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APPENDIX

6.1 Sources of cloned ORFs

6.1.1 ORFs cloned from public cDNA clones

I.M.A.G.E. clones

[For more information, see <http://image.llnl.gov>]

Symbol	Accession	IMAGE CloneID	Tissue origin and state
ABCC13	AF418600.1	IMAGE:460420	Liver+Spleen, fetal normal
ABCG1	X91249.1	IMAGE:5198758	Brain, normal
AGPAT3	BC011971.1	IMAGE:4148915	Brain, cancer
ATP5A1	AL110183.1	IMAGE:3357779	Retina, cancer
ATP5O	X83218.1	IMAGE:4103001	Brain, cancer
BACE2	NM_012105.3	IMAGE:4868925	Melanocyte, cancer
BTG3	D64110.1	IMAGE:3859781	Ovary, cancer
C21orf4	AF045606.2	IMAGE:2161387	Kidney, normal
C21orf7	AF269164.1	IMAGE:4212641	Brain, cancer
C21orf9	AY077697.1	IMAGE:2630949	Uterus, cancer
C21orf13	BC031059.2	IMAGE:5271223	Testis, normal
C21orf19	AF363446.1	IMAGE:4851517	B-cell, normal
C21orf33	BC003587.1	IMAGE:2822714	Lung, cancer
C21orf56	AL136871.1	IMAGE:3949357	Ovary, cancer
C21orf59	AF282851.1	IMAGE:2782693	Brain, normal
C21orf63	BC038710.1	IMAGE:4813873	Brain, normal
C21orf69	AY035381.1	IMAGE:1705552	Heart, normal
C21orf74	AY077696.1	IMAGE:1734396	Testis, normal
C21orf97	AK024977.1	IMAGE:3536686	Lung, cancer
C21orf119	NM_032910.2	IMAGE:3945901	Lung, cancer
C21orf121	NM_198078.1	IMAGE:5271985	Testis, normal
C21orf122	NM_032653.1	IMAGE:3633193	Uterus, cancer
C21orf127	AF139682.1	IMAGE:4640080	Melanocyte, cancer
C21orf128	NM_152507.1	IMAGE:5207414	Pool, normal
CBR1	J04056.1	IMAGE:3050837	Melanocyte, cancer
CBR3	BC002812.2	IMAGE:3637434	Placenta, cancer
CBS	L00972.1	IMAGE:2675094	Uterus, cancer
CCT8	D13627.1	IMAGE:2266509	Gingiva, normal
CHODL	BC009418.1	IMAGE:3509743	Brain, cancer
CLDN8	NM_012132.3	IMAGE:4594155	Kidney, normal
CLDN14	AF314090.1	IMAGE:2832338	Pancreas, cancer
COL6A1	NM_001848.1	IMAGE:6598940	Ovary, cancer
COL6A2	BC002484.2	IMAGE:3347413	Kidney, cancer
CSTB	L03558.1	IMAGE:2900656	Placenta, cancer
CXADR	BC010536.1	IMAGE:3456544	HeLa, cancer
CYYR1	AF401639.1	IMAGE:5588436	Ovary, normal
D21S2056E	BC000380.2	IMAGE:2820455	Lung, cancer

DNMT3L	BC002560.2	IMAGE:3138514	Placenta, cancer
DSCR2	AJ006291.1	IMAGE:2961575	Muscle, cancer
DSCR4	AB000099.1	IMAGE:2369711	Pool, normal
DSCR5	NM_016430.2	IMAGE:4281552	Brain, normal
HMG1	J02621.1	IMAGE:6501871	Uterus, cancer
IFNAR1	NM_000629.1	IMAGE:4932084	Brain, cancer
IFNAR2	BC002793.2	IMAGE:3626374	Uterus, cancer
IFNGR2	BC003624.2	IMAGE:2967074	Melanocyte, cancer
IL10RB	Z17227.1	IMAGE:3544611	Kidney, cancer
ITGB2	BC005861.2	IMAGE:3532902	Muscle, cancer
ITSN1	AF114488.1	IMAGE:6420600	Lung, cancer
JAM2	AF255910.1	IMAGE:4616238	Lung, normal
KCNE1	BC036452.1	IMAGE:5266786	Testis, normal
KIAA0179	XM_035973.5	IMAGE:4821672	Testis, normal
LRRC3	AB058646.1	IMAGE:6178213	Ganglion, normal
MCM3AP	AB005543.1	IMAGE:4099986	Brain, cancer
MRPS6	BC010076.2	IMAGE:4304420	Uterus, cancer
MX2	NM_002463.1	IMAGE:5182160	Pool, normal
NCAM2	NM_004540.1	IMAGE:5315109	Brain, normal
NDUFV3	BC021217.2	IMAGE:4302265	Uterus, cancer
OLIG1	XM_170977.2	IMAGE:4944525	Brain, cancer
OLIG2	AF221520.1	IMAGE:5300879	Brain, normal
PCBP3	BC012061.1	IMAGE:4637826	Lung, cancer
PCP4	X93349.1	IMAGE:4345740	Adrenal gland, cancer
PDE9A	BC009047.1	IMAGE:3874635	Retina, cancer
PDXK	BC000123.1	IMAGE:3352536	Retina, cancer
PFKL	BC009919.2	IMAGE:3009907	Muscle, cancer
PKNOX1	BC007746.2	IMAGE:4099156	Muscle, cancer
PRMT2	BC000727.2	IMAGE:3506339	Kidney, cancer
PTTG1IP	Z50022.1	IMAGE:2823814	Lung, cancer
RBM11	BC030196.1	IMAGE:5199053	Brain, normal
S100B	NM_006272.1	IMAGE:3543825	Melanocyte, cancer
SH3BGR	BC006371.2	IMAGE:4138452	Muscle, cancer
SLC19A1	BC003068.2	IMAGE:3509422	Brain, cancer
SOD1	X02317.1	IMAGE:3140145	Placenta, cancer
SUMO3	BC008420.1	IMAGE:3505840	Kidney, cancer
TCP10L	NM_144659.3	IMAGE:5163416	Brain, normal
TFF1	X00474.1	IMAGE:2223790	Pancreas, cancer
TFF2	BC032820.1	IMAGE:5184770	Pool, normal
TFF3	L08044.1	IMAGE:4696566	Lung, normal
U2AF1	BC001923.1	IMAGE:2823296	Lung, cancer
UBE2G2	AF032456.1	IMAGE:3536171	Lung, cancer
USP25	NM_013396.2	IMAGE:3920963	Melanocyte, cancer
WDR4	BC006341.2	IMAGE:4080041	Uterus, cancer
WRB	Y12478.1	IMAGE:3865141	Ovary, cancer

DKFZ clones

For more information, see <http://www.imagenes-bio.de>

Symbol	Accession	IMAGE CloneID	Tissue origin and state
C21orf30	AL117578.1	DKFZp434C128	Testis, normal
C21orf25	XM_032945.3	DKFZp686G1128	Pool, normal
MRPL39a	NM_017446.3	DKFZp762L094	Melanocyte, cancer

6.1.2 ORFs cloned from cDNA

Symbol	Accession	cDNA tissue origin and state
ADAMTS1	NM_006988.2	HeLa, cancer
ADAMTS5	NM_007038.2	HeLa, cancer
ADARB1	NM_001112.2	Brain, normal
AIRE-1	NM_000383.1	Pool, normal
ANKRD21	NM_174981.2	Pool, normal
APP	NM_000484.2	Lung, normal
B3GALT5	NM_006057.1	Pancreas, normal
BACH1	NM_001186.2	Pool, normal
BRWD1	NM_018963.1	Brain, normal
C21orf2	NM_004928.1	HeLa, cancer
C21orf5	NM_005128.1	HeLa, cancer
C21orf18	NM_017438.2	Placenta, normal
C21orf41	AY081145.1	HeLa, cancer
C21orf42	AY035382.1	HeLa, cancer
C21orf45	AF231921.1	Testis, normal
C21orf51	NM_058182.3	HeLa, cancer
C21orf55	NM_017833.1	Testis, normal
C21orf58	AY039243.1	Pool, normal
C21orf62	AF231922.1	Brain, normal
C21orf66	AF153208.1	Testis, normal
C21orf67	AF380178.1	HeLa, cancer
C21orf70	BC009341.2	HeLa, cancer
C21orf77	NM_018277.1	Ovary, normal
C21orf79	AL117624.1	Pool, normal
C21orf81	NM_153750.1	Pool, normal
C21orf82	NM_153751.1	Pool, normal
C21orf84	NM_153752.1	Pool, normal
C21orf86	NM_153454.1	Pool, normal
C21orf87	NM_153455.1	Pool, normal
C21orf88	NM_153754.1	Pool, normal
C21orf90	NM_153204.1	Pool, normal
C21orf91	AF239726.1	Brain, normal
C21orf93	NM_145179.1	Pool, normal
C21orf94	NM_145180.2	Pool, normal
C21orf96	NM_025143.1	Thymus, normal
C21orf98	AK023499.1	Pool, normal
C21orf99	NM_153773.1	Pool, normal
C21orf100	NM_145033.2	Pool, normal
C21orf106	D80006.1	Lung, normal
C21orf109	AF490769.1	HeLa, cancer
C21orf114	AF304443.1	Pool, normal
C21orf115	AF269287.1	Pool, normal
C21orf116	AF130090.1	Pool, normal
C21orf117	BC009878.2	Pool, normal
C21orf118	NM_199174.1	Pool, normal
C21orf123	NM_199175.1	Pool, normal
C21orf129	AK057397.1	Pool, normal
CHAF1B	NM_005441.2	Brain, normal
CLIC6	AK092733.1	Pool, normal
COL18A1	NM_030582.2	HeLa, cancer
CRYAA	U05569.1	Placenta, normal
CRYZL1	AK001293.1	HeLa, cancer
DONSON	AL157441.1	HeLa, cancer
DSCAM	NM_001389.3	HeLa, cancer
DSCR3	NM_006052.1	Brain, normal
DSCR6	NM_018962.1	Brain, normal
DSCR8	NM_032589.2	Testis, normal
DSCR9	NM_148675.2	Pool, normal

DSCR10	NM_148676.1	Pool, normal
DYRK1A	NM_001396.2	HeLa, cancer
ERG	M17254.1	HeLa, cancer
ETS2	NM_005239.4	Placenta, normal
FAM3B	AF375989.1	Pool, normal
FTCD	AF169017.1	Kidney, normal
GABPA	NM_002040.1	Brain, normal
GART	NM_000819.3	HeLa, cancer
GRIK1	L19058.1	HeLa, cancer
HLCS	NM_000411.3	Testis, normal
HUNK	NM_014586.1	Brain, normal
ICOSLG	AB014553.1	Brain, normal
KCNE2	NM_005136.2	Heart, normal
KCNJ6	NM_002240.2	Pancreas, normal
KCNJ15	NM_002243.3	Leukocyte, normal
LSS	NM_002340.1	HeLa, cancer
MCM3APAS	NM_018118.1	Brain, normal
MORC3	NM_015358.1	HeLa, cancer
MX1	NM_002462.2	Lung, normal
PCNT2	NM_006031.3	HeLa, cancer
POFUT2	NM_015227.3	HeLa, cancer
PRDM15	XM_029600.2	Pool, normal
PRSS7	NM_002772.1	Small intestine, normal
PSMD4	AF050199.1	Placenta, normal
PWP2	NM_005049.1	HeLa, cancer
RIPK4	NM_020639.1	HeLa, cancer
RPS5L	U14970.1	HeLa, cancer
RUNX1	NM_001754.3	Pool, normal
SAMSN1	NM_022136.2	Small intestine, normal
SFRS15	AB032998.1	HeLa, cancer
SIM2	NM_005069.2	Pool, normal
SLC5A3	AF027153.1	Brain, normal
SLC37A1	NM_018964.2	Pancreas, normal
SNF1LK	U11494.2	HeLa, cancer
SON	AF380180.1	HeLa, cancer
STCH	NM_006948.3	Placenta, normal
SYNJ1	NM_003895.1	HeLa, cancer
TIAM1	NM_003253.1	HeLa, cancer
TMEM1	U19252.1	HeLa, cancer
TMPRSS2	NM_005656.2	Prostate, normal
TMPRSS3a	NM_024022.1	Liver, normal
TPTE	NM_013315.1	Testis, normal
TRPC7	NM_003307.3	HeLa, cancer
TSGA2	NM_080860.2	Testis, normal
TTC3	D83077.1	HeLa, cancer
UBASH3A	NM_018961.2	Leukocyte, normal
UMODL1	AK093654.1	Pool, normal
URB1	NM_014825.1	Brain, normal
USP16	NM_006447.2	Small intestine, normal
ZNF294	XM_047829.3	HeLa, cancer
ZNF295	XM_016999.2	Pool, normal

6.1.3 ORFs cloned from genomic DNA

Symbol	Accession	genomic DNA tissue origin and state
C21orf71	AF086441.1	HeLa, cancer
H2BFS	NM_017445.1	HeLa, cancer
KRTAP6-1	NM_181602.1	HeLa, cancer

6.1.4 ORFs obtained from public Gateway clones

Gateway clones from the RZPD

[For more information, see <http://www.imagenes-bio.de>]

Symbol	Accession	RZPD CloneID	Tissue origin and state
C21orf6	NM_016940.1	IOH12821	unknown
DSCR1	NM_004414.5	RZPDo834H126D	Lung, cancer
HSF2BP	CR457067.1	RZPDo834H0411D	HeLa, cancer
NRIP1	BC040361.1	IOH25775	unknown
PPIAL3	CR456707.1	RZPDo834F113D	Bone marrow, cancer

Gateway ORFeome clones from the Harvard Institute of Proteomics

[For more information, see <http://www.hip.harvard.edu>]

Symbol	Accession	ORFeome CloneID
ADAMTS1	BC036515.2	11025@F05
ATP50	BC021233.2	11046@A07
C21orf2	BC031300.1	31016@D09
C21orf29	BC021197.2	11068@C10
C21orf45	BC042917.1	31023@C02
C21orf51	BC015596.2	11081@B05
C21orf70	BC009341.2	31040@E12
COL6A1	BC052575.1	31025@B07
CRYAA	BC069528.1	31026@D03
DIP2A	BC038443.1	11025@B06
DIP2A	BC046176.1	31028@G04
DIP2A	BC033718.1	31045@F07
DSCR8	BC015981.1	11081@G01
ERG	BC040168.1	31006@E07
ICOSLG	BC064637.1	31013@F03
JAM2	BC017779.1	31020@A06
LSS	BC035638.1	11024@D04
MRAP	BC062721.1	31034@G01
POFUT2	BC011044.1	31027@A09
SETD4	BC002898.2	11053@B02
TMEM1	BC046241.1	31033@A01
TMPRSS2	BC051839.1	31010@D03
TPTE	BC028719.1	11089@E03
USP25	BC015930.1	11063@F10
USP25	BC075792.1	31032@G06

6.2 List of primer sequences

6.2.1 Primer for ORF cloning

To allow for the introduction into Gateway entry vectors by recombinatorial cloning, the following extensions were added to all primers for ORF cloning:

Forward primer extension (partial attB1 site): 5'– AAAA GCA GGC ... –3'

Reverse primer extension (partial attB2 site): 5'– AA GAA AGC TGG GT ... –3'

In a second PCR, the full attB sites were installed using these adapter primers:

Forward adapter: 5'– GGGGACAAGTTTGTAC AAA AAA GCA GGC ATG –3'

Reverse adapter: 5'– GGGGACCACTTTGTA CAA GAA AGC TGG GT –3'

Pre-synthesized primers obtained from the RZPD

Symbol	Accession	Forward primer (5'–3')	Reverse primer (5'–3')
ADAMTS1	NM_006988	ATGGGGAACCGGGAGCGG	TGCACCAGCCCTTCCTCACT
ADAMTS5	NM_007038	ATGCTGCTCGGGTGGGCG	GCATCGGTGCTGAATCCTCC
ADARB1a	NM_001112	ATGGATATAGAAGATGAAGAAAACATGAGTTC	CCGTGTCCCCTACTCCCTC
ADARB1c	NM_015834	ATGGATATAGAAGATGAAGAAAACATGAGTTC	CCTCAGTGTACCTTGGCGGC
AIRE-1	NM_000383	ATGGCGACGGACGCGCG	CGGCTTCCAGGACTGAGGAA
AIRE-2	NM_000658	ATGTGGTTGGGTGTACAGTTCCGG	CGGCTTCCAGGACTGAGGAA
AIRE-3	NM_000659	ATGTGGTTGGGTGTACAGTTCCGG	CGAAGGTGTGCTCGCTCAGA
ANKRD3	NM_020639	ATGGAGGGCGACGGCGG	GATCGTTCATCCCCACGAG
APP	NM_000484	ATGCTGCCCGTTTGGCAC	GCACAGCTGTCAAAGGCGA
B3GALT5	NM_006057	ATGGCTTCCCGAAGATGAGATG	ACCGACATCTGGCGTGGAT
BACE2	NM_012105	ATGGGCGCACTGGCCCC	AGATTGAAGACGGGTGGGCA
BRWD1	NM_018963	ATGAACCCAATTTTCAGGAAATCTGAACTG	GCCAGCTTTCACCATAAATGCC
C21orf2	NM_004928	ATGAAGCTGACGCGGAAGATGG	AACCGGGAGGCTTTTGTGT
C21orf5	NM_005128	ATGGATCCAGAAGAGCAGGAGC	CCACCGCACCTAGCTGAAA
C21orf18	NM_017438	ATGCAGAAAGGAAAAGGGAGAACAAG	GCGCTTCGGTGAATCAGGT
C21orf66	NM_013329	ATGGCAGATCACCTTGAAGGCC	AGGCATGCAGAAACATGACTGG
C21orf77	NM_018277	ATGGAGCGCCCTCTCATCTG	GACAGATGGCACCAGCCTCA
C21orf78	NM_017833	ATGAATACAATGTATGTGATGATGGCTCAG	CATCAAAATGGACTTTTTGCCTGGT
C21orf91	NM_017447	ATGAACGAAGAGGAGCAGTTTGTAAAC	AGCTGTTTCGATGGCAACGTG
C21orf96	NM_025143	ATGGCCTCGGCCAAGGATG	CCCCTGAGCTTGGGCCTATC
CHAF1B	NM_005441	ATGAAAGTCATCACTTGTGAAATAGCCTG	TCCATGGAGCCCTGGTCTC
CLDN8	NM_012132	ATGGCAACCCATGCCTTAGAAATC	CTACACATACTGACTTCTGGAGTAGACGCT
COL18A1	NM_030582	ATGGCTCCCTACCCCTGTG	CTACTTGGAGGCAGTCAAGAAGCTGT
CRYZL1	AK001293	ATGAAAGGCTTATATTTCCAAC	TAATTAACCCACTGAGGTCTGAAAAC
DSCAM	NM_001389	ATGTGGATACTGCTCTCTCTTG	CGTGGAGCGATCATCAATGT
DSCR3	NM_006052	ATGGGACCGCCCTGGAC	CAGATGGCCACTCCCGTTCT
DSCR6	NM_018962	ATGGAGCCCGAAGCGGCG	AGTGTCTGGCTCGGGTGTG
DSCR8	NM_032589	ATGAAGGAGCCTGGACCCAAC	TCACGGCATGAATGAATGGACT
DYRK1A	NM_001396	ATGCATACAGGAGGAGAGACTTCA	GCCTTGGCCCTTGTAGCCG
ETS2	NM_005239	ATGAATGATTTTCGGAATCAAGAATATGGACC	GCCACTGCTTCTTGGCCACT
GABPA	NM_002040	ATGACTAAAAGAGAAGCAGAGGAGC	GGGGCTCAATTATCCTTTTCCG
GART	NM_000819	ATGGCAGCCGAGTACTTATAATG	TCATTCTCTTTAACCCACAGATCTTGCC
HLCS	NM_000411	ATGGAAGATAGACTCCACATGGATAATG	GATTTCAGATGCATGGGCAC
HUNK	NM_014586	ATGCCGCGCGCGCGG	GGTTGTGCAAGGCTTTGGGTG
IFNAR1	NM_000629	ATGATGGTTCCTCCTGGG	AGGACCTCAGGCTCCCAGTGT
KCNE2	NM_005136	ATGTCTACTTTATCCAATTTACACAGACG	CGTGGCACTGGCATCTCTTC
KCNJ15	NM_002243	ATGGATGCCATTCACATCGGCATG	TGTGGAACAGCTTGCAGGG
KCNJ6	NM_002240	ATGGCCAAGCTGACAGAATCCATG	GAAGAGAAGGGTTTGCCCAGC
KIAA0539	NM_014825	ATGCTCCTCACCCCGGTAC	CCGGCAGGAGTCAAGCATCT
KIAA0958	NM_015227	ATGGCGACACTGACTTCGTC	TGCCAACAGCCTGCTATGGA
LSS	NM_002340	ATGACGGAGGGCACGTGTC	CTGGCCCCAGATTCACATC
MCM3APAS	NM_018118	ATGACATATAACATCCAACAAGGGG	TCCATGTTCCCTCTGTCTG
MX1	NM_002462	ATGGTTGTTTCCGAAGTGGACATC	TCTGAGGGTGGGGCTCTGTC
MX2	NM_002463	ATGTCTAAGGCCCCACAAGCCTTG	CAAAGCAGAAGCGGCATCTC
NCAM2	NM_004540	ATGAGCCTCCTCTCTCTTC	GGATCCATGGGCCAGGAGTA
PCNT2	NM_006031	ATGGAAGTTGAGCAAGAGCAGCG	CGCAGGAAAGAGCCATGACA
PRSS7	NM_002772	ATGGGGTCGAAAAGAGGCATATCT	TTTGTTCCTGGCCCCCTA

6. Appendix

PWP2H	NM_005049	ATGAAGTTCGCTTACCGGTTTTCAAATTTG	CACAATCCAACGCTGCAACC
RUNX1	NM_001754	ATGCGTATCCCCGTAGATGCC	GGGCTGACCTACAGCGAGA
SAMSN1	NM_022136	ATGCTCAAGAGAAGCCATCCAATG	AATGCGGTTCAGTCACTTGGG
SIM2	NM_005069	ATGAAGGAGAAGTCCAAGAATGCG	GCGGGTCCAATTC AACAG
SIM2s	NM_009586	ATGAAGGAGAAGTCCAAGAATGCG	TCTCAGCACATGGGAGCTGG
SLC37A1	NM_018964	ATGGCTCGACTCCCCGCT	GGGGTGGGGTGTCACTGTTC
STCH	NM_006948	ATGGCCAGAGAGATGACGATCTTA	TCAAACAGGATCAATCTGGTCACG
SYNJ1	NM_003895	ATGGCGTTCAGTAAAGGATTCGGG	CGGGCTGGCGTTATCTTTCTGT
TIAM1	NM_003253	ATGGGAAACGCAGAAATCAACATG	GGGACATCTTTGTCGACGG
TMPRSS2	NM_005656	ATGGCTTTGAACTCAGGGTCACC	GGATTAGCCGCTGCGCCCTCA
TMPRSS3a	NM_024022	ATGGGGGAAAAATGATCCGCGCTG	TCTGCTCGTGTGCAGGTTCC
TMPRSS3c	NM_032404	ATGTGCTCCGATGACTGGAAGG	TCTGCTCGTGTGCAGGTTCC
TPTE	NM_013315	ATGAATGAAAGTCTGATCCGACTG	GAACATGTGGCAGGTTGGGA
TRPC7	NM_003307	ATGGAGCCCTCAGCCCTG	AGAAGCCCTGGTTTCTGGGG
UBASH3A	NM_018961	ATGGCAGCGGGGAGACG	TTACAAAGGCGAAAGCCGGA
USP16	NM_006447	ATGGGAAAGAAACGGACAAGGGA	CCATAAATGTGTTTCCAGAAAAAGTGC
USP25	NM_013396	ATGACCGTGGAGCAGAACGTG	CGCCATGCGATTTTTCAGCTT

Primers designed using GenomePRIDE

Symbol	Accession	Forward primer (5'-3')	Reverse primer (5'-3')
ABCC13	AF418600	ATGCTCTCCAGTACGCAGAAC	CTCTTTCATCATGATGGAGCCAA
ABCG1	X91249	ATGGCCGCTTTCTCGGCT	GCATTCAGGTGTTTTACCTCTC
AGPAT3	BC011971	ATGGCCGCTGTTGGCCTT	GCCATTAATTAATTCCTTTAAAC
ATP5A	AL110183	ATGATTCCTCAGAGGCTCTTCA	TTTATTTCTCAGGCTGGGG
ATP50	X83218	ATGGCTGCCCCAGCAGT	ACTTTTAGACAATCTCCCGCAT
BANP	BC009424	ATGATGTCGGAAACACGACCTG	TCACTGAATCTGGATGGCCCC
BTG3	D64110	ATGAAGAATGAAATGCTGCC	AAGTAGTGAGGTGCTAACATGT
C21orf4	AF045606	ATGGCAGGCTTCCTAGATAAT	AGAAGTGATCTCAGGTCCATAG
C21orf6	BC012546	ATGAAAATTGAGCTGTCCATGCA	ACTACTCTTGATGTCATTTGCTTC
C21orf7	AF269164	ATGATCAGCACAGCCAGGTA	AAAAATTTAAAGTTAGGACGAGCC
C21orf9	AY077697	ATGGAGGATGCAGCAAAAGG	GCTGAAACCCCTAAATTAGAGC
C21orf11	AF375989	ATGCGCCATTGGCTGG	GCAGTGTACAGTTCGTTCT
C21orf13	BC031059	ATGTCTTTGGCTGATCTAACAAAA	AGAATGCATTAGGATATTGATATTT
C21orf19	AF363446	ATGTCCAACCGAGTGGTCTGC	GAGCTTCAGTGGACCGGTGAT
C21orf25	XM_032945	ATGCAGGGCTACACGGCCT	CCTACGTGCAGGGCTCCAC
C21orf30	AL117578	ATGAGCTGCCACCGTCTCT	CGGCATCAGGAAGCTAAGCC
C21orf33	BC003587	ATGGCGGCTGTGAGGGC	TCCATGCGCGTCACTTTC
C21orf41	AY081145	ATGTTGTTGAGAGAGATAACATATTCA	GAATGTCAATGGAAAGCCGTGTG
C21orf42	AY035382	ATGTTTTCTCTGTTTATTGAGAACAGAT	TTATTTCAGGAGTCATCTTTCTTGC
C21orf45	AF231921	ATGGCAGGCGTTTCGGTCT	CTAGAGTTCAGCTTTTACAAGTG
C21orf51	BC015596	ATGAATTGGAAGGTTCTTGAGCAC	ATGGCAGAATCTTCAGTTATCTTTTT
C21orf55	AF462153	ATGAATACAATGTATGTGATGATGG	TAAACATCAAAATGATCGTATTTTAAATAA
C21orf56	AL136871	ATGGTCCGGCCTAAGAAGG	CTCACAGGCGAAGAGGG
C21orf58	AY039243	ATGCTGGACTCATCAGCAGC	AAAACCTCAGGGTGGGCCAGG
C21orf59	AF282851	ATGGTTCGCTGCACGTGA	TGGTGAACCTCATCTTGGTCTC
C21orf62	AF231922	ATGGCACCACTTCCAGGCA	GATACCTATCTCACGGCCTTATTTCT
C21orf63	BC038710	ATGCTTCTGCGGGACGCGCACGCCAACC	GTTTTTCAGTAGAAGTGGCCCATG
C21orf67	AF380178	ATGGGGTGGGACTGCAGAAAG	ATGGCTCAGCCCATAGCTCC
C21orf68	BC009418	ATGAGCCGCTGGTCTCT	AGTTATTACTTCCATGGCCACTTT
C21orf69	AY035381	ATGGCTTGCCCTGCGTCACA	AGGTCATGGCTCCCTGCTATC
C21orf70	BC009341	ATGGGGAAAGTGAAGGGGTT	TTGTGGCATGCCCGCTG
C21orf71	AF086441	ATGGGCTCACCAATTAGACATAA	ATAAAATGGCTCACAAGTCACAG
C21orf73	AP001660	ATGCTCTCCAGTACGCAGA	ACCTTTAACTTTTTTATTTTAGTTGCA
C21orf74	AY077696	ATGGCTTATGCTTTAATCTCAGCT	CATTCATTTATTTAGTGTCTCATGTAA
C21orf79	AL117624	ATGATGTACAAAATTTGGATGAAAAGA	TATATATTGCTAAGTTTGTCTTTTAAACAG
C21orf81	NM_153750	ATGAAGTTGTTTCGGCTTCAGGA	TTTCCATTGACTATTTCTGTTTCCCTTTT
C21orf82	AF426258	ATGAGACAAGGCTGCAAAATTCAG	GTTGGTGTGTCAATTTAGTGTCTTG
C21orf84	NM_153752	ATGACAACCTCTGAGCAAGTCAAAA	GGAAACTGTCACGCAAGCCT
C21orf86	AF426264	ATGACCCCTGCTCGCCCCC	CTCAGGGCCAGGGTCCACT
C21orf87	NM_153455	ATGCTTGGATGGATCCAGCCG	CACAAGAGGGGGCATTACAC
C21orf88	NM_153754	ATGAGACGACTCCGGCACAG	GGAGAGAGTCACAGTCAAGAG
C21orf90	NM_153204	ATGGGAAATCCCAGGCTGCC	ACGTAGGCAGTCACTTCCAATC
C21orf93	NM_145179	ATGGACAGCCTCAGGGAGAG	CTCTGCTTAGGCCCCAG
C21orf94	NM_145180	ATGTTGAAGATTGCAGTATGAA	ATCAACATATTAGAAATGTTAAATAACAGAA
C21orf97	AK024977	ATGTCCCTTCCATCTCTGACC	ACCTCTGCCTCCCATCACAA
C21orf98	AK023499	ATGCAGGAATTTGGAACCATGTG	CTGTGTTGATTACTGATCATTGACG
C21orf99	NM_153773	ATGCAAAATGCAAAATGGAGTTGATAA	AGGAATTCAGTGTATCCTATTCGTC
C21orf100	NM_145033	ATGCACATATTTCTTTGATTTTAA	ACCCACCTCACTCAAGTATGAC
C21orf103	D86419	ATGTGTGGCAGTACTACGGA	ATGGCATCTCAATAATAGTAGCC
C21orf109	AF490769	ATGACTATCTGGATGACACAGGAA	TTTCATGCCATTTTATAGCCAGTT
C21orf114	AF304443	ATGGGAGAAATACTCAATGAAATAGAT	AAGATTAGTTTCACTGGATACAAATCT
C21orf115	AF269287	ATGAAAGAGTTGCTGGCCCT	AGGGTGAAGTGGGTTGACTG
C21orf127	AF139682	ATGGCAGGGGAGAACTTCGC	GTATGCTAAGACTTGGTGAAGTTGA

CALM1	BC047523	ATGGCTGATCAGCTGACCGA	TCATTTTGCAGTCATCATCTGTACG
CBR1	J04056	ATGTCGTCGGCATCCAT	AGCCAGCTCACCAGTGT
CBR3	BC002812	ATGTCGTCCTGCAGCCG	AAGCAGACGTTTACCAGTTTTG
CBS	L00972	ATGGCCAAGTGTGAGTTCTTC	CTCCGGACTTCACTTCTGTGT
CCT8	D13627	ATGAGTAAACAATATGGTAATGAAGTA	TTCAATCATTTTTGGTCATCATCCC
CLDN8	BC020866	ATGGCAACCCATGCCTTAGAAAT	AAACATACACAACATACACATACCTGACT
CLDN14	AF314090	ATGGCCAGCACGGCCGTGCAGTTCTG	TGTGGGGACTCACAGCTAGT
CLDN17	AJ250712	ATGGCATTTTATCCCTTGCAAATTG	TTAGACATAAAGTGGGAGGTCTTAC
CLIC6	AK092733	ATGACTTTTGTAGGTGAAGTCAAGA	CAGCCAGCTTCATTTTCTTCTT
COL6A1	NM_001848	ATGAGGGCGGCCGTGCTC	GACAGGGTTTGGTGCCGGC
COL6A2	BC002484	ATGACCTACGTGAGGGAGAC	CGGCCTAGCAGATCCA
COPS6	BC002520	ATGGCGGCGGGCGGGCGGGCTGCAGCTA	CCTTCAAGTACCCTCATCAGAAAA
CRYAA	U05569	ATGGACGTGACCATCCAGC	GGCAATGCCTGCTTAGGAC
CSTB	L03558	ATGATGTGCGGGGGCGCC	AAGTCAGGATCAGAAAATAGGTCA
CTDBP	AB032998	ATGGCTCAGGTTTCAAGCTATCA	CTCTAACGAGGAGCCTCTGC
CXADR	BC010536	ATGGCGCTCCTGCTGTG	AGGCTCTATACTATAGACCATC
CYR1	BC036761	ATGGACGCTCCGAGGCTAC	ATAGATTATTTCTTGCCTTTCCAG
D21S2056E	BC000380	ATGGTTTTCGCGCGTGCA	CACATCACTCCCTGCGTTTC
DKFZP56400	BC044570	ATGGCGTCGAGCGGGCGGAG	CTCTATATCTTCTTCTTTGTTTTAATGG
DNMT3A	BC043617	ATGCCCGCCATGCCCTCCAG	TTACACACACGCAAAATACTCCTTC
DNMT3L	BC002560	ATGGCGGCCATCCAGC	TGACTCATTTATAAAGAGGAAGTGA
DONSON	AL157441	ATGGCCCTTTCGGTGCCCG	TTCAGGATCTCCAATTATAAATGTAGTC
DSCR10	NM_148676	ATGCAGATTGTGCAGGGGTTT	CACATATTCTCACACAGGCATACAC
DSCR2	AJ006291	ATGGCGGCCACGTTCTTC	TGTTAAGATCATGTATAAATGTTACTC
DSCR4	AB000099	ATGTCGTTAATCATCTTGACGAG	CCTTCAGGTTGATGGGCTTG
DSCR5	NM_016430	ATGGTACTTTTACCTCGTGTGG	CAGTTTCTGTTTTGGTGAAGTT
DSCR9	NM_148675	ATGGGCAGGATTTGCCCGC	ATTTCTACCGTCCACATAATTCCTG
EEF1A1	BC018641	ATGGGAAAGGAAAGACTCATATCAA	TCATTTAGCCTTCTGAGCTTCT
ERG	M17254	ATGATTCAGACTGTCCCGGACC	CCGCCAGGCTTTAGTAGTAAGT
FAM3B	AF375989	ATGCGCCCATTTGGCTGTGT	CAGTGTCACTTCCGTTCTTTGG
FLJ32835	AK057397	ATGGACGGAGGAGCCTTGGA	GACATGCTGTTTACTTCTCTATCCT
FLJ33471	NM_152507	ATGGCCTGGGGGCTGCCTT	CAGTGGTCACTGTGAGTCCCC
FTCD	AF169017	ATGTCCCAGCTGGTGGAATGC	AGGGAGGGGCCACAGAGCC
GIT1	BC067358	ATGTCCCGAAAGGGGCCCG	GCTGGACCTTGGACTTTAAGCC
GMNN	BC005185	ATGAATCCCAGTATGAAGCAGAAAC	TCATATACATGGCTTGCATCCG
GRIK1	L19058	ATGGAGCACGGCACACTCC	TAAACTGATTACACAGTATGAAGTGAG
H2BFS	NM_017445	ATGCCGGAGCCAGCGAA	TTACTTAGCGCTGGTGTACTT
H3F3B	BC001124	ATGGCCCGAACCAAGCAGAC	TTAAGCTCTCTCTCCCCGATC
HBUCE1	BC004104	ATGGCGTAAAGCGGATCC	TTACATAGCATATTTTTGTGTCCACTC
HDAC1	BC000301	ATGGCGCAGACCGAGGGCA	TCAGGCCAAGTGCCTTCT
HMG14	J02621	ATGCCAAGAGGAAGGTGAG	GGTTATTAATCAGACTTGGCTTCT
HNRPR	BC001449	ATGGCTAATCAGGTGAATGGTAATG	CTACTTCCACTGTTGCCATAAG
HSPC152	BC017172	ATGAAACTGCTTACCCACAATCTG	TCAACTCTCAGTTTCTCTTCTACT
HTATIP	BC064912	ATGGCGGAGGTGGGGGAGA	GGTCACCACTTCCCCCTCTTG
IFNAR2	BC002793	ATGCTTTTGGAGCCAGAATGC	AAAACCTAATCACTGGGGCACA
IFNGR2	BC003624	ATGCGACCGACGCTGCT	TTGGTTCAAAGCGTTTGGAGA
IL10RB	Z17227	ATGGCGTGGAGCCTTGG	TTCTCAGAGCCTAGCTTTGG
ITGB2	BC005861	ATGCTGGGCCTGCGCCC	GCTCCTAACTCTCAGCAAAT
ITSN	AF114488	ATGGCTCAGTTTCCAAACCTTT	TGATTTCATGCTGGCTTGGGTG
JAM2	AF255910	ATGGCGAGGAGGAGCCG	AGTGGAGTCTTTAAATTAATAAGGATT
KCNE1	BC036452	ATGATCCTGTCTAACACCACAGC	ACATATCAGACCTGTAGCTCTC
KIAA0136	D50926	ATGGCGGCGCAGCCACCCCGGGATACGCC	CTTTAAGTACTACTGATTTCACTCATTT
KIAA0179	XM_035973	ATGGCCCCCGCCATGCAGCCGGCCGAGATC	TCCTCAGAAAGAAATCCATAGCC
KIAA0184	D80006	ATGCCTGGAGCTAATGTATGTGT	CTCATATGTTGTAGCGCATAG
KIAA0653	AB014553	ATGCGGCTGGGAGTCTCT	ACATCTATGTTGCTCCTGGAAT
KIAA1377	BC036525	ATGCTGGCGGGAGGCCCGGAACCCGGAGCG	TCACATTTTTTTAFTCTAGTACAACATGG
LRRC3	AB058646	ATGGGCACCGTGCGCCACCTCGCCCTC	CTAGGGCCCCGGGCGGATGGGGTC
MCM3AP	AB005543	ATGCGGGCTTTCCTGTCTG	TCAAATGTCCACCATGTCTAGCAGCG
MRPL39	AK000458	ATGGAGGCGCTGGCCAT	AGAAAGTTATTAGGTAGATGTACATTC
MRPS6	BC010076	ATGCCCGCTACGAGT	AATCTTCTCACTTCTTCTCTTCT
NDUFV3	BC021217	ATGGCTGCCCGTGTTTGC	CTCAGTGTGAGGTGACTCCC
NXF1	BC004904	ATGGCGGACGAGGGGAAGT	TCACTTCATGAATGCCACTTCTG
OLIG1	XM_170977	ATGCTGCGGCCACAGCGGCCCGGAGACTTG	CCCGCCCTCACTTGGAGAAAT
OLIG2	AF221520	ATGGACTCGGACGCCAGCC	GCTCCCCGTGCGCCAGAAC
OTUB1	BC007519	ATGGCGGCGGAGGAACCTC	CTATTTGTAGAGGATATCGTAGTGT
PABPC1	BC023520	ATGAACCCAGTCCCCCAG	TTAAACAGTTGGAACCCGGTGG
PCBP3	BC012061	ATGGAGTCCAAGGTCTCAGAA	CTGGGTAGGATTACAGCGTG
PCP4	X93349	ATGAGTGAGCCACAAGGTG	TCCCACTAGGACTGAGACCC
PDE9A	BC009047	ATGGGATCCGGTCTCTCCA	CCGCTTTCCTCAGGCACA
PDXK	BC000123	ATGGAGGAGGAGTGCCGG	CGGGGCCCTCACAGCAC
PFKL	BC009919	ATGGCCGCGTGGACCT	CCTCAGAAGCCCTTGTCCA
PKNOX1	BC007746	ATGATGGCTACACAGACATTAAG	CCCCTACTGCAGGGAGTCA
POLR2D	BC017205	ATGGCGCGGGTGGCAGCGATCCG	TTAATACTGAAAGTGCCTTTG
POTE	NM_174981	ATGGTGGCTGAGTTTGTTCAT	CCACTGTACTTAAATATGGTTTTCTG
PPP3CA	BC025714	ATGTCGAGCCCAAGCAATT	TCACTGAATATGCTGCTTACTCTG
PRDM15	XM_029600	ATGCTCAAGCACTGCAAGC	GCAGCTCAGTAGCTGTACATC
PRED80	AK096071	ATGCCTTTTGTCTGCCCTGC	AACCACAGGCCCTCAGGAGAG
PRED82	AF130090	ATGATGGTTTTGACTCCTTTCTGG	ATACAGGCTCTAAACTGTAAGAGTG

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PRED84	NM_032910	ATGGGGCGAGCGGACACTC	AACTACTCATTGTGCTGCTTGG
PRED85	AF304442	ATGGCTGAAAGGGGCCAACA	TTTCATGGGCTGGTGTGTCTG
PRED87	BC029588	ATGAAAGATAAAATGTGGTGTGAGGA	TGTGATCTAAGGCCGTGGAGA
PRED89	BC009878	ATGATGGGAGGGCATTACCTC	GCCATGCCCTAGTCAATGTCACC
PRED90	NM_032653	ATGCAGCAGGCTGCCCGCTTCAGTC	TATTTAGCCGTCACCGTTGCG
PRKCBP2	AF221520	ATGGACTCGGACGCCAGCC	GCTCCCCGTGCGCCAGAAC
PRMT2	BC000727	ATGGCAACATCAGGTGACTGT	CAACTGTCATCTCCAGATGGG
PSMD4	AF050199	ATGGTTACAGATAACACACATCTAACC	GCTCTCATCAGTTCTCCGATTTT
PTN	BC005916	ATGCAGGCTCAACAGTACCAG	ATCTTTTAAATCCAGCATCTTCTCCT
PTTG1IP	Z50022	ATGGCGCCCGGAGTGGC	TTTAGTTGTTTTCAAATCTAGCATAC
RBBP5	BC037284	ATGAACCTCGAGTTGCTGGAGT	TCATAACAGTTCTGAGATGTCTCC
RBM11	BC030196	ATGTTCCCTGCTCAGGAGGAG	TACTAGTATCTTTTCTTCTTCTAGACT
RIF1	BC008115	ATGCCACCATTGAGTACCATCG	TTTTATTTTTGGTGCATCTTCTTACG
RPS5L	U14970	ATGCAGATCAATGGCATTPTCCC	GAAAATCAGCGGTTGGACTTGT
S100B	NM_006272	ATGTCTGAGCTGGAGAAGG	CTTTCTAATCTCACTCATGTTCAA
SH3BGR	BC006371	ATGCCTCTGCTGCTCCTT	GAAAAGGCCCTAGGAATCTTCG
SLC19A1	BC003068	ATGGTGCCTCCAGCCC	AGGTCAGGATGGACACACTTC
SLC5A3	AF027153	ATGAGAGCTGTACTGGACACAG	CATATCCCTAAGTTCATAAGGAGAAATA
SNF1LK	U11494	ATGGTTATCATGTCGGAGTTTCCAG	GTCTGCTCCTCCTCTAGGC
SOD1	X02317	ATGGCGACGAAGGCCGT	GAATGTTTATTGGGCGATCCC
SON	AF380180	ATGGCGACCAACATCGAGCA	GCTACCACAAAATCTAGAGCTATA
SUMO3	BC008420	ATGTCCGAGGAGAAGCCCA	CCCTCTAGAACTGTGCCCT
TCP10L	AK058078	ATGCTGGCAGGTCAACTCGA	TTTCCATCTTCAGACACCCCC
TFF1	X00474	ATGGCCACCATGGAGAACA	TGCTAAAATTCACACTCCTCTTC
TFF2	BC032820	ATGGGACGGCGAGACGCC	TCTTAGTAATGGCAGCTTCCACA
TFF3	L08044	ATGCTGGGGCTGCTCCTG	TGGAGGTGCCCTCAGAAGT
TLE1	BC010100	ATGTTCCCGCAGAGCCGGCACCCGACGCCG	TCAGTAGATGACTTCATAGACTGTAG
TLE2	BC017364	ATGTACCCCCAGGAAGGCAC	TCAGTAGACCACCTCATACACG
TMEM1	U19252	ATGGACGCCTCTGAGGAGCC	GTCTGCCCGTCTGCTT
TP53	BC003596	ATGGAGGAGCCGAGTCTAG	GTCTAGTCTGAGTCAAGCCCTT
TSGA2	NM_080860	ATGTCGGACCTGGGCTCGG	CATCTTAGTCTGGAGGTCTGAC
TTC3	D83077	ATGGACAATTTTGTGAGGGAGA	GACTACCTAGAAGAGCAGGAAGG
U2AF1	BC001923	ATGGCGGAGTATCTGGCCT	GGCTCAGAACTGCCCCAGA
UBE2G2	AF032456	ATGGCGGGGACCGGCTCAAGAGG	GTCTCACAGTCCCAGAGACTT
UBE2H	BC006277	ATGTCATCTCCAGTCCGGG	CTACAACCTCATATCTCTGGGCC
UBE2I	BC000427	ATGTCGGGGATCGCCCTCAG	TTATGAGGGCGCAAATCTTGT
UMODL1	AK093654	ATGCAGAGCAACATGACGAAC	GCGCCTCCTATTCTGTAAGACA
UNC119	BC027176	ATGAAGGTGAAGAAGGGCGG	GCCGTGGGGTCAAGGTTGTC
WDR4	BC006341	ATGGCGGGCTCTGTGGG	CACGATCAGCAACTTAGCG
WRB	Y12478	ATGAGCTCAGCCGCGCCGACACTGGGC	CCTGTTCACTGAAACGGATGA
ZNF294	XM_047829	ATGAAAAGAAAAAAGTCTTGATGA	AAAATCTCAGAAAAACGCTCACGA
ZNF295	AB033053	ATGGAGGATTACTGCATTACATCA	TCTTTCAATGTGTGTTTTGTTCTG

6.2.2 Primer for C-terminal epitope tagging

To allow for expression of fusion proteins with native N-terminus and C-terminal epitope tag, the following extensions were added to the primers for subcloning:

Forward primer extension (attB1 site + Kozak): 5'– A AAA GCA GGC ACC ... –3'

Reverse primer extension (attB2 site in frame): 5'– AA GAA AGC TGG GTT ... –3'

In a second PCR, the full attB sites were installed using these adapter primers:

Forward adapter: 5'– GGGGACAAGTTTGTAC AAA AAA GCA GGC ACC ATG –3'

Reverse adapter: 5'– GGGGACCACTTTGTA CAA GAA AGC TGG GTT –3'

Symbol	Accession	Forward primer (5'–3')	Reverse primer (5'–3')
AGPAT3_KC	BC011971	ATGGGCCTGCTGGCCTT	TTCTTTTTTCTTAAACTCTTGG
B3GALT5_KC	NM_006057	ATGGCTTTCCCGAAGATGAG	GACAGGCGGACAATCTTCC
C21orf7_KC	AF269164	ATGATCAGCACAGCCAGGGTAC	GGACGAGCCCTGCCTCTTC
CCT8_KC	D13627	ATGAGTAAACAATATGGTAATGAAG	ATCATTTTGGTCATCATCCAGTC
CLDN8_KC	NM_012132	ATGGCAACCCATGCCTTAGAAAT	CACATACTGACTTCTGGAGTAG
CLDN14_KC	AF314090	ATGGCCAGCACGGCCGTGACGCTTCTG	CACGTAGTCGTTACGCCGTGAC
CLDN17_KC	AJ250712	ATGGCATTATCCCTTGCAAATG	GACATAACTGGTGGAGGTTCTAC
ETS2_KC	NM_005239	ATGAATGATTTTCGGAATCAAGAAT	GTCTCCGTGTCGGGCTGG
HLCS_KC	NM_000411	ATGGAAGATAGACTCCACATGG	CCGCCGTTTGGGGAGGATG
HMGNI_KC	J02621	ATGCCCAAGAGGAAGGTCAG	ATCAGACTTGGCTTCTTTCTCTC

KCNE1_KC	BC036452	ATGATCCTGTCTAACACCACAG	CGACCTGTAGCTCTCCAGG
KCNE2_KC	NM_005136	ATGTCTACTTTTATCCAATTTACACACAGACG	GGGGGACATTTTGAACCCAGCCG
KCNJ6_KC	NM_002240	ATGGCCAAGCTGACAGAATCCATG	AAC TTTGGATTCAATCTCCAGG
KCNJ15_KC	NM_002243	ATGGATGCCATTACATCGGGCATG	GACATTGCTCTGTGTAAATAAAAAGTG
MX1_KC	NM_002462	ATGGTTGTTTCCGAAGTGGAC	ACCGGGAACTGGGCAAGC
PCBP3_KC	BC012061	ATGGAGTCCAAGGTCTCAGAAG	CAGCGTGCCCATCCCGGTG
PDE9A_KC	BC009047	ATGGGATCCGGTCCCTCCAG	GGCACAGTCTCCTTCACTG
PP1AL3_KC	XM_926499	ATGGTCAACCCACCGTGTTC	TTCGAGTTGTCCACAGTCAGC
RRP1_KC	BC000380	ATGGTTTCGCGCGTGCA	CTCCCTGCGTTTCTTCTTCTTC

6.2.3 Primer for insert verification and sequencing

Vector name	Forward insert primer (5'-3')	Reverse insert primer (5'-3')
pDONR201	TCGCGTTAACGCTAGCATGGATCTC	GTAACATCAGAGATTTTGAGACAC
pDONR221 & pDONR/zeo	GTAAAACGACGGCCAGT (M13_fwd)	TAATACGACTCACTATAGGG (T7_fwd)
pDEST17	TAATACGACTCACTATAGGG (T7_fwd)	CCAACTCAGCTTCCTTTC
pDEST26	CGGACCATGGCGTACTACC	TAATACGACTCACTATAGGG (T7_fwd)
pDEST474	GCCTGCAGGTACCGGATCA	GCTTTTGTTCGCTAGCCATTC
pDEST475	TAGCCTCGGGTACCGGATCA	GCTTTTGTTCGCTAGCCATTC
pDEST515	ACAAAGACGATGACGACAAGC	GCCACCCGGGATCCTCTA
pBTM116-D9	TCGTAGATCTTCGTCAGCAG	AGCAACCTGACCTACAGG
pGAD426-D3	TACCACTACAATGGATGATGT	GCACAGTTGAAGTGAACCTGC
pACT2	CCGGGGATCCGAATTCGAG	GAGGCCCGGGGATCCGAATTC
pACT4-1b	ATCTCGTCGACCACGCGTCC	GATTCATAGATCTGCGGCCGC

6.3 Bacterial and fungal strains and mammalian cell lines

6.3.1 *Escherichia coli* strains

DH5 α

Genotype: F⁻ Φ 80/*lacZ* Δ M15 Δ (*lacZYA-argF*)U169 *recA1 endA1 hsdR17*(r_k⁻, m_k⁺)
phoA supE44 thi-1 gyrA96 relA1 λ ⁻

Description: DH5 α is a well-known, versatile strain that can be used in many everyday cloning applications. In addition to supporting blue/white screening, *recA1* and *endA1* mutations in DH5 α increase insert stability and improve the quality of plasmid DNA prepared from minipreps (Source: Invitrogen).

DB3.1

Genotype: F⁻ *gyrA462 endA1* Δ (*sr1-recA*) *mcrB mrr hsdS20*(r_B⁻, m_B⁻) *supE44 ara-14 galk2 lacY1 proA2 rpsL20*(Sm^R) *xyl-5* λ ⁻ *leu mtl1*

Description: Suitable for propagation of plasmids containing the *ccdB* gene. Designed for use with the Gateway Vector Conversion System. Used for propagating Gateway pDONR and pDEST vectors (Source: Invitrogen).

Rosetta(DE3)pLysS

Genotype: F⁻ *ompT hsdS_B(r_B- m_B-) gal dcm* (DE3) pLysSRARE (Cam^R)

Description: BL21 derivative designed to enhance the expression of eukaryotic proteins that contain codons rarely used in *E. coli*. This strain supplies tRNAs for the codons AUA, AGG, AGA, CUA, CCC, GGA on a compatible chloramphenicol-resistant plasmid (pRARE). Thus the Rosetta strain provides for "universal" translation which is otherwise limited by the codon usage of *E. coli*. The tRNA genes are driven by their native promoters. In Rosetta(DE3)pLysS, the rare tRNA genes are present on the same plasmids that carries the T7 lysozyme and *lac* repressor genes, respectively. This Rosetta strain also is deficient in *lon* and *OmpT* proteases (Source: Novagen).

6.3.2 *Saccharomyces cerevisiae* strains

L40ccua

Genotype: *MATa his3Δ200 trp1-901 leu2-3,112 LYS2::(lexAop)₄-HIS3 ura3::(lexAop)₈-lacZ ADE2::(lexAop)₈-URA3 GAL4 gal80 can1 cyh2*

Description: Haploid yeast strain carrying Y2H-inducible auxotrophy markers for growth on minimal medium lacking histidine and uracil as well as Y2H-inducible expression of β-galactosidase (Source: E. Wanker, MDC Berlin).

L40ccα

Genotype: *MATα his3Δ200 trp1-910 leu2-3,112 ade2 LYS2::(lexAop)₄-HIS3 URA3::(lexAop)₈-lacZ GAL4 gal80 can1 cyh2*

Description: Haploid yeast strain carrying Y2H-inducible auxotrophy marker for growth on minimal medium lacking histidine as well as Y2H-inducible expression of β-galactosidase (Source: E. Wanker, MDC Berlin).

6.3.3 *Cercopithecus aethiops* cell line

COS-1

Origin: African green monkey kidney fibroblast-like cell line (ATCC No. CRL-1650)

Description: This fibroblast line grows adherently to glass and plastic in culture and is generally utilized as a transfection host for virus genomes and recombinant plasmids. COS-1 cells contain T antigen, retain complete permissiveness for lytic growth of SV40, support the replication of ts A209 virus at 40°C, and support the replication of pure populations of SV40 mutants with deletions in the early region. The line was derived from the CV-1 cell line by transformation with an origin defective mutant of SV40 which codes for wild type T antigen. The cells contain a single integrated copy of the complete early region of the SV40 genome.

6.3.4 *Homo sapiens* cell line

HEK293T/17

Origin: Human fetal kidney fibroblast-like cell line (ATCC No. CRL-11268)

Description: This fibroblast line is a derivative of the 293T cell line. 293T is a highly transfectable derivative of the 293 cell line into which the temperature sensitive gene for SV40 T-antigen was inserted. These cells constitutively express the simian virus 40 (SV40) large T antigen, and clone 17 was selected specifically for its high transfectability.