10. Appendix

10.1. Preparation of Poly-l-lysine-coated glass slides for cell array use

1) Clean the normal microscopy slides with the cleaning solution (70 ml 1,75 M NaOH, 240 ml Ethanol and 160 ml sterile H_2O) for 2 hours at room temperature, followed by three times wash with sterile H_2O.
2) Wash the slides with Acetone for 5 minutes, and let them dry shortly in the air.
3) Immerse the slides in the Vectabond Solution (350 ml Acetone and 7 ml Vectabond™ (VECTOR Laboratories, Inc., Burlingame, USA)) for 5 minutes.
4) Rinse the slides shortly by sterile H_2O for three times
5) Dry the slides in a 37 °C oven
6) Treat the slides with Poly-l-lysine Solution (20 ml Poly-l-lysine, 20 ml PBS, and 160 ml H_2O) in a plastic containers at 4°C for 45 minutes
7) Wash the slides with H_2O and let them dry in a sterile environment
8) Incubate the slide at 55°C for 40 minutes
9) Keep the slides in dark with vacuum before use

10.2. List of primer pairs used for the construction of Chr21 protein expression clones

Table A. 1 Primers used for the amplification of 89 Chr21 ORFs

Gene	Accession	Primer Name[a]	Fwd[b]	Rev
SAMSN1	NM_022136	SAMSN1_NM_022136	AAAAGCAGGCATGCTCAAGAGAAAGCCATCCAATG	AAGAAAGCTGGGTAATGCGTGTTCAGTCACTTGGC
NRIP1	X84373		Gateway™ entry clone obtained from RZPD	
NRIP1	X84373	NRIP1_KC_fwd	AAAAGCAGGCACCATGACTCATGGAGAAGAGCTTGG	AAGAAAGCTGGGTTTTCTGATTCTTTCTTTATCGTTAGCAC
BTG3	D64110	BTG3_D64110	AAAAGCAGGCATGAAGAATGAAATTGCTGCC	AAGAAAGCTGGGTAAGTTAGTGAGGTGCTAACATGT
C21orf91	AF239726	C21orf91_NM_017447	AAAAGCAGGCATGAACGAAGAGGAGCAGTTTGTAAAC	AAGAAAGCTGGGTAGCTGTTCGATGGCAACGTG
PPIA3L	X52851		Gateway™ entry clone obtained from RZPD	
PPIA3L	X52851	PPIAL3_C	AAAAGCAGGCACCATGGTCAACCCCACCGTGTTC	AAGAAAGCTGGGTTTTCGAGTTGTCCACAGTCAGC
C21orf74	AY077696	C21orf74_AY077696	AAAAGCAGGCATGGCTTATGTCTTTAATCTCAGCT	AAGAAAGCTGGGTCATTCATTTATTTAGCTGCTCATGTAA

ATP5A1	AL110183	ATP5A_AL110183	AAAAGCAGGCATGATTCTTCA GAGGCTCTTCA	AAGAAAGCTGGGTTTTATTTCTT CAGGCCTGGGG
GABPA	NM_002040	GABPA_KC_fwd	AAAAGCAGGCACCATGACTA AAAGAGAAGCAGAGGAGC	AAGAAAGCTGGGTTATTATCCTT TTCCGTTTGCAGAGAAG
GABPA	NM_002040	GABPA_NM_002040	AAAAGCAGGCATGACTAAAA GAGAAGCAGAGGAGC	AAGAAAGCTGGGTGGGGCTCAA TTATCCTTTTCCG
C21orf127	AF139682	DNMTA1_AF139682	AAAAGCAGGCATGGCAGGGG AGAACTTCGC	AAGAAAGCTGGGTGTATGCTAA GACTTGGTGAACTTGA
C21orf6	AK000056	C21orf6_BC012546	AAAAGCAGGCATGAAAATTG AGCTGTCCATGCA	AAGAAAGCTGGGTACTACTCTT GATGTCATTGTCCTTC
USP16	NM_006447	USP16_NM_006447	AAAAGCAGGCATGGGAAAGA AACGGACAAAGGGA	AAGAAAGCTGGGTCCATAAATG TGTTTCCAGAAAAAGTGC
CCT8	D13627	CCT8_C	AAAAGCAGGCACCATGAGTA AACAATATGGTAATGAAG	AAGAAAGCTGGGTTATCATTTTG GTCATCATCCCAGTC
CCT8	D13627	CCT8_D13627	AAAAGCAGGCATGAGTAAAC AATATGGTAATGAAGTA	AAGAAAGCTGGGTTTCAATCAT TTTGGTCATCATCCC
C21orf7	AF269164	C21orf7_AF269164	AAAAGCAGGCATGATCAGCA CAGCCAGGGTA	AAGAAAGCTGGGTAAAAATTTA AAGTTAGGACGAGCCC
C21orf7	AF269164	C21orf7_C	AAAAGCAGGCACCATGATCA GCACAGCCAGGGTAC	AAGAAAGCTGGGTTGGACGAGC CCTGCCTCTTC
BACH1	AB002803	BACH1_KC_fwd	AAAAGCAGGCACCATGTCTCT GAGTGAGAACTCGG	AAGAAAGCTGGGTTCTCATCAG TAGTACATTTATCAGTC
C21orf9	AY077697	C21orf9_AY077697	AAAAGCAGGCATGGAGGATG CAGCAAAAGG	AAGAAAGCTGGGTGCTGAAACC CCTAAATTAGAGC
C21orf108	NM_014825	KIAA0539_NM_014825_	AAAAGCAGGCATGCTCCTCAC CGCCGTAC	AAGAAAGCTGGGTCCGGCAGGA GTCAAGCATCT
C21orf63	BC038710	C21orf63_BC038710	AAAAGCAGGCATGCTTCTGCC GGGACGCGCACGCCAACC	AAGAAAGCTGGGTGTTTTCAGT AGAACTGGCCCATG
C21orf77	NM_018277	C21orf77_NM_018277_	AAAAGCAGGCATGGAGCGCC CTCTCATCTG	AAGAAAGCTGGGTGACAGATGG CACCAGCCTCA
C21orf59	AF282851	C21orf59_AF282851	AAAAGCAGGCATGGTTCTGCT GCACGTGA	AAGAAAGCTGGGTTGGTGAACT TCATCTTGGTCTC
C21orf66	AF153208	C21orf66_KC_fwd	AAAAGCAGGCACCATGGCAG ATCACCTTGAAGGC	AAGAAAGCTGGGTTAGAGAAGA CAACACAAGGCCTG
C21orf66	AF153208	C21orf66_NM_013329_	AAAAGCAGGCATGGCAGATC ACCTTGAAGGCC	AAGAAAGCTGGGTAGGCATGCA GAAACATGACTGG
C21orf55	NM_017833	C21orf55_AF462153	AAAAGCAGGCATGAATACAA TGTATGTGATGATGG	AAGAAAGCTGGGTTAAACATCA AAATGATCGTATTTTAATAA
CRYZL1	AK001293	CRYZL1_ak001293_	AAAGCAGGCATGAAAGGCTT ATATTTCCAAC	GCTGGGTTAATTAACCCACTGA GGTCTGAAAAC
ITSN1	AF114488	ITSN_AF114488	AAAAGCAGGCATGGCTCAGTT TCCAACACCTTT	AAGAAAGCTGGGTTGATTCATT GCTGGCTTGGGTC
MRPS6	BC010076	MRPS6_BC010076	AAAAGCAGGCATGCCCCGCT ACGAGCT	AAGAAAGCTGGGTAATCTTCTC ACTTCTTCCTCTTC
DSCR1	NM_004414		Gateway™ entry clone obtained from RZPD	
C21orf96	NM_025143	C21orf96_NM_025143_	AAAAGCAGGCATGGCCTCGG CCAAGGATG	AAGAAAGCTGGGTCCCCTGAGC TTGGGCCTATC
C21orf19	AF363446	C21orf19_AF363446	AAAAGCAGGCATGTCCAACC GAGTGGTCTGC	AAGAAAGCTGGGTGAGCTTCAG TGGACCGTGAGT
CHAF1B	NM_005441	CHAF1B_NM_005441_	AAAAGCAGGCATGAAAGTCA TCACTTGTGAAATAGCCTG	AAGAAAGCTGGGTTCCATGGAA GCCCTGGTCTC
HLCS	NM_000411	HLCS_C	AAAAGCAGGCACCATGGAAG ATAGACTCCACATGG	AAGAAAGCTGGGTTCCGCCGTT TGGGGAGGATG
HLCS	NM_000411	HLCS_NM_000411_	AAAAGCAGGCATGGAAGATA GACTCCACATGGATAATG	AAGAAAGCTGGGTGATTTCCAG ATGCATGGGCAC
DSCR3	NM_006052	DSCR3_NM_006052_	AAAAGCAGGCATGGGGACCG CCCTGGAC	AAGAAAGCTGGGTCAGATGGCC ACTCCCGTTCT
DYRK1A	NM_001396	DYRK1A_NM_001396_	AAAAGCAGGCATGCATACAG GAGGAGAGACTTCA	AAGAAAGCTGGGTGCTTTGCCC TCTTGTAGCGG
DSCR4	AB000099	DSCR4_AB000099	AAAAGCAGGCATGTCGTTAAT CATCTTGACGAG	AAGAAAGCTGGGTCCTTCAGGT TGATGGGCTTG
ETS2	NM_005239	ETS2_C	AAAAGCAGGCACCATGAATG ATTTCGGAATCAAGAAT	AAGAAAGCTGGGTTGTCCTCCG TGTCGGGCTGG

ETS2	NM_005239	ETS2_NM_005239_	AAAAGCAGGCATGAATGATTTCGGAATCAAGAATATGGACC	AAGAAAGCTGGGTGCCACTGCTTCTTGGCCACT
DSCR2	AJ006291	DSCR2_AJ006291	AAAAGCAGGCATGGCGGCCACGTTCTTC	AAGAAAGCTGGGTTGTTTAAGATCATGTATAAATGTTACTC
WDR9_3'	NM_033656_5663..6949	WDR9_NM_018963_	AAAAGCAGGCATGAACCCAATTTCAGGAAATCTGAACTG	AAGAAAGCTGGGTGCCAGCTTTCACCATAAATGCC
SH3BGR	BC006371	SH3BGR_BC006371	AAAAGCAGGCATGCCTCTGCTGCTCCTT	AAGAAAGCTGGGTGAAAAGGCCTAGGAATCTTCG
PCP4	X93349	PCP4_X93349	AAAAGCAGGCATGAGTGAGCGACAAGGTG	AAGAAAGCTGGGTTCCCACTAGGACTGAGACCC
MX1	NM_002462	MX1_C	AAAAGCAGGCACCATGGTTGTTTTCCGAAGTGGAC	AAGAAAGCTGGGTTACCGGGGAACTGGGCAAGC
MX1	NM_002462	MX1_NM_002462_	AAAAGCAGGCATGGTTGTTTCCGAAGTGGACATC	AAGAAAGCTGGGTTCTGAGGGTGGGGCTCTGTC
C21orf25	XM_032945	C21orf25_XM-032945	AAAAGCAGGCATGCAGGGCTACACGGCCT	AAGAAAGCTGGGTCCTACGTGCAGGGCTCCAC
TFF3	L08044	TFF3_L08044	AAAAGCAGGCATGCTGGGGCTGGTCCTG	AAGAAAGCTGGGTTGGAGGTGCCTCAGAAGGT
TFF2	BC032820	TFF2_BC032820	AAAAGCAGGCATGGGACGGCGAGACGCCC	AAGAAAGCTGGGTTCTTAGTAATGGCAGTCTTCCACA
TFF1	X00474	TFF1_X00474	AAAAGCAGGCATGGCCACCATGGAGAACAA	AAGAAAGCTGGGTTGTCTAAAATTCACACTCCTCTTC
UBASH3A	NM_018961	UBASH3A_NM_018961_	AAAAGCAGGCATGGCAGCGGGGGAGACG	AAGAAAGCTGGGTTTACAAAGGCGAAAGCCGGA
PDE9A	BC009047	PDE9A_BC009047	AAAAGCAGGCATGGGATCCGGCTCCTCCA	AAGAAAGCTGGGTCCGCTTTCCTCAGGCACA
PDE9A	BC009047	PDE9A_C	AAAAGCAGGCACCATGGGATCCGGCTCCTCCAG	AAGAAAGCTGGGTTGGCACAGTCTCCTTCACTG
WDR4	BC006341	WDR4_BC006341	AAAAGCAGGCATGGCGGGCTCTGTGGG	AAGAAAGCTGGGTCACGATCAGCAACTTAGCG
PKNOX1	BC007746	PKNOX1_BC007746	AAAAGCAGGCATGATGGCTACACAGACATTAAG	AAGAAAGCTGGGTCCCCTACTGCAGGGAGTCA
PKNOX1	BC007746	PKNOX1_KC_fwd	AAAAGCAGGCACCATGATGGCTACACAGACATTAAG	AAGAAAGCTGGGTTCTGCAGGGAGTCACTGTTCTC
U2AF1	BC001923	U2AF1_BC001923	AAAAGCAGGCATGGCGGAGTATCTGGCCT	AAGAAAGCTGGGTGGCTCAGAATCGCCCAGA
SNF1LK	U11494_ex	SNF1LK_U11494ex	AAAAGCAGGCATGGTTATCATGTCGGAGTTCAG	AAGAAAGCTGGGTGTCCTGCTCCTCCTCTAGGC
HSF2BP	AB007131_ex		Gateway™ entry clone obtained from RZPD	
HSF2BP	AB007131_ex	HSF2BP_KC_fwd	AAAAGCAGGCACCATGGGCGAAGCGGGCGCCGC	AAGAAAGCTGGGTTCACATTATGCTCCAGAGTGCGGAG
KIAA0179	XM_035973	KIAA0179_XM-035973	AAAAGCAGGCATGGCCCCCGCCATGCAGCCGGCCGAGATC	AAGAAAGCTGGGTTCCTCAGAAGAAATCCATAGCCC
PDXK	BC000123	PDXK_BC000123	AAAAGCAGGCATGGAGGAGGAGTGCCGG	AAGAAAGCTGGGTCGGGGCCCTCACAGCAC
C21orf97	AK024977	C21orf97_AK024977	AAAAGCAGGCATGTCCCCTTCCATCTCTGACC	AAGAAAGCTGGGTACCTCTGCCTCCCATCACCAA
D21S2056E	BC000380	D21S2056E_BC000380	AAAAGCAGGCATGGTTTCGCGCGTGCA	AAGAAAGCTGGGTCACATCACTCCCTGCGTTTC
C21orf33	BC003587	C21orf33_BC003587	AAAAGCAGGCATGGCGGCTGTGAGGGC	AAGAAAGCTGGGTTCCATGCGCGTCACTTTC
DNMT3L	BC002560	DNMT3L_BC002560	AAAAGCAGGCATGGCGGCCATCCCAGC	AAGAAAGCTGGGTTGACTCATTTATAAAGAGGAAGTGA
DNMT3L	BC002560	DNMT3L_KC_fwd	AAAAGCAGGCACCATGGCGGCCATCCCAGCCCTG	AAGAAAGCTGGGTTTAAAGAGGAAGTGAGTTCTGTTGAAAAATAC
C21orf30	AL117578_ex	C21orf30_AL117578ex	AAAAGCAGGCATGAGCTGCCCACCGTCCT	AAGAAAGCTGGGTCGGCATCAGGAAGCTAAGCC
UBE2G2	AF032456	UBE2G2_AF032456	AAAAGCAGGCATGGCGGGGACCGCGCTCAAGAGG	AAGAAAGCTGGGTGTCTCACAGTCCCAGAGACTT
C21orf69	AY035381	C21orf69_AY035381	AAAAGCAGGCATGGCTTGCCTGCGTCACA	AAGAAAGCTGGGTAGGTCATGGCTCCCTGCTATC

ADARB1a	NM_001112	ADARB1a_NM_001112_	AAAAGCAGGCATGGATATAGAAGATGAAGAAAACATGAGTTC	AAGAAAGCTGGGTCCGTGTCCCCCTACTCCCTC
PCBP3	BC012061	PCBP3_BC012061	AAAAGCAGGCATGGAGTCCAAGGTCTCAGAA	AAGAAAGCTGGGTCTGGGTAGGATTACAGCGTG
PCBP3	BC012061	PCBP3_C	AAAAGCAGGCACCATGGAGTCCAAGGTCTCAGAAG	AAGAAAGCTGGGTTCAGCGTGCCCATCCCGGTG
MCM3APAS	NM_018118	MCM3APAS_NM_018118_	AAAAGCAGGCATGACATATAACATCCAACAAGGGGC	AAGAAAGCTGGGTTCCATGTTCCCTCTGTCCTGG
MCM3AP	AB005543	MCM3AP_AB005543	AAAAGCAGGCATGCGGGCTTTCCCTGCTG	AAGAAAGCTGGGTTCAAATGTCCACCATGTCTAGCAGCG
RBM11	BC030196	RBM11_BC030196	AAAAGCAGGCATGTTCCCTGCTCAGGAGGAG	AAGAAAGCTGGGTTACTAGTATCTTTTCTTCTTCTTAGACT
STCH	NM_006948	STCH_NM_006948_	AAAAGCAGGCATGGCCAGAGAGATGACGATCTTA	AAGAAAGCTGGGTTCAAACAGGATCAATCTGGTCACG
CXADR	BC010536	CXADR_BC010536	AAAAGCAGGCATGGCGCTCCTGCTGTG	AAGAAAGCTGGGTAGGCTCTATACTATAGACCCATC
CHODL	BC009418	C21orf68_BC009418	AAAAGCAGGCATGAGCCGCGTGGTCTC	AAGAAAGCTGGGTAGTTATTATACTTCCATGCCACTTT
C21orf71	AF086441_ex	C21orf71_AF086441	AAAAGCAGGCATGGGCTCACCAATTAGACATAA	AAGAAAGCTGGGTATAAAATGGCTCACAAGTCACAG
MRPL39a	NM_017446	MRPL39_AK000458	AAAAGCAGGCATGGAGGCGCTGGCCAT	AAGAAAGCTGGGTAGAAAGTTATTAGGTAGATGTACATTC
APP	NM_000484	APP_NM_000484_	AAAAGCAGGCATGCTGCCCGGTTTGGCAC	AAGAAAGCTGGGTGCACAGCTGTCAAAAGGCGA
CYYR1	AF401639	CYYR1_BC036761	AAAAGCAGGCATGGACGCTCCGAGGCTAC	AAGAAAGCTGGGTATAGATTATTTCCTTGCGTTTCCAG
CLDN17	AJ250712	CLDN17_AJ250712	AAAAGCAGGCATGGCATTTTATCCCTTGCAAATTG	AAGAAAGCTGGGTTTAGACATAACTGGTGGAGGTCTTAC
CLDN17	AJ250712	CLDN17_Kozak_C	AAAAGCAGGCACCATGGCATTTTATCCCTTGCAAATTG	AAGAAAGCTGGGTTGACATAACTGGTGGAGGTCTTAC
CLDN8	NM_012132	CLDN8_BC020866	AAAAGCAGGCATGGCAACCCATGCCTTAGAAAT	AAGAAAGCTGGGTAAACATACACAACTACACATACTGACT
CLDN8	NM_012132	CLDN8_Kozak_C	AAAAGCAGGCACCATGGCAACCCATGCCTTAGAAAT	AAGAAAGCTGGGTTCACATACTGACTTCTGGAGTAG
KRTAP6-1	D86419_ex	C21orf103_D86419ex	AAAAGCAGGCATGTGTGGCAGCTACTACGGA	AAGAAAGCTGGGTATGGCATCCTCAATAATAGTAGCC
SOD1	X02317	SOD1_X02317	AAAAGCAGGCATGGCGACGAAGGCCGT	AAGAAAGCTGGGTGAATGTTTATTGGGCGATCCC
C21orf62	AF231922	C21orf62_AF231922	AAAAGCAGGCATGGCACCACCTTCCAGGCA	AAGAAAGCTGGGTGATACCTATCTCACGGCCTTATTTC
IL10RB	Z17227	IL10RB_Z17227	AAAAGCAGGCATGGCGTGGAGCCTTGG	AAGAAAGCTGGGTTTCTCAGAGCCTAGCTTTGG
IFNGR2	BC003624	IFNGR2_BC003624	AAAAGCAGGCATGCGACCGACGCTGCT	AAGAAAGCTGGGTTTGGTTCAAAGCGTTTGGAGA
C21orf4	AF045606	C21orf4_AF045606	AAAAGCAGGCATGGCAGGCTTCCTAGATAAT	AAGAAAGCTGGGTAGAAGTGATCTCAGGTCCATAG
RPS5L	U14970_ex	RPS5L_U14970ex	AAAAGCAGGCATGCAGATCAATGGCATTTCCC	AAGAAAGCTGGGTGAAAATCAGCGGTTGGACTTGT
KCNE2	NM_005136	KCNE2_Kozak_C	AAAAGCAGGCACCATGTCTACTTTATCCAATTTCACACAGACG	AAGAAAGCTGGGTTGGGGGACATTTTGAACCCAGCCG
KCNE2	NM_005136	KCNE2_NM_005136_	AAAAGCAGGCATGTCTACTTTATCCAATTTCACACAGACG	AAGAAAGCTGGGTCGTGGCACTGGCATCTCTTC
KCNE1	BC036452	KCNE1_BC036452	AAAAGCAGGCATGATCCTGTCTAACACCACAGC	AAGAAAGCTGGGTACATATCACGACCTGTAGCTCTC
KCNE1	BC036452	KCNE1_C	AAAAGCAGGCACCATGATCCTGTCTAACACCACAG	AAGAAAGCTGGGTTCGACCTGTAGCTCTCCAGG
CLDN14	AF314090	CLDN14_AF314090	AAAAGCAGGCATGGCCAGCACGGCCGTGCAGCTTCTG	AAGAAAGCTGGGTTGTGGGGACTCACACGTAGT
PSMD4	AF050199	PSMD4_AF050199	AAAAGCAGGCATGGTTACAGATAACACACATCTAACC	AAGAAAGCTGGGTGCTCTCATCAGTTCTCCGATTTT
DSCR5	NM_016430	DSCR5_NM-016430	AAAAGCAGGCATGGTACTTTACCTCGTGTGG	AAGAAAGCTGGGTCAGTTCAGTTTTTGGTGTAAAGTT

KCNJ6	NM_002240	KCNJ6_Kozak_C	AAAAGCAGGCACCATGGCCA AGCTGACAGAATCCATG	AAGAAAGCTGGGTTAACTTTGG ATTCATTCTCCAGG
KCNJ6	NM_002240	KCNJ6_NM_002240 _	AAAAGCAGGCATGGCCAAGC TGACAGAATCCATG	AAGAAAGCTGGGTGAAGAGAAG GGTTTGCCCAGC
KCNJ15	NM_002243	KCNJ15_Kozak_C	AAAAGCAGGCACCATGGATG CCATTCACATCGGCATG	AAGAAAGCTGGGTTGACATTGC TCTGTTGTAATAAAAGTG
KCNJ15	NM_002243	KCNJ15_NM_00224 3_	AAAAGCAGGCATGGATGCCA TTCACATCGGCATG	AAGAAAGCTGGGTTGTGGAAAC AGCTTGCAGGG
HMGN1	J02621	HMG14_J02621	AAAAGCAGGCATGCCCAAGA GGAAGGTCAG	AAGAAAGCTGGGTGGTTATTAA TCAGACTTGGCTTCT
HMGN1	J02621	HMGN1_C	AAAAGCAGGCACCATGCCCA AGAGGAAGGTCAG	AAGAAAGCTGGGTTATCAGACT TGGCTTCTTTCTCTC
WRB	Y12478	WRB_Y12478	AAAAGCAGGCATGAGCTCAG CCGCGGCCGACCACTGGGC	AAGAAAGCTGGGTCCTGTTCAG CTGAACGGATGA
B3GALT5	NM_006057	B3GALT5_C	AAAAGCAGGCACCATGGCTTT CCCGAAGATGAG	AAGAAAGCTGGGTTGACAGGCG GACAATCTTCC
B3GALT5	NM_006057	B3GALT5_NM_0060 57_	AAAAGCAGGCATGGCTTTCCC GAAGATGAGATTG	AAGAAAGCTGGGTACCGACATT CTGGCGTGGAT
ABCG1	X91249	ABCG1_X91249	AAAAGCAGGCATGGCCGCTTT CTCGGTC	AAGAAAGCTGGGTGCATTCAGG TGTTTTACCTCTC
TMPRSS3a	NM_024022	TMPRSS3a_NM_024 022_	AAAAGCAGGCATGGGGGAAA ATGATCCGCCTG	AAGAAAGCTGGGTTCTGCTCGT GTGCAGGTTCC
TSGA2	NM_080860	TSGA2_NM-080860	AAAAGCAGGCATGTCGGACC TGGGCTCGG	AAGAAAGCTGGGTCATCTTAGT CCTGGAGGTCTGAC
SLC37A1	NM_018964	SLC37A1_NM_0189 64_	AAAAGCAGGCATGGCTCGAC TCCCCGCT	AAGAAAGCTGGGTGGGGTGGGG TGTCACTGTTC
CBS	L00972_ex	CBS_L00972	AAAAGCAGGCATGGCCAAGT GTGAGTTCTTC	AAGAAAGCTGGGTCTCCGGACT TCACTTCTGGT
AGPAT3	BC011971	AGPAT3_BC011971	AAAAGCAGGCATGGGCCTGC TGGCCTT	AAGAAAGCTGGGTGCCATTAAT TATTCCTTTTTCTTAAAC
AGPAT3	BC011971	AGPAT3_Kozak_C	AAAAGCAGGCACCATGGGCC TGCTGGCCTT	AAGAAAGCTGGGTTTTCCTTTTT CTTAAACTCTTGG
PFKL	BC009919	PFKL_BC009919	AAAAGCAGGCATGGCCGCGG TGGACCT	AAGAAAGCTGGGTCCTCAGAAG CCCTTGTCCA

[a] The primer pairs used for the construct of N-terminal His_6-tagged expression clones were named after the gene symbol followed by gene accession number. The primer pairs used for the construct of C-terminal Myc-tagged expression clones were named after the gene symbol followed by "Kozak_C". [b] The Gateway™ entry clones of 4 genes could be ordered from RZPD, thus no PCR amplification was needed for the entry clones construction.

Table A. 2 Adapter primers used to install the complete *att*B sequences

Primers name	Primers sequence
*att*B1_adapter [a]	5' - G GGG ACA AGT TTG TAC AAA AAA GCA GGC T - 3' (forward)
*att*B2_adapter [a]	5' - GGG GAC CAC TTT GTA CAA GAA AGC TGG GT - 3' (reverse)
*att*B1_adap_ Kozak_C [b]	5' - G GGG ACA AGT TTG TAC AAA AAA GCA GGC ACC ATG- 3' (forward)
*att*B2_adap_ Kozak_C [b]	5' - GGG GAC CAC TTT GTA CAA GAA AGC TGG GTT- 3' (reverse)

[a] The pair of *att*B_adapter primers was used for construction of N-terminal His_6-tagged expression clones. [b] The pair of *att*B_adap_Kozak_C primers was used for construction of C-terminal Myc-tagged expression clones.