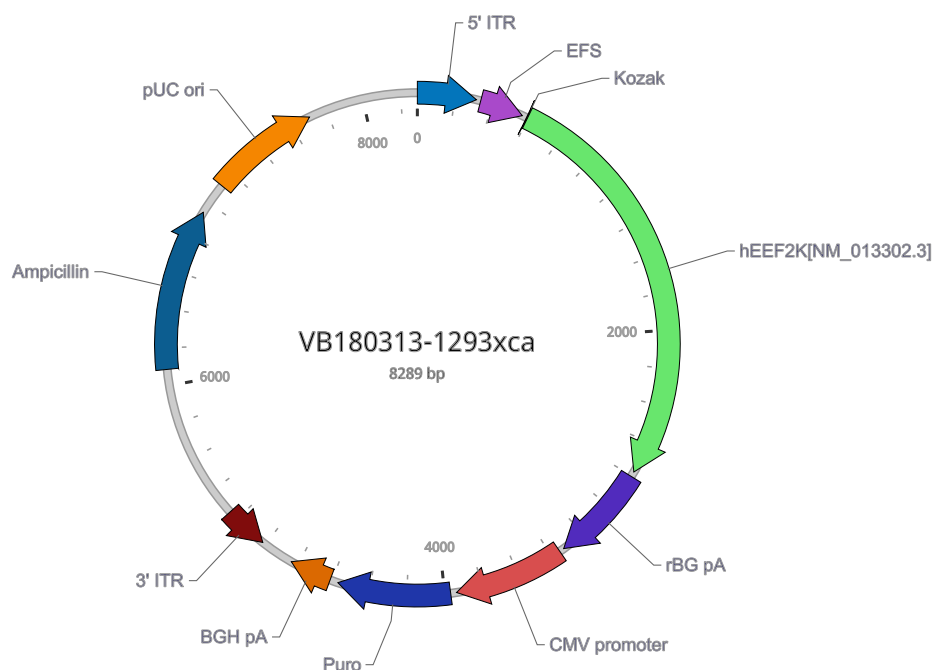


Vector Summary

Vector ID	VB180313-1293xca
Vector Name	pPB[Exp]-Puro-EFS>hEEF2K[NM_013302.3]
Date Created (Pacific Time)	2018-03-13
Size	8289 bp
Vector Type	PiggyBac transposon gene expression vector
Inserted Promoter	EFS
Inserted ORF	hEEF2K[NM_013302.3]
Inserted Marker	Puro
Plasmid Copy Number	High
Antibiotic Resistance	Ampicillin
Cloning Host	Stbl3 (or alternative strain)

Vector Map



Vector Components

Name	Position	Size (bp)	Type	Description	Application notes
5' ITR	■ 1-313	313	ITR	piggyBac 5' inverted terminal repeat	Recognized by PBase transposase; DNA flanked by piggyBac 5' ITR and 3' ITR can be transposed by PBase into TTAA sites.
EFS	■ 337-568	232	Promoter	Human eukaryotic translation elongation factor 1 α 1 short form	Strong promoter.
Kozak	■ 593-598	6	Miscellaneous	Kozak translation initiation sequence	Facilitates translation initiation of ATG start codon downstream of the Kozak sequence.
hEEF2K[NM_013302.3]	■ 599-2776	2178	ORF	None	None
rBG pA	■ 2804-3325	522	PolyA_signal	Rabbit beta-globin polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.

Name	Position	Size (bp)	Type	Description	Application notes
CMV promoter	■ 3351-3938	588	Promoter	Human cytomegalovirus immediate early enhancer/promoter	Strong promoter; may have variable strength in some cell types.
Puro	■ 3970-4569	600	ORF	Puromycin resistance gene	Allows cells to be resistant to puromycin.
BGH pA	■ 4613-4837	225	PolyA_signal	Bovine growth hormone polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.
3' ITR	■ complement (5019-5253)	235	ITR	piggyBac 3' inverted terminal repeat	Recognized by PBase transposase; DNA flanked by piggyBac 5' ITR and 3' ITR can be transposed by PBase into TTAA sites.
Ampicillin	■ 6085-6945	861	ORF	Ampicillin resistance gene	Allows E. coli to be resistant to ampicillin.
pUC ori	■ 7116-7704	589	Rep_origin	pUC origin of replication	Facilitates plasmid replication in E. coli; regulates high-copy plasmid number (500-700).

Note: Components added by user are listed in **bold red** text.

Vector Sequence

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1  TTAACCTAG AAAGATAGTC TGCCTAAAAT TGACGCATGC ATTCTTGAAA TATTGCTCTC TCTTTCTAAA TAGCGCGAAT CCGTCGCTGT GCATTTAGGA
101 CATCTCAGTC GCCGCTTGGG GCTCCCGTGA GCGGTGCTTG TCAATGCGGT AAGTGTCACT GATTTTGAAC TATAACGACC GCGTGAGTCA AAATGACGCA
201 TGATTATCTT TTACGTGACT TTAAAGATTT AACTCATACG ATAATTATAT TGTATTTCAT TGTCTACTTT ACGTGATAAC TTATTATATA TATATTTTCT
301 TGTATAGAT ATCATCAACT TTGTATAGAA AAGTGGGCTT CCGGTGCCCG TCAGTGGGCA GAGCGCACAT CGCCACAGT CCCCAGAGAAG TTGGGGGGAG
401 GGGTCGGCAA TTGATCCGGT GCCTAGAGAA GGTGGCGCGG GGTAACTGGG GAAAGTGATG TCGTGTACTG GCTCCGCCCT TTTCCCGAGG GTGGGGGAGA
501 ACCGTATATA AGTGCAGTAG TCGCCGTGAA CGTTCTTTTT CGCAACGGGT TTGCCGCCAG AACACAGGCA AGTTTGTAAC AAAAAGCAGG CTGCCACCAT
601 GGCAGACGAA GATCTCATCT TCCGCTGGA AGCGTGTGAT GCGCGCCAGT CCCCCGAGC TGGCCATGAT GGTGATTCTG ATGGGGACAG CGACGATGAG
701 GAAGGTTACT TCATCTGCCC CATCACGGAT GACCCAAGCT CGAACCAGAA TGTCAATTCC AAGGTTAATA AGTACTACAG CAACCTAACA AAAAGTGAGC
801 GGTATAGCTC CAGCGGGTCC CCGGCAAACCT CCTTCCACTT CAAGGAAGCC TGGAAGCAGC CAATCCAGAA GGCCAAGCAC ATGCCCGACC CCTGGGCTGA
901 GTTCCACCTG GAAGATATTG CCACCGAAGC TGCTACTCGA CACAGGTACA ACGCCGTCAC CGGGGAATGG CTGGATGATG AAGTTCTGAT CAAGATGGCA
1001 TCTCAGCCCT TCGGCCGAGG AGCAATGAGG GAGTGCTTCC GGACGAAGAA GCTCTCCAAC TTCTTGTCATG CCCAGCAGTG GAAGGGCGCC TCCAACACG
1101 TGGCGAAGCG CTACATCGAG CCCGTAGACC GGGATGTGTA CTTTGAGGAC GTGCGTCTAC AGATGGAGGC CAAGCTCTGG GGGGAGGAGT ATAATCGGCA
1201 CAAGCCCCCC AAGCAGGTGG ACATCATGCA GATGTGCATC ATCGAGCTGA AGGACAGACC GGGCAAGCCC CTCTTCCACC TGGAGACTA CATCGAGGGC
1301 AAGTACATCA AGTACAACCT CAACTCTGGC TTTGTCCGGG ATGACAACAT CCGCCTGACG CCGCAGGCCT TCAGCCACTT CACTTTTGTG CGTTCCGGCC
1401 ATCAGCTGAT AGTGGTGGAC ATCCAGGGAG TTGGGGATCT CTACACTGAC CCACAGATCC ACACGGAGAC GGGCACTGAC TTTGGAGACG GCAACCTAGG
1501 TGTCCGCGGG ATGGCGCTCT TCTTCTACTC TCATGCCTGC AACCGGATTT GCGAGAGCAT GGGCCTTGCT CCTTTGACC TCTCGCCCCG GGAGAGGGAT
1601 GCAGTGAATC AGAACACCAA GCTGTGTCAG TCAGCCAAGA CCATCTTGAG AGGAACAGAG GAAAAATGTG GGAGCCCCCG AGTAAGGACC CTCTCTGGGA
1701 GCCGGCCACC CCGTCTCCGT CCCCTTTTCAG AGAACTCTGG AGACGAGAAC ATGAGCGACG TGACCTTCGA CTCTCTCCCT TCTTCCCCAT CTTCGGCCAC
1801 ACCACACAGC CAGAAGCTAG ACCACCTCCA TTGGCCAGTG TTCAGTGACC TCGATAACAT GGCATCCAGA GACCATGATC ATCTAGACAA CCACCGGGAG
1901 TCTGAGAATA GTGGGGACAG CGGATACCCC AGTGAGAAGC GGGGTGAGCT GGTGACCCCT GAGCCCCGAG AACATGGCCA CTCATACAGT AATCGGAAGT
2001 ACGAGTCTGA CGAAGACAGC CTGGGCAGCT CTGGACGGGT ATGTGTAGAG AAGTGGAAAT TCCTCAACTC CTCCCGCTC CACCTGCCGA GGGCTTCGGC
2101 CGTGGCCCTG GAAGTGCAAA GGCTTAATGC TCTGGACCTC GAAAAGAAAA TCGGGAAGTC CATTTTGGGG AAGGTCCATC TGGCCATGGT GCGCTACCAC
2201 GAGGGTGGGC GCTTCTGCGA GAAGGGCGAG GAGTGGGACC AGGAGTCGGC TGTCTTCCAC CTGGAGCAGC CAGCCAACCT GGGCGAGCTG GAGGCCATCG
2301 TGGGCTGGG ACTCATGTAC TCGCAGTTGC CTCATCACAT CCTAGCCGAT GTCTCTCTGA AGGAGACAGA AGAGAACAAA ACCAAAGGAT TTGATTACTT
2401 ACTAAAGGCC GCTGAAGCTG GCGACAGGCA GTCCATGATC CTAGTGGCGC GAGCTTTTGA CTCTGGCCAG AACCTCAGCC CGGACAGGTG CCAAGACTGG
2501 CTAGAGGCCG TGCATGGTA CAACACTGCC CTGGAGATGA CCGACTGTGA TGAGGGCGGT GAGTACGACG GAATGCAGGA CGAGCCCCGG TACATGATGC
2601 TGGCCAGGGA GGCCGAGATG CTGTTACAGG GAGGCTACGG GCTGGAGAAG GACCCGCAGA GATCAGGGGA CTTGTATACC CAGGCAGCAG AGGCAGCGAT
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2901 TATGGGGACA TCATGAAGCC CCTTGAGCAT CTGACTTCTG GCTAATAAAG GAAATTTATT TTCATTGCAA TAGTGTGTG GAAATTTTGT TGTCTCTCAC
3001 TCGGAAGGAC ATATGGGAGG GCAAAATCATT TAAACATCA GAATGAGTAT TTGGTTTAGA GTTTGGCAAC ATATGCCCAT ATGCTGGCTG CCATGAACAA
3101 AGGTTGGCTA TAAAGAGGTC ATCAGTATAT GAAACAGCCC CCGTCTGTCC ATTCCTTATT CCATAGAAAA GCCTTGACTT GAGGTTAGAT TTTTATATA
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3401	TTAGTTCATA	GCCCATATAT	GGAGTTCGCG	GTTACATAAC	TTACGGTAAA	TGGCCCCGCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	ACGTCAATAA
3501	TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGGTGGAGT	ATTTACGGTA	AACTGCCCCC	TTGGCAGTAC	ATCAAGTGTA
3601	TCATATGCCA	AGTACGCCCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATTG	TGCCCAGTAC	ATGACCTTAT	GGGACTTTCC	TACTTGGCAG
3701	TACATCTACG	TATTAGTCAT	CGCTATTACC	ATGGTGATGC	GGTTTTGGCA	GTACATCAAT	GGGCGTGAT	AGCGGTTTGA	CTCACGGGGA	TTTCCAAGTC
3801	TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	GACTTTCCAA	AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG
3901	TAGGCGTGTA	CGGTGGGAGG	TCTATATAAG	CAGAGCTCTC	TGGCTAACTA	GAGAACCAC	TGCGCCACCA	TGACCGAGTA	CAAGCCCACG	GTGCGCTCTG
4001	CCACCCGCGA	CGACGTCCCC	AGGGCCGTAC	GCACCCTCGC	CGCCGCGTTC	GCCGACTACC	CCGCCACGCG	CCACACCGTC	GATCCGGACC	GCCACATCGA
4101	GCGGGTCAAC	GAGCTGCAAG	AACTCTTCCT	CACGCGCGTC	GGGCTCGACA	TCGGCAAGGT	GTGGGTCGCG	GACGACGGCG	CCGCGGTGGC	GGTCTGGACC
4201	ACGCCGGAGA	GCGTCGAAGC	GGGGGCGGTG	TTCGCCGAGA	TCGGCCCCGCG	CATGGCCGAG	TTGAGCGGTT	CCCGGCTGGC	CGCGCAGCAA	CAGATGGAAG
4301	GCCTCCTGGC	GCCGCACCGG	CCCAAGGAGC	CCGCGTGGTT	CCTGGCCACC	GTCGGCGTCT	CGCCCGACCA	CCAGGGCAAG	GGTCTGGGCA	GCGCCGTCGT
4401	GCTCCCCGGA	GTGGAGGCGG	CCGAGCGCGC	CGGGGTGCCC	GCCTTCCTGG	AGACCTCCGC	GCCCCGCAAC	CTCCCTTCT	ACGAGCGGCT	CGGCTTCACC
4501	GTCACCGCCG	ACGTCGAGGT	GCCCCAAGGA	CCGCGCACCT	GGTGCATGAC	CCGCAAGCCC	GGTGCTGAC	TCGAGTCTAG	AGGGCCCCGT	TAAACCCGCT
4601	GATCAGCCTC	GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	CCTGGAAGGT	GCCACTCCCA	CTGTCTTTTC
4701	CTAATAAAAT	GAGGAAATTG	CATCGCATTG	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGTGGGGG	CAGGACAGCA	AGGGGGAGGA	TTGGGAAGAC
4801	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGCTC	GAGTTAAATTA	ACGAGAGCAT	AATATTGATA	TGTGCCAAAG	TTGTTTCTGA	CTGACTAATA
4901	AGTATAATTT	GTTTCTATTA	TGTATAGGTT	AAGCTAATTA	CTTATTTTAT	AATACAACAT	GACTGTTTTT	AAAGTACAAA	ATAAGTTTAT	TTTTGTAAAA
5001	GAGAGAATGT	TTAAAAGTTT	TGTTACTTTA	TAGAAGAAAT	TTTGAGTTT	TGTTTTTTTT	TAATAAATAA	ATAAACATAA	ATAAATGT	TGTTGAATTT
5101	ATTATTAGTA	TGTAAGTGTA	AATATAATAA	AACTTAATAT	CTATTCAAAT	TAATAAATAA	ACCTCGATAT	ACAGACCGAT	AAAACACATG	CGTCAATTTT
5201	ACGCGATGAT	ATCTTTTAACG	TACGTCACAA	TATGATTATC	TTTCTAGGGT	TAAATAATAG	TTTCTAATTT	TTTTATTATT	CAGCCTGCTG	TCGTGAATAC
5301	CGAGCTCCAA	TTCGCCCTAT	AGTGAGTCGT	ATTACAATTC	ACTGGCCGTC	GTTTTACAAC	GTCGTGACTG	GGAAAACCCT	GGCGTTACCC	AACTTAATCG
5401	CCTTGCGAGC	CATCCCCCTT	TCGCCAGCTG	GCGTAATAGC	GAAGAGGCC	GCACCGATCG	CCCTTCCCAA	CAGTTGCGCA	GCCTGAATGG	CGAATGGGAC
5501	GCGCCCTGTA	GCGGCGCATT	AAGCGCGGCG	GGTGTTGGTG	TTACGCGCAG	CGTGACCGCT	ACACTTGCCA	GCGCCCTAGC	GCCCGCTCCT	TTCGCTTTCT
5601	TCCTTCTCTT	TCTCGCCACG	TTCGCCGGCT	TTCCCCGTCA	AGCTCTAAAT	CGGGGGCTCC	CTTTAGGGTT	CCGATTTAGT	GCTTTACGGC	ACCTCGACCC
5701	CAAAAACTT	GATTAGGGTG	ATGGTTCACG	TAGTGGGCCA	TCGCCCTGAT	AGACGGTTTT	TCGCCCTTTG	ACGTGAGAGT	CCACGTTCTT	TAATAGTGGA
5801	CTCTTGTTCC	AAACTGGAAC	AACACTCAAC	CCTATCTCGG	TCTATTCTTT	TGATTTATAA	GGGATTTTGC	CGATTTGCGC	CTATTGGTTA	AAAAATGAGC
5901	TGATTTAACA	AAAATTTAAC	GCGAATTTTA	ACAAAATATT	AACGCTTACA	ATTTAGGTGG	CACTTTTCGG	GGAAATGTGC	GCGGAACCCC	TATTTGTTTA
6001	TTTTTCTAAA	TACATTCAAA	TATGTATCCG	CTCATGAGAC	AATAACCCTG	ATAAATGCTT	CAATAATATT	GAAAAAGGAA	GAGTATGAGT	ATTCAACATT
6101	TCCGTGTGCG	CCTTATTTCC	TTTTTTGCGG	CATTTTGCCT	TCCTGTTTTT	GCTCACCCAG	AAACGCTGGT	GAAAGTAAAA	GATGCTGAAG	ATCAGTTGGG
6201	TGCACGAGTG	GGTTACATCG	AACTGGATCT	CAACAGCGGT	AAGATCCTTG	AGAGTTTTTCG	CCCCGAAGAA	CGTTTTCCAA	TGATGAGCAC	TTTTAAAGTT
6301	CTGCTATGTG	GCGCGGTATT	ATCCCGTATT	GACGCGGGCG	AAGAGCAACT	CGGTGCGCGC	ATACACTATT	CTCAGAATGA	CTTGGTTGAG	TACTCACCAG
6401	TCACAGAAAA	GCATCTTACG	GATGGCATGA	CAGTAAGAGA	ATTATGCAGT	GCTGCCATAA	CCATGAGTGA	TAACACTGCG	GCCAACTTAC	TTCTGACAAC
6501	GATCGGAGGA	CCGAAGGAGC	TAACCGCTTT	TTTGACACAAC	ATGGGGGATC	ATGTAACCTG	CCTTGATCGT	TGGGAACCGG	AGCTGAATGA	AGCCATACCA
6601	AACGACGAGC	GTGACACCAC	GATGCCTGTA	GCAATGGCAA	CAACGTTGCG	CAAACATATTA	ACTGGCGAAC	TACTTACTCT	AGCTTCCCGG	CAACAATTAA
6701	TAGACTGGAT	GGAGGCGGAT	AAAGTTGCAG	GACCACCTTCT	GCCTCGGCC	CTTCCGGCTG	GCTGTTTAT	TGCTGATAAA	TCTGGAGCCG	GTGAGCGTGG
6801	GTCTCGCGGT	ATCATTGACG	CACTGGGGCC	AGATGGTAAG	CCCTCCCGTA	TCGTAGTTAT	CTACACGACG	GGGAGTCAGG	CAACTATGGA	TGAACGAAAT
6901	AGACAGATCG	CTGAGATAGG	TGCCTCACTG	ATTAAGCATT	GGTAACTGTC	AGACCAAGTT	TACTCATATA	TACTTTAGAT	TGATTTAAAA	CTTCATTTTT
7001	AATTTAAAG	GATCTAGGTG	AAGATCCTTT	TTGATAATCT	CATGACCAA	ATCCCTTAAC	GTGAGTTTTC	GTTCCACTGA	GCGTCAGACC	CCGTAGAAAA
7101	GATCAAAGGA	TCTTCTTGAG	ATCCTTTTTT	TCTGCGCGTA	ATCTGCTGCT	TGCAAACAAA	AAAACCACCG	CTACCAGCGG	TGGTTTGTTT	GCCGATCAA
7201	GAGCTACCAA	CTCTTTTTTC	GAAGGTAAC	GGCTTCAGCA	GAGCGCAGAT	ACCAAATACT	GTTCTTCTAG	TGTAGCCGTA	GTTAGGCCAC	CACTTCAAGA
7301	ACTCTGTAGC	ACCGCCTACA	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG	GCTGCTGCCA	GTGGCGATAA	GTCGTGTCTT	ACCGGGTTGG	ACTCAAGACG
7401	ATAGTTACCG	GATAAGGCGC	AGCGGTGCGG	CTGAACGGGG	GGTTCGTGCA	CACAGCCAG	CTTGAGCGA	ACGACCTACA	CCGAACCTGAG	ATACCTACAG
7501	CGTGAGCTAT	GAGAAAGCGC	CACGCTTCCC	GAAGGGAGAA	AGGCGGACAG	GTATCCGGTA	AGCGGCAGGG	TCGGAACAGG	AGAGCGCAGC	AGGGAGCTTC
7601	CAGGGGAAAA	CGCCTGGTAT	CTTTATAGTC	CTGTCCGGTT	TCGCCACCTC	TGACTTGAGC	GTCGATTTTT	GTGATGCTCG	TCAGGGGGGC	GGAGCCTATG
7701	GAAAAACGCC	AGCAACGCGG	CCTTTTTACG	GTTCTGCGCC	TTTGTCTGGC	CTTTTGCTCA	CATGTTCTTT	CCTGCGTTAT	CCCCTGATTC	TGTGGATAAC
7801	CGTATTACCG	CCTTTGAGTG	AGCTGATACC	GCTCGCCGCA	GCCGAACGAC	CGAGCGCAGC	GAGTCAGTGA	GCGAGGAAGC	GGAAGAGCGC	CCAATACGCA
7901	AACCGCCTCT	CCCCGCGCGT	TGGCCGATTC	ATTAATGCAG	CTGGCACGAC	AGGTTTCCCG	ACTGGAAGC	GGGCAGTGAG	CGCAACGCAA	TTAATGTGAG
8001	TTAGCTCACT	CATTAGGCAC	CCCAGGCTTT	ACACTTTATG	CTTCCGGCTC	GTATGTTGTG	TGGAATTGTG	AGCGGATAAC	AATTTACAC	AGGAAACAGC
8101	TATGACCATG	ATTACGCCAA	GCTCGAAATT	AACCCTCACT	AAAGGGAACA	AAAGCTGGTA	CCTCGCGCGA	CTTGGTTTGC	CATTCTTTAG	CGCGCGTCGC
8201	GTCACACAGC	TTGGCCACAA	TGTGGTTTTT	GTCAAACGAA	GATTCTATGA	CGTGTTTAAA	GTTTAGGTCG	AGTAAAGCGC	AAATCTTTT	

Validation by Restriction Enzyme Digestion

Cutters	Locations	Fragments (bp)
NaeI	1704, 5627	3923, 4366
NdeI	3012, 3072, 3080, 3604	60, 8, 524, 7697
ApaLI	6201, 7447	1246, 7043
ApaLI+NaeI	1704, 5627, 6201, 7447	3923, 574, 1246, 2546
ApaLI+NdeI	3012, 3072, 3080, 3604, 6201, 7447	60, 8, 524, 2597, 1246, 3854