

Table SII. Customized primers and amplicons for 29 targeted genes in the present study.

Amplicon_I D	Ion_AmpliSeq_Fwd_Primer ^a	Ion_AmpliSeq_Rev_Primer ^a	Gene name	Location ^a	Length (bp)	Accession number
AMPL7153 134585	GGGTGACATAAAATGTGCACAG ACA	GGATCTAGGGAGGCTGAACT GA	<i>DUOX</i> 2	chr15:45387172-4 5387344	172	NM_01408 0.4
AMPL7153 212168	TAGGTGGCGATGACCCTCT	GATCACGCTACCGCTCGT	<i>DUOX</i> 2	chr15:45403313-4 5403524	211	
AMPL7153 212232	GGGCTGTCTAAGGCTAGACA	CCAGGACCTATCCCAGCTAG A	<i>DUOX</i> 2	chr15:45400167-4 5400391	224	
AMPL7155 234979	CCTTTAACAGCTGACCTCATC CT	CCCATTCTCTGTCTCTTGGGC TA	<i>DUOX</i> 2	chr15:45386621-4 5386979	358	
AMPL7155 234981	CACCTCCACCTTTGACACAGA G	GTCACTGGTAACCACATTAG ATAATCTGG	<i>DUOX</i> 2	chr15:45394003-4 5394292	289	
AMPL7155 234982	G TTCCTTGAGCCTGGTCTCAA A	GAAGACAGATGATACCTTGG TCCTT	<i>DUOX</i> 2	chr15:45398927-4 5399270	343	
AMPL7155 234983	GGCTTGTCCTGAAGGCTAGAA A	TACAGAGGGTGGAACCATGG AA	<i>DUOX</i> 2	chr15:45390087-4 5390437	350	
AMPL7155 234987	CCCGGATAATTCCTCTACCCT TCA	AATCTCTGCCGTGTTCAAGG AA	<i>DUOX</i> 2	chr15:45401950-4 5402315	365	
AMPL7155 234995	GATAGGGAAGGGCAGAGATC CT	GGTGCCTATCAGTCCTCAGG TA	<i>DUOX</i> 2	chr15:45387958-4 5388329	371	
AMPL7155	GCAGGTCATCTCCTTGCTGAA	ATATGAAGGGTCACTGAACT	<i>DUOX</i>	chr15:45396272-4	371	

234996	A	GCTTC	2	5396643	
AMPL7155	GCAGCTGGAATGTTTGTGCTA	AGTGAGTGCTTAGTCTAGGG	<i>DUOX</i>	chr15:45393257-4	364
235001	C	AATGA	2	5393621	
AMPL7155	CTCTCCCATGCAGACTCTTAG	GTCACCTTTCATGGAGTGGC	<i>DUOX</i>	chr15:45392151-4	353
235002	G	AT	2	5392504	
AMPL7155	GCGAAATGACCTTCCAGTCTC	TCCAGTACTAGCTGTAGGAA	<i>DUOX</i>	chr15:45405434-4	284
235003	A	CAAGAG	2	5405718	
AMPL7155	GGCCTCGCTTGTGATAATGGA	GACTCACAGAGGAATTGACC	<i>DUOX</i>	chr15:45398257-4	347
235004	G	TGAAG	2	5398604	
AMPL7155	CTGCTCAGAGGCCACCACAAA	TGACCCTTCCTGGTCTCATCT	<i>DUOX</i>	chr15:45402664-4	352
235008	T	C	2	5403016	
AMPL7155			<i>DUOX</i>	chr15:45404936-4	336
235009	GGCTCTGTCTAAGCACTCCAT	AGTCAGGACGCACTCTCACT	2	5405272	
AMPL7155	AATGAGTCAACATATGTAAAG	GTGCCAATAGTCAGATACAA	<i>DUOX</i>	chr15:45400903-4	330
235016	GGTTTGGA	GGCT	2	5401233	
AMPL7155			<i>DUOX</i>	chr15:45404073-4	125
399284	CAGGTGGGATGCGGATGTT	CGCAATACGGACGGTTTGTC	2	5404198	
AMPL7155	CCAGCTTGTCACCTCCATAGA	CCAAGATCTCAGAATGAGAC	<i>DUOX</i>	chr15:45389496-4	237
415877	TG	TTTGAGATT	2	5389733	
AMPL7155	GAGTGGGCTGACTGAGAAGAT	CATGTTCTCTTATATCTTGCT	<i>DUOX</i>	chr15:45391625-4	374
435721	G	CACCATGT	2	5391999	
AMPL7153	CGTACAAACTGGTCGAGGACA	GCTTGCCTAAGAAGAGGAAA	<i>DUOX</i>	chr15:45400290-4	266

212237	A	TCAGG	2	5400556	246
AMPL7153	AGGTTGTTAAACCAGCCGTCA	CCTGAGACTGGAAGGTCATT	<i>DUOX</i>	chr15:45405211-4	
212528	TAG	TCG	2	5405457	339
AMPL7155	CTGAGGCCTAAGGTGGATTCT	CTGGGCTTGAAGCCTTAGTC	<i>DUOX</i>	chr15:45386240-4	
234972	G	ATT	2	5386579	320
AMPL7155	CTGAGCAGAGCGCCAGATCAA	GGTTCTGTCAGTGAAGTGGG	<i>DUOX</i>	chr15:45404703-4	
234973	C	AT	2	5405023	373
AMPL7155	ATTTTCTTCTTATGGCTCCTTG	GGGACAACAGTTCAAGAGA	<i>DUOX</i>	chr15:45401578-4	
234975	AAGTCT	GTCT	2	5401951	372
AMPL7155	CGCCTTCAGGTCAATTCCTCT	GTTTGAGACCAGGCTCAAGG	<i>DUOX</i>	chr15:45398577-4	
234977	G	AA	2	5398949	369
AMPL7155	CCTCTTCCTCTGGCCAGATAC	GCTGACATGGGAGGATTTTC	<i>DUOX</i>	chr15:45393719-4	
234980	AT	ACTT	2	5394088	328
AMPL7155	GCAGGTCAGACCAAAGACAG	ATCCAAGAGGTGGAGGAGA	<i>DUOX</i>	chr15:45386904-4	
234984	TC	ACGA	2	5387232	373
AMPL7155	GGAACAAATGGAATGAGACT	GCCAGAATCATTCTACAAAA	<i>DUOX</i>	chr15:45392832-4	
234988	CAGGAT	CAAATCATGA	2	5393205	374
AMPL7155	GAGTGCGAGGAGCCATAGAT	CCGAGTTCCTCAACATCCGC	<i>DUOX</i>	chr15:45403728-4	
234991			2	5404102	367
AMPL7155	GGCATCTCAACCACTGGGTAA	TGTCTCCGTTTCTGGTCTCAG	<i>DUOX</i>	chr15:45387494-4	
235005	G	A	2	5387861	343
AMPL7155	GGGTCTTAAATCTCAAAGTCT	ATGAGAGAGGAAGGAGGGA	<i>DUOX</i>	chr15:45389697-4	

235006	CATTCTGA	AGGATAG	2	5390040	
AMPL7155	GAATGACCCAGCTGCTAGACA	CAGGATACCGTCCTTTCCTA	<i>DUOX</i>	chr15:45402384-4	341
235007	A	GAC	2	5402725	
AMPL7155	CGGCCTGCCTATTTCTTTTTCT	CCTTATACCTCCATCTCTCCT	<i>DUOX</i>	chr15:45391503-4	278
235010	ATT	CCCTAT	2	5391781	
AMPL7155	CCAGTCAGGTAAATATTTGAA	CCTGGTGGTCTTCATGAAAG	<i>DUOX</i>	chr15:45395984-4	373
235017	GGTGGA	GTAG	2	5396357	
AMPL7155	GGTGATAAATAATCATCACCA	GTTCCGCTACCACAACCTGT	<i>DUOX</i>	chr15:45403103-4	314
235019	GCCAGAT		2	5403417	
AMPL7155	GAAAGTCTCTCGCAGGAAGGT	CCCTCTGATCCTAAGAGTCT	<i>DUOX</i>	chr15:45391936-4	245
415875	TAT	GCAT	2	5392181	
AMPL7155	CCTCCTAGCCCAACACAGAAG	CCCTCTGGGTCTCTTTTCTCA	<i>DUOX</i>	chr15:45399421-4	339
435713		C	2	5399760	
AMPL7155	CCACCTCTTCTCAGGTCCTTC	CCCACTTTCCACATCTACTTC	<i>DUOX</i>	chr15:45389195-4	358
435722		CTG	2	5389553	
AMPL7156	CCATAGAGCGGAAGCTTAGTT	CCCTCAACCCAAGATCCATT	<i>DUOX</i>	chr15:45397737-4	374
642760	CA	GA	2	5398111	
AMPL7155	CATGCAACCACATTGGACCTC	ACGAGGACCACAAGCTATTT	<i>DUOX</i>	chr15:45408203-4	NM_20758
221429	TA	GAG	<i>A2</i>	5408576	1.3
AMPL7155	GCATCAGCTGAACGAGACCAT	GCAGATCTCGTGGATCTTCT	<i>DUOX</i>	chr15:45408724-4	367
221454	T	AACC	<i>A2</i>	5409091	
AMPL7155	GGGTAGGCTCCAAAAGATGG	CCCTCACAGGTTAGTGGTGA	<i>DUOX</i>	chr15:45409748-4	362

223000	AA	TAC	A2	5410110	
AMPL7156	GCGTTCCACTGCTCATCGTTAT	AGCCTCAATTCGACTATTCA	DUOX	chr15:45406865-4	204
640855		TGGAG	A2	5407069	
AMPL7154	GCCGCTCTCCCAGACTTAAAA	AGCCATGAAAATTAATGGGA	DUOX	chr15:45410066-4	265
275000	T	AAAACAGTTT	A2	5410331	
AMPL7155	GGATAAAGAAGAGCGCAGCT	CTGTAAACTGGAAAGTGCAC	DUOX	chr15:45409208-4	374
221433	GT	ACC	A2	5409582	
AMPL7155	GGGCCTGGAGGGCATTAAATAT	CCAGGTGAACTGCTCGTTGT	DUOX	chr15:45408425-4	344
221453	T	AG	A2	5408769	
AMPL7155	CCAGAGGGACTTGCAGGAAA	CATGGTAAGGGCCAAAAAGT	DUOX	chr15:45407850-4	356
221462	AG	GG	A2	5408206	
AMPL7155	CCAGGAAAGTAACGGCTACA	GCTTGCTGCTAGAGCCAAAA	DUOX	chr15:45406541-4	373
223002	GA	AC	A2	5406914	
AMPL7155	CGCCGTCTATGCAGGCTAC	GCGGCAAAGATCGCACTG	FOXE1	chr9:100616778-1	314
235125				00617092	
AMPL7155	GCTGGCTACCGTGAAGGAAG	GAGGAAGCAGTCGTTGAGTG	FOXE1	chr9:100616238-1	294
235129		T		00616532	
AMPL7160	CCGGCAGTGCGATCTTTG	CGTGTGAACAGCCGATGTGT	FOXE1	chr9:100617071-1	293
331243				00617364	
AMPL7155	AAAAAGTGGCAGAACAGCAT	GGGTAGTAGACTGGAGGCG	FOXE1	chr9:100616479-1	358
235124	CC	G		00616837	
AMPL7155	ACTCCCGAGCCTCTGTCTGC	GCGCTCTTCCTTCACGGT	FOXE1	chr9:100615979-1	283

NM_00447

3.3

235128				00616262		
AMPL7155	TCAGCTCTGGTAAGCCGTCTA	CCCTGTGGGTGGAAGAAGTT	<i>FOXII</i>	chr5:169532706-1	374	NM_01218
546677		C		69533080		8.4
AMPL7155	TCGCAGGAGGAGCTGATGA	GAGGAAGGAAGTGAGTCTTC	<i>FOXII</i>	chr5:169533301-1	289	
546679		CTTG		69533590		
AMPL7156	CCCTTGCCTTAACAGCTTCCTT	CTACTGCTTTTCTCTCTGGCA	<i>FOXII</i>	chr5:169535303-1	363	
335358		TGT		69535666		
AMPL7155	TTTATGACAATAAGGAGGAAC	CCGCTCACATAGGCTGTCAT	<i>FOXII</i>	chr5:169534977-1	373	
546664	AGAAGCA	AG		69535350		
AMPL7155	CCCGAGATGAACCTCTACTAT	GAGAGCCGAGTAGGAATAG	<i>FOXII</i>	chr5:169533037-1	317	
546678	GA	GGT		69533354		
AMPL7154	CCTGCCTTCTGAAAGAACATC	CCTCACTTGGTGAGCTGCAT	<i>GLIS3</i>	chr9:3828127-382	374	NM_15262
848923	AGT	TA		8501		9.3
AMPL7154	AACAGAGCATCTGAAATCCAC	TATAGCCAGAATGGGAGGTG	<i>GLIS3</i>	chr9:3855912-385	371	
848926	GA	AGAAT		6283		
AMPL7154	AAAGAACAACACAGACGATC	GCTTGATAAATTTTTGTGGG	<i>GLIS3</i>	chr9:3898576-389	372	
848931	TTAGGAAA	CTGAGTT		8948		
AMPL7154	CATTGTCCCTGTAACCTGCAG	CCAGACTCAAACATTCAAGG	<i>GLIS3</i>	chr9:3936912-393	334	
848933	A	TCCT		7246		
AMPL7154	GACTCTCATGTGGATCAGCAG	GGCAGCACCGTAGACCTA	<i>GLIS3</i>	chr9:4117798-411	368	
848935	T			8166		
AMPL7154	AGGCGTTCGGTCTTGAACAG	CATCGGGATAGATTTCATA	<i>GLIS3</i>	chr9:4118180-411	365	

848937		CCATCATCC		8545		
AMPL7154	CTAGGGTAAGGAGAGTGGCTA	CAATCCGTATCCTGCTAAAA	<i>GLIS3</i>	chr9:4118624-411	319	
848939	CT	TGTTTATCTT		8943		
AMPL7154	CATCTTTGACCCTGACACTGA	CAGCACATCGAGTCCCATA	<i>GLIS3</i>	chr9:4285921-428	373	
848942	ATCA	TG		6294		
AMPL7156	GGCATCTTGAGATGGAGGTTG	CTGAAAGGAGTCATTAGTGA	<i>GLIS3</i>	chr9:4286238-428	246	
997970	TTA	CATTGGATAT		6484		
AMPL7154		GTTGGAATGATCTGTGGAAC	<i>GLIS3</i>	chr9:3829255-382	302	
848924	CCTGGTCTCTCCTGTCAGTTGA	TTGTG		9557		
AMPL7154	GTA ACTCAACCCACCAACGGA	CAAATATGCTTGCTGTCAGG	<i>GLIS3</i>	chr9:3879313-387	370	
848930	T	CTT		9683		
AMPL7154	CCTCAAACGGTCTAAAGCAGG	GAGTATTAGCTAGCATTTCA	<i>GLIS3</i>	chr9:3932230-393	374	
848932	T	CATCAGTCA		2604		
AMPL7154	GCTGGCATCTCCTTTCCAAGA	CCTCGAAGATACAAGCCCTT	<i>GLIS3</i>	chr9:4117496-411	358	
848934	T	CAAC		7854		
AMPL7154			<i>GLIS3</i>	chr9:4117894-411	370	
848936	CTGGTCGATGTGGACCTTCT	CAGGCCTGGTCAACCACAT		8264		
AMPL7154		TGTCTCTAACTCATTACCATC	<i>GLIS3</i>	chr9:4118473-411	213	
848938	CCTCGACCCGTTGATGTAGG	CTACCTTT		8686		
AMPL7154	TGTGTGTATTCAGAAAGAGAA	CTGATATAAGCGTGCACATG	<i>GLIS3</i>	chr9:4125649-412	374	
848941	CGGAA	TCTG		6023		
AMPL7154	CTGTGATTCTCTATGGGACCTT	CCAGGTAATCATTTTTAAAA	<i>HESX1</i>	chr3:57232270-57	373	NM_00386

674251	TTCA	AGGCATCCA		232643	5.2
AMPL7154	CAGTCTTGGCAACAAGACCAA	GCTCCTTTTCAATTGAGAGA	<i>HESX1</i>	chr3:57233616-57	275
674275	C	ATCTTAGGAC		233891	
AMPL7153	GGGTTTCATTAATGGAACACA	AGGAAGATCCCAGCCCTATA	<i>HESX1</i>	chr3:57233824-57	199
377021	GTCTTT	CAC		234023	
AMPL7154	GAGATACCAAAGTGAGTGGG	TGAAAGATGAGTTCCTGAAA	<i>HESX1</i>	chr3:57232695-57	374
674247	CTTT	CTACCTCT		233069	
AMPL7154	CAGATTAAATGCAGGAAAGA	AGGAAGACAGAATCCAGGT	<i>HESX1</i>	chr3:57232120-57	315
674272	AAACATCACA	AATTTTCAAAT		232435	
AMPL7154	CTTCATCCTCAGGTGTCAGGT	CCTAGACAGTACTATCCTTG	<i>IGSF1</i>	chrX:130419237-1	257
279716	T	CTTTACCTA		30419494	NM_001170961.1
AMPL7154	ATGAGTAAGGGAGGACCCAG	CTCCCACGTGAACCCTAAAG	<i>IGSF1</i>	chrX:130407924-1	365
811805	AA	AA		30408289	
AMPL7154	CTCGGCACCAGAGAGTAACAT	CAGAGGACTCTGGGAACTAT	<i>IGSF1</i>	chrX:130409659-1	371
811811	T	AGCT		30410030	
AMPL7154	CAGGGTCCCTGTGAGTTCATT	GAACCTAACCCTCTGGTGCA	<i>IGSF1</i>	chrX:130412338-1	320
811815	C	GAA		30412658	
AMPL7154	GTCTTGTTCCCTAAGCCCAGA	CACTTCTGCCTCACCTTCTCA	<i>IGSF1</i>	chrX:130415062-1	372
811819	A	AT		30415434	
AMPL7154	TGTGCAGAAATAGGGCAAGTT	GGTGATGGAGGGAATTACAG	<i>IGSF1</i>	chrX:130410624-1	373
811822	GA	CTG		30410997	
AMPL7154	AGGCAAAGTTGGAGGCTGAAT	GGTCTCACTAGAGAAGCCTG	<i>IGSF1</i>	chrX:130412954-1	372

811824	T	GTT		30413326	
AMPL7154	AATTAAATCACCCCTCCACGAA	GAGAAGCCTTCTTTACAATC	<i>IGSF1</i>	chrX:130411601-1	357
811836	CCAA	CAGAGA		30411958	
AMPL7154	CCCAGACTCATCCCTGAAAAG	GGGTTGTCAAGTGCAATTTA	<i>IGSF1</i>	chrX:130420425-1	374
811837	AG	GCC		30420799	
AMPL7157	GTTTCATGGCATACCCGTCTCT	ACAACAGGAAAGAATCATCT	<i>IGSF1</i>	chrX:130416929-1	362
792940	T	TGCCT		30417291	
AMPL7157	AGCTGCAGCTGTAGTTTCCAA	ATCACAGTGACTCCCTGGAG	<i>IGSF1</i>	chrX:130408642-1	363
792941	T	AT		30409005	
AMPL7157	GAGTTGATTCTTGAGTATCAC	GGAGAGGGTTGGACTGCTCA	<i>IGSF1</i>	chrX:130419709-1	360
792944	TGTCATCT	TA		30420069	
AMPL7157	CCCTCCTTCAACAGGACAAAT	CTGGACCAGTTCTATCAAGA	<i>IGSF1</i>	chrX:130409140-1	367
792945	GT	TACAACC		30409507	
AMPL7157	CACTGCGATGTGACCAGATGT	GTACTGGGTTTGAGGTCACT	<i>IGSF1</i>	chrX:130415667-1	300
792950	TA	TCTC		30415967	
AMPL7157	TAAAAACAGTTGTTAACACTT	GGAGCAGGAAGTGAAATCA	<i>IGSF1</i>	chrX:130416395-1	366
792951	GCCTACAAC	CTAGTG		30416761	
AMPL7154	GCAGCTGTAATTGCCTTCGTC	GGCAACTGCAAACCTTCTGAC	<i>IGSF1</i>	chrX:130411900-1	256
279735	T	TC		30412156	
AMPL7154	GCTCAGGTGATTAGAGACCAA	GAACCAGGTGGTGCTAGAAA	<i>IGSF1</i>	chrX:130407649-1	374
811798	GGA	AAC		30408023	
AMPL7157	TCAGCAACACAAACTCCTTAG	GTGATCTGGGTAGAGGGTTC	<i>IGSF1</i>	chrX:130412600-1	210

791283	TTGA	AAG		30412810	
AMPL7157	GTAGGCTCACATTCTGACCCA	CACTCCTTAGTGATGTCCTG	<i>IGSF1</i>	chrX:130416640-1	349
792939	T	AAAATCT		30416989	
AMPL7157	TGTACTGAAGTCTCCAGGACC	CACTGGAAAGTGACCTCTTC	<i>IGSF1</i>	chrX:130408948-1	360
792942	TTAC	TCT		30409308	
AMPL7157	GGTCTCAGCCTGAATCCAGAA	AGCCCAGTAAAGTTCTAGAG	<i>IGSF1</i>	chrX:130419400-1	373
792943	G	TTGGA		30419773	
AMPL7154	ACTCACCAGTCTCTTCTATCA	CCCTCAAAAAGAAAAGTCAT	<i>IGSF1</i>	chrX:130413111-1	374
811799	ATACCC	TGATGTCAAA		30413485	
AMPL7154	CTTTTCCATCTGAGATAAAGC	AGACATTCACTGTTTTGCTCT	<i>IGSF1</i>	chrX:130420236-1	372
811814	TTTTTCACC	TTTGC		30420608	
AMPL7154	TGGGCTCAGACCAGATAGAAA	GCTTTCTCTCTTTCTTGTCT	<i>IGSF1</i>	chrX:130410940-1	340
811823	AGT	TAATTTGGT		30411280	
AMPL7154	GGTGATCTAAAGATTCCTGGT	TAGGATGCCATCACACAACA	<i>IGSF1</i>	chrX:130416085-1	373
811829	TCCTT	CTG		30416458	
AMPL7154	GTTGGCTGGGCTCCTTTACTA	CCAACCTGGGACAATGGCCAT	<i>IGSF1</i>	chrX:130418927-1	364
811833	G	AT		30419291	
AMPL7157	CCTTACCTGTGACTAGGAGTT	CAGGAACTCATAAGTTTCTA	<i>IGSF1</i>	chrX:130409446-1	347
792946	CCA	TAGTCACCA		30409793	
AMPL7157	CCCTGTTTGACATGGTTGTCTC	GATGTGAGGGCTGGGTTTAT	<i>IGSF1</i>	chrX:130409974-1	295
792947		CT		30410269	
AMPL7157	AGAGTTTATGCTGAAGCAGAA	TGGAGACTTTGTCATCAACA	<i>IGSF1</i>	chrX:130408326-1	374

792948	GCA	ACGTAG		30408700		
AMPL7157	GGGTGAGGACAATCTGGTTAC	CTACAGTTGCAGCTATCGCG	<i>IGSF1</i>	chrX:130415378-1	344	
792949	T	TA		30415722		
AMPL7155	AGGTTAGAGGGAGAGCAGTC	GACCTGACACCTGGAGAAAG	<i>IYD</i>	chr6:150719125-1	356	NM_20339
234941	AT	AG		50719481		5.2
AMPL7155		CCATAAGCCCTGCCATTGAC	<i>IYD</i>	chr6:150690059-1	366	
234945	ACACCTGTGTCTGCATTCCTTC	TC		50690425		
AMPL7155	GACAAAAACAAAAATTCTGCA	TGTCCCTGAATTGAAAACCTC	<i>IYD</i>	chr6:150715089-1	374	
234952	GCTTTTCA	AGCT		50715463		
AMPL7155	GATGAATGGCAAGAATCAGA	ACACCAGTAAGGTGACTAAC	<i>IYD</i>	chr6:150710493-1	237	
413470	AGAAAATGTT	ATTTCC		50710730		
AMPL7155	CTACAGGGATGAGCCTCTCCT	TTACAACAAAGCCAGGACAT	<i>IYD</i>	chr6:150713398-1	328	
234938	TA	GGT		50713726		
AMPL7155	GCTTCTTCACTATCTCAAAGA	GCTTCATGGAGATTTTCTTT	<i>IYD</i>	chr6:150716453-1	374	
234942	AAAACATGT	CCTCCA		50716827		
AMPL7155	TGCACCCAGCTGGAGTTTTAA	CCTTCTCAGGATAGTGGTTA	<i>IYD</i>	chr6:150710295-1	267	
232622	G	TGAGAGAAG		50710562		
AMPL7156	GGAGGAACTAAGTCCAGTAG	GGGAGAGCGTTTACTGCAAG	<i>LHX3</i>	chr9:139092103-1	358	NM_01456
708648	AATCC			39092461		4.3
AMPL7156		CCTCCTGGCTGGATGAGGTA	<i>LHX3</i>	chr9:139088852-1	356	
335363				39089208		
AMPL7156	GACGCAGCTCTCGGTACT	GCCATGCTCCAACAGTAGAA	<i>LHX3</i>	chr9:139089434-1	313	

335365		GG		39089747		
AMPL7156	CTCCTGAACGCTGTCCTTGT	TGAAGAGCGCTTACAACACC	<i>LHX3</i>	chr9:139090532-1	313	
335368		T		39090845		
AMPL7156	AACTTCGGACCGAACGAA	CCCAGGACTTCGTGTACCA	<i>LHX3</i>	chr9:139091313-1	348	
335369				39091661		
AMPL7156	ACAACCTCACTCACTCCCTGA	CCGGGAAAGTTCGGGACTG	<i>LHX3</i>	chr9:139094590-1	343	
335371				39094933		
AMPL7153	CCACCCTGGGATCTGGAAAC	CGCGATGCTGCTGGAAAC	<i>LHX3</i>	chr9:139096616-1	246	
412458				39096862		
AMPL7153	GGGAGCAGGTTCTGTAAGTGA	GCAGTATTTCCGCAACATGA	<i>LHX3</i>	chr9:139090344-1	254	
990366	A	AGC		39090598		
AMPL7156	TCTCGGACGAGAGCTGCT	GCCTTCCGAGAAGCCTGTG	<i>LHX3</i>	chr9:139090780-1	264	
330356				39091044		
AMPL7156	GGTCAGAACTGAGCGTGGT	GCAACTTCTCCCTGGAGCAT	<i>LHX3</i>	chr9:139089169-1	324	
335364		G		39089493		
AMPL7156	GGGCTCACTTGAAAAAGTCGT	AAGAGGGTGTGTAGGGAAA	<i>LHX3</i>	chr9:139092420-1	322	
335367		GGA		39092742		
AMPL7156	GGCTGTCCTCCATGAGGTAGA	TGAGATTGAGGTTCCCTTCT	<i>LHX3</i>	chr9:139091566-1	354	
335370	A	CAGT		39091920		
AMPL7157	GGCATCAGCTTTGGAAAAGGT	GGTTGCAGATGATGCAAGCA	<i>LHX4</i>	chr1:180235268-1	374	NM_03334
082244	AC	AAG		80235642		3.3
AMPL7157	GAAAGGACTGCTGTCCTCACT	AGTTCTTGTATGCATTCTTTA	<i>LHX4</i>	chr1:180240291-1	307	

082246	TT	ATGTCTCCA		80240598		
AMPL7156	CAAAGCAAGGGTTGGCTTTCA	CAGGATGAACTTGTCCAGGA	<i>LHX4</i>	chr1:180217207-1	265	
371403	G	TGT		80217472		
AMPL7156	CCATTCAGGCTTCAGTCTGCTT	GCCAAGGCCTCAAGAAAGAT	<i>LHX4</i>	chr1:180240865-1	374	
371440		CC		80241239		
AMPL7156	ACAATCCTATCAGGACTTGAG	GCAAGTCTCTTTTGATCCTTG	<i>LHX4</i>	chr1:180243429-1	356	
371446	GGAT	AAGATATTC		80243785		
AMPL7153	CAAGGCCCAAGGACTTTGTCTA	CATGAGTAGGGCTCTGAGGG	<i>LHX4</i>	chr1:180235587-1	259	
824990	C	AT		80235846		
AMPL7156	TCTCCTCTTCCTCACAGAGATT	CTCTCAGCTCCAGGATTTAC	<i>LHX4</i>	chr1:180217403-1	328	
371442	CC	CTG		80217731		
AMPL7156	CAGATAGGCCGAAGCCAGTA	CTGTCTTCAGTTCTGGCAAA	<i>LHX4</i>	chr1:180240474-1	331	
371443	AG	AGC		80240805		
AMPL7156	GCGAGATCAAAGGGACTGGA	GAGGCTGCTAGCTGTCTTGT	<i>LHX4</i>	chr1:180199449-1	346	
371444	AA	TA		80199795		
AMPL7156	CCTCTGGATATCAGGCTGCCA	GGACGATATGGAGGATGGA	<i>LHX4</i>	chr1:180243152-1	346	
371445	TA	GACT		80243498		
AMPL7154	GCACGGTTTGCCGTCTTTC	GCCAGCATGATCCACCTGAC	<i>NKX2-</i>	chr14:36986789-3	227	NM_00107
832248			<i>1</i>	6987016		
AMPL7154	TGTTCTCATGGTGTCTGGTA	GTTCTCAGTGTCTGACATCTT	<i>NKX2-</i>	chr14:36988244-3	289	
832722		GAGTC	<i>1</i>	6988533		
AMPL7154	TGGAAAACCCATTTGAATCAC	ACTACGGCACCATGTCCTG	<i>NKX2-</i>	chr14:36986158-3	374	

832856	CAAAAA		1	6986532	
AMPL7154	CCATGCCGCTCATGTTTCATG	TCGAAAGAGGGAACTGAGA	NKX2-	chr14:36987178-3	305
832859		CTGA	1	6987483	
AMPL7155	GGGAGTAACAGAGGAGGAGA	CCAGACTCGCTCGCTCATT	NKX2-	chr14:36989091-3	296
234653	GATG		1	6989387	
AMPL7154	CCATGCCCACCTTTCTTGTAAGCT	CCAGAATATTTGGCAAAGGG	NKX2-	chr14:36988475-3	191
832010		AGAAAAA	1	6988666	
AMPL7154	GCCTAGGAGACGCCGAGTA	CTACTGCAACGGCAACCTG	NKX2-	chr14:36987945-3	363
832721			1	6988308	
AMPL7154	TCACCAGGTCCGACCGTATA	GTGCCGGTCCTGGTGAAA	NKX2-	chr14:36986483-3	338
832857			1	6986821	
AMPL7154	CCTGGCGCTTCATTTTGTAGC	GCTTACAGTCTCCCGCTTCAT	NKX2-	chr14:36986941-3	292
832860			1	6987233	
AMPL7154	GACGCCGAAGTTCACGAAG	AGCGTGCTGAAACTCACGT	NKX2-	chr5:172659656-1	374
603293			5	72660030	NM_00438 7.3
AMPL7154	CGTAGGCCTCTGGCTTGAAG	CTTGTGCTCAGCGCTACCT	NKX2-	chr5:172661918-1	321
603297			5	72662239	
AMPL7154	GCAGAGAGACGCTTGGTAAG	ACCAAAGTAGCCCTAATTCA	NKX2-	chr5:172660231-1	365
603298	AG	GTTAC	5	72660596	
AMPL7154	CCGCAGGAGTGAATGCAAAAT	TCAATCCCTACGGTTATAAC	NKX2-	chr5:172659451-1	362
603292	C	GCCTA	5	72659813	
AMPL7154	CCTAGGCATGGCTTGCCAT	GGTGGAGCTGGAGAAGACA	NKX2-	chr5:172659852-1	338

603294		GA	5	72660190		
AMPL7156	TCCTGGCCCTGAGTTTCTTG	CAGTCAAAGACATCCTAAAC	NKX2-	chr5:172661682-1	367	
591694		CTGGA	5	72662049		
AMPL7155	CACACCTTCCGCCTGACA	CAAGTCCTAAGACACAGGCT	PAX8	chr2:113994100-1	283	NM_00346
234639		CAG		13994383		6
AMPL7155	CCCGTCACAGAGAACTTCATG	CCTTCGCCATAAAGCAGGAA	PAX8	chr2:113992802-1	345	
234641	T	AC		13993147		
AMPL7155	GAATTCTCTAGCTGCCCTGAG	CCAGCACCTGTACTCATAGC	PAX8	chr2:114004251-1	327	
234643	AT	TAATC		14004578		
AMPL7155	CATCTCCCAGGCCCTCTGTAT	GGACCTTCTGAGCTCCATTG	PAX8	chr2:113977545-1	365	
234644	A	TC		13977910		
AMPL7155	GGGTTTGTGAATGGTACTGTG	TGACTGTGGACAGTTGAGTT	PAX8	chr2:114000135-1	354	
234647	CA	TCAAG		14000489		
AMPL7155	GCAGCTATCCTGATCACCTGG	GCTCCACCTACTCCATCAAT	PAX8	chr2:113999287-1	369	
234651	TA	GG		13999656		
AMPL7153	CTGACGCTCTCGAGATCCAA	CATCGCATCTCATGCCCTTCT	PAX8	chr2:114035857-1	225	
508036				14036082		
AMPL7155	CCAGGCCTTTCTTGTCTCTTTC	GGCTCTGGCTAAATCCCTGT	PAX8	chr2:114001923-1	352	
234640	C	CTA		14002275		
AMPL7155	GGCGGAGCTAGATAAAGAGG	TCTCTCCATTTTCGCTGCAGA	PAX8	chr2:113993074-1	308	
234642	AAG	A		13993382		
AMPL7155	GCAACTTCCAGCTGCTTTGAT	TCAGCTTGGAGTCAGTCCTC	PAX8	chr2:113999028-1	361	

234645	G	TA		13999389		
AMPL7155	GCAATGCTGGACTTGTGGTTA	GATCAGATAGGCCAGAGAA	<i>PAX8</i>	chr2:113975988-1	328	
234648	T	ATGAATGATTA		13976316		
AMPL7155	CCCTCTTTGGTCCATCCTTCAA	GGAGGAAGTGGGTTTGGAG	<i>PAX8</i>	chr2:113984596-1	370	
234650		AATG		13984966		
AMPL7155	CATCCATTTTCCTCTTGTCGCT	GTGTCACTCTCACTCCCTGA	<i>PAX8</i>	chr2:113999588-1	331	
234652	G	C		13999919		
AMPL7157	CCCTCAAACCTCCTGCTTTAG	GTTGACAAAGATACACAGAT	<i>POU1</i>	chr3:87311126-87	351	NM_00030
507742	C	TTGTGTGAC	<i>F1</i>	311477		6.2
AMPL7160	CCCGGTCATATGTAAACTGTC	ATATGCAGGTAGTGAGAATT	<i>POU1</i>	chr3:87325436-87	280	
337849	ATAGG	GAATCGG	<i>F1</i>	325716		
AMPL7155	GAAATCAAATTTTCATGTCACA	CCCAAAATGAGAAAAACAT	<i>POU1</i>	chr3:87322393-87	359	
697318	CTCTGATCA	ATTGGCATGTA	<i>F1</i>	322752		
AMPL7155	CAACCAAGTAATTTCTGTTTTT	ACCTACCTTAATTTTGAGCT	<i>POU1</i>	chr3:87308964-87	367	
697587	GTTGAGG	GCCAAA	<i>F1</i>	309331		
AMPL7157	CAGATTTTCTTCCTTACAACA	CATGCCACCAATGTGATGTC	<i>POU1</i>	chr3:87325228-87	267	
507340	AAGCCA	TAC	<i>F1</i>	325495		
AMPL7155	CTTGGCCTCCCAATTCACCTTA	CTCTAAGGTCTGTAATAGAA	<i>POU1</i>	chr3:87310303-87	343	
697310		AAAGACTGCA	<i>F1</i>	310646		
AMPL7155	ACAGCAATAAAGATTTGCAAA	GCTAAGTCAGGCAAAACCCT	<i>POU1</i>	chr3:87313379-87	369	
697381	CCAAGT	TTCTTATATA	<i>F1</i>	313748		
AMPL7154	GGGATCACCTTGGTGGTACTT	TTCCAGAACCGCAGAGCTAA	<i>PROPI</i>	chr5:177419681-1	361	NM_00626

870067	G	GCAA		77420042		1.4
AMPL7154	CCATTTAGGTTAGGGTTATAA	AGGAGCGTCCTCCTCAGAA	<i>PROPI</i>	chr5:177421013-1	373	
870070	TGCCCA			77421386		
AMPL7157	GTAGGGTACCAGTCCTCAGAC	TGTCACCACCTATGTCAAGT	<i>PROPI</i>	chr5:177419801-1	300	
082098	T	GTG		77420101		
AMPL7154	ACAGTTTTTAACATGATAGGAT	CTACACACACATTTCAGAGAC	<i>PROPI</i>	chr5:177422701-1	374	
870069	TCGGGTT	AGAGT		77423075		
AMPL7156	AGAAAGAGCTGGGATCTTCTT	CAAGTCCTGGAAGTGGAGGTC	<i>PROPI</i>	chr5:177419357-1	368	
603831	CAATC	AA		77419725		
AMPL7154	CATGCAAAGCAGTCCTCCAAA	GTCCTTATCTATGCTTATTCT	<i>SECIS</i>	chr9:91956358-91	172	NM_02407
342368	C	AGCATCACA	<i>BP2</i>	956530		7.3
AMPL7157	GTTTCTTACGGACTTCCAGCTC	AGCCAGGCACTGAGTAAACA	<i>SECIS</i>	chr9:91940111-91	373	
792845	AT	TTC	<i>BP2</i>	940484		
AMPL7157	CCAGTATCTTTATAACCAACC	TGTCAAACTTTTGCTGATCAT	<i>SECIS</i>	chr9:91940486-91	374	
792847	CAGTTGT	ACGTTTTT	<i>BP2</i>	940860		
AMPL7157	CAACAATTTTGGTTATCTTTGA	ACCATCCATCTTCAGAAACT	<i>SECIS</i>	chr9:91949411-91	368	
792849	GCAGAGTT	CATTTCC	<i>BP2</i>	949779		
AMPL7157	CTGCCCACCTTTTCTTCCAGGAT	GCATCTGGCTGCAGTAACTG	<i>SECIS</i>	chr9:91965211-91	352	
792850	A	AA	<i>BP2</i>	965563		
AMPL7155	CAGGCTGAGAACAGTGAGTG	CATTGTCATGAAAAACAGAA	<i>SECIS</i>	chr9:91973475-91	353	
234869	AAT	GAAAAAGCC	<i>BP2</i>	973828		
AMPL7155	ATCATAGATGGGTGTGTTGCT	CAATGACAGCCTACTGGAGG	<i>SECIS</i>	chr9:91972222-91	374	

234874	AAGAAAA	TT	BP2	972596	
AMPL7155	AAAGTGGCTGTAACGTTTTTC	CTAACACTGATGTTAGGTTA	SECIS	chr9:91947681-91	363
234875	ATTCTT	CCCACAAT	BP2	948044	
AMPL7155	CGTAATCCATTGCTGATCAGA	AAACTCAGGTTTGGAGGTAG	SECIS	chr9:91943278-91	370
234878	CCA	ATACATTTTT	BP2	943648	
AMPL7155	CTCAGGGCACTAAGAGGCACA	ACTTTCACCACAAAAGGAAG	SECIS	chr9:91962876-91	373
234893	T	AGGA	BP2	963249	
AMPL7155	GCGGAAACGCTTTGTCTGT	GTGACATCGCACCCACAGAC	SECIS	chr9:91933413-91	354
234896			BP2	933767	
AMPL7155	GCAGAAGCTCTTATGTGAGAG	TCTCATGAAGGAATGAATCA	SECIS	chr9:91954629-91	374
234897	TTTCG	AAACAAAACC	BP2	955003	
AMPL7157	GCTTTTTAATCTTTCCTGCAGA	GCTGTATACATAGCAGGAAT	SECIS	chr9:91940791-91	238
791168	AGAAAACC	GTTTCTGG	BP2	941029	
AMPL7157	ATCCATATGCCTATTCTCCTTA	AAAAGCAACATGAAATAAA	SECIS	chr9:91940422-91	374
792846	TACCCTT	ACCACCACT	BP2	940796	
AMPL7157	GCTTGCCACGTGGACATTTAT	GTCTGTCTGAACAACATAACC	SECIS	chr9:91949115-91	361
792848	T	CATTG	BP2	949476	
AMPL7157	CCCAATGTTCTGAAAGAAGGA	TGAGATGGAAAGACTCTCTT	SECIS	chr9:91956049-91	367
792851	AGACA	ACCTGA	BP2	956416	
AMPL7155	TGTCCTCTGTAGCTGGGATGT	ACCTAGGGACTCCTAATTAA	SECIS	chr9:91972865-91	315
234870	T	AGTCAGTAAA	BP2	973180	
AMPL7155	TTTCCTTCAGAACTATTCTAGT	ACCCAAGTTTCTTTTAAGAA	SECIS	chr9:91953190-91	373

234877	GAATGCTG	AGACCCA	BP2	953563		
AMPL7155	ATAAGCGAACAGACAGGAAA	CCACAGCAAGATTTAATGTG	SECIS	chr9:91943584-91	305	
234879	TCCA	TAATGTTTGA	BP2	943889		
AMPL7155	TTTTAAACAACATCGGGAACA	TCTCATCATCTGCAGAACTTT	SECIS	chr9:91934448-91	374	
234887	TTTCTGG	AGTGC	BP2	934822		
AMPL7155	GGTGACTTGGCAAACCTCCTTC	AATCTAAGAGCTGGGAGAAT	SECIS	chr9:91961680-91	365	
234895	A	AACTATGGA	BP2	962045		
AMPL7155	TGTTGTCTGTGAATGTGGTGG	CCCAGCAACAAGGATTTATG	SECIS	chr9:91964564-91	374	
234900	TT	GG	BP2	964938		
AMPL7155	CCAGTGGCACAATTCCTGATG	AGAAAACGAGTTGTCAAGAC	SECIS	chr9:91965509-91	374	
234901	T	CTGT	BP2	965883		
AMPL7154	GGATAAGATCAAGCTGGCCCA	GCAGGTTGAGGGTAGCTTCT	SLC16	chrX:73744380-73	323	NM_00651
726552	AA	TG	A2	744703		7.4
AMPL7154	CCTGTGAAAGGCCAGAGAAG	GGGATTCTGCAGTGAGAAAA	SLC16	chrX:73740731-73	331	
726555	AAG	GTAAC	A2	741062		
AMPL7154	TAGAACGGGCTGAGAGTACCT	TGGCAAAAATGTAAATGCTG	SLC16	chrX:73751096-73	369	
726556	T	AGCA	A2	751465		
AMPL7154	CTGCAGCAGCAGAAACAAGT	GGGTCTCTACCGTAGGCGT	SLC16	chrX:73641400-73	328	
733837	ACCA		A2	641728		
AMPL7155	AATCCCAACAGAATCACAGTT	CCATGATGGTGATGAAGAAG	SLC16	chrX:73748818-73	353	
364058	AAGTAGG	CCAT	A2	749171		
AMPL7154	TCTGTCCTGCTCCAGGAAAGT	CTTTCCCATGCGACACAACA	SLC16	chrX:73745472-73	363	

726549	A	AG	A2	745835		
AMPL7154	CGGAGGAATGGAAGTCTCAG	AGCATAAGAACAAACATGA	SLC16	chrX:73744102-73	340	
726551	GA	AGGTACTCAG	A2	744442		
AMPL7155	CCTTATCGTCGTCTGTCTTTTC	GCTGCTTAAATAGACGATAA	SLC16	chrX:73749113-73	280	
364059	CT	GAGGAAAAGG	A2	749393		
AMPL7155	AGCTGGAGTTCGAGTCCGA	CCAACCTTGCCCCAAAATGCC	SLC16	chrX:73641669-73	278	
364507			A2	641947		
AMPL7152	TTTCCTAGGAACATAACAAAAC	AGACTAGACTTGTGTAATGT	SLC26	chr7:107350458-1	270	NM_00044
997850	ATTGTGTCT	TTGCCATTTA	A4	07350728		1.1
AMPL7152	AGGTAGTTATCACATGATGGT	CAAAATGGTATAAGGAAGCT	SLC26	chr7:107336310-1	243	
997946	ACCTGA	CAGAGTGT	A4	07336553		
AMPL7157	ACTACCCACCATAGAAAGGCAG	ATCAGGCTCAAAAGCATTAT	SLC26	chr7:107341951-1	371	
604914	T	TTGTTGAA	A4	07342322		
AMPL7154	TTTGAAAACCTCCATGGTTTT	GGAATGAAGCAGTGCCAGAT	SLC26	chr7:107344619-1	373	
850825	GCA	TC	A4	07344992		
AMPL7154	GTGGGAAGATTCATATGAGAA	GCAGTAGCAATTATCGTCTG	SLC26	chr7:107323546-1	370	
850830	TTGATTGTG	AAATAAAACA	A4	07323916		
AMPL7154	TGAGCAAATAACTATCACTTT	AGAGAGACAGAGAAGGCTG	SLC26	chr7:107334685-1	374	
850838	TCTCGACA	TGTTA	A4	07335059		
AMPL7154	ACAGTGAGTGAGATTCAGTCT	GCCTAGAAGCAGTCTTAGTG	SLC26	chr7:107355660-1	371	
850848	CCA	CT	A4	07356031		
AMPL7154	CTTTCATGTCTAATATGTGACT	CAATAAGGTCTGGTGAAAGA	SLC26	chr7:107329394-1	370	

850857	GAGCAGA	ATCCAAC	A4	07329764	
AMPL7154	AACCCTATGCAGACACATTGA	GGGTTCCAGGAAATTACTTT	SLC26	chr7:107314539-1	369
850861	ACA	GTTTTGTTTT	A4	07314908	
AMPL7154	AAACATCAGCAGAATCCAGTT	GGTAAGCAACCATCTGTCAC	SLC26	chr7:107303647-1	326
850864	CATAAC	AGA	A4	07303973	
AMPL7154	GAAAAGAAAGAAAAGTTGAG	CTCATTGCCCTACACAAAGG	SLC26	chr7:107340389-1	358
850867	TGCTGCTA	GA	A4	07340747	
AMPL7154			SLC26	chr7:107301812-1	
850868	GGGCTTACTCGCTTCAAGTT	GAAAGCGAGCTCGCTGTAGA	A4	07302182	370
AMPL7157	GTGTTTTCTTCGTTTAGAATGG	CATTTTACTATTGCCAAAGC	SLC26	chr7:107342255-1	301
775959	CATCATA	TCCAAATGT	A4	07342556	
AMPL7154	AGATCTACTCCATCAGACCTT	TGATACGTACATGTCATTTG	SLC26	chr7:107341396-1	374
850820	ACAATTTCT	TTCATTCACA	A4	07341770	
AMPL7154	AGAACAATACAGCTGAAGAG	GCTATGAAGCCATCTTTTCT	SLC26	chr7:107352848-1	355
850823	GATTCTG	GCATTTG	A4	07353203	
AMPL7154	GGTATAACCCTGCTTCTCTGC	CCACAATTCTAATTTCTCCTC	SLC26	chr7:107334925-1	372
850828	A	TGGAGTT	A4	07335297	
AMPL7154	GCAGAGTAGGCATGGGAGTTT	TTAGGAAGTACAAGTCTGAA	SLC26	chr7:107330460-1	338
850833	T	AGGCAAATT	A4	07330798	
AMPL7154	CATATTGCTTTTGCATCATCAT	TTGCACCAACCTAATAGAGG	SLC26	chr7:107312465-1	320
850837	AAAGGC	TATAATGC	A4	07312785	
AMPL7154	ATGATCGGTTTAGACACAAAA	AGATCACACACAAATAGGAC	SLC26	chr7:107323747-1	365

850840	TCCCA	TATTGAAGG	A4	07324112	
AMPL7154	GTATTTTTGTGCTATAGGCAG	GGCCCAGACTCAGAGAATGA	SLC26	chr7:107315265-1	367
850842	GCTACTA	AT	A4	07315632	
AMPL7154	TTCAGAGTTAGCTACAGGAAA	CACTGGATCAAAAGTTTTCA	SLC26	chr7:107338336-1	374
850846	ATGTCATC	TGACACTC	A4	07338710	
AMPL7154	CGAGTACAGCTGCAGCTACAT	AGTTTCCCAGGTAAGTTCAT	SLC26	chr7:107302128-1	350
850869	G	TTCGG	A4	07302478	
AMPL7154	TGGAAGAAAGAACTGTCATTTC	CATTGCTCCAGCTTTTCTATC	SLC26	chr7:107350175-1	351
894585	AAATCTGG	ACATAAT	A4	07350526	
AMPL7153	CCATATTCTGGGACCACCCTT	CGGTCACTATGCAAAAAGAG	SLC5A	chr19:17985211-1	267
508092	CT	GTC	5	7985478	NM_00045 3.2
AMPL7155	GGGCAAATATCTCCTTCACCT	CGATCCGTAGATGAGTGCTG	SLC5A	chr19:17992631-1	343
234960	TTG	TA	5	7992974	
AMPL7155	GAGTTCCTGAGGTCTCGCTT	CAGGACCCTCATGGTCTGC	SLC5A	chr19:17994396-1	361
234961			5	7994757	
AMPL7155	CGGACATCGACAGCCCATA	ATGCCAGTGGACACCAGGA	SLC5A	chr19:17982930-1	287
234963			5	7983217	
AMPL7155	GGGACTGGAGCCTGTTAGACT	AATAGAGTCTTTTGACTGGA	SLC5A	chr19:18001571-1	372
234968	T	GATAATGAGC	5	8001943	
AMPL7155	GCGTGGCTCTCTCAGTCAAC	CCCTTCAAGATCACACCATC	SLC5A	chr19:17994777-1	136
231906		CA	5	7994913	
AMPL7155	TATGGCCTCAAGTTCCTCTGG	CATCCGCGTCCTCCTGTA	SLC5A	chr19:17983375-1	216

232628	AT		5	7983591	
AMPL7155	CGCTATACATTCTGGACTTTTG	CAGTGTAGAACACAAACATG	<i>SLC5A</i>	chr19:17988554-1	304
433062	TGG	ACGATG	5	7988858	
AMPL7155	AACTTAATTCTTACAACAACA		<i>SLC5A</i>	chr19:17986603-1	349
433065	CAGTAAGAAGG	CCCATCCTGCTGGAGTATCC	5	7986952	
AMPL7155	CCAGGTCATCAGTAGCCCATC	TACAAGGCAATCCAGCCAAT	<i>SLC5A</i>	chr19:18004427-1	367
234956	T	CA	5	8004794	
AMPL7155	GGATACCTGGAGGGAAGGAA	GCCTTGAGGCAGAGAGATGA	<i>SLC5A</i>	chr19:17998965-1	358
234957	CAT	AT	5	7999323	
AMPL7155	ACAAAACCACAGACAAAAAC	TCTTCTAGGGATCAAGCAGG	<i>SLC5A</i>	chr19:17991523-1	374
234959	TAAATGCA	AACT	5	7991897	
AMPL7155	GCATCCACCAGCATCAATGCT	GAAGTGAGTTCTGCCACTGA	<i>SLC5A</i>	chr19:17992773-1	370
234964	A	CA	5	7993143	
AMPL7155	CTCATCCTGAACCAAGGTGTG	CAGCAATAAGCTTTTCAGAT	<i>SLC5A</i>	chr19:17985339-1	364
234967	A	CATTTTTCAC	5	7985703	
AMPL7155			<i>SLC5A</i>	chr19:17984723-1	351
234970	GTGCACACGCATGGACCAGT	CGGGCTAGTGAAGGCTGA	5	7985074	
AMPL7155		CCCTACCCTCAAGTCTGCTC	<i>SLC5A</i>	chr19:17994531-1	346
234971	GGGAGCCTTCATCTTGGAAT	A	5	7994877	
AMPL7155		TGAGGACCGAGTTCAGAAGC	<i>SLC5A</i>	chr19:17983160-1	269
232627	CCTTCGGAGCCTGGGACTA	T	5	7983429	
AMPL7156	CCAACAAAACCCACTCCAAAT	CATACATGGAGAGCCACACC	<i>SLC5A</i>	chr19:17988415-1	196

640661	GT	AA	5	7988611		
AMPL7154	GGTGGCAGGTACATGCTGATC	CTGCAGTACAGCCCAATGAT	SOX3	chrX:139586006-1	301	NM_00563
809600		G		39586307		4.2
AMPL7154	ACTTATCTTTCTTGAGCAGCGT	GATGCACAATTCTGAGATCA	SOX3	chrX:139586559-1	178	
809602	CTT	GCAAG		39586737		
AMPL7154	GCTGCGTTCGCACTACTCTT	GAGAACTCATCAGGTGCGAG	SOX3	chrX:139586885-1	325	
809604		AA		39587210		
AMPL7154	CCCATCATCGGTACAAGGCAA	GGCTCGGTAGTGAAGTCTGA	SOX3	chrX:139585760-1	355	
809599		G		39586115		
AMPL7154	GCGACGTTCATGTAGCTCTGA	GAGTATCCGGACTACAAGTA	SOX3	chrX:139586255-1	367	
809601		CCGA		39586622		
AMPL7154	GTCGGTCAGCAGTTTCCAGT	CTTCTGGAGACTGAACTCAA	SOX3	chrX:139586680-1	311	
809603		GAACC		39586991		
AMPL7154	GGAAGGGTAGGCTTATCAAAA	GGAATCCGAGCAGGTATATA	SOX3	chrX:139587135-1	142	
809605	TGCTC	AGGG		39587277		
AMPL7155	CTGTCCAACCTCTGCCATGTTTT	GTGTAGGCACTCACACTGTA	TG	chr8:133953538-1	363	NM_00323
234769	G	CTC		33953901		5.4
AMPL7155	GCTTGGAGGAAGGATGCAGA	GTGACACCTCCTTCCTAGGT	TG	chr8:134107183-1	352	
234770	AC	CT		34107535		
AMPL7155	TGATGTCAATGGTGCTGATTT	CGTTGGTACAACCTCGAAGAC	TG	chr8:133900038-1	374	
234771	AGTCA	CT		33900412		
AMPL7155	CTAGCAGCACTGGAAGGGAA	TACCCTCCCACTAGACATCC	TG	chr8:133900591-1	319	

234773	AC	TTTTT		33900910	
AMPL7155	GAGGAGTCCTGTGTCAACCAA	ATTTCCACTGTGTGCCTAGCT	TG	chr8:134034145-1	374
234775	G	T		34034519	
AMPL7155	TTTTGAGCTCAATGAGGAAGG	CTGTCTCCAGCCTCTGTGTTA	TG	chr8:133920326-1	359
234776	GTT	AT		33920685	
AMPL7155	CTCTATCTCTGACACTTTCTCT	ATGACACAAAATTTGGCCTT	TG	chr8:133978675-1	374
234782	CTCTGT	ATCTGTG		33979049	
AMPL7155	GGGAAGGGAGCATGAGTTTTTC	CAGGAAACCCTAAATGTGTT	TG	chr8:133883509-1	374
234783	C	GGATC		33883883	
AMPL7155	TGTCCTCAGAGATTCTACCTCT	CCCAGGCTGAGAACATCATG	TG	chr8:133910901-1	374
234784	CTATGA	TG		33911275	
AMPL7156	AAAGTGTGCTTAGCTGCCAAA	GCCTCACATGCACAAAGGAG	TG	chr8:133880213-1	368
642724	TTT	TT		33880581	
AMPL7155	CCTTTTCACTAGGCGTGGACT	GCTAAGGTTGTGTCCTCCTC	TG	chr8:133894007-1	356
234788	T	AATG		33894363	
AMPL7155	TTGCACAGGAATGGAGACCAA	GCATCCTAGGTTATCGTAGT	TG	chr8:134024016-1	374
234791	GA	GTCTCA		34024390	
AMPL7155	GTCTGAGTTAGATGTGTGACT	CCTCCAGCTTCTCTCCCTTTC	TG	chr8:133935469-1	371
234792	TGGA	TAA		33935840	
AMPL7155	GCTGCAAGAAGCTTCTGGGTT	TGGAGCCCTTCTATTCCACA	TG	chr8:133973099-1	373
234818	A	GA		33973472	
AMPL7155	ATTTGTGTATCTGCATATTTGT	ATCAGCTCTCGACAACCTCA	TG	chr8:133945661-1	374

234833	GTGTGTG	TTC		33946035	
AMPL7155	CATTCAGAATGCCAGTGGAGA	TGAGTCCCATTGATAGAT	TG	chr8:134029945-1	374
234835	GA	TAGAATGGA		34030319	
AMPL7155	GTTAAGAGCAAACAGCAGTGC	ACACTAGAAGGCAGTTGAAT	TG	chr8:133894977-1	373
234841	AT	TAATGGG		33895350	
AMPL7155	TCTCTCTCCTCTGTAGGCTCC	GGACTCCACTCTTGAGCACA	TG	chr8:133913272-1	361
234843	TA	TTG		33913633	
AMPL7155	GCCATCATTTTAGTGAGATT	AGTGCTGGGTATGCTTCTGT	TG	chr8:133981539-1	374
234846	GAGTTAGG	TTT		33981913	
AMPL7155	TAAATAAGAAGGCCTCCTTAT	GCTAAAGAGGAGCCTAAGA	TG	chr8:133909782-1	361
234850	GTTGGAAC	GTCCA		33910143	
AMPL7155	GGCATCTCTGCCCTGCTTAAT	GCTGAGGTGGCCTTTCCTAA	TG	chr8:133925211-1	367
234852	C	AG		33925578	
AMPL7155	GCTTCCCAGAGAGAAAATTCT	CGTGCCTTTATTTCTCATTC	TG	chr8:134125567-1	374
234857	AGAGC	TGACC		34125941	
AMPL7155	CCCTCTAAAGGGCATTAGCAA	TCACACATTAGAGTCAACAA	TG	chr8:134146794-1	372
234858	GA	TGCTTCA		34147166	
AMPL7155	TCCCAAATGTCTGCTGAACAA	CTTGAACCCAATGAGTCTTC	TG	chr8:133984731-1	373
234860	TGTA	ATTAATCTAC		33985104	
AMPL7155	GCCCTAAACAGGATACTTGGA	GATGAGTCTATCGATGCAAA	TG	chr8:134143915-1	374
234864	TATGA	TTGGG		34144289	
AMPL7155	GCAGATGGGCTCATCCAAGTA	TATCAATGGCCCTGGTGGAA	TG	chr8:133918731-1	356

433012	G	AC		33919087	
AMPL7155	AAGAGTAGCCAGATTTGCCAC	GTAAATGTGCCTCTTGTGC	TG	chr8:133898814-1	291
433015	AT	CAA		33899105	
AMPL7155	CAACATGCTATCTCTGTGCCA	GTAGCACTCTGAGTTGAAGC	TG	chr8:133899361-1	368
433017	GAA	ACT		33899729	
AMPL7155	CATAGATGGATAACCAGTATT	TCAGCAATTGGTCAATATCT	TG	chr8:134108343-1	374
234768	GGCATTCA	CTTGATCA		34108717	
AMPL7155	GGAGACAAGTGCAATGCAAT	GCTCCAGGAGGATATTCTCC	TG	chr8:133900358-1	287
234772	GG	CT		33900645	
AMPL7155	TCAAAGCTAAGAATCCACTCA	CCATTTCCTTATCTGTGAACG	TG	chr8:133983869-1	372
234778	TGCA	AGGAT		33984241	
AMPL7155	GCTCCTTTTGACCAGCAGAGA	AGCAAATCACTGACATGTGG	TG	chr8:133879085-1	356
234780	A	GAA		33879441	
AMPL7155	GGCTTGCACTGCTATGAGTGA	CCTTCCAAGTAGGAAGTGCC	TG	chr8:133910312-1	372
234781	A	AA		33910684	
AMPL7155	CTGCCATAGACAGCACCATGA	AGCCAAGTAGACTTTTGCAG	TG	chr8:134041987-1	367
234790	T	CA		34042354	
AMPL7155	GTATGTTGGAGCTACCTTACA	GTTTTAATGGTTTGATTGGT	TG	chr8:133941158-1	373
234806	AAGGA	TTGTCTCGA		33941531	
AMPL7155	GGTGAAGGCTGTCTCTCTCAG	TCTTTTCATCTCTGCCCTCAC	TG	chr8:133894617-1	356
234809	T	TTTG		33894973	
AMPL7155	GATCCATGTCAGGGCATCTGT	GGTTAAAAGATTAAAGGAG	TG	chr8:133975090-1	369

234815	T	AGTCCATGGA		33975459	
AMPL7155	CCTGAGACGCTGTCACCTATC	CCACAAGGAGGGCTCATAAG	TG	chr8:133960910-1	368
234824	T	AA		33961278	
AMPL7155	GCTAAGGGACACGAGTGCATA	AGCTCTTAATTCCTTATCATG	TG	chr8:133885219-1	362
234825	T	CTGCA		33885581	
AMPL7155	TTCATGGGAGTCAGAGGGAAG	GAGAGACGAATTTAAGCTCC	TG	chr8:133905869-1	374
234834	T	TGCTT		33906243	
AMPL7155	CTCCACTCTCTCCCTAATTTAA	GGGATGATTCTTATTCACAG	TG	chr8:133881839-1	374
234842	ACGAAC	AGGAGAAG		33882213	
AMPL7155	CATCTGGCTTGTCTCTGTGTCA	AGTCTGGATCAAAGAACAGA	TG	chr8:133913575-1	283
234844		TATGCAG		33913858	
AMPL7155	TGTTTGTTAGCTCAGCATCATC	GTTTAATTCATAGGAGCTGG	TG	chr8:133995422-1	372
234845	CA	AATTAATGCG		33995794	
AMPL7155	TGAATGAGCTCTTGAACTGGT	CTGCACAAAGAATTATCTGT	TG	chr8:133931510-1	374
234847	TTGA	CCCAAAAT		33931884	
AMPL7155	CCACATCTCTCCGTCTGGAGA	CCCACAGCTATGGAAGCAGT	TG	chr8:133912352-1	343
234849	A	AG		33912695	
AMPL7155	CATTTCCTGAAGCTGCCTAAT	GAGTGTCTTAGGCAAATCA	TG	chr8:134031706-1	374
234851	TTCTG	CCTAA		34032080	
AMPL7155	CTCTGCCCTAACTAGGAGGGA	TTCTAAAACACAGAGCCAG	TG	chr8:133979920-1	361
234853	T	CAGAA		33980281	
AMPL7155	TGGAGGATTGAAGGAAGTAA	ACAAGAAGACATCATGGGCT	TG	chr8:133923512-1	374

234854	CATAAGC	TCTTC		33923886		
AMPL7155	CAGCCTTGACACCTACAGATA	GCACAGCAGATGCTGAGATC	TG	chr8:134145589-1	374	
234861	CA	AA		34145963		
AMPL7155	GGGAATGGGAAGAAGGTGTT	GGTTAAGTGGTGTGTCCCAT	TG	chr8:134128708-1	337	
234865	CTT	GT		34129045		
AMPL7155	CTGCTTGTACTAGTGAGGGAC	GATTTCTATTACTGTACTGCA	TG	chr8:133899671-1	204	
413419	ATTT	TTGGGTCA		33899875		
AMPL7155	GGAGGTGGTTGGTGGACAAT	GAAAATGCTCCATGGGACTC	TG	chr8:133918964-1	346	
433013	C	TCT		33919310		
AMPL7155	TGGTTTCAAACGTAGGTGTCC	CCACAAAGAGCTCCTTGATC	TG	chr8:133898566-1	303	
433014	TT	GT		33898869		
AMPL7155	GGTGAATGTTGGCCAGTTTAA	CCGTTTCCATCACATCACCT	TG	chr8:133899048-1	373	
433016	CTT	AAATCT		33899421		
AMPL7156	ATGCATGAGTGAAGTAACATC	AACTCACCAAGTGTTTAAAT	TG	chr8:134025784-1	304	
642723	TCTGAG	AGTCCCTT		34026088		
AMPL7156	GGCTGCAAGTTACTGCTTACA	GCTGGAAACCAGCTCCAAAC	TG	chr8:133947837-1	344	
642725	C	AT		33948181		
AMPL7157	CTGGACAGGACAAGACTCCGA	TTGGCATGACCTAGTTGCTG	THRA	chr17:38230451-3	373	NM_19933
792783	A	AA		8230824		4.3
AMPL7154	AAAACATGTAGCCTGATGCCT	TTGGTAAACTCGCTGAAGGC	THRA	chr17:38242688-3	354	
976347	GAT	TT		8243042		
AMPL7155	TGGGAGGTAGAATGAGGACA	GCACATCCCACATTACCTTT	THRA	chr17:38232999-3	362	

235082	CAA	CTCA		8233361	
AMPL7155	CCCTAGTAAACTGCATGGTTG	ACCTAGACTGGATTGCCACT	<i>THRA</i>	chr17:38240010-3	348
235089	GT	CT		8240358	
AMPL7155	CATGCACATGGCCCAATACAA	CACTTCCGTGTCATCCAGGT	<i>THRA</i>	chr17:38244350-3	369
235095	G	TAAA		8244719	
AMPL7155	TTGAGACAGGAACAGAACAA	GAGACTTCCCGCTTCACCAA	<i>THRA</i>	chr17:38249066-3	374
235097	ATCAGAG			8249440	
AMPL7155	TTCTCCTGTCCACGTCTCTCA	GGTCAGTCACCTTCATCAGC	<i>THRA</i>	chr17:38245294-3	302
235101		A		8245596	
AMPL7153	CCAGTCACCCATTGTCTCCAT	AGAACCTCAGATGAGCCTGT	<i>THRA</i>	chr17:38242974-3	221
529749	G	ACT		8243195	
AMPL7156	GTGGGTCAGACCCAGAGGAG	ATCCCACAGAGGTGCTTAAA	<i>THRA</i>	chr17:38230770-3	126
749592	AA	GG		8230896	
AMPL7154	GCCATCTTTGAACTGGGCAAG	AGAAGAAGATTCAGGAGGG	<i>THRA</i>	chr17:38244663-3	190
342403	T	AGTTGA		8244853	
AMPL7157	CTTCTCGGAATGCATGTTGTTC	GGAGAAGGTATGGCACTCCT	<i>THRA</i>	chr17:38249366-3	319
792784	AG	TCT		8249685	
AMPL7154	AGATTCTTCATACTCTTAGGG	CGGGCTTTAGGTGACATAGG	<i>THRA</i>	chr17:38233575-3	359
976349	CAGAGAT	GA		8233934	
AMPL7155	GTTTCTCCAACCTGTACTCTAG	AGACTCCGAGCTCACTCTCT	<i>THRA</i>	chr17:38240763-3	374
235092	GAAG	TC		8241137	
AMPL7155	GCAAACACAACATTCCGCACT	CTATCCAAGGACGAGAGGA	<i>THRA</i>	chr17:38245543-3	288

235102	T	AGGAGAGAAG		8245831		
AMPL7155	ACACTTATTGGTTTGGAAATA	AGTTGAGAGTAACAAATATT	<i>THRB</i>	chr3:24270305-24	306	NM_00046 1.4
234911	ACGGTT	GCTTCAAGGT		270611		
AMPL7155	GCAATGGAATGAAATGACACC	GGAATTGGACAAAGCAAGC	<i>THRB</i>	chr3:24164314-24	371	
234912	CAGTA	CTT		164685		
AMPL7155	GGTATTCCCTTCTCTGTCTTCT	AAGGTCCAAAACGATTCATC	<i>THRB</i>	chr3:24188046-24	373	
234913	TGG	TCATAGTT		188419		
AMPL7155	ACGTTGCTTTCATATGATTAA	AGGATATCAGTTCAGAAGAG	<i>THRB</i>	chr3:24174684-24	370	
234923	GTCCCT	ATTTTCTGC		175054		
AMPL7156	CTTCATAAAAATACAGCGATG	CGGAGGAGAAGAAATGTAA	<i>THRB</i>	chr3:24231225-24	360	
629819	CCTGTT	AGGTAACC		231585		
AMPL7155	CTTGTTGAAACACATGATAAT	AGCAAAATCTTGACAATGCC	<i>THRB</i>	chr3:24231522-24	358	
234915	GGGCT	AACA		231880		
AMPL7155	GGATGATCACAGACCATGGAT	GTTTGGTTTCACTAAGTCTTT	<i>THRB</i>	chr3:24193749-24	372	
234921	GT	ACTGTTGTT		194121		
AMPL7155	GAGGCAATAACACCAGTATCC	GAAGTGCAGCTTGCTGTGTA	<i>THRB</i>	chr3:24184892-24	372	
234930	CA	TC		185264		
AMPL7155	TTAGCGCTAGACAAGCAAAAG	GTTCTGACTGGCATTTTTGC	<i>THRB</i>	chr3:24168931-24	374	
234935	CT	A		169305		
AMPL7155	CCTCCAGCATGACAAGCAAGA	CATTTATTCATCCATGCCTGA	<i>TPO</i>	chr2:1546037-154	373	NM_00054 7.5
234746	A	GAGTAACTA		6410		
AMPL7155	CTTTTCTGGGCAGATAAATGT	TTTGAGATACCAGTAACCTG	<i>TPO</i>	chr2:1520499-152	374	

234747	CCCT	TGTTAGC	0873		
AMPL7155	CCACTTATTCTCCCTGAGAAT	CTGGGAGGATCTGAAGGGAT	chr2:1457367-145		
234750	GGT	TG	7722		355
AMPL7154	CTCAAGGCCCTCAATGCG	CTGGGAGAGAGAAGCCACG	chr2:1481299-148		
067858		ATG	1469		170
AMPL7156	CGTTGGTGTGTGGTTTTCTTTT	GCGAAGAAATTTTCAATGAC	chr2:1500304-150		
642706	CTC	ATTGCATT	0624		320
AMPL7155	CATCTCCTTCGGGTCCTCAGT	CGTGAAGACGTGGCTGTTCT	chr2:1499447-149		
433050	A		9791		344
AMPL7155	GTCACATTGTCTGGGACACAG	CACAAAGTCAAGGTGTCCTC	chr2:1437092-143		
234726	TA	CTT	7444		352
AMPL7155	TCCCTATGAAGGCTATGACTC	GCACATGTATACCCTACGTA	chr2:1488433-148		
234728	CA	ACAAACC	8758		325
AMPL7155	GGACCATGGCATGAGTGAGAT	TCTGGATAGGAACGTACCAG	chr2:1497496-149		
234731	G	TCA	7828		332
AMPL7155	GCAGTTTCTGTAACCTCCTGA	AGGAGCTACCATTATGCCCT	chr2:1417986-141		
234732	CA	CTA	8359		373
AMPL7155	GCCTCGAACTTCCAGAGTCTT	CGAGGTCAACCCGTTTCATCT	chr2:1480785-148		
234737	A		1004		219
AMPL7155	CCCAGTTACATATGAATCCCA	ATACAGATCCACCAGTGGTG	chr2:1439904-144		
234742	AATTCAG	GTA	0257		353
AMPL7155	CCAGGAAGTGCATGATCCCAA	CCATTCTGTTTGACGTTTAA	chr2:1459763-146		360

234745	A	ATAGCACT		0123		
AMPL7155	ATTGTTGTTTCTCTAGAACTGA	TCTCTCTAGCAGCAGGTTGC	<i>TPO</i>	chr2:1491532-149	309	
234751	GCCAA	TA		1841		
AMPL7153	GCAAGATGGGCTTGAGGAAC	TCATCTGCAATTGCGAAAAT	<i>TPO</i>	chr2:1426729-142	271	
464249	AA	CAGG		7000		
AMPL7157	CTTACTCACTGTCTCCTTCTCT	TGATGAGATGCACGTGCTGT	<i>TPO</i>	chr2:1499735-150	284	
651842	GGA	AA		0019		
AMPL7155	TGTCTCATTGGGAAGCAGATG	GCTTACGTAAGAGTTGAATG	<i>TPO</i>	chr2:1497768-149	166	
231694	AAG	GTGGA		7934		
AMPL7155	TGGGAAGGAGGCTCTCTAGTC	CTGTGGAGAACACGTTGGAC	<i>TPO</i>	chr2:1488143-148	348	
234727		A		8491		
AMPL7155	GCTCCTCATCACCTTTTCGGAT	TCTTCATTTTACAAAACTC	<i>TPO</i>	chr2:1507537-150	372	
234730		GCAAATGGA		7909		
AMPL7155	GAACCTGTCCACGGCCAA	CTCCAGTGCGCATTGAGG	<i>TPO</i>	chr2:1480956-148	368	
234738				1324		
AMPL7155	GGAGTGTTTCCTGCCAAAGACA	GGACTAGGAAACACGGAGT	<i>TPO</i>	chr2:1544248-154	368	
234741	A	AAACAG		4616		
AMPL7157	TCTCCAGTCCTTTCCAAGAAA	GACTGCACAGATTCTCATTT	<i>TRHR</i>	chr8:110131362-1	374	NM_00330
792880	ATTGG	TCTTTGT		10131736		1.5
AMPL7157	TGTATGCTCTGGTTCTTCTTGC	AGGAACTCTATCCCACATTT	<i>TRHR</i>	chr8:110100210-1	373	
792882	TG	CCTCTATT		10100583		
AMPL7155	GGCGCTGGAAAGAAGATGTTT	TAATGCAGAGGCATCCAACA	<i>TRHR</i>	chr8:110099681-1	364	

235022	T	TAGC		10100045		
AMPL7157	CACACTGCTTTGGCTTTTCCTA	ACTGTTGAGATAAATGCAAA	<i>TRHR</i>	chr8:110131053-1	373	
792879	C	TTCTGCAA		10131426		
AMPL7157	CCAACATAACAGACAGTATCT	GATATCACAATAGCATCTTT	<i>TRHR</i>	chr8:110099983-1	291	
792881	ACGGTTC	GTAGGTGCTA		10100274		
AMPL7156	CAATGGCAAACACTGTTTCTTCC	CCTGTGTAGGTATGGGTATG	<i>TSHB</i>	chr1:115576599-1	374	NM_00054
642936	CAAAT	GATTAAATAG		15576973		
AMPL7155	TGCATTGGGATGGTACTGAAG	CATTAGATTTGGGAAATGAG	<i>TSHB</i>	chr1:115575884-1	374	
235105	TTT	GTTGTGATTT		15576258		
AMPL7156	TTATGTGAATCTACTCAGCAC	TGAAGTCTCTATATGTGCAA	<i>TSHB</i>	chr1:115576299-1	364	
642935	AATGGATAC	ACATCCTG		15576663		
AMPL7156	GAAGGTGTTGGGAGTTTGACT	TGTAGTCACACCTGATCATT	<i>TSHR</i>	chr14:81557280-8	342	
642703	ACA	GCTTAC		1557622		
AMPL7154	GTTTTGGCCAGGAGCTCAAAA	CCAGTCGATGGCATGGTTGT	<i>TSHR</i>	chr14:81609496-8	370	NM_00036
824249	A	AG		1609866		
AMPL7155	GTATACAGTGGACCAAGCTTG	CAAAGACTAGAGTGCCTTCC	<i>TSHR</i>	chr14:81574774-8	373	
234612	CT	ATCTAG		1575147		
AMPL7155	ATTTGGCAGAATCCATGAGGG	AACATGAACTGAGAATGAG	<i>TSHR</i>	chr14:81534460-8	371	
234628	TT	AACAGGTTAAT		1534831		
AMPL7155	TGCCCTTCAGTTAACAAATAA	CAGATTAGAAAATGCATGAC	<i>TSHR</i>	chr14:81528191-8	355	
234634	AGTGTGA	TTGGAATAGT		1528546		
AMPL7155	TTGTACTGGAAAGTTTCTTGT	CCAAGTTCCTTGACCTCATTT	<i>TSHR</i>	chr14:81562828-8	374	

234636	GGGAT	CCA		1563202	
AMPL7155	TCGTGGGTTTTAAACAAGCAT	CATCAAGGACTCAAGGATTC	<i>TSHR</i>	chr14:81608928-8	374
433070	TCTTTT	TGCA		1609302	
AMPL7155	CCCTCTTGCTCTGGCATATATT	GGAAGGCCTTGGTGAAAATA	<i>TSHR</i>	chr14:81610130-8	328
788309	GTT	GCA		1610458	
AMPL7156	CAGAGCTGAGAATGAGGCGA	GTTATTGAGCTGCTTTTGTGC	<i>TSHR</i>	chr14:81421966-8	316
723623	TT	ACTT		1422282	
AMPL7155	GCCTGGCACTGACTCTTTTCTG	GGCTGTCAAAGCTTGTAGA	<i>TSHR</i>	chr14:81609251-8	301
234590		GTCT		1609552	
AMPL7155	AACCTCAGGCCTGTTTGAGTT	GGTTTTCAAACCAGGAAGCA	<i>TSHR</i>	chr14:81605933-8	374
234609	T	TCTTC		1606307	
AMPL7155	CTCTGAGCCACTAGCGGTAA	TATATATGATAAGGCAGTAT	<i>TSHR</i>	chr14:81558716-8	339
234610	G	GGCTCTTGGA		1559055	
AMPL7155	ACCCTGTGGCGTAAATGCATA	TGGATCATTTACCCGATAC	<i>TSHR</i>	chr14:81554174-8	354
234629	T	CTTG		1554528	
AMPL7155	ACTGTTATTTTCACAGGAAGC	CATCGAGAATTATGAACTGC	<i>TSHR</i>	chr14:81528476-8	341
234635	TTATTGAGA	TCAAAATCAA		1528817	
AMPL7155	AAGTGCTCAAGCCAGAAGAA	GAGGGACTTGACAGAAGCCTT	<i>TSHR</i>	chr14:81574564-8	374
234637	GATAAA	TA		1574938	
AMPL7155	GCCTCTGTAGACCTCTACACT	GACGAAGGCAACTATGTTGA	<i>TSHR</i>	chr14:81609813-8	374
788308	CA	GC		1610187	
AMPL7155	CTATCCACTTAACTCCTGTGCC	TGGGATTGGAATGCATATTC	<i>TSHR</i>	chr14:81610400-8	371

788310	AAT	AAGAAACTAT		1610771		
AMPL7153	CACATAATTTACAGGTTGTAT	GTCCTACATGAGACAAAATG	<i>UBRI</i>	chr15:43328353-4	192	NM_17491 6
557478	ACCTGGTCT	TTTCTCCATA		3328545		
AMPL7158	ACTCAGTAAAATCTAGGAACA	CGTCATCTAGTTCAAGCTCTT	<i>UBRI</i>	chr15:43329874-4	329	
797561	CAGGGTA	CCATTTT		3330203		
AMPL7158	ATGGAGCAAAAGACCCTCCAA	GGCTCCAGGAACATCTCAAG	<i>UBRI</i>	chr15:43237415-4	354	
797574	T	AG		3237769		
AMPL7160	CTGTTTATCTTTTGAGGTTGCA	TGTAGAGATGCATGTGTAGT	<i>UBRI</i>	chr15:43294753-4	202	
337843	AAGGA	TCTGAATG		3294955		
AMPL7160	TCAGGGTTACCTATGTTTTAA	GACAGAGTGAGACCAGTCTC	<i>UBRI</i>	chr15:43314765-4	334	
337844	GGACTGA	TGA		3315099		
AMPL7160	GCATCTTTTTTCGCTACTCGATA	ACTCGGAGAATCCCTGTCTC	<i>UBRI</i>	chr15:43350969-4	373	
337845	ATGG	ATAA		3351342		
AMPL7155	TTGGCCTCACCTTTAACCTAC	GGGATATGTTTAAATCTAGG	<i>UBRI</i>	chr15:43258180-4	374	
234655	AC	GCTTTAGTCT		3258554		
AMPL7155	CAGTGACGTGACCGGAGAT	CAGCTTTGTGGGAGGGTTTT	<i>UBRI</i>	chr15:43378054-4	177	
234656		C		3378231		
AMPL7155	GTAAAATCTGTGCTTTTGTGA	TATTTGTGCTGTGCACACAT	<i>UBRI</i>	chr15:43324625-4	351	
234663	AGGTGA	ACAAAAA		3324976		
AMPL7155	TAAGGAATAAATGGAGAGGA	CCCACAGGTTGGAAACTACA	<i>UBRI</i>	chr15:43359976-4	373	
234671	TGGTCAGA	CAG		3360349		
AMPL7155	TTTAATTACACAGGCATGAAA	AAATATGAAGACAAGTGACC	<i>UBRI</i>	chr15:43299218-4	323	

234674	AGAAATGCA	AAAACATGTG		3299541	
AMPL7155	CAAGGCAGCGCCTAGTTAACT	TTATAGATAGAAACAAACCT	<i>UBRI</i>	chr15:43348377-4	361
234675	A	GCAGCAGTT		3348738	
AMPL7155	GATCTATCAAAACAGGATGAG	CAACATTGTCTATAACCCTG	<i>UBRI</i>	chr15:43340430-4	341
234676	TGAGTCA	AGAACCT		3340771	
AMPL7155	CCCTCATTCTCACCCCTTTCTAA	CCCAAACGTAAGATAATTGG	<i>UBRI</i>	chr15:43319829-4	367
234679	TCTG	TTTGTAGACCT		3320196	
AMPL7155	ACAGATCTCATATACTTCACA	GTTTGTCTACAGTCAGAGTCA	<i>UBRI</i>	chr15:43309166-4	374
234681	ATCAACAGG	CTTTTT		3309540	
AMPL7155	TATGTGAATAAGAAGCAAAA	TTTTGCATTAGGTTTCTCTAG	<i>UBRI</i>	chr15:43317434-4	371
234685	AGCTCTTTGC	AACACAATT		3317805	
AMPL7155	CTTAAGAGGAACTGCTGGCTT	AAAAAGAGAATGGCTTGTTG	<i>UBRI</i>	chr15:43252614-4	365
234689	CT	ACAAATCA		3252979	
AMPL7155	ATTCAAGAAATCTGTACTTGC	AGGAAATTAATCTGGAGGAA	<i>UBRI</i>	chr15:43290256-4	333
234699	AAACCA	CTCAACTTTT		3290589	
AMPL7155	GCATGGCTTCTGTAGGTGGTA	AAGGTATATAATGAGTCTGC	<i>UBRI</i>	chr15:43275943-4	374
234700	A	AGCTAATTCC		3276317	
AMPL7155	AGCATGTCTGTACATATTGAG	ACAGGACAGGCTGTCTCAAA	<i>UBRI</i>	chr15:43335303-4	374
234702	CACA	AC		3335677	
AMPL7155	CTATCAACACACTGTCCCACC	TGATGAAAACATGCTTGATT	<i>UBRI</i>	chr15:43244385-4	357
234704	ATA	GCTAACAG		3244742	
AMPL7155	AATGCAACCCTGAAAATTAAT	GGAAGTGGCAGGGTTATGTG	<i>UBRI</i>	chr15:43351751-4	374

234707	CAAAGTGT	AT		3352125	
AMPL7155	CGTAGACTTGGCTGGCAGAAA	GTAAAAGTGTCGTCCCTGTC	<i>UBRI</i>	chr15:43397957-4	356
234714	T	TCT		3398313	
AMPL7155	AAAAAGCCTCCTTACACCTAA	CATTGAACTCAATTAAGGTT	<i>UBRI</i>	chr15:43367040-4	365
234716	ATATGAGA	GGAGTATTGG		3367405	
AMPL7155	AAGTCAAATTATTCTGGGCCA	GAGCAGTTTACTTATGTTGA	<i>UBRI</i>	chr15:43280913-4	371
234717	TCAGT	AAGCAGTTAA		3281284	
AMPL7155	TAATTAATTTTGCCAGTAAAG	CTGCCCTTCACATTTAGTTAT	<i>UBRI</i>	chr15:43268848-4	299
234723	CATGGCAA	GACATTAAT		3269147	
AMPL7153	ATGATTCAAATGTTACGTTGC	ACGTTGTTTATTGTCTTGGA	<i>UBRI</i>	chr15:43262636-4	262
557475	CAAACA	CAATGAAAT		3262898	
AMPL7160	AAAAATTGAGTTGGTAATTTT	GCCATCCAAACAGCGTATAT	<i>UBRI</i>	chr15:43307847-4	290
337842	TGGTTTGC	AAATGTTTAA		3308137	
AMPL7160	CTTACCTTTATAAAGCTTTGCA	TTGCCTCAAATGTGGGAGGA	<i>UBRI</i>	chr15:43351278-4	374
337846	TCCCAAAG	TTAATATTAT		3351652	
AMPL7160	TGTAAGGAAGGGATCCAGAA	GACCAGGTATACAACCTGTA	<i>UBRI</i>	chr15:43328008-4	373
337847	CAAAAA	AATTATGTGA		3328381	
AMPL7155	TCTAATTCTTACCTGCAAGAA	CCCTAGATGATTAAGAAGGA	<i>UBRI</i>	chr15:43378170-4	328
234657	TAGGTTGTC	ACTTGTAAGT		3378498	
AMPL7155	AAACAAACGAGAAAGAAACA	GAAGCTACAGATGATCATGC	<i>UBRI</i>	chr15:43282089-4	372
234660	AGATAATGGG	CACT		3282461	
AMPL7155	ACCAGTAGTAAATGTCTACAA	GCATTAGTGGACTTTGATGT	<i>UBRI</i>	chr15:43313367-4	312

234661	TGGTACAGT	CCACA		3313679	
AMPL7155	GGTGTCTGGCCTCAATTACCT	GAATATCTAACAGATATTGG	<i>UBRI</i>	chr15:43242326-4	345
234662	T	CCACGTCTT		3242671	
AMPL7155	GCTCTAGATGTGGTTCCAAC	GCATGTGTTGTTTTGCATGTA	<i>UBRI</i>	chr15:43316927-4	374
234664	GA	ACCTATTAT		3317301	
AMPL7155	CTCGACTCACTGGAGCTTCAA	TTTGCAAATCTCTGTGCAAT	<i>UBRI</i>	chr15:43294478-4	338
234665	T	ACTGTG		3294816	
AMPL7155	GTAACCTAGGAATCTCCTATA	AATAAGCAATATACCCTCTA	<i>UBRI</i>	chr15:43255998-4	367
234667	CTTTTGCCA	CAAGGAGAGT		3256365	
AMPL7155	ACACACATTTTGCAATACAAA	CGATGTTGTAATGAATTCAG	<i>UBRI</i>	chr15:43362930-4	303
234669	TAACCATCA	CAAAGTGATT		3363233	
AMPL7155	CTTTACACACCACTTTCCAAC	ACACTTTGCTTGACATTCCT	<i>UBRI</i>	chr15:43295849-4	374
234670	TTGATAAT	AAGA		3296223	
AMPL7155	CCACTAAAGGATGAAGGTGAT	AATTTAATGCAGTGTTCTGT	<i>UBRI</i>	chr15:43321993-4	374
234672	TGGT	GTGTAAGTG		3322367	
AMPL7155	AGAAAAAGCAGAAAATTTTCT	GCTTTGTGTTTACAATGTAG	<i>UBRI</i>	chr15:43318678-4	363
234673	GTGGAGT	GTTTTTAGTT		3319041	
AMPL7155	GCAGGGCCAAGAACAACCTTT	ATACTATTTGAGGTCTGTTTG	<i>UBRI</i>	chr15:43350400-4	356
234678	T	CATGTGA		3350756	
AMPL7155	TCTGTAAAGCAACACACATCC	GAAGCATTTTCATATTCAGT	<i>UBRI</i>	chr15:43374671-4	366
234680	CTT	TTGTGTACCA		3375037	
AMPL7155	ACAAAAACAAGGAAGTGTGTT	GGATTGCAAGTGTAGATCCT	<i>UBRI</i>	chr15:43250115-4	289

234691	AGTTATGG	TTTGTTATTT		3250404		
AMPL7155	TATAAGACACAGCAAATAAGC	AGTGAAACTAAGGACTGTGT	<i>UBRI</i>	chr15:43346872-4	366	
234693	AACTGA	TTAACATTCA		3347238		
AMPL7155	GTTTGCAGAAGATAATGTAGT	AACTTATTTTTGCCACTAAG	<i>UBRI</i>	chr15:43328562-4	359	
234696	AGTCCCTT	GATTTTGAGG		3328921		
AMPL7155	AAGAAATCACATAACCCTGCC	CATCTGTCTTTCAGATATTGT	<i>UBRI</i>	chr15:43352099-4	368	
234697	AGTT	TCCGGTAT		3352467		
AMPL7155	CCTATTTGTAAACAATGGACA	TGGTTTTCATATCTCAAAGG	<i>UBRI</i>	chr15:43269929-4	364	
234703	GGAGAGA	TGTGATGT		3270293		
AMPL7155	GCTATTCAGTTTCCTATAAGA	TTTGGCATAGACTTAAAACA	<i>UBRI</i>	chr15:43276920-4	371	
234711	CTGATGCA	CAAGACTTTG		3277291		
AMPL7155	ACTTTACATCAAGGAAGCTGC	TGACCCAGTGTAACAACCAT	<i>UBRI</i>	chr15:43339265-4	341	
234713	AACA	GTAAAAT		3339606		
AMPL7155	GGAAGAGCTTGAAGTAGATGA	CCAGCCAAATCAAATCGCAC	<i>UBRI</i>	chr15:43330181-4	349	
234719	CGT	AA		3330530		
AMPL7156	TCCATCCAAGTTGTTGCAAGT	GGCATTATCCCAGAAAATG	<i>ZNF25</i>	chr8:146221805-1	302	NM_00046
642941	ATCTT	AAAATGTGT	<i>2P</i>	46222107		5.2
AMPL7156	CCTGTGCAACATGATACAGCA	GGTGTTTACTTAAGTAAAGAA	<i>ZNF25</i>	chr8:146199767-1	341	
642951	TGATA	CCTCGGTATT	<i>2P</i>	46200108		
AMPL7156	GCCTCAGAGGAAAAGCTTCCT	CCCAAGGATCTCTTCTTTGA	<i>ZNF25</i>	chr8:146200176-1	369	
642953	AA	GGT	<i>2P</i>	46200545		
AMPL7156	TTGACTTAACTTCAGGAGATT	CAAGGAATAAGGTGAGTCTT	<i>ZNF25</i>	chr8:146200674-1	371	

642955	AAGGTTTCC	TGTGTAGAT	2P	46201045	
AMPL7156	GCAAAGTAAGTGGTCTCCAGT	TCTAGCGCACAGTCATCTTT	ZNF25	chr8:146201263-1	366
642957	GAAATA	CATTC	2P	46201629	
AMPL7156	TGTTGGATAAGGGATAAGCAT	GAAAACCTTTGGGCAGATAT	ZNF25	chr8:146201860-1	371
642959	GCA	CCAC	2P	46202231	
AMPL7156	CTTCTCACCATTGTGTGTTCTT	ACTCTTACTGTCCATCAGAG	ZNF25	chr8:146202423-1	374
642961	TGATG	AATTCACA	2P	46202797	
AMPL7156	TCTCTCCACTATGAATTCTCTG	ACCAGCACCAGAGATTTTCAT	ZNF25	chr8:146203013-1	365
642963	ATGATGAA	AGTG	2P	46203378	
AMPL7156	GCGTCCTCTACGGGTCACT	CTGGAAGGGACGTAACCGG	ZNF25	chr8:146228077-1	338
642997		GAA	2P	46228415	
AMPL7160	GCCAAGGTCAACCTAAGAAGT	GGAGGAGTTTATGCCTGTA	ZNF25	chr8:146199188-1	374
337868	CT	CCA	2P	46199562	
AMPL7160	TCTAAGATGTTTGGCAGGATT	TCCATAGTAAAATGCAAGCG	ZNF25	chr8:146203617-1	374
337870	TGAGT	ATTCACT	2P	46203991	
AMPL7156	CAGTGTTATCTGACTTTTTAGC	ATTCATGGCACCAGACCCT	ZNF25	chr8:146200977-1	346
642956	AAGGTCT	AAG	2P	46201323	
AMPL7156	GACTAATCAGTTACTCTCCAC	CCCTACATGTGCAATGAGTG	ZNF25	chr8:146201566-1	352
642958	TGTGAAC	TGAG	2P	46201918	
AMPL7156	CTTCTCTCCATTGTGTGTTCTC	TGGAAAAGCTTTCAGCCAGA	ZNF25	chr8:146202171-1	315
642960	TCAT	GTTTTA	2P	46202486	
AMPL7156	GGATTTCCCACATTCATTACA	TCATGAGTGTAATCAGTGTG	ZNF25	chr8:146202729-1	363

642962	CCTATAAGG	GGAAAG	2P	46203092	
AMPL7156	GCTTTTCCACATTCATTGTGCT	CAGAAGTTCAATGCTGTTGG	ZNF25	chr8:146203318-1	361
642964	CATA	AGAAAA	2P	46203679	
AMPL7156	GGCTTGTAGAGAAGGGATTCG	GCTAGTTTTGACCTTTCCTCA	ZNF25	chr8:146219792-1	353
642998	T	GCTTAG	2P	46220145	
AMPL7160	GCCTCATAAATTGGGATTAGA	TGTTCTGCAGCATTTCCATTG	ZNF25	chr8:146198873-1	372
337867	GGCA	ATG	2P	46199245	
AMPL7160	AGTATGGATCATGATGAGATT	ATCATACACTTGGTACTTCCT	ZNF25	chr8:146199498-1	335
337869	CCTGGAA	AGCATTTTT	2P	46199833	
AMPL7156	CCCAAGCTTGATCCTCAAGGT	TGCCTCAAAGAGTTCACATT	ZNF25	chr8:146224922-1	323
642942	T	AGTGG	2P	46225245	
AMPL7156	AGAAATGTTTTAGCCATAAAA	GTGAAACCACATTTCTACAA	ZNF25	chr8:146200038-1	362
642952	CCCAAAACC	AATGCAAAAA	2P	46200400	
AMPL7156	CCAGCCTCCTTTTGTCTCTCT	GCAAGAACAGAGTTCATGGC	ZNF25	chr8:146200494-1	245
642954	T	TTTTC	2P	46200739	

^aPhysical position of the amplicons was obtained from the human assembly (GRCh37/hg19). Fwd, forward; Rev, reverse; bp, base pair.