

REFERENCES

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APPENDIX

APPENDIX A CERTIFICATE OF APPROVAL



EC 017-54

เอกสารรับรองโครงการวิจัย
โดย
คณะกรรมการจัดธรรมการวิจัย โรงพยาบาลประสาทเชียงใหม่

ชื่อโครงการ	การศึกษาความถี่ของ Single Nucleotide Polymorphisms ใน Presenilin 1 gene ในผู้ป่วยชนชาติเชื้อชาติไทยและต่างด้าว
หัวหน้าโครงการ/ หน่วยงานที่ดูแล	นายก้อนหลา ใจกลาง นักศึกษาปริญญาโท คณะวิทยาศาสตร์การแพทย์ มหาวิทยาลัยเชียงใหม่
สถานที่ที่ทำวิจัย	โรงพยาบาลประสาทเชียงใหม่
ระยะเวลาดำเนินการ	๒ ปี
ผู้ทรงคุณวุฒิ	- ศาสตราจารย์พิเศษ - ศาสตราจารย์และผู้ช่วยศาสตราจารย์พิเศษ - ผู้เชี่ยวชาญในด้านวิชาการให้รางวัลเกียรติ - อาจารย์และอาจารย์มหาวิทยาลัยที่มีคุณสมบัติเหมาะสม

รับรองโดยคณะกรรมการวิจัย ๑๖๓ สำนักงาน พ.ศ. ๒๕๕๔
การรับรองโดยคณะกรรมการผลิติจารนี ๑๖๓ สำนักงาน พ.ศ. ๒๕๕๔



(นายสุจารุณ์ ลักษณ์ ที่นักวิจัย
เอกสารควบคุมของคณะกรรมการวิจัย ๑๖๓)

APPENDIX B CERTIFICATE OF APPROVAL



เอกสารรับรองโครงการวิจัยในมนุษย์ คณะกรรมการจัดการวิจัยในมนุษย์ มหาวิทยาลัยแม่ฟ้า

ชื่อโครงการ	การศึกษาความถี่ที่พบของ Single Nucleotide polymorphisms ใน Presenilin 1 gene ในผู้ป่วย痴呆ที่เป็นไปเพื่อให้ผลลัพธ์ Single Nucleotide Polymorphisms Association Studies of Presenilin 1 gene in Thai Alzheimer's Disease Patients
ชื่อผู้นำโครงการ	นายกิตติ์มูล ไกรพันธุ์
ชื่ออาจารย์ที่ปรึกษา	ดร. พชร ชูภักดี นฤาเสตร์ศรีสุข
เลขที่โครงการภาษาไทย	54-02-02-0061
ลักษณะป้ายงาน/คณบ	วิจัยทางชีววิทยาและเคมี
การรับรอง	อนุมัติโครงการวิจัยที่เข้ามาดำเนินการที่มีวัตถุประสงค์ในการศึกษาและวิเคราะห์ หาผลลัพธ์ของการวิจัยและผลการวิจัยในมนุษย์ มหาวิทยาลัยแม่ฟ้า ลงวันที่ 10/2559 เมื่อวันที่ 21 ธันวาคม 2559
วันสืบต่อการรับรอง	วันที่ 21 ธันวาคม 2559
ประมวลผลการรับรอง	วิจัยทางชีววิทยา

ลงนาม



APPENDIX C Solution preparation

0.5 M EDTA

EDTA (disodium ethylene diamine tetraacetate H₂O)

Distilled H₂O

Adjust pH to 8.0 with NaOH and adjust the volume to 1 liter with distilled H₂O.

5X TBE buffer

445 mM Tris-base 54.0 g

445 mM Boric acid 27.5 g of boric acid

10 mM EDTA 20 ml of 0.5 M (pH 8.0)

Adjust volume with distilled H₂O to 1 liter.



2% agarose gel

Agarose gel 2 g

Adjust volume with 1XTBE buffer to 100 ml

6X DNA loading dye

10 mM Tris-HCl (pH 7.6)

0.03% bromophenol blue

0.03% xylene cyanol FF

60% glycerol

60 mM EDTA

APPENDIX D Composition of Buffers and Solutions (Promega Corporation, USA)

Membrane Wash Solution (after ethanol addition)

10mM potassium acetate (pH 5.0)

80% ethanol

16.7 μ M EDTA (pH 8.0)

Membrane Binding Solution

4.5M guanidine isothiocyanate

0.5M potassium acetate (pH 5.0)

1X TE buffer

10mM Tris-HCl (pH 7.5)

1mM EDTA (pH 8.0)

1X TBE buffer

89mM Tris base

89mM boric acid

2 mM EDTA (pH 8.0)

1X TEA

40mM Tris base

5mM sodium acetate

1mM EDTA (pH 8.0)

APPENDIX E Measurement of nucleic acid concentration

Concentration of extracted DNA was estimated by spectrophotometry method. Light absorbance was measured at the wavelength of 260 nm (A_{260}). An A_{260} value 1.0 corresponds to concentration of 50 $\mu\text{g}/\text{ml}$ double-strand DNA (Sambrook et al., 2001). Therefore, concentration of nucleic acids was estimated in $\mu\text{g}/\text{ml}$ by using the following equation:

$$\text{DNA} = A_{260} \times 50$$

Purity of the nucleic acid samples can be inferred from the ratio of A_{260}/A_{280} . The ratio is much lower than 1.8 indicates contamination of residual proteins or organic solvents.

APPENDIX F Alignment of 5 tagSNPs of AD and CT in PSEN1 with rsSNPs

rs3025780

	19	20	30	40	50	60	70	80	90	100
rs3025780 master	GTCCTCTTCCCT CTTAATCTCA GCTACACG	GGTACGAGA GGTATGCCA	AGTCTCTAAC AGCTCTAA	AAA	TACGGTTTC	TGTTTTTTTT	TTTGCTCTCA			
GC9200571 (CT001-2) -F-RS3025780	-CGGTGAGA AGGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG10150004 (CT002-2) -F-RS3025780	CGTGTGAGC TAGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG10150005 (CT004-2) -F-RS3025780	GCTTGAAGA AGGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210131 (CT005-2) -F-RS3025780	GG TTGGGAGGAA AGGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210132 (CT006-2) -F-RS3025780	GGGGTAGGAA GTTGTCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210133 (CT007-2) -F-RS3025780	C GGGGAGGAAA GTATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG10150006 (CT008-2) -F-RS3025780	CTTGACGA AGGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG10150007 (CT009-2) -F-RS3025780	CGGGTAGC TGTTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210136 (CT012-2) -F-RS3025780	CGAA GTATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210138 (CT014-2) -F-RS3025780	AGGGAA GGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210139 (CT015-2) -F-RS3025780	GGGGAGGAAA GGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210140 (CT016-2) -F-RS3025780	GGTIGAGA GTTA GCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210141 (CT017-2) -F-RS3025780	CGGYGAAGAA GGTATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210142 (CT018-2) -F-RS3025780	GGG GTGGGAGGAA GGGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210137 (CT019-2) -F-RS3025780	CG GGGGAGGAAA GGGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG11210045 (AD002-2) -F-RS3025780	AA GTGGGAGGAA GTATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210046 (AD003-2) -F-RS3025780	CGG GTGGCAGGAA AGGTGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210047 (AD005-2) -F-RS3025780	CCGII 9GGCAGGATG GTGGTCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
GG9200577 (AD007-2) -F-RS3025780	CGGGAG AGGTGCTC -C	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210048 (AD008-2) -F-RS3025780	CG GTGGGAGGAA GGGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210049 (AD010-2) -F-RS3025780	CAA GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA						
G11210051 (AD014-2) -F-RS3025780	C GTGGGAGGAA GTT TCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210052 (AD015-2) -F-RS3025780	CG GGGGAGGAAA GTT GCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210053 (AD019-2) -F-RS3025780	CG IIAGGAGGAA GGGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210054 (AD020-2) -F-RS3025780	CG GTGGGAGGAA GT TCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210055 (AD021-2) -F-RS3025780	CG IGGAG -AA GTGATGCTCA	GTCCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					
G11210056 (AD022-2) -F-RS3025780	AA GTTGTCTAAC AGCTCTAA	TAACGGTTTC	GGTTTTTTTT	TTTGCTCTCA						
G11210057 (AD025-2) -F-RS3025780	AA GTTGTCTAAC AGCTCTAA	TAACGGTTTC	GGTTTTTTTT	TTTGCTCTCA						
G11210058 (AD027-2) -F-RS3025780	CCCT IGTAAAGGAA GGGTGTCTCA	AGTCTCTAAC AGCTCTAA	TAACGGTTTC	TGTTTTTTTT	TTTGCTCTCA					

rs165932

rs10146743

rs10146743 master

G09200573 (CT001-4) F-RS10146743

G11210157 (CT002-4) F-RS10146743

G01050014 (CT004-4) F-RS10146743

G11210159 (CT005-4) F-RS10146743

G11210161 (CT007-4) F-RS10146743

G11210162 (CT008-4) F-RS10146743

G11210163 (CT009-4) F-RS10146743

G11210164 (CT012-4) F-RS10146743

G11210166 (CT014-4) F-RS10146743

G11210167 (CT015-4) F-RS10146743

G11210168 (CT016-4) F-RS10146743

G11210169 (CT017-4) F-RS10146743

G11210170 (CT018-4) F-RS10146743

G11210165 (CT019-4) F-RS10146743

G11210073 (AD002-4) F-RS10146743

G11210074 (AD003-4) F-RS10146743

G11210075 (AD005-4) F-RS10146743

G09200579 (AD007-4) F-RS10146743

G11210076 (AD008-4) F-RS10146743

G11210077 (AD010-4) F-RS10146743

G11210078 (AD012-4) F-RS10146743

G11210079 (AD014-4) F-RS10146743

G11210080 (AD015-4) F-RS10146743

G01050015 (AD019-4) F-RS10146743

G11210082 (AD020-4) F-RS10146743

G01050016 (AD021-4) F-RS10146743

G11210084 (AD022-4) F-RS10146743

G11210085 (AD025-4) F-RS10146743

G11210086 (AD027-4) F-RS10146743

rs10146743 master

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G01050014 (CT004-4) F-RS10146743

G11210159 (CT005-4) F-RS10146743

G11210161 (CT007-4) F-RS10146743

G11210162 (CT008-4) F-RS10146743

G11210163 (CT009-4) F-RS10146743

G11210164 (CT012-4) F-RS10146743

G11210166 (CT014-4) F-RS10146743

G11210167 (CT015-4) F-RS10146743

G11210168 (CT016-4) F-RS10146743

G11210169 (CT017-4) F-RS10146743

G11210170 (CT018-4) F-RS10146743

G11210073 (AD002-4) F-RS10146743

G11210074 (AD003-4) F-RS10146743

G11210075 (AD005-4) F-RS10146743

G11210077 (AD007-4) F-RS10146743

G11210078 (AD008-4) F-RS10146743

G11210079 (AD010-4) F-RS10146743

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G11210086 (AD022-4) F-RS10146743

rs10146743 master

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G11210157 (CT002-4) F-RS10146743

G01050014 (CT004-4) F-RS10146743

G11210159 (CT005-4) F-RS10146743

G11210161 (CT007-4) F-RS10146743

G11210162 (CT008-4) F-RS10146743

G11210163 (CT009-4) F-RS10146743

G11210164 (CT012-4) F-RS10146743

G11210166 (CT014-4) F-RS10146743

G11210167 (CT015-4) F-RS10146743

G11210168 (CT016-4) F-RS10146743

G11210169 (CT017-4) F-RS10146743

G11210170 (CT018-4) F-RS10146743

G11210165 (CT019-4) F-RS10146743

G11210073 (AD002-4) F-RS10146743

G11210074 (AD003-4) F-RS10146743

G11210075 (AD005-4) F-RS10146743

G11210076 (AD007-4) F-RS10146743

G11210077 (AD010-4) F-RS10146743

G11210078 (AD012-4) F-RS10146743

G11210079 (AD014-4) F-RS10146743

G11210080 (AD015-4) F-RS10146743

G01050015 (AD019-4) F-RS10146743

G11210082 (AD020-4) F-RS10146743

GC11210081 (AD021-4) F-RS10146743

G11210084 (AD022-4) F-RS10146743

G11210085 (AD025-4) F-RS10146743

G11210086 (AD027-4) F-RS10146743

rs10146743 (cont.)

rs10146743 (cont.)

	610	620	630	640	650	660	670	680
rs10146743 master	AGGGGAGGGG	AAATGAAGGG	TCTGTTAATG	GGTGTAGAGI	ITCAGTTTTA	CAAGATGGAA	AGAGTCCTG	GGAGGGACCA
G09200573 (CT001-4) F-RS10146743	GGGGAGGGG	AAAAGGGGGG	GCCTTTAAGG	GGGGGGAGGT	ITCCTTTTTA	AAAAAGGAAA	AAATCTCG	GGAGGGACCA
G11210157 (CT002-4) F-RS10146743	GGGGAGGGG	AAAAAAAGGG	CCTTAAAGG	GGGGGAAGAT	ITCCTTTTTA	AAAAAAAAGA	AAATITGG	GGAGGGAAAA
G01050014 (CT004-4) F-RS10146743	AGGGGGGGG	AAAAGGGGG	GTCTTITAGG	GGGGGGAGGT	ITTCATTITTA	CCAAAAGAGA	AGAATTCTG	TGAGGGACCA
G11210159 (CT005-4) F-RS10146743	AGGGGGGGG	AAAAGGGGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACCA
G11210161 (CT007-4) F-RS10146743	AGGGGGGGG	AAAARAGGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACCA
G11210162 (CT008-4) F-RS10146743	GGGGGGGG	AAAAGGGGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACCA
G11210163 (CT009-4) F-RS10146743	AGGGGGGGG	AAAAGGGGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACCA
G11210164 (CT012-4) F-RS10146743	GGGGGGGGG	AAAAGAAGGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACCA
G11210166 (CT014-4) F-RS10146743	GGGGGGGGG	AAAAGGGGG	CCTTITAGG	GGGGGAAGGT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACAC
G11210167 (CT015-4) F-RS10146743	GGGGGGGGG	AAAAGGGGG	CCTTITAGG	GGGGGAAGGT	ITCCTTTTTA	CCAAAAGAGA	AGAATTCTG	GGAGGGACAC
G11210168 (CT016-4) F-RS10146743	GGGGGGGGG	AAAATGAGGG	TCTTITAGG	GGGGGAAGGT	ITCCTTTTTA	AA GAGGAA	AGATITGGG	GAGGGACACA
G11210169 (CT017-4) F-RS10146743	GGGGGGGGG	AAATGAGGG	TCTTITAGG	GGGTGAAGAT	ITCCTTTTTA	AAATGATGAA	ATTTITGGG	AAGGGACACA
G11210170 (CT018-4) F-RS10146743	GGGGGGGGG	AAATGAGGG	TCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	AAATGATGAA	AGAGTTCTG	GAGGGACACA
G11210165 (CT019-4) F-RS10146743	GGGGGGGGG	AAATGAGGG	TCTTITAGG	GGGGGAAGGT	ITCCTTTTTA	AAAGAAGAAA	AGAGTTCTG	GAGGGACACA
G11210073 (AD002-4) F-RS10146743	GGGGGGGGG	AAITGAGGG	CITTAAGGGG	GGGGGAAGGT	ITCATTITTA	AAAGAAGAAA	AGAGTTCTG	GAGGGACACA
G11210074 (AD003-4) F-RS10146743	AGGGGGGGG	AAATAGAGG	CCTTITAGG	GGGGGAAGAT	ITCCTTTTTA	CCAAAAGAAA	AAATCTCTG	GGAGGGACAC
G11210075 (AD005-4) F-RS10146743	GGGGGAGGG	AAATAGAGGG	CCTTITAGG	GGTGTAAAGT	ITCATTITTA	AAAGAAGAAA	AAATCTCTG	GGAGGGACACA
G09200579 (AD007-4) F-RS10146743	AGGGGGAGGG	AAAAGGGGGG	GCCTTTAGG	GGGTGAAGAT	ITTCCTTTTA	AAAGAAGAAA	AGAATTITGT	GGGGGGACCA
G11210076 (AD008-4) F-RS10146743	GGGGGGGGG	AAAAGGGGG	CTCTTAAAGG	GGGGGAAGAT	ITTCCTTTTA	AAAGAAGAAA	AAATCTCTG	GGGGGGACCA
G11210077 (AD010-4) F-RS10146743	AGGGGGGGGG	AAATRAAGGG	CTTTTTAGG	GGGGGGAAATI	ITTCCTTTTA	AAAGAAGAAA	AGAGTTCTG	GGGGGGACCA
G11210078 (AD012-4) F-RS10146743	GGGGGGGGG	AAAAGAAGGG	CTTTTTAGG	GGGGGGAAATI	ITTCCTTTTA	AAAGAAGAAA	AAATITTTGG	GGATGGAG
G11210079 (AD014-4) F-RS10146743	GGGGGGGGG	AAATAGAGGG	CTTTTTAGG	GGGGGAAGAT	ITTCCTTTTA	CCAAAAGAAA	AAATCTCTG	GGAGGGACACA
G11210080 (AD015-4) F-RS10146743	AGGGGGGGG	AAAAGAAGGG	TTTTTAAAGG	GGTTAGGATT	ITCCCTTTT	CCAGAAGAAA	AAATTTTGA	AGGGGGACACA
G01050015 (AD019-4) F-RS10146743	GGGGGGGGG	AAAATGAGGG	CTCTTTAATG	GGGTGAGAGA	TTT ATTTT	AAAGAAGAAA	AGAGTTCTG	GAAGGGACACA
G11210082 (AD020-4) F-RS10146743	AGGGGGGGG	AAAAGAAGGG	GCCTTTAAGG	GGGGGAAGAT	TTT ATTTT	AAAGAAGAAA	AAATCTCTG	GGAGGGACACA
G01050016 (AD021-4) F-RS10146743	AGGGGGGGG	AAAATGAGGG	GTCTTTAAGG	GGGGGAAGAT	TTCCCATTTTA	ACAAAAGAAA	AAATTTTGT	GAAGGGACACA
G11210084 (AD022-4) F-RS10146743	AGGGGAAGGG	AAAAGAAGGG	CCCTTAAAGG	GGGGGAAGAT	TTCCATTTTA	AAAGAAGAAA	AAATTTTGT	GGAGGGACACA
G11210085 (AD025-4) F-RS10146743	AGGGGGGGG	AAATGAGGG	CCGTITTTAG	GGTGTAAGGT	TTCCATTTTA	AAAGAAGAAA	AGAGTTCTG	GATGGGACACA
G11210086 (AD027-4) F-RS10146743	GGGGGGGGG	AAATAAGGG	CCTTAAAGGG	GGTAGGAAATI	TTATTTTT	AAAGAAGAAA	AAAGITCTGG	GGAGGGACACA

rs214273

rs214273 (cont.)

rs165933

rs165933 (cont.)

rs165933 (cont.)

rs165933 (cont.)

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BIOGRAPHY

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Sopachai, K., Nonglak, Y. and Yasothornsrikul, S. (2010). Identification of single nucleotide polymorphisms in Presenilin1 gene and primer design for Multiplex Polymerase Chain Reaction: A possible Tool in Alzheimer's diagnosis in Thai population. In Proceeding publication in The 3rd SUT Graduate Conference 2010 (pp.121-124). Nakhon Ratchasima: Suranaree University of Technology.	

