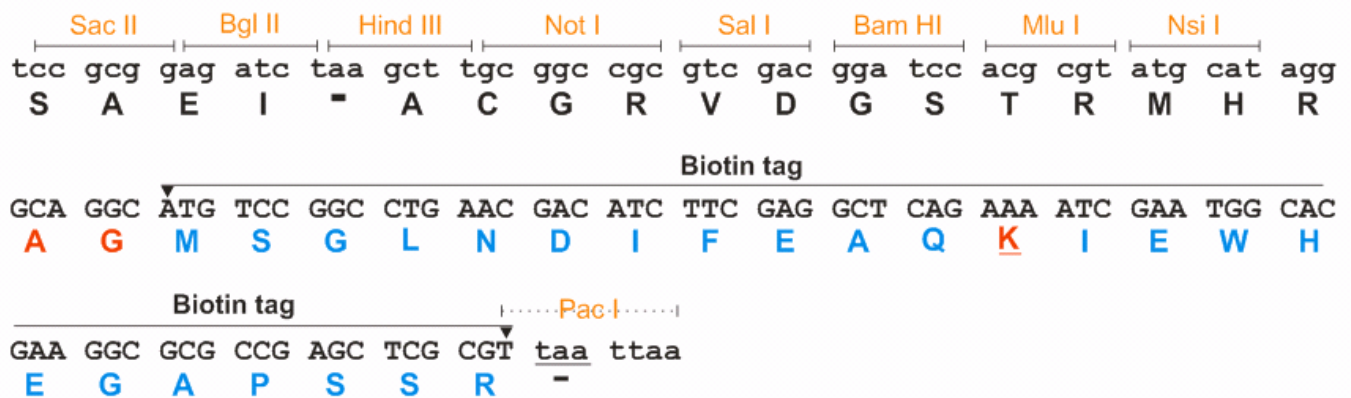
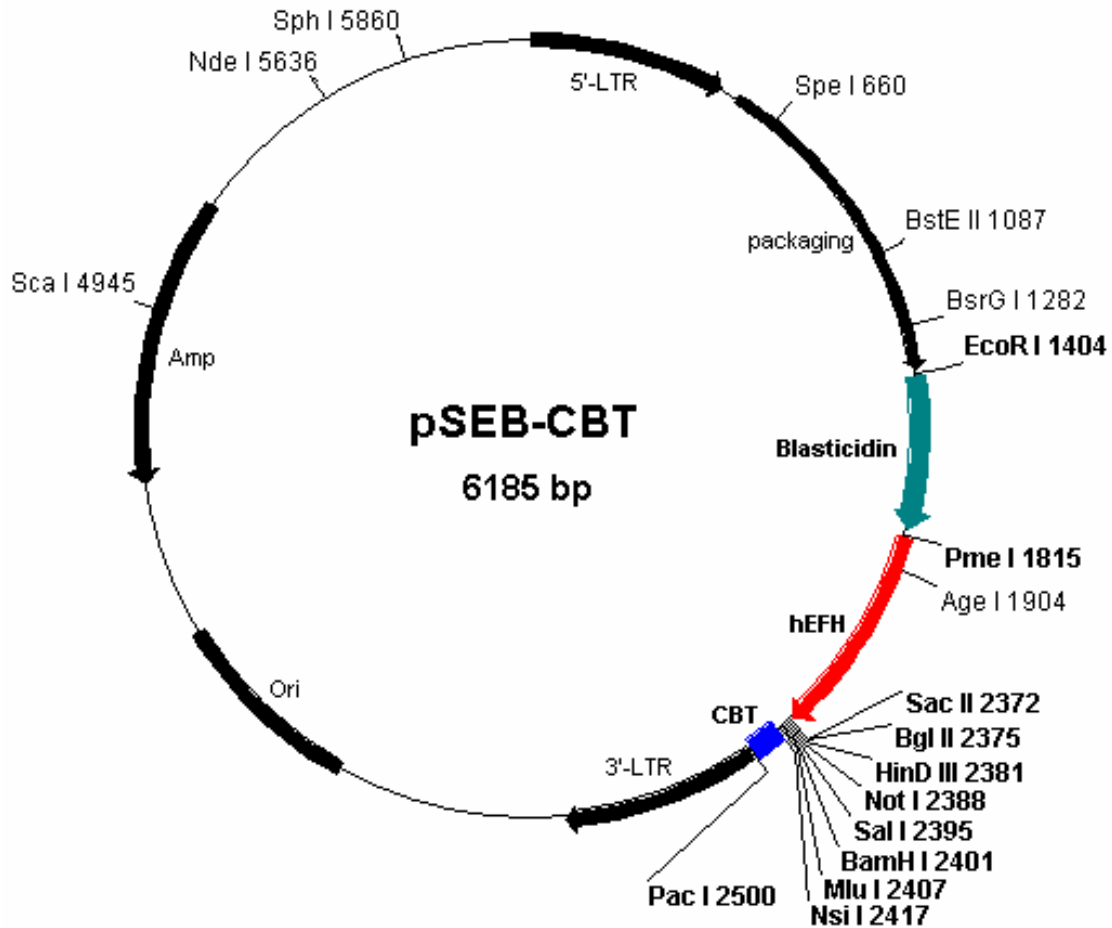


Vector: pSEB-CBT (C-terminal Biotin tag)

Antibiotic Selection: Amp

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

Date of Construction: April, 2008



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

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGAACAGAGACAGACAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCGGTCCTCCG
 CCTACAGCACTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCCCAAGGACCTGAAATGACCTTGCCCTATTGAACTAACCAACTCAGCTTCGCTTCTCGCTTCT
 GTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGGCCAGTCTCCGATAGACTGCGTCGCGGGTACCCGATATCCCAAT
 AAAGCCTCTG CTGTTTGCAT CGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG
 GTTCCACCAG GATTTGGAGACCCTGCCCA GGGACCACCGACCCCGCCG CCGGAGGTAA GCTGGCCAGC GGTGTTTCTGTGTCTGTCT TGTCTTTGTG
 CGTGTTTGTGCCGGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTTAGCTAAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGAGACGAGAACC AAAACGATCT CCGCTCCGT CTGAATTTTGTCTTCCGGT TGGAACCGAAGCCGCGCTG TTGTCTGTG CAGCGCTGA
 GCATCGTTCT GTGTTGTCT TGTCTACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTACCTTAGGTCATG
 GAAAGATGTGCGAGCGGATCG CTCACAACCA GTCGGTAGAT GTCAAGAAAGAGACCTTGGGT GACTTCTGC TCTGCAAAAT GGCAACCTTAAACGTCGGA
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 CCCCCTGAACCTCCTCGTTTCGACCCCGCTCGATCTCCTTTATCCAGCCCTCACTCCTTCTTAGGCGCCGGAATTCACCATG GCCAAGCCTTTGTCTCAAGA
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AGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGCGCCATCCACCGGGTTGAGTCCGCTTCTGCCGCTCCCGCTGTGGTCCCTCTGAAT
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g9gg c9g c9t c9a c9g atc cA CGC GT atgcat AGG GCAGGC ATG TCC GGC CTG AAC GAC ATC TTC GAG GCT
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 CCGTCAGGGCGCGTCAAGCG GTGTTGGCGG GTGTCGGGGC TGGCTTAACTATGCGGCATC AGAGCAGATT GTACTGAGAG TGCACCATATGCGGTGTGAA
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 TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGAA

Unique enzymes in pSEB-CBT:

Spe I	A`CTAG,T	660
BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
EcoR I	G`AATT,C	1404
Nco I	C`CATG,G	1411
Bbv II	GAAGC 7/11	1497
Bbs I	GAAGC 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,GC`GG	2372
Bgl II	A`GATC,T	2375
HinD III	A`AGCT,T	2381
Not I	GC`GGCC,GC	2388
Sal I	G`TCGA,C	2395
Acc I	GT`MK,AC	2396
HinC II	GTY RAC	2397
Hind II	GTY RAC	2397
BamH I	G`GATC,C	2401
Mlu I	A`CGCG,T	2407
Nsi I	A,TGCA`T	2417
Pac I	TTA,AT`TAA	2500

		5042						4757	4999	5500	5534
Drd I	(3)	1500	3680	5549				5886	6009	6018	6033
Dsa I	(4)	694	1411	2369	5890	Hph I	(13)	1157	1183	1401	4309
Eae I	(11)	582	724	1109	1130			4536	4950	5158	5191
		1414	1529	2388	3411			5475	5484	5977	6022
		4853	5887	6019				6103			
Eag I	(3)	724	1529	2388		Kas I	(6)	1397	2354	5687	5870
Ear I	(6)	1070	1311	3194	3456			5984	6005		
		5260	5748			Kpn I	(2)	405	2954		
Eco47 III	(3)	923	1826	5926		Mae I	(16)	31	219	661	673
Eco57 I	(5)	1509	2077	4119	5133			1394	1522	1912	2063
		6137						2189	2251	2578	2768
EcoN I	(4)	784	1392	1915	2110			4067	4320	4655	6090
EcoO109 I	(6)	254	1219	1572	2803	Mae II	(10)	742	1081	1122	2019
		5441	5895					2302	4275	4691	5064
								5384	5826		
EcoR I	(1)	1404				Mae III	(20)	39	994	1022	1087
EcoR II	(17)	239	546	733	746			1231	2331	2347	2586
		1167	1192	1215	1235			3064	3928	3991	4107
		1265	1715	2788	3310			4390	4721	4779	4932
		3598	3719	3732	5805			5120	5508	5799	5819
		6082				Mbo I	(28)	92	457	1044	1176
EcoR V	(3)	140	2688	6073				1361	1645	1706	1720
Ehe I	(6)	1399	2356	5689	5872			2337	2365	2375	2401
		5986	6007					2640	4138	4213	4224
Fnu4H I	(41)	727	901	917	920			4232	4310	4322	4427
		925	928	1133	1513			4768	4786	4832	5090
		1532	1606	1609	1612			5107	5143	5728	5952
		1615	1618	1782	1823			1086	1299	1445	1502
		2043	2102	2117	2148	Mbo II	(15)	1530	2440	3210	3444
		2388	2391	3397	3478			4233	4306	5061	5139
		3496	3499	3617	3772			5248	5736	5948	
		3915	3980	3983	4189			2407			
		4517	4856	4883	4978	Mlu I	(1)	829	1106	3011	3063
		5207	5494	5603	5707	Mme I	(6)	3786	3970		
		5780						167	216	368	387
Fok I	(12)	423	1140	1300	1464	Mnl I	(53)	432	460	484	506
		1699	2107	2971	4431			510	566	776	872
		4612	4899	5542	5786			1168	1271	1304	1310
Fsp I	(2)	4687	5710					1313	1319	1349	1352
Gdi II	(11)	723	725	1129	1528			1367	1374	1390	1454
		1530	2387	2389	3412			1795	1796	1880	1969
		4852	5888	6020				2064	2106	2160	2176
Gsu I	(3)	2516	4536	6154				2445	2765	2917	2936
Hae I	(6)	584	1111	1416	3587			2981	3008	3032	3092
		3598	4050					3421	3470	3680	3753
Hae II	(12)	925	1401	1828	2235			4004	4404	4485	4631
		2358	3450	3820	5691			4837	5432	5490	5750
		5874	5928	5988	6009			6034			
Hae III	(31)	129	173	584	726			584	1111	1416	
		762	774	987	1111	Msc I	(3)	36	1007	1119	1149
		1132	1197	1416	1531	Mse I	(26)	1173	1814	2199	2496
		2116	2221	2390	2435			2500	2583	3117	3215
		2677	2722	3413	3587			3343	3402	4278	4330
		3598	3616	4050	4508			4335	4349	4402	4637
		4588	4855	5442	5740			4676	5041	5413	5594
		5889	5897	6021				5791	6061		
Hga I	(12)	381	642	895	1491	Msl I	(2)	4717	4876		
		2168	2383	2930	3682	Msp I	(32)	163	398	569	630
		4260	4992	5550	6019			723	1401	1830	1905
HgiA I	(7)	338	2491	2887	3890			2129	2217	2229	2261
		5051	5136	5633				2352	2432	2712	2947
HgiE II	(2)	4151	5631					3290	3779	3926	3952
Hha I	(45)	319	321	370	372			4142	4546	4580	4647
		648	905	924	1400			4757	4999	5500	5534
		1512	1827	1854	1926			5886	6009	6018	6033
		2097	2234	2329	2357			588	1620	2056	2371
		2482	2484	2868	2870	MspAl I	(12)	3048	3396	3914	4159
		2919	2921	3196	3356			5100	5566	5760	6116
		3421	3449	3482	3752			1897			
		3819	3919	4093	4202	Mun I	(1)	631	2262	6019	
		4595	4688	5025	5357	Nae I	(3)	1398	2355	5688	5871
		5457	5560	5690	5711	Nar I	(6)	5985	6006		
		5844	5873	5927	5987			163	398	399	570
		6008				Nci I	(15)	723	2218	2712	2947
HinC II	(1)	2397						2948	3952	4648	4999
Hind II	(1)	2397						5500	5535	5886	
Hind III	(1)	2381						1411			
Hinf I	(17)	442	450	791	802	Nco I	(1)	5636			
		1437	1769	2135	2254	Nde I	(1)	629	2260	6017	
		3107	3129	3150	3407	Ngom I	(3)	30	2062	2577	
		3472	3547	3943	4460	Nhe I	(3)	62	1205	1415	1822
		6098				Nla III	(19)	2430	2609	3063	3230
HinI I	(9)	742	1398	2355	5002			3576	4296	4787	4797
		5384	5688	5871	5985			4875	4911	5304	5409
		6006						5493	5860	5933	
HinP I	(45)	317	319	368	370			188	201	246	403
		646	903	922	1398	Nla IV	(38)	521	552	692	761
		1510	1825	1852	1924			893	1144	1221	1399
		2095	2232	2327	2355			1573	1689	1834	1909
		2480	2482	2866	2868			1961	2165	2244	2356
		2917	2919	3194	3354			2403	2737	2750	2795
		3419	3447	3480	3750			2952	3318	3604	3643
		3817	3917	4091	4200			4415	4509	4550	4761
		4593	4686	5023	5355			5351	5689	5872	5896
		5455	5558	5688	5709			5986	6007		
		5842	5871	5925	5985			2388			
		6006				Not I	(1)	1644			
Hpa II	(32)	163	398	569	630	Nru I	(1)	2417			
		723	1401	1830	1905	Nsi I	(1)	1818	2426	3572	5489
		2129	2217	2229	2261	Nsp7524 I	(5)	5856			
		2352	2432	2712	2947			588	1620	2056	2371
		3290	3779	3926	3952	NspB II	(12)	3048	3396	3914	4159
		4142	4546	4580	4647						

		5100	5566	5760	6116	Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
NspH I	(5)	1822	2430	3576	5493	Age I	A`CCGG,T	1	Aha II	GR`CG,YC	9
		5860				Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	34
Pac I	(1)	2500				Alw I	GGATC 8/9	16	AlwN I	CAG,NNN`CTG	2
Pal I	(31)	129	173	584	726	Apa I	G,GGCC`C	-	Apal I	G`TGCA,C	3
		762	774	987	1111	Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	3
		1132	1197	1416	1531	Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
		2116	2221	2390	2435	Ava I	C`YCGR,G	7	Ava II	G`GWC,C	13
		2677	2722	3413	3587	Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
		3598	3616	4050	4508	Ban I	G`GYRC,C	17	Ban II	G,RCY`C	9
		4588	4855	5442	5740	Bbe I	G,CGCG`C	6	Bbs I	GAAGAC 8/12	1
		5889	5897	6021		Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Ple I	(4)	799	2143	3115	3951	Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	15
Pme I	(1)	1815				Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2
PpuM I	(4)	254	1219	1572	2803	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Psp1406 I	(3)	2019	4691	5064		Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
PspA I	(2)	397	2946			BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	1
Pst I	(3)	921	929	1105		BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	33
Pvu I	(3)	1648	4835	5731		BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
Pvu II	(5)	1620	2056	3396	5760	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
		6116				BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	7
Rsa I	(8)	403	659	1284	1955	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
		2952	4945	5621	6132	BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
Sac I	(3)	338	2491	2887		BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	41
Sac II	(1)	2372				Bspl20 I	G`GGCC,C	-	Bspl286 I	G,DCGH`C	-
Sal I	(1)	2395				BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
Sap I	(2)	3194	3456			BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
Sau3A I	(28)	92	457	1044	1176	BarB I	GAG CGG	4	BsrD I	GCAATG, 8	2
		1361	1645	1706	1720	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	5
		2337	2365	2375	2401	BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
		2640	4138	4213	4224	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
		4232	4310	4322	4427	BstN I	CC`W,GG	17	BstU I	CG CG	28
		4768	4786	4832	5090	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
		5107	5143	5728	5952	Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	40
Sau96 I	(27)	127	171	186	199	Cfr10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
		254	551	690	760	Csp6 I	G`TA,C	8	Dde I	C`TNA,G	24
		773	985	1196	1219	Dpn I	GA TC	28	DpnII	`GATC,	28
		1572	2219	2675	2720	Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
		2735	2748	2803	4507	Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
		4586	4603	4825	5441	Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
		5738	5895	6080		Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	3
Sca I	(1)	4945				Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
ScrF I	(32)	163	241	398	399	EcoN I	CCTNN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	6
		548	570	723	735	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
		748	1169	1194	1217	EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
		1237	1267	1717	2218	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	41
		2712	2790	2947	2948	Fok I	GGATG 14/18	12	Fse I	GG,CCGG`CC	-
		3312	3600	3721	3734	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
		3952	4648	4999	5500	Gau I	CTGGAG 21/19	3	Hae I	WGG CCW	6
		5535	5807	5886	6084	Hae II	R,CGCG`Y	12	Hae III	GG CC	31
Sec I	(33)	161	240	250	397	Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	7
		461	497	546	547	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	45
		694	733	734	746	HinC II	GTY RAC	1	Hind II	GTY RAC	1
		747	1167	1236	1245	HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	17
		1265	1266	1411	1716	HinI I	GR`CG,YC	9	HinP I	G`CG,C	45
		1974	2238	2369	2710	Hpa I	GTT AAC	-	Hpa II	C`CG,G	32
		2789	2799	2946	3009	Hph I	GGTGA 12/11	13	Kas I	G`GCGC,C	6
		3311	3732	5806	5884	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
		5890				Mae II	A`CG,T	10	Mae III	`GTNAC,	20
SfaN I	(21)	185	444	641	938	Mbo I	`GATC,	28	Mbo II	GAAGA 12/11	15
		1485	1542	1674	1720	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
		2088	2734	2992	3668	Mnl I	CCTC 10/10	53	Msc I	TGG CCA	3
		4720	4913	5160	5521	Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	2
		5613	5651	5689	6005	Msp I	C`CG,G	32	MspAl I	CMG CKG	12
		6017				Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Sfc I	(10)	15	917	925	1101	Nar I	GG`CG,CC	6	Nci I	CC`S,G	15
		1496	2562	3837	4028	Nco I	C`CATG,G	1	Nde I	CA`TA,TG	1
		4706	6124			NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3
Sma I	(2)	399	2948			Nla III	,CATG`	19	Nla IV	GGN NCC	38
Spe I	(1)	660				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Sph I	(1)	5860				Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	5
Ssp I	(2)	3115	5269			NspB II	CMG CKG	12	NspH I	R,CATG`Y	5
Sty I	(7)	250	461	1245	1411	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
		2238	2799	3009		Pal I	GG CC	31	PflM I	CCAN,NNN`NTGG	-
Taq I	(14)	794	1038	1349	1360	Ple I	GAGTC 9/10	4	Pme I	C TTT AAAC	1
		1705	2069	2211	2364	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
		2396	2450	2465	3110	Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
		3672	5116			Pst I	C,TGCCA`G	3	Pvu I	CG,AT`CG	3
Tfi I	(7)	442	802	1437	1769	Pvu II	CAG CTG	5	Rsa I	GT AC	8
		3150	3407	3547		Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	3
Tsp45 I	(7)	1022	1231	2347	4721	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
		4932	5508	5819		Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	28
Tth111 I	(4)	390	811	1217	2939	Sau96 I	G`GNC,C	27	Sca I	AGT ACT	1
Tth111 II	(9)	146	422	613	632	ScrF I	CC`N,GG	32	Sec I	C`CNNG,G	33
		2278	2694	4161	4170	SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	10
		4200				Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
Vsp I	(4)	3215	3343	3402	4637	SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Xba I	(2)	218	2767			Sph I	G,CATG`C	1	SpI I	C`GTAC,C	2
Xho II	(9)	2337	2375	2401	4213	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	-
		4224	4310	4322	5090	Stu I	AGG CCT	-	Sty I	C`CWG,G	7
		5107				Taq I	T`CG,A	14	Tfi I	G`AWT,C	7
Xma I	(2)	397	2946			Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Xma III	(3)	724	1529	2388		Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	4
Xmn I	(3)	3178	3216	5064		Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
						Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
						Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	2
						Xma III	C`GGCC,G	3	Xmn I	GAANN NNITC	3

Site usage in pSEB-CBT:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	68