

Table S1

Sample	Mapped Pairs	Fragments
gDNA_Pilot_Rep1	447816	189741
gDNA_Pilot_Rep2	480134	203572
gDNA_Pilot_Rep3	342594	143817
Plasmid_Pilot_Rep1	276964	472
Plasmid_Pilot_Rep2	399114	481
Plasmid_Pilot_Rep3	573080	540
gDNA_Final_Rep1	1317646	522946
gDNA_Final_Rep2	1035946	413343
gDNA_Final_Rep3	1466722	575167
Plasmid_Final_Batch1_Rep1	1500958	92822
Plasmid_Final_Batch1_Rep2	1318560	90347
Plasmid_Final_Batch1_Rep3	1501272	93088
Plasmid_Final_Batch2_Rep1	1457526	126868
Plasmid_Final_Batch2_Rep2	1723194	134349
Plasmid_Final_Batch2_Rep3	1740592	132963
Plasmid_Final_Batch3_Rep1	1467720	129278
Plasmid_Final_Batch3_Rep2	2712002	153399
Plasmid_Final_Batch3_Rep3	2207970	143289
Plasmid_Final_Batch4_Rep1	1588276	40770
Plasmid_Final_Batch4_Rep2	1418664	38870
Plasmid_Final_Batch4_Rep3	2323702	44937

Table S2

Accession	Annotation	Final gDNA	Final Plasmid	Paralogs	RNAseq, FPKM	Proteomics, Spectra
EHI_026690	protein kinase domain containing protein	-	-	-	0.01	2
EHI_093470	hypothetical protein	-	-	-	0.01	-
EHI_142370	hypothetical protein, conserved	-	-	1	0.01	-
EHI_052510	hypothetical protein	-	-	5	0.01	-
EHI_027230	hypothetical protein, conserved	-	-	2	0.01	-
EHI_009130	hypothetical protein	-	-	58	0.01	-
EHI_065120	hypothetical protein, conserved	-	-	1	0.01	-
EHI_073780	DNAJ homolog subfamily A member 2, putative	-	-	2	0.01	-
EHI_167840	WH2 motif domain containing protein	-	-	-	0.01	-
EHI_149330	hypothetical protein, conserved	-	-	2	0.01	-
EHI_162670	hypothetical protein	-	-	-	0.01	-
EHI_130360	modulator of drug activity B homolog, putative	-	-	-	0.01	-
EHI_126760	hypothetical protein	-	-	-	0.01	-
EHI_008920	hypothetical protein	-	-	4	0.01	-
EHI_040950	hypothetical protein	-	-	1	0.01	-
EHI_185010	ribosomal protein L10, putative	-	-	2	0.17	1
EHI_046900	4-alpha-glucanotransferase, putative	-	-	1	0.01	-
EHI_115050	protein kinase, putative	-	-	58	0.01	-
EHI_093460	hypothetical protein	-	-	-	0.01	-
EHI_200340	hypothetical protein	-	-	-	0.01	-
EHI_159040	plasma membrane calcium ion-transporting ATPase, putative	-	-	6	0.01	-
EHI_077770	UDP-glucose:glyco protein glucosyltransferase 1 precursor, putative	-	-	-	0.1	-
EHI_157570	tRNA-Asp (anticodon: GTC)	+	-	-	0.5	-
EHI_087110	hypothetical protein, conserved	+	-	3	432.1	-
EHI_153620	prolyl oligopeptidase family protein	+	-	2	0.05	-
EHI_157670	hypothetical protein	+	-	4	0.56	-

Table S3

Accession	Annotation	Final gDNA	Final Plasmid	Paralogs	RNAseq, FPKM	Proteomics, Spectra
EHI_148050	hypothetical protein, conserved	+	+	-	169.21	22
EHI_148280	p21-activated kinase	+	+	1	404.02	28
EHI_148450	hypothetical protein	+	+	-	17.41	-
EHI_148490	hypothetical protein, conserved	+	+	-	7.62	-
EHI_148550	protein tyrosine kinase domain-containing protein	+	+	13	3.55	-
EHI_148680	hypothetical protein, conserved	+	+	-	18.06	7
EHI_148770	hypothetical protein, conserved	+	+	-	7.66	4
EHI_148840	RhoGAP domain containing protein	+	+	-	16.71	-
EHI_148870	hypothetical protein	+	+	-	38.06	4
EHI_149020	hypothetical protein	+	+	-	3.46	-

Table S4

Primer	Purpose	Sequence
BAR_1FF_F	Cloning	TTAAAAACAAAAATTGCAGCATCAACGCCACCAGATGCAGGAAGATCATCA
BAR_1FF_R	Cloning	GTTTAAAAAAGAAGAGTTCAACTCGAGCCCCTCCACTCCACCAATCACCT
BAR_RTPCR_F	RT-PCR	AGGCTTGTTGAGGCATGTACTA
BAR_RTPCR_R	RT-PCR	AAGTTCTCCACTCCACCAATCA
MSP1_1FF_F	Cloning	TTGCAGCATCAACGCCCGGAATAATCAGAAACGAAATATTTTTGG
MSP1_1FF_R	Cloning	AAAGAAGAGTTCAACTCGAGACTAGATGAAAAACATCTTGAATCTT
MSP1_RTPCR_F	RT-PCR	GGTGAGACTCAAGCAAGGGG
MSP1_RTPCR_R	RT-PCR	GGCCATTCTTCTACTTCGCCA
Adaptor1primer_F	Library construction	ACACTCTTCCCTACACGAC
Adaptor2primer_R	Library construction	GTGACTGGAGTTCAGACGTGT
SG0_F	Cloning	TTAAAAACAAAAATTGCAGCATCAACGCCCATGTCTTCCAATTACCAC
SG0_R	Cloning	GTTTAAAAAAGAAGAGTTCAACTCGAGCCCTTGAGGGGAAAAGTGAA
SG1i_F	Cloning	TTAAAAACAAAAATTGCAGCATCAACGCCCGTGATGATACTTCTGTCTCTAAC
SG1i_R	Cloning	GTTTAAAAAAGAAGAGTTCAACTCGAGCCCCGATACAACGCTCAGTATCTC
SG2i_F	Cloning	TTAAAAACAAAAATTGCAGCATCAACGCCCCATTACCACATTAAGTCTTC
SG2i_R	Cloning	GTTTAAAAAAGAAGAGTTCAACTCGAGCCCGGATAAACAAGAACTAAGTTTTG
SG0_RTPCR_F	RT-PCR	GCTCTTGAGCCTCATATTAGT
SG0_RTPCR_R	RT-PCR	CAACGAACTTCCAGTTGACTAC
SG1_RTPCR_F	RT-PCR	GGAGATACTGAGCGTTGTATCG
SG1_RTPCR_R	RT-PCR	GCATACTGTGTTTCTCC
SG2_RTPCR_F	RT-PCR	CATGCCTCACCACATTTACT
SG2_RTPCR_R	RT-PCR	ACCAAATCCCATCCTTCAA
GAPDH_RTPCR_F	RT-PCR	CGTCCACAGACAATTCGAAGGAAC
GAPDH_RTPCR_R	RT-PCR	AAGGCAGTTGGTTGTGCATGA
CS5'_F	Sanger sequencing	TCAGTCTTACCACGTCATAAAGT
CS3'_R	Sanger sequencing	TGCAAGAAGATGTTACAAAGCA
LibraryRNAiSeq_F	Sanger sequencing	ACACTCTTCCCTACACGACG
LibraryRNAiSeq_R	Sanger sequencing	GTGACTGGAGTTCAGACGTGT