

Appendix A

Preparation of Reagents and Buffers

Reagent for DNA isolation and electrophoresis

Digestion buffer :

2M NaCl (116.9 mg/ml)	25.0	ml
1M Tris pH 8.0 (121.1 mg/ml)	25.0	ml
0.5M EDTA (186.1 mg/ml)	2.0	ml

Adjust the volume to 0.5 liter with distilled water

EDTA (0.5 M)

EDTA ($\text{Na}_2 \cdot 2\text{H}_2\text{O}$) 186.1 g

Adjust pH to 8.0 with NaOH

Adjust the volume to 1 liter with distilled water

Autoclave

PBS :

Sodium chloride 8.0 g

di-Sodium hydrogen phosphate 1.44 g

Potassium dihydrogen phosphate 0.24 g

Potassium chloride 0.20 g

Adjust pH to 7.4

Adjust the volume to 1 liter with distilled water

Autoclave

1X TBE buffer:

Tris 108.0 g

Boric acid 55.0 g

EDTA (0.5 M) 40.0 ml

Adjust the volume to 1 liter with distilled water

1x TE buffer:

1M Tris pH 8.0 (121.1 mg/ml)	10.0	ml
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0.5M EDTA (186.1 mg/ml)	2.0	ml
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Adjust the volume to 1 liter with distilled water

Tris (pH 8.0)

Tris base	121.0	g
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Adjust the volume to 1 liter with distilled water

Reagent for Isolation and Purification of Plasmid DNA**Resuspension buffer (Buffer P1)**

50 mM Tris-Cl	6.06 g Tris base
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10 mM Na ₂ EDTA.2H ₂ O	3.72 g Na ₂ EDTA.2H ₂ O
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100 µg/ml RNaseA	pH 8.0 (HCl)
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Adjust the volume to 1 liter with distilled water

Lysis buffer (Buffer P2)

200 mM NaOH	8.0 g NaOH
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1 % SDS (w/v)	50 ml 20% SDS (w/v)
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Adjust the volume to 1 liter with distilled water

Neutralization buffer (Buffer P3)

3.0 M potassium acetate	294.5 g potassium acetate
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pH 5.5 (Acetic acid)

Adjust the volume to 1 liter with distilled water

Equilibration buffer (Buffer QBT)

750 mM NaCl	43.83 g NaCl
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50 M MOPS	10.46 g MOPS
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15% isopropanol (v/v)	pH 7.0 (NaOH)
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0.15% Triton X-100 (v/v)	150 ml pure isopropanol
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	15 ml 10% Triton X-100
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Adjust the volume to 1 liter with distilled water

Wash buffer (Buffer QC)

1.0 M NaCl	58.44 g NaCl
50 mM MOPS	10.46 g MOPS
15% isopropanol (v/v)	pH 7.0 (NaOH)
	150 ml pure isopropanol

Adjust the volume to 1 liter with distilled water

Elution buffer (Buffer QF)

1.25 M NaCl	73.05 g NaCl
50 mM Tris-Cl	6.06 g Tris base
15% isopropanol (v/v)	pH 7.0 (HCl)

Adjust the volume to 1 liter with distilled water

Reagent for southern blot and hybridization**Denaturing solution**

1.5 M NaCl	87.6 g NaCl
0.5 M NaOH	20 g NaOH

Adjust the volume to 1 liter with distilled water

Neutralized solution

1.5 M NaCl	87.6 g NaCl
0.5 M Tris-base	60.57 g Tris-base
	pH 7.5 (HCl)

Adjust the volume to 1 liter with distilled water

20X SSC

0.3 M Na ₃ Citrate	98.0 g Na ₃ Citrate
3.0 M NaCl	175.32 g NaCl

Adjust the volume to 1 liter with distilled water

10X TBE

890 mM Tris-Base

890 mM Boric Acid

20 mM EDTA

Adjust the volume to 1 liter with distilled water

Primary wash buffer

0.4% SDS 4 g SDS

0.5X SSC 25 ml 20X SSC

Adjust the volume to 1 liter with distilled water

Secondary wash buffer

2X SSC 100 ml 20X SSC

Adjust the volume to 1 liter with distilled water

Media**1. TYM –Medium**

Tryptone 20 g

Yeast extracts 5 g

NaCl 5 g

MgSO₄·7H₂O 2 g

Adjust the volume to 1 liter with distilled water

2. NZCYM-Medium

NZ-Amine A 10 g

Yeast extracts 5 g

Cassminoacids 1 g

NaCl 5 g

MgSO₄·7H₂O 2 g

Adjust the volume to 1 liter with distilled water

3. Luria Broth Medium

Tryptone	10 g
Yeast extracts	5 g
NaCl	5 g

Adjust the volume to 1 liter with distilled water

4. Luria Broth Agar plate

Tryptone	10 g
Yeast extracts	5 g
NaCl	5 g
Bacto Agar	15 g

Adjust the volume to 1 liter with distilled water

Antibiotic

Ampicillin (50 mg/ml); 0.5 g Ampicillin dissolved in 10 ml H₂O

Tetracyclin (12.5 mg/ml); 0.125 g Tetracycline dissolved in 10 ml 70% Ethanol

X-Gal (40 mg/ml); 0.4 g X-Gal dissolved in 10 ml N,N-Dimethylformamide (DMF)

IPTG (100 mM); 236 mg IPTG dissolved in 10 ml H₂O

Carbinicilin (50 mg/ml); 0.5 g Carbinicilin dissolved in 10 ml H₂O

Kanamycin (10 mg/ml); 0.1 g Kanamycin dissolved in 10 ml H₂O

All antibiotic kept at -20 °C

DNA Ladder

1. 100 bp DNA Ladder (Fermentas, Germany)
2. 1 Kb DNA Ladder (Invitrogen, USA)
3. Midrange I PFG Marker (New England Biolabs Inc. USA)

Appendix B

(S0220; GenBank accession No. L31355)

1	TCTAGATGCT	ACAAATACAG	CCCTAAAAAG	CGCACGCACA	CACACACACA	CTCATA CACA
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121	ACAGAGTAGG	GAACATATAG	CACCATAATC	AATTTTCAGAA	AATCTTGGAG	TTCCCATCAT
181	GGTGCAGCGG	AAACAAATCT	GACTGGGAAC	CATGAGGTTG	CAGGTTCAAT	CCCTGGCCTT
241	GATGCGTGGG	TTAAGGATCC	AGCATTGCCA	TGCGCTGTGG	TGTAGGTCGC	AGACGTGGCT
301	TGGATCCAC	ATTGCTGTGG	CTGTGGTGTA	GGCTGGTGGC	TGCAGCTCCG	ATTGGACCCC
361	TAGCCTGGGA	ACCTCCATAT	ACCGCAGGTG	AACCCCCCGC	CCAAAAAATA	AAAGAAAAGA
421	AAAATCTTCA	TGACTCCAAA	AAACCTCACA	CCTAATTCCT	CCATCCTCCT	GGGCCCTAAG
481	CAACCACAGA	TCTCCTCTCT	GGCTCTGTGG	ATTTGCCAAA	TATTGGCCAC	TGCACAGGGA
541	TGACATCCTG	TGCCATGTGA	CCTTTGACGT	CTGTCTGCTT	TCATTTGACG	AAGAGTGGAA
601	AGGGGTGCTG	TCCCTCCCCG	TGGTAGCACT	CATCACCATG	TCAGTCTCCT	TCCTGGCCAT
661	GCTACAGATG	AGATCTCCTG	CCAAGTTCC	GCAGGCAGGA	TGTGAGGCTA	GCCCTGAGCT
721	GTCTGTGCC	TTTCCCCAGG	TGTGGACGAC	ACGGTCAGCG	TGCTACTCCA	GTACCCAGGA
781	GGGGTCCAGG	GCAGCTTCAC	CTGCAGCATC	ACTTCCCAGC	TCTCCAATAC	AGTCTCTGTG
841	AGCGGTACCA	AGGGCATGGC	CCAGGTGAGG	TTCGATTGGT	CAAGCCGGGA	GGGGTGGCCAT
901	GCTCCTCAGC	CCGAGGAAGG	GCCAGCTGT	GGCTGCTGCA	GCTGGATGTG	GACTCAACATA
961	ACCTCTCCCC	GCCCTGTTCG	TAAGGAACCC	ATCCTCAACC	ACCAGGCCGT	GGGATGGGGT
1021	CTGGACTTCT	AGGTTCCCTC	CCGAGGGCGA	ACCATTGGTC	TGTCAAAAAC	CCTTAGTCCCT
1081	TTTAACCATC	GTGGCTCAGC	AGTTAACAAA	CCCAGCTAGC	ATCCATGAGG	ACGCAGGTTT
1141	GATCCCTGGC	CTCATTCAGT	GGGCTAAGGA	TTCGGCTTTG	CTGAGAACCT	TGGCAGTAGT
1201	CACAGACACG	GCTCGGATCC	TGTGTTGCTG	TGGCTGTGGT	GTAGTCTGGT	GGCTACGGCT
1261	CTGATTGCAC	CCTAACCTAG	GAACCTCCAC	ATGCCGTGGG	TGCGGCCCCA	AAAAGACAAA
1321	AAGGCAAAAA	AAAAAAGAAA	GAAAGAAAGC	CTTTATTCTT	TTCTTCGAAG	AAACCAGTTT
1381	TTATCAACCA	TCCTCGGAAA	GCAGCTGTAA	CCTTTGGGAT	TGCTTTCACC	ATGGAGTATG
1441	GCCAGGACCA	AAGAGCAGTT	TCACTGATCT	TCCTAGAGCC	CTGTTGCTGG	CAGAAATTCT
1501	ATTCTCAACA	GAATTTGGAC	CTTGCCCTGG	GTATATTTCC	ATTTTGACCT	ACATGACTTG
1561	GGTACGGAAT	AATTTAGGTT	TCCGAGAGCC	CTGGGGGCC	CCCCAAAAA	GTCTCCTAGT
1621	AGATAGGAAG	GTGCTGGATT	ATCTAAGCCT	CCTCCTTGCA	AAGGGGATTC	ACACAGATGT
1681	GAAGAGAAGC	CGTCTTCATG	AGACCCGAGC	AAGGTGTTAG	AGAGGGATTT	GCTCCTGGGA
1741	AACAAACAGG	ACAGGTTTCT	AGTGCGGCAA	CTGTTGCTAG	GGAGCAACCC	CCCAGCAACC
1801	AGGGGTGGGG	TGGGGACCCA	AACCTTGAGG	ATGGAGGGCA	ATCCGTCTTT	GGCCACCAGG
1861	TGGCAGGGGG	AGGCTCCCCG	GCATCCCCAA	GCAGGAGCCC	CCTGTTGGTG	AGAGCAGTAG
1921	GGCCACCTCT	TATCTCCCCT	CAGATCCTCG	ACCCCTGCTG	GTGCCCAACA	GAGCTGGTGG
1981	TGAAGGGGGA	GCATAAGGAG	TTCCCCTGCT	CCTCAGCCCC	AGGCGAGGAG	TTCAATTATA
2041	CAAATGGAAT	GGGCATGTGT	TACGAGGCCA	AGCACGTCCG	GGAATGCTTG	AAGAAGGGTA
2101	AGAATGTGGA	GGACGGGGTG	GCAGGTGGCA	GGGTGGCAGA	GCAAGCCTGA	TAGGGAGGTG
2161	GGTATCTTCC	CCACCCCTTA	GCCACTCAAG	AAGCTATGTA	GAACTACATC	TCCCAGGAGC
2221	CCTTGGGGGG	ATCCATCTGC	CCAAATCATA	CCTCATGGGA	TTCTGGGAAT	TGTAGTTCCT
2281	TGGGGACATG	AGTAGGAGAA	GTTCTTAATT	GCCTCTCCC	CCAGGCCTGA	AGGAAAGCCC
2341	TATGATTACT	CTGGCTGAAA	GTGAGCTCCT	GGCTGCATC	CCTGAGGAGG	TGAGGAGGCG
2401	TATTGGAGTC	ACCTTCCCCC	AGGATAAATG	CTGATATATA	CCCTGAATAA	ATAAAGATGT
2461	GCTTTCACCA	GAGATTATGA	TGGTTTGC'TG	GGAGCTGGAG	AAAGCCCACC	ACTAAAGGGA
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2701	CTCGCCCCCA	GCCTCCCTCT	GCCTTTGTCT	CTTCATCAGT	AGAGGGGAGA	TACTGTACTG
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3001	GCAATGCCAG	ATCCTTAACC	CCTGCAGGGA	GGCCAGGGAT	CAAACCTGCG	TCCTGAATAC
3061	TAGACAGATT	CATTTCCACT	GAGTCGTGCC	AGGAACTCCT	GCCATTCATC	TTGAGGTCAG
3121	GCCTCCATTA	AGGTACAGAG	AGGCATTTCA	GTGGAAGTGT	TCTGGAGCGT	TCCCATGGCC
3181	TGACTGGCAA	AGCCTGGGTC	CCTGGCAAAG	CCTATTTGTG	TGGCAGGGGT	AGGAGGTAAT
3241	TCCCACCCAA	ATGACAAGCA	CTTGGAAAGG	GGCTATATGT	GGGGGCTTAG	TCAACAAATT
3301	AGGGTTAACT	CTATGCTCTA	GGAAAGATCT	AACCTTTGTA	TTTTGCTACA	GTAGTGAGTA
3361	GAGGTTCCGT	TATGCTGTCA	TAACAACCCCT	CAAAGAGTTC	CCTTGTGGTG	CAGCAGGTTA
3421	AGGATCCAGT	GTGTGCCCTG	CAGCAGCCCC	AGATCGCTGC	TGTGGCCAAAG	GTTCAAGCCC
3481	TGGCCTGGGA	ACTTCCACCT	GCTATGGCTG	CAGCCAAAAA	CACAACAAA	CAAAACAACA
3541	AAAAAATAAA	CCCAGATCTC	AGCTTCATAC	ACGTTTTTTT	CCTCACTTGT	GTTATATGTT
3601	GGCTGAGGGT	TCTGGACTGT	GTCTGTCTGG	GACCCACACT	GACAGAGCCT	GCACCATACA

3661 GAGCCGCGCC GTCAAGGTCA CCCGGGAAAG AACCCCCAG AAGCTCTTGT AACAACTT
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 3781 GTCACGTCTG TGGCTTGAGT CATTGCTAGG GTGTAGGGTT CGATCCCCTGG TCCCAGAACT
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 3961 CCAGAAGATA GAGATGGATA TATTGGGCTT ATGATGCTCA TAACTCTCGC TCTGAGCAA
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 6421 CAGGACCCCTG GTTCTCTTTT ACACACTGCT TTGCTTTTCCAG CTTATCATTT AGTTGTCCCC
 6481 TAGACCCAC TCTTCTTCA AATCCTATAA TAACTCTGTC TTTTCTTTGT CAAGAGGCTC
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6635 (TATA Box)

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 6721 CCAGCTTATT TTTCTTTTTA ATTTTATTTA TTTTAAATTA TAGCTGGTTT AACAGTGTTC
 6781 TGT**CAAT**TTT CTGCTGCACA GCATGGTGC CCAGTTACAC ATACACGTAT AGAATCTATT
 6841 TTCTCACACT ATCCTGCTCC ATCATAAGTG ACTAGATATA GTTCCCCATG CTACACAGCA
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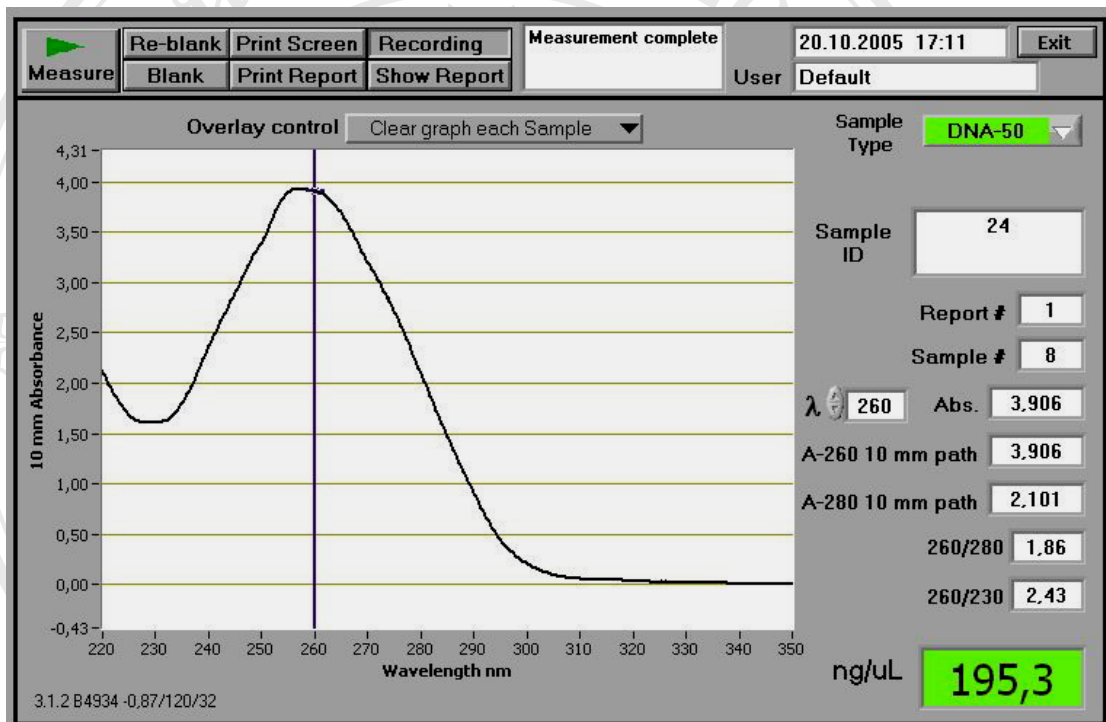
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 7021 AGCTCAGTGA ATTTTAAAT ACGTGTATGT CCAAGTAATC ACCGCCAGA TCAAGATATA
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 7261 GTGCCCGCCC GAAAACCTGG GGAATATTG CCGGAATGAA TGAATGAATG AATGAATAAA
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 7501 GCGATCACGT GACAGGACGC GCGCCTAGCG GGGCGCTCAC GTGACCGGGG GCGT**GCTGCC**
 7561 **GCCGCCCGGG CGGACCCGGC GAGAGGCCGG GGCGGGAGCG GCGGTGATGG ACGGGTCCGG**
 7621 **GGAGCAACCC AGAGGCCGGG GTGAGGCCGG AGGTGGACGG GCGGGAGGAG GGGGAGCCCC**
 7681 TCGCCGGCTG ACCCCGCGAT TCCCTCCTGC CCGTCTGGGG CCGTGCATC TCCAGGCACT
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 8221 **AGCAGATCAT GAAGACAGGG GCCCTTTTGC TTCAGGGGTG** AGTGTGAGGT CTGATTATTTG
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 8341 CACTCT**ACTT** **TCATCCAGGA TCGAGCAGGG CGAATGGGGG GAGAGACACC TGAGCTGGGG**
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 8881 **GAGAAGTCTT TTTCCGAGTG GCGGCCGAAA TGTTTGCTGA CCGCAACTTC AACTGGGGCC**
 8941 **GGTGGTCCGC GCTTTTCTAC TTTGCCAGTA AACTGGTGCT CAAGTGGGGC** GATTGCAAGG
 9001 CCGTGAGCCC AGCGAGGCTC CCCTCAGACC TGTGAGGACC TGGGAGTTGT GAGGCCAAGC
 9061 CCTGTGGCAG CCTAGGAACC ACAGAGGGGA ACGGAGAGAG TCCGCTGTGG GCCAGTTATC
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 9601 CAAGAAATAT AAGGATGGGG GAAAGGCATC TGGTAGAGGC CACAGCAAT GCAAAGGCC
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 9841 CCCTCGCACC CTCGGCATGT GGAAGTTCCC GAGCCAGGGA TCAACCTATG TGCAGCAGTG
 9901 ACAACACTGG ATCCTTAACC CAGTAGGCAG CCAGGGAAC TCCAGCTATT TTGGGGGATT
 9961 TGTTTGTTTG TTTGTTTGT TCTTTTGTAG GCCACATATG GAAGTTCTCA GGCCAGGGGT
 10021 TGAATCAGAG CTATAGTGGC CGGCCTACAC CACAGCCACA CAACAAGCAG ATCCAAGCTG
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 10141 CAGGGATCGA ACCCATATCC TCGTGGATAC TAGTTGGGCT CATTACTGCT GAGCCAATAT
 10201 ATGAACTCCT CCCAGCTAGT TTTAAACGTT CATTGGGCAT GGAACCGAAC AGGCTGGGCC
 10261 CCTGCTTTCA TGGAGCCCAG GTTGTGGGAT GAATGCTGAG AGTGATAAGA CCTGATTTAT
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 10381 CACCTGTGGC ATATGGAGGT TCCCAGGCTA GGGGTGGAAT CAGAGCTGTA GCTGCCGGCC
 10441 TATGCCAGAG CAACACAGGA TCCATAACCC ACTAAGCAAG GCCAGGGATC GAAGCCACAA
 10501 CCTCATGGTT CCTAGTCAGA TTCGTTAAC ACTGAGTCAC AACAGGAAC TCTAAATAGA
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 10621 TGCTGTTCCT CTGTGAAATT TTTTAACTT TTCTATAAAG ATTCTCATGC TAAAATATTTG
 10681 TGGGAGGGGA AGCCCAACAA ATTTGTTTAG CCCTGTGGG TAGAAAAAGG GATTATGGGA
 10741 A

DNA quality

The ratio of sample absorbance at 260 and 280 nm is used to assess the purity of DNA. A ratio of about 1.8 is generally accepted as pure for DNA, the ratio of sample absorbance at 260 and 230 nm is a secondary measurement of nucleic acid purity. A ratio commonly in the range of 1.8-3.3 is generally values for pure nucleic acid.



PAC-Genbank (IVM PAC 714)

96-well		
ssp	sp	pp
	1	1--10
	2	11--20
1	3	21--30
	4	31--40
	5	41--50
	6	51--60
	7	61--70
2	8	71--80
	9	81--90
	10	91--100
	11	101--110
	12	111--120
3	13	121--130
	14	131--140
	15	141--150
	16	151--160
	17	161--170
4	18	171--180
	19	181--190
	20	191--200
	21	201--210
	22	211--220
5	23	221--230
	24	231--240
	25	241--250

ssp	sp	pp
	26	251--260
	27	261--270
6	28	271--280
	29	281--290
	30	291--300
	31	301--310
	32	311--320
7	33	321--330
	34	331--340
	35	341--350
	36	351--360
	37	361--370
8	38	371--380
	39	381--390
	40	391--400
	41	401--410
	42	411--420
9	43	421--430
	44	431--440
	45	441--450
	46	451--460
	47	461--470
10	48	471--480
	49	481--490
	50	491--500

ssp	sp	pp
	51	501--510
	52	511--520
11	53	521--530
	54	531--530
	55	541--550
	56	551-560

384-well		
ssp	sp	pp
	57	001--0010
	58	0011--0020
12	59	0021--0030
	60	0031--0040
	61	0041--0050
	62	0051--0060
	63	0061--0070
13	64	0071--0080
	65	0081--0090
	66	0091--0095

ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่
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Genotype Data					
Pig ID	Sex	State of affection	Breed	Intron 1	Intron 3
				Genotype (CT)	Genotype (AT)
95	2	1	CB	CC	TT
926	1	1	CB	CT	TT
54	1	1	CB	CC	TT
53	2	1	CB	CC	TT
140	1	1	CB	CC	TT
TH-15	2	1	CB	CT	TT
TH-16	2	1	CB	CC	TT
TH-17	2	1	CB	CC	TT
TH-18	2	1	CB	CC	TT
TNP-1	na	1	TNP	CC	TT
TNP-2	na	1	TNP	CC	TT
TNP-3	na	1	TNP	CC	TT
TNP-4	na	1	TNP	CC	TT
TNP-5	na	1	TNP	CC	TT
WP-1	na	1	WP	CC	TT
WP-2	na	1	WP	CC	TT
WP-3	na	1	WP	CC	TT
WP-4	na	1	WP	CC	TT
WP-5	na	1	WP	CC	TT
Veltins	1	1	AS	CC	TT
Hektor	1	1	AS	CC	TT
Pier	1	1	AS	CC	TT
Vegler	1	1	Pit	CC	TT
Vulpino	1	1	Pit	CT	TT
Heftig	1	1	BB	CC	TT
Robust	1	1	Pit	CT	TT
Ass	1	1	DLS	CC	TT
Grunhagen	1	1	Pit	CT	TT
Vivaldi	1	1	Pit	CC	TT
Crestax	1	1	Pit	TT	TT
Jubel	1	1	Pit	CC	TT
Flagrant	1	1	DE	CC	TT
Fred	1	1	Pit	CT	TT
Flodder	1	1	DE	CC	TT
Taco	1	1	DE	CC	TT
Pierre	1	1	DE	CT	TT
Jaque	1	1	DE	CC	TT
Zauberer	1	1	DE	CT	TT
Michel	1	1	DE	CC	TT
Hotzenplott	1	1	SHS	CC	TT
Holgi	1	1	SHS	CT	TT
Räuber	1	1	SHS	CC	TT

Genotype Data					
Pig ID	Sex	State of affection	Breed	Intron 1 Genotype (CT)	Intron 3 Genotype (AT)
Grandel	1	1	SHS	CT	TT
Orca	1	1	SHS	CT	TT
Hartmann	1	1	SHS	CT	TT
Obelix	1	1	SHS	CC	TT
Extra	1	1	DLS	CC	TT
Lotto	1	1	DLS	CC	TT
Telur	1	1	DLS	CT	TT
Lukas	1	1	DLS	CC	TT
Gaub	1	1	DLS	CT	TT
Leon	1	1	DLS	CC	TT
Orkan	1	1	DLS	CC	TT
Hacho	1	1	BB	CC	TT
Hansel	1	1	BB	CC	TT
Stummel	1	1	BB	CC	TT
Salto	1	1	BB	CC	TT
Zapfmann	1	1	Pit	CT	TT
Zampano	1	1	Pit	CC	TT
Voyeur	1	1	Pit	TT	TT
Mykro	1	1	Pit	TT	TT
El Verraco	1	1	Pit	CT	TT
Zackig	1	1	Pit	TT	TT
Vorzug	1	1	Pit	CT	TT
Ys-18	na	1	YS	CC	TT
LC-15	na	1	LC	CC	TT
LC-16	na	1	LC	CC	TA
RC-13	na	1	RC	CC	TT
RC-14	na	1	RC	CC	TT
957	1	1	CB	CC	TT
YS25	1	1	YS	CC	TT
YS26	na	1	YS	CC	TT
YS27	na	1	YS	CC	TT
YS28	na	1	YS	CC	TT
YS29	na	1	YS	CC	TT
YS30	na	1	YS	CC	TT
JQH25	na	1	JQH	CC	TT
JQH26	na	1	JQH	CT	TT
JQH27	na	1	JQH	CT	TT
JQH28	na	1	JQH	CC	TT
JQH29	na	1	JQH	CC	TT
JQH30	na	1	JQH	TT	TT
RC19	na	1	RC	CC	TT

Genotype Data					
Pig ID	Sex	State of affection	Breed	Intron 1	Intron 3
				Genotype (CT)	Genotype (AT)
RC27	na	1	RC	CC	TT
RC28	na	1	RC	CC	TT
RC29	na	1	RC	CC	TT
RC30	na	1	RC	CC	TT
LC19	na	1	LC	CC	TT
LC21	na	1	LC	CC	TT
LC22	na	1	LC	CC	TT
LC23	na	1	LC	CC	TT
LC24	na	1	LC	CC	TA
LC26	na	1	LC	CC	TA
LC27	na	1	LC	CC	TA
LC28	na	1	LC	CC	TT
LC29	na	1	LC	CC	TT
LC30	na	1	LC	CC	AA
Gustav	1	1	AS	CC	TT
Pescal	1	1	AS	CC	TA
Garfeld	1	1	AS	CT	TT
Sokrates	1	1	AS	CC	TT
<i>TH-5</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>TH-9</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>TH-10</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>TH-23</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>55</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>141</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>97</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>939</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>936</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>1307</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>1601</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>1309</i>	<i>1</i>	<i>2</i>	HIP	TT	TT
<i>1312</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>1314</i>	<i>1</i>	<i>2</i>	HIP	TT	TT
<i>1291</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>1294</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>1372</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>925</i>	<i>1</i>	<i>2</i>	HIP	TT	TT
<i>967</i>	<i>1</i>	<i>2</i>	HIP	TT	TT
<i>1286</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>1268</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>1271</i>	<i>1</i>	<i>2</i>	HIP	CT	TT
<i>1274</i>	<i>1</i>	<i>2</i>	HIP	CC	TT
<i>1277</i>	<i>1</i>	<i>2</i>	HIP	CC	TT

Genotype Data					
Pig ID	Sex	State of affection	Breed	Intron 1	Intron 3
				Genotype (CT)	Genotype (AT)
1280	1	2	HIP	CT	TT
1300	1	2	HIP	CC	TT
1303	1	2	HIP	CT	TT
1382	1	2	HIP	CT	TT
1388	1	2	HIP	TT	TT
1402	1	2	HIP	TT	TT
1391	1	2	HIP	CC	TT
1389	1	2	HIP	CC	TT
1408	1	2	HIP	CC	TT
1411	1	2	HIP	TT	TT
1429	1	2	HIP	CC	TT
1433	1	2	HIP	CT	TT
1516	1	2	HIP	CC	TT

HIP = Hernia inguinalis piglets

TNP= Thai Native Pig

WP= Thai Wild Pig

AS= Angler Saddleback

Pit= Pietrain

DLS= German Landrasse

DE= German Edelschwein

SHS= Swabian- Haellian swine

BB= Bunte Bentheimer

YS= Yushanhei

LC = Luchuan

RC = Rongehang

JQH = Jiangquhar

CB= Cross bred

Sex; 1= Male, 2= Female

State of affection; 1=Normal, 2=Hernia

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1988-1993 Primary School (Bandon School, Chiang Rai, Thailand)
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Publication

C. Knorr, J. Beck, C. Beuermann, K. Chen, N. Ding, K. Gatphayak, L.S. Huang,
W. Laenoi and B. Brenig. 2006. Chromosomal assignment of porcine
oncogenic and apoptotic genes (CACNA2D2, TUSC4, ATP2A1, COL1A1,
TAC1, BAK1, and CASP9). *Animal Genetics*. (in press)

Poster Presentation:

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Beck J., **W. Laenoi**, H. Täubert, C. Knorr and B. Brenig. 2006. Porcine Hernia–Functional/Positional Candidate Genes. *1st European Conference on Pig Genomics*, February 20-21, 2006, Lodi, Italy

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