XII. Appendix E

Polymerase chain reaction primers

All DNA primers (Table XII-1) were purchased from MWG Biotech. They were kept at -20°C as 100 µM stocks and were diluted ten-fold to obtain 10 µM working solutions. Primers were named according to the following general scheme:

Template-Use-Position in template of the last base-Endonuclease site/other addition-F/Rn

Where applicable, the size of a PCR product can be derived by subtracting the positions of the corresponding reverse and forward primers. Endonuclease sites and other additions such as tags are printed in lower case. Mismatches between primer and template sequence are under-scored. Identities between a primer and its nested primer are printed in boldface. Please note that indication of exon numbers in primer names used for amplification of genes/cDNAs for which the intron – exon structure has not been elucidated yet, is based on the human homologue.

Table XII-1 | **PCR primers used in this study**

Primer	**Sequence (5' – 3')**	**T_a[§] (°C)**	**Application**
	General		
hG3PDH-Contr-137-F	ACCCCTTCATTGACCTCAACTAC	60.0	Positive control on genomic DNA
hG3PDH-Contr-824-R	TGCTTCACCACCTTCTTGATGTC	60.0	
*hMSL3L1*mRNA-Contr-704-F	TTCCATGCCAGACCAACATC	56.0	Check of cDNA integrity
*hMSL3L1*mRNA-Contr-1149-R	CAGAGACTGCAATGCTTCTG	52.0	
RACE-T_{18}-AP	C**TAATACGACTCACTATAGGGCTCGAGCGG** CTTTTTTTTTTTTTTTT	50.0	Second-strand cDNA synthesis

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
RACE-AP1n	**TAATACGACTCACTATAGGGC**	55.9	RACE (in combination with a GSP)
RACE-AP2n	**ACTCACTATAGGGCTCGAGCGG**	64.0	
Adaptor (long)	CTAATACGACTCACTATAGGGCTC GAGCGGCCGCCC**GGGCAGGT**	NA	Adaptors for use in suppression PCR[756]
Adaptor (NH_2-modified, blunt)	Ⓟ-**ACCTGCCC**-N_2H	NA	
Adaptor (NH_2-modified, -GATC)	Ⓟ-GATC**ACCTGCCC**-N_2H	NA	
AP1-F	GGATCCTAATACGACTCACT**ATAGGGC**	65.0	APs for suppression PCR[756], which were combined with a *hKIAA1202* GSP
AP2-Fn	A**ATAGGGC**TCGAGCGGC	57.6	
88O18-68036-F	CAAGGGAAATGATGGAAAGG	55.2	Southern hybridisation probe 1, proximal to the t(X;8) BP
88O18-68614-R	ACAGCAATGTTCTGGGAAGG	57.3	
88O18-79597-F	CCTTGACTGATGCTTTGGGAG	59.8	Southern hybridisation probe 2, proximal to the t(X;8) BP
88O18-80166-R	CTCACAATTCCTGGGTCATGG	59.8	
88O18-81254-F	CTTTTCTCCAACCTGCACAGC	59.8	Southern hybridisation probe 3, spanning the t(X;8) BP
88O18-81845-R	TCTCTGCTATTTCTGTGTGGTC	58.4	
88O18-81254-F	CTTTTCTCCAACCTGCACAGC	59.8	Southern hybridisation probe 4, spanning the t(X;8) BP
88O18-82454-R	GAGACTAGCTGCCATAGAAGC	59.8	
88O18-82174-F	GCCATAGGAAAGCAGCTTAGG	59.8	Southern hybridisation probe 5, distal to the t(X;8) BP
88O18-82454-R	GAGACTAGCTGCCATAGAAGC	59.8	
88O18-82610-F	GCGATTGATGAAAGAGTTTGG	55.9	Southern hybridisation probe 6, distal to the t(X;8) BP
88O18-83376-R	GATTACCTGTGGCTGCTGTG	59.4	
88O18-90523-F	ACGGATGCCTGGAGTGTTAG	59.4	Southern hybridisation probe 7, distal to the t(X;8) BP
88O18-91382-R	CCATTGTACTCTGCCTTCACC	59.8	
88O18-81257-F	TTCTCCAACCTGCACAGCAG	59.4	Amplification across the t(X;8) BP on der(X)

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
91J19-82124-F	CCTCTTATTGGTGAGAAACAGG	58.4	Amplification across the t(X;8) BP on der(8)
88O18-81478-R	TGAAATCAGAGCTGTCCCAGG	59.8	
91J19-82395-R	AGGCCAACTGAGGTTATCAGC	59.8	
EGFPC1-Seq-1267-F	CATGGTCCTGCTGGAGTTCGTG	64.0	Sequencing primer for EGFP-C1 5' of the MCS
EGFPC1-Seq-1432-R	GGTATGGCTGATTATGATCAG	55.9	Sequencing primer for EGFP-C1 3' of the MCS
EGFPN3-Seq-466-F	GGCACCAAAATCAACGGGAC	59.4	Sequencing primer for EGFP-N3 5' of the MCS
EGFPN3-Seq-761-R	CTGAACTTGTGGCCGTTAC	56.7	Sequencing primer for EGFP-N3 3' of the MCS
pBTM117c-Seq-957-F	TCGTAGATCTTCGTCAGCAG	57.3	Sequencing primer for pBTM117c 5' of the MCS
pBTM117c-Seq-1218-R	AGCAACCTGACCTACAGG	56.0	Sequencing primer for pBTM117c 3' of the MCS
pGAD426-Seq-758-F	TACCACTACAATGGATGATGT	54.0	Sequencing primer for pGAD426 5' of the MCS
pGAD426-Seq-919-R	GCACAGTTGAAGTGAACTTGC	57.9	Sequencing primer for pGAD426 3' of the MCS
M13F(-20)pGEM-T easy-Seq-2976-F	GTAAAACGACGGCCAG	51.7	Sequencing primer for pGEM-T easy 5' of the MCS
M13pGEM-T easy-Seq-192-R	CAGGAAACAGCTATGAC	50.4	Sequencing primer for pGEM-T easy 3' of the MCS
T7pcDNA4/V5 HisB-Seq-863-F	TAATACGACTCACTATAGGG	53.2	Sequencing primer for pcDNA4/V5 HisB 5' of the MCS
BGHpcDNA4/V5 HisB-Seq-1121-R	TAGAAGGCACAGTCGAGG	56.0	Sequencing primer for pcDNA4/V5 HisB 3' of the MCS
pSG5pTL1-HA3-Seq-929-F	TCTGCTAACCATGTTCATGCC	57.9	Sequencing primer for pTL1-HA3 5' of the MCS
pSG5pTL1-HA3-Seq-1173-R	GGACAAACCACAACTAGAATG	55.9	Sequencing primer for pTL1-HA3 3' of the MCS
pTL1-HA3-HA-*Not*I-F	TATgcggccgcACTATAGGGCGAATTGCCGCCGTG	76.5 66.1	Amplification and subcloning of the HA-tag from pTL1-HA3
pTL1-HA3-HA-*Age*I-R	TATaccggtAATTCCCGATCCGGATCTCAAG	68.2 60.3	

Table XII-1 | **PCR primers used in this study**

Primer	**Sequence (5' – 3')**	**T_a [§] (°C)**	**Application**
*scMOM*pcDNA3-scMOM-896-*Nhe*I-F	CCTAgctagcGCCGCCACCATGAAGAGCTTCAT TACAAG	74.7 51.1	Subcloning of scMOM in pGEM-T easy
*scMOM*pcDNA3-scMOM-983-*Hin*dIII-R	CCCCaagcttCGTAATAATAGTAGGCACCG	68.1 52.4	
pcDNA4/V5 HisB-FLAG-929-*Nhe*I-F	CTAAgctagcGCCGCCACCATGgattacaaggatga cgacgataagcAAGCTTGGTACCGAGCTCG	81,8 61,4	Cloning of a FLAG-tag in pcDNA4/V5 HisB 5' of the MCS
pcDNA4/V5 HisB-cMyc-929-*Nhe*I-F	CTAAgctagcGCCGCCACCATGgagcagaaactcatct ctgAAGAGGATCTGCAAGCTTGGTACCGAGCTCG	83,0 61,4	Cloning of a cMyc-tag in pcDNA4/V5 HisB 5' of the MCS
hFBXO4/hFBXO7/hFBXO25			
*hFBXO25*mRNA-ex1-222-F	GCGCGTCAGGTGAAGACTG	61.0	Inter-exon RT-PCR
*hFBXO25*mRNA-ex2-376-F	ACCGTTGTAACATCAGTCACAG	58.4	
*hFBXO25*mRNA-ex3-436-F	ATGAAGAGCATGAATATGCATCG	57.1	
*hFBXO25*mRNA-ex3-460-R	TTCGATGCATATTCATGCTCTTC	57.1	
*hFBXO25*mRNA-ex5-624-F	TATCCGAAGGTTCAATTATGTGG	57.1	
*hFBXO25*mRNA-ex5-648-R	GACCACATAATTGAACCTTCGG	58.4	
*hFBXO25*mRNA-ex6-694-F	GGCGTGGCACAGAAGAATTAC	59.8	
*hFBXO25*mRNA-ex6-714-R	GTAATTCTTCTGTGCCACGCC	59.8	
*hFBXO25*mRNA-ex7-782-F	ATCTTCTGCAAGACCTAAGCTCT	58.9	
*hFBXO25*mRNA-ex7-802-R	AGCTTAGGTCTTGCAGAAGATC	58.4	
*hFBXO25*mRNA-ex8-982-F	AACATCCTATACCGGTTCTCAG	58.4	
*hFBXO25*mRNA-ex8-1002-R	TGAGAACCGGTATAGGATGTTG	58.4	
*hFBXO25*mRNA-ex9-1224-R	ATGCAGTGTGTCTCCGTACTG	59.8	
*hFBXO25*mRNA-ex10-1354-R	GCAGCCCTTAAAACTTGAAGAG	58.4	
*hFBXO25*mRNA-5'RACEex1-69-R	GTGGCAATGTTGCTGCCTGGTCCTG	67.9	5' RACE from *hFBXO25* exon 1

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
*hFBXO25*mRNA-5'RACEex1-30-Rn	CGCCTGCGTAGTAGGCACTG	63.5	3' RACE from *hFBXO25* exon 10
*hFBXO25*mRNA-3'RACEex10-1960-F	GGCAGTGGTCTCTGTGCTCCTAGG	67.8	
*hFBXO25*mRNA-3'RACEex10-2008-Fn	GGGTCTGTGCATAATCCTGGACTG	64.4	
*hFBXO25*mRNA-ex1-222-F	GCGCGTCAGGTGAAGACTG	61.0	Northern hybridisation probe to assess *hFBXO25* expression
*hFBXO25*mRNA-ex7-802-R	AGCTTAGGTCTTGCAGAAGATC	58.4	
hFBXO25ORF1-EGFP-1-*Xho*I-F	TTCCGctcgagCTATGCCATTTTTGGGTCAGGAC	71.9 57.9	Cloning of hFBXO25 ORFs 1 and 2 in EGFP-N3 and EGFP-C1
hFBXO25ORF2-EGFP-1-*Xho*I-F	TTCCGctcgagCTATGGAGAAATATTCAATAATGAAGAG	68.4 55.3	
hFBXO25ORF1/2-EGFP-1101/873-*Sac*II-R	AAGGCccgcggTAAACTTGAAGAGGTCGATGAAG	71.9 56.5	
hFBXO25ORF1-S244L-716-F	CCTATACCGGTTCTTAGACGGATGGGACATC	69.5	*In vitro* mutagenesis of the hFBXO25 ORF1 F-box (S244L)
hFBXO25ORF1-S244L-747-R	GATGTCCCATCCGTCTAAGAACCGGTATAGG	69.5	
hFBXO25ORF1-EGFP-1-*Xho*I-F	TTCCGctcgagCTATGCCATTTTTGGGTCAGGAC	71.9 57.9	Subcloning of hFBXO25 ORF1 ΔF, fragment I
hFBXO25ORF1-ΔF-654-*Eco*RI-R	GTgaattcGCCATTGTTCACTTGCTTAGTC	65.4 58.4	
hFBXO25ORF1-ΔF-832-*Eco*RI-F	CAgaattcGCTGAAAAGCAGTTTTGTAGAC	64.0 56.5	Subcloning of hFBXO25 ORF1 ΔF, fragment II
hFBXO25ORF1-ΔF-1367-*Xba*I-R	GCtctagaACAAACTTGAAGAGGTCGATGAAG	66.9 56.5	
T7pcDNA4/V5 HisB-Seq-863-F	TAATACGACTCACTATAGGG	53.2	Subcloning of the hFBXO4/7 ORFs[765]
hFBXO4/7ORF-1180/1465-*Not*I-R	ATTAgcggccgcCATCGTCGTCCTTGTAGTC	72.1 56.7	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
hFBXO4ORF-Seq-419-F	TGGCAGTCTATAGAATGTGCTG	58.4	Sequencing of hFBXO4/7 ORFs in pcDNA3[765]
hFBXO7ORF-Seq-361-F	ACAGGTTTCTATCCCTCAGAAC	58.4	
hFBXO7ORF-Seq-747-F	ACTAGGGGAAAATGTAGCCAAC	58.4	
	mFbxo25		
*mFbxo25*mRNA-ex1-27-F	TTGGTGGCTGTCTCGTCTGG	61.4	Inter-exon RT-PCR
*mFbxo25*mRNA-ex2-198-R	GCTGTGGTTGATGGTGTACTGG	62.1	
*mFbxo25*mRNA-ex2-176-F	GCCAGTACACCATCAACCACAG	62.1	
*mFbxo25*mRNA-ex4-342-R	GCTTTCCTTATGGACGTAGATC	58.4	
*mFbxo25*mRNA-ex4-320-F	GGATCTACGTCCATAAGGAAAG	58.4	
*mFbxo25*mRNA-ex6-513-R	GTTGAAGTAGTTCTTCTGTGCC	58.4	
*mFbxo25*mRNA-ex6-492-F	GGCACAGAAGAACTACTTCAAC	58.4	
*mFbxo25*mRNA-ex7-654-R	GTTGATGTTCCCGACTAGCAC	59.8	
*mFbxo25*mRNA-ex7-634-F	GTGCTAGTCGGGAACATCAAC	59.8	
*mFbxo25*mRNA-ex9-957-R	CAGCTTCCACTCGATATGACC	59.8	
*mFbxo25*mRNA-ex9-937-F	GGTCATATCGAGTGGAAGCTG	59.8	
*mFbxo25*mRNA-ex10-1122-R	AATGAAGTGCTCCGGAGACAC	59.8	
*mFbxo25*mRNA-5'RACEex1-54-R	GGTCCCTTCCAGACGAGACAGCCACC	71.1	5' RACE from *mFbxo25* exon 1
*mFbxo25*mRNA-5'RACEex1-29-Rn	CAACCACACCGAGCCGCAG	63.1	
*mFbxo25*mRNA-3'RACEex10-1757-F	CAGACTCGGGATGTGGGCTCCAAACC	69.5	3' RACE from *mFbxo25* exon 10
*mFbxo25*mRNA-3'RACEex10-1788-Fn	AGAGCCTCTGCCAAGGAGCTG	63.7	
*mFbxo25*mRNA-ex6-492-F	GGCACAGAAGAACTACTTCAAC	58.4	Northern hybridisation and ISH probe to assess *mFbxo25* expression
*mFbxo25*mRNA-ex10-1122-R	AATGAAGTGCTCCGGAGACAC	59.8	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
	hKIAA1202		
*hKIAA1202*mRNA-ex1-11-F	CTGAGCCCAGCCGAGGATG	63.1	Inter-exon RT-PCR
*hKIAA1202*mRNA-ex3-472-R	ATGAGTGCGGCCTACTGAC	58.8	
*hKIAA1202*mRNA-ex2-181-R	ATCTTCTGGGACAAAGCTGCC	59.8	
*hKIAA1202*mRNA-ex2-233-R	GGAGCCATATAATGGAGTGCC	59.8	
*hKIAA1202*mRNA-ex2-243-F	GCCCTCATTCTCATCAAAGGC	59.8	
*hKIAA1202*mRNA-ex2a-310-F	GGCCCCTGGTATAAAGCATTC	59.8	
*hKIAA1202*mRNA-ex2a-374-F	CTGAAAGAGAACCATCGTAGTC	58.4	
SHAP-A-ex2b-F	AGAACTGGAACCTGACTGTGC	59.8	
*hKIAA1202*mRNA-ex3-556-F	CATTCTGGCTGCAACACAAG	57.3	
*hKIAA1202*mRNA-ex4-728-R	CGCTGGTTAGGGTACATGTTC	59.8	
*hKIAA1202*mRNA-ex4-2922-F	GATGCCAAATTGCTACAACTGC	58.4	
*hKIAA1202*mRNA-ex5-3092-R	GGATTCCATTTGTCCCCAGGA	59.8	
*hKIAA1202*mRNA-ex5-3072-F	TCCTGGGGACAAATGGAATCC	59.8	
*hKIAA1202*mRNA-ex6-3222-R	TGCTCGGTAGCTTGACAAGTC	59.8	
*hKIAA1202*mRNA-ex6-3202-F	GACTTGTCAAGCTACCGAGCA	59.8	
*hKIAA1202*mRNA-ex6-3429-R	CTCATCACCTTTGCTAAAGAGC	58.4	
*hKIAA1202*mRNA-ex7-4032-F	CAAGGCAGAGCTGCTGAACAA	59.8	
*hKIAA1202*mRNA-ex7-4052-R	TTGTTCAGCAGCTCTGCCTTG	59.8	
*hKIAA1202*mRNA-ex8-4195-F	GAGGACATCAATGCCAATTCTG	58.4	
*hKIAA1202*mRNA-ex8-4216-R	CAGAATTGGCATTGATGTCCTC	58.4	
*hKIAA1202*mRNA-ex9-4423-R	GCTGCTTCTTCTCTATCAGTAC	58.4	
*hKIAA1202*mRNA-ex9-4451-R	TTGGCATCTGCCAACTGCCC	61.4	

Table XII-1 | **PCR primers used in this study**

Primer	**Sequence (5' – 3')**	**T_a[§] (°C)**	**Application**
*hKIAA1202*mRNA-ex9-5572-F	AACTAATAAGGCGAGAAGAGGG	58.4	Verification by RT-PCR of predicted *hKIAA1202* exons
*hKIAA1202*mRNA-ex10-6159-R	GATGCTATTGTAAATGGAACTG	56.0	
hKIAA1202-BF724335-20-F	ACAGTGTCTTGCCCAGTCTAG	59.8	
hKIAA1202-BF724335-626-R	TTGAGATGTAGTCTCCTTGCTG	58.4	
hKIAA1202-BF724336-1-F	CCCCAGTAAAGCAAGGACTTC	59.8	
hKIAA1202-BF724336-114-R	GCTTGGCAACAACAAATGCAAG	58.4	
hKIAA1202-BF914967-18-F	TGTATCCTCCTTGCGTCTCAC	59.8	
hKIAA1202-BF914967-412-R	AAATTGCCTGCCAAGACCAGG	59.8	
hKIAA1202-AW945473-51-F	TCTAGGAGGTAGGAATGTGGC	59.8	
hKIAA1202-AW945473-402-R	CTTTCTAGCTGTGTGTCCTTTGG	60.6	
hKIAA1202-BF922581-16-F	GCCAAAACAGTGTCTTGTCAAG	58.4	
hKIAA1202-BF922581-289-R	AGTGCTTCGTGTGTTGAGAGG	59.8	
hKIAA1202-BF362446-5-F	AGAGGGAAATGTCTCCTTTCTG	58.4	
hKIAA1202-BF362446-134-R	ATATCCAGGAGAGAGGTGAAAC	58.4	
554P16-89029-F	AGTAAAGAGGAGGACCAAAGAG	58.4	
554P16-89282-R	CAAGGAGGAAATGACACGGAG	59.8	
554P16-101990-F	ATCAGGGAGAGTTAATTCCCAC	58.4	
554P16-102118-R	CCTGTTCCAGATCACTGTCAC	59.8	
554P16-103791-F	AAGCAAGCTCTGACATGTTGTG	58.4	
554P16-103941-R	TTGGCCCTTCTCAGCATTCTC	59.8	
554P16-104394-F	GTTGTTATCAAAGGGACAGAGC	58.4	
554P16-104615-R	GCATTTCCATTCCCTTGACCC	59.8	
554P16-136617-F	ATTTTGGATAGTCAGCTTCATC	54.7	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
554P16-136908-R	ACTTGAATAAATTCCAGATGGG	54.7	
554P16-89881-F	GCTGTTGGGGATTTCTCCTTG	59.8	
554P16-90363-R	TTCCAGCAGATCACAGACTCC	59.8	
554P16-91043-F	TGAGATGCGTTTGTCATCCAC	57.9	
554P16-91615-R	ACTGTACATTCAGTGGAAAGGG	58.4	
554P16-99048-F	GAGTATCTATTCCTCAGAGGTC	58.4	
554P16-99372-R	CCTGTTTAATAAGGGACACCTG	58.4	
554P16-123423-F	CCTAACAGCCACACAAAGAGG	59.8	
554P16-123744-R	TGGACATTGCTATCTCTGGTTC	58.4	
554P16-147643-F	CCTACTACCATGGACCTATTTC	58.4	
554P16-147911-R	TCATCACAGGGCCAAGTTCAC	59.8	
88O18-20647-F	ATATATTCTATCCTTTTGTCCTC	53.5	
88O18-20778-R	GAAAGCAAGCGAAGACTTGC	57.3	
88O18-21341-F	TTGCCATAGGAAAGCAGCTTAG	58.4	
88O18-21591-R	AGGGCAGAAACCACAGGATTC	59.8	
88O18-22405-F	AACTGAAATTGTCTTGGGGTG	55.9	
88O18-22646-R	TATGGCCACCATGATATGGC	57.3	
119E20-34337-F	TTCAGGCATCTTTAATAGGG	53.2	
119E20-34497-R	GTAAGAATTATAGCAAAAGCAC	52.8	
119E20-55402-F	CTGCTGGAAGTGCCTTTCATC	59.8	
119E20-55558-R	AGGCAAGGTATGACCATCAGC	59.8	
119E20-24513-F	TCCATTCTGAGGTTTTGTGTGC	58.4	
119E20-24744-R	GGTATTGGTAGAGGGTCAGAC	59.8	

Table XII-1 | **PCR primers used in this study**

Primer	**Sequence (5' – 3')**	**T_a[§] (°C)**	**Application**
119E20-28159-F	GGCGAAAGATATCAACAGACAC	58.4	
119E20-28676-R	CTGCAAAGGACATGAACTCATC	58.4	
119E20-45496-F	CATAGTATTGGAAGTTCTGGCC	58.4	
119E20-45914-R	TTCTTCCTATCCATGAGCATGG	58.4	
119E20-46942-F	TGGCGATTCCTCAAGGATCTG	59.8	
119E20-47238-R	ACCTAGAATGATGGTTTCCAGC	58.4	
119E20-59515-F	TGCTACCAGTGCCTAGTCTG	59.4	
119E20-60003-R	GGCCATGACTCTGAATACAGC	59.8	
119E20-80862-F	TTCCTTAATGAAGCTCCTTGCC	58.4	
119E20-80958-R	ATCAGGCCTCCTAAATGTACAG	58.4	
119E20-96145-F	ACATTTGAACAGTGCCTTCTCC	58.4	
119E20-106365-F	CTTCTAGCTGATAGTCCAATC	55.9	
*hKIAA1202*mRNA-5'RACEex1-34-R	TTCTCCATCCTCGGCTGGGCTCAG	67.8	
*hKIAA1202*mRNA-5'RACEex1$_{ext.}$--5-Rn	CTTTTCCGAGGGGGCTACGTTG	64.0	5' RACE from *hKIAA1202* exon 1
*hKIAA1202*mRNA-5'RACEex2-197-R	CTCATCACCAGTCCTCATCTTCTGGG	66.4	
*hKIAA1202*mRNA-5'RACEex2-169-Rn	AAAGCTGCCTTGCCTCCATCTTC	62.4	5' RACE from *hKIAA1202* exon 2
*hKIAA1202*mRNA-5'RACEex3-489-R	CAGCTTGGCCACATGCCATGAGTG	66.1	
*hKIAA1202*mRNA-5'RACEex3-461-Rn	CTACTGACAGGGGCGTTCCTC	63.7	5' RACE from *hKIAA1202* exon 3
*hKIAA1202*mRNA-5'RACEex6-3213-R	GCTTGACAAGTCCAGTGCTGGGTTC	66.3	5' RACE from *hKIAA1202* exon 6

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
*hKIAA1202*mRNA-5'RACEex6-3186-Rn	AAGGCAAGGATGGAAAGGGGTTG	62.4	
*hKIAA1202*mRNA-3'RACEex1$_{ext.}$--26-F	CAACGTAGCCCCCTCGGAAAAGG	66.0	3' RACE from *hKIAA1202* exon 1
*hKIAA1202*mRNA-3'RACEex1-16-Fn	CCCAGCCGAGGATGGAGAAC	63.5	
*hKIAA1202*mRNA-3'RACEex2-147-F	GAAGATGGAGGCAAGGCAGCTTTGTC	66.4	3' RACE from *hKIAA1202* exon 2
*hKIAA1202*mRNA-3'RACEex2-178-Fn	AGATGAGGACTGGTGATGAGCTG	62.4	
*hKIAA1202*mRNA-3'RACEex2a-307-F	GCTGGCCCCTGGTATAAAGCATTCTC	66.4	
*hKIAA1202*mRNA-3'RACEex2a-339-Fn	GAAGACCTTGAGGCTCTCTCTAAAG	63.0	3' RACE from *hKIAA1202* exon 2a
*hKIAA1202*mRNA-3'RACEex5-3073-F	CCTGGGGACAAATGGAATCCAATAACAGG	66.7	
*hKIAA1202*mRNA-3'RACEex5-3102-Fn	AAACAGGAAGACCAGCCAGTCAG	62.4	3' RACE from *hKIAA1202* exon 5
554P16-5'RACE-98999-R	CCTCC**GTCTGTCCCCCAACCTCTC**	69.5	Verification of predicted *hKIAA1202* exons using RACE
554P16-5'RACE-98994-Rn	**GTCTGTCCCCCAACCTCTC**ATTC	64.2	
554P16-3'RACE-98985-F	GGGGAC**AGACGGAGGGAGGGAAATG**	69.5	
554P16-3'RACE-98991-Fn	**AGACGGAGGGAGGGAAATG**AGG	64.0	
88O18-5'RACE-21956-R	GGGATTCTGCCACAGATTCCTGGCATCAC	69.5	
88O18-5'RACE-21915-Rn	GAGACAGTGGACAAAGGCCAAGTG	64.4	
88O18-3'RACE-22094-F	AAGTTGGCCTGCAGGGTGGGTCCAG	69.5	
88O18-3'RACE-22130-Fn	GGGTGAATTGGATATATCTGATGGCAC	63.4	
119E20-5'RACE-45427-R	CTGTCCATTCAGTAT**GATACTGGCTGTGGGTTTG**	69.5	
119E20-5'RACE-45412-Rn	**GATACTGGCTGTGGGTTTG**TCATATATAG	63.9	

Table XII-1 | **PCR primers used in this study**

Primer	**Sequence (5' – 3')**	**T_a[§] (°C)**	**Application**
119E20-3'RACE-46941-F	GTGGCGATTCCTCAAGGATCTGGAACCAG	69.5	
119E20-3'RACE-46976-Fn	CGTTTGATCTAGCAATCCCATTACTGG	63.4	
119E20-5'RACE-105427-R	GCTACTGGCAGAGCAGCACTGTCAGG	69.5	
119E20-5'RACE-105396-Rn	TCGGGTTCAGGATGTGGCTCTG	64.0	
119E20-3'RACE-105017-F	TCTCCCGTCAAATACTTATACAGGCCCCCATG	69.5	
119E20-3'RACE-105062-Fn	CATGATGGCTGATAGAGAAGTCAGTG	63.2	
554P16-ex1/1-89264-F	CCGTGTCATTTCCTCCTTGC	59.4	Mutation analysis *hKIAA1202* 'Exon 1/1'
554P16-ex1/1-89483-R	GCACAGGGACGTACTGGAAGG	63.7	
554P16-ex1/2-89350-F	AGAGCTGGAGGGCGATGGTG	63.5	Mutation analysis *hKIAA1202* 'Exon 1/2'
554P16-ex1/2-89619-R	CGCACCCGCTTGTCCATTC	61.0	
554P16-ex1a-98699-F	ACCGCTGTATAGCAAATACTGC	58.4	Mutation analysis *hKIAA1202* 'Exon 1a'
554P16-ex1a-98906-R	GGGATTTGAAGTTGGACAGAAG	58.4	
119E20-ex2-3096-F	CAAGTAGAATTTTGGGGAGA	53.2	Mutation analysis *hKIAA1202* 'Exon 2'
119E20-ex2-3379-R	TTGAGCTTTATTACCAACCA	51.1	
119E20-ex2a-11843-F	GCAAAGTTGAATAGTTGCAACAG	57.1	Mutation analysis *hKIAA1202* 'Exon 2a'
119E20-ex2a-12134-R	GTACCAACCACATCATTGCCC	59.8	
119E20-ex3-60722-F	GAAGCTGCCTGGGAAGTG	58.2	Mutation analysis *hKIAA1202* 'Exon 3'
119E20-ex3-60990-R	AGAGGAGGAGGAGTGTCCAA	59.4	
119E20-ex4/1-63357-F	GCTGGCCTGCCCTCTCCTAT	63.5	Mutation analysis *hKIAA1202* 'Exon 4/1'
119E20-ex4/1-63639-R	GAAAGGGCACAGTCAGAAGCATTT	61.0	
119E20-ex4/2-63588-F	CAGCCTACAGCTCCTTCTC	58.8	Mutation analysis *hKIAA1202* 'Exon 4/2'
119E20-ex4/2-63828-R	GTGGGCCCCTGACTGCTT	60.5	
119E20-ex4/3-63795-F	GTCCACAGGAGGGATACCAG	61.4	Mutation analysis *hKIAA1202* 'Exon 4/3'

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
119E20-ex4/3-64043-R	GATGGCCCTCACTTGTCACT	59.4	
119E20-ex4/4-63975-F	TACCCGCAAGGAACCCTAAT	57.3	Mutation analysis *hKIAA1202* 'Exon 4/4'
119E20-ex4/4-64237-R	TCCTATGAGATGTGGAGGTCTG	60.3	
119E20-ex4/5-64171-F	CCCACTCAATGAGGCTTCTG	59.4	Mutation analysis *hKIAA1202* 'Exon 4/5'
119E20-ex4/5-64433-R	GGTCATGGGTTCCTCCTGTA	59.4	
119E20-ex4/6-64382-F	AGCCACAAAGGGAAGAAAAG	55.2	Mutation analysis *hKIAA1202* 'Exon 4/6'
119E20-ex4/6-64612-R	GTTGAACAAGGGAGCCAGAG	59.4	
119E20-ex4/7-64570-F	AAGCAGAGCAGCCAGTGAA	56.7	Mutation analysis *hKIAA1202* 'Exon 4/7'
119E20-ex4/7-64827-R	GCCTTCCTCCTCTGAATTTC	57.3	
119E20-ex4/8-64772-F	CGGAAGAGTGAGCGTTTTG	56.7	Mutation analysis *hKIAA1202* 'Exon 4/8'
119E20-ex4/8-65009-R	AGGCACTCGGAAGACCTAGC	61.4	
119E20-ex4/9-64970-F	CCCAGAGACAAGCTCTTCAAC	59.8	Mutation analysis *hKIAA1202* 'Exon 4/9'
119E20-ex4/9-65236-R	AAGTGGCTGTGAATTATGCTC	55.9	
119E20-ex4/10-65183-F	GGAGTCCGTGGAGGTCATT	58.8	Mutation analysis *hKIAA1202* 'Exon 4/10'
119E20-ex4/10-65441-R	GTTTTGGTCTCTGGGTAAAAGTC	58.9	
119E20-ex4/11-65381-F	ACATCTCATTTGCCAGGTTT	53.2	Mutation analysis *hKIAA1202* 'Exon 4/11'
119E20-ex4/11-65633-R	TGGAATTTTCTAGACCTTTGCTT	55.3	
119E20-ex4/12-65563-F	CATGTCACCCCTTCAGTCAG	59.4	Mutation analysis *hKIAA1202* 'Exon 4/12'
119E20-ex4/12-65802-R	CACCGGCAGTTGTAGCAAT	56.7	
119E20-ex4/13-65747-F	ATCTGCCCTGCCTTGCTA	56.0	Mutation analysis *hKIAA1202* 'Exon 4/13'
119E20-ex4/13-65980-R	GTAGCTTTCCCCTCTCAAAG	57.3	
119E20-ex5-71337-F	CGGCTCCTGACCTCTTCAC	61.0	Mutation analysis *hKIAA1202* 'Exon 5'
119E20-ex5-71576-R	TCAAAGGAAACTAAGCAAACCA	54.7	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
119E20-ex6/1a-90844-F	GTTGTCATCCAAAATATGGGCC	58.4	Mutation analysis *hKIAA1202* 'Exon 6/1a'
119E20-ex6/1a-91043-R	ATGTTTGAAGTCTCCAAGGAGG	58.4	
119E20-ex6/1b-90961-F	ATCCTTGCCTTGAGAACCCAG	59.8	Mutation analysis *hKIAA1202* 'Exon 6/1b'
119E20-ex6/1b-91201-R	CTAAAGAGCTCCCTCCTATGC	59.8	
119E20-ex6/2-91132-F	CAGAGAGTCACATCAGCTTGG	59.8	Direct sequencing of 'Exon 6/2' repeat
119E20-ex6/2-91486-R	TCAGGATTGAGAGCACAGGA	57.3	
119E20-ex6/3-91431-F	TGCCACCCCAGTATTTCAGT	57.3	Mutation analysis *hKIAA1202* 'Exon 6/3'
119E20-ex6/3-91783-R	GGAGGTAAAATTCAAACTTGTGC	57.1	
119E20-ex7-96229-F	AAATGTCAGCAGCCTCTCAAC	57.9	Mutation analysis *hKIAA1202* 'Exon 7'
119E20-ex7-96534-R	GGCTGGTCATCCTCCAGATA	59.4	
119E20-ex8/1a-100482-F	CAAAACAGAGGTTACAGGCACA	58.4	Mutation analysis *hKIAA1202* 'Exon 8/1a'
119E20-ex8/1a-100650-R	CAGAATTGGCATTGATGTCCTC	58.4	
119E20-ex8/1b-100565-F	ACAGCTTATCGAAAGCATCAGC	58.4	Mutation analysis *hKIAA1202* 'Exon 8/1b'
119E20-ex8/1b-100740-R	GTCCAGGTCCCCAACAAAC	58.8	
119E20-ex8/2-100684-F	CCGTCTGCAAATCCAATGA	54.5	Mutation analysis *hKIAA1202* 'Exon 8/2'
119E20-ex8/2-100905-R	CTTGAAAGAGGGAGCCCTGA	59.4	
119E20-ex9/1-102065-F	GCTAGGCAGCACTGTTGGA	58.8	Mutation analysis *hKIAA1202* 'Exon 9/1'
119E20-ex9/1-102321-R	TCTCGCTGTTCAATGATGAGA	55.9	
119E20-ex9/2-102260-F	CAGCTCCAAGATTACCAGCAC	59.8	Mutation analysis *hKIAA1202* 'Exon 9/2'
119E20-ex9/2-102518-R	AGGGCTGGAACAAACTGCTA	57.3	
119E20-ex9/3-102463-F	TCTTTGTTAGCAGTTTCTCAGCA	57.1	Mutation analysis *hKIAA1202* 'Exon 9/3'
119E20-ex9/3-102713-R	CAAAGCAGAATGAAGGCACT	55.2	
119E20-ex9/4-102627-F	TCTTAGAACCACACTCTCCTTC	58.4	Mutation analysis *hKIAA1202* 'Exon 9/4'

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
119E20-ex9/4-102936-R	TTCAGTGTAATTCCTCCCTCTG	58.4	
119E20-ex9/5-102874-F	ACCAGTTTCAGGGCCTCAC	58.8	Mutation analysis *hKIAA1202* 'Exon 9/5'
119E20-ex9/5-103135-R	CCCCAGCAATGTAAAGGAAA	55.2	
119E20-ex9/6-103063-F	GTGTGACCCTCTTCCTGTCCTAA	62.4	Mutation analysis *hKIAA1202* 'Exon 9/6'
119E20-ex9/6-103242-R	AATAAGAACCCCCTCCCCCAAT	60.3	
119E20-ex9/7-103174-F	GCCATTAATAGCTCTACTAAAACTGA	58.5	Mutation analysis *hKIAA1202* 'Exon 9/7'
119E20-ex9/7-103469-R	AGGGGAAAACTCCTTCCTAGAC	60.3	
119E20-ex10/1-106848-F	GAACATATTACAGCATGGGAAGT	57.1	Mutation analysis *hKIAA1202* 'Exon 10/1'
119E20-ex10/1-107192-R	GCTAACACGGTGAAACCCTAT	57.9	
119E20-ex10/2-107146-F	GAGGTCAGGAGATCAAGACC	59.4	Mutation analysis *hKIAA1202* 'Exon 10/2'
119E20-ex10/2-107509-R	GAAGTGCGAAACTTTTACACTG	56.5	
554P16-102096-F	AAGTGACAGTGATCTGGAACAG	58.4	Analysis of intragenic variable repeats in a ~1900 kb genomic region encompassing *hKIAA1202*
554P16-102326-R	TTGCTGCAACAGAATCAGTTGG	58.4	
554P16-108227-F	TTTGTTCCCAGGTACTCTCAG	57.9	
554P16-108917-R	TTAGCACAGAAGACAAGGAAGC	58.4	
88O18-23553-F	ATAGGGTGATATCCTGAGATCC	58.4	
88O18-24144-R	TAAACAGCAGCAGATCAGAAGC	58.4	
119E20-38381-F	CACTTGAGCCAGAGTTTAAGTC	58.4	
119E20-38742-R	GAGTAGCAAGGTATAAGAGCAC	58.4	
119E20-52432-F	CCAGAGAGTATTCATCTCTCAG	58.4	
119E20-52832-R	CAAACAGCACATTCCACCTGC	59.8	
119E20-80164-F	GGATGAATGTAGCACAAGTACC	58.4	
119E20-80907-R	AAGGATTCTTTCCTTGGAGTGG	58.4	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a[§] (°C)	Application
119E20-106944-F	CTTATCCCAGGCATATTCTTGC	58.4	
119E20-107680-R	AACTTACACAAGGAAGCCACTG	58.4	
56H2-114883-F	CAAAGTTGCATGATCGGACATG	58.4	Southern hybridisation probe to investigate large genomic rearrangements – direct repeat 1
56H2-115350-R	TTAGGTGTTCTGCACTATGAGG	58.4	
339K12-50379-F	ATGAGGCGTTCAGCAAACACC	59.8	Southern hybridisation probe to investigate large genomic rearrangements – direct repeat 2
339K12-50628-R	CTTTAGAAGAGTCTTTCCGTGC	58.4	
104D21-23337-F	TCTAGGAGCAACTGATGATGAC	58.4	Southern hybridisation probe to investigate large genomic rearrangements – inverted repeat 1
104D21-23774-R	TCAGGATCTGTGATAGATGACC	58.4	
637B23-39085-F	GCACTGGCTACACTGAACATG	59.8	Southern hybridisation probe to investigate large genomic rearrangements – inverted repeat 2
637B23-39709-R	TATGTCCCTTTAGCATAGCCTG	58.4	
119E20-ex4/9-64970-F	CCCAGAGACAAGCTCTTCAAC	59.8	Northern hybridisation probe to assess *hKIAA1202* expression
119E20-ex4/12-65802-R	CACCGGCAGTTGTAGCAAT	56.7	
hKIAA1202ORF1-EGFPC1/N3-1-*Eco*RI-F	ACgaattcTATGGAGAACCGGCCTGGG	68.0 60.5	Subcloning of hKIAA1202 ORF1, fragment I
hKIAA1202ORF1-EGFPC1/N3-1111-*Bam*HI-R	TTGGGGATCCAACAGCTTTGG	59.8	
hKIAA1202ORF1-EGFPC1/N3-4178-*Cla*I-F	GGGTGGAGAATGCTCTGAACAGC	64.2	Subcloning of hKIAA1202 ORF1, fragment II
hKIAA1202ORF1-EGFPC1/N3-4494-*Sal*I-R	CAAGgtcgacGAAATTGCTGGGCCCCAGGAG	73.5 63.7	
*hKIAA1202*mRNA-Oligo-2335-*Hin*dIII/ATG_{Kozak}-F	CCCaagcttGCCACCatgGAACGTGGAGG TCATTGGAGATG	76.4 59.4	Subcloning of hKIAA1202 Y2H-4 in pcDNA4/V5 HisB for use in chemical cross-linking assays
*hKIAA1202*mRNA-Oligo-3120-*Apa*I-R	ATgggcccTTCTGGCTGGTCTTCCTGTTTC	70.9 59.4	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
*hKIAA1202*mRNA-Y2H-39-*Sal*I-F	ACGCgtcgacACCTGGGTCCTTCCAGTAC	72.3 58.2	Subcloning of partial hKIAA1202 ORF1 in pBTM117c and pGAD426
*hKIAA1202*mRNA-Y2H-1056-*Not*I-R	AAGAAAAAgcggccgCTGCTCTCCATTGAGGAGTTG	72.9 59.8	
*hKIAA1202*mRNA-Y2H-39-*Sal*I/semi-myc-F	ACGCgtcgacagaggtacagaaattactcatcggtt cagaagaggatgctctgCCTGGGTCCTTCCAGTAC	81.5 58.2	
*hKIAA1202*mRNA-Y2H-928-*Sal*I-F	ACGCgtcgacaCAGATGTCATCCCGTCCACAG	73.3 61.8	
*hKIAA1202*mRNA-Y2H-1712-*Not*I-R	AAGAAAAAgcggccgcCTGTTTGGGTCCAGGAAACC	74.0 59.4	
*hKIAA1202*mRNA-Y2H-1674-*Sal*I-F	ACGCgtcgacTGGACACCCCTCAGAAAAAGG	72.1 59.8	
*hKIAA1202*mRNA-Y2H-2427-*Not*I-R	CAGAATAAgcggccgCTTGTTGTCACCTGGGTTGGAAG	73.8 62.4	
*hKIAA1202*mRNA-Y2H-2335-*Sal*I-F	ACGCgtcgacaCGTGGAGGTCATTGGAGATG	72.1 59.4	
*hKIAA1202*mRNA-Y2H-3120-*Not*I-R	AAGAAAAAgcggccgCTGGCTGGTCTTCCTGTTTC	73.0 59.4	
*hKIAA1202*mRNA-Y2H-3102-*Sal*I-F	ACGCgtcgacAAACAGGAAGACCAGCCAGTC	72.1 59.8	
*hKIAA1202*mRNA-Y2H-3870-*Not*I-R	AAGAAAAAgcggccgCTCAGGTTGAGATCCCAAGTG	72.9 59.8	
*hKIAA1202*mRNA-Y2H-3849-*Sal*I-F	ACGCgtcgacTCACTTGGGATCTCAACCTG	70.9 57.3	

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a § (°C)	Application
*hKIAA1202*mRNA-Y2H-4638-*Not*I-R	CAGAATAAgcggccgCTCCCTGAGACATTTGAGTTG	71.7 57.9	
	mKiaa1202/drKiaa1202		
*mKiaa1202*mRNA-ex1$_{ext.}$-19-F	GAGGACGATGGTGGCTGAG	61.0	Inter-exon and exonic RT-PCR
*mKiaa1202*mRNA-ex4-967-R	CCACTGTACACTCACGTCAC	59.4	
*mKiaa1202*mRNA-ex3-913-F	CTTCAGCTTGTCCTGGCATTC	59.8	
*mKiaa1202*mRNA-ex4-1653-R	GGGGAATCAAGAGCTTTGGAG	59.8	
*mKiaa1202*mRNA-ex4-1588-F	TGAATCCAGCCAGGATGACTG	59.8	
*mKiaa1202*mRNA-ex4-2378-R	CTTCGTTCGTGTCACACAATTG	58.4	
*mKiaa1202*mRNA-ex4-2320-F	GAAAGCCCAGCTCCAGAAAAG	59.8	
*mKiaa1202*mRNA-ex4-3102-R	GCAAAGCATTCTGGGTAAGTAG	58.4	
*mKiaa1202*mRNA-ex4-3032-F	GCTGCAGACCAATCCTATCATTC	60.6	
*mKiaa1202*mRNA-ex6-3795-R	CCAAGTGTATCTGGCTGAGTC	59.8	
*mKiaa1202*mRNA-ex6-3735-F	GGGGAAAACATCAGAGAGAATC	58.4	
*mKiaa1202*mRNA-ex7-4318-R	ATAAGCTGAGTAAGAGGTAGGG	58.4	
*mKiaa1202*mRNA-ex7-4253-F	CAAGAGTTTCAGCACTTCTCAC	58.4	
*mKiaa1202*mRNA-ex9-4953-R	AAGTGCAGGCTCTCTTTGAGG	59.8	
*mKiaa1202*mRNA-ex9-4890-F	AGCTGGAGGAGAAGATCAAAC	57.9	
*mKiaa1202*mRNA-ex9-8239R	CCTGTGCATCCAATTTCTCCC	59.8	
*mKiaa1202*mRNA-ex9-8165-F	CCAAGTGGAGTCTAAAGGAATG	58.4	
*mKiaa1202*mRNA-ex4-3032-F	GCTGCAGACCAATCCTATCATTC	60.6	Northern hybridisation probe and ISH probe 1 to assess *mKiaa1202* expression
*mKiaa1202*mRNA-ex6-3795-R	CCAAGTGTATCTGGCTGAGTC	59.8	
*mKiaa1202*mRNA-ISH-ex7-4038-F	GGGAGTTGACTATGAACTGGC	59.8	*mKiaa1202* ISH probe 2

Table XII-1 | **PCR primers used in this study**

Primer	Sequence (5' – 3')	T_a [§] (°C)	Application
*mKiaa1202*mRNA-ISH-ex9-4649-R	AAGTGCAGGCTCTCTTTGAGG	59.8	
*drKIAA1202*mRNA-ISH-ex2-34-*Eco*RI-F	GgaattcAGAGACGGCAAACTCAGGAAG	66.6 59.8	*drKiaa1202* ISH probe
*drKIAA1202*mRNA-ISH-ex4-684-*Xba*I-R	GCtctagaACTCTCCTTCCTCATTGGTGG	68.1 59.8	
*mKiaa1202*mRNA-Skip ex2-126-F	GCCGCTCACGGTGTCGAAGGAG	67.7	Exon-skipping PCR for screening a library of ENU-mutagenised E14.1 ES cells
*mKiaa1202*mRNA-ex2-371-F	ATTGAAGATGGAGGCAAGGCAGCC	64.4	
*mKiaa1202*mRNA-Skip ex3-499-F	GATCCTCAAGCTGATTGTCAGGAGTGAC	66.6	
*mKiaa1202*mRNA-ex4-993-R	GTGCTGCAATGCCGGGAGAGG	65.7	
*mKiaa1202*mRNA-ex4-1315-R	GTAGGATGATGCATGGGAAGTGGAG	64.6	
*mKiaa1202*mRNA-Skip ex4-3433-R	CCACTTGTCCACAGGAAATTCCTAG	63.0	
*mKiaa1202*mRNA-ex4-3116-F	GACAATTCCCTGTGCTGTAAGCCAG	64.6	
*mKiaa1202*mRNA-Skip ex5-3495-R	GCCTTAGAATGAGCCATTTCCCTG	62.7	
*mKiaa1202*mRNA-Skip ex7-4455-R	CTAATGCTTTCAATGAGCTGAATTTTGG	60.7	
*mKiaa1202*mRNA-Skip ex8-4726-R	CTGCTTCTTCTCTATCAGCACCAACTTTTT	64.0	
*mKiaa1202*mRNA-ex9-4753-R	GGCATCTGCCAACTGGTTCGTC	64.0	

[§] Primers introducing endonuclease sites or other additions such as tags have two annealing temperatures indicated: the T_a of the entire primer is underscored, the T_a of the gene-specific part alone is printed in normal face.