

Appendices

APPENDIX I Primers used to screen vectorette cDNA libraries for the expression of novel genes

GENE	stSG number	Sense (5' → 3')	Antisense (5' → 3')
FOXP3	stSG156841	CATCATCCGACAAGGGCTC	AATGTGCTGTTTCCATGGCT
UBE1	stSG156840	TCTGGAGTCACGAACAGGTG	CTTCTTCAGGGGAGGTTGTG
PHF16	stSG156758	CTTTCCTCTTTTGGCTGCAC	GGAGCTGGAGGAGGAGTTCT
N.A.	stSG156806	CATGACTCCAGAGCAGCAAG	GGGCTGAGCTCATAGTCTGG
bA637B23.1	stSG156802	GAGGATTGCCCAAAAATCA	GGTGCTTGTCATCTTCAGCA
RP11-1145B22.1	stSG388756	AGGATTGGTGAACATGGAGG	TCCTAGCACCCCTATCCACA
RP11-54B20.4	stSG156037	GGGCTAGTGACATTTGAAGATG	GACCAAGTTGCTGTAGGTCTCC
RP11-38O23.2	stSG187910	AAGTGATTCGAAGGGAGTGC	CTCTCGTGAATCTTCTCAGAGCTA
AC115617.1	stSG486758	CCTCCATCACGAGGAGATG	CATCTCCTCGTGATGGAGG
AC115617.1	stSG486759	TGATGACGGTGAAGAGCATC	GATGCTCTTCACCGTCATCA
AC115617.1	stSG486760	TTTGGTCCCAAACCTGTCTT	AAGACAGTTTGGGACCAAA
AC115617.1	stSG529890	GGACATATGTCTGATCACAG	CTGTGATCAGACATATGTCC
RP11-348F1.1	stSG156807	AAGTGCAAACCCAACCAGAC	GACTCCCCTTCTTCGTACA
RP11-348F1.1	stSG172512	AAACATTGATGTGAACCCAGTG	CAACAAAAGGCTATAGGTGCTG
AF196971.4	stSG156785	TGCCTGAGTACAAGGCTGT	TGTCCAGGGTCAACTCCTT
AF196971.4	stSG498780	TGCCTGAGTACAAGGCTGTG	AGCACACCATCACAGACAGC
RP11-54B20.3	stSG156035	TCTCTTCATATGCACACAGCTG	GCCTTCGATGATATTGCCAA
AF238380.5	stSG156846	GCTTTAGCCCCTTGGAGAAA	GATCCTATCTTCACCCACGC
RP11-1148L6.5	stSG486773	TCTGCTTTCCGTCTCGCTAT	TGTGGGAAGAACATGAAGAATG
RP11-805H4.2	stSG156812	ATCAACTCCAAAAGTGGCGA	CTTCAGGTCCACCCTTCAAT
AF196970.3	stSG380014	TGGGTAGAAGGAAACATGCC	AATTACACCACAGGCAGCG
AF196970.3	stSG380015	CGGACACTGACAGTAGAAGCC	AACTCTGGACACTCTGGCCT
AF196970.3	stSG172510	GCTTTGGCTACTGGAGATCG	CTGTGCCAGCCCTTGAGTA
AF235097.6	stSG380006	CACTTCTCCCTCCTGTGCTC	GCTAACACTTACGGGGGTGA
RP11-258C19.5	stSG156811	GAGGAAGAGGAAGACGCTCA	TTCTGCATAGAAAATGGCCC
RP11-576P23.4	stSG156810	CAGGCCTAGAGGCACTGCT	CACCTCCTCCTGCTTTCATC
RP1-30G7.2	stSG156783	ATGAGTGTTTCATGTCTGG	TGTCTTGTGAGGCTCTGGAA
RP5-1158E12.2	stSG156757	GCACATTCACACGGAACACT	CTGAGGGCTGATACTGCACA
bA104D21.3	stSG156804	ACCTCCAAAGCAGACCTTCA	ATACTGGGAATACTCGGCCA
RP1-71L6.2	stSG400506	GAGGTTTCAGGCTGTCTGGCA	CGACTAAGTGGGGAAGCCGA
AF196972.9	stSG387162	AATGACCCACAGCACCTACC	ATGGAAACAATCAAGTCCGC
bA56H2.2	stSG156798	GGGAGACGTTTCAGGAAACTG	CCGATAGGTGACGATGCTTT
RP11-1158E12.1	stSG156871	AAGAGGTGGCTGGGAAAGTT	CCCACAGTTTCTGAACGTC
bA258C19.6	stSG156809	GCTGGAGCTGAACAACATCA	GTTCTGGTACTGGCTCTCGC

APPENDIX II Primers used to identify transcript variants

GENE	stSG number	Sense (5'→3')	Antisense (5'→3')
EBP			
A	487013	GCTCCGTAAGGCAAGAGAAC	GGCTCCGGGCTCTCTTTAG
B	487014	CCTATACACACGCAGCCATC	TCACGACTAAGACCCCTGTG
C	487015	GTTGTCCCATTGGGGACTT	GAACCAGCCCTCGATCACC
D	487016	GGTGGTGATCGCCTTTCTC	CCACAGAGACCACAAGCTGTA
E	487017	GCCAAGAGCAAGAAGAAGTGA	CAAACCTGTGGGAGCAGGACT
F	498791	TTGAGGGTCTTCATGCCAAT	GCAGCGGTCAATTCTCTCTC
OATL1			
A	487003	CTCCGGAGCCAGACAAGT	ACTTGTCTGGCTCCGGAG
B	487004	TGCTGTAGATCCCCAGATCA	AAAGGCTCGGATGAGGATGT
C	487005	TCGTCAGTGATGACCGTTTC	AATCAGCCCCAAAGATGTCA
D	487006	CAAGTGCTGAGCTGGTCGTA	TCGTGGTTCAGGTACGTGTG
E	487007	GCGCTGATGACCTCTTCTTC	GAAGAAGAGGTCATCAGCG
F	487008	TGGGTCTGGGGAGTTCAAT	TATTGAACTCCCAGACCCA
G	487009	CCCAGGCCTAAGTATGTGGA	TCCACATACTTAGGCCTGGG
H	487010	AAGACAGGTGCTGTGAGCTG	CAGCTCACAGCACCTGTCT
I	487011	TTGAGCCCCCTAGACACAGA	TCTGTGTCTAGGGGGCTCAA
J	487012	GGATCTTGGCCTCTCTGTGA	TGCACGGTACCTGTCTGAAG
WDR13			
A	486663	CGGCGACAGTGGTCTCAGG	CCTGAGACCACTGTCGCCG
B	486664	TCGCGTCCACTGCTAAGACT	AGTCTTAGCAGTGGACGCGA
C	486665	GGCAGTACCTGAGGCTTCG	TGCTATAGGCACGAGCACTG
D	486666	GACACGTCCTGAGCGAGAA	GTAGCACGCGAAGCACTGT
E	486667	ATCCTCGTGTCCACCTCACT	GCAGAGCAGTTCAGCGCTAT
F	486668	ACCGTGGCAGTGTCTTCTCT	CTTGTTGAGGCAAGCATTGA
G	486669	AGAGAAGCTTCCCCATCGAG	GACATGAGGGGACAGAAGATG
H	486670	ACATGTGCGTGCACCTTCTT	AAAGAAGTGCACGCACATGT
I	486671	AAGTTTCGGTGGTCTATGCTG	CAGCATGACCACCGAAACTT
RBM3			
A	486772	CCTCCGAGCTCGCTGTTC	GAACAGCGAGCTCGGAGG
B	486773	TCTGCTTCCGTCTCGCTAT	TGTGGGAAGAACATGAAGAATG
C	486774	GTGGGAGGGCTCAACTTTAAC	CCTGCTCGTCCGTGTTAAAG
D	486775	TGTCAAGGACCGGGAGACT	CTCTCATGGCAACTGAAGCA
E	486776	CGGAGAGGACCTCGTGAGTT	TCCTCTAAGCTGCCCGACTA
F	486777	AAGTCTGCTCGGGGAACC	GTTCCCCGAGCAGACTTG
G	486778	GACAGTCGACCTGGAGGGTA	CTCTGGAACGTCCATATCCAT
H	486779	GGGTGGTTATGACCGCTACT	TGTGCATGTCTATTTCAAGTTG
I	486780	TATGGGACGTTTGTAGAACCTG	CAGGTTCTACAAACGTCCATA
J	486781	CAAGAACATGATTATCCAGGGG	CCCCTGGATAATCATGTTCTTG
K	457763	GGGGAAGCGTCTTTGGGATTAGTG	TGGGGTACTGACTGGTCCACATTG
L	498793	TCAGTGGGAATATGCATACAGTT	TGGCATGAAGTCTTTTAAACAAT

GENE	stSG number	Sense (5'→3')	Antisense (5'→3')
WAS			
A	486751	AGATGCTTGGACGAAAATGC	GCATTTTCGTCCAAGCATCT
B	486752	GGAACAGGAGCTGTA CTACA	TGTGAGTACAGCTCCTGTTCC
C	486753	ACTTTGCAGACGAGGACGAG	CTCGTCCTCGTCTGCAAAGT
D	486754	CGACAGTGGACATCCAGAAC	GTTCTGGATGTCCACTGTCCG
E	486755	GGGGTAACAAGGGTCGTTCT	GCCGGATTTGATCCAAAAG
F	486756	GAGAAGCAGAGCCATCCACT	AGTGGATGGCTCTGCTTCTC
G	486757	CAACCCCTCCAATGCTGTTA	TAACAGCATTGGAGGGGTTG
H	486762	AGAACGACCCTTGTTACCCC	CTTTTGGATCAAATCCGGC
AC115617.1			
A	486758	CCTCCATCACGAGGAGATG	CATCTCCTCGTGATGGAGG
B	486759	TGATGACGGTGAAGAGCATC	GATGCTCTTACCAGTCATCA
C	486760	TTTGGTCCCAAACCTGTCTT	AAGACAGGTTTGGGACCAA
GATA1			
A	486656	GAACCCTCCGCAACCACCAG	CTGGTGGTTGCGGAGGGTTC
B	486657	TTAATCCCCAGAGGCTCCAT	ATAGGCTGCTGAATTGAGGG
C	486658	CCACTACCTATGCAACGCCT	GGCAGTTGGTGCCTGAGTA
D	486659	GCTTTGAAGGTTCAAGCCA	TGGCTTGAACCTTCAAAGC
E	486660	GCTCAACTGTATGGAGGGGA	TCCCTCCATACAGTTGAGC
F	486661	GCGGAAGGATGGTATTGAGA	TCTGAATACCATCCTTCCGC
G	511595	TGCTCCTGCAGTTACAATCG	TCAGATCATGTTTATTGTGGGG
SUV39H1			
A	487030	TGCTAAGCCAGGAAGCAGAAT	ATTCTGCTTCTGGCTTAGCA
B	487031	CTGCTCGTGCTTACAGTGCT	ACAGCTCTTAGGGCCAACAC
C	487032	GAGCTCACCTTTGATTACAA	TTGTAATCAAAGGTGAGCTC
D	367547	ATTTCGAAGAAGCAGCTTCGT	TTGTAATCAAAGGTGAGCTC
E	367548	TAAGAAGCGGGTCCGTATT	AACCAGATTGAGTCCATGC
F	433850	CTAGGCCCGAATGTCGTTAG	CGGGAGTTGCACTCGTAGAT
G	498794	CTGGTGACCGTTACCCATTC	CGCACAGGTA CTGACTTCA
H	498806	CTTAGAGGTCTGCTGCTCCA	CTGGGACATCCCAAAGACTG
HDAC6			
A	486638	GGGGCTGCGTCCAATGAGTG	CACTCATTGGACGCAGCCCC
B	486639	GGCTGGTTGAAACGCTAGGG	CCCTAGCGTTTCAACCAGCC
C	486640	TGATTATCCCGGGAGATAGG	CCTATCTCCCGGGATAATCA
D	486641	ACCAGGCAGCGAAGAAGTAG	CCTTGCAGTCCCACGATTAG
E	486642	GCTGAAAAGGAAGAGCTGATG	CATCAGCTCTTCTTTTCAGC
F	486643	TGGCTATTCTTCAGGTTGAC	GTCAACCTGAAGGAATAGCCA
G	486644	GGGAGCCAGAAAGGGAGTAA	TACTCCCTTTCTGGCTCCC
H	486645	GGCTGAGATCCGGAATGG	CCATTCCGGATCTCAGCC
I	486646	AGTTCACCTTCGACCAGGAC	TCCAAGGCACATTGATGGTA
J	486647	CAGCTAACCCACCTGCTCAT	AGAAGGGTGTGGAGCGAAG
K	486648	GATCATGTGCCGTCTGGAG	TGTGCACAGGCCGAAGGTA
L	486649	CACAGGCTTACCAGTCAAC	TAAGGATAATGCGGCCACTG
M	486650	GGATGACCACAGAGAAAAGA	TCTTTTCTCGTGTGGTCTATCC
N	486651	GACCTTGGAGCTAGGCAGC	GCTGCCTAGCTCCAAGGTC
O	486652	CCCCATTTGGTGGCAGTAT	GGCTGACAGGTGATGTAGC
P	486653	CACCACTACTCCAGCCCAGAA	TTCTGGGCTGGAGTAGTGGTG

GENE	stSG number	Sense (5'→3')	Antisense (5'→3')
PCSK1N			
A	484537	GTCGGCCTTTTGGTGCTG	CAGCACAAAAGGCCGAC
B	484538	CCGTGTGCACATTCCATAGT	TGCTCCTGCAGTTACAATCG
C	484539	CCTAAGCGCAGCGTCTCC	GGAGACGCTGCGCTTAGG
D	484540	GGACCCCGAGCTGTTGAG	GTCCACGTCGGGTGTCTC
E	484541	TACTTGCTGGGACGGATTCT	GGTAAGTTGCTCTGGACGTG
PIM2			
A	487044	ACCAGTTTCTCTGCTTTCCAC	GCCCACTGAACCCGCTAA
B	487045	AGTCACATGCCACTCGAAG	CATAGCAGTGGGACTTCGAG
C	487046	AAGCTGCTTACCTGCCTCAG	GAAGCCTTGGGGTAACAACA
D	487047	TTCGAGGCCGAGTATCGACT	AGTCGATACTCGGCCTCGAA
E	487048	GGTACATCCTCGGCTGGTGT	CGACCCTACTGGAAGAGAT
F	530013	CCGGACAAACAACCTACCAGC	GCGACCTTCTGTCAAGACT
G	499718	GAGCTTTCGCCTATTACCG	CGGTAATAGGCGGAAAGCTC
TIMM17B			
B	483753	GGTTGAGAGGTAGTGCCAATG	CATTGGCACTACCTCTCAACC
C	483754	GGGAGGGAACCGAGAAGTAG	CTACTTCTCGTTCCCTCCC
D	483755	CCACCCCAACGTTACCAATA	TATTGGTAACGTTGGGGTGG
H	485476	CAGCGCCATGGAGGAGTAC	GTACTCCTCCATGGCGCTG
I	485477	TAAAGCCCGTTTTGAAATGC	GCATTTCAAACGGGCTTTA
J	485479	TAATTGGCAGACGGAAGACAG	CTGTCTTCCGTCTGCCAATTA
PQBP1			
A	483740	GAAGAGATCATTGCCGAGGA	TCCTCGGCAATGATCTCTTC
B	483741	GGAAGGGTCAACACCTTGTA	TACAAGGTGTTCCGACCCTTCC
C	483742	TAGACCCCATGGACCCTAGC	GCTAGGGTCCATGGGGTCTA
D	483743	ATGCTGAAGAAAAGTTGGACCG	CGGTCCAACTTTTCTTCAGCAT
E	483744	CTTCTTGCTCTTGGGATAGGG	CCCTATCCCAAGAGCAAGAAG
F	483745	GGGCAGGATCACCAGAAAG	CTTTCTGGTGATCCTGCCC
G	483746	CAATCCTGCTGCTTGTTTC	GAACCAAGCAGCAGGATTG
H	483747	AAGACTGGCGCTGACACC	GGTGTGAGCGCCAGTCTT
I	483748	CCTTCCACTACCTGCACGA	TCGTGCAGGTAGTGGAAGG
J	483749	GTGAAGGCCTCGTTGAGAGA	TCTCTCAACGAGGCCTTAC
K	483750	TGGGAGTTGCGATGATATTG	CAATATCATCGCAACTCCCA
L	483751	CCAAGAGAGGCATCCTCAA	TTTGAGGATGCCTCTTTGG
M	499719	CCTTCACAACCTCCTTGCCCA	TGGGGCAAGGAGTTGTGAAGG
N	498795	TCTTCGCACTCTGTTTATTTCG	GTAACGTTGGGGTGGGTGCAC
SLC35A2			
A	482243	TCTTCCTCCATGAGGCTGTC	GAGGTGGGTCATGAGAGAGC
C	482245	CTCATCACGGAGCCCTTTCT	AGAAAGGGCTCCGTGATGA
D	482244	GATCCTCAAAGGCAGCTCA	TGGCATTGGATATCCTGACA
G	482277	AGCGTGTCCACATACTGCAC	TTTCCGCGGGTGCATTGGAG
H	482278	CTCCAATGCACCCGCGGAAA	AATCCCGGGGCTATTTCATC
J	486761	TCACGTGCAGTGCCTAGAAC	ATTCAGCATGAGCACGGAG

GENE	stSG number	Sense (5'→3')	Antisense (5'→3')
AF207550.5			
A	487022	CTACGGCACCACCCACAC	CTCAAGGCCCGCTACCAG
B	487023	GCAACCACATTGAGATGCAG	ACCTCCACAGGACGGTTGTA
C	487024	ACGAACCCATTTCGTGTTAGC	TGGCCTTGTTAGGATTCACC
D	487025	GACCGGCTAGTCCACTCCTC	CGGGATCAGGAGAAACAGG
E	487026	TGATGATGAGATCCTAGCTTCG	CCTGGGTCTCCATCAACTCT
F	487027	CTCAGACGTTCTTGGGGGTA	GGGTGCCGAAGATAGACAAG
G	487028	TGCTCCACACTCCCTACAC	GGGGTCATCTTTGGGGATTA
H	487029	AGGTGTATGGAGACCAGGACA	TAGTCCATGCAATGCTTTCCG
I	498796	GGGCCCTGTAACAGTGAGAA	GTTTTGTTGGAGGGGAGAAT
KCND1			
A	487033	GACACACCCAACTCCCTTTC	ATCTAGACGGGCCAACAAG
B	487034	TGTCTAGGGCAGATGCTGTG	CAACTGTGAGACATGGGCAG
C	487035	CAGGCTCTTTGTGTCAGGAAC	GAGGTGCTACGGCTGGTG
D	487036	TGGGTGACCTTCCAAAACCTC	TCTTTGTCAGCCACCAGCTC
E	487037	TCCCTTTCCAGATCCATGAG	GAAGTGGGGGTTCTAGAGGG
F	487038	ATTCTCCTAAACGCCACCCT	ATCTCCTCGAGATGCCTTCA
G	487039	GCTGCCTTGAAGAGTATCGG	GATGAAGAAGCCGGTCACAT
H	487040	GTTCTGATTGGTTCTGCGGT	GACCCCTTTTCATTCCCCTA
I	487041	AGGGCACAAACAAGACCAAC	GAAAATCTTGCCAGCAATGG
J	487042	GACTTCGTGGCTGCCATTAT	GATCTTGACAGTCTCGGGGA
K	487043	CTTGGGCTCTCAGATGAAGG	CTCCAAAGCTCCATATCCCA
GRIPAP1			
A	530014	ACAGCCAGGAGGAGGACTTC	GAAGTCCTCCTCCTGGCTGT
B	530015	AGCTGATCACAAAGCCCAGT	CTGATTGGCAGCCTCAAGTT
C	530016	ACAGGATGTACGGGATCAGC	GCTTCAGGCTGCTAATGGTC
D	530017	CTTATCCAGCAGCCCTCAAG	GCTGAAAGAGCTCAGCCACT
E	530018	GCAGCGTCCTGAGAGACCTA	TCTTGTTTATCTCCCGAAGG
F	487049	CAGCAAAGACCCAAGAAGT	CTCGTACTCAGCCTGCTGCT
M13 F & R		GTAAAACGACGGCCAGTG	GGAAACAGCTATGACCATG

APPENDIX III Primer pairs used to screen human cDNA samples for novel transcript variants

EBP

Number	Primer 1		Primer 2		Product Size		
1	A	487013S	B'	487014A	328	273	
2	B	487014S	C'	487015A	282		
3	A	487013S	C'	487015A	444	389	220
4	C	487015S	E'	487017A	613		
5	F	498791S	B'	487014A	287		

OATL1

Number	Primer 1		Primer 2		Product Size		
1	A	487003A	B'	487004A	257	209	
2	B	487004S	C'	487005A	317		
3	C	487005S	E'	487007S	802		
4	D	487006S	G'	487009A	1671		
5	D	487006S	I'	487001S	3019		

RBM3

Number	Primer 1		Primer 2		Product size				
1	A	486772S	C'	486774A	566	237			
2	B	486773S	C'	486774A	228				
3	D	486775S	E'	486776A	480	329	219		
4	D	486775S	F'	486777A	646	425	318	156	
5	C	486774S	F'	486777A	655	508	401	239	132
6	C	486774S	E'	486776A	840	562	416	309	
7	K'	457763A	H'	486779A	323				
8	F	486777S	H'	486779A	233				
9	H	486779S	I'	486780A	654	299			
10	H	486779S	J'	486781A	1096	733			
11	G	486778S	J'	486781A	1155	800			
12	L	498796A	K	498794S	1104	1000			

WDR13

Number	Primer 1		Primer 2		Product Size		
1	A	486663S	B'	486664S	482	139	
2	B	486664A	C'	486665A	897	218	185
3	C	486665S	D'	486666A	486		
4	D	486666S	F'	486668A	693		
5	F	486668S	H'	486670A	339		
6	F	486668S	I'	486671A	674		

WAS

Number	Primer 1		Primer 2		Product Size
1	A	486751S	C'	486753A	290
2	B	486752S	D'	486754A	352 220
3	C	486753S	D'	486754A	233 101
4	D	486754S	E'	486755A	725 656
5	E	486755S	E'	486755A	320 251
6	H'	486762A	G'	486757A	350

SUV39H1

Number	Primer 1		Primer 2		Product Size
1	F	433850S	F'	433850A	706
2	D	367547S	D'	367547A	400 308 134
3	A	487030S	D'	367547A	248 74
4	C	487032S	E'	367548A	749

AC115617.1

Number	Primer 1		Primer 2		Product Size
1	A'	486758A	C	486760S	200
2	B	486759S	D'	529890A	150
3	C	4869760S	D'	529890A	230

GATA1

Number	Primer 1		Primer 2		Product size
1	A	486656S	B'	486657A	599
2	B	486657S	C'	486658A	802
3	C	486658S	D'	486659A	695 475 354

HDAC6

Number	Primer 1		Primer 2		Product size
1	A	486638S	D'	486641A	311
2	B	486639S	D'	486641A	290 559
3	C	486640S	D'	486641A	280
4	B	486639S	C'	486640A	160
5	D	486641S	E'	486642A	396
6	E	486642S	H'	486645A	1052 858 162
7	H	486645S	I'	486646A	260
8	I	486646S	J'	486647A	427
9	J	486647S	K'	486648A	647
10	K	486648S	L'	486649A	803
11	L	486649S	N'	486651A	1093
12	M	486650S	O'	486652A	947
13	O	486652S	P'	486653A	547
14	L	486649S	P'	486653A	1799 253

PCSK1N

Number	Primer 1		Primer 2		Product Size
1	A	484537S	C'	484539A	101
2	B	484538S	C'	484539A	256
3	C	484539S	E'	484541A	754 451
4	D	484540S	E'	484541A	310
5	A	484537S	D'	484540A	545

TIMM17B

Number	Primer 1		Primer 2		Product Size
1	D'	483755A	H'	485476A	115
2	G'	483757A	H'	485476A	93
3	H	485476S	B	483753S	167 317 788
4	B'	483753A	C'	483754A	423 509
5	B'	483753A	I	485477S	548 745

PQBP1

Number	Primer 1		Primer 2		Product Size
1	J	483749S	I'	476748A	144
2	J	486749S	L'	483751A	203 135
3	I	483748S	L'	483751A	99
4	K	483750S	L'	483751A	260
5	L	483751S	B	483741S	143
6	A	483740S	D	483743A	239
7	A	483740S	C'	483742A	251 285 546 763
8	A	483740S	E	483744S	501
9	C	483742S	G	483746S	198 328
10	C	483742S	F	483745S	216
11	D	483743S	E	483744S	284
12	D	483743S	C'	483742A	329 543
13	D	483743S	H'	483747A	329 621 753
14	B'	483741A	C'	483742A	170 204 465 682

SLC35A2

Number	Primer 1		Primer 2		Product Size
1	A	482243S	C'	482245A	272 731 1600 620
2	D	482244S	C'	482245A	492
3	C	482245S	F	482244A	1135
4	D	482244S	F	482244A	1707 560
5	D	482244S	B	482243A	732
6	C	482245S	B	482243A	260
7	H	482277S	G	482277A	282
8	I	482278S	G	482277A	542

PIM2

Number	Primer 1		Primer 2		Product Size
1	A	487044S	B'	487045A	336
2	B	487045S	C'	487046A	1262

AF207550.5

Number	Primer 1		Primer 2		Product Size
1	A	487022A	B'	487023A	694
2	B	487023S	C'	487024A	205 180
3	C	487024S	D'	487025S	391
4	D	487025A	E'	487026A	494
5	E	487026S	F'	487027S	596 370
6	E	487026S	G'	487028S	977 851

KCND1

Number	Primer 1		Primer 2		Product Size
1	A	487033S	I'	487041A	2154
2	I	4870141S	C'	487035A	507
3	C	487035S	D'	487036A	1715
4	B	487034S	I'	487041A	1188

GRIPAP1

Number	Primer 1		Primer 2		Product Size
1	A	530013S	B'	530014A	248
2	B	530014S	C'	530015A	622
3	C	530015S	G'	487049A	465
4	G	487049S	D'	530016A	708 630
5	D	530016S	E'	530017A	445
6	E	530017S	F'	530018A	316

APPENDIX IV Transcript variants identified for 18 genes in human Xp11.23
(Blue - reference transcript, pink transcripts identified in this study)

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
EBP.1	NM_006579		n.a.	n.a.	n.a.	n.a.
EBP.2	AL583368		3' gain	-54	exon 2	5' UTR
EBP.3	BE300348		3' gain	-223	exon 2	5' UTR
EBP.4	BI224033		novel first exon	108	exon 1a	5' UTR
EBP.5	AJ973496	EBP- 2	internal deletion	-81	exon 2	5' UTR
EBP.6	AJ973494	EBP- 5	first exon extension	408	exon 1	5' UTR
EBP.7	AJ973495 AJ973491	EBP- 6	first exon extension	124	exon 1	5' UTR
EBP.8	AJ973492 AJ973493	EBP- 6	first exon extension	323	exon 1	5' UTR
OATL1.1	NM_001006113		n.a.	n.a.	n.a.	n.a.
OATL1.2	BG480179		3' gain	48	exon 2	CDS
OATL1.3	AJ973528 AJ973590	OATL1-6	5' loss 3' loss	-57	exon 1,2	CDS
OATL1.4	AJ973529 AJ973530	OATL1-6	whole exon addition	30	exon 4a	CDS
OATL1.5	AJ973532	OATL1-2	5' gain	72	exon 2	CDS
OATL1.6	AJ973532	OATL1-5	internal deletion	768	exon 6	3' UTR
OATL1.7	AJ973532	OATL1-1	5' gain	12	exon 1	CDS
RBM3.1	AK000859		n.a.	n.a.	n.a.	n.a.
RBM3.2	BM702340		novel first exon	415	exon 1	5' UTR
RBM3.3	AU137487		5' gain	416	exon1	5' UTR
RBM3.4	CB110977		whole exon deletion	107	exon 1	5' UTR
RBM3.5	BG708929		whole exon addition	269	exon 3a	CDS
RBM3.6	AL540984		intron retention	424	intron 2,3	CDS
RBM3.7	AL539019		intron retention	147	intron 3	CDS
RBM3.8	BM786866		first exon extension	322	exon 2	5' UTR

Appendices

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
RBM3.9	AV703485		first exon extension	364	exon 4	5' UTR
RBM3.10	AJ973551 AJ973552	RBM3-7	internal deletion	1001	exon 7	CDS
RBM3.11	AJ973553	RBM3-5	intron retention	278	intron 2	CDS
RBM3.12	AJ973555	RBM3-5	whole exon deletion, whole exon addition	101	exon 3, 3a	CDS
RBM3.13	AJ973556	RBM3-5	intron retention	230	intron 3a	CDS
RBM3.14	AJ973585	RBM3-12	internal deletion 5' loss final exon extension	-619	exon 8	3' UTR
RBM3.15	AJ973558	RBM3-12	antisense	559	antisense	n.a.
RBM3.16	AJ973560	RBM3-12	5' loss, final exon extension	231	exon 8b	3' UTR
RBM3.17	AJ973562	RBM3-12	5' loss final exon extension	446	exon 8c	3' UTR
RBM3.18	AJ973564 AJ973565	RBM3-12	internal deletion 5' loss final exon extension	-616	exon 8d	3' UTR
WDR13.1	AF329819		n.a.	n.a.	n.a.	n.a.
WDR13.2	AF158978		first exon extension	1149	exon 1	5' UTR
WDR13.3	BM791753		internal deletion 3' loss	-375	exon 1	5' UTR
WDR13.4	AL552544		internal deletion	-363	exon 1	5' UTR
WDR13.5	AL544291		3' loss	-34	exon 1	5' UTR
WDR13.6	BM193349		internal deletion first exon extension	256, -343	exon 1	5' UTR
WDR13.7	BM921240		whole exon deletion	-241	exon 2	CDS
WDR13.8	BE253921		novel first exon 3' loss	52	exon 1	5' UTR
WDR13.9	BU158146		3' gain	85	exon 4	CDS
WDR13.10	AU408073		whole exon deletion	181	exon 6	CDS
WDR13.11	AJ973583	WDR13-3	3' loss	-56	exon 6	CDS

Appendices

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
WDR13.12	AJ973579	WDR13-4	whole exon deletion 3' loss	-423	exon 5, 6	CDS
WDR13.13	AJ973577 AJ973578	WDR13-2	antisense	80,98	n.a.	n.a.
WDR13.14	AJ973581	WDR13-5	antisense	18585	n.a.	n.a.
WAS.1	NM_000377		n.a.	n.a.	n.a.	n.a.
WAS.2	BI833034		whole exon deletion	-132	exons 5,6	CDS
WAS.3	AJ973571	WAS-4	intron retention	1099	intron 7	CDS
WAS.4	AJ973572	WAS-4	internal deletion	90	exon 9	CDS
ERAS	NM_181532		n.a.	n.a.	n.a.	n.a.
GATA1.1	NM_002049		n.a.	n.a.	n.a.	n.a.
GATA1.2	BC009797		3' loss	-341	exon 6	3' UTR
GATA1.3	AI022182		internal deletion	-217	exon6	3' UTR
GATA1.4	Sccd21402	GATA1-1	whole exon deletion	-239	exon2	CDS
GATA1.5	AJ973499	GATA1-2	5' loss	-137	exon 3	CDS
SUV39H1.1	NM_003173		n.a.	n.a.	n.a.	n.a.
SUV39H1.2	AL549893		novel first exon	93	exon 2a	5' UTR
SUV39H1.3	BG285236		5' loss, 3' loss	-174	exon 3,4	CDS
SUV39H1.4	AJ973548	SUV39H1.1	whole exon deletion	-147	exon 2	5' UTR
SUV39H1.5	AJ973549	SUV39H1.5	first exon extension	352	exon 2	5' UTR
AC115617.1.	t.b.c.		n.a.	n.a.	n.a.	n.a.
AC115617.1.2	AJ973481	AC115617.1-1	whole exon addition	69	exon 1a	CDS
AC115617.1.3	AJ973482	AC115617.1-1	whole exon addition 5' loss	118, 47	exon 1b	CDS
AC115617.1.4	AJ973484	AC115617.1-1	5' loss	47	exon 3	CDS
HDAC6.1	AK024083		n.a.	n.a.	n.a.	n.a.
HDAC6.2	AL137696		intron retention	696	intron 6	CDS
HDAC6.3	BC005872		novel first exon	59	exon 1a	5'
HDAC6.4	BC011498		novel first exon final exon extension	83, 1313	exon 6	CDS

Appendices

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
HDAC6.5	AJ973509	HDAC6-1	novel first exon	24	exon 1b	CDS
HDAC6.6	AJ973527	HDAC6.10	whole exon deletion 3' loss	925	exons 22-24	CDS
HDAC6.7	AJ973511	HDAC6.14	whole exon deletion	150	exon 22	CDS
HDAC6.8	AJ973513	HDAC6.10	internal deletion	229	exon 25	CDS
HDAC6.9	AJ973515	HDAC6.10	whole exon deletion 3' loss	486	exons 23-24	CDS
HDAC6.10	AJ973516	HDAC6.10	whole exon deletion 3' loss	374	exons 23-24	CDS
HDAC6.11	AJ973526	HDAC6.13	whole exon deletion	123	exon 2	CDS
HDAC6.12	AJ973517 AJ973518	HDAC6.14	5' loss 3' loss	633	exons 23-24	CDS
HDAC6.13	AJ973519 AJ973520	HDAC6.14	whole exon deletion 3' loss	24	exons 22-23	CDS
HDAC6.14	AJ973521	HDAC6.10	3' loss	396	exon 25	CDS
HDAC6.15	AJ973523	HDAC6.14	whole exon deletion whole exon deletion 5' loss 3' loss	837	exons 22-25	CDS
HDAC6.16	AJ973524 AJ973525	HDAC6.10	whole exon deletion 5' loss 3' loss	797	exons 23-25	CDS
HDAC6.17	AJ973507 AJ973508	HDAC6.10	whole exon deletion 5' loss 3' loss	818	exons 23-25	CDS
TIMM17B.1	NM_005854		n.a.	n.a.	n.a.	n.a.
TIMM17B.2	AL529917		whole exon addition	103	exon 4a	CDS
TIMM17B.3	BF530129		whole exon addition 3' gain	150, 188	exon 4b , exon 1	CDS
TIMM17B.4	BC028017		whole exon deletion intron retention	621, 87	exon 4c, intron 5	CDS

Appendices

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
TIMM17B.5	AJ973566 AJ973567	TIMM17B-1	intron retention	246	intron 2	5' UTR
TIMM17B.6	AJ973568 AJ973569	TIMM17B-5	internal deletion	-170	exon 6	3' UTR
TIMM17B.7	AJ973570	TIMM17B-4	antisense	69, 71	n.a.	Anti
PQBP1.1	NM_005170		n.a.	n.a.	n.a.	n.a.
PQBP1.2	AB041836		whole exon deletion	285	exon 5	CDS
PQBP1.3	AB041834		intron retention	2113	introns 5,6	CDS
PQBP1.4	AB041835		intron retention	211	intron 5	CDS
PQBP1.5	BC012358		5' loss	-68	exon1	5' UTR
PQBP1.6	BC255007		5' loss	-132	exon 5	CDS
PQBP1.7	AB041837		3' gain	14	exon 5	CDS
PQBP1.8	AJ973535	PQBP1-2	3' gain	11	exon 1	5' UTR
PQBP1.9	AJ973536	PQBP1-2	intron retention	410	intron 1	5' UTR
PQBP1.10	AJ973538	PQBP1-7	whole exon addition	87	exon 3a	CDS
PQBP1.11	AJ973541	PQBP1-4	novel first exon	46	exon 1a	5' UTR
PQBP1.12	AJ973540	PQBP1-4	novel first exon	102	exon 1b	5' UTR
PQBP1.13	AJ973543	PQBP1-6	5' loss	-48	exon 3	CDS
PQBP1.14	AJ973545	PQBP1-7	internal deletion	21	exon 5	CDS
SLC35A2.1	D88146		n.a.	n.a.	n.a.	
SLC35A2.2	BI820134		final exon extension	1871	exon4	3' UTR
SLC35A2.3	D84454		3' loss	-590	exon 4	3' UTR
SLC35A2.4	BE902730		3' loss final exon	165	exon 4	3' UTR
PIM2.1	NM_002648		n.a.	n.a.	n.a.	n.a.
PCSK1N.1	NM_013271		n.a.	n.a.	n.a.	n.a.
PSCK1N.2	AW163271		novel first exon	297	5' UTR	5' UTR
AF207550.5.1	NM_017602		n.a.	n.a.	n.a.	n.a.
AF207550.5.2	AL137509		5' loss	-15	exon 4	CDS

Appendices

Variant	Sequence	Identified in screen	Description	Size change (+/- bp)	Location	Coding
AF207550.5.3	AK026260		novel final exon	-414	exon9	3' UTR
AF207550.5.4	BC011738		internal deletion	-211	exon 9	3' UTR
AF207550.5.5	AJ973485	AF207550.5-2	3' loss	-60	exon 4	CDS
AF207550.5.6	AJ973487	AF207550.5-3	intron retention	84	intron 4	CDS
AF207550.5.7	AJ973489 AJ973490	AF207550.5-3	5' gain 3' loss	-72	exons4,5	CDS
KCND1.1	NM_004979		n.a.	n.a.	n.a.	n.a.
KCND1.2	AJ005898		novel first exon	1278	5' UTR	5' UTR
GRIPAP1.1	NM_020137		n.a.	n.a.	n.a.	n.a.
GRIPAP1.2	AJ973501	GRIPAP1-3	3' loss	-97	exon 7	CDS
GRIPAP1.3	AJ973502	GRIPAP1-3	whole exon addition	75	exon 13a	CDS
GRIPAP1.4	AJ973504	GRIPAP1-2	intron retention	1413	intron 11	CDS
GRIPAP1.5	AJ973505	GRIPAP1-2	whole exon deletion	-151	exon 6	CDS

APPENDIX V Multiple sequence alignment of *PQBP1* transcripts

Alternating exon sequences are displayed in blue and black. Retained intron sequences are shown in aqua, deletions located within exons are displayed in red. The start and stop codons are also highlighted in green.

		*	20	*	40	*	60	*	80	*	100	*	120	
Reference	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 1	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 2	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 3	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 4	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 5	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 6	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 7	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 8	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 9	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 10	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 11	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 12	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 13	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 14	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								
Transcript 15	:	TCTCTGCTTCAGCT	ATGCCGCTGCCCGTTGCGCTGCAGACCCGCTTGGCCAAGAGAGGGCATCCTCAAACATCTGGAGCCTG	AACCAGAGGAAGAGATCATTGCCGAGGACTATGACGATG	:	120								

		*	140	*	160	*	180	*	200	*	220	*	240	
Reference	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 1	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 2	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 3	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 4	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 5	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 6	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 7	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 8	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 9	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 10	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	GTGAGCCTGGGTGAGGGGGAGCTAACTTCTGGCTTCACCCTTCCTGT	:	240									
Transcript 11	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 12	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 13	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 14	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAGGTGTTTCGACCCCTTCCTG	-----	:	193									
Transcript 15	:	ATCCTGTGGACTACGAGGCCACCAGGTTGGAGGGCCTACCACCAAGCTGGTACAAG	-----	:	176									

Appendices

	*	260	*	280	*	300	*	320	*	340	*	360		
Reference	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 1	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 2	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 3	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 4	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 5	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 6	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 7	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 8	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 9	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 10	:	GCTGACCTTGGTTGTGAGGTTTAGGGGGACACAAGGGAGGGAGCCTCGGGTGGAGGGTGTGGCATTAGGTATCTGCAGGACTCAAGTTGCTGCCTGCTGGGGCCTGGCTCCTCTGGGGT											:	360
Transcript 11	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 12	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 13	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 14	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 15	:	-----		-----		-----		-----		-----		-----	:	-

	*	380	*	400	*	420	*	440	*	460	*	480		
Reference	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 1	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 2	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 3	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 4	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 5	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 6	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 7	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 8	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 9	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 10	:	TGGAAGACTGTCTTTTCTCTCTTTTGAACGGAGTTTCACTCTTGTAG											:	480
Transcript 11	:	-----		-----		-----		-----		-----		-----	:	263
Transcript 12	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 13	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 14	:	-----		-----		-----		-----		-----		-----	:	-
Transcript 15	:	-----		-----		-----		-----		-----		-----	:	-

Appendices

Reference : -----* 500 * 520 * 540 * 560 * 580 * 600
Transcript 1 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 2 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 3 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 4 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 5 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 6 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 7 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 8 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 9 : CTGTCTCAGCCTCCCAGCGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 383
Transcript 10 : CTGTCTCAGCCTCCCAGCGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 600
Transcript 11 : CTGTCTCAGCCTCCCAGCGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 383
Transcript 12 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 13 : -----CGGGCTCCCTTACTACTGGAATGCAGAC----- : 221
Transcript 14 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 296
Transcript 15 : -----CGGGCTCCCTTACTACTGGAATGCAGACACAGACCTTGTATCCTGGCTCTCCCCACATGACCCCAACTCCGTGGTTACCAAATCGGCCAAGAAGCTCAGAAGC : 279

Reference : * 620 * 640 * 660 * 680 * 700 * 720
Transcript 1 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 416
Transcript 1 : AGTAATGCAG----- : 306
Transcript 2 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTC-----GGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 395
Transcript 3 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTC-----GGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 395
Transcript 4 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTC-----GGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 395
Transcript 5 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTC-----GGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 395
Transcript 6 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 416
Transcript 7 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 416
Transcript 8 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 416
Transcript 9 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 503
Transcript 10 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 720
Transcript 11 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 503
Transcript 12 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGC----- : 395
Transcript 13 : ----- : -
Transcript 14 : AGTAATGCAGATGCTGAAGAAAAGTTGGACCGGAGCCATGACAAGTCGGACAGGGGCCATGACAAGTCGGACCGCAGCCATGAGAAACTAGACAGGGGCCACGACAAGTCAGACCGGGGC : 416
Transcript 15 : AGTAATGCAG----- : 289

Appendices

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Reference      : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 536
Transcript 1  : ----- : -
Transcript 2  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 515
Transcript 3  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 515
Transcript 4  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAG----- : 437
Transcript 5  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 515
Transcript 6  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAG----- : 458
Transcript 7  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 536
Transcript 8  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 536
Transcript 9  : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 623
Transcript 10 : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 840
Transcript 11 : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 623
Transcript 12 : ----- : -
Transcript 13 : -----CGGGAAGAGGGCAAA : 236
Transcript 14 : CACGACAAGTCTGACAGGGATCGAGAGCGTGGCTATGACAAGGTAGACAGAGAGAGAGAGCGAGACAGGGAACGGGATCGGGACCGGGGTATGACAAGGCAGACCGGGAAGAGGGCAAA : 536
Transcript 15 : ----- : -

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Reference      : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 591
Transcript 1  : ----- : -
Transcript 2  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 570
Transcript 3  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGGGTAAGCTGGGCAGAATGGGGCTCGGTGAGACCAACAAGGTGCAGGGTGCCTGCGTGAGGAAGCC : 635
Transcript 4  : ----- : -
Transcript 5  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 570
Transcript 6  : ----- : -
Transcript 7  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGGGTAAGCTGGGCAGAATGGGGCTCGGTGAGACCAACAAGGTGCAGGGTGCCTGCGTGAGGAAGCC : 656
Transcript 8  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGGGTAAGCTGGGCAGAATGGGGCTCGGTGAGACCAACAAGGTGCAGGGTGCCTGCGTGAGGAAGCC : 656
Transcript 9  : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 678
Transcript 10 : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 895
Transcript 11 : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGGGTAAGCTGGGCAGAATGGGGCTCGGTGAGACCAACAAGGTGCAGGGTGCCTGCGTGAGGAAGCC : 743
Transcript 12 : ----- : -
Transcript 13 : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 291
Transcript 14 : GAACGGCGCCACCATCGCCGGGAGGAGCTGGCTCCCTATCCCAAGAGCAAGAAGG----- : 591
Transcript 15 : ----- : -

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Appendices

	*	980	*	1000	*	1020	*	1040	*	1060	*	1080		
Reference	:	-----											:	-
Transcript 1	:	-----											:	-
Transcript 2	:	-----											:	-
Transcript 3	:	TTCCCTCAAAAAGATGCCTGGACCTGGGGCTAGAGGAGGGTGTCTGTGGTACATGGCAGCCAGGGGCTTCATTTCTTCTTTGGGGTGGGGCTCAGTGATCAGGGGCTCCTGGTGCCTCTA											:	755
Transcript 4	:	-----											:	-
Transcript 5	:	-----											:	-
Transcript 6	:	-----											:	-
Transcript 7	:	TTCCCTCAAAAAGATGCCTGGACCTGGGGCTAGAGGAGGGTGTCTGTGGTACATGGCAGCCAGGGGCTTCATTTCTTCTTTGGGGTGGGGCTCAGTGATCAGGGGCTCCTGGTGCCTCTA											:	776
Transcript 8	:	TTCCCTCAAAAAGATGCCTGGACCTGGGGCTAGAGGAGGGTGTCTGTGGTACATGGCAGCCAGGGGCTTCATTTCTTCTTTGGGGTGGGGCTCAGTGATCAGGGGCTCCTGGTGCCTCTA											:	776
Transcript 9	:	-----											:	-
Transcript 10	:	-----											:	-
Transcript 11	:	TTCCCTCAAAAAGATGCCTGGACCTGGGGCTAGAGGAGGGTGTCTGTGGTACATGGCAGCCAGGGGCTTCATTTCTTCTTTGGGGTGGGGCTCAGTGATCAGGGGCTCCTGGTGCCTCTA											:	863
Transcript 12	:	-----											:	-
Transcript 13	:	-----											:	-
Transcript 14	:	-----											:	-
Transcript 15	:	-----											:	-

	*	1100	*	1120	*	1140	*	1160	*	1180	*	1200		
Reference	:	-----											:	656
Transcript 1	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	371
Transcript 2	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	635
Transcript 3	:	TTGAAGACTTTGCCCTGCCACTTCCACAGCAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	849
Transcript 4	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	502
Transcript 5	:	-----TAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	632
Transcript 6	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	523
Transcript 7	:	TTGAAGACTTTGCCCTGCCACTTCCACAGCAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	870
Transcript 8	:	TTGAAGACTTTGCCCTGCCACTTCCACAGCAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGGTAAGTGACAACCCCTCTTGACTCAGT											:	896
Transcript 9	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	743
Transcript 10	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	960
Transcript 11	:	TTGAAGACTTTGCCCTGCCACTTCCACAGCAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	957
Transcript 12	:	-----											:	-
Transcript 13	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	356
Transcript 14	:	-----TAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	653
Transcript 15	:	-----CAGTAAGCCGAAAGGATGAAGAGTTAGACCCCATGGACCCTAGCTCATACTCAGACGCCCCCGG-----											:	354

Appendices

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Reference      : -----*-----1220-----*-----1240-----*-----1260-----*-----1280-----*-----1300-----*-----1320-----GGCACGTGGTCAAC : 670
Transcript 1  : -----GGCACGTGGTCAAC : 385
Transcript 2  : -----GGCACGTGGTCAAC : 649
Transcript 3  : -----GGCACGTGGTCAAC : 863
Transcript 4  : -----GGCACGTGGTCAAC : 516
Transcript 5  : -----GGCACGTGGTCAAC : 646
Transcript 6  : -----GGCACGTGGTCAAC : 537
Transcript 7  : -----GGCACGTGGTCAAC : 884
Transcript 8  : ACGTGGACACCATCCTCCGGCCTCCTTCCTCCATTCTCATTGGGACCAGGTGGGCTGTGTCCGCCACATCACCCATCCCCATCCCCTGACTCTTTCACCGGCAGGGCACGTGGTCAAC : 1016
Transcript 9  : -----GGCACGTGGTCAAC : 757
Transcript 10 : -----GGCACGTGGTCAAC : 974
Transcript 11 : -----GGCACGTGGTCAAC : 971
Transcript 12 : ----- : -
Transcript 13 : -----GGCACGTGGTCAAC : 370
Transcript 14 : -----GGCACGTGGTCAAC : 667
Transcript 15 : -----GGCACGTGGTCAAC : 368
```

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Reference      : -----*-----1340-----*-----1360-----*-----1380-----*-----1400-----*-----1420-----*-----1440-----AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 789
Transcript 1  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 504
Transcript 2  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 768
Transcript 3  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 982
Transcript 4  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 635
Transcript 5  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 765
Transcript 6  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 656
Transcript 7  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 1003
Transcript 8  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 1136
Transcript 9  : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 876
Transcript 10 : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 1093
Transcript 11 : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 1090
Transcript 12 : -----TGTGCTCCGGGCCAATGCAGAGGCCT : 421
Transcript 13 : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGTTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 489
Transcript 14 : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 786
Transcript 15 : AGGACTCCCCAAGCGGAATGAGGCCAAGACTGGCGCTGACACCACAGCAGCTGGGCCCCCTCTCCAGCAGCGGCCGTATCCATCCCCAGGGGCTGTGCTCCGGGCCAATGCAGAGGCCT : 487
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Appendices

Reference	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 817
Transcript 1	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 533
Transcript 2	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 797
Transcript 3	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 1011
Transcript 4	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 665
Transcript 5	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 794
Transcript 6	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 685
Transcript 7	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 1032
Transcript 8	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 1165
Transcript 9	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 905
Transcript 10	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 1122
Transcript 11	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 1119
Transcript 12	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 450
Transcript 13	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 520
Transcript 14	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 815
Transcript 15	: CCCGAACCAAGCAGCAGGATTGAAGCTTC	: 516

APPENDIX VI Primers used to quantify *PQBP1* alternative transcripts

NAME	Targeted transcript	Sense (5' → 3')	Antisense (5' → 3')
<i>PQBP1.Q1</i>	all	CCTCAAACATCTGGAGCCTGAAC	TCGTCATAGTCCTCGGCAATG
<i>PQBP1.Q2</i>	1, 15	CCCAACTCCGTGGTTACCAA	GGCTTACTGCTGCATTACTGCTT
<i>PQBP1.Q2b</i>	1, 1,5	GGGCTCCCTTACTACTGGAA	GGCTTACTGCTGCATTACTGCTT
<i>PQBP1.Q3</i>	4, 6	GACCGCAGCCATGAGAACTAGA	CTTTCGGCTTACTGCTTGTGCATAGC
<i>PQBP1.Q4</i>	3, 7, 8, 11	GGCTCCTGGTGCCTCTATTG	CATCCTTTCGGCTTACTGCTG
<i>PQBP1.Q5</i>	8	CCTTCCTCCATTCCCTCATTGG	GGTGATGTGGCGGACACAG
<i>PQBP1.Q6</i>	9, 10, 11	CTGCCCGGGCTGGAGTG	GAGAGCCAGGATACAAGGTCTGTGT
<i>PQBP1.Q7</i>	12	GCTGAAGAAAAGTTGGACCGG	GGAGCACAGCCCCTGTCTAGT
<i>PQBP1.Q8</i>	13	GGAATGCAGACCGGGAAGAG	CCTCCCGCGATGGTG
<i>PQBP1.Q8b</i>	13	GGAATGCAGACCGGGAAGAG	CTTTCGGCTTACTGCCTTCT
<i>PQBP1.Q9</i>	5, 14	ATCGAGAGCGTGGCTATGG	CACCCTTTCGGCTTACCTTCT
<i>PQBP1.Q10</i>	all	CAGACCCGCTTGCCAAGA	TGGTGGTAGGCCCTCCAA
<i>PQBP1.Q11</i>	all	CTATGCCGCTGCCCGTTG	TTGTACCAGCTTGGTGGTA

APPENDIX VII Multiple sequence alignment of *PQBP1* peptides

Predicted open reading frames from the *PQBP1* alternative transcripts were identified and the amino acid sequences extracted from orf-Finder at NCBI. Transcript numbers refer to those outlined in section 5.2. Sequences were aligned using clustalw and edited in GeneDoc. Alternating exons are shown in grey, amino acids resulting from retained introns are shown in yellow, deleted regions are shown in red while alternative translation start sites are shown in green.

```

Ref   : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 1  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 2  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 3  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 4  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 5  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 6  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 7  : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 9a : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr10a : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr10b : ----- :
Tr11b : ----- :
Tr 12 : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 13 : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 14 : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :
Tr 15 : MPLPVALQTRLAKRGILKHLEPEPEEEEEIIAEDYDDDPVDYEATRLEGLPP :

```

```

Ref   : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 1  : WLSPHDPNSVVTKSAKKLRSSNA ----- :
Tr 2  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRSHEKL :
Tr 3  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRSHEKL :
Tr 4  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRSHEKL :
Tr 5  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRSHEKL :
Tr 6  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 7  : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 9a : ----- :
Tr10a : ----- :
Tr10b : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr11b : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 12 : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 13 : SWYKVFNPSCGLPYYWN ----- :
Tr 14 : WLSPHDPNSVVTKSAKKLRSSNADAEKLD RSHDKSDRGHDKSDRSHEKL :
Tr 15 : SWYKRAPLLLECRHRPCILALPT----- :

```

```

Ref   : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 1  : ----- :
Tr 2  : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 3  : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 4  : DRG-----HDKSDRGHDKSDRDRERGYDKQ----- :
Tr 5  : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 6  : DRG-----HDKSDRGHDKSDRDRERGYDKQ----- :
Tr 7  : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 9a : ----- :
Tr10a : ----- :
Tr10b : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr11b : DRG-----HDKSDRGHDKSDRDRERGYDKVDRERERD :
Tr 12 : DRG CAPGQCRGLPNQAAGLKI ----- :
Tr 13 : ----- :
Tr 14 : DRG-----HDKSDRGHDKSDRDRERGYGKVDRERERD :
Tr 15 : ----- :

```

Ref : RERDRDRGYDKADREEGKERRHHRREELAPYPKSKK----- :
 Tr 1: ----- :
 Tr 2: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKK----- :
 Tr 3: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKKGKLG RMGLGETNKV :
 Tr 4: ----- :
 Tr 5: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKK----- :
 Tr 6: ----- :
 Tr 7: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKKGKLG RMGLGETNKV :
 Tr 9a: ----- :
 Tr10a: ----- :
 Tr10b: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKK----- :
 Tr11b: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKKGKLG RMGLGETNKV :
 Tr 12: ----- :
 Tr 13: -----ADREEGKERRHHRREELAPYPKSKK----- :
 Tr 14: RERDRDRGYDKADREEGKERRHHRREELAPYPKSKK----- :
 Tr 15: ----- :

Ref : -----AVSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 1: -----AVSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 2: -----AVSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 3: QGALREEAFPQKDAWTWG----- :
 Tr 4: ----- :
 Tr 5: -----VSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 6: ----- :
 Tr 7: QGALREEAFPQKDAWTWG----- :
 Tr 9a: ----- :
 Tr10a: ----- :
 Tr10b: -----AVSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr11b: QGALREEAFPQKDAWTWG----- :
 Tr 12: ----- :
 Tr 13: -----AVSRKDEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 14: -----VSRKGEELDPMDPSSYS DAPRG TWSTGLPKR :
 Tr 15: ----- :

Ref : NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 1: NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 2: NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 3: ----- :
 Tr 4: ----- :
 Tr 5: NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 6: ----- :
 Tr 7: ----- :
 Tr 9a: ----- :
 Tr10a: ----- :
 Tr10b: NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr11b: ----- :
 Tr 12: ----- :
 Tr 13: NEAKTGADTTAVGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 14: NEAKTGADTTAAGPLFQQRYPYSPGAVLRANA EASRTKQQD----- :
 Tr 15: ----- :

APPENDIX VIII Primer combinations and sequences used in the preparation of T7 epitope::PBQP1 (variant) pCDNA.3 constructs

Primer combinations

Transcript	N-tag primers		C-tag primers	
Reference	N1S	N1A	C1S	C1A
1	N1S	N1A	C1S	C1A
2	N1S	N1A	C1S	C1A
3	N1S	N3A	C1S	C3A
4	N1S	N2A	C1S	C2A
5	N1S	N1A	C1S	C1A
6	N1S	N2A	C1S	C2A
7	N1S	N3A	C1S	C3A
9a	N1S	N4A	C1S	C4A
10a	N1S	N5A	C1S	C5A
10b	N2S	N1A	C2S	C1A
11b	N2S	N3A	C2S	C3A
12	X1S	X1A	X1S	X1A
13	N1S	N1A	C1S	C1A
14	N1S	N1A	C1S	C1A
15	N1S	N6A	C1S	C6A

Primer Sequences

Direction	Name	Sequence (5' → 3')
Sense	N1S	GGCCAAGCTTTAGGCTATGCCGCTGCCCGTTG
	N2S	GGCCAAGCTTTAGCTTATGGCAACCTCCGCCT
	C1S	GGCCGCGGCCGCTATGCCGCTGCCCGTGG
	C2S	GGCCGCGGCCGCTATGGCAACCTCCGCCT
	X1S	ATGCCGCTGCCCGTTGCGCT
	Antisense	N1A
N2A		GGCCGCTAGCCTGCTTGTTCATAGCCACGCTCT
N3A		GGCCGCTAGCGCCCCAGGTCCAGGCATCTTTT
N4A		GGCCGCTAGCCACCATTGCACTCCAGCCCGGG
N5A		GGCCGCTAGCTGTGGGAGAGCCAGGATACAA
N6A		GGCCGCTAGCGGAGGAAGGGTCGAACACCTTG
C1A		GGCCTCTAGATCAATCCTGCTGCTTGG
C2A		GGCCTCTAGATTACTGCTTGTTCATAGC
C3A		GGCCTCTAGACTAGCCCCAGGTCCAGG
C4A		GGCCTCTAGATCACACCATTGCACTCC
C5A		GGCCTCTAGATCATGTGGGAGAGCCA
C6A		GGCCTCTAGATCACCAGGAAGGGTCGA
X1A		CCAAGCTTCAATCCTGCTGCTT

APPENDIX IX Control primers used in real-time PCR analysis

Gene	Species	Sense (5' → 3')	Antisense (5' → 3')
GAPDH	Human Chinese	GAAGGTGAAGGTCGGAGTC	GAAGATGGTGATGGGATTTTC
ActB	Hamster	ACCAACTGGGACGACATGGAGAAGA	TACGACCAGAGGCATACAGGGACAA
LacZ		TTGAAAATGGTCTGCTGCTG	TATTGGCTTCATCCACCACA
Luc		TGCAGAGATCCTGTGTTTGG	GTACCAGCAACGCACTTTGA

