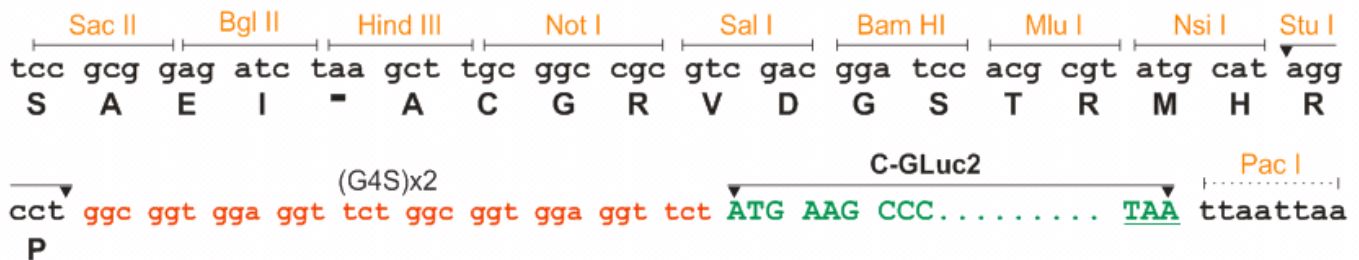
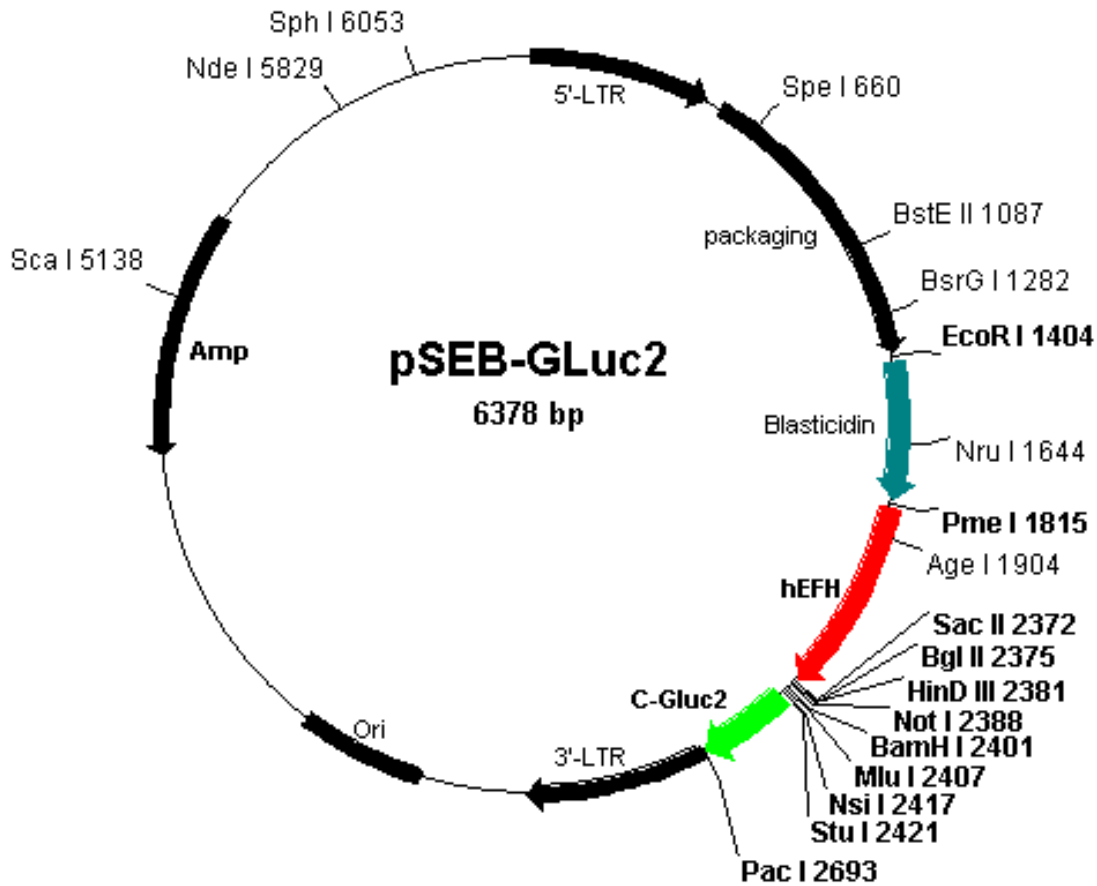


Vector: pSEB-GLuc2 (C-terminal half of Gaussia Luciferase for PCA)

Antibiotic Selection: Amp

Creator(s): Bai-Cheng He, Molecular Oncology Lab of The University of Chicago

Date of Construction: November, 2008



pSEB-GLuc2 (C-terminal half of Gaussia Luciferase) Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGAAGACAGAGACAGCAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTCCCGGGTCAAGGCAAGAACAGATGGTCCCAGATGCGGTCGCCG
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 GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCGACCCCGCG CGGGAGGTAA GCTGGCCAGC GGTGTTTCGTGTCTGTCTC TGCTTTTGTG
 CTTGTTTGTGCCGGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTTGGTGAACAGTTCGAAACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
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gcg ccg cgt cga cgg atc c GC GT atgcat **AGCCCT ggc ggt gga ggt tct ggc ggt gga ggt tct**
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Unique enzymes in pSEB-GLuc2:

Spe I	A`CTAG,T	660	Mun I	C`AATT,G	1897
BstE II	G`GTNAC,C	1087	Age I	A`CCGG,T	1904
BsrG I	T`GTAC,A	1282	Cla I	AT`CG,AT	2364
EcoR I	G`AATT,C	1404	Sac II	CC,GC`GG	2372
Bbv II	GAAGAC`7/11	1497	Bgl II	A`GATC,T	2375
Bbs I	GAAGAC`8/12	1498	Hind III	A`AGCT,T	2381
Nru I	TCG CGA	1644	Not I	GC`GGCC,GC	2388
BsaB I	GATNN NNATC	1711	BamH I	G`GATC,C	2401
Pme I	CTTT AAAC	1815	Mlu I	A`CGCG,T	2407
			Nsi I	A,TGCA`T	2417
			Stu I	AGG CCT	2421
			BspM I	ACCTGC`10/14	2603

DpnII	(32)	92	457	1044	1176			4284	4393	4786	4879
		1361	1645	1706	1720			5216	5548	5648	5751
		2337	2365	2375	2401			5881	5902	6035	6064
		2462	2532	2642	2663			6118	6178	6199	
		2833	4331	4406	4417		Hpa II (32)	163	398	569	630
		4425	4503	4515	4620			723	1401	1830	1905
		4961	4979	5025	5283			2129	2217	2229	2261
		5300	5336	5921	6145			2352	2675	2905	3140
Dra I	(5)	1815	2200	4524	4543			3483	3972	4119	4145
		5235						4335	4739	4773	4840
Drd I	(3)	1500	3873	5742				4950	5192	5693	5727
Dsa I	(5)	694	1411	2369	2507			6079	6202	6211	6226
		6083					Hph I (14)	1157	1183	1401	2691
Eae I	(11)	582	724	1109	1130			4502	4729	5143	5351
		1414	1529	2388	3604			5384	5668	5677	6170
		5046	6080	6212				6215	6296		
Eag I	(3)	724	1529	2388			Kas I (6)	1397	2354	5880	6063
Ear I	(6)	1070	1311	3387	3649			6177	6198		
		5453	5941				Kpn I (2)	405	3147		
Eco47 III	(3)	923	1826	6119			Mae I (16)	31	219	661	673
Eco57 I	(5)	1509	2077	4312	5326			1394	1522	1912	2063
		6330						2189	2251	2771	2961
EcoN I	(4)	784	1392	1915	2110			4260	4513	4848	6283
EcoO109 I	(6)	254	1219	1572	2996		Mae II (11)	742	1081	1122	2019
		5634	6088					2302	2579	4468	4884
EcoR I	(1)	1404						5257	5577	6019	
EcoR II	(21)	239	546	733	746		Mae III (21)	39	994	1022	1087
		1167	1192	1215	1235			1231	2331	2347	2680
		1265	1715	2421	2484			2779	3257	4121	4184
		2645	2651	2981	3503			4300	4583	4914	4972
		3791	3912	3925	5998			5125	5313	5701	5992
		6275						6012			
EcoR V	(3)	140	2881	6266			Mbo I (32)	92	457	1044	1176
Ehe I	(6)	1399	2356	5882	6065			1361	1645	1706	1720
		6179	6200					2337	2365	2375	2401
Fnu4H I	(44)	727	901	917	920			2462	2532	2642	2663
		925	928	1133	1513			2833	4331	4406	4417
		1532	1606	1609	1612			4425	4503	4515	4620
		1615	1618	1782	1823			4961	4979	5025	5283
		2043	2102	2117	2148		Mbo II (14)	5300	5336	5921	6145
		2388	2391	2559	2611			1086	1299	1445	1502
		2614	3590	3671	3689			1530	3403	3637	4426
		3692	3810	3965	4108			4499	5254	5332	5441
		4173	4176	4382	4710			5929	6141		
		5049	5076	5171	5400		Mlu I (1)	2407			
		5687	5796	5900	5973		Mme I (6)	829	1106	3204	3256
Fok I	(12)	423	1140	1300	1464			3979	4163		
		1699	2107	3164	4624		Mnl I (56)	167	216	368	387
		4805	5092	5735	5979			432	460	484	506
		4880	5903					510	566	776	872
Fsp I	(2)	4880	5903					1168	1271	1304	1310
Gdi II	(11)	723	725	1129	1528			1313	1319	1349	1352
		1530	2387	2389	3605			1367	1374	1390	1454
		5045	6081	6213				1795	1796	1880	1969
Gsu I	(3)	2709	4729	6347				2064	2106	2160	2176
Hae I	(7)	584	1111	1416	2421			2425	2440	2451	2571
		3780	3791	4243				2958	3110	3129	3174
Hae II	(12)	925	1401	1828	2235			3201	3225	3285	3614
		2358	3643	4013	5884			3663	3873	3946	4197
		6067	6121	6181	6202			4597	4678	4824	5030
Hae III	(33)	129	173	584	726			5625	5683	5943	6227
		762	774	987	1111			584	1111	1416	
		1132	1197	1416	1531		Msc I (3)	36	1007	1119	1149
		2116	2221	2390	2421		Mse I (26)	1173	1814	2199	2689
		2651	2674	2870	2915			2693	2776	3310	3408
		3606	3780	3791	3809			3536	3595	4471	4523
		4243	4701	4781	5048			4528	4542	4595	4830
		5635	5933	6082	6090			4869	5234	5606	5787
		6214						5984	6254		
Hga I	(12)	381	642	895	1491		Msl I (2)	4910	5069		
		2168	2383	3123	3875		Msp I (32)	163	398	569	630
		4453	5185	5743	6212			723	1401	1830	1905
HgiA I	(6)	338	3080	4083	5244			2129	2217	2229	2261
		5329	5826					2352	2675	2905	3140
HgiE II	(2)	4344	5824					3483	3972	4119	4145
Hha I	(43)	319	321	370	372			4335	4739	4773	4840
		648	905	924	1400			4950	5192	5693	5727
		1512	1827	1854	1926			6079	6202	6211	6226
		2097	2234	2329	2357			588	1620	2056	2371
		3061	3063	3112	3114		MspAl I (12)	3241	3589	4107	4352
		3389	3549	3614	3642			5293	5759	5953	6309
		3675	3945	4012	4112			1897			
		4286	4395	4788	4881		Mun I (1)	631	2262	6212	
		5218	5550	5650	5753		Nae I (3)	1398	2355	5881	6064
		5883	5904	6037	6066		Nar I (6)	6178	6199		
		6120	6180	6201			Nci I (15)	163	398	399	570
HinC II	(2)	2397	2469					723	2218	2905	3140
Hind II	(2)	2397	2469					3141	4145	4841	5192
HinD III	(1)	2381						5693	5728	6079	
Hinf I	(18)	442	450	791	802		Nco I (2)	1411	2507		
		1437	1769	2135	2254		Nde I (1)	5829			
		2481	3300	3322	3343		NgoM I (3)	629	2260	6210	
		3600	3665	3740	4136		Nhe I (3)	30	2062	2770	
		4653	6291				Nla III (19)	62	1205	1415	1822
HinI I	(9)	742	1398	2355	5195			2511	2802	3256	3423
		5577	5881	6064	6178			3769	4489	4980	4990
		6199						5068	5104	5497	5602
HinP I	(43)	317	319	368	370			5686	6053	6126	
		646	903	922	1398			188	201	246	403
		1510	1825	1852	1924		Nla IV (40)	521	552	692	761
		2095	2232	2327	2355			893	1144	1221	1399
		3059	3061	3110	3112			1573	1689	1834	1909
		3387	3547	3612	3640			1961	2165	2244	2356
		3673	3943	4010	4110						

