Table 2 Oligonucleotides used for RT-PCR, EMSA, and ChIP in the identification of of HNF4α target genes in the liver

		RT-PCR Oligonucleotides		EMSA				ChIP Oligonucleotides	
Gene Symbol	Entrez ID	Forward	Reverse	H4 site[4]	Position	Sequence	Shift Oligo	Forward	Reverse
Cdh1	12550	cgcgcccgggactccag	ctccaccgcttccccatttga	n/a	64530	agtcccaaggcca	n/a	n/a	n/a
				n/a	64469	aggttacagttca	n/a	n/a	n/a
				n/a	3875	ggcttaaagtca	n/a	n/a	n/a
				n/a	11616	agtctaaaggtca	n/a	n/a	n/a
				H4.120	25249	agggcagaggcca	ttttggggcagggcagaggccatcagg	ctcaaactcttacctgctcccgactcctg	taactaaaacattttggggataaggggaagat
				n/a	33399	aggcccaaggcca	n/a	n/a	n/a
				n/a	20005	agggcttagttca	n/a	n/a	n/a
				n/a	45165	aggtcagaggcca	n/a	n/a	n/a
				H4.182	-6134	agtccaaaggccg	ttttgtttaagtccaaaggccggggaa	ctgctgaggggtccccacaagataa	taaatgactagagcacttccaaagaacagg
Ceacam1	26365	caatctgccccctggcgcttgga	tgaaatcgcacagtcgcctgag	n/a	3914	gtcacaaaggcca	n/a	n/a	n/a
				H4.114	-2681	gggccagggtcca	ttttttgagggggccagggtccactcat	aagagctgttgaaatcttctaatgggtggt	gatctgcgcgggcagtggtggtg
Cldn1	12737	aagcgtaaaaccagtaagaatcccatagtc	aaqcaaacaagacaagctccaagaccaaaqtq	H4.29	13561	agaccaaagtgca	ttttgctccagaccaaagtgcaaagac	tcagatgatgttttcccgatgacctttc	aagcacagtttgcaggactcgggatgga
				n/a	11654	tgatcaaagagca	n/a	n/a	n/a
				H4.161	2488	ggggcaaagttca	ttttgctctgggcaaagttcacgagt	gctatgggtttcctaatattgtactcgtga	cctctttatgctatttccagtgttctcgt
				H4.60	3566	ggatcaaaggtcc	ttttgggatggatcaaagtccactgg	tgcattccaacaagtaagaataggggc	caatttgtaacgtagggcagagtagga
				n/a	-2290	aggtaagaggtca	ttttgaataaggtaagaggtcactttg	n/a	n/a
Cldn2	12738	gattgtgcttgaggtgggagaacggaga	ttgccggtgctgaagttttgatgaggt	n/a	5317	aggataaagtcca	n/a	n/a	n/a
				n/a	-1995	aggtcagaggcct	tttttgctcaggtcagaggcctctaag	n/a	n/a
				n/a	7617	aggtcaaaaaggca	n/a	n/a	n/a
Cldn12	64945	ctgctctcctgctgttcgtttggtattgtg	qtqaqtaaqtqtqcatcccaqqaqcqtqaq	n/a	n/a	n/a	n/a	n/a	n/a
Crb3	224912	tccgggggcagcttgaggttgg	gagtccaacgggggcctgtcttca	H4.172	-5505	aggccagaggtca	tttttgaagaggccagaggtcaatggc	cccaggagacacccaaaccatacatag	acccagcaccggtgaggtagagact
Cxadr	13052	cgcgcctactgtgcttcgtgctcttg	ttccccttqqcctttttcqatcctctqttc	H4.183	-6919	agatcaaagtgca	ttttacactagatcaaagtgcagatac	caaatcaggttaaactagaattatgtggagag	acactggggtggcctttggtgataca
				n/a	24374	aggtagaggtca	n/a	n/a	n/a
				n/a	25276	agagcaaaagtcc	n/a	n/a	n/a
				n/a	23557	agttcaagggttg	n/a	n/a	n/a
				n/a	10720	agtccaaagtctt	n/a	n/a	n/a
				n/a	9740	aggtcaaaggtca	n/a	n/a	n/a
				n/a	6477	ggggcaatggtca	n/a	n/a	n/a
				n/a	45616	agttcaaagttct	n/a	n/a	n/a
				H4.184	-2346	agatcaatgtccca	ttttttgacagatcaatgtccagaatg	ctgggggaaataaccacaggatgacc	gaggtaacggagtccaagtggcaaca
Dsc2	13506	tgcagttcccattcggattacagacaga	ttgatgcccgggaaacactacagactaat	H4.41	16746	agggcaaagtca	ttttattccagggcaaagtgcaatggc	tctatggaatcccacagcttgaagagt	agggcgagagcagcactgtgttattac
Dusp16	70686	cacagaggccagggaaacaacgagagaac	tqaaqcqaaqqttqcaacaqqacaqaqtat	n/a	30529	agtccagagtcca	n/a	n/a	n/a
				n/a	38519	aggtcagaggaca	n/a	n/a	n/a
				n/a	42667	gggccaaaagaca	n/a	n/a	n/a
				n/a	43092	agaacagagtcca	n/a	n/a	n/a
Eppk1	223650	tqtcctqtacctqttctcccqctttctctcttqt	gcacatgcccttaatcccagtcctccaga	n/a	1668	ggggcaaaggcca	n/a	n/a	n/a
				n/a	8002	tgggcaaggtcca	n/a	n/a	n/a
				n/a	6490	aaagcaggtcca	n/a	n/a	n/a
				n/a	-2364	agggcagaggcaa	ttttctggaagggcagaggcaagattc	n/a	n/a
				H4.81	14313	aggtcagaggtca	tttttgctgaggtcagaggtcatcaca	aacccgggcactgcagaaggtggtaga	cagctggttcccttgaggtatctcttcacg
Eva1	14012	catgggccaaagactacctaaatggaaataacc	atcacatcqcaaaqattcaccctqqacctq	n/a	-1284	aggtcaaaaggca	ttttgtgtaggtcaaaaggcagtttt	n/a	n/a
F11r	16456	cgagggggaaagccgggaggaaactgttgtt	ccqcataqqqaactqtqatctqqctcttat	n/a	18695	ggtccagagttca	n/a	n/a	n/a
				H4.35	4038	tgtccaaagtcca	tttgtttctgtccaaagtccagcttg	ggtggggcggaggctgtgggtag	accggccaggacatcactcactcaaga
				n/a	11117	agtccaaagattt	n/a	n/a	n/a
				n/a	25793	tgggcaagagtcc	n/a	n/a	n/a
Gjb1	14618	ctgctctacccccggctatgc	caggctgagcatcggtcgctctt	H4.185	-6501	agtccaaaggttc	ttttagggtagtccaaaggttctttca	gtatcagggcggtacttgttcttccc	aatctgcctgctggtctctgtgaa
				n/a	2598	aggttaaagtcca	n/a	n/a	n/a
				n/a	9066	aaagcagagtcca	n/a	n/a	n/a
Gjb2	14619	aggatcagccggcgacccatttc	cggcttgctcatctcccccacacc	n/a	2845	agtccacagtgca	n/a	n/a	n/a
Gpld1	14756	cgcatatcaggctgggaccgtgtt	aatggatgctggcgttaagaaatggag	n/a	43085	aggtcagagggca	n/a	n/a	n/a
				H4.186	-2056	gggtcagaggtca	tttttatagggggtcagaggtcaacatc	tggccagccatcctaatcaaatcaat	gcatgtacgatataggggtcagaggtcaa
				n/a	14257	gggtcacagttca	n/a	n/a	n/a
				n/a	17157	tgtccagagtcca	n/a	n/a	n/a
				n/a	29057	tgatcaaaggcaa	n/a	n/a	n/a
Gsn	227753	ccccaggcagacccaggtttcagttc	ccatggcggtggaggtgtgcagcgtagc	n/a	22663	cgggcagaggtca	n/a	n/a	n/a
				H4.77	1821	aggtcaaagggca	ttttatcacaggtcaaagggcagagct	atccccgaccccccaactgtatg	ggctcctagctgggaagagaaaatga
				n/a	1512	aggccaggctcct	n/a	n/a	n/a
				n/a	21780	gggtcaagggttt	n/a	n/a	n/a
Krt2-8	16691	ctggcggctttggcgggctggtgtc	cagctgccggcggaggttgttgatgta	n/a	-916	tgggcagacaaag	tttttaacctgggcagacaaagcaaac	n/a	n/a
Lgals9	16859	ccggtttgaggaaggaggggtatgtggt	ccgtgggaactggactggctgagag	n/a	20648	aaactaaagtccca	n/a	n/a	n/a
				H4.187	-4626	tgggcaaaggtct	tttttccactgggcaaagtctgtgccc	agcattcctcaaacggcttattcatcta	ctccctttttctctgcccgtttctcttt
				H4.49	-1077	ggtccaaagttca	ttttatgaaggtccaaagttcaaatccc	ttaagagcgctaattgcccgaaaaaca	agctgtcttcagacacaccagtagaggatg
				H4.41	11946	agggcaaaggtca	ttttggcagagggcaaagtcacatct	accccccggtttgaggaaggagg	gtaaggcagaggggcaaagtcacatc
				n/a	1257	aggcagaggctgac	n/a	n/a	n/a
				n/a	1747	ggggccaagggca	n/a	n/a	n/a
				n/a	3182	ggtcagagttca	n/a	n/a	n/a
				H4.94	11830	aggtcagagttca	ttttgcagaggtcagagttcaaggtg	accccggtttgaggaaggagg	gtaaggcagaggggcaaagtcacatc
				n/a	15433	gggccaaaagtct	n/a	n/a	n/a
Mbl2	17195	ccggggttaaaaggagcagtgggac	cacagagccctggaattcggagcaca	n/a	n/a	n/a	n/a	n/a	n/a
Npnt	114249	acgaggggggatggactgaactgtgtgt	gatggccttttctgggggtggtggtagt	n/a	65513	agctcaaggggca	n/a	n/a	n/a
				H4.188	-7251	ggctcaaagtcca	tttactctcggctcaaagttcaaaagt	aattatttcttttacatccctggtccctttat	cctgattgtggatgtcctatgaagagttgc
				n/a	3474	aggccaagggca	n/a	n/a	n/a
				n/a	7127	ggttcaaagtgca	n/a	n/a	n/a
				n/a	30353	gggcaaaagttca	n/a	n/a	n/a
				n/a	33332	agaccaaaagtca	n/a	n/a	n/a
				n/a	36727	ggggaaaagtcca	n/a	n/a	n/a
				n/a	15434	aggccagggccca	n/a	n/a	n/a
				n/a	44363	aaaccaaaggcca	n/a	n/a	n/a
Ocln	18260	ctatggcggatatacagacccaagagcag	tctqtqaqccqtacataqatccaaagcct	H4.189	-8995	aggtcaaggggca	ttttgtggaggtcagagggcaatttg	ggtgcctgccccaaagcctactg	tttgtatttaaaatccccaggtcgtga
				n/a	50280	aggtttaaggtca	n/a	n/a	n/a
				n/a	43957	tgggaaaaggtca	n/a	n/a	n/a
				n/a	8225	aggtcagggaca	n/a	n/a	n/a
				n/a	29446	tgggagagctgac	n/a	n/a	n/a
				n/a	23816	aggtcaaaattca	n/a	n/a	n/a
				n/a	19626	aggctaaagttca	n/a	n/a	n/a
				n/a	29149	gggcagaggggca	n/a	n/a	n/a
				H4.169	15440	aggtcaaaggtca	ttttagaggaggtcaaaggtcaataac	aaaaatgagaatgagaagtgatggaggaa	atctgtaatgggattcaatgccttcttcta
				H4.95	2254	agttcacagttca	ttttagttcagttcacagttcaaacat	ccagcatgtaacgctaaggaccagta	ctccgccccagtgagcatcttga
				n/a	-464	gagtcagaggtca	ttttgaggagagtcagaggtcaggagg	n/a	n/a
Pkp2	67451	cgcctcaccctgccacgctatgctc	gcgggcggttctgctctgcgtgctttga	n/a	50688	agaacaatgttca	n/a	n/a	n/a
				n/a	47823	agtgtaaaggtca	n/a	n/a	n/a
				n/a	25371	gtaccaaaagccc	n/a	n/a	n/a
				H4.190	-7328	ggggtagagtcca	ttttccagagggtagagtccatggtg	ttcattggtagatgagccatgcattagtta	gttctctgcctcctcggttgtgatttga
Rhpn2	52428	agccgctggagaaagagggtgacgactact	tcaggccgagaggaatcagaggaatggtg	n/a	32117	ggtccagagttca	n/a	n/a	n/a
				H4.191	-672	ggtccagagttca	ttttccgaaggtccagagttcaaatccc	aaattatcttttcgggctggtgag	ggaggaaagggagggaagggaacaat
				n/a	22671	aggtcaaaggcct	n/a	n/a	n/a
				n/a	9347	aggtcaaaaggct	n/a	n/a	n/a
				n/a	19640	agtcctagggtca	n/a	n/a	n/a
				H4.191	-6371	ggtccagagttca	ttttccaaagtccagagttcaaatccc	ccgaaggtccagagttcaaatcccagc	agcaactagtggaaaagcagccgtgaat
				n/a	36043	aggtcaaaggtca	n/a	n/a	n/a
				n/a	-8018	agggcagagggca	ttttcgggagggcagagggcaggtgg	n/a	n/a
				n/a	17186	tgggcaaggggca	n/a	n/a	n/a
				n/a	-3879	tgggtaaaggcca	ttttcccagtgggtaaaggccagtggc	n/a	n/a
				n/a	-1417	ctgaagagctgac	ttttaaggactgaagagctgacttcag	n/a	n/a
				n/a	9320	ggggcagggtcca	n/a	n/a	n/a
Sdc1	20969	ctgactccagccggcgaaacctaca	tggagctgtgggcgtggctgtcaac	n/a	3317	aggtcaaagtcta	n/a	n/a	n/a
				H4.172	-7406	aggccagaggtca	ttttgtggaggccagaggtcacatgt	ccccccaaaaatcaaactgtgt	taaagaaatgacagccgtaaggaaca
				n/a	-69	aaactaaagtcca	ttttggaggaactaaagtccatgttg	n/a	n/a
				n/a	20526	agtccaaagattt	n/a	n/a	n/a
				n/a	25317	aggttagagttca	n/a	n/a	n/a
				n/a	1009	agcttaaaggttg	n/a	n/a	n/a
Spp1	20750	cgatgtccccaacggccgaggtgata	ctcatggctgccctttccgttgttgtcct	H4.192	-6793	aggggaaaggttt	tttgagccagggcaaaggttttgaca	gggaaataacattgagaaacctgcctgc	tatctctggcctccttctcttcttcctcaa
				H4.193	-4419	agtccaaagtcaa	tttttacctagtccaaagtcaagatgg	cctccaaatggccaaacgggtctgaac	ctccagtcctgagatgatttcttacgcac
Timd2	171284	aaccagaaatttccacgagtccaccaac	agtgttatcatcccaagggtcatctg	n/a	n/a	n/a	tttgttgactaagtcaataatcaqaatcaq	n/a	n/a
				H4.21	n/a	tqqqcaaaqtca	n/a	n/a	n/a
				H4.221	n/a	n/a	n/a	cqtqaaaaqcatqqqcaatc	aqqqataaaactqaqcaqgc
Vtn	22370	gcgttcgcccttcctgcccaccgttaca	ccggccatagcagcgtccactttccc	n/a	n/a	n/a	n/a	agcgcaagttgaatctgc	agcgacaatctaccagag
Ttr[1]	22139	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
APOC3[2]	345	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Apoc3[2]	11814	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Hprt1	15452	agcgcaagttgaatctgc	agcgacaatctaccagag	n/a	n/a	n/a	n/a	n/a	n/a
Hnf4a	15378	cttccttcttcatgccag	acacgtccccatctgaag	n/a	n/a	n/a	n/a	n/a	n/a
Afp	11576	tcgtattccaacaggagg	aggctttgcttcaccag	n/a	n/a	n/a	n/a	n/a	n/a
Alb1	11657	cttaaacgatggcgatctcact	cccctactagcctctggcaaaat	n/a	n/a	n/a	n/a	n/a	n/a
Apoa1	11806	acacacgtagactctctg	ctgggctttggtcttaag	n/a	n/a	n/a	n/a	n/a	n/a
Apoa2	11807	gccatcatgaagctgctcgc	ccagactagttcctgctgac	n/a	n/a	n/a	n/a	n/a	n/a
Apob	238055	ctctcaggggacaaagcag	tcaaggggtgagctgattg	n/a	n/a	n/a	n/a	n/a	n/a
Apoc2	11813	ttactggacctctgccaagg	cctaacttgggcttgcctg	n/a	n/a	n/a	n/a	n/a	n/a
Apoc4	11425	ctgagagcagccgctggagcctggtaag	caggctgtgggtcttgtttaggaggtggtc	n/a	n/a	n/a	n/a	n/a	n/a
Apoh	11818	tgctcgccttgttctccgcctcctc	atttttcctcctccgtgcacttagatga	n/a	n/a	n/a	n/a	n/a	n/a
Apom	55938	tgaaggcgcccagacatgaaacag	tcgacagcgggcaggcctcttgattc	n/a	n/a	n/a	n/a	n/a	n/a
Acox1	11430	agtcggggaagctggtggtggtatggtgt	cacqcctctacqqctctqtcttgaatctt	n/a	n/a	n/a	n/a	n/a	n/a
Agpat3	28169	cactttgggaaggacatgtggttgttatc	atgctgatgcgatgctggtctctgtg	n/a	n/a	n/a	n/a	n/a	n/a
Aldh3a2	11671	taaaaggggtaaaggggggaaagcgtcaa	ttcaqgaqaqqcaacaaqgaaqtcattaca	n/a	n/a	n/a	n/a	n/a	n/a
Amacr	17117	ggaaacagcctcgaggacaaaacatcttag	cctcctcaaacqtcaqcactqqqqtcacac	n/a	n/a	n/a	n/a	n/a	n/a
Decr1	67460	gctgctgggccgtgcgttctt	gaagttccctgccgcgttgtttatcac	n/a	n/a	n/a	n/a	n/a	n/a
Ech1	51798	gcccgcatagcctggtacctccgtgac	acctccgccaatgcagcctccgtgaat	n/a	n/a	n/a	n/a	n/a	n/a
Elovl2	54326	cctgctctctgatatggctgggtaacaagt	qgacqcqtqqtqatagacatqaagqaaqgt	n/a	n/a	n/a	n/a	n/a	n/a
Fapb1	14080	ctcatccagaaaggaagga	cccaatgtcatggtattggtg	n/a	n/a	n/a	n/a	n/a	n/a
Acsl1	14081	ccatagggatagtcgagggcacggaaca	caqcaaqcaqcaqacatatcaqaaaqaat	n/a	n/a	n/a	n/a	n/a	n/a
Lcat	16816	ccgccagtcgcagcccgtacatttg	gggctggcagctggcgacttaggagtg	n/a	n/a	n/a	n/a	n/a	n/a
Lipc	15450	gctgtcgtctcagacctcagc	gagcaggtgaactcgccgatc	n/a	n/a	n/a	n/a	n/a	n/a
Ehhadh	74147	gaaccccgcaggatcctaaacaagccagtc	cccaagccaagaacaaccagcaggag	n/a	n/a	n/a	n/a	n/a	n/a
Mttp	17777	catgatcctcttggcagtgcttttctct	attcctccacaqtaacacaacqtccacatc	n/a	n/a	n/a	n/a	n/a	n/a
Pemt	18618	ttctggttctggctgatcttcttcgttatga	ggagcggaggatgttcaaaagcaggatg	n/a	n/a	n/a	n/a	n/a	n/a
Phyh	16922	aggatctgcactatttcccctccgaccta	acttgggggaatcatgtggcttcagagtg	n/a	n/a	n/a	n/a	n/a	n/a
Pon1	18979	agaaccatcggtcttcctatcaaacaa	gaatctctaagtcttcagcacccgtctc	n/a	n/a	n/a	n/a	n/a	n/a
Scp2	20280	aaccctcagtcggcctctcttcaa	tcatgctattcgggaggtgtcagtctaa	n/a	n/a	n/a	n/a	n/a	n/a
Slc27a2	26458	gccctcctgctgttccgagcagaga	acaqcccagtttqaqtcccaqccaqcaat	n/a	n/a	n/a	n/a	n/a	n/a
Slc27a5	26459	gcccccaagttctctgctcccgattctg	caca agttcatcaagcccacattgccctc	n/a	n/a	n/a	n/a	n/a	n/a
Thb	235674	agaagctaggaattcctgcag	qaqacaqtacacatttactqcatccctccc	n/a	n/a	n/a	n/a	n/a	n/a
Aldob	230163	atggcctctctgaacgctgt	tctccgtcaggaagcacctc	n/a	n/a	n/a	n/a	n/a	n/a
Fbp1	14121	gacagggggcgagactggagactat	cgcaccgcagacggagatggcttctgat	n/a	n/a	n/a	n/a	n/a	n/a
G6pc	14377	ccatgggcgcagcaggtgtat	aggctggcaaagggtgtagtgtca	n/a	n/a	n/a	n/a	n/a	n/a
Slc37a4	14385	gtggatttctggctggcttacccttca	agccgctctcctttccgtgcctgcca	n/a	n/a	n/a	n/a	n/a	n/a
Galk1	14635	gccgaggcccgccgtgtcatggaggagttt	ccatctgtccqqqqctqccaaccatcacq	n/a	n/a	n/a	n/a	n/a	n/a
Pcx	18563	ttggcagcctttgggaatggagcgtgtttt	qqcqqqaattqacctcqatqaagtaqtqct	n/a	n/a	n/a	n/a	n/a	n/a
Pck1	18534	gcccccgggagtcaccatcac	tttgccgaagttgtagccgaagaa	n/a	n/a	n/a	n/a	n/a	n/a
Pfkfb1	18639	gtgccttctagcatacttcctggataaaag	tgcagccataagccacaggtgtgagtttg	n/a	n/a	n/a	n/a	n/a	n/a
F5	14067	tggcgagccgaccctacagcatttaccct	aqqcactqqqcatcqttttccqtqqqttca	n/a	n/a	n/a	n/a	n/a	n/a
F9	14071	agccacatgcctaggtccacaaca	ggtcccccactatctccttcacacg	n/a	n/a	n/a	n/a	n/a	n/a
F10	14058	cgaggacgacgagaagacgaaagaatactg	atgcaggacttgccatcattacccaggaa	n/a	n/a	n/a	n/a	n/a	n/a
F12	58992	acggctctgttgttcctggggtctctgc	ctqqccqcccttttqtqqatqcatttqtqqt	n/a	n/a	n/a	n/a	n/a	n/a
F13b	14060	tacttattgaaggggtcggaaacatctcgc	taggtgcgggctgctgaactaacaata	n/a	n/a	n/a	n/a	n/a	n/a

[1] *Foxa* binding site in the mouse *Ttr* gene used as a negative control for EMSA
[2] *Hnf4a* binding site in the human *APOC3* gene used as a positive control for EMSA
[3] *Hnf4a* binding site in the mouse *Apoc3* gene used as a positive control for ChIP
[4] Binding site numbers were assigned according to the nomenclature previously given to the 169 known binding sites (C.Y. and F.M.S., submitted). Sites designated with numbers beyond 181 represent novel binding sites identified in this