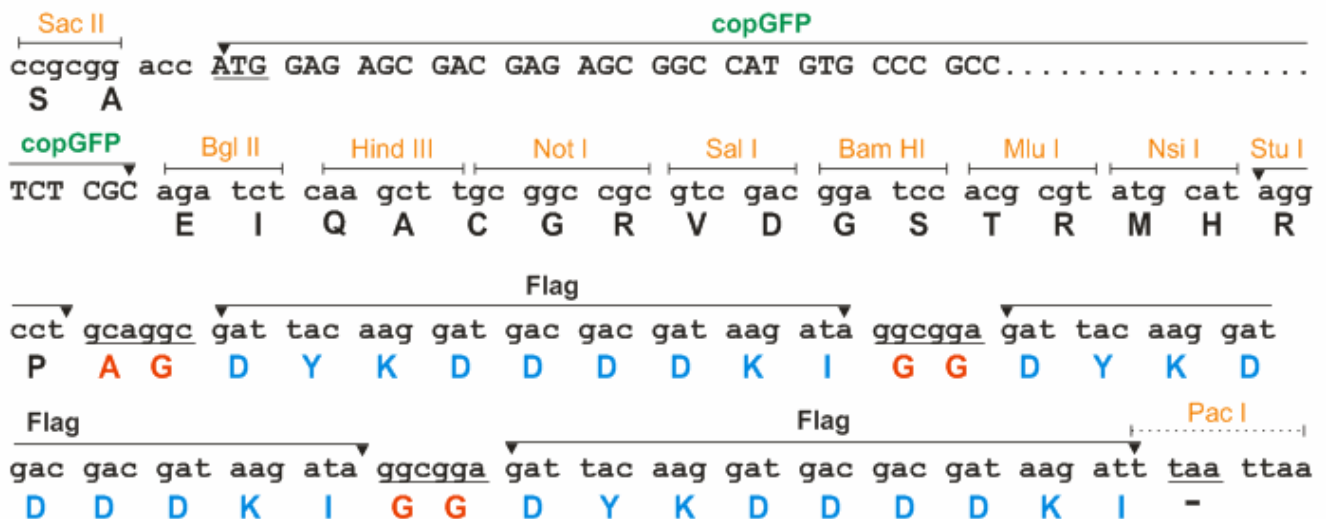
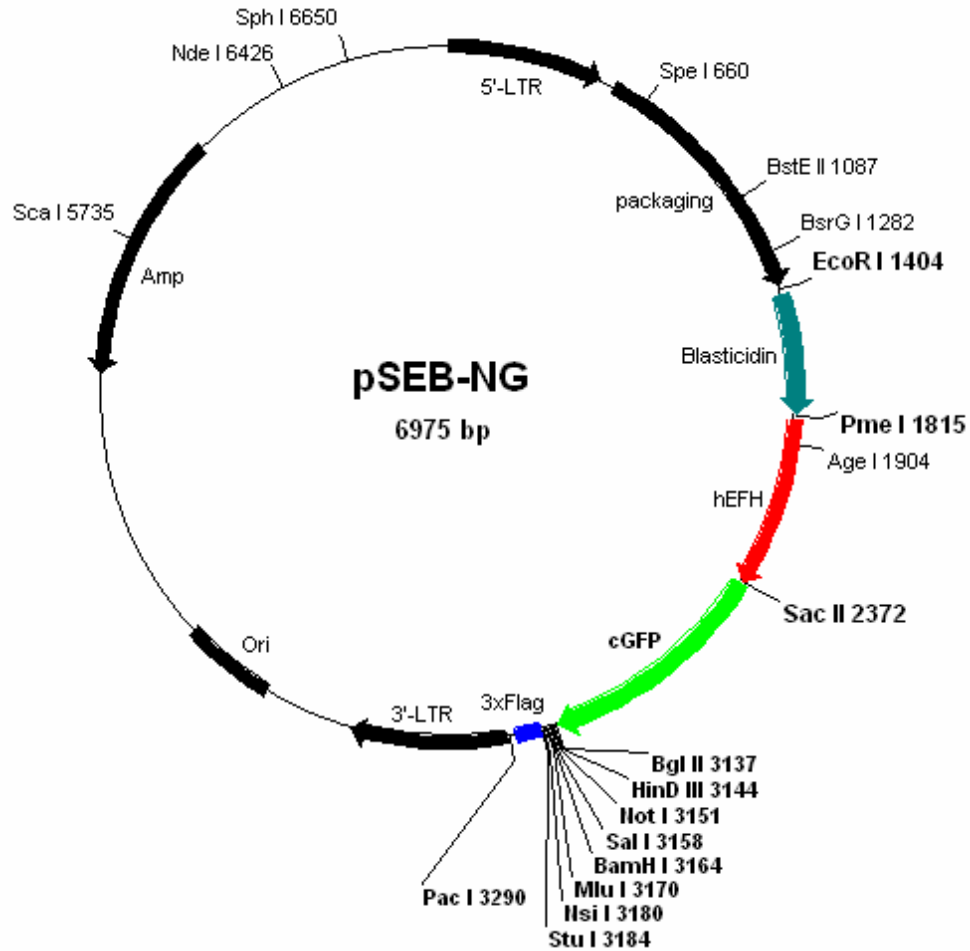


Vector: pSEB-NG (N-terminal copGFP tag)

Antibiotic Selection: Amp

Creator(s): Hong Yin, Molecular Oncology Lab of The University of Chicago

Date of Construction: December, 2007



pSEB-NG (N-terminal copGFP tag) Full-Length Sequence

TGAAAGACCC CACGTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGC AAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
TTCAGAACACAGACAGCAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAAAGAACAGATGGTCCCAGCATGCGGTCGCCG
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GTTCCACCGA GATTTGGAGACCCTGCCCA GGGACCACCGACCCCCCGC CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGTCTTTGTG
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GCATCGTTCT GTGTTGTCT TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTACCTTAGTCTACTG
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gac gac gat aag ata **ggcgga** gat tac aag gat gac gac gat aag ata **ggcgga** gat tac aag gat gac gac gat aag
at**TTAATTAA**
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AGTCCAATTT GTTAAAGACA GGAATCAAGTGGTCCAGGCT CTAGTTTTG CTCAACAATA TCACCAGTGAAGCCATATAG AGTACGAGCCATAGATAAAA

Unique enzymes in pSEB-NG:

Spe I A`CTAG,T 660

BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
EcoR I	G`AATT,C	1404
Bbv II	GAAGAC 7/11	1497

Bbs I	GAAGAC 8/12	1498			1687	1832	1907	2163
Nru I	TCG CGA	1644			2354	2435	2480	2528
BsaB I	GATNN NNATC	1711			2591	2753	3104	3583
Pme I	CTTT AAAC	1815			3740	4106	5203	6477
Mun I	C`AATT,G	1897			6660	6774	6795	
Age I	A`CCGG,T	1904		Ban II (9)	338	351	1677	2078
Cla I	AT`CG,AT	2364			2969	3677	3690	6727
Sac II	CC,GC`GG	2372			6741			
Blp I	GC`TNA,GC	2555		Bbe I (7)	1401	2358	2532	6481
Esp I	GC`TNA,GC	2555			6664	6778	6799	
Pf1M I	CCAN,NN`NTGG	2566		Bbs I (1)	1498			
Fse I	GG,CCGG`CC	2724		Bbv I (12)	931	939	1524	1629
Bsp120 I	G`GGCC,C	2965			1834	2814	2868	4781
Apa I	G,GGCC`C	2969			4784	4990	5684	6295
Xcm I	CCANNNN,N`NNNTGG3094			Bbv II (1)	1497			
Bgl II	A`GATC,T	3137		Bcn I (16)	164	399	400	571
Hind III	A`AGCT,T	3144			724	2219	3118	3503
Not I	GC`GGCC,GC	3151			3738	3739	4743	5439
Sal I	G`TCGA,C	3158			5790	6291	6326	6677
Acc I	GT`MK,AC	3159		Bfa I (16)	31	219	661	673
HinC II	GTY RAC	3160			1394	1522	1912	2063
Hind II	GTY RAC	3160			2189	2251	3368	3558
BamH I	G`GATC,C	3164			4857	5110	5445	6880
Mlu I	A`CGCG,T	3170		Bgl I (2)	5375	6493		
Nsi I	A,TGCA`T	3180		Bgl II (1)	3137			
Stu I	AGG CCT	3184		Blp I (1)	2555			
Pac I	TTA,AT`TAA	3290		Bpm I (3)	3305	5325	6943	
Sca I	AGT ACT	5735		Bsa I (7)	476	530	1149	2207
Nde I	CA`TA,TG	6426			3793	3814	5316	
Sph I	G,CATG`C	6650		BsaA I (2)	2563	2695		
Number of enzymes = 35				BsaB I (1)	1711			
				BsaH I (10)	742	1398	2355	2529
					5792	6174	6478	6661
					6775	6796		

The following enzymes do not cut in pSEB-NG:

Avr II	Bcl I	BsiC I	BsiW I	Bsm I	BsaJ I (39)	161	240	250	397
BspM II	Bst1107 I	BstB I	BstX I	Dra III		461	497	546	547
Hpa I	PaeR7 I	Rsr II	Sfi I	SnaB I		694	733	734	746
						747	1167	1236	1245
						1265	1266	1411	1716
						1974	2238	2369	2376
						2409	2766	2814	2832
						3096	3500	3579	3589
						3736	3799	4101	4522
						6596	6674	6680	
					BsaW I (6)	1829	1904	3125	4568
						4715	5546		
					BseR I (5)	464	1293	1332	3008
						3802			
					Bsg I (6)	1600	2022	2609	2675
						2810	2984		
					BsiE I (11)	592	727	1532	1648
						2725	3154	4278	4702
						5625	5774	6521	
					BsiHKA I (8)	338	2522	2823	3677
						4680	5841	5926	6423
					BsmA I (22)	107	475	531	609
						734	832	949	1073
						1132	1150	1328	1431
						2208	3322	3445	3792
						3813	5317	6091	6244
						6288	6960		
					BsmB I (7)	733	831	1072	1131
						1329	6245	6287	
					BsmF I (11)	172	185	564	729
						764	1205	1585	1853
						3511	3524	6656	
					BsoF I (55)	727	901	917	920
						925	928	1133	1513
						1532	1606	1609	1612
						1615	1618	1782	1823
						2043	2102	2117	2148
						2395	2425	2470	2497
						2605	2644	2683	2690
						2725	2803	2857	2890
						2986	2999	3151	3154
						4187	4268	4286	4289
						4407	4562	4705	4770
						4773	4979	5307	5646
						5673	5768	5997	6284
						6393	6497	6570	
					Bsp120 I (1)	2965			
					Bsp1286 I (2)	2522	2823		
					BspH I (4)	5082	6090	6195	6719
					BspM I (2)	2559	2832		
					Bsr I (18)	374	1030	1058	1546
						1570	1939	1960	3713
						4163	4769	4782	4896
						5302	5420	5463	5730
						5902	6608		
					BsrB I (5)	1042	2394	4054	4295
						6096			
					BsrD I (2)	5316	5490		
					BsrG I (1)	1282			
					Bssh II (4)	317	368	3656	3707
					BssS I (4)	1587	4535	5919	6226
					BstE II (1)	1087			
					BstN I (17)	241	548	735	748
						1169	1194	1217	1237
						1267	1717	3580	4102
						4390	4511	4524	6597
						6874			
					BstU I (30)	317	319	370	903
						905	1135	1644	1926

pSEB-NG: sites sorted by name:

Aat II	(2)	745	6177						
Acc I	(1)	3159							
Acc65 I	(2)	401	3740						
Aci I	(89)	197	203	566	588				
		688	727	860	901				
		1042	1133	1199	1298				
		1317	1355	1532	1614				
		1681	1926	1963	2043				
		2099	2102	2117	2148				
		2155	2182	2369	2371				
		2394	2406	2425	2469				
		2472	2497	2604	2643				
		2659	2682	2710	2725				
		2800	2866	2889	2983				
		2986	3073	3108	3150				
		3154	3222	3255	3536				
		3542	3838	4052	4155				
		4211	4221	4245	4288				
		4295	4316	4407	4435				
		4562	4581	4702	4812				
		4947	4956	5318	5409				
		5600	5646	5767	5811				
		5888	5997	6096	6143				
		6317	6356	6366	6392				
		6430	6443	6469	6526				
		6785							
Afl II	(3)	35	1006	3372					
Afl III	(2)	3170	4362						
Age I	(1)	1904							
Aha II	(10)	742	1398	2355	2529				
		5792	6174	6478	6661				
		6775	6796						
Ahd I	(4)	1020	3785	3831	5255				
Alu I	(40)	30	34	336	580				
		668	676	1515	1620				
		2056	2062	2066	2204				
		2345	2461	2700	2706				
		2859	2901	2998	3016				
		3146	3367	3371	3675				
		3994	4027	4122	4186				
		4304	4530	4620	4666				
		4923	5444	5544	5607				
		6286	6305	6550	6906				
Alw I	(18)	453	1051	1357	1727				
		2333	2361	3064	3135				
		3160	3171	4924	5010				
		5010	5107	5108	5572				
		5887	5893						
AlwN I	(2)	3496	4778						
Apa I	(1)	2969							
ApaL I	(3)	4676	5922	6419					
Apo I	(2)	872	1404						
Asc I	(2)	368	3707						
Ase I	(4)	4005	4133	4192	5427				
Asp718	(2)	401	3740						
Ava I	(8)	331	397	498	1871				
		1973	2765	3670	3736				
Ava II	(15)	186	199	254	551				
		690	1219	1572	2373				
		3113	3525	3538	3593				
		5393	5615	6870					
BamH I	(1)	3164							
Ban I	(23)	244	401	1142	1397				

		2095	2140	2371	2727	Fsp I	(2)	5477	6500		
		2883	2988	3075	3156	Gdi II	(14)	723	725	1129	1528
		3172	3656	3658	3709			1530	2396	2721	2723
		4209	4211	4409	4990			3150	3152	4202	5642
		5320	5813	6145	6245			6678	6810		
		6247	6350			Gsu I	(3)	3306	5326	6944	
BstY I	(11)	2337	3068	3128	3137	Hae I	(7)	584	1111	1416	3184
		3164	5003	5014	5100			4377	4388	4840	
		5112	5880	5897		Hae II	(14)	925	1401	1828	2235
Bsu36 I	(3)	781	1018	2111				2358	2532	2937	4240
Cac8 I	(46)	28	32	319	370			4610	6481	6664	6718
		582	586	631	650			6778	6799		
		1199	1508	1622	2064	Hae III	(36)	129	173	584	726
		2078	2099	2262	2290			762	774	987	1111
		2406	2628	2687	2722			1132	1197	1416	1531
		2866	2879	3039	3148			2116	2221	2397	2496
		3186	3190	3365	3369			2720	2724	2967	3153
		3658	3709	4155	4184			3184	3467	3512	4203
		4293	4379	4416	4976			4377	4388	4406	4840
		5367	6380	6528	6548			5298	5378	5645	6232
		6552	6648	6689	6737			6530	6679	6687	6811
		6779	6809			Hga I	(12)	381	642	895	1491
Cfr10 I	(11)	629	1904	2128	2260			2168	3146	3720	4472
		2351	2432	2720	2756			5050	5782	6340	6809
		5335	6798	6807		HgiA I	(8)	338	2522	2823	3677
		2364						4680	5841	5926	6423
Cla I	(1)	402	658	1283	1954	HgiE II	(2)	4941	6421		
Csp6 I	(10)	2671	3031	3741	5734	Hha I	(47)	319	321	370	372
		6410	6921					648	905	924	1400
		75	167	208	476			1512	1827	1854	1926
Dde I	(24)	781	1018	1290	1808			2097	2234	2329	2357
		2111	2205	2256	2555			2531	2883	2936	3077
		3078	3412	3506	3547			3658	3660	3709	3711
		3816	3887	4637	5046			3986	4146	4211	4239
		5212	5752	6178	6413			4272	4542	4609	4709
Dpn I	(34)	94	459	1046	1178			4883	4992	5385	5478
		1363	1647	1708	1722			5815	6147	6247	6350
		2339	2367	2417	2732			6480	6501	6634	6663
		2780	2795	3070	3130			6717	6777	6798	
		3139	3166	3432	4930	HinC II	(1)	3160			
		5005	5016	5024	5102	Hind II	(1)	3160			
		5114	5219	5560	5578	Hind III	(1)	3144			
		5624	5882	5899	5935	Hinf I	(17)	442	450	791	802
		6520	6744					1437	1769	2135	2254
DpnII	(34)	92	457	1044	1176			3897	3919	3940	4197
		1361	1645	1706	1720			4262	4337	4733	5250
		2337	2365	2415	2730			6888			
		2778	2793	3068	3128	HinI I	(10)	742	1398	2355	2529
		3137	3164	3430	4928			5792	6174	6478	6661
		5003	5014	5022	5100			6775	6796		
		5112	5217	5558	5576			317	319	368	370
		5622	5880	5897	5933	HinP I	(47)	646	903	922	1398
		6518	6742					1510	1825	1852	1924
Dra I	(5)	1815	2200	5121	5140			2095	2232	2327	2355
		5832						2529	2881	2934	3075
		1500	4470	6339				3656	3658	3707	3709
Drd I	(3)	694	1411	2369	2376			3984	4144	4209	4237
Dsa I	(9)	2409	2814	2832	3096			4270	4540	4607	4707
		6680						4881	4990	5383	5476
Eae I	(13)	582	724	1109	1130			5813	6145	6245	6348
		1414	1529	2395	2722			6478	6499	6632	6661
		3151	4201	5643	6677			6715	6775	6796	
		6809				Hpa II	(37)	163	398	569	630
Eag I	(4)	724	1529	2722	3151			723	1401	1830	1905
Ear I	(7)	1070	1311	2510	3984			2129	2217	2229	2261
		4246	6050	6538				2352	2433	2721	2757
Eco47 III	(3)	923	1826	6716				3111	3117	3126	3502
Eco57 I	(8)	1509	2077	2525	2687			3737	4080	4569	4716
		2858	4909	5923	6927			4742	4932	5336	5370
Eco72 I	(2)	2563	2695					5437	5547	5789	6290
EcoN I	(4)	784	1392	1915	2110			6324	6676	6799	6808
EcoO109 I	(8)	254	1219	1572	2965			6823			
		2966	3593	6231	6685	Hph I	(15)	1157	1183	1401	2423
EcoR I	(1)	1404						2777	5099	5326	5740
EcoR II	(17)	239	546	733	746			5948	5981	6265	6274
		1167	1192	1215	1235			6767	6812	6893	
		1265	1715	3578	4100	Kas I	(7)	1397	2354	2528	6477
		4388	4509	4522	6595			6660	6774	6795	
		6872				Kpn I	(2)	405	3744		
EcoR V	(3)	140	3478	6863		Mae I	(16)	31	219	661	673
Ehe I	(7)	1399	2356	2530	6479			1394	1522	1912	2063
		6662	6776	6797				2189	2251	3368	3558
		2555						4857	5110	5445	6880
Esp I	(1)	727	901	917	920			742	1081	1122	2019
Fnu4H I	(55)	925	928	1133	1513	Mae II	(13)	2302	2562	2694	2844
		1532	1606	1609	1612			5065	5481	5854	6174
		1615	1618	1782	1823			6616			
		2043	2102	2117	2148			39	994	1022	1087
		2395	2425	2470	2497			1231	2331	2347	3376
		2605	2644	2683	2690			3854	4718	4781	4897
		2725	2803	2857	2890			5180	5511	5569	5722
		2986	2999	3151	3154			5910	6298	6589	6609
		4187	4268	4286	4289	Mbo I	(34)	92	457	1044	1176
		4407	4562	4705	4770			1361	1645	1706	1720
		4773	4979	5307	5646			2337	2365	2415	2730
		5673	5768	5997	6284			2778	2793	3068	3128
		6393	6497	6570				3137	3164	3430	4928
Fok I	(18)	423	1140	1300	1464			5003	5014	5022	5100
		1699	2107	2783	2924			5112	5217	5558	5576
		2936	3215	3248	3281			5622	5880	5897	5933
		3761	5221	5402	5689			6518	6742		
		6332	6576			Mbo II	(16)	1086	1299	1445	1502
Fse I	(1)	2724						1530	2526	2774	4000

		4234	5023	5096	5851	Pst I	(5)	921	929	1105	2958
		5929	6038	6526	6738			3190			
Mlu I	(1)	3170				Pvu I	(3)	1648	5625	6521	
Mme I	(6)	829	1106	3801	3853	Pvu II	(5)	1620	2056	4186	6550
		4576	4760					6906			
Mnl I	(57)	167	216	368	387	Rsa I	(10)	403	659	1284	1955
		432	460	484	506			2672	3032	3742	5735
		510	566	776	872			6411	6922		
		1168	1271	1304	1310	Sac I	(2)	338	3677		
		1313	1319	1349	1352	Sac II	(1)	2372			
		1367	1374	1390	1454	Sal I	(1)	3158			
		1795	1796	1880	1969	Sap I	(3)	2510	3984	4246	
		2064	2106	2160	2176	Sau3A I	(34)	92	457	1044	1176
		2470	2668	2710	2761			1361	1645	1706	1720
		2986	3555	3707	3726			2337	2365	2415	2730
		3771	3798	3822	3882			2778	2793	3068	3128
		4211	4260	4470	4543			3137	3164	3430	4928
		4794	5194	5275	5421			5003	5014	5022	5100
		5627	6222	6280	6540			5112	5217	5558	5576
		6824						5622	5880	5897	5933
Msc I	(3)	584	1111	1416				6518	6742		
Mse I	(26)	36	1007	1119	1149	Sau96 I	(32)	127	171	186	199
		1173	1814	2199	3286			254	551	690	760
		3290	3373	3907	4005			773	985	1196	1219
		4133	4192	5068	5120			1572	2219	2373	2494
		5125	5139	5192	5427			2965	2966	3113	3465
		5466	5831	6203	6384			3510	3525	3538	3593
		6581	6851					5297	5376	5393	5615
Msl I	(2)	5507	5666					6231	6528	6685	6870
Msp I	(37)	163	398	569	630	Sca I	(1)	5735			
		723	1401	1830	1905	ScrF I	(33)	163	241	398	399
		2129	2217	2229	2261			548	570	723	735
		2352	2433	2721	2757			748	1169	1194	1217
		3111	3117	3126	3502			1237	1267	1717	2218
		3737	4080	4569	4716			3117	3502	3580	3737
		4742	4932	5336	5370			3738	4102	4390	4511
		5437	5547	5789	6290			4524	4742	5438	5789
		6324	6676	6799	6808			6290	6325	6597	6676
		6823						6874			
MspAl I	(13)	588	1620	2056	2371	Sec I	(39)	161	240	250	397
		2604	3838	4186	4704			461	497	546	547
		4949	5890	6356	6550			694	733	734	746
		6906						747	1167	1236	1245
Mun I	(1)	1897						1265	1266	1411	1716
Nae I	(4)	631	2262	2722	6809			1974	2238	2369	2376
Nar I	(7)	1398	2355	2529	6478			2409	2766	2814	2832
		6661	6775	6796				3096	3500	3579	3589
Nci I	(16)	163	398	399	570			3736	3799	4101	4522
		723	2218	3117	3502			6596	6674	6680	
		3737	3738	4742	5438	SfaN I	(25)	185	444	641	938
		5789	6290	6325	6676			1485	1542	1674	1720
Nco I	(4)	1411	2376	2409	2832			2088	2435	2669	2957
Nde I	(1)	6426						3029	3524	3782	4458
NgoM I	(4)	629	2260	2720	6807			5510	5703	5950	6311
Nhe I	(3)	30	2062	3367				6403	6441	6479	6795
Nla III	(25)	62	1205	1415	1822			6807			
		2380	2402	2413	2503	Sfc I	(13)	15	917	925	1101
		2836	2923	2974	3399			1496	2896	2954	3186
		3853	4020	4366	5086			3352	4627	4818	5496
		5577	5587	5665	5701			6914			
		6094	6199	6283	6650	Sma I	(2)	399	3738		
		6723				Spe I	(1)	660			
Nla IV	(49)	188	201	246	403	Sph I	(1)	6650			
		521	552	692	761	Ssp I	(2)	3905	6059		
		893	1144	1221	1399	Stu I	(1)	3184			
		1573	1689	1834	1909	Sty I	(10)	250	461	1245	1411
		1961	2165	2244	2356			2238	2376	2409	2832
		2437	2482	2530	2593			3589	3799		
		2755	2966	2967	2968	Taq I	(15)	794	1038	1349	1360
		3106	3115	3121	3166			1705	2069	2211	2364
		3527	3540	3585	3742			2418	2457	2664	3159
		4108	4394	4433	5205			3900	4462	5906	
		5299	5340	5551	6141	Tfi I	(7)	442	802	1437	1769
		6479	6662	6686	6776			3940	4197	4337	
		6797				Tsp45 I	(7)	1022	1231	2347	5511
Not I	(1)	3151						5722	6298	6609	
Nru I	(1)	1644				Tth111 I	(4)	390	811	1217	3729
Nsi I	(1)	3180				Tth111 II	(10)	146	422	613	632
Nsp7524 I	(5)	1818	2919	4362	6279			2278	2503	3484	4951
		6646						4960	4990		
NspB II	(13)	588	1620	2056	2371	Vsp I	(4)	4005	4133	4192	5427
		2604	3838	4186	4704	Xba I	(2)	218	3557		
		4949	5890	6356	6550	Xcm I	(1)	3094			
		6906				Xho II	(11)	2337	3068	3128	3137
NspH I	(5)	1822	2923	4366	6283			3164	5003	5014	5100
		6650						5112	5880	5897	
Pac I	(1)	3290				Xma I	(2)	397	3736		
Pal I	(36)	129	173	584	726	Xma III	(4)	724	1529	2722	3151
		762	774	987	1111	Xmn I	(4)	2618	3968	4006	5854
		1132	1197	1416	1531						
		2116	2221	2397	2496						
		2720	2724	2967	3153						
		3184	3467	3512	4203						
		4377	4388	4406	4840						
		5298	5378	5645	6232						
		6530	6679	6687	6811						
PflM I	(1)	2566				Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Ple I	(4)	799	2143	3905	4741	Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	89
Pme I	(1)	1815				Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Pml I	(2)	2563	2695			Age I	A`CCGG,T	1	Aha II	GR`CG,YC	10
PpuM I	(4)	254	1219	1572	3593	Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	40
Psp1406 I	(3)	2019	5481	5854		Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
PspA I	(2)	397	3736			Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	3
						Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
						Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
						Ava I	C`YCGR,G	8	Ava II	G`GWC,C	15
						Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1

Site usage in pSEB-NG:

Ban I	G`GYRC,C	23	Ban II	G,RCY`C	9	HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	17
Bbe I	G,CGC`C	7	Bbs I	GAAGAC 8/12	1	HinI I	GR`CG,YC	10	HinP I	G`CG,C	47
Bbv I	GCAGC 13/17	12	Bbv II	GAAGAC 7/11	1	Hpa I	GTT AAC	-	Hpa II	C`CG,G	37
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	16	Hph I	GGTGA 12/11	15	Kas I	G`GGCC,C	7
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	1	Mae II	A`CG,T	13	Mae III	`GTNAC,	20
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7	Mbo I	`GATC,	34	Mbo II	GAAGA 12/11	16
Bsaa I	YAC GTR	2	BsaB I	GATNN NNATC	1	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Bsah I	GR`CG,YC	10	BsaH I	C`CNNG,G	39	Mnl I	CCTC 10/10	57	Msc I	TGG CCA	3
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	5	Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	2
Bsg I	GTGCAG 22/20	6	Bsic I	TT`CG,AA	-	Msp I	C`CG,G	37	MspAl I	CMG CKG	13
BsiE I	CG,RY`CG	11	BsiHKA I	G,WGCW`C	8	Mun I	C`AATT,G	1	Nae I	GCC GGC	4
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-	Nar I	GG`CG,CC	7	Nci I	CC`S,GG	16
Bsma I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7	Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	55	Ngom I	G`CCGG,C	4	Nhe I	G`CTAG,C	3
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G, DGCH`C	2	Nla III	,CATG`	25	Nla IV	TGN NCC	49
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	2	Not I	GC`GGCC,GC	1	Nru I	TGG CGA	1
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18	Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	5
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2	NspB II	CMG CKG	13	NspH I	R,CATG`Y	5
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-	Pal I	GG CC	36	Pflm I	CCAN,NNN`NTGG	1
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1	Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
BstN I	CC`W,GG	17	BstU I	CG CG	30	Pml I	CA GTG	2	PpuM I	RG`GWC,CY	4
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	11	Psp1406 I	AA`CG,TT	3	PspA I	C`CGGG,G	2
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	46	Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	3
Cfr10 I	R`CCGG,Y	11	cla I	AT`CG,AT	1	Pvu II	CAG CTG	5	Rsa I	GT AC	10
Csp6 I	G`TA,C	10	Dde I	C`TNA,G	24	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Dpn I	GA TC	34	DpnII	`GATC,	34	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-	Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	34
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	9	Sau96 I	G`GNC,C	32	Sca I	AGT ACT	1
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	4	ScrF I	CC`N,GG	33	Sec I	C`CNNG,G	39
Ear I	CTCTTC 7/10	7	Eco47 III	AGC GCT	3	SfaN I	GCATC 9/13	25	Sfc I	C`TRYA,G	13
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	2	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
EcoN I	CCTNN`N,NNAGG	4	Eco109 I	RG`GNC,CY	8	SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17	Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
EcoR V	GAT ATC	3	Ehe I	GGC GCC	7	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	55	Stu I	AGG CCT	1	Sty I	G`CWVG,G	10
Fok I	GGATG 14/18	18	Fse I	GG,CCGG`CC	1	Taq I	T`CG,A	15	Tfi I	G`AWT,C	7
Fsp I	TGC GCA	2	Gdi II	YGGC,CG	14	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7	Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	4
Hae II	R,GCGC`Y	14	Hae III	GG CC	36	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	8	Xcm I	CCANNNN,N`NNNNTGG1	-	Xho I	C`TCGA,G	-
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	47	Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	2
Hinc II	GTY RAC	1	Hind II	GTY RAC	1	Xma III	C`GGCC,G	4	Xmn I	GAANN NNTTC	4