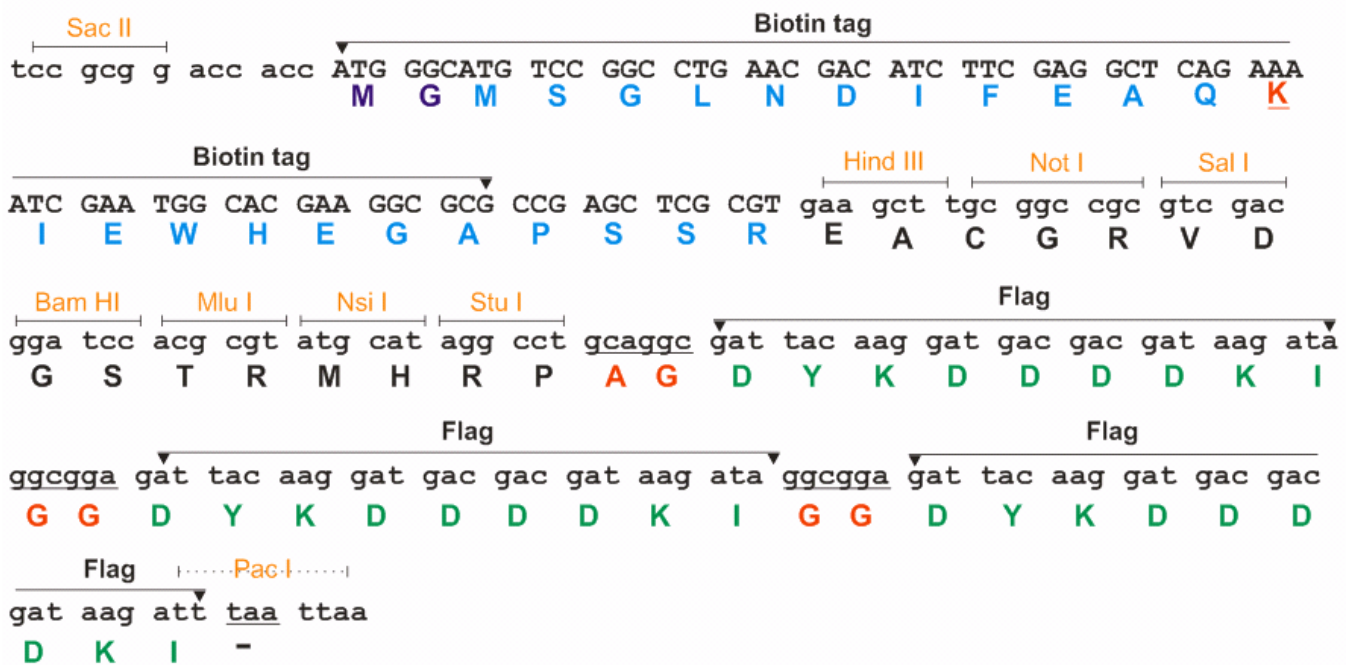
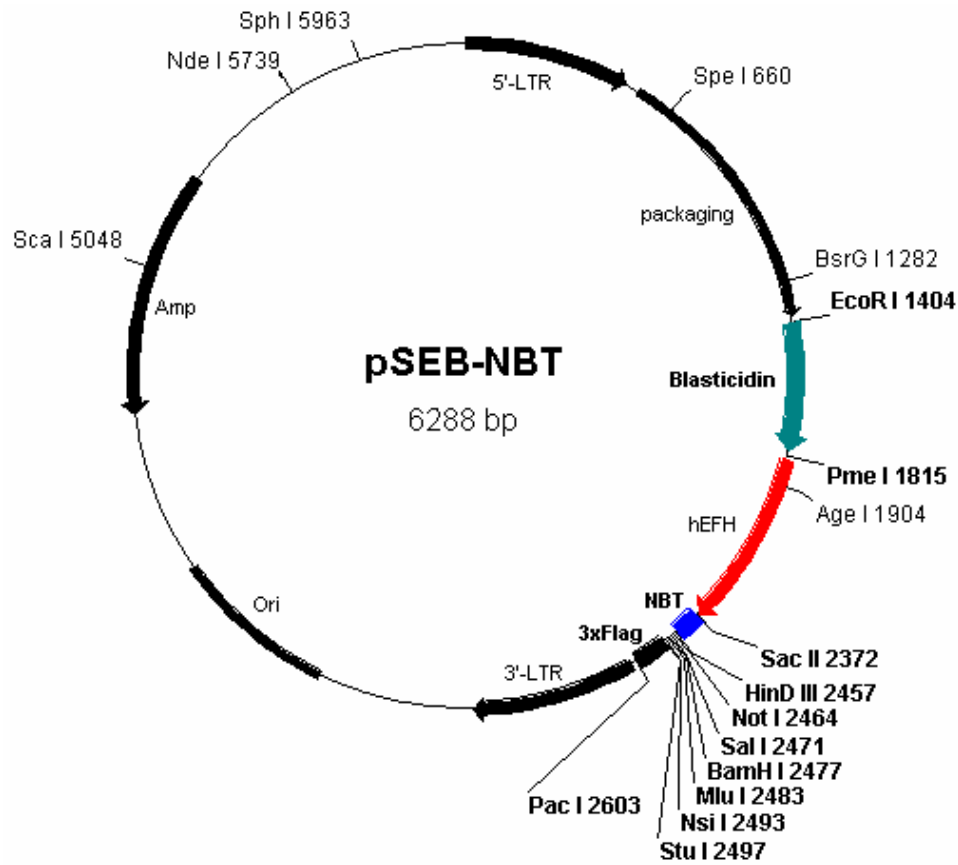


**Vector:** pSEB-NBT (N-terminal Biotin tag)

**Antibiotic Selection:** Amp

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

**Date of Construction:** April, 2008



# pSEB-NBT (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG  
 TTAGGAACAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTCTCCCGGCTCAGGGCCAAAGACAGATGGTCCCAGATGCGGTCCC  
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCAAGGACCTGAAATGACCTTGTGCCATTATTGAACCTAACCAATCAGTCTCGCTTCT  
 GTTCGCGCGTCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATTTCCCAAT  
 AAAGCCTCTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG  
 GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCGACCCCGCG CGGGAGGTA GCTGGCCAGC GGTGTTTCTGTCTGTCTC TGTCTTTGTG  
 CGTGTGTGCGCGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTTAGCTAACCTAGCTCTGTATCTGGCGGACCCGTTGGTGAACCTGACGAGTCTGAACACCCG  
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCGGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT  
 CTGGTAGGAGACGAGAACC TAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTTCGGTT TGAACCCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA  
 GCATCGTCT GTGTGTCTC TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTGACCTTAGGTCCTG  
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 TCGTAGCCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT  
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 GCCGACGGCAGTTGGGATTGCTGAATTGCTGCCCTCTGTTTATGTTGGGAGGGCTaa**gtttaaacatg****cagCGTCCGGTGCCCGTCACTGGGGCAGAGCGCACAT**  
**CGCCACAGTCCCGAGAAGTTGGGGGAGGGTCCGCAATGAACCGGTGCTAGAGAAGTGGCGCGGGTAAACTGGGAAAGTATGCTGTACTGGTCTCCG**  
**CGTTTTCCGAGGGTGGGGAGAACCGTATAAAGTGCAGTAGTCCCGTGAACGTTCTTTTCGCAAGCGGGTTGGCCCAAGAACACAGCTG**AGCTAGCTTCG****  
**AGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGCGCCATCCAGCCGGTTGAGTCCGCTTCTGCGCCTCCCGCTGTGGTCCCTCTGAAT**  
**GCGTCCGCTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCTTTGTCCGCGCTCCCTTGAGGCTACCTAGACTCAGCCGCTCTCCAGCTTTGCCTGA**  
**CCCTGCTGCTCAACTCTACGTCTTTGTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTAC atcgat cgcgg ACCACC**  
**ATG GGC ATG TCC GGC CTG AAC GAC ATC TTC GAG GCT CAG AAA ATC GAA TGG CAC GAA GGC GCG**  
**CCG AGC TCG CGT GAagett gcg cgc cgt cga cgg atc ca CGC GT atgcat AGGCCT gcaggc** gat tac aag gat 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**tt**  
**TAATTAA**  
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 GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCTTCTCCCTTCGGG AAGCGTGGCGTTCCTCATA GCTCAGCTGTAGTATCTC  
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 CCCGATCTTCCCCTCGGTG ATGTCGGCA TATAGCGCC AGCAACCGA CTTGTGGCG CGGTGATGCCGGCCAGATG CGTCCGCGGTAGAGCGGATT  
 AGTCCAATTT GTTAAAGACA GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTAACAATA TCACCAGCTGAAGCTATAG AGTACGAGCCATAGATAAAAA

## Unique enzymes in pSEB-NBT:

Enzyme	Recognition Sequence	Frequency
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	GAGAC 8/12	1498
Nru I	TCG CGA	1644
BsaB I	GATNN NNATC	1711
Pme I	CTTT AAAC	1815
Mun I	C`AATT,G	1897
Age I	A`CCGG,T	1904
Cla I	AT`CG,AT	2364
Sac II	CC,CG`GG	2372
HinD III	A`AGCT,T	2457
Not I	GC`GGCC,GC	2464
Sal I	G`TCGA,C	2471
Acc I	GT`MK,AC	2472
HinC II	GTV RAC	2473
HinD II	GTV RAC	2473
BamH I	G`GATC,C	2477
Mlu I	A`CCGC,T	2483
Nsi I	A,TGCA`T	2493
Stu I	AGG CCT	2497

Pac I	TTA,AT`TAA	2603
Sca I	AGT ACT	5048
Nde I	CA`TA,TG	5739
Sph I	G,CATG`C	5963

Number of enzymes = 27

			1132	1150	1328	1431
			2208	2635	2758	3105
			3126	4630	5404	5557
			5601	6273		
BsmB I	(7)	733	831	1072	1131	
		1329	5558	5600		
BsmF I	(11)	172	185	564	729	
		764	1205	1585	1853	
		2824	2837	5969		
BsoF I	(41)	727	901	917	920	
		925	928	1133	1513	
		1532	1606	1609	1612	
		1615	1618	1782	1823	
		2043	2102	2117	2148	
		2464	2467	3500	3581	
		3599	3602	3720	3875	
		4018	4083	4086	4292	
		4620	4959	4986	5081	
		5310	5597	5706	5810	
		5883				
BspH I	(4)	4395	5403	5508	6032	
Bsr I	(18)	374	1030	1058	1546	
		1570	1939	1960	3026	
		3476	4082	4095	4209	
		4615	4733	4776	5043	
		5215	5921			
BsrB I	(4)	1042	3367	3608	5409	
BsrD I	(2)	4629	4803			
BsrG I	(1)	1282				
BssH II	(5)	317	368	2439	2969	
		3020				
BssS I	(4)	1587	3848	5232	5539	
BstE II	(1)	1087				
BstN I	(17)	241	548	735	748	
		1169	1194	1217	1237	
		1267	1717	2893	3415	
		3703	3824	3837	5910	
		6187				
BstU I	(28)	317	319	370	903	
		905	1135	1644	1926	
		2095	2140	2371	2441	
		2452	2469	2485	2969	
		2971	3022	3522	3524	
		3722	4303	4633	5126	
		5458	5558	5560	5663	
BstY I	(8)	2337	2477	4316	4327	
		4413	4425	5193	5210	
Bsu36 I	(3)	781	1018	2111		
Cac8 I	(41)	28	32	319	370	
		582	586	631	650	
		1199	1508	1622	2064	
		2078	2099	2262	2290	
		2441	2450	2461	2499	
		2503	2678	2682	2971	
		3022	3468	3497	3606	
		3692	3729	4289	4680	
		5693	5841	5861	5865	
		5961	6002	6050	6092	
		6122				
Cfr10 I	(8)	629	1904	2128	2260	
		2351	4648	6111	6120	
Cla I	(1)	2364				
Csp6 I	(8)	402	658	1283	1954	
		3054	5047	5723	6234	
		75	167	476		
Dde I	(23)	781	1018	1290	1808	
		2111	2205	2256	2415	
		2725	2819	2860	3129	
		3200	3950	4359	4525	
		5065	5491	5726		
Dpn I	(27)	94	459	1046	1178	
		1363	1647	1708	1722	
		2339	2367	2479	2745	
		4243	4318	4329	4337	
		4415	4427	4532	4873	
		4891	4937	5195	5212	
		5248	5833	6057		
DpnII	(27)	92	457	1044	1176	
		1361	1645	1706	1720	
		2337	2365	2477	2743	
		4241	4316	4327	4335	
		4413	4425	4530	4871	
		4889	4935	5193	5210	
		5246	5831	6055		
Dra I	(5)	1815	2200	4434	4453	
		5145				
Drd I	(3)	1500	3783	5652		
Dsa I	(5)	694	1411	2369	2379	
		5993				
Eae I	(11)	582	724	1109	1130	
		1414	1529	2464	3514	
		4956	5990	6122		
Eag I	(3)	724	1529	2464		
Ear I	(6)	1070	1311	3297	3559	
		5363	5851			
Eco47 III	(3)	923	1826	6029		
Eco57 I	(5)	1509	2077	4222	5236	
		6240				
EcoN I	(4)	784	1392	1915	2110	
EcoO109 I	(6)	254	1219	1572	2906	
		5544	5998			
EcoR I	(1)	1404				
EcoR II	(17)	239	546	733	746	
		1167	1192	1215	1235	
		1265	1715	2891	3413	
		3701	3822	3835	5908	
		6185				
EcoR V	(3)	140	2791	6176		
Ehe I	(6)	1399	2356	5792	5975	
		6089	6110			
Fnu4H I	(41)	727	901	917	920	
		925	928	1133	1513	
		1532	1606	1609	1612	
		1615	1618	1782	1823	
		2043	2102	2117	2148	
		2464	2467	3500	3581	
		3599	3602	3720	3875	
		4018	4083	4086	4292	
		4620	4959	4986	5081	
		5310	5597	5706	5810	
		5883				
Fok I	(15)	423	1140	1300	1464	
		1699	2107	2528	2561	
		2594	3074	4534	4715	

The following enzymes do not cut in pSEB-NBT:

Apa I	Avr II	Bcl I	Bgl II	Blp I
BsaA I	BsiC I	BsiW I	Bsm I	Bsp120 I
Bsp1286 I	BspM I	BspM II	Bst1107 I	BstB I
BstX I	Dra III	Eco72 I	Esp I	Fse I
Hpa I	PaeR7 I	PflM I	Pml I	Rsr II
Sfi I	SnaB I	Spl I	Srf I	Xca I

pSEB-NBT: sites sorted by name:

Aat II	(2)	745	5490				
Acc I	(1)	2472					
Acc65 I	(2)	401	3053				
Aci I	(70)	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		
		2463	2467	2535	2568		
		2849	2855	3151	3365		
		3468	3524	3534	3558		
		3601	3608	3629	3720		
		3748	3875	3894	4015		
		4125	4260	4269	4631		
		4722	4913	4959	5080		
		5124	5201	5310	5409		
		5456	5630	5669	5679		
		5705	5743	5756	5782		
		5839	6098				
Afl II	(3)	35	1006	2685			
Afl III	(2)	2483	3675				
Age I	(1)	1904					
Aha II	(9)	742	1398	2355	5105		
		5487	5791	5974	6088		
		6109					
Ahd I	(4)	1020	3098	3144	4568		
Alu I	(34)	30	34	336	580		
		668	676	1515	1620		
		2056	2062	2066	2204		
		2345	2448	2459	2680		
		2684	2988	3307	3340		
		3435	3499	3617	3843		
		3933	3979	4236	4757		
		4857	4920	5599	5618		
		5863	6219				
Alw I	(16)	453	1051	1357	1727		
		2333	2361	2473	2484		
		4237	4323	4323	4420		
		4421	4885	5200	5206		
AlwN I	(2)	2809	4091				
Apal I	(3)	3989	5235	5732			
Apo I	(2)	872	1404				
Asc I	(3)	368	2439	3020			
Ase I	(4)	3318	3446	3505	4740		
Asp718	(2)	401	3053				
Ava I	(7)	331	397	498	1871		
		1973	2983	3049			
Ava II	(14)	186	199	254	551		
		690	1219	1572	2373		
		2838	2851	2906	4706		
		4928	6183				
BamH I	(1)	2477					
Ban I	(17)	244	401	1142	1397		
		1687	1832	1907	2163		
		2354	2896	3053	3419		
		4516	5790	5973	6087		
		6108					
Ban II	(9)	338	351	1677	2078		
		2450	2990	3003	6040		
		6054					
Bbe I	(6)	1401	2358	5794	5977		
		6091	6112				
Bbs I	(1)	1498					
Bbv I	(10)	931	939	1524	1629		
		1834	4094	4097	4303		
		4997	5608				
Bbv II	(1)	1497					
Bcn I	(15)	164	399	400	571		
		724	2219	2816	3051		
		3052	4056	4752	5103		
		5604	5639	5990			
Bfa I	(16)	31	219	661	673		
		1394	1522	1912	2063		
		2189	2251	2681	2871		
		4170	4423	4758	6193		
Bgl I	(2)	4688	5806				
Bpm I	(3)	2618	4638	6256			
Bsa I	(7)	476	530	1149	2207		
		3106	3127	4629			
BsaB I	(1)	1711					
BsaH I	(9)	742	1398	2355	5105		
		5487	5791	5974	6088		
		6109					
BsaJ I	(34)	161	240	250	397		
		461	497	546	547		
		694	733	734	746		
		747	1167	1236	1245		
		1265	1266	1411	1716		
		1974	2238	2369	2379		
		2813	2892	2902	3049		
		3112	3414	3835	5909		
		5987	5993				
BsaW I	(5)	1829	1904	3881	4028		
		4859					
BseR I	(4)						

		5002	5645	5889		Msp I	(32)	163	398	569	630
Fsp I	(2)	4790	5813					723	1401	1830	1905
Gdi II	(11)	723	725	1129	1528			2129	2217	2229	2261
		1530	2463	2465	3515			2352	2391	2815	3050
		4955	5991	6123				3393	3882	4029	4055
Gsu I	(3)	2619	4639	6257				4245	4649	4683	4750
Hae I	(7)	584	1111	1416	2497			4860	5102	5603	5637
		3690	3701	4153				5989	6112	6121	6136
Hae II	(12)	925	1401	1828	2235	MspAl I	(12)	588	1620	2056	2371
		2358	3553	3923	5794			3151	3499	4017	4262
		5977	6031	6091	6112			5203	5669	5863	6219
Hae III	(32)	129	173	584	726	Mun I	(1)	1897			
		762	774	987	1111	Nae I	(3)	631			
		1132	1197	1416	1531	Nar I	(6)	1398	2262	6122	
		2116	2221	2394	2466			6088	6109		
		2497	2780	2825	3516	Nci I	(15)	163	398	399	570
		3690	3701	3719	4153			723	2218	2815	3050
		4611	4691	4958	5545			3051	4055	4751	5102
		5843	5992	6000	6124			5603	5638	5989	
Hga I	(12)	381	642	895	1491	Nco I	(2)	1411	2379		
		2168	2459	3033	3785	Nde I	(1)	5739			
		4363	5095	5653	6122	NgoM I	(3)	629	2260	6120	
HgiA I	(7)	338	2450	2990	3993	Nhe I	(3)	30	2062	2680	
		5154	5239	5736		Nla III	(20)	62	1205	1415	1822
HgiE II	(2)	4254	5734					2383	2389	2712	3166
Hha I	(45)	319	321	370	372			3333	3679	4399	4890
		648	905	924	1400			4900	4978	5014	5407
		1512	1827	1854	1926			5512	5596	5963	6036
		2097	2234	2329	2357	Nla IV	(38)	188	201	246	403
		2441	2443	2971	2973			521	552	692	761
		3022	3024	3299	3459			893	1144	1221	1399
		3524	3552	3585	3855			1573	1689	1834	1909
		3922	4022	4196	4305			1961	2165	2244	2356
		4698	4791	5128	5460			2479	2840	2853	2898
		5560	5663	5793	5814			3055	3421	3707	3746
		5947	5976	6030	6090			4518	4612	4653	4864
		6111						5454	5792	5975	5999
		6089						6089	6110		
Hinc II	(1)	2473				Not I	(1)	2464			
Hind II	(1)	2473				Nru I	(1)	1644			
Hind III	(1)	2457				Nsi I	(1)	2493			
Hinf I	(17)	442	450	791	802	Nsp7524 I	(5)	1818	2385	3675	5592
		1437	1769	2135	2254			5959			
		3210	3232	3253	3510	NspB II	(12)	588	1620	2056	2371
		3575	3650	4046	4563			3151	3499	4017	4262
		6201						5203	5669	5863	6219
HinI I	(9)	742	1398	2355	5105	NspH I	(5)	1822	2389	3679	5596
		5487	5791	5974	6088			5963			
		6109						2603			
HinP I	(45)	317	319	368	370	Pac I	(1)	2603			
		646	903	922	1398	Pal I	(32)	129	173	584	726
		1510	1825	1852	1924			762	774	987	1111
		2095	2232	2327	2355			1132	1197	1416	1531
		2439	2441	2969	2971			2116	2221	2394	2466
		3020	3022	3297	3457			2497	2780	2825	3516
		3522	3550	3583	3853			3690	3701	3719	4153
		3920	4020	4194	4303			4611	4691	4958	5545
		4696	4789	5126	5458			5843	5992	6000	6124
		5558	5661	5791	5812	Ple I	(4)	799	2143	3218	4054
		5945	5974	6028	6088	Pme I	(1)	1815			
		6109				PpuM I	(4)	254	1219	1572	2906
Hpa II	(32)	163	398	569	630	Psp1406 I	(3)	2019	4794	5167	
		723	1401	1830	1905			397	3049		
		2129	2217	2229	2261	Pst I	(4)	921	929	1105	2503
		2352	2391	2815	3050	Pvu I	(3)	1648	4938	5834	
		3393	3882	4029	4055	Pvu II	(5)	1620	2056	3499	5863
		4245	4649	4683	4750			6219			
		4860	5102	5603	5637	Rsa I	(8)	403	659	1284	1955
		5989	6112	6121	6136			3055	5048	5724	6235
Hph I	(13)	1157	1183	1401	4412	Sac I	(3)	338	2450	2990	
		4639	5053	5261	5294	Sac II	(1)	2372			
		5578	5587	6080	6125	Sal I	(1)	2471			
		6206				Sap I	(2)	3297	3559		
Kas I	(6)	1397	2354	5790	5973	Sau3A I	(27)	92	457	1044	1176
		6087	6108					1361	1645	1706	1720
Kpn I	(2)	405	3057					2337	2365	2477	2743
Mae I	(16)	31	219	661	673			4241	4316	4327	4335
		1394	1522	1912	2063			4413	4425	4530	4871
		2189	2251	2681	2871			4889	4935	5193	5210
		4170	4423	4758	6193			5246	5831	6055	
Mae II	(10)	742	1081	1122	2019	Sau96 I	(28)	127	171	186	199
		2302	4378	4794	5167			254	551	690	760
		5487	5929					773	985	1196	1219
Mae III	(20)	39	994	1022	1087			1572	2219	2373	2778
		1231	2331	2347	2689			2823	2838	2851	2906
		3167	4031	4094	4210			4610	4689	4706	4928
		4493	4824	4882	5035			5544	5841	5998	6183
		5223	5611	5902	5922	Sca I	(1)	5048			
Mbo I	(27)	92	457	1044	1176	ScrF I	(32)	163	241	398	399
		1361	1645	1706	1720			548	570	723	735
		2337	2365	2477	2743			748	1169	1194	1217
		4241	4316	4327	4335			1237	1267	1717	2218
		4413	4425	4530	4871			2815	2893	3050	3051
		4889	4935	5193	5210			3415	3703	3824	3837
		5246	5831	6055				4055	4751	5102	5603
Mbo II	(15)	1086	1299	1445	1502			5638	5910	5989	6187
		1530	2399	3313	3547	Sec I	(34)	161	240	250	397
		4336	4409	5164	5242			461	497	546	547
		5351	5839	6051				694	733	734	746
Mlu I	(1)	2483						747	1167	1236	1245
Mme I	(6)	829	1106	3114	3166			1265	1266	1411	1716
		3889	4073					1974	2238	2369	2379
Mnl I	(53)	167	216	368	387			2813	2892	2902	3049
		432	460	484	506			3112	3414	3835	5909
		510	566	776	872			5987	5993		
		1168	1271	1304	1310	SfaN I	(21)	185	444	641	938
		1313	1319	1349	1352			1485	1542	1674	1720
		1367	1374	1390	1454			2088	2837	3095	3771
		1795	1796	1880	1969			4823	5016	5263	5624
		2064	2106	2160	2176			5716	5754	5792	6108
		2404	2868	3020	3039			6120			
		3084	3111	3135	3195	Sfc I	(11)	15	917	925	1101
		3524	3573	3783	3856			1496	2499	2665	3940
		4107	4507	4588	4734			4131	4809	6227	
		4940	5535	5593	5853			399	3051		
		6137				Sma I	(2)	660			
Msc I	(3)	584	1111	1416		Spe I	(1)	660			
Mse I	(26)	36	1007	1119	1149	Sph I	(1)	5963			
		1173	1814	2199	2599	Ssp I	(2)	3218	5372		
		2603	2686	3220	3318	Stu I	(1)	2497			
		3446	3505	4381	4433	Sty I	(8)	250	461	1245	1411
		4438	4452	4505	4740			2238	2379	2902	3112
		4779	5144	5516	5697	Taq I	(14)	794	1038	1349	1360
		5894	6164					1705	2069	2211	2364
Msl I	(3)	2384	4820	4979				2409	2424	2472	3213
								3775	5219		

Tfi I	(7)	442	802	1437	1769
		3253	3510	3650	
Tsp45 I	(7)	1022	1231	2347	4824
		5035	5611	5922	
Tth111 I	(4)	390	811	1217	3042
Tth111 II	(9)	146	422	613	632
		2278	2797	4264	4273
		4303			
Vsp I	(4)	3318	3446	3505	4740
Xba I	(2)	218	2870		
Xho II	(8)	2337	2477	4316	4327
		4413	4425	5193	5210
Xma I	(2)	397	3049		
Xma III	(3)	724	1529	2464	
Xmn I	(3)	3281	3319	5167	

Site usage in pSEB-NBT:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Acc I	C`CG,C	70
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	9
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	34
Alw I	GGATC 8/9	16	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	2	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	3
Ase I	AT`TA,AT	4	Asp118	G`GTAC,C	2
Ava I	C`YCGR,G	7	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	7	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RGY`C	9
Bbe I	G,CGC`C	6	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	7	Bcn I	CC,S`GG	15
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	7	Blp I	GC`TNA,GC	7
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	34
BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
Bsp I	GTCCAG 22/20	2	BsIC I	TT`CG,AA	-
BsiE I	CG,R`CG	10	BsiHKA I	G,WGCW`C	7
BsiW I	C`GTAC,G	-	Bsm I	GATC,C 7	-
BsmA I	GTCCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	41
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	5
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	1
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	17	BstU I	CG CG	28
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	8
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	41
Cfr10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	8	Dde I	C`TNA,G	23
Dpn I	GA TC	27	DpnII	`GATC,	27
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	5

Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	6
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	41
Fok I	GGATG 14/18	15	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7
Hae II	R,GGCC`Y	12	Hae III	GG CC	32
Hga I	GAAGC 9/14	12	HgaI I	G,WCCW`C	7
HgiE II	ACCCNNNNNGGT -1/132	1	Hha I	G,CG`C	45
Hinc II	GTY RAC	1	Hind II	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	17
HinI I	GR`CG,YC	9	HinP I	G`CG,C	45
Hpa I	GTT AAC	-	Hpa II	C`CG,G	32
Hph I	GGTGA 12/11	13	Kas I	G`GGCC,C	6
Kpn I	G,GTAC`C	2	Mae I	G`TA,G	16
Mae II	A`CG,T	10	Mae III	`GTNAC,	20
Mbo I	`GATC,	27	Mbo II	GAAGA 12/11	15
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	53	Msc I	TGG CCA	3
Mse I	T`TA,A	26	Msl I	CAYANN`NNRTG	3
Msp I	C`CG,G	32	MspAl I	CMG CKG	12
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	15
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3
Nla III	,CATG`	20	Nla IV	GGN NCC	38
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	5
NspB II	CMG CRG	12	NspH I	R,CATG`Y	5
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-
Pal I	BG CC	32	Pf1M I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`WGC,CY	4
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Pvu II	CAG CTG	5	Rsa I	GT AC	8
Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	3
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	27
Sau96 I	G`GNC,C	28	Sca I	AGT ACT	1
ScrF I	CC`N,GG	32	Sec I	C`CNNG,G	34
SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	11
Sfi I	GCCN,NNN`NGGCC	-	Sma I	CCC GG	2
SnaB I	TRC GTA	-	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
Srf I	GGCC GGCC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	-	Sty I	C`MWG,G	8
Taq I	T`CG,A	14	Tfi I	G`AWT,C	7
Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	4
Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNNTGG-	-	Xho I	C`TCAG,G	-
Xho II	R`GATC,Y	8	Xma I	C`CCGG,G	2
Xma III	C`GGCC,G	3	Xmn I	GAANN NNITTC	3