

PFC	Dist to 3' gene	Length	Sequence
PseB _{AC2}	16,089	26	AAACAACGTACCTTTCTGGAGAAAT
PseB _{AC3}	5,963	28	AATTAATTAGTCAATACGATTAGTGCT
PseB _{AC4}	3,355	22	TTAATGTCACGTTGAATACAT
PseB _{CF16}	-107	14	TTTTTGCTTTTGTT
PseB _{CF17}	-1,106	27	AAATCAGTGTTTAACCTTGACCTTGAA
PseB _{CF18}	7,372	27	TTTGTTACGTTACTGCGGTTTCATCAGT
PseB _{CF19}	336	24	TTGAAATGGTCAATGTGTACATTT
PseB _{CF20}	53	53	TTGAAAAGTCAATTGAGAAGAACCCTTTGCCTTCGTTAAAAATATG TCCACGCA
PseB _{FH21}	in 10	16	TGATCTGATTCATATT
PseB _{FH42}	2,782	26	ATGAAACCTGTATTTGAGAATGCAGA
PseB _{FH49}	2,104	34	TTTGTAATGTTTCATTAAGTTTCCGCAGAATTTT
			CTCGTAAAAATTTAACAGCTTGTGTTCCCTTTGCATTCTGTATAAAA CAACGCGCAACCTTGCCGTTTATGGGATTTGTAAACCATTTACC GCTTTATTTTCTATTACGGCAGATACAATATCCACGGGTATACA ACTTAAATATACATGAAACACATATTTATAACAAATCATTAAAAAC GTTAAATATGACCACCTCGTTTGCTTTATATAAACGTTTACTGGTG GAATACTGCGTTTTTCATAAGATGTTCTAAAAATGCCAATTACATTTA TATGACCTGCTAAAACCTGATAGTAATTAAGTCGTGTACTTTTACA
PseB _{FH50_{abef}}	986	342	ATGTGCTAAAGCGACCCTGACATT
PseB _{FH51_{abcd}}	528	74	TGATTTGATGCAAAGCGGCAGATATCTCATTAACTAACCCGGTTG AACATATTAATGCGCATATTCTCCCCTCC
			GTCCGTGTGGAAAACCTGAAGCCAATGGGATGGAGATCCGGTAA TAGATGCAAATTATCATGAAAAGACTCTGCAAAATATGAAACAAC TCATTTGCGGCGGAGTAAATCACAGAAAACCTGTTTATGAACTGGC
PseB _{FH52_{acd}}	352	163	ACCCCTTCTTGAAATGCAATGCGAGAAC
PseB _{HI58}	1,944	27	TTGGTGTGTGAAGAAACAAAGAACTGA
PseB _{HI59}	1,815	36	AAATGTGAAACTTTTTATTAGAATGGTTTCTTAATT
PseB _{HI60_{ab}}	1,680	24	CAACATGAAACTGCCTATTTATGC
PseB _{HI61}	1,624	16	AAATCAAGATATTTTT
			AGCATGCGCACAGTTAAAAAAAATGTAACGTGACCCTCTGTTTAC TGTGAAAAGAATGTATACTGTACTCGTGAATTACTTTATGGGGAC TCCGTGATATACTCTGTTGTTTTGCGCTACTTTGTTCTATGTCTAA ACCTGGAAGCAGCGGAAGAAAGGGGCACAATAAAAGTTTACAAGC
PseB _{HI62_{abc}}	1,586	219	GAGAATCCGTGACATCATTGCTGCGCTCTGGTTCATTT
			ATTATTAGACATATTTTATACATTTAAACTGTATTACAAATTTTCC ACATTACTGGAGCTGCAGGGATCCCGAATTCTATTGGATCAGCGA GAAGCACGTGTCTTGTACGTGTCTCCACAAGAAAAAGGGGTGCT TTTTGGTGTAAATCTGGACTCTAATTCGTAATATATCACGGTACA TCGTA AAAACCGACACTAAAACGTCCAGACCTACAAATCACTCGGT
PseB _{HI63_{ab}}	233	233	CAAATT
PseB _{IK78}	779	25	CATTTGGCTGACTTTATATATGTTT

			CCTAACAAATTCTCATCTCGTCATTATTTGTAACCATAGAGCATGA ATTACCTCTTGAAGTCATCAGTGAGAATTTACGACTGGTCAACAA AAGCACGTGATTCCCTAACGCACCCCCACCCCATATTTGGCCGC ATACATAGCAAAAACGAAGTACAGTGCATTGCTATAATTCATTA TACATCATAAAATCGTGAAGCACAGCGTTATAACGACCAAGATCTA
PseB _{KL} 79 _{abc}	252	231	CAAATC AACATTATTCCAAGTCTGGAGTACTGTAAAAGCACCTTTTGGCAT
PseB _{KL} 83	12,413	65	GCTCGTGATGTTATAGGCAT
PseB _{KL} 84	12,176	17	GTTTCATGTGAACCTCT
			GTTGTTATCGTTATAAAATCTTATGTGACAAGTGCGATGTTGATGCT TTCTTAAAAGTCGGCATGTTTCATGTGAACTTCTAAGTGTATAAC
PseB _{KL} 85	12,239	133	TTATTTCCAATCTATACCAACTGTATAATTTAAGTTTACA
			GTTTCATGTGTATACTTTTACTCGAATGACAAATGTACAATATGT TATTATTCATGTGCGAAAAAGTTGTAAATAATTATACATTTTTAA TGTGATCAAGAATATTTGTAGTAAGCAGTGTGAATGACAAGCATT CTGTGGAAAATGGCATCTGTCATGTGCGACTGCCACTTAGTATTT TGCGAATAAGCTTTTTTGTATTTGTTGTAGCTTAACTTG
PseB _{KL} 86	11,914	222	
			AAAAGTAGGTATGACATTTTCGATGTCAAATGGATGAGGGTTTTAT CTAGAAGTTAGATCGTAAAAATCGCCAGACCATAGACAGATAC CCCTCACTGGCTCTCAAAAGTACCGTGGGGTCCATAAAGTTAGTT TTATGGTTTTGGGGAGTTGACAATGTACTATATATTTCCCGTTCTA GAATGTAAGTGACGGTTTAAAC
PseB _{KL} 87 _{abcdef}	10,865	201	
PseB _{KL} 89	10,359	31	GGGAAAAGATTTTTTGTCAATTATGCTCCCT
			ATAATGTGGTTTGCATATTGATAGGAGTAATCTGCGCTCATATCTC ATCAATAATTCATTGAAGCAGGGATCATTTTCGAGGTCA
PseB _{KL} 90 _{abcd}	8,221	84	
PseB _{KL} 91	6,830	19	CAGAGCCCGCTTCAGACCA
			AAGTTTATGTGGTGTGATTTCCTGTATACTATTATTATT
PseB _{KL} 94	5,703	39	
PseB _{KL} 95	1,593	20	ATTTTTTACTGTTTGTTC
			AAGTAATGACCTGGGCAAAAATTC AATATGACCGAGCAAGCGGTA TGCATTAATAGAAAGTCGCAAGTGGGAGAGCCCTCTAGAAGGG GTGAAACGCAGGTCAGCGCGTCTAACAAATATTA AAAATGTACTGG GATGCATGACACGCCTAGCTGTTAACAAAGACTGCCAAAGTATT AGATTAATACGAAAACCT
PseB _{KL} 102 _{ab}	3,824	195	
			TCTATATATACCCTGTAGATCCGAATTTGTGTGAACAGAGAAGCG GTCACAAATTCGTATCTAGGGGAGTATGTAGT
PseB _{KL} 104 _{abcde}	1,219	77	
			GTGATTTAGGAGCTTGGTATCCCGAATTAGTTGATGAATTTTTTAT CGATCCAAACAAGCCCAGATTTATCTCTG
PseB _{KL} 105 _{abc}	621	75	
PseB _{KL} 106	441	13	TTTTTCATGAACAC
			AAACGAGTAAAGGGATAGAAATAAATTTTAGTATATTTTTGTGTG CAATTC AAAGAAAT
PseB _{KL} 108	61	60	