Supplemental Figures:

Supplemental Figure 1. Blood plate phenotypes for select avirulent strains

Bacteria were struck on LB-G1P agar containing 5% defibrinated sheep's blood and incubated for 48 hr. at 37°C.

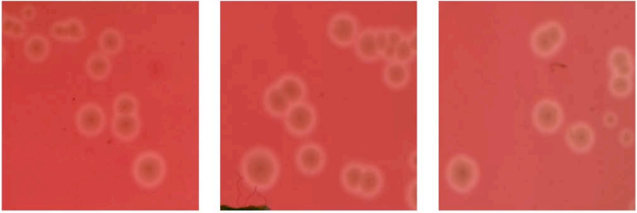
Supp. Table 1: Signature-tagged *L. monocytogenes* strains

Supp. Table 2: Signature tag sequences

Supp. Table 3: Mutagenic primers for site-directed mutagenesis

Supp. Table 4: Signature-tag-specific amplification primers

Supp. Table 5: Primers used for signature tag sequence insertion into pPL2


WT
A374G
I204A

Supplemental Table 1.
Signature-tagged *L. monocytogenes* strains

Name	Residue	ST #
1.1A	K25A	5
1.1B	D26A	6
1.1C	A27G	11
1.1D	S28A	20
1.1E	A29G	58
1.1F	F30A	102
1.1G	N31A	116
1.1H	K32A	119
1.2A	E33A	122
1.2B	N34A	128
1.2C	S35A	146
1.2D	I36A	150
1.2E	S37A	159
1.2F	S38A	168
1.2G	M39A	169
1.2H	A40G	177
1.3A	P41A	184
1.3B	P42A	191
1.3C	A43G	201
1.3D	S44A	204
1.3E	P45A	205
1.3F	P46A	208
1.3G	A47G	209
1.3H	S48A	210
1.4A	P49A	211
1.4B	K50A	212
1.4C	T51A	213
1.4D	P52A	219
1.4E	I53A	230
1.4F	E54A	231
1.4G	K55A	234
1.4H	K56A	242
1.5A	H57A	249
1.5B	A58G	282
1.5C	D59A	288
1.5D	E60A	290
1.5E	I61A	295
1.5F	D62A	296
1.5G	K63A	297
1.5H	Y64A	298
1.6A	I65A	5
1.6B	Q66A	6
1.6C	G67A	11
1.6D	L68A	20
1.6E	D69A	58
1.6F	Y70A	102
1.6G	N71A	116
1.6H	K72A	119
1.7A	N73A	122
1.7B	N74A	128
1.7C	V75A	146
1.7D	L76A	150
1.7E	V77A	159
1.7F	Y78A	168
1.7G	H79A	169
1.7H	G80A	177
1.8A	D81A	184
1.8B	A82G	191
1.8C	V83A	201
1.8D	T84A	204
1.8E	N85A	205
1.8F	V86A	208
1.8G	P87A	209
1.8H	P88A	210
1.9A	R89A	211
1.9B	K90A	212

1.9C	G91A	213	1.12H	A120G	177	2.4E	R149A	58
1.9D	Y92A	219	2.1A	I121A	184	2.4F	D150A	102
1.9E	K93A	230	2.1B	S122A	191	2.4G	S151A	116
1.9F	D94A	231	2.1C	S123A	201	2.4H	L152A	119
1.9G	G95A	234	2.1D	L124A	204	2.5A	T153A	122
1.9H	N96A	242	2.1E	T125A	205	2.5B	L154A	128
1.10A	E97A	249	2.1F	Y126A	208	2.5C	S155A	146
1.10B	Y98A	282	2.1G	P127A	209	2.5D	I156A	150
1.10C	I99A	288	2.1H	G128A	210	2.5E	D157A	159
1.10D	V100A	290	2.2A	A129G	211	2.5F	L158A	168
1.10E	V101A	295	2.2B	L130A	212	2.5G	P159A	169
1.10F	E102A	296	2.2C	V131A	213	2.5H	G160A	177
1.10G	K103A	297	2.2D	L132A	219	2.6A	M161A	184
1.10H	K104A	298	2.2E	A133G	230	2.6B	T162A	191
1.11A	K105A	5	2.2F	N134A	231	2.6C	N163A	201
1.11B	K106A	6	2.2G	S135A	234	2.6D	Q164A	204
1.11C	S107A	11	2.2H	E136A	242	2.6E	D165A	205
1.11D	I108A	20	2.3A	L137A	249	2.6F	N166A	208
1.11E	N109A	58	2.3B	V138A	282	2.6G	K167A	209
1.11F	Q110A	102	2.3C	E139A	288	2.6H	I168A	210
1.11G	N111A	116	2.3D	N140A	290	2.7A	V169A	211
1.11H	N112A	119	2.3E	Q141A	295	2.7B	V170A	212
1.12A	A113G	169	2.3F	P142A	296	2.7C	K171A	213
1.12B	D114A	122	2.3G	D143A	297	2.7D	N172A	219
1.12C	I115A	128	2.3H	V144A	298	2.7E	A173G	230
1.12D	Q116A	146	2.4A	L145A	5	2.7F	T174A	231
1.12E	V117A	150	2.4B	P146A	6	2.7G	K175A	234
1.12F	V118A	159	2.4C	V147A	11	2.7H	S176A	242
1.12G	N119A	168	2.4D	K148A	20	2.8A	N177A	249

2.8B	V178A	282	2.11G	D207A	209	3.3D	F236A	150
2.8C	N179A	288	2.11H	D208A	210	3.3E	F237A	159
2.8D	N180A	290	2.12A	E209A	211	3.3F	A238G	168
2.8E	A181G	295	2.12B	M210A	212	3.3G	I239A	169
2.8F	V182A	296	2.12C	A211G	213	3.3H	S240A	177
2.8G	N183A	297	2.12D	Y212A	219	3.4A	E241A	184
2.8H	T184A	298	2.12E	S213A	230	3.4B	G242	191
2.9A	L185A	5	2.12F	E214A	231	3.4C	K243A	201
2.9B	V186A	6	2.12G	S215A	234	3.4D	M244A	204
2.9C	E187A	11	2.12H	Q216A	242	3.4E	Q245A	205
2.9D	R188A	20	3.1A	L217A	249	3.4F	E246A	208
2.9E	W189A	58	3.AB	I218A	282	3.4G	E247A	209
2.9F	N190A	102	3.1C	A219G	288	3.4H	V248A	210
2.9G	E191A	116	3.1D	K220A	290	3.5A	I240A	211
2.9H	K192A	119	3.1E	F221A	295	3.5B	S250A	212
2.10A	Y193A	122	3.1F	G222A	296	3.5C	F251A	213
2.10B	A194A	128	3.1G	T223A	297	3.5D	K252A	219
2.10C	Q195A	146	3.1H	A224G	298	3.5E	Q253A	230
2.10D	A196G	150	3.2A	F225A	5	3.5F	I254A	231
2.10E	Y197A	159	3.2B	K226A	6	3.5G	Y255A	234
2.10F	P198A	168	3.2C	A227G	11	3.5H	Y256A	242
2.10G	N199A	169	3.2D	V228A	20	3.6A	N257A	249
2.10H	V200A	177	3.2E	N229A	58	3.6B	V258A	282
2.11A	S201A	184	3.2F	N230	102	3.6C	N259A	288
2.11B	A202G	191	3.2G	S231A	116	3.6D	V260A	290
2.11C	K203A	201	3.2H	L232A	119	3.6E	N261A	295
2.11D	I204A	204	3.3A	N233A	122	3.6F	E262A	296
2.11E	D205A	205	3.3B	V234A	128	3.6G	P263A	297
2.11F	Y206A	208	3.3C	N235A	146	3.6H	T264A	298

3.7A	R265A	5
3.7B	P266A	6
3.7C	S267A	11
3.7D	R268A	20
3.7E	F269A	58
3.7F	F270A	102
3.7G	G271A	116
3.7H	K272A	119
3.8A	A273G	122
3.8B	V274A	128
3.8C	T275A	146
3.8D	K276A	150
3.8E	E277A	159
3.8F	Q278A	168
3.8G	L279A	169
3.8H	Q280A	177
3.9A	A281G	184
3.9B	L282A	191
3.9C	G283A	201
3.9D	V284A	204
3.9E	N285A	205
3.9F	A286G	208
3.9G	E287A	209
3.9H	N288A	210
3.10A	P289A	211
3.10B	P290A	212
3.10C	A291G	213
3.10D	Y292A	219
3.10E	I293A	230
3.10F	S294A	231
3.10G	S295A	234
3.10H	V296A	242
3.11A	A297G	249
3.11B	Y298A	282
3.11C	G299A	288
3.11D	R300A	290
3.11E	Q301A	295
3.11F	V302A	296
3.11G	Y303A	297
3.11H	L304A	298
3.12A	K305A	5
3.12B	L306A	6
3.12C	S307A	11
3.12D	T308A	20
3.12E	N309A	58
3.12F	S310A	102
3.12G	H311A	116
3.12H	S312A	119
4.1A	T313A	122
4.1B	K314A	128
4.1C	V315A	146
4.1D	K316A	150
4.1E	A317G	159
4.1F	A318G	168
4.1G	F319A	169
4.1H	D320A	177
4.2A	A321G	184
4.2B	A322G	191
4.2C	V323A	201
4.2D	S324A	204
4.2E	G325A	205
4.2F	K326A	208
4.2G	S327A	209
4.2H	V328A	210
4.3A	S329A	211
4.3B	G330A	212
4.3C	D331A	213
4.3D	V332A	219
4.3E	E333A	230
4.3F	L334A	231
4.3G	T335A	234
4.3H	N336A	242
4.4A	I337A	249
4.4B	I338A	282
4.4C	K339A	288
4.4D	N340A	290
4.4E	S341A	295
4.4F	S342A	296
4.4G	F343A	297
4.4H	K344A	298
4.5A	A345G	5
4.5B	V346A	6
4.5C	I347A	11
4.5D	Y348A	20
4.5E	G349A	58
4.5F	G350A	102
4.5G	S351A	116

4.5H	A352G	119	4.9E	P381A	295	5.1B	T410A	212
4.6A	K353A	122	4.9F	G382A	296	5.1C	S411A	213
4.6B	D354A	128	4.9G	V383A	297	5.1D	K412A	219
4.6C	E355A	146	4.9H	P384A	298	5.1E	A413G	230
4.6D	V356A	150	4.10A	I385A	5	5.1F	Y414A	231
4.6E	Q357A	159	4.10B	A386G	6	5.1G	T415A	234
4.6F	I358A	168	4.10C	Y387A	11	5.1H	D416A	242
4.6G	I359A	169	4.10D	T388A	20	5.2A	G417A	249
4.6H	D360A	177	4.10E	T389A	58	5.2B	K418A	282
4.7A	G361A	184	4.10F	N390A	102	5.2C	I419A	288
4.7B	N362A	191	4.10G	F391A	116	5.2D	N420A	290
4.7C	L363A	201	4.10H	L392A	119	5.2E	I421A	295
4.7D	G364A	204	4.11A	K393A	122	5.2F	D422A	296
4.7E	D365A	205	4.11B	D394A	128	5.2G	H423A	297
4.7F	L366A	208	4.11C	N395A	146	5.2H	S424A	298
4.7G	R367A	209	4.11D	E396A	150	5.3A	G425A	5
4.7H	D368A	210	4.11E	L397A	159	5.3B	G426A	6
4.8A	I369A	211	4.11F	A398G	168	5.3C	Y427A	11
4.8B	L370A	212	4.11G	V399A	169	5.3D	V428A	20
4.8C	K371A	213	4.11H	I400A	177	5.3E	A429G	58
4.8D	K372A	219	4.12A	K401A	184	5.3F	Q430A	102
4.8E	G373A	230	4.12B	N402A	191	5.3G	F431A	116
4.8F	A374G	231	4.12C	N403A	201	5.3H	N432A	119
4.8G	T375A	234	4.12D	S404A	204	5.4A	I433A	122
4.8H	F376A	242	4.12E	E405A	205	5.4B	S434A	128
4.9A	N377A	249	4.12F	Y406A	208	5.4C	W435A	146
4.9B	R378A	282	4.12G	I407A	209	5.4D	D436A	150
4.9C	E379A	288	4.12H	E408A	210	5.4E	E437A	159
4.9D	T380A	290	5.1A	T409A	211	5.4F	V438A	168

5.4G	N439A	169	5.8D	I468A	20	5.12A	D497A	249
5.4H	Y440A	177	5.8E	Y469A	58	5.12B	D498A	282
5.5A	D441A	184	5.8F	L470A	102	5.12C	R499A	288
5.5B	P442A	191	5.8G	P471A	116	5.12D	N500A	290
5.5C	E443A	201	5.8H	G472A	119	5.12E	L501A	295
5.5D	G444A	204	5.9A	N473A	122	5.12F	P502A	296
5.5E	N445A	205	5.9B	A474G	128	5.12G	L503A	297
5.5F	E446A	208	5.9C	R475A	146	5.12H	V504A	298
5.5G	I447A	209	5.9D	N476A	150	6.1A	K505A	5
5.5H	V448A	210	5.9E	I477A	159	6.1B	N506A	6
5.6A	Q449A	211	5.9F	N478A	168	6.1C	R507A	11
5.6B	H450A	212	5.9G	V479A	169	6.1D	N508A	20
5.6C	K451A	213	5.9H	Y480A	177	6.1E	I509A	58
5.6D	N452A	219	5.10A	A481G	184	6.1F	S510A	102
5.6E	W453A	230	5.10B	K482A	191	6.1G	I511A	116
5.6F	S454A	231	5.10C	E483A	201	6.1H	W512A	119
5.6G	E455A	234	5.10D	C484A	204	6.2A	G513A	122
5.6H	N456A	242	5.10E	T485A	205	6.2B	T514A	128
5.7A	N457A	249	5.10F	G486A	208	6.2C	T515A	146
5.7B	K458A	282	5.10G	L487A	209	6.2D	L516A	150
5.7C	S459A	288	5.10H	A488G	210	6.2E	Y517A	159
5.7D	K460A	290	5.11A	W489A	211	6.2F	P518A	168
5.7E	L461A	295	5.11B	E490A	212	6.2G	K519A	169
5.7F	A462G	296	5.11C	W491A	213	6.2H	Y520A	177
5.7G	H463A	297	5.11D	W492A	219	6.3A	S521A	184
5.7H	F464A	298	5.11E	R493A	230	6.3B	N522A	191
5.8A	T465A	5	5.11F	T494A	231	6.3C	K523A	201
5.8B	S466A	6	5.11G	V495A	234	6.3D	V524A	204
5.8C	S467A	11	5.11H	I496A	242	6.3E	D525A	205

6.3F	N526A	208	6.3H	I528A	210
6.3G	P527A	209	6.4A	E529A	211

Supplemental Table 2.
Signature tag sequences

ST	Sequence
5	ATCTACAACCAACCCCCGCAAACTCTCCCGCCCTCTAGCA
6	CCATAGCTACCACACGATAGCTCCCCCTAGCCCCCTACTC
11	CGGGGTGGTGTGTGGGAGGTTTAGAGGTTTATTTCGTGTG
20	ATCAACAACTACCGACCACGATCGACATCCAACGCCCCAT
58	CGCAAAATCACTAGCCCTATAGCGACCCCTCTACCCCAAC
102	AACCATAGCGATATCTACCCCAATCTCTCGCCCCCTCTAC
116	GGATGGCGGAGATGGAGCTCTTGGGTGCTCTTGCGGTTG
119	CGCCCCCTCCCCACATAAAGAGAGCTAAACAAAAACATCA
122	ACAGCTCCAAACCTCGCTAAACAGCCCACCCACTCTCCAC
128	TTAGGTAGGTGTATGTGGCGAGGGCGCTGGAGAGAGATAG
146	CGCCATATCGCCACCCCACTAGCCCCCCCTCACCACCTCT
150	ATATACCGCTCAACATACACCCCCATCCCCCCACCTCGCA
159	AAACACCGAACACCCCCCCACGCACCAGACACACAACCAG
168	ATATAACAATCCCTAGCCCCCTATCCAGCCATCTCTCCCC
169	GGTTCGGGATAGTGATATAGATGTGGGGGGGTGGGCTCG
177	AGATGGAGATGGGGAGTTGGTGGTCGGGGTGGCGGGTAT
184	CTCTATCTAGCTCGAGCCATATATCGCCACCTACCCCCCC
191	AACTACCGCAAACGCTCGCTAAAAACATCCATATCTAAC
201	CTCCCTCCCTCCACCTACCCTCTATCTCGAGAAAGCTCC
204	TTAGCGATCTCTCGCGCTTGGGGGATAGCTATATGGGTAT
205	CCCCCGCTACCCTGATATCCCCCTTTCCGCTCTCTAGCA
208	GTCGAGCTATAGGGATCTAGTGGTATAGGGGTTTGGGTCG
209	TTATGGGTAGAGCGAGATTGTGCTATTGCTAGAGTGATAG
210	GGAGCGGGATGGAGCGTTGTGGCGGGCTCTAGATCGGGTG
211	GGAGAGCGGTCGCTTTATAGCGATTTATATATATCTAGTT
212	GTAGAGATATAGAGCGATCGCGTTATAGATGTATTGCTGG
213	ACATAGACACATCAAAATCCCCAGCTCTCTAGCGCCATAA
219	CCCTAAAACCCTACAGCAATCACGATATACCGCTCCCGAC
230	CCAGACCCAGACCTATCGCCCTACCTACATAGAAACACCA
231	CTAAAGCACTCTTAGCCCGAGAGATCCCAACATCACGCGAC
234	AACCCCCGAACCAGCCAGCACTCCGATATATCTCACCAACC

242	ATTTCGATGTATATATGTAGCGATAGGGGTGTCGCTTTAG
249	ATATATATGTCGATCGCTGGCGCGCGATGGATATGGTGAT
282	ACAGAACGCGATAACTCTCTATAGCAAAACCAATCCCACC
288	CTATCCAACTAGACCTCTAGCTACATCGCTCACTACCCCC
290	ATCTCTCACCACCGCGACCGACAGCTCGAACAAGCAAGAG
295	ACACCTACATCAAACCCTCCCCAGAGAAAGATAAACCTCC
296	GTGGATAGTGAGGGCGGGCGAGAGCTTGCTTGCGCGAGTG
297	GATCCGTCGCCAAATCGAGTCAGAGGTCTAGCTATCGCGACACTG
298	GATCCGTCTTTGGCAAAGAGTACCCTGGATCAGTCTCGAGTGCG

Supplemental Table 3.
Mutagenic primers for site-directed mutagenesis

K2A-F	AGAGTGAAACCCATGGCAAAAATAATGCTAGTT
K2A-R	AACTAGCATTATTTTTGCCATGGGTTTCACTCT
K3A-F	GTGAAACCCATGAAAGCAATAATGCTAGTTTTT
K3A-R	AAAAACTAGCATTATTGCTTTCATGGGTTTCAC
I4A-F	AAACCCATGAAAAAAGCAATGCTAGTTTTTATT
I4A-R	AATAAAAACTAGCATTGCTTTTTTCATGGGTTT
M5A-F	CCCATGAAAAAAATAGCGCTAGTTTTTATTACA
M5A-R	TGTAATAAAAACTAGCGCTATTTTTTTCATGGG
L6A-F	ATGAAAAAAATAATGGCAGTTTTTATTACACTT
L6A-R	AAGTGTAATAAAAACTGCCATTATTTTTTTCAT
V7A-F	AAAAAAATAATGCTAGCTTTTATTACACTTATA
V7A-R	TATAAGTGTAATAAAAGCTAGCATTATTTTTTT
F8A-F	AAAATAATGCTAGTTGCTATTACACTTATATTA
F8A-R	TAATATAAGTGTAATAGCAACTAGCATTATTTT
I9A-F	ATAATGCTAGTTTTTGCTACACTTATATTAGTT
I9A-R	AACTAATATAAGTGTAGCAAAAACTAGCATTAT
T10A-F	ATGCTAGTTTTTATTGCACTTATATTAGTTAGT
T10A-R	ACTAACTAATATAAGTGCAATAAAAACTAGCAT
L11A-F	CTAGTTTTTATTACAGCTATATTAGTTAGTCTA
L11A-R	TAGACTAACTAATATAGCTGTAATAAAAACTAG
I12A-F	GTTTTTATTACACTTGCATTAGTTAGTCTACCA
I12A-R	TGGTAGACTAACTAATGCAAGTGTAATAAAAAC
L13A-F	TTTATTACACTTATAGCAGTTAGTCTACCAATT
L13A-R	AATTGGTAGACTAACTGCTATAAGTGTAATAAA
V14A-F	ATTACACTTATATTAGCTAGTCTACCAATTGCG
V14A-R	CGCAATTGGTAGACTAGCTAATATAAGTGTAAT
S15A-F	ACACTTATATTAGTTGCTCTACCAATTGCGCAA
S15A-R	TTGCGCAATTGGTAGAGCAACTAATATAAGTGT
L16A-F	CTTATATTAGTTAGTGCACCAATTGCGCAACAA
L16A-R	TTGTTGCGCAATTGGTGCACTAACTAATATAAG
P17A-F	ATATTAGTTAGTCTAGCAATTGCGCAACAAACT
P17A-R	AGTTTGTTGCGCAATTGCTAGACTAACTAATAT
I18A-F	TTAGTTAGTCTACCAGCTGCGCAACAAACTGAA
I18A-R	TTCAGTTTGTTGCGCAGCTGGTAGACTAACTAA
A19G-F	GTTAGTCTACCAATTGGGCAACAAACTGAAGCA
A19G-R	TGCTTCAGTTTGTTGCCCAATTGGTAGACTAAC
Q20A-F	AGTCTACCAATTGCGGCACAAACTGAAGCAAAG
Q20A-R	CTTTGCTTCAGTTTGTGCCGCAATTGGTAGACT
Q21A-F	CTACCAATTGCGCAAGCAACTGAAGCAAAGGAT
Q21A-R	ATCCTTTGCTTCAGTTGCTTGCGCAATTGGTAG
T22A-F	CCAATTGCGCAACAAGCTGAAGCAAAGGATGCA

T22A-R	TGCATCCTTTGCTTCAGCTTGTTGCGCAATTGG
E23A-F	ATTGCGCAACAAACTGCAGCAAAGGATGCATCT
E23A-R	AGATGCATCCTTTGCTGCAGTTTGTTGCGCAAT
A24G-F	GCGCAACAAACTGAAGGAAAGGATGCATCTGCA
A24G-R	TGCAGATGCATCCTTTCCTTCAGTTTGTTGCGC
K25A-F	CAACAAACTGAAGCAGCGGATGCATCTGCATTC
K25A-R	GAATGCAGATGCATCCGCTGCTTCAGTTTGTTG
D26A-F	CAAACTGAAGCAAAGGCTGCATCTGCATTCAAT
D26A-R	ATTGAATGCAGATGCAGCCTTTGCTTCAGTTTG
A27G-F	ACTGAAGCAAAGGATGGATCTGCATTCAATAAA
A27G-R	TTTATTGAATGCAGATCCATCCTTTGCTTCAGT
A29G-F	GAAGCAAAGGATGCAGCTGCATTCAATAAAGAA
A27G-R	TTCTTTATTGAATGCAGCTGCATCCTTTGCTTC
S28A-F	GCAAAGGATGCATCTGGATTCAATAAAGAAAAT
S28A-R	TTCTTTATTGAATGCAGCTGCATCCTTTGCTTC
A29G-F	GCAAAGGATGCATCTGGATTCAATAAAGAAAAT
A29G-R	ATTTTCTTTATTGAATCCAGATGCATCCTTTGC
F30A-F	AAGGATGCATCTGCAGCCAATAAAGAAAATTCA
F30A-R	TGAATTTTCTTTATTGGCTGCAGATGCATCCTT
N31A-F	GATGCATCTGCATTCGCTAAAGAAAATTCAATT
N31A-R	AATTGAATTTTCTTTAGCGAATGCAGATGCATC
K32A-F	GCATCTGCATTCAATGCAGAAAATTCAATTTCA
K32A-R	TGAAATTGAATTTTCTGCATTGAATGCAGATGC
E33A-F	TCTGCATTCAATAAAGCAAATTCAATTTCATCC
E33A-R	GGATGAAATTGAATTTGCTTTATTGAATGCAGA
N34A-F	GCATTCAATAAAGAAGCTTCAATTTCATCCATG
N34A-R	CATGGATGAAATTGAAGCTTCTTTATTGAATGC
S35A-F	TTCAATAAAGAAAATGCAATTTCATCCATGGCA
S35A-R	TGCCATGGATGAAATTGCATTTTCTTTATTGAA
I36A-F	AATAAAGAAAATTCAGCTTCATCCATGGCACCA
I36A-R	TGGTGCCATGGATGAAGCTGAATTTTCTTTATT
S37A-F	AAAGAAAATTCAATTGCATCCATGGCACCACCA
S37A-R	TGGTGGTGCCATGGATGCAATTGAATTTTCTTT
S38A-F	GAAAATTCAATTTCAGCCATGGCACCACCAGCA
S38A-R	TGCTGGTGGTGCCATGGCTGAAATTGAATTTTC
M39A-F	AATTCAATTTCATCCGCGGCACCACCAGCATCT
M39A-R	AGATGCTGGTGGTGCCGCGGATGAAATTGAATT
A40G-F	TCAATTTCATCCATGGGACCACCAGCATCTCCG
A40G-R	CGGAGATGCTGGTGGTCCCATGGATGAAATTGA
P41A-F	ATTTCATCCATGGCAGCACCAGCATCTCCGCCT
P41A-R	AGGCGGAGATGCTGGTGCTGCCATGGATGAAAT
P42A-F	TCATCCATGGCACCAGCAGCATCTCCGCCTGCA
P42A-R	TGCAGGCGGAGATGCTGCTGGTGCCATGGATGA
A43G-F	TCCATGGCACCACCAGGATCTCCGCCTGCAAGT

A43G-R	ACTTGCAGGCGGAGATCCTGGTGGTGCCATGGA
S44A-F	ATGGCACCACCAGCAGCTCCGCCTGCAAGTCCT
S44A-R	AGGACTTGCAGGCGGAGCTGCTGGTGGTGCCAT
P45A-F	GCACCACCAGCATCTGCGCCTGCAAGTCCTAAG
P45A-R	CTTAGGACTTGCAGGCGCAGATGCTGGTGGTGC
P46A-F	CCACCAGCATCTCCGGCTGCAAGTCCTAAGACG
P46A-R	CGTCTTAGGACTTGCAGCCGGAGATGCTGGTGG
A47G-F	CCAGCATCTCCGCCTGGAAGTCCTAAGACGCCA
A47G-R	TGGCGTCTTAGGACTTCCAGGCGGAGATGCTGG
S48A-F	GCATCTCCGCCTGCAGCTCCTAAGACGCCAATC
S48A-R	GATTGGCGTCTTAGGAGCTGCAGGCGGAGATGC
P49A-F	TCTCCGCCTGCAAGTGCTAAGACGCCAATCGAA
P49A-R	TTCGATTGGCGTCTTAGCACTTGCAGGCGGAGA
K50A-F	CCGCCTGCAAGTCCTGCGACGCCAATCGAAAAG
K50A-R	CTTTTCGATTGGCGTCGCAGGACTTGCAGGCGG
T51A-F	CCTGCAAGTCCTAAGGCGCCAATCGAAAAGAAA
T51A-R	TTTCTTTTCGATTGGCGCCTTAGGACTTGCAGG
P52A-F	GCAAGTCCTAAGACGGCAATCGAAAAGAAACAC
P52A-R	GTGTTTCTTTTCGATTGCCGTCTTAGGACTTGC
I53A-F	AGTCCTAAGACGCCAGCCGAAAAGAAACACGCG
I53A-R	CGCGTGTTTCTTTTCGGCTGGCGTCTTAGGACT
E54A-F	CCTAAGACGCCAATCGCAAAGAAACACGCGGAT
E54A-R	ATCCGCGTGTTTCTTTGCGATTGGCGTCTTAGG
K55A-F	AAGACGCCAATCGAAGCGAAACACGCGGATGAA
K55A-R	TTCATCCGCGTGTTTCGCTTCGATTGGCGTCTT
K56A-F	ACGCCAATCGAAAAGGCACACGCGGATGAAATC
K56A-R	GATTTCATCCGCGTGTGCCTTTTCGATTGGCGT
H57A-F	CCAATCGAAAAGAAAGCCGCGGATGAAATCGAT
H57A-R	ATCGATTTCATCCGCGGCTTTCTTTTCGATTGG
A58G-F	ATCGAAAAGAAACACGGGGATGAAATCGATAAG
A58G-R	CTTATCGATTTCATCCCCGTGTTTCTTTTCGAT
D59A-F	GAAAAGAAACACGCGGCTGAAATCGATAAGTAT
D59A-R	ATACTTATCGATTTCAGCCGCGTGTTTCTTTTC
E60A-F	AAGAAACACGCGGATGCAATCGATAAGTATATA
E60A-R	TATATACTTATCGATTGCATCCGCGTGTTTCTT
I61A-F	AAACACGCGGATGAAGCCGATAAGTATATACAA
I61A-R	TTGTATATACTTATCGGCTTCATCCGCGTGTTT
D62A-F	CACGCGGATGAAATCGCTAAGTATATACAAGGA
D62A-R	TCCTTGTATATACTTAGCGATTTCATCCGCGTG
K63A-F	GCGGATGAAATCGATGCGTATATACAAGGATTG
K63A-R	CAATCCTTGTATATACGCATCGATTTCATCCGC
Y64A-F	GATGAAATCGATAAGGCTATACAAGGATTGGAT
Y64A-R	ATCCAATCCTTGTATAGCCTTATCGATTTCATC
I65A-F	GAAATCGATAAGTATGCACAAGGATTGGATTAC

I65A-R	GTAATCCAATCCTTGTGCATACTTATCGATTTC
Q66A-F	ATCGATAAGTATATAGCAGGATTGGATTACAAT
Q66A-R	ATTGTAATCCAATCCTGCTATATACTTATCGAT
G67A-F	GATAAGTATATACAAGCATTGGATTACAATAAA
G67A-R	TTTATTGTAATCCAATGCTTGTATATACTTATC
L68A-F	AAGTATATACAAGGAGCGGATTACAATAAAAAC
L68A-R	GTTTTTATTGTAATCCGCTCCTTGTATATACTT
D69A-F	TATATACAAGGATTGGCTTACAATAAAAACAAT
D69A-R	ATTGTTTTTATTGTAAGCCAATCCTTGTATATA
Y70A-F	ATACAAGGATTGGATGCCAATAAAAACAATGTA
Y70A-R	TACATTGTTTTTATTGGCATCCAATCCTTGTAT
N71A-F	CAAGGATTGGATTACGCTAAAAACAATGTATTA
N71A-R	TAATACATTGTTTTTAGCGTAATCCAATCCTTG
K72A-F	GGATTGGATTACAATGCAAACAATGTATTAGTA
K72A-R	TACTAATACATTGTTTGCATTGTAATCCAATCC
N73A-F	TTGGATTACAATAAAGCCAATGTATTAGTATAC
N73A-R	GTATACTAATACATTGGCTTTATTGTAATCCAA
N74A-F	GATTACAATAAAAACGCTGTATTAGTATACCAC
N74A-R	GTGGTATACTAATACAGCGTTTTTATTGTAATC
V75A-F	TACAATAAAAACAATGCATTAGTATACCACGGA
V75A-R	TCCGTGGTATACTAATGCATTGTTTTTATTGTA
L76A-F	AATAAAAACAATGTAGCAGTATACCACGGAGAT
L76A-R	ATCTCCGTGGTATACTGCTACATTGTTTTTATT
V77A-F	AAAAACAATGTATTAGCATACCACGGAGATGCA
V77A-R	TGCATCTCCGTGGTATGCTAATACATTGTTTTT
Y78A-F	AACAATGTATTAGTAGCCCACGGAGATGCAGTG
Y78A-R	CACTGCATCTCCGTGGGCTACTAATACATTGTT
H79A-F	AATGTATTAGTATACGCCGGAGATGCAGTGACA
H79A-R	TGTCACTGCATCTCCGGCGTATACTAATACATT
G80A-F	GTATTAGTATACCACGCAGATGCAGTGACAAAT
G80A-R	ATTTGTCACTGCATCTGCGTGGTATACTAATAC
D81A-F	TTAGTATACCACGGAGCTGCAGTGACAAATGTG
D81A-R	CACATTTGTCACTGCAGCTCCGTGGTATACTAA
A82G-F	GTATACCACGGAGATGGAGTGACAAATGTGCCG
A82G-R	CGGCACATTTGTCACTCCATCTCCGTGGTATAC
V83A-F	TACCACGGAGATGCAGCGACAAATGTGCCGCCA
V83A-R	TGGCGGCACATTTGTCGCTGCATCTCCGTGGTA
T84A-F	CACGGAGATGCAGTGGCAAATGTGCCGCCAAGA
T84A-R	TCTTGGCGGCACATTTGCCACTGCATCTCCGTG
N85A-F	GGAGATGCAGTGACAGCTGTGCCGCCAAGAAAA
N85A-R	TTTTCTTGGCGGCACAGCTGTCACTGCATCTCC
V86A-F	GATGCAGTGACAAATGCGCCGCCAAGAAAAGGT
V86A-R	ACCTTTTCTTGGCGGCGCATTTGTCACTGCATC
P87A-F	GCAGTGACAAATGTGGCGCCAAGAAAAGGTTAC

P87A-R	GTAACCTTTTCTTGGCGCCACATTTGTCACTGC
P88A-F	GTGACAAATGTGCCGGCAAGAAAAGGTTACAAA
P88A-R	TTTGTAACCTTTTCTTGCCGGCACATTTGTCAC
R89A-F	ACAAATGTGCCGCCAGCAAAAGGTTACAAAGAT
R89A-R	ATCTTTGTAACCTTTTGCTGGCGGCACATTTGT
K90A-F	AATGTGCCGCCAAGAGCAGGTTACAAAGATGGA
K90A-R	TCCATCTTTGTAACCTGCTCTTGGCGGCACATT
G91A-F	GTGCCGCCAAGAAAAGCTTACAAAGATGGAAAT
G91A-R	ATTTCCATCTTTGTAAGCTTTTCTTGGCGGCAC
Y92A-F	CCGCCAAGAAAAGGTGCCAAAGATGGAAATGAA
Y92A-R	TTCATTTCCATCTTTGGCACCTTTTCTTGGCGG
K93A-F	CCAAGAAAAGGTTACGCAGATGGAAATGAATAT
K93A-R	ATATTCATTTCCATCTGCGTAACCTTTTCTTGG
D94A-F	AGAAAAGGTTACAAAGCTGGAAATGAATATATT
D94A-R	AATATATTCATTTCCAGCTTTGTAACCTTTTCT
G95A-F	AAAGGTTACAAAGATGCAAATGAATATATTGTT
G95A-R	AACAATATATTCATTTGCATCTTTGTAACCTTT
N96A-F	GGTTACAAAGATGGAGCTGAATATATTGTTGTG
N96A-R	CACAACAATATATTCAGCTCCATCTTTGTAACC
E97A-F	TACAAAGATGGAAATGCATATATTGTTGTGGAG
E97A-R	CTCCACAACAATATATGCATTTCCATCTTTGTA
Y98A-F	AAAGATGGAAATGAAGCTATTGTTGTGGAGAAA
Y98A-R	TTTCTCCACAACAATAGCTTCATTTCCATCTTT
I99A-F	GATGGAAATGAATATGCTGTTGTGGAGAAAAAG
I99A-R	CTTTTTCTCCACAACAGCATATTCATTTCCATC
V100A-F	GGAAATGAATATATTGCTGTGGAGAAAAAGAAG
V100A-R	CTTCTTTTTCTCCACAGCAATATATTCATTTCC
V101A-F	AATGAATATATTGTTGCGGAGAAAAAGAAGAAA
V101A-R	TTTCTTCTTTTTCTCCGCAACAATATATTCATT
E102A-F	GAATATATTGTTGTGGCGAAAAAGAAGAAATCC
E102A-R	GGATTTCTTCTTTTTCGCCACAACAATATATTC
K103A-F	TATATTGTTGTGGAGGCAAAGAAGAAATCCATC
K103A-R	GATGGATTTCTTCTTTGCCTCCACAACAATATA
K104A-F	ATTGTTGTGGAGAAAGCGAAGAAATCCATCAAT
K104A-R	ATTGATGGATTTCTTCGCTTTCTCCACAACAAT
K105A-F	GTTGTGGAGAAAAAGGCGAAATCCATCAATCAA
K105A-R	TTGATTGATGGATTTCGCCTTTTTCTCCACAAC
K106A-F	GTGGAGAAAAAGAAGGCATCCATCAATCAAAAT
K106A-R	ATTTTGATTGATGGATGCCTTCTTTTTCTCCAC
S107A-F	GAGAAAAAGAAGAAAGCCATCAATCAAAATAAT
S107A-R	ATTATTTTGATTGATGGCTTTCTTCTTTTTCTC
I108A-F	AAAAAGAAGAAATCCGCCAATCAAAATAATGCA
I108A-R	TGCATTATTTTGATTGGCGGATTTCTTCTTTTT
N109A-F	AAGAAGAAATCCATCGCTCAAAATAATGCAGAC

N109A-R	GTCTGCATTATTTTGAGCGATGGATTTCTTCTT
Q110A-F	AAGAAATCCATCAATGCAAATAATGCAGACATT
Q110A-R	AATGTCTGCATTATTTGCATTGATGGATTTCTT
N111A-F	AAATCCATCAATCAAGCTAATGCAGACATTCAA
N111A-R	TTGAATGTCTGCATTAGCTTGATTGATGGATTT
N112A-F	TCCATCAATCAAAATGCTGCAGACATTCAAGTT
N112A-R	AACTTGAATGTCTGCAGCATTTTGATTGATGGA
A113G-F	ATCAATCAAAATAATGGAGACATTCAAGTTGTG
A113G-R	CACAACTTGAATGTCTCCATTATTTTGATTGAT
D114A-F	AATCAAAATAATGCAGCCATTCAAGTTGTGAAT
D114A-R	ATTCACAACTTGAATGGCTGCATTATTTTGATT
I115A-F	CAAAATAATGCAGACGCTCAAGTTGTGAATGCA
I115A-R	TGCATTCACAACTTGAGCGTCTGCATTATTTTG
Q116A-F	AATAATGCAGACATTGCAGTTGTGAATGCAATT
Q116A-R	AATTGCATTCACAACTGCAATGTCTGCATTATT
V117A-F	AATGCAGACATTCAAGCTGTGAATGCAATTTCG
V117A-R	CGAAATTGCATTCACAGCTTGAATGTCTGCATT
V118A-F	GCAGACATTCAAGTTGCGAATGCAATTTCGAGC
V118A-R	GCTCGAAATTGCATTCGCAACTTGAATGTCTGC
N119A-F	GACATTCAAGTTGTGGCTGCAATTTCGAGCCTA
N119A-R	TAGGCTCGAAATTGCAGCCACAACTTGAATGTC
A120G-F	ATTCAAGTTGTGAATGGAATTTCGAGCCTAACC
A120G-R	GGTTAGGCTCGAAATTCCATTCACAACTTGAAT
I121A-F	CAAGTTGTGAATGCAGCTTCGAGCCTAACCTAT
I121A-R	ATAGGTTAGGCTCGAAGCTGCATTCACAACTTG
S122A-F	GTTGTGAATGCAATTGCGAGCCTAACCTATCCA
S122A-R	TGGATAGGTTAGGCTCGCAATTGCATTCACAAC
S123A-F	GTGAATGCAATTTCGGCCCTAACCTATCCAGGT
S123A-R	ACCTGGATAGGTTAGGGCCGAAATTGCATTCAC
L124A-F	AATGCAATTTCGAGCGCAACCTATCCAGGTGCT
L124A-R	AGCACCTGGATAGGTTGCGCTCGAAATTGCATT
T125A-F	GCAATTTCGAGCCTAGCCTATCCAGGTGCTCTC
T125A-R	GAGAGCACCTGGATAGGCTAGGCTCGAAATTGC
Y126A-F	ATTTCGAGCCTAACCGCTCCAGGTGCTCTCGTA
Y126A-R	TACGAGAGCACCTGGAGCGGTTAGGCTCGAAAT
P127A-F	TCGAGCCTAACCTATGCAGGTGCTCTCGTAAAA
P127A-R	TTTTACGAGAGCACCTGCATAGGTTAGGCTCGA
G128A-F	AGCCTAACCTATCCAGCTGCTCTCGTAAAAGCG
G128A-R	CGCTTTTACGAGAGCAGCTGGATAGGTTAGGCT
A129G-F	CTAACCTATCCAGGTGGTCTCGTAAAAGCGAAT
A129G-R	ATTCGCTTTTACGAGACCACCTGGATAGGTTAG
L130A-F	ACCTATCCAGGTGCTGCCGTAAAAGCGAATTCG
L130A-R	CGAATTCGCTTTTACGGCAGCACCTGGATAGGT
V131A-F	TATCCAGGTGCTCTCGCAAAAGCGAATTCGGAA

V131A-R	TTCCGAATTCGCTTTTGCGAGAGCACCTGGATA
K132A-F	CCAGGTGCTCTCGTAGCAGCGAATTCGGAATTA
K132A-R	TAATTCCGAATTCGCTGCTACGAGAGCACCTGG
A133G-F	GGTGCTCTCGTAAAAGGGAATTCGGAATTAGTA
A133G-R	TACTAATTCCGAATTCCCTTTTACGAGAGCACC
N134A-F	GCTCTCGTAAAAGCGGCTTCGGAATTAGTAGAA
N134A-R	TTCTACTAATTCCGAAGCCGCTTTTACGAGAGC
S135A-F	CTCGTAAAAGCGAATGCGGAATTAGTAGAAAAT
S135A-R	ATTTTCTACTAATTCCGCATTCGCTTTTACGAG
E136A-F	GTAAAAGCGAATTCGGCATTAGTAGAAAATCAA
E136A-R	TTGATTTTCTACTAATGCCGAATTCGCTTTTAC
L137A-F	AAAGCGAATTCGGAAGCAGTAGAAAATCAACCA
L137A-R	TGGTTGATTTTCTACTGCTTCCGAATTCGCTTT
V138A-F	GCGAATTCGGAATTAGCAGAAAATCAACCAGAT
V138A-R	ATCTGGTTGATTTTCTGCTAATTCCGAATTCGC
E139A-F	AATTCGGAATTAGTAGCAAATCAACCAGATGTT
E139A-R	AACATCTGGTTGATTTGCTACTAATTCCGAATT
N140A-F	TCGGAATTAGTAGAAGCTCAACCAGATGTTCTC
N140A-R	GAGAACATCTGGTTGAGCTTCTACTAATTCCGA
Q141A-F	GAATTAGTAGAAAATGCACCAGATGTTCTCCCT
Q141A-R	AGGGAGAACATCTGGTGCATTTTCTACTAATTC
P142A-F	TTAGTAGAAAATCAAGCAGATGTTCTCCCTGTA
P142A-R	TACAGGGAGAACATCTGCTTGATTTTCTACTAA
D143A-F	GTAGAAAATCAACCAGCTGTTCTCCCTGTAAAA
D143A-R	TTTTACAGGGAGAACAGCTGGTTGATTTTCTAC
V144A-F	GAAAATCAACCAGATGCTCTCCCTGTAAAACGT
V144A-R	ACGTTTTACAGGGAGAGCATCTGGTTGATTTTC
L145A-F	AATCAACCAGATGTTGCCCCTGTAAAACGTGAT
L145A-R	ATCACGTTTTACAGGGGCAACATCTGGTTGATT
P146A-F	CAACCAGATGTTCTCGCTGTAAAACGTGATTCA
P146A-R	TGAATCACGTTTTACAGCGAGAACATCTGGTTG
V147A-F	CCAGATGTTCTCCCTGCAAAACGTGATTCATTA
V147A-R	TAATGAATCACGTTTTGCAGGGAGAACATCTGG
K148A-F	GATGTTCTCCCTGTAGCACGTGATTCATTAACA
K148A-R	TGTTAATGAATCACGTGCTACAGGGAGAACATC
R149A-F	GTTCTCCCTGTAAAAGCTGATTCATTAACACTC
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D150A-F	CTCCCTGTAAAACGTGCTTCATTAACACTCAGC
D150A-R	GCTGAGTGTTAATGAAGCACGTTTTACAGGGAG
S151A-F	CCTGTAAAACGTGATGCATTAACACTCAGCATT
S151A-R	AATGCTGAGTGTTAATGCATCACGTTTTACAGG
L152A-F	GTAAAACGTGATTCAGCAACACTCAGCATTGAT
L152A-R	ATCAATGCTGAGTGTTGCTGAATCACGTTTTAC
T153A-F	AAACGTGATTCATTAGCACTCAGCATTGATTTG

T153A-R	CAAATCAATGCTGAGTGCTAATGAATCACGTTT
L154A-F	CGTGATTCATTAACAGCCAGCATTGATTTGCCA
L154A-R	TGGCAAATCAATGCTGGCTGTTAATGAATCACG
S155A-F	GATTCATTAACACTCGCCATTGATTTGCCAGGT
S155A-R	ACCTGGCAAATCAATGGCGAGTGTTAATGAATC
I156A-F	TCATTAACACTCAGCGCTGATTTGCCAGGTATG
I156A-R	CATACCTGGCAAATCAGCGCTGAGTGTTAATGA
D157A-F	TTAACACTCAGCATTGCTTTGCCAGGTATGACT
D157A-R	AGTCATACCTGGCAAAGCAATGCTGAGTGTTAA
L158A-F	ACACTCAGCATTGATGCGCCAGGTATGACTAAT
L158A-R	ATTAGTCATACCTGGCGCATCAATGCTGAGTGT
P159A-F	CTCAGCATTGATTTGGCAGGTATGACTAATCAA
P159A-R	TTGATTAGTCATACCTGCCAAATCAATGCTGAG
G160A-F	AGCATTGATTTGCCAGCTATGACTAATCAAGAC
G160A-R	GTCTTGATTAGTCATAGCTGGCAAATCAATGCT
M161A-F	ATTGATTTGCCAGGTGCGACTAATCAAGACAAT
M161A-R	ATTGTCTTGATTAGTCGCACCTGGCAAATCAAT
T162A-F	GATTTGCCAGGTATGGCTAATCAAGACAATAAA
T162A-R	TTTATTGTCTTGATTAGCCATACCTGGCAAATC
N163A-F	TTGCCAGGTATGACTGCTCAAGACAATAAAATC
N163A-R	GATTTTATTGTCTTGAGCAGTCATACCTGGCAA
Q164A-F	CCAGGTATGACTAATGCAGACAATAAAATCGTT
Q164A-R	AACGATTTTATTGTCTGCATTAGTCATACCTGG
D165A-F	GGTATGACTAATCAAGCCAATAAAATCGTTGTA
D165A-R	TACAACGATTTTATTGGCTTGATTAGTCATACC
N166A-F	ATGACTAATCAAGACGCTAAAATCGTTGTAAAA
N166A-R	TTTTACAACGATTTTAGCGTCTTGATTAGTCAT
K167A-F	ACTAATCAAGACAATGCAATCGTTGTAAAAAAT
K167A-R	ATTTTTTACAACGATTGCATTGTCTTGATTAGT
I168A-F	AATCAAGACAATAAAGCCGTTGTAAAAAATGCC
I168A-R	GGCATTTTTTACAACGGCTTTATTGTCTTGATT
V169A-F	CAAGACAATAAAATCGCTGTAAAAAATGCCACT
V169A-R	AGTGGCATTTTTTACAGCGATTTTATTGTCTTG
V170A-F	GACAATAAAATCGTTGCAAAAAATGCCACTAAA
V170A-R	TTTAGTGGCATTTTTTGCAACGATTTTATTGTC
K171A-F	AATAAAATCGTTGTAGCAAATGCCACTAAATCA
K171A-R	TGATTTAGTGGCATTTGCTACAACGATTTTATT
N172A-F	AAAATCGTTGTAAAAGCTGCCACTAAATCAAAC
N172A-R	GTTTGATTTAGTGGCAGCTTTTACAACGATTTT
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A173G-R	AACGTTTGATTTAGTGCCATTTTTTACAACGAT
T174A-F	GTTGTAAAAAATGCCGCTAAATCAAACGTTAAC
T174A-R	GTTAACGTTTGATTTAGCGGCATTTTTTACAAC
K175A-F	GTAAAAAATGCCACTGCATCAAACGTTAACAAC

K175A-R	GTTGTTAACGTTTGATGCAGTGGCATTTTTTAC
S176A-F	AAAAATGCCACTAAAGCAAACGTTAACAACGCA
S176A-R	TGCGTTGTTAACGTTTGCTTTAGTGGCATTTTT
N177A-F	AATGCCACTAAATCAGCCGTTAACAACGCAGTA
N177A-R	TACTGCGTTGTTAACGGCTGATTTAGTGGCATT
V178A-F	GCCACTAAATCAAACGCTAACAACGCAGTAAAT
V178A-R	ATTTACTGCGTTGTTAGCGTTTGATTTAGTGGC
N179A-F	ACTAAATCAAACGTTGCCAACGCAGTAAATACA
N179A-R	TGTATTTACTGCGTTGGCAACGTTTGATTTAGT
N180A-F	AAATCAAACGTTAACGCCGCAGTAAATACATTA
N180A-R	TAATGTATTTACTGCGGCGTTAACGTTTGATTT
A181G-F	TCAAACGTTAACAACGGAGTAAATACATTAGTG
A181G-R	CACTAATGTATTTACTCCGTTGTTAACGTTTGA
V182A-F	AACGTTAACAACGCAGCAAATACATTAGTGGAA
V182A-R	TTCCACTAATGTATTTGCTGCGTTGTTAACGTT
N183A-F	GTTAACAACGCAGTAGCTACATTAGTGGAAAGA
N183A-R	TCTTTCCACTAATGTAGCTACTGCGTTGTTAAC
T184A-F	AACAACGCAGTAAATGCATTAGTGGAAAGATGG
T184A-R	CCATCTTTCCACTAATGCATTTACTGCGTTGTT
L185A-F	AACGCAGTAAATACAGCAGTGGAAAGATGGAAT
L185A-R	ATTCCATCTTTCCACTGCTGTATTTACTGCGTT
V186A-F	GCAGTAAATACATTAGCGGAAAGATGGAATGAA
V186A-R	TTCATTCCATCTTTCCGCTAATGTATTTACTGC
E187A-F	GTAAATACATTAGTGGCAAGATGGAATGAAAAA
E187A-R	TTTTTCATTCCATCTTGCCACTAATGTATTTAC
R188A-F	AATACATTAGTGGAAGCATGGAATGAAAAATAT
R188A-R	ATATTTTTCATTCCATGCTTCCACTAATGTATT
W189A-F	ACATTAGTGGAAAGAGCGAATGAAAAATATGCT
W189A-R	AGCATATTTTTCATTCGCTCTTTCCACTAATGT
N190A-F	TTAGTGGAAAGATGGGCTGAAAAATATGCTCAA
N190A-R	TTGAGCATATTTTTCAGCCCATCTTTCCACTAA
E191A-F	GTGGAAAGATGGAATGCAAAATATGCTCAAGCT
E191A-R	AGCTTGAGCATATTTTGCATTCCATCTTTCCAC
K192A-F	GAAAGATGGAATGAAGCATATGCTCAAGCTTAT
K192A-R	ATAAGCTTGAGCATATGCTTCATTCCATCTTTC
Y193A-F	AGATGGAATGAAAAAGCTGCTCAAGCTTATCCA
Y193A-R	TGGATAAGCTTGAGCAGCTTTTTCATTCCATCT
A194G-F	TGGAATGAAAAATATGGTCAAGCTTATCCAAAT
A194A-R	ATTTGGATAAGCTTGACCATATTTTTCATTCCA
Q195A-F	AATGAAAAATATGCTGCAGCTTATCCAAATGTA
Q195A-R	TACATTTGGATAAGCTGCAGCATATTTTTCATT
A196G-F	GAAAAATATGCTCAAGGTTATCCAAATGTAAGT
A196G-R	ACTTACATTTGGATAACCTTGAGCATATTTTTC
Y197A-F	AAATATGCTCAAGCTGCTCCAAATGTAAGTGCA

Y197A-R	TGCACTTACATTTGGAGCAGCTTGAGCATATTT
P198A-F	TATGCTCAAGCTTATGCAAATGTAAGTGCAAAA
P198A-R	TTTTGCACTTACATTTGCATAAGCTTGAGCATA
N199A-F	GCTCAAGCTTATCCAGCTGTAAGTGCAAAAATT
N199A-R	AATTTTTGCACTTACAGCTGGATAAGCTTGAGC
V200A-F	CAAGCTTATCCAAATGCAAGTGCAAAAATTGAT
V200A-R	ATCAATTTTTGCACTTGCATTTGGATAAGCTTG
S201A-F	GCTTATCCAAATGTAGCTGCAAAAATTGATTAT
S201A-R	ATAATCAATTTTTGCAGCTACATTTGGATAAGC
A202G-F	TATCCAAATGTAAGTGGAAAAATTGATTATGAT
A202G-R	ATCATAATCAATTTTTCCACTTACATTTGGATA
K203A-F	CCAAATGTAAGTGCAGCAATTGATTATGATGAC
K203A-R	GTCATCATAATCAATTGCTGCACTTACATTTGG
I204A-F	AATGTAAGTGCAAAAGCTGATTATGATGACGAA
I204A-R	TTCGTCATCATAATCAGCTTTTGCACTTACATT
D205A-F	GTAAGTGCAAAAATTGCTTATGATGACGAAATG
D205A-R	CATTTCGTCATCATAAGCAATTTTTGCACTTAC
Y206A-F	AGTGCAAAAATTGATGCTGATGACGAAATGGCT
Y206A-R	AGCCATTTCGTCATCAGCATCAATTTTTGCACT
D207A-F	GCAAAAATTGATTATGCTGACGAAATGGCTTAC
D207A-R	GTAAGCCATTTCGTCAGCATAATCAATTTTTGC
D208A-F	AAAATTGATTATGATGCCGAAATGGCTTACAGT
D208A-R	ACTGTAAGCCATTTCGGCATCATAATCAATTTT
E209A-F	ATTGATTATGATGACGCAATGGCTTACAGTGAA
E209A-R	TTCACTGTAAGCCATTGCGTCATCATAATCAAT
M210A-F	GATTATGATGACGAAGCGGCTTACAGTGAATCA
M210A-R	TGATTCACTGTAAGCCGCTTCGTCATCATAATC
A211G-F	TATGATGACGAAATGGGTTACAGTGAATCACAA
A211G-R	TTGTGATTCACTGTAACCCATTTCGTCATCATA
Y212A-F	GATGACGAAATGGCTGCCAGTGAATCACAATTA
Y212A-R	TAATTGTGATTCACTGGCAGCCATTTCGTCATC
S213A-F	GACGAAATGGCTTACGCTGAATCACAATTAATT
S213A-R	AATTAATTGTGATTCAGCGTAAGCCATTTCGTC
E214A-F	GAAATGGCTTACAGTGCATCACAATTAATTGCG
E214A-R	CGCAATTAATTGTGATGCACTGTAAGCCATTTC
S215A-F	ATGGCTTACAGTGAAGCACAATTAATTGCGAAA
S215A-R	TTTCGCAATTAATTGTGCTTCACTGTAAGCCAT
Q216A-F	GCTTACAGTGAATCAGCATTAATTGCGAAATTT
Q216A-R	AAATTTCGCAATTAATGCTGATTCACTGTAAGC
L217A-F	TACAGTGAATCACAAGCAATTGCGAAATTTGGT
L217A-R	ACCAAATTTCGCAATTGCTTGTGATTCACTGTA
I218A-F	AGTGAATCACAATTAGCTGCGAAATTTGGTACA
I218A-R	TGTACCAAATTTCGCAGCTAATTGTGATTCACT
A219G-F	GAATCACAATTAATTGGGAAATTTGGTACAGCA

A219G-R	TGCTGTACCAAATTTCCCAATTAATTGTGATTC
K220A-F	TCACAATTAATTGCGGCATTTGGTACAGCATTT
K220A-R	AAATGCTGTACCAAATGCCGCAATTAATTGTGA
F221A-F	CAATTAATTGCGAAAGCTGGTACAGCATTTAAA
F221A-R	TTTAAATGCTGTACCAGCTTTCGCAATTAATTG
G222A-F	TTAATTGCGAAATTTGCTACAGCATTTAAAGCT
G222A-R	AGCTTTAAATGCTGTAGCAAATTTCGCAATTAA
T223A-F	ATTGCGAAATTTGGTGCAGCATTTAAAGCTGTA
T223A-R	TACAGCTTTAAATGCTGCACCAAATTTCGCAAT
A224G-F	GCGAAATTTGGTACAGGATTTAAAGCTGTAAAT
A224G-R	ATTTACAGCTTTAAATCCTGTACCAAATTTCGC
F225A-F	AAATTTGGTACAGCAGCTAAAGCTGTAAATAAT
F225A-R	ATTATTTACAGCTTTAGCTGCTGTACCAAATTT
K226A-F	TTTGGTACAGCATTTGCAGCTGTAAATAATAGC
K226A-R	GCTATTATTTACAGCTGCAAATGCTGTACCAAA
A227G-F	GGTACAGCATTTAAAGGTGTAAATAATAGCTTG
A227G-R	CAAGCTATTATTTACACCTTTAAATGCTGTACC
V228A-F	ACAGCATTTAAAGCTGCAAATAATAGCTTGAAT
V228A-R	ATTCAAGCTATTATTTGCAGCTTTAAATGCTGT
N229A-F	GCATTTAAAGCTGTAGCTAATAGCTTGAATGTA
N229A-R	TACATTCAAGCTATTAGCTACAGCTTTAAATGC
N230A-F	TTTAAAGCTGTAAATGCTAGCTTGAATGTAAAC
N230A-R	GTTTACATTCAAGCTAGCATTTACAGCTTTAAA
S231A-F	AAAGCTGTAAATAATGCCTTGAATGTAAACTTC
S231A-R	GAAGTTTACATTCAAGGCATTATTTACAGCTTT
L232A-F	GCTGTAAATAATAGCGCGAATGTAAACTTCGGC
L232A-R	GCCGAAGTTTACATTCGCGCTATTATTTACAGC
N233A-F	GTAAATAATAGCTTGGCTGTAAACTTCGGCGCA
N233A-R	TGCGCCGAAGTTTACAGCCAAGCTATTATTTAC
V234A-F	AATAATAGCTTGAATGCAAACTTCGGCGCAATC
V234A-R	GATTGCGCCGAAGTTTGCATTCAAGCTATTATT
N235A-F	AATAGCTTGAATGTAGCCTTCGGCGCAATCAGT
N235A-R	ACTGATTGCGCCGAAGGCTACATTCAAGCTATT
F236A-F	AGCTTGAATGTAAACGCCGGCGCAATCAGTGAA
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S240A-R	TTGCATTTTCCCTTCAGCGATTGCGCCGAAGTT
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G242A-R	TTCTTCTTGCATTTTCGCTTCACTGATTGCGCC
K243A-F	GCAATCAGTGAAGGGGCAATGCAAGAAGAAGTC
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M244A-R	AATGACTTCTTCTTGCGCTTTCCCTTCACTGAT
Q245A-F	AGTGAAGGGAAAATGGCAGAAGAAGTCATTAGT
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V248A-F	AAAATGCAAGAAGAAGCCATTAGTTTTAAACAA
V248A-R	TTGTTTAAAACTAATGGCTTCTTCTTGCATTTT
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I249A-R	AATTTGTTTAAAACTAGCGACTTCTTCTTGCAT
S250A-F	CAAGAAGAAGTCATTGCTTTTAAACAAATTTAC
S250A-R	GTAAATTTGTTTAAAAGCAATGACTTCTTCTTG
F251A-F	GAAGAAGTCATTAGTGCTAAACAAATTTACTAT
F251A-R	ATAGTAAATTTGTTTAGCACTAATGACTTCTTC
K252A-F	GAAGTCATTAGTTTTGCACAAATTTACTATAAC
K252A-R	GTTATAGTAAATTTGTGCAAAACTAATGACTTC
Q253A-F	GTCATTAGTTTTAAAGCAATTTACTATAACGTG
Q253A-R	CACGTTATAGTAAATTGCTTTAAAACTAATGAC
I254A-F	ATTAGTTTTAAACAAGCTTACTATAACGTGAAT
I254A-R	ATTCACGTTATAGTAAGCTTGTTTAAAACTAAT
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Y255A-R	AACATTCACGTTATAGGCAATTTGTTTAAAACT
Y256A-F	TTTAAACAAATTTACGCTAACGTGAATGTTAAT
Y256A-R	ATTAACATTCACGTTAGCGTAAATTTGTTTAAA
N257A-F	AAACAAATTTACTATGCCGTGAATGTTAATGAA
N257A-R	TTCATTAACATTCACGGCATAGTAAATTTGTTT
V258A-F	CAAATTTACTATAACGCGAATGTTAATGAACCT
V258A-R	AGGTTCATTAACATTCGCGTTATAGTAAATTTG
N259A-F	ATTTACTATAACGTGGCTGTTAATGAACCTACA
N259A-R	TGTAGGTTCATTAACAGCCACGTTATAGTAAAT
V260A-F	TACTATAACGTGAATGCTAATGAACCTACAAGA
V260A-R	TCTTGTAGGTTCATTAGCATTCACGTTATAGTA
N261A-F	TATAACGTGAATGTTGCTGAACCTACAAGACCT
N261A-R	AGGTCTTGTAGGTTCAGCAACATTCACGTTATA
E262A-F	AACGTGAATGTTAATGCACCTACAAGACCTTCC
E262A-R	GGAAGGTCTTGTAGGTGCATTAACATTCACGTT
P263A-F	GTGAATGTTAATGAAGCTACAAGACCTTCCAGA

P263A-R	TCTGGAAGGTCTTGTAGCTTCATTAACATTCAC
T264A-F	AATGTTAATGAACCTGCAAGACCTTCCAGATTT
T264A-R	AAATCTGGAAGGTCTTGCAGGTTCATTAACATT
R265A-F	GTTAATGAACCTACAGCACCTTCCAGATTTTTC
R265A-R	GAAAAATCTGGAAGGTGCTGTAGGTTCATTAAC
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P266A-R	GCCGAAAAATCTGGAAGCTCTTGTAGGTTCATT
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S267A-R	TTTGCCGAAAAATCTGGCAGGTCTTGTAGGTTC
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A273G-R	CTGCTCTTTAGTAACACCTTTGCCGAAAAATCT
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K276A-R	CGCTTGCAACTGCTCTGCAGTAACAGCTTTGCC
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Q280A-F	ACTAAAGAGCAGTTGGCAGCGCTTGGAGTGAAT
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L282A-F	GAGCAGTTGCAAGCGGCTGGAGTGAATGCAGAA
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G283A-F	CAGTTGCAAGCGCTTGCAGTGAATGCAGAAAAT
G283A-R	ATTTTCTGCATTCACTGCAAGCGCTTGCAACTG
V284A-F	TTGCAAGCGCTTGGAGCGAATGCAGAAAATCCT
V284A-R	AGGATTTTCTGCATTCGCTCCAAGCGCTTGCAA
N285A-F	CAAGCGCTTGGAGTGGCTGCAGAAAATCCTCCT

N285A-R	AGGAGGATTTTCTGCAGCCACTCCAAGCGCTTG
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E287A-F	CTTGGAGTGAATGCAGCAAATCCTCCTGCATAT
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N288A-F	GGAGTGAATGCAGAAGCTCCTCCTGCATATATC
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V328A-F	GTAAGCGGAAAATCTGCCTCAGGTGATGTAGAA
V328A-R	TTCTACATCACCTGAGGCAGATTTTCCGCTTAC
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S329A-R	TAGTTCTACATCACCTGCGACAGATTTTCCGCT
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G330A-R	TGTTAGTTCTACATCAGCTGAGACAGATTTTCC
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D331A-R	ATTTGTTAGTTCTACAGCACCTGAGACAGATTT
V332A-F	TCTGTCTCAGGTGATGCAGAACTAACAAATATC
V332A-R	GATATTTGTTAGTTCTGCATCACCTGAGACAGA
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E333A-R	GATGATATTTGTTAGTGCTACATCACCTGAGAC
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L334A-R	TTTGATGATATTTGTTGCTTCTACATCACCTGA
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T335A-R	ATTTTTGATGATATTTGCTAGTTCTACATCACC
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N336A-R	AGAATTTTTGATGATAGCTGTTAGTTCTACATC
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Y348A-R	TTTTGCGGAACCTCCGGCAATTACGGCTTTGAA
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A352G-R	TTGAACTTCATCTTTTCCGGAACCTCCGTAAAT
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K353A-R	GATTTGAACTTCATCTGCTGCGGAACCTCCGTA
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D354A-R	GATGATTTGAACTTCAGCTTTTGCGGAACCTCC
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I359A-F	GATGAAGTTCAAATCGCCGACGGCAACCTCGGA
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G364A-F	ATCGACGGCAACCTCGCAGACTTACGCGATATT
G364A-R	AATATCGCGTAAGTCTGCGAGGTTGCCGTCGAT
D365A-F	GACGGCAACCTCGGAGCCTTACGCGATATTTTG
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R367A-R	TTTTTTCAAAATATCGGCTAAGTCTCCGAGGTT
D368A-F	CTCGGAGACTTACGCGCTATTTTGAAAAAAGGC
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K372A-R	ATTAAAAGTAGCGCCTGCTTTCAAAATATCGCG
G373A-F	GATATTTTGAAAAAAGCCGCTACTTTTAATCGA

G373A-R	TCGATTAAAAGTAGCGGCTTTTTTCAAAATATC
A374G-F	ATTTTGAAAAAAGGCGGTACTTTTAATCGAGAA
A374G-R	TTCTCGATTAAAAGTACCGCCTTTTTTCAAAAT
T375A-F	TTGAAAAAAGGCGCTGCTTTTAATCGAGAAACA
T375A-R	TGTTTCTCGATTAAAAGCAGCGCCTTTTTTCAA
F376A-F	AAAAAAGGCGCTACTGCTAATCGAGAAACACCA
F376A-R	TGGTGTTTCTCGATTAGCAGTAGCGCCTTTTTT
N377A-F	AAAGGCGCTACTTTTGCTCGAGAAACACCAGGA
N377A-R	TCCTGGTGTTTCTCGAGCAAAAGTAGCGCCTTT
R378A-F	GGCGCTACTTTTAATGCAGAAACACCAGGAGTT
R378A-R	AACTCCTGGTGTTTCTGCATTAAAAGTAGCGCC
E379A-F	GCTACTTTTAATCGAGCAACACCAGGAGTTCCC
E379A-R	GGGAACTCCTGGTGTTGCTCGATTAAAAGTAGC
T380A-F	ACTTTTAATCGAGAAGCACCAGGAGTTCCCATT
T380A-R	AATGGGAACTCCTGGTGCTTCTCGATTAAAAGT
P381A-F	TTTAATCGAGAAACAGCAGGAGTTCCCATTGCT
P381A-R	AGCAATGGGAACTCCTGCTGTTTCTCGATTAAA
G382A-F	AATCGAGAAACACCAGCAGTTCCCATTGCTTAT
G382A-R	ATAAGCAATGGGAACTGCTGGTGTTTCTCGATT
V383A-F	CGAGAAACACCAGGAGCTCCCATTGCTTATACA
V383A-R	TGTATAAGCAATGGGAGCTCCTGGTGTTTCTCG
P384A-F	GAAACACCAGGAGTTGCCATTGCTTATACAACA
P384A-R	TGTTGTATAAGCAATGGCAACTCCTGGTGTTTC
I385A-F	ACACCAGGAGTTCCCGCTGCTTATACAACAAAC
I385A-R	GTTTGTTGTATAAGCAGCGGGAACTCCTGGTGT
A386G-F	CCAGGAGTTCCCATTGGTTATACAACAAACTTC
A386G-R	GAAGTTTGTTGTATAACCAATGGGAACTCCTGG
Y387A-F	GGAGTTCCCATTGCTGCTACAACAAACTTCCTA
Y387A-R	TAGGAAGTTTGTTGTAGCAGCAATGGGAACTCC
T388A-F	GTTCCCATTGCTTATGCAACAAACTTCCTAAAA
T388A-R	TTTTAGGAAGTTTGTTGCATAAGCAATGGGAAC
T389A-F	CCCATTGCTTATACAGCAAACTTCCTAAAAGAC
T389A-R	GTCTTTTAGGAAGTTTGCTGTATAAGCAATGGG
N390A-F	ATTGCTTATACAACAGCCTTCCTAAAAGACAAT
N390A-R	ATTGTCTTTTAGGAAGGCTGTTGTATAAGCAAT
F391A-F	GCTTATACAACAAACGCCCTAAAAGACAATGAA
F391A-R	TTCATTGTCTTTTAGGGCGTTTGTTGTATAAGC
L392A-F	TATACAACAAACTTCGCAAAAGACAATGAATTA
L392A-R	TAATTCATTGTCTTTTGCGAAGTTTGTTGTATA
K393A-F	ACAACAAACTTCCTAGCAGACAATGAATTAGCT
K393A-R	AGCTAATTCATTGTCTGCTAGGAAGTTTGTTGT
D394A-F	ACAAACTTCCTAAAAGCCAATGAATTAGCTGTT
D394A-R	AACAGCTAATTCATTGGCTTTTAGGAAGTTTGT
N395A-F	AACTTCCTAAAAGACGCTGAATTAGCTGTTATT

N395A-R	AATAACAGCTAATTCAGCGTCTTTTAGGAAGTT
E396A-F	TTCCTAAAAGACAATGCATTAGCTGTTATTAAA
E396A-R	TTTAATAACAGCTAATGCATTGTCTTTTAGGAA
L397A-F	CTAAAAGACAATGAAGCAGCTGTTATTAAAAAC
L397A-R	GTTTTTAATAACAGCTGCTTCATTGTCTTTTAG
A398G-F	AAAGACAATGAATTAGGTGTTATTAAAAACAAC
A398G-R	GTTGTTTTTAATAACACCTAATTCATTGTCTTT
V399A-F	GACAATGAATTAGCTGCTATTAAAAACAACTCA
V399A-R	TGAGTTGTTTTTAATAGCAGCTAATTCATTGTC
I400A-F	AATGAATTAGCTGTTGCTAAAAACAACTCAGAA
I400A-R	TTCTGAGTTGTTTTTAGCAACAGCTAATTCATT
K401A-F	GAATTAGCTGTTATTGCAAACAACTCAGAATAT
K401A-R	ATATTCTGAGTTGTTTGCAATAACAGCTAATTC
N402A-F	TTAGCTGTTATTAAAGCCAACTCAGAATATATT
N402A-R	AATATATTCTGAGTTGGCTTTAATAACAGCTAA
N403A-F	GCTGTTATTAAAAACGCCTCAGAATATATTGAA
N403A-R	TTCAATATATTCTGAGGCGTTTTTAATAACAGC
S404A-F	GTTATTAAAAACAACGCAGAATATATTGAAACA
S404A-R	TGTTTCAATATATTCTGCGTTGTTTTTAATAAC
E405A-F	ATTAAAAACAACTCAGCATATATTGAAACAACT
E405A-R	AGTTGTTTCAATATATGCTGAGTTGTTTTTAAT
Y406A-F	AAAAACAACTCAGAAGCTATTGAAACAACTTCA
Y406A-R	TGAAGTTGTTTCAATAGCTTCTGAGTTGTTTTT
I407A-F	AACAACTCAGAATATGCTGAAACAACTTCAAAA
I407A-R	TTTTGAAGTTGTTTCAGCATATTCTGAGTTGTT
E408A-F	AACTCAGAATATATTGCAACAACTTCAAAAGCT
E408A-R	AGCTTTTGAAGTTGTTGCAATATATTCTGAGTT
T409A-F	TCAGAATATATTGAAGCAACTTCAAAAGCTTAT
T409A-R	ATAAGCTTTTGAAGTTGCTTCAATATATTCTGA
T410A-F	GAATATATTGAAACAGCTTCAAAAGCTTATACA
T410A-R	TGTATAAGCTTTTGAAGCTGTTTCAATATATTC
S411A-F	TATATTGAAACAACTGCAAAAGCTTATACAGAT
S411A-R	ATCTGTATAAGCTTTTGCAGTTGTTTCAATATA
K412A-F	ATTGAAACAACTTCAGCAGCTTATACAGATGGA
K412A-R	TCCATCTGTATAAGCTGCTGAAGTTGTTTCAAT
A413G-F	GAAACAACTTCAAAAGGTTATACAGATGGAAAA
A413G-R	TTTTCCATCTGTATAACCTTTTGAAGTTGTTTC
Y414A-F	ACAACTTCAAAAGCTGCTACAGATGGAAAAATT
Y414A-R	AATTTTTCCATCTGTAGCAGCTTTTGAAGTTGT
T415A-F	ACTTCAAAAGCTTATGCAGATGGAAAAATTAAC
T415A-R	GTTAATTTTTCCATCTGCATAAGCTTTTGAAGT
D416A-F	TCAAAAGCTTATACAGCTGGAAAAATTAACATC
D416A-R	GATGTTAATTTTTCCAGCTGTATAAGCTTTTGA
G417A-F	AAAGCTTATACAGATGCAAAAATTAACATCGAT

G417A-R	ATCGATGTTAATTTTTGCATCTGTATAAGCTTT
K418A-F	GCTTATACAGATGGAGCAATTAACATCGATCAC
K418A-R	GTGATCGATGTTAATTGCTCCATCTGTATAAGC
I419A-F	TATACAGATGGAAAAGCTAACATCGATCACTCT
I419A-R	AGAGTGATCGATGTTAGCTTTTCCATCTGTATA
N420A-F	ACAGATGGAAAAATTGCCATCGATCACTCTGGA
N420A-R	TCCAGAGTGATCGATGGCAATTTTTCCATCTGT
I421A-F	GATGGAAAAATTAACGCCGATCACTCTGGAGGA
I421A-R	TCCTCCAGAGTGATCGGCGTTAATTTTTCCATC
D422A-F	GGAAAAATTAACATCGCTCACTCTGGAGGATAC
D422A-R	GTATCCTCCAGAGTGAGCGATGTTAATTTTTCC
H423A-F	AAAATTAACATCGATGCCTCTGGAGGATACGTT
H423A-R	AACGTATCCTCCAGAGGCATCGATGTTAATTTT
S424A-F	ATTAACATCGATCACGCTGGAGGATACGTTGCT
S424A-R	AGCAACGTATCCTCCAGCGTGATCGATGTTAAT
G425A-F	AACATCGATCACTCTGCAGGATACGTTGCTCAA
G425A-R	TTGAGCAACGTATCCTGCAGAGTGATCGATGTT
G426A-F	ATCGATCACTCTGGAGCATACGTTGCTCAATTC
G426A-R	GAATTGAGCAACGTATGCTCCAGAGTGATCGAT
Y427A-F	GATCACTCTGGAGGAGCCGTTGCTCAATTCAAC
Y427A-R	GTTGAATTGAGCAACGGCTCCTCCAGAGTGATC
V428A-F	CACTCTGGAGGATACGCTGCTCAATTCAACATT
V428A-R	AATGTTGAATTGAGCAGCGTATCCTCCAGAGTG
A429G-F	TCTGGAGGATACGTTGGTCAATTCAACATTTCT
A429G-R	AGAAATGTTGAATTGACCAACGTATCCTCCAGA
Q430A-F	GGAGGATACGTTGCTGCATTCAACATTTCTTGG
Q430A-R	CCAAGAAATGTTGAATGCAGCAACGTATCCTCC
F431A-F	GGATACGTTGCTCAAGCCAACATTTCTTGGGAT
F431A-R	ATCCCAAGAAATGTTGGCTTGAGCAACGTATCC
N432A-F	TACGTTGCTCAATTCGCCATTTCTTGGGATGAA
N432A-R	TTCATCCCAAGAAATGGCGAATTGAGCAACGTA
I433A-F	GTTGCTCAATTCAACGCTTCTTGGGATGAAGTA
I433A-R	TACTTCATCCCAAGAAGCGTTGAATTGAGCAAC
S434A-F	GCTCAATTCAACATTGCTTGGGATGAAGTAAAT
S434A-R	ATTTACTTCATCCCAAGCAATGTTGAATTGAGC
W435A-F	CAATTCAACATTTCTGCGGATGAAGTAAATTAT
W435A-R	ATAATTTACTTCATCCGCAGAAATGTTGAATTG
D436A-F	TTCAACATTTCTTGGGCTGAAGTAAATTATGAT
D436A-R	ATCATAATTTACTTCAGCCCAAGAAATGTTGAA
E437A-F	AACATTTCTTGGGATGCAGTAAATTATGATCCT
E437A-R	AGGATCATAATTTACTGCATCCCAAGAAATGTT
V438A-F	ATTTCTTGGGATGAAGCAAATTATGATCCTGAA
V438A-R	TTCAGGATCATAATTTGCTTCATCCCAAGAAAT
N439A-F	TCTTGGGATGAAGTAGCTTATGATCCTGAAGGT

N439A-R	ACCTTCAGGATCATAAGCTACTTCATCCCAAGA
Y440A-F	TGGGATGAAGTAAATGCTGATCCTGAAGGTAAC
Y440A-R	GTTACCTTCAGGATCAGCATTTACTTCATCCCA
D441A-F	GATGAAGTAAATTATGCTCCTGAAGGTAACGAA
D441A-R	TTCGTTACCTTCAGGAGCATAATTTACTTCATC
P442A-F	GAAGTAAATTATGATGCTGAAGGTAACGAAATT
P442A-R	AATTTCGTTACCTTCAGCATCATAATTTACTTC
E443A-F	GTAAATTATGATCCTGCAGGTAACGAAATTGTT
E443A-R	AACAATTTCGTTACCTGCAGGATCATAATTTAC
G444A-F	AATTATGATCCTGAAGCTAACGAAATTGTTCAA
G444A-R	TTGAACAATTTCGTTAGCTTCAGGATCATAATT
N445A-F	TATGATCCTGAAGGTGCCGAAATTGTTCAACAT
N445A-R	ATGTTGAACAATTTCGGCACCTTCAGGATCATA
E446A-F	GATCCTGAAGGTAACGCAATTGTTCAACATAAA
E446A-R	TTTATGTTGAACAATTGCGTTACCTTCAGGATC
I447A-F	CCTGAAGGTAACGAAGCTGTTCAACATAAAAAC
I447A-R	GTTTTTATGTTGAACAGCTTCGTTACCTTCAGG
V448A-F	GAAGGTAACGAAATTGCTCAACATAAAAACTGG
V448A-R	CCAGTTTTTATGTTGAGCAATTTCGTTACCTTC
Q449A-F	GGTAACGAAATTGTTGCACATAAAAACTGGAGC
Q449A-R	GCTCCAGTTTTTATGTGCAACAATTTCGTTACC
H450A-F	AACGAAATTGTTCAAGCTAAAAACTGGAGCGAA
H450A-R	TTCGCTCCAGTTTTTAGCTTGAACAATTTCGTT
K451A-F	GAAATTGTTCAACATGCAAACTGGAGCGAAAAC
K451A-R	GTTTTCGCTCCAGTTTGCATGTTGAACAATTTC
N452A-F	ATTGTTCAACATAAAGCCTGGAGCGAAAACAAT
N452A-R	ATTGTTTTCGCTCCAGGCTTTATGTTGAACAAT
W453A-F	GTTCAACATAAAAACGCGAGCGAAAACAATAAA
W453A-R	TTTATTGTTTTCGCTCGCGTTTTTATGTTGAAC
S454A-F	CAACATAAAAACTGGGCGGAAAACAATAAAAGC
S454A-R	GCTTTTATTGTTTTCCGCCCAGTTTTTATGTTG
E455A-F	CATAAAAACTGGAGCGCAAACAATAAAAGCAAG
E455A-R	CTTGCTTTTATTGTTTGCGCTCCAGTTTTTATG
N456A-F	AAAAACTGGAGCGAAGCCAATAAAAGCAAGCTA
N456A-R	TAGCTTGCTTTTATTGGCTTCGCTCCAGTTTTT
N457A-F	AACTGGAGCGAAAACGCTAAAAGCAAGCTAGCT
N457A-R	AGCTAGCTTGCTTTTAGCGTTTTCGCTCCAGTT
K458A-F	TGGAGCGAAAACAATGCAAGCAAGCTAGCTCAT
K458A-R	ATGAGCTAGCTTGCTTGCATTGTTTTCGCTCCA
S459A-F	AGCGAAAACAATAAAGCCAAGCTAGCTCATTTC
S459A-R	GAAATGAGCTAGCTTGGCTTTATTGTTTTCGCT
K460A-F	GAAAACAATAAAAGCGCGCTAGCTCATTTCACA
K460A-R	TGTGAAATGAGCTAGCGCGCTTTTATTGTTTTC
L461A-F	AACAATAAAAGCAAGGCAGCTCATTTCACATCG

L461A-R	CGATGTGAAATGAGCTGCCTTGCTTTTATTGTT
A462G-F	AATAAAAGCAAGCTAGGTCATTTCACATCGTCC
A462G-R	GGACGATGTGAAATGACCTAGCTTGCTTTTATT
H463A-F	AAAAGCAAGCTAGCTGCTTTCACATCGTCCATC
H463A-R	GATGGACGATGTGAAAGCAGCTAGCTTGCTTTT
F464A-F	AGCAAGCTAGCTCATGCCACATCGTCCATCTAT
F464A-R	ATAGATGGACGATGTGGCATGAGCTAGCTTGCT
T465A-F	AAGCTAGCTCATTTCGCATCGTCCATCTATTTG
T465A-R	CAAATAGATGGACGATGCGAAATGAGCTAGCTT
S466A-F	CTAGCTCATTTCACAGCGTCCATCTATTTGCCA
S466A-R	TGGCAAATAGATGGACGCTGTGAAATGAGCTAG
S467A-F	GCTCATTTCACATCGGCCATCTATTTGCCAGGT
S467A-R	ACCTGGCAAATAGATGGCCGATGTGAAATGAGC
I468A-F	CATTTCACATCGTCCGCCTATTTGCCAGGTAAC
I468A-R	GTTACCTGGCAAATAGGCGGACGATGTGAAATG
Y469A-F	TTCACATCGTCCATCGCTTTGCCAGGTAACGCG
Y469A-R	CGCGTTACCTGGCAAAGCGATGGACGATGTGAA
L470A-F	ACATCGTCCATCTATGCGCCAGGTAACGCGAGA
L470A-R	TCTCGCGTTACCTGGCGCATAGATGGACGATGT
P471A-F	TCGTCCATCTATTTGGCAGGTAACGCGAGAAAT
P471A-R	ATTTCTCGCGTTACCTGCCAAATAGATGGACGA
G472A-F	TCCATCTATTTGCCAGCTAACGCGAGAAATATT
G472A-R	AATATTTCTCGCGTTAGCTGGCAAATAGATGGA
N473A-F	ATCTATTTGCCAGGTGCCGCGAGAAATATTAAT
N473A-R	ATTAATATTTCTCGCGGCACCTGGCAAATAGAT
A474G-F	TATTTGCCAGGTAACGGGAGAAATATTAATGTT
A474G-R	AACATTAATATTTCTCCCGTTACCTGGCAAATA
R475A-F	TTGCCAGGTAACGCGGCAAATATTAATGTTTAC
R475A-R	GTAAACATTAATATTTGCCGCGTTACCTGGCAA
N476A-F	CCAGGTAACGCGAGAGCTATTAATGTTTACGCT
N476A-R	AGCGTAAACATTAATAGCTCTCGCGTTACCTGG
I477A-F	GGTAACGCGAGAAATGCTAATGTTTACGCTAAA
I477A-R	TTTAGCGTAAACATTAGCATTTCTCGCGTTACC
N478A-F	AACGCGAGAAATATTGCTGTTTACGCTAAAGAA
N478A-R	TTCTTTAGCGTAAACAGCAATATTTCTCGCGTT
V479A-F	GCGAGAAATATTAATGCTTACGCTAAAGAATGC
V479A-R	GCATTCTTTAGCGTAAGCATTAATATTTCTCGC
Y480A-F	AGAAATATTAATGTTGCCGCTAAAGAATGCACT
Y480A-R	AGTGCATTCTTTAGCGGCAACATTAATATTTCT
A481G-F	AATATTAATGTTTACGGTAAAGAATGCACTGGT
A481G-R	ACCAGTGCATTCTTTACCGTAAACATTAATATT
K482A-F	ATTAATGTTTACGCTGCAGAATGCACTGGTTTA
K482A-R	TAAACCAGTGCATTCTGCAGCGTAAACATTAAT
E483A-F	AATGTTTACGCTAAAGCATGCACTGGTTTAGCT

E483A-R	AGCTAAACCAGTGCATGCTTTAGCGTAAACATT
C484A-F	GTTTACGCTAAAGAAGCCACTGGTTTAGCTTGG
C484A-R	CCAAGCTAAACCAGTGGCTTCTTTAGCGTAAAC
T485A-F	CGCTAAAGAATGCGCTGGTTTAGCTTGGG
T485A-R	CCCAAGCTAAACCAGCGCATTCTTTAGCG
G486A-F	GCTAAAGAATGCACTGCTTTAGCTTGGGAATGG
G486A-R	CCATTCCCAAGCTAAAGCAGTGCATTCTTTAGC
L487A-F	GAATGCACTGGTGCAGCTTGGGAATGGTGG
L487A-R	CCACCATTCCCAAGCTGCACCAGTGCATTC
A488G-F	GAATGCACTGGTTTAGGTTGGGAATGGTGG
A488G-R	CCACCATTCCCAACCTAAACCAGTGCATTC
W489A-F	GCACTGGTTTAGCTGCGGAATGGTGGAGAACG
W489A-R	CGTTCTCCACCATTCCGCAGCTAAACCAGTGC
E490A-F	GGTTTAGCTTGGGCATGGTGGAGAACGG
E490A-R	CCGTTCTCCACCATGCCCAAGCTAAACC
W491A-F	GTTTAGCTTGGGAAGCGTGGAGAACGGTAAATG
W491A-R	CATTTACCGTTCTCCACGCTTCCCAAGCTAAAC
W492A-F	GCTTGGGAATGGGCGAGAACGGTAATTGATG
W492A-R	CATCAATTACCGTTCTCGCCCATTCCCAAGC
R493A-F	GGGAATGGTGGGCAACGGTAATTGATGACCG
R493A-R	CGGTCATCAATTACCGTTGCCCACCATTCCC
T494A-F	TGGGAATGGTGGAGAGCGGTAATTGATGACCGGAAC
T494A-R	GTTCCGGTCATCAATTACCGCTCTCCACCATTCCCA
V495A-F	GAATGGTGGAGAACGGCAATTGATGACCGGAACTTA
V495A-R	TAAGTTCCGGTCATCAATTGCCGTTCTCCACCATTC
I496A-F	TGGTGGAGAACGGTAGCTGATGACCGGAACTTACCA
I496A-R	TGGTAAGTTCCGGTCATCAGCTACCGTTCTCCACCA
D497A-F	TGGAGAACGGTAATTGCTGACCGGAACTTACCACTT
D497A-R	AAGTGGTAAGTTCCGGTCAGCAATTACCGTTCTCCA
D498A-F	AGAACGGTAATTGATGCCCGGAACTTACCACTTGTG
D498A-R	CACAAGTGGTAAGTTCCGGGCATCAATTACCGTTCT
R499A-F	ACGGTAATTGATGACGCGAACTTACCACTTGTGAAA
R499A-R	TTTCACAAGTGGTAAGTTCGCGTCATCAATTACCGT
N500A-F	GTAATTGATGACCGGGCCTTACCACTTGTGAAAAAT
N500A-R	ATTTTTCACAAGTGGTAAGGCCCGGTCATCAATTAC
L501A-F	ATTGATGACCGGAACGCACCACTTGTGAAAAATAGA
L501A-R	TCTATTTTTCACAAGTGGTGCGTTCCGGTCATCAAT
P502A-F	GATGACCGGAACTTAGCACTTGTGAAAAATAGAAAT
P502A-R	ATTTCTATTTTTCACAAGTGCTAAGTTCCGGTCATC
L503A-F	GACCGGAACTTACCAGCTGTGAAAAATAGAAATATC
L503A-R	GATATTTCTATTTTTCACAGCTGGTAAGTTCCGGTC
V504A-F	CGGAACTTACCACTTGCGAAAAATAGAAATATCTCC
V504A-R	GGAGATATTTCTATTTTTCGCAAGTGGTAAGTTCCG
K505A-F	AACTTACCACTTGTGGCAAATAGAAATATCTCCATC

K505A-R	GATGGAGATATTTCTATTTGCCACAAGTGGTAAGTT
N506A-F	TTACCACTTGTGAAAGCTAGAAATATCTCCATCTGG
N506A-R	CCAGATGGAGATATTTCTAGCTTTCACAAGTGGTAA
R507A-F	CCACTTGTGAAAAATGCAAATATCTCCATCTGGGGC
R507A-R	GCCCCAGATGGAGATATTTGCATTTTTCACAAGTGG
N508A-F	CTTGTGAAAAATAGAGCTATCTCCATCTGGGGCACC
N508A-R	GGTGCCCCAGATGGAGATAGCTCTATTTTTCACAAG
I509A-F	GTGAAAAATAGAAATGCCTCCATCTGGGGCACCACG
I509A-R	CGTGGTGCCCCAGATGGAGGCATTTCTATTTTTCAC
S510A-F	AAAAATAGAAATATCGCCATCTGGGGCACCACGCTT
S510A-R	AAGCGTGGTGCCCCAGATGGCGATATTTCTATTTTT
I511A-F	AATAGAAATATCTCCGCCTGGGGCACCACGCTTTAT
I511A-R	ATAAAGCGTGGTGCCCCAGGCGGAGATATTTCTATT
W512A-F	AGAAATATCTCCATCGCGGGCACCACGCTTTATCCG
W512A-R	CGGATAAAGCGTGGTGCCCGCGATGGAGATATTTCT
G513A-F	AATATCTCCATCTGGGCCACCACGCTTTATCCGAAA
G513A-R	TTTCGGATAAAGCGTGGTGGCCCAGATGGAGATATT
T514A-F	ATCTCCATCTGGGGCGCCACGCTTTATCCGAAATAT
T514A-R	ATATTTCGGATAAAGCGTGGCGCCCCAGATGGAGAT
T515A-F	TCCATCTGGGGCACCGCGCTTTATCCGAAATATAGT
T515A-R	ACTATATTTCGGATAAAGCGCGGTGCCCCAGATGGA
L516A-F	ATCTGGGGCACCACGGCTTATCCGAAATATAGTAAT
L516A-R	ATTACTATATTTCGGATAAGCCGTGGTGCCCCAGAT
Y517A-F	TGGGGCACCACGCTTGCTCCGAAATATAGTAATAAA
Y517A-R	TTTATTACTATATTTCGGAGCAAGCGTGGTGCCCCA
P518A-F	GGCACCACGCTTTATGCGAAATATAGTAATAAAGTA
P518A-R	TACTTTATTACTATATTTCGCATAAAGCGTGGTGCC
K519A-F	ACCACGCTTTATCCGGCATATAGTAATAAAGTAGAT
K519A-R	ATCTACTTTATTACTATATGCCGGATAAAGCGTGGT
Y520A-F	ACGCTTTATCCGAAAGCTAGTAATAAAGTAGATAAT
Y520A-R	ATTATCTACTTTATTACTAGCTTTCGGATAAAGCGT
S521A-F	CTTTATCCGAAATATGCTAATAAAGTAGATAATCCA
S521A-R	TGGATTATCTACTTTATTAGCATATTTCGGATAAAG
N522A-F	TATCCGAAATATAGTGCTAAAGTAGATAATCCAATC
N522A-R	GATTGGATTATCTACTTTAGCACTATATTTCGGATA
K523A-F	CCGAAATATAGTAATGCAGTAGATAATCCAATCGAA
K523A-R	TTCGATTGGATTATCTACTGCATTACTATATTTCGG
V524A-F	AAATATAGTAATAAAGCAGATAATCCAATCGAATAA
V524A-R	TTATTCGATTGGATTATCTGCTTTATTACTATATTT
D525A-F	TATAGTAATAAAGTAGCTAATCCAATCGAATAATTG
D525A-R	CAATTATTCGATTGGATTAGCTACTTTATTACTATA
N526A-F	AGTAATAAAGTAGATGCTCCAATCGAATAATTGTAA
N526A-R	TTACAATTATTCGATTGGAGCATCTACTTTATTACT
P527A-F	AATAAAGTAGATAATGCAATCGAATAATTGTAAAAG

P527A-R	CTTTTACAATTATTCGATTGCATTATCTACTTTATT
I528A-F	AAAGTAGATAATCCAGCCGAATAATTGTAAAAGTAA
I528A-R	TTACTTTTACAATTATTCGGCTGGATTATCTACTTT
E529A-F	GTAGATAATCCAATCGCATAATTGTAAAAGTAATAA
E529A-R	TTATTACTTTTACAATTATGCGATTGGATTATCTAC

Supplemental Table 4.
Signature-tag-specific amplification primers
(each used in combination with primer pPL2-359R)

Tag5	CCAACCCCCGCAAACTCTC
Tag6	CCATAGCTACCACACGATAGC
Tag11	GGTTTAGAGGTTTATTTCGTGTG
Tag20	ATCCAACGCCCCATGCTATT
Tag58	GACGTCCGCAAAATCACTAG
Tag102	CGATATCTACCCCAATCTCTC
Tag116	GGAGATGGAGCTCTTGGGT
Tag119	ATAAAGAGAGCTAAACAAAAACATC
Tag122	GACGTCACAGCTCCAAACC
Tag128	TAGGTGTATGTGGCGAGGG
Tag146	CCATATCGCCACCCCACTA
Tag150	ATATACCGCTCAACATACACC
Tag159	CAGACACACAACCAGGCTATT
Tag168	GACGTCATATAACAATCCCTAG
Tag169	GGTTCGGGATAGTGATATAGA
Tag177	AGATGGGGAGTTGGTGGTC
Tag184	GTCCTCTATCTAGCTCGAGC
Tag191	GACGTCAACTACCGCAAACG
Tag201	TATCTCGAGAAAGCTCCGCT
Tag204	GACGTCTTAGCGATCTCTCG
Tag205	GCTACCCTGATATCCCCCT
Tag208	CTAGAGGTATAGGGGTTTGGGTCG
Tag209	GTGCTATTGCTAGAGTGATAG
Tag210	TTGTGGCGGGCTCTAGATC
Tag211	GGTCGCTTTATAGCGATTTATA
Tag212	GATCGCGTTATAGATGTATTGC
Tag213	ACATAGACACATCAAAATCCCCAG
Tag219	CTACAGCAATCACGATATACC
Tag230	CGTCCCAGACCCAGACCTA
Tag231	GACGTCCTAAAGCACTCTTAG

Tag234	CAGCCAGCACTCCGATATAT
Tag242	ATTTCGATGTATATATGTAGCGA
Tag249	CGTCATATATATGTCGATCGC
Tag282	ACAGAACGCGATAACTCTCTA
Tag288	CTAGACCTCTAGCTACATCG
Tag290	ACCGACAGCTCGAACAAGC
Tag295	CCCCAGAGAAAGATAAACCTCC
Tag296	GACGTCGTGGATAGTGAGG
Tag297	CGAGTCAGAGGTCTAGCTAT
Tag298	CAGTCTCGAGTGCGGCTAT
pPL2-359R	CTTAATGAATTACAACAGTACTGC

Supplemental Table 5.
Primers used for signature tag sequence insertion to pPL2

Tag5-F	GTGAGTCGTATTGACGTCATCTACACCCAAACCCCGCAAACTCTCCCGCCCTCTAGCA GCTATTTAACGACCCTGCCC
Tag5-R	GGGCAGGGTCGTTAAATAGCTGCTAGAGGGCGGGAGAGTTTGCGGGGTTTGGGTGTAGATGACGTCAATACGACTCAC
Tag6-F	GTGAGTCGTATTGACGTCCCATAGCTACCACACGATAGCTCCCCCTAGCCCCCTACACGCTATTTAACGACCCTGCCC
Tag6-R	GGGCAGGGTCGTTAAATAGCGTGTAGGGGGCTAGGGGGAGCTATCGTGTGGTAGCTATGGGACGTCAATACGACTCAC
Tag11-F	GTGAGTCGTATTGACGTCCGGGGTGGTGTGTGGGAGGTTTAGAGGTTTATTTCGTGTGGCTATTTAACGACCCTGCCC
Tag11-R	GGGCAGGGTCGTTAAATAGCCACACGAAATAAACCTCTAAACCTCCCACACACCACCCCGGACGTCAATACGACTCAC
Tag20-F	GTGAGTCGTATTGACGTCATCAACAACTACCGACCACGATCGACATCCAACGCCCCATGCTATTTAACGACCCTGCCC
Tag20-R	GGGCAGGGTCGTTAAATAGCATGGGGCGTTGGATGTCGATCGTGGTCGGTAGTTGTTGATGACGTCAATACGACTCAC
Tag58-F	GTGAGTCGTATTGACGTCCGCAAAATCACTAGCCCTATAGCGACCCCTCTACCCCAACGCTATTTAACGACCCTGCCC
Tag58-R	GGGCAGGGTCGTTAAATAGCGTTGGGGTAGAGGGGTCGCTATAGGGCTAGTGATTTTGCGGACGTCAATACGACTCAC
Tag102-F	GTGAGTCGTATTGACGTCAACCATAGCGATATCTACCCCAATCTCTCGCCCCCTCTACGCTATTTAACGACCCTGCCC
Tag102-R	GGGCAGGGTCGTTAAATAGCGTAGAGGGGGCGAGAGATTGGGGTAGATATCGCTATGGTTGACGTCAATACGACTCAC
Tag116-F	GTGAGTCGTATTGACGTCGGATGGCGGAGATGGAGCTCTTGGGTGCTCTTGCGGTTGGCTATTTAACGACCCTGCCC

Tag116-R	GGGCAGGGTCGTTAAATAGCCAACCGCAAGAGCACCCAAGAGCTCCATCTCCGCCATCCGACGTCAATACGACTCAC
Tag119-F	GTGAGTCGTATTGACGTCCGCCCCCTCCCCACATAAAGAGAGCTAAACAAAAACATCAGCTATTTAACGACCCTGCCC
Tag119-R	GGGCAGGGTCGTTAAATAGCTGATGTTTTTGTTTAGCTCTCTTTATGTGGGGAGGGGGCGGACGTCAATACGACTCAC
Tag122-F	GTGAGTCGTATTGACGTCACAGCTCCAAACCTCGCTAAACAGCCCACCCACTCTCCACGCTATTTAACGACCCTGCCC
Tag122-R	GGGCAGGGTCGTTAAATAGCGTGGAGAGTGGGTGGGCTGTTTAGCGAGGTTTGGAGCTGTGACGTCAATACGACTCAC
Tag128-F	GTGAGTCGTATTGACGTCTTAGGTAGGTGTATGTGGCGAGGGCGCTGGAGAGAGATAGGCTATTTAACGACCCTGCCC
Tag128-R	GGGCAGGGTCGTTAAATAGCCTATCTCTCTCCAGCGCCCTCGCCACATACACCTACCTAAGACGTCAATACGACTCAC
Tag146-F	GTGAGTCGTATTGACGTCCGCCATATCGCCACCCCACTAGCCCCCCCTCACCACCTCTGCTATTTAACGACCCTGCCC
Tag146-R	GGGCAGGGTCGTTAAATAGCAGAGGTGGTGAGGGGGGGCTAGTGGGGTGGCGATATGGCGGACGTCAATACGACTCAC
Tag150-F	GTGAGTCGTATTGACGTCATATACCGCTCAACATACACCCCCATCCCCCCACCTCGCAGCTATTTAACGACCCTGCCC
Tag150-R	GGGCAGGGTCGTTAAATAGCTGCGAGGTGGGGGGATGGGGGTGTATGTTGAGCGGTATATGACGTCAATACGACTCAC
Tag159-F	GTGAGTCGTATTGACGTCAAACACCGAACACCCCCCCACGCACCAGACACACAACCAGGCTATTTAACGACCCTGCCC
Tag159-R	GGGCAGGGTCGTTAAATAGCCTGGTTGTGTGTCTGGTGCGTGGGGGGGTGTTCGGTGTTTGACGTCAATACGACTCAC
Tag168-F	GTGAGTCGTATTGACGTCATATAACAATCCCTAGCCCCCTATCCAGCCATCTCTCCCCGCTATTTAACGACCCTGCCC

Tag168-R	GGGCAGGGTCGTTAAATAGCGGGGAGAGATGGCTGGATAGGGGGCTAGGGATTGTTATATGACGTCAATACGACTCAC
Tag169-F	GTGAGTCGTATTGACGTCGGTTCGGGATAGTGATATAGATGTGGGGGGGGTGGGCTCGGCTATTTAACGACCCTGCCC
Tag169-R	GGGCAGGGTCGTTAAATAGCCGAGCCCACCCCCCCCACATCTATATCACTATCCCGAACCGACGTCAATACGACTCAC
Tag177-F	GTGAGTCGTATTGACGTCAGATGGAGATGGGGAGTTGGTGGTCGGGGTGGCGGGTATGCTATTTAACGACCCTGCCC
Tag177-R	GGGCAGGGTCGTTAAATAGCATACCCGCCACCCCGACCACCAACTCCCCATCTCCATCTGACGTCAATACGACTCAC
Tag184-F	GTGAGTCGTATTGACGTCCTCTATCTAGCTCGAGCCATATATCGCCACCTACCCCCCCGCTATTTAACGACCCTGCCC
Tag184-R	GGGCAGGGTCGTTAAATAGCGGGGGGGTAGGTGGCGATATATGGCTCGAGCTAGATAGAGGACGTCAATACGACTCAC
Tag191-F	GTGAGTCGTATTGACGTCAACTACCGCAAACGCTCGCTAAAAACATCCATATCTAACGCTATTTAACGACCCTGCCC
Tag191-R	GGGCAGGGTCGTTAAATAGCGTTAGATATGGATGTTTTTAGCGAGCGTTTGCGGTAGTTGACGTCAATACGACTCAC
Tag201-F	GTGAGTCGTATTGACGTCCTCCCTCCCTCCACCTCACCCTCTATCTCGAGAAAGCTCCGCTATTTAACGACCCTGCCC
Tag201-R	GGGCAGGGTCGTTAAATAGCGGAGCTTTCTCGAGATAGAGGGTGAGGTGGAGGGAGGGAGGACGTCAATACGACTCAC
Tag204-F	GTGAGTCGTATTGACGTCTTAGCGATCTCTCGCGCTTGGGGGATAGCTATATGGGTATGCTATTTAACGACCCTGCCC
Tag204-R	GGGCAGGGTCGTTAAATAGCATACCCATATAGCTATCCCCCAAGCGCGAGAGATCGCTAAGACGTCAATACGACTCAC
Tag205-F	GTGAGTCGTATTGACGTCCCCCCGCTACCCCGATATCCCCCTCTCCGCTCTCTAGCAGCTATTTAACGACCCTGCCC

Tag205-R	GGGCAGGGTCGTTAAATAGCTGCTAGAGAGCGGAGAGGGGGATATCGGGGTAGCGGGGGGACGTCAATACGACTCAC
Tag208-F	GTGAGTCGTATTGACGTCGTCGAGCTATAGGGATCTAGTGGTATAGGGGTTTGGGTCGGCTATTTAACGACCCTGCCC
Tag208-R	GGGCAGGGTCGTTAAATAGCCGACCCAAACCCCTATACCACTAGATCCCTATAGCTCGACGACGTCAATACGACTCAC
Tag209-F	GTGAGTCGTATTGACGTCTTATGGGTAGAGCGAGATTGTGCTATTGCTAGAGTGATAGGCTATTTAACGACCCTGCCC
Tag209-R	GGGCAGGGTCGTTAAATAGCCTATCACTCTAGCAATAGCACAATCTCGCTCTACCCATAAGACGTCAATACGACTCAC
Tag210-F	GTGAGTCGTATTGACGTCGGAGCGGGATGGAGCGTTGTGGCGGGCTCTAGATCGGGTGGCTATTTAACGACCCTGCCC
Tag210-R	GGGCAGGGTCGTTAAATAGCCACCCGATCTAGAGCCCGCCACAACGCTCCATCCCGCTCCGACGTCAATACGACTCAC
Tag211-F	GTGAGTCGTATTGACGTCGGAGAGCGGTCGCTTTATAGCGATTTATATATATCTAGTTGCTATTTAACGACCCTGCCC
Tag211-R	GGGCAGGGTCGTTAAATAGCAACTAGATATATATAAATCGCTATAAAGCGACCGCTCTCCGACGTCAATACGACTCAC
Tag212-F	GTGAGTCGTATTGACGTCGTAGAGATATAGAGCGATCGCGTTATAGATGTATTGCTGGGCTATTTAACGACCCTGCCC
Tag212-R	GGGCAGGGTCGTTAAATAGCCCAGCAATACATCTATAACGCGATCGCTCTATATCTCTACGACGTCAATACGACTCAC
Tag213-F	GTGAGTCGTATTGACGTCACATAGACACATCAAAATCCCCAGCTCTCTAGCGCCATAAGCTATTTAACGACCCTGCCC
Tag213-R	GGGCAGGGTCGTTAAATAGCTTATGGCGCTAGAGAGCTGGGGATTTTGATGTGTCTATGTGACGTCAATACGACTCAC
Tag219-F	GTGAGTCGTATTGACGTCCCCTAAAACCCTACAGCAATCACGATATACCGCTCCCGACGCTATTTAACGACCCTGCCC

Tag219-R	GGGCAGGGTCGTTAAATAGCCAGTGTCGCGATAGCTAGACCTCTGACTCGATTTGGCGACGGATCGACGTCAATACGACTCAC