAACCTG	TCTTAATGTGTTTCTTGT	ÇAA 105
Sbjct	1784	ATTCGATGGTTGTGTTAG	TGATGGGAAGAGGAAACCTG	TCTTAATGTGTTTCTTGT0	IIII ICAA 1843
Query	106	ATTGTCTTTTGGCTATAT	CAGGTCATTTGTAACCCATG	CTGTACATGATCATCGGA	TGAC 165
Sbjct	1844	ATTGTCTTTTGGCTATAT	caggtcatttgtaacccatd	CTGTACATGATCATCGGA	GAC 1903
Query	166	TCTCAATGATGAGGAGCA	GAGGCTCCTCAGTAATAAAT	GCGTCTCCGCCATAATAC	AGGG 225
Sbjct	1904	TCTCAATGATGAGGAGCA	GAGGCTCCTCAGTAATAAAT	GCGTCTCCGCCATAATAC	AGGG 1963
Query	226	GATTGGCAAAAACAAAGA	ACCTCTTATAAGCTTTCTGG	AACCaaaaaaaTCCACTT(TGT 285
Sbjct	1964	GATTGGCAAAGACAAAGA	ACCTCTTATAAGCTTTCTGG	AACCAAAAAAAATCCACTT	TGT 2023
Query	286	TTATCCCAATTTTTCTAC	TACAAACCTCATAGGACCTG	ATCCAA 329	
Sbjct	2024	ttatcccaatttttctac	tacaaacctcataggacctd	ATCCAA 2067	

ZH002 (N1 from founder 17) in pGEM-Teasy: clone #1

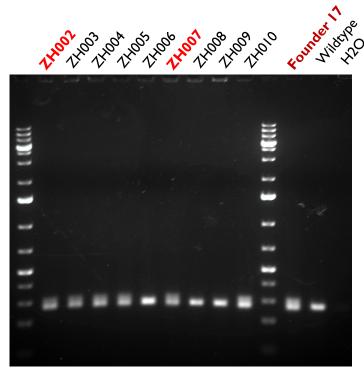
51	 TGGT	TGTGTTAGTG	 ATGGGAAGAG	. GAAACCTGTC	 TTAATGTGTT	TCTTGTGCAA	2189 104 104	No definition line found major minor	I
2190	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	2249	No definition line found	
105	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	164	major	
105	ATTGTCTTTT	GGCTATATCA	GGTCATTTGT	AACCCATGCT	GTACATGATC	ATCGGATGAC	164	minor	
2250	TCTCAATGAT	GAGGAGCAGA	GGCTCCTCAG	TAATAAATGC	GTCTCCGCCA	TAATACAGGG	2309	No definition line found	
165	TCTCAATGAT	GAGGAGCAGA	HIIIIIIIII	TAATAAATGC	HIIIIIIIIII		224		
		GAGGAGCAGA					224 217	major minor	
103	rerearioni	unuunuchun	docreerend	TATTAATIGE	diciccocca	444	217	milition	
2310	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	2369	No definition line found	
	11111111111	11111111111	11111111111		11111111111				
225	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	284	major	
218	GATTGGCAAA	GACAAAGAAC	CTCTTATAAG	CTTTCTGGAA	CCAAAAAAAT	CCACTTCTGT	277	minor	
0270						N- 4-6		- f d	
23/0	TTATCCCAAT	IIIICIACIA	CAAACCTCAT	AGGACCIGAT	CCAA 2413	NO deti	inition lin	e Touna	
285	TTATCCCAAT	TTTTCTACTA	CAAACCTCAT	AGGACCTGAT	CCAA 328	major			
	TIMICCCANI	TTTTCTACTA	CAMACCICAI	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		minor			
-/-									

PREDICTED: Mus musculus zinc finger homeodomain 4 (Zfhx4), transcript variant X3, mRNA Sequence ID: XM 017319816.1 Length: 14533 Number of Matches: 1

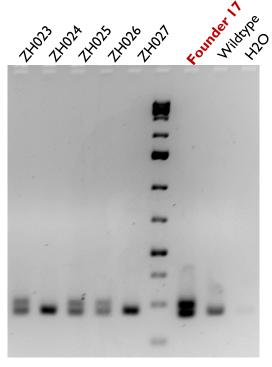
Range	1: 178	4 to 2067 GenBank Gra	<u>ohics</u>	▼	Next Match 🛕 Previous Matcl
Score		Expect	Identities	Gaps	Strand
508 bi	ts(562) 4e-141	283/284(99%)	0/284(0%)	Plus/Plus
Query	45	ATTCGATGGTTGTGTTAG	GATGGGAAGAGGAAACCT	TCTTAATGTGTTTCTTG	TGCAA 104
Sbjct	1784	ATTCGATGGTTGTGTTAG	GATGGGAAGAGGAAACCT	stettaatetettte	TGCAA 1843
Query	105	ATTGTCTTTTGGCTATATO	AGGTCATTTGTAACCCAT	GCTGTACATGATCATCGG	ATGAC 164
Sbjct	1844	ATTGTCTTTTGGCTATAT	AGGTCATTTGTAACCCAT	sctgtacatgatcatcgg	ATGAC 1903
Query	165	TCTCAATGATGAGGAGCAG	AGGCTCCTCAGTAATAAA	TGCGTCTCCGCCATAATA	CAGGG 224
Sbjct	1904	TCTCAATGATGAGGAGCAG	AGGCTCCTCAGTAATAAA	rdcdtctccdccataata	CAGGG 1963
Query	225	GATTGGCAAAAACAAAGAA	ACCTCTTATAAGCTTTCTG	SAACCaaaaaaaTCCACT	TCTGT 284
Sbjct	1964	GATTGGCAAAGACAAAGA	ACCTCTTATAAGCTTTCTG	SAACCAAAAAAAATCCACT	tctdt 2023
Query	285	TTATCCCAATTTTTCTACT	ACAAACCTCATAGGACCT	SATCCAA 328	
Sbjct	2024	ttatcccaatttttctac	ACAAACCTCATAGGACCT	SATCCAA 2067	

^{*}Progeny of Founder No. 17

Genotyping results

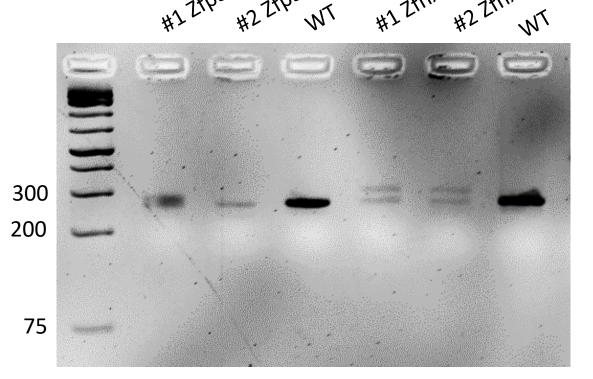


Founder no. 17 x C56BI/6J



ZH002 x ZH007

Leesa Sampson
Screening of mice used for cryopreservation
3.5% agarose gel



Zfp92 genotyping failed: incorrect primer set?

