Vector Summary

Vector ID	VB160216-10057
Vector Name	pRP[Exp]-mCherry-CAG>hyPBase
Date Created (Pacific Time)	2017-06-14
Size	7467 bp
Cloning Host	Stbl3 (or alternative strain)

Vector Map
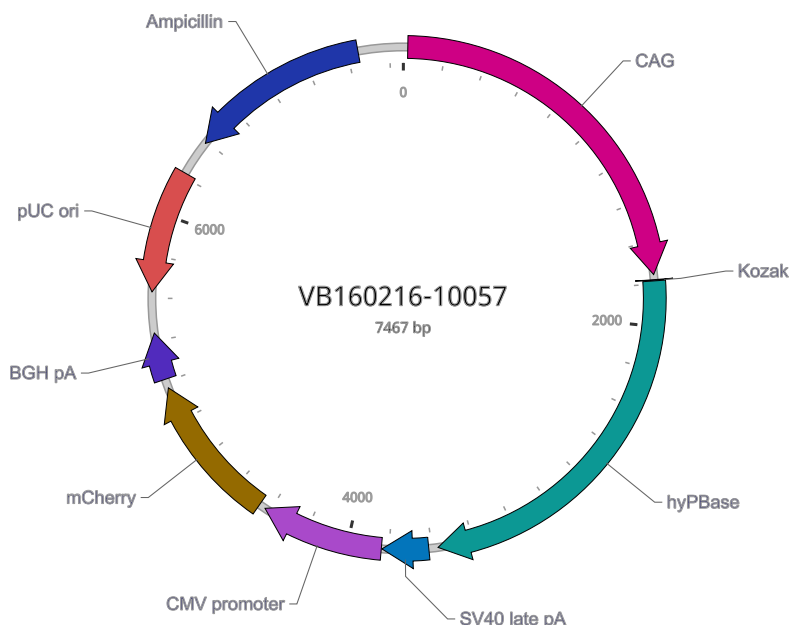
Vector Components

Name	Position	Size (bp)	Type	Description	Application notes
CAG	■ 22-1754	1733	Promoter	CMV early enhancer fused to modified chicken β-actin promoter	Strong promoter.
Kozak	■ 1779-1784	6	kozak	Kozak translation initiation sequence	Facilitates translation initiation of ATG start codon downstream of the Kozak sequence.
hyPBase	■ 1785-3569	1785	ORF	Hyperactive version of piggyBac transposase (PBase) created by mutagenesis	Higher efficiency compared to its predecessor, PBase, in mammalian cells.
SV40 late pA	■ 3614-3835	222	PolyA_signal	Simian virus 40 late polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.
CMV promoter	■ 3839-4426	588	promoter	Human cytomegalovirus immediate early enhancer/promoter	Strong promoter; may have variable strength in some cell types.
mCherry	■ 4458-5168	711	ORF	Variant of mRFP1 generated by mutagenesis	Commonly used red fluorescent protein; fast maturation compared to its predecessor, mRFP1.
BGH pA	■ 5212-5436	225	PolyA_signal	Bovine growth hormone polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.

Name	Position	Size (bp)	Type	Description	Application notes
pUC ori	■ complement (5632-6220)	589	rep_origin	pUC origin of replication	Facilitates plasmid replication in E. coli; regulates high-copy plasmid number (500-700).
Ampicillin	■ complement (6391-7251)	861	ORF	Ampicillin resistance gene	Allows E. coli to be resistant to ampicillin.

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

Vector Sequence

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   1  CAACTTTGTA TAGAAAAGTT GCTCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG
 101  CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA
 201  GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG
 301  TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC
 401  CATGGTCGAG GTGAGCCCCA CGTTCTGCTT CACTCTCCCC ATCTCCCCCC CCTCCCCACC CCCAATTTTG TATTTATTTA TTTTTTAATT ATTTTGTGCA
 501  GCGATGGGGG CGGGGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG CGGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC
 601  AGAGCGGCGC GCTCCGAAAG TTTCCTTTTA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGCGCTG
 701  CCTTCGCCCC GTGCCCCGCT CCGCCGCCGC CTCGCGCCGC CCGCCCCGGC TCTGACTGAC CGCGTTACTC CCACAGGTGA GCGGGCGGGA CGGCCCTTCT
 801  CCTCCGGGCT GTAATTAGCG CTTGGTTTAA TGACGGCTTG TTTCTTTTCT GTGGCTGCGT GAAAGCCTTG AGGGGCTCCG GGAGGGCCCT TTGTGCGGGG
 901  GGAGCGGCTC GGGGGGTGCG TGCGTGTGTG TGTGCGTGGG GAGCGCCGCG TGCGGCTCCG CGCTGCCCGG CGGCTGTGAG CGCTGCGGGC GCGGCGCGGG
1001  GCTTTGTGCG CTCCGCAGTG TGCGCGAGGG GAGCGCGGCC GGGGGCGGTG CCCCGCGGTG CGGGGGGGGC TGCGAGGGGA ACAAAGGCTG CGTGCGGGGT
1101  GTGTGCGTGG GGGGGTGAGC AGGGGGTGTG GGCGCGTCGG TCGGGCTGCA ACCCCCCCTG CACCCCCCTC CCCGAGTTGC TGAGCACGGC CCGGCTTCGG
1201  GTGCGGGGCT CCGTACGGGG CGTGGCGCGG GGCTCGCCGT GCCGGGCGGG GGGTGGCGGC AGGTGGGGGT GCCGGGCGGG GCGGGGCCGC CTCGGGCCGG
1301  GGAGGGCTCG GGGGAGGGGC GCGGCGGCCC CCGGAGCGCC GGCGGCTGTC GAGGCGCGGC GAGCCGCAGC CATTGCCTTT TATGGTAATC GTGCGAGAGG
1401  GCGCAGGGAC TTCCTTTGTC CCAAATCTGT GCGGAGCCGA AATCTGGGAG GCGCCGCCGC ACCCCCTCTA GCGGGCGCGG GGCGAAGCGG TGCGGCGCCG
1501  GCAGGAAGGA AATGGGCGGG GAGGGCCTTC GTGCGTCGCC GCGCCGCCGT CCCCTTCTCC CTCTCCAGCC TCGGGGCTGT CCGCGGGGGG ACGGCTGCCT
1601  TCGGGGGGGA CGGGGCAGGG CGGGGTTCGG CTTCTGGCGT GTGACCGGCG GCTCTAGAGC CTCTGCTAAC CATGTTCATG CCTTCTTCTT TTTCCTACAG
1701  CTCCTGGGCA ACGTGCTGGT TATTGTGCTG TCTCATCATT TTGGCAAAGA ATTGCAAGTT TGTACAAAAA AGCAGGCTGC CACCATGGGC AGCAGCCTGG
1801  ACGACGAGCA CATCCTGAGC GCCCTGCTGC AGAGCGACGA CGAGCTGGTC GGCGAGGACA GCGACAGCGA GGTGAGCGAC CACGTGAGCG AGGACGACGT
1901  GCAGTCCGAC ACCGAGGAGG CCTTCATCGA CGAGGTGCAC GAGGTGCAGC CTACCAGCAG CGGCTCCGAG ATCCTGGACG AGCAGAACGT GATCGAGCAG
2001  CCCGGCAGCT CCCTGGCCAG CAACAGGATC CTGACCCTGC CCCAGAGGAC CATCAGGGGC AAGAACAAGC ACTGCTGGTC CACCTCCAAG CCCACCAGGC
2101  GGAGCAGGGT GTCCGCCCTG AACATCGTGA GAAGCCAGAG GGGCCCCACC AGGATGTGCA GGAACATCTA CGACCCCCTG CTGTGCTTCA AGCTGTTCTT
2201  CACCGACGAG ATCATCAGCG AGATCGTGAA GTGGACCAAC GCCGAGATCA GCCTGAAGAG GCGGGAGAGC ATGACCTCCG CCACCTTCAG GGACACCAAC
2301  GAGGACGAGA TCTACGCCTT CTTCGGCATC CTGGTGATGA CCGCCGTGAG GAAGGACAAC CACATGAGCA CCGACGACCT GTTCGACAGA TCCCTGAGCA
2401  TGGTGTACGT GAGCGTGATG AGCAGGGACA GATTCGACTT CCTGATCAGA TGCCTGAGGA TGGACGACAA GAGCATCAGG CCCACCCTGC GGGAGAACGA
2501  CGTGTTCACC CCCGTGAGAA AGATCTGGGA CCTGTTCATC CACCAGTGCA TCCAGAACTA CACCCCTGGC GCCCACCTGA CCATCGACGA GCAGCTGCTG
2601  GGCTTCAGGG GCAGGTGCCC CTTCAGGGTC TATATCCCCA ACAAGCCCAG CAAGTACGGC ATCAAGATCC TGATGATGTG CGACAGCGGC ACCAAGTACA
2701  TGATCAACGG CATGCCCTAC CTGGGCAGGG GCACCCAGAC CAACGGCGTG CCCCTGGGCG AGTACTACGT GAAGGAGCTG TCCAAGCCCG TCCACGGCAG
2801  CTGCAGAAAC ATCACCTGCG ACAACTGGTT CACCAGCATC CCCCTGGCCA AGAACCTGCT GCAGGAGCCC TACAAGCTGA CCATCGTGGG CACCGTGAGA
2901  AGCAACAAGA GAGAGATCCC CGAGGTCCTG AAGAACAGCA GGTCCAGGCC CGTGGGCACC AGCATGTTCT GCTTCGACGG CCCCCTGACC CTGGTGTCCT
3001  ACAAGCCCAA GCCCGCCAAG ATGGTGTACC TGCTGTCCAG CTGCGACGAG GACGCCAGCA TCAACGAGAG CACCGGCAAG CCCCAGATGG TGATGTACTA
3101  CAACCAGACC AAGGGCGGCG TGGACACCCT GGACCAGATG TGCAGCGTGA TGACCTGCAG CAGAAAGACC AACAGGTGGC CCATGGCCCT GCTGTACGGC
3201  ATGATCAACA TCGCCTGCAT CAACAGCTTC ATCATCTACA GCCACAACGT GAGCAGCAAG GGCGAGAAGG TGCAGAGCCG GAAAAAGTTC ATGCGGAACC
3301  TGTACATGGG CCTGACCTCC AGCTTCATGA GGAAGAGGCT GGAGGCCCCC ACCCTGAAGA GATACCTGAG GGACAACATC AGCAACATCC TGCCCAAAGA
3401  GGTGCCCGGC ACCAGCGACG ACAGCACCGA GGAGCCCGTG ATGAAGAAGA GGACCTACTG CACCTACTGT CCCAGCAAGA TCAGAAGAAA GGCCAGCGCC
3501  AGCTGCAAGA AGTGTAAGAA GGTCATCTGC CGGGAGCACA ACATCGACAT GTGCCAGAGC TGTTTCTGAA CCCAGCTTTC TTGTACAAAG TGGTGATGGC
3601  CGGCCGCTTC GAGCAGACAT GATAAGATAC ATTGATGAGT TTGGACAAAC CACAACTAGA ATGCAGTGAA AAAAATGCTT TATTTGTGAA ATTTGTGATG
3701  CTATTGCTTT ATTTGTAACC ATTATAAGCT GCAATAAACA AGTTAACAAC AACAATTGCA TTCATTTTAT GTTTCAGGTT CAGGGGGAGG TGTGGGAGGT
3801  TTTTTAAAGC AAGTAAAACC TCTACAAATG TGGTACGCGT TGACATTGAT TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC
3901  CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCCCGCCTGG CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC
4001  CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGAGTAT TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCCAAG
4101  TACGCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA
4201  TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTG
4301  ACGTCAATGG GAGTTTGTTT TGGCACCAAA ATCAACGGGA CTTTCCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGTA GGCGTGTACG
4401  GTGGGAGGTC TATATAAGCA GAGCTCTCTG GCTAACTAGA GAACCCACTG CGCCACCATG GTGAGCAAGG GCGAGGAGGA TAACATGGCC ATCATCAAGG
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4501  AGTTCATGCG CTTCAAGGTG CACATGGAGG GCTCCGTGAA CGGCCACGAG TTCGAGATCG AGGGCGAGGG CGAGGGCCGC CCCTACGAGG GCACCCAGAC
4601  CGCCAAGCTG AAGGTGACCA AGGGTGGCCC CCTGCCCTTC GCCTGGGACA TCCTGTCCCC TCAGTTCATG TACGGCTCCA AGGCCTACGT GAAGCACCCC
4701  GCCGACATCC CCGACTACTT GAAGCTGTCC TTCCCCGAGG GCTTCAAGTG GGAGCGCGTG ATGAACTTCG AGGACGGCGG CGTGGTGACC GTGACCCAGG
4801  ACTCCTCCCT GCAGGACGGC GAGTTCATCT ACAAGGTGAA GCTGCGCGGC ACCAACTTCC CCTCCGACGG CCCCGTAATG CAGAAGAAGA CCATGGGCTG
4901  GGAGGCCTCC TCCGAGCGGA TGTACCCCGA GGACGGCGCC CTGAAGGGCG AGATCAAGCA GAGGCTGAAG CTGAAGGACG GCGGCCACTA CGACGCTGAG
5001  GTCAAGACCA CCTACAAGGC CAAGAAGCCC GTGCAGCTGC CCGGCGCCTA CAACGTCAAC ATCAAGTTGG ACATCACCTC CCACAACGAG GACTACACCA
5101  TCGTGGAACA GTACGAACGC GCCGAGGGCC GCCACTCCAC CGGCGGCATG GACGAGCTGT ACAAGTAACT CGAGTCTAGA GGGCCCGTTT AAACCCGCTG
5201  ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT GTTTGCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC
5301  TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA
5401  ATAGCAGGCA TGCTGGGGAT GCGGTGGGCT CTATGGGCGG CCGCGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT TCGGCTGCGG
5501  CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA
5601  GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT GGCGAAACCC
5701  GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC
5801  CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG
5901  TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG GTAACAGGAT
6001  TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACTACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG
6101  AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC
6201  GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT
6301  ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TTACCAATGC
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6501  CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG
6601  TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA CGTTGTTGCC
6701  ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT
6801  GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC ATAATTCTCT
6901  TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG CTCTTGCCCG
7001  GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC
7101  TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA
7201  AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG TTATTGTCTC
7301  ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTA
7401  TTATCATGAC ATTAACCTAT AAAAATAGGC GTATCACGAG GCCCTTTCGT CGGCGCGCCG CGGCCGC
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Validation by Restriction Enzyme Digestion

Cutters	Locations	Fragments (bp)
FspI	6687	7467
DrdI	1846, 2994, 4999, 5680	1148, 2005, 681, 3633
ApaLI	1936, 4519, 5886, 7132	2583, 1367, 1246, 2271
ApaLI+DrdI	1846, 1936, 2994, 4519, 4999, 5680, 5886, 7132	90, 1058, 1525, 480, 681, 206, 1246, 2181
ApaLI+FspI	1936, 4519, 5886, 6687, 7132	2583, 1367, 801, 445, 2271