

Supplementary file 1: DNA DNA sequencing files

R13L

A6

>7951850.seq - ID: A6-T7 on 2011/5/21-8:50:45 automatically edited with PhredPhrap, start with base no.: 7 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

gaTaATTCCcTCtnanaaATTTtGTTtAaCTTtAAGAAGGAGaTATACCATgGgCAG
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CTTTTTATATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCA
TGGGGGGACACGCCGCGGCGaGGAAGCCAGTCGTTTAGCCGTCGATCAC
ATTGCGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGT
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GCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGA
TTCTACTTGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGCGAC
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TCATCAGTATCTACCTCAGTGAACCCAATGTTCAAAAAGCTGCTGCTGCCC
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AGCTgaantTGGCTGCTnnncncngCTgaaGcAATAAaGCATaaCCCCCTTggggnc
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nna

C3

>7951861.seq - ID: C3-T7 on 2011/5/21-8:50:45 automatically edited with PhredPhrap, start with base no.: 20 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

AaanaTTTtGTtTaCTTtAaGAAGGAGATATACCATGGGCAGCAGCCATCATCAT
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ATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGGGACAC
GCCGGCGGcgagGAAGCCAGTCGTTTAGCCgtcGATCACATTCGGCAGTATTT
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AGGGCGATCGCGCtTGGTGTGCCCATGTGGGCGACTCCCGCATCTACCGCT
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GTGGCGCCATGTGCTCTCCCAGTGTTTAGGACGCGAGGACCTCAGCCAAA
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CAGTGAACCCAATGTTCAAAAAGCTGCTGCTGCCCTTGTGGATGCAGCCA
AAACCCATGGCGGGCGTGACAATGTCACCGTCGTTGTCATCAGTGTTTAA
CCGCTCGAGGATCCGGCTGCTAACAAAGCCCgaAAGGAAGCTGAGTTGGC
TGCTGCCACCGCTGAGCAATAACTAGCATAACCcCTTGGGGCCTCTAAACG
GGTCTTGAGGgGTtTTTTGCTGAAAGGAGGAAGTATATCCGGATATCCCGC
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TGAcgGtnc

E6

>8055299.seq - ID: E6-T7 on 2011/6/15-10:18:43 automatically edited with PhredPhrap, start with base no.: 10 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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TCACATTCGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACC
CCGTCACCTACTCCGCCAAGCCTTTCTTGACGCCAATCATGCTATTGTTG
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GCGACCACACGTGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATT
GAGCAGGCGCGGCAGCATCCGTGGCGCCATGTGCTCTCCCAGTGTTTAGG
ACGCGAGGACCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGG
GCGATCGCCTGCTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGAT
GACGTCATCAGTATCTACCTCAGTGAACCCAATGTTCAAAAAGCTGCTGC
TGCCCTTGTGGATGCAGCCAAAACCCATGGCGGGCGTGACAATGTCACCG
TCGTTGTCATCAGTGTTTAAACCGCTCGAGGATCCGGCTGCTAACAAAGCCC
GaAaGGAAGCTGAGTTGGCTGCTGCCACCGCTGancAATAACTagCATAACcc
cTTGGGGCCTCTAAACGGGTcTTGAGGgGTTTTTTGCTGAAAGGagGAAGTat
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E7

>8055300.seq - ID: E7-T7 on 2011/6/15-10:18:47 automatically edited with PhredPhrap, start with base no.: 15 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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CGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCAC
TCTACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCA
GCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTC
TACTTGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGCGACTCC
CGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCA
CACGTGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGAccaTTGAGCAGGC
GCGGcagCATCCGTGGCGCCATGTGCTCtnccAGTGTTTAGgACGCGAGGACC
TCaGccaAatTGAatattcAGCCCATCgaccTAgagCCGGGCGatcgcCTGCTGCTgngcA
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F1

>8055302.seq - ID: F1-T7 on 2011/6/15-10:18:43 automatically edited with
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GATGCTTTTTTATATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGAT
GGCATGGGGGGACACGCCGGCGGCGAGGAAGCCAGTCGTTTAGCCGTCG
ATCACATTCGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGAC
CCCGTCACTCTACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTT
GAGCAGCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGT
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GCGACTCCCGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACC
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GACGCGAGGACCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCG
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TGCCCTTGTGGATGCAGCCAAAACCCATGGCGGGCGTGACAATGTCACCG
TCGTTGTCATCAGTGTTTAACCGCTCGAGGATCCGGCTGCTAACAnAGCCC
GAAAGGAAGCTGagtTGGCTGCTGCCACCGCTGancAATAACTAGCATAACC
CCTTGGGGGCCtCTAAACGGGTCTTGAGGGGtTTTTTGCTGAAAGGAGGAAC
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F5

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GATGCTTTTTTATATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGAT
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CCCGTCACTCTACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTT
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GCGACTCCCGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACC
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GACGCGAGGACCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCG
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TGACGTCATCAGTATCTACCTCAGTGAACCCAATGTTCAAnAAGCTGCTGC
TGCCCTTGTGGATGCAGCCAAAACCCATGGCGGGCGTGACAATGTCACCG
TCGTTGTCATCAGTGTTTAACCGCTCGAGGATCCGGCTGCTAACAAAGCcC
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F8

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ACACGCCGCGGCGAGGAAGCCAGTCGTTTAGCCGTCGATCACATTCGGC
AGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCTA
CTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGCGC
CAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTACT
TGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGCGACTCCCGCA
TCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACAG
TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
GCAGCATCCGTGGCGCCATGTGCTCTCCCAGTGTTTAGGACGCGAGGACC
TCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCCTG
CTGCTGTGCAGTGATGGCCTGACCGAAGAAGCTCACAGATGACGTCATCAG
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GTGTTTAACCGCTCGAGGATCCGGCTGCTAACAAAGCCCCGanaGGAAGCTG
AGTTGGCTGCTgccACCGCTGAGCAATAACTAGCATAAaCCCCCTTGgGGCCTC
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caaannGGCCCGGGCAGTACcgggcannaaccaa

R13R

B1

>7951853.seq - ID: B1-T7 on 2011/5/21-8:12:39 automatically edited with
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ATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGGG
ACACGCCGGCGGGCGAGGAAGCCAGTCGTTTAGCCGTCGATCACATTCGGC
AGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCTA
CTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGCGC
CAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTACT
TGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGCGACTCCCGCA
TCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACACG
TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
GCAGCATCCGTGGCGCCATGTGCTCTCCAGTGTTTAGGACGCGAGGACC
TCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCCTG
CTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGACGTCATCAG
TATCTACCTCAGTGAACCCAATGTTCAAAAAGCTGCTGCTGCCCTTGTGGA
TGCAGCCAAAACCCATGGCGGGCGTGACAATGTCACCGTCGTTGTCATCA
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GAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGC
CTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCG
GATATCCCGCAAGAGGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTA
CAGCATCCAGGGTGACGGTGCCGAGGATGA_cgATGAG_cGCATTGTTAGATT
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C8

>7951866.seq - ID: C8-T7 on 2011/5/21-8:12:44 automatically edited with PhredPhrap, start with base no.: 17 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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ATATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGG
GACACGCCGGCGGGCGAGGAAGCCAGTCGTTTAGCCGTCGATCACATTCGG
CAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCT
ACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGCG
CCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTAC
TTGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGCGACTCCCGC
ATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACAC
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GGCAGCATCCGTGGCGCCATGTGCTCTCCAGTGTTTAGGACGCGAGGAC
CTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCCT
GCTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGACGTCATCA
GTATCTACCTCAGTGAACCCAATGTTCAAAAAGCTGCTGCTGCCCTTGTGG
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AGTGTTTAACCGCTCGAGGATCCGGCTGCTAACAAAGCCCGAAAGGAAGC
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CCTCTAAACGGGTCTTGAGGgGTTTTTTGCTGAAAGGAGGAACTATATCCG
GATATCCCGCAAgAGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTA
CAGCATCCAGGGTGACGGTGCCGAGGATGACGATGancGCATTGTTAgaTTT
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E3

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ACCCCGTCACTCTACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTG
TTGAGCAGCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCT
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GGGCGACTCCCGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTA
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ATTGAGCAGGCGCGGCAGCATCCGTGGCGCCATGTgCTCTCCAGtGtttAGG
ACgCgaGGAacctCaGcCAAattGaTaTTCagcCcaTcgaCCTagaGCCGGgcgATCGcctgc
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F3

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TATATTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGG
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GCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTC
TACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGC
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CCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCC
TGCTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGAcGTCATC
AGTATCTACCTCAGTGAACCCAATGTTCAAAAAGCTGCTGCTGCCCTTGTG
GATGCAGCCaAAACCCATGGCGGGCGTGACAATGTCACCGTCGTTGTCAT
CAGTGTTTAACCGCTCGAGGatcCGGCTGCTAACAAAGCCCGAAAGGAAGc

TGAnTTGGCTGCTGCCACCGCTGA_gCAATAACTAGCATAACCCCTTGGGG_c
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CC

R13P

A7

>7954464.seq - ID: A7-T7 on 2011/5/23-16:15:47 automatically edited with
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B4

>7951856.seq - ID: B4-T7 on 2011/5/21-8:50:49 automatically edited with
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CTCTAAACGGGTCTTGAG_{gg}GTTtTTTGCTGAAAGGAGGA_gACTATATCCGG
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D7

>8055292.seq - ID: D7-T7 on 2011/6/15-8:25:28 automatically edited with PhredPhrap, start with base no.: 29 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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AGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCTA
CTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGCGC
CAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTACT
TGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGGCGACTCCCGCA
TCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACAG
TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
GCAGCATCCGTGGCGCCATGTGCTCTCCCAGTGTTTAGGACGCGAGGACC
TCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCCTG
CTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGACGTCATCAG
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GTGtTTAACCGCTCGAGGATcCGGCTGCTAACAAAGCCCGAAAGGA_gCTG
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CcgGcaGTACcGGc

F4

>8055305.seq - ID: F4-T7 on 2011/6/15-10:18:47 automatically edited with PhredPhrap, start with base no.: 11 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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CAGCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGT
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GCGAGGACCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGC
GATCGCCTGCTGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGA
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TTGGGGCCTCTAAACGGGTcTTGAGGgGTtTTTTGCTGAAAGGAGGAACTAT
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R13Q

B2

>7951854.seq - ID: B2-T7 on 2011/5/21-8:12:44 automatically edited with
PhredPhrap, start with base no.: 24 Internal Params: Window size: 20, Goodqual: 19,
Badqual: 10, Minseq length: 50, nbadelimit: 1

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CGCCGGCGGCGAGGAAGCCAGTCGTTTAGCCGTCGATCACATTCGGCAGT
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B8

>7951859.seq - ID: B8-T7 on 2011/5/21-8:12:44 automatically edited with PhredPhrap, start with base no.: 20 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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TGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGGGAC
ACGCCGCGCGGAGGAAGCCAGTCGTTTAGCCGTCGATCACATTCGGCAG
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GTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGgGGCCTC
TAAACGGGTCTTGAGGGGTTTTtTGCTGAAAGGAGGAACTATATCCGGATA
TCCCGCAAGangCCCGGCAGTACCGGCATAACCAAGCCTATGCCTACAGCA
TCCAGGGTGACGGTGCCGAGGATGACGATGagcgCATTGTTagaTTtCatACAC
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TcGatganaa

C5

>7951863.seq - ID: C5-T7 on 2011/5/21-8:12:39 automatically edited with PhredPhrap, start with base no.: 18 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
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GAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGgGGC
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GATATCCCGCAAGAGGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTA
CAGCATCCAGGGTGACGGTGCCGAGGATGACGATGAgcGCATTGTTAGAT
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R13H

A2

>7951846.seq - ID: A2-T7 on 2011/5/21-8:50:49 automatically edited with
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TGATGAAAAGGGCGATCGCGCTTGGTGTGCCCATGTGGGGCGACTCCCGCA
TCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACAG
TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
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CTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCG
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D4

>8055289.seq - ID: D4-T7 on 2011/6/15-10:18:47 automatically edited with
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Badqual: 10, Minseq length: 50, nbadlimit: 1

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TCACATTCGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACC
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AGCAGCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTG
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E5

>8055298.seq - ID: E5-T7 on 2011/6/15-10:18:47 automatically edited with PhredPhrap, start with base no.: 19 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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CGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCAC
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CGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCA
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R13G

A3

>7951847.seq - ID: A3-T7 on 2011/5/21-8:12:39 automatically edited with PhredPhrap, start with base no.: 10 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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ATTCGGCAGTATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGT

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GCAGCGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGA
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CCACACGTgGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGC
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A4

>7951848.seq - ID: A4-T7 on 2011/5/21-8:50:45 automatically edited with
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Badqual: 10, Minseq length: 50, nbadelimit: 1

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R13N

A8

>7951852.seq - ID: A8-T7 on 2011/5/21-8:12:44 automatically edited with PhredPhrap, start with base no.: 20 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseqlength: 50, nbadelimit: 1

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CAGCATCCAGGGTGACGGTGcgaGGAAtgACGATGAGcGCATTGTTAgaTTTC
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C7

>7951865.seq - ID: C7-T7 on 2011/5/21-8:12:39 automatically edited with PhredPhrap, start with base no.: 20 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseqlength: 50, nbadelimit: 1

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CTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACACGT
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GCATCCAGGGTGAcgGTGCcgaGGATGACGATGAGCGCATTGTTAgatTTTCAT
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R13S

B5

>7951857.seq - ID: B5-T7 on 2011/5/21-8:12:44 automatically edited with
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D6

>8055291.seq - ID: D6-T7 on 2011/6/15-10:18:43 automatically edited with
PhredPhrap, start with base no.: 22 Internal Params: Window size: 20, Goodqual: 19,
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AGTGTTTAACCGCTCGAGGATCCGGCTGCTAACAAAGCCCGAAAGGAAGC
TGAGTTGGCTGCTGCCACCGCTGancAATAACTAGCATAACCCCTtngGGGC
CTCTAAancGGGTcTTGAGgngTTTTTTGCTGAAAGGaggAACTATATcnngGat
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R13T

C1

>7951860.seq - ID: C1-T7 on 2011/5/21-8:12:39 automatically edited with PhredPhrap, start with base no.: 22 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseq length: 50, nbadelimit: 1

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TGCTGTGCAGTGATGGCCTGACCGAAGAACTCACAGATGACGTCATCAGT
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GCAGCCAAAACCCATGGCGGGCGTGACAATGTCACCGTCGTTGTCATCAG
TGTTTAACCGCTCGAGGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTG
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D8

>8055293.seq - ID: D8-T7 on 2011/6/15-10:18:47 automatically edited with
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Badqual: 10, Minseqlength: 50, nbadelimit: 1

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AATAATATTGAAnAAGGAAGAGTATGAGTATTCAACATTTCCGTGTGCGC
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E8

>8055301.seq - ID: E8-T7 on 2011/6/15-8:25:30 automatically edited with
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R13D

C6

>7951864.seq - ID: C6-T7 on 2011/5/21-8:12:44 automatically edited with
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CAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTACT
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TGGATTGCTCAAGCCGTGCAACTGGGTAGCTTGACCATTGAGCAGGCGCG
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GATATCCCGCAAGAGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTA
CAGCATCCAGGGTGACGGTGCCGAGGATGACGATGancGCATTGTTAgaTTT
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E4

>8055297.seq - ID: E4-T7 on 2011/6/15-8:25:30 automatically edited with
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Badqual: 10, Minseq length: 50, nbadelimit: 1

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CTACTCCGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAG
CGCCAAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCT
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GCGGCAGCATCCGTGGCGCCATGTGCTCTCCCAGTGTTTAGGACGCGAGG
ACCTCAGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGC
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F7

>8055308.seq - ID: F7-T7 on 2011/6/15-10:18:43 automatically edited with PhredPhrap, start with base no.: 9 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseqlength: 50, nbadelimit: 1

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CATGGGGGGACACGCCGGCGGCGAGGaAGCCAGTCGTTTAGCCGTCGATC
ACATTCGGCAGTATTTGGAAACCCACCTtGAAGACCTGCAGCACGACCCCG
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TCCCGCATCTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGA
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R13F

B6

>7951858.seq - ID: B6-T7 on 2011/5/21-8:12:39 automatically edited with PhredPhrap, start with base no.: 23 Internal Params: Window size: 20, Goodqual: 19, Badqual: 10, Minseqlength: 50, nbadelimit: 1

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TTGATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGGGA
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AAAACAGTGCCCGTGCCGATATGGGTACGACGGCTGTGGTGATTCTACTT
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CTACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACACGT
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CAGCATCCGTGGCGCCATGTGCTCTCCAGTGTTTAGGACGCGAGGACCT
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GCATCCAGGGTGACGGTGCCGAGGATGACGATGAgcgCATTGTTAgaTTtCA
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E1

>8055294.seq - ID: E1-T7 on 2011/6/15-8:25:29 automatically edited with
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Badqual: 10, Minseq length: 50, nbadelimit: 1

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GATGAAAAGCATCAGCGCTTTTTTATTGTTGCAGATGGCATGGGGGGACA
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ATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCTACTC
CGCCAAGCCTTTCTTGCAGCCAATCATGCTATTGTTGAGCAGCAGCGCCA
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R13W

A5

>7951849.seq - ID: A5-T7 on 2011/5/21-8:50:49 automatically edited with

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TACCGCTGGCGCAAAGATCAACTCCAGCAGATTACCAGCGACCACACGTG
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R13I

A1

>7951845.seq - ID: A1-T7 on 2011/5/21-8:50:45 automatically edited with
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Badqual: 10, Minseq length: 50, nbadelimit: 1

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R13K

C4

>7951862.seq - ID: C4-T7 on 2011/5/21-8:12:44 automatically edited with
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R13M

D3

>8055288.seq - ID: D3-T7 on 2011/6/15-10:18:43 automatically edited with
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R13Y

F2

>8055303.seq - ID: F2-T7 on 2011/6/15-8:25:25 automatically edited with
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Badqual: 10, Minseq length: 50, nbadelimit: 1

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gCa

Unknown variants

B3

>7951855.seq - ID: B3-T7 on 2011/5/21-8:12:39 automatically edited with
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AGCCAAATTGATATTCAGCCCATCGACCTAGAGCCGGGCGATCGCCTGCT
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GTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGgGGCCTC
TAAACGGGTCTTGAgGgGTTTTTTGCTGAAAGGAGGAAGTATATCCGGATA
TCCCGCAAGAGGCCCGGCAGTACCGGCATAACCAAGCCTATGCCTACAGC
ATCCAGGGTGACGGTGCCgaGGATGAcGATGAGCgCATTGTTAGATTtCATA
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D1

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TATTTGGAAACCCACCTTGAAGACCTGCAGCACGACCCCGTCACTCTACTC
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E2

>8055295.seq - ID: E2-T7 on 2011/6/15-8:25:30 automatically edited with
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F6

>8055307.seq - ID: F6-T7 on 2011/6/15-10:18:47 automatically edited with
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TGATATTtCAGCCCAAtcgAcctaGagcCggGcg

Supplementary file 2:**The generated tPphA variants from random site-directed mutagenesis and the gene codes of variants amino acids replacing wild type tPphA Arg-13.**

The gene code of Arg-13 of Wild type tPphA is CAC. The plasmids extracted from *E.coli* X-10 Gold colony B7, C2, D2, D5 did not yield any results in DNA sequencing.

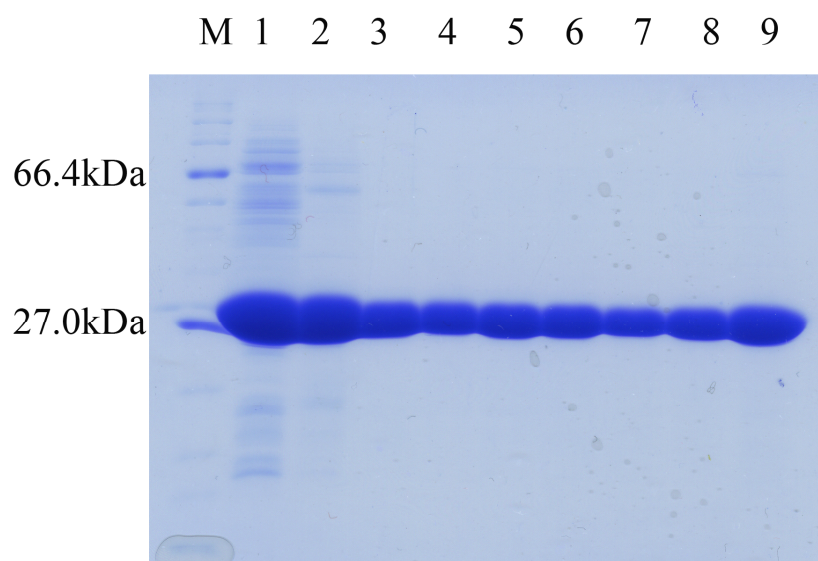
Variants name	The gene codes of variants amino acids replacing wild type tPphA Arg-13	The name of <i>E.coli</i> X-10 Gold colony
R13L	CCT	A6
	CTC	C3
	TTA	E6
	CTT	E7
	CTC	F1
	TTA	F5
	CTT	F8
R13R	CAC	B1
	CGT	C8
	CAC	E3
	CGT	F3
R13P	CCC	A7
	CCC	B4
	CCC	D7
	CCT	F4
R13Q	CAA	B2
	CAA	B8
	CAG	C5
R13H	CAT	A2
	CAC	D4
	CAC	E5
R13G	GGA	A3
	GGG	A4
R13N	AAC	A8
	AAT	C7
R13S	TCG	B5
	TCA	D6
R13T	ACA	C1
	ACT	D8
	ACC	E8
R13D	GAT	C6
	GAC	E4
	GAC	F7
R13F	TTT	B6
	TTC	E1
R13W	TGG	A5
R13I	ATT	A1

R13K	AAA	C4
R13M	ATG	D3
R13Y	TAT	F2
Unknown variants	N*AT	B3
	NNN	D1
	CTN	E2
	CNG	F6

N* means four nucleotides AGCT could randomly appear at that position

Supplementary file 3:

SDS-PAGE of wild type tPphA and R13 variants



M: ProteinMarker

1: wild type tPphA

2: R13K

3: R13H

4: R13D

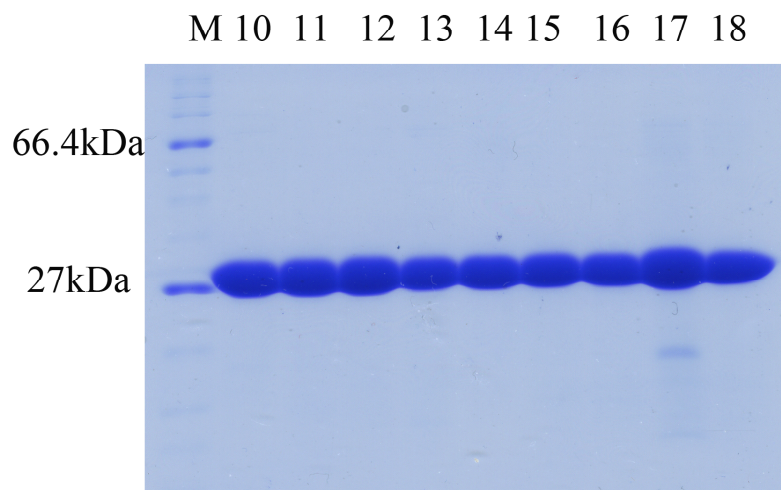
5: R13S

6: R13T

7: R13N

8: R13Q

9: R13A



M: ProteinMarker

10: R13L

11: R13I

12: R13M

13: R13F

14: R13W

15: R13Y

16: R13G

17: R13C

18: R13P