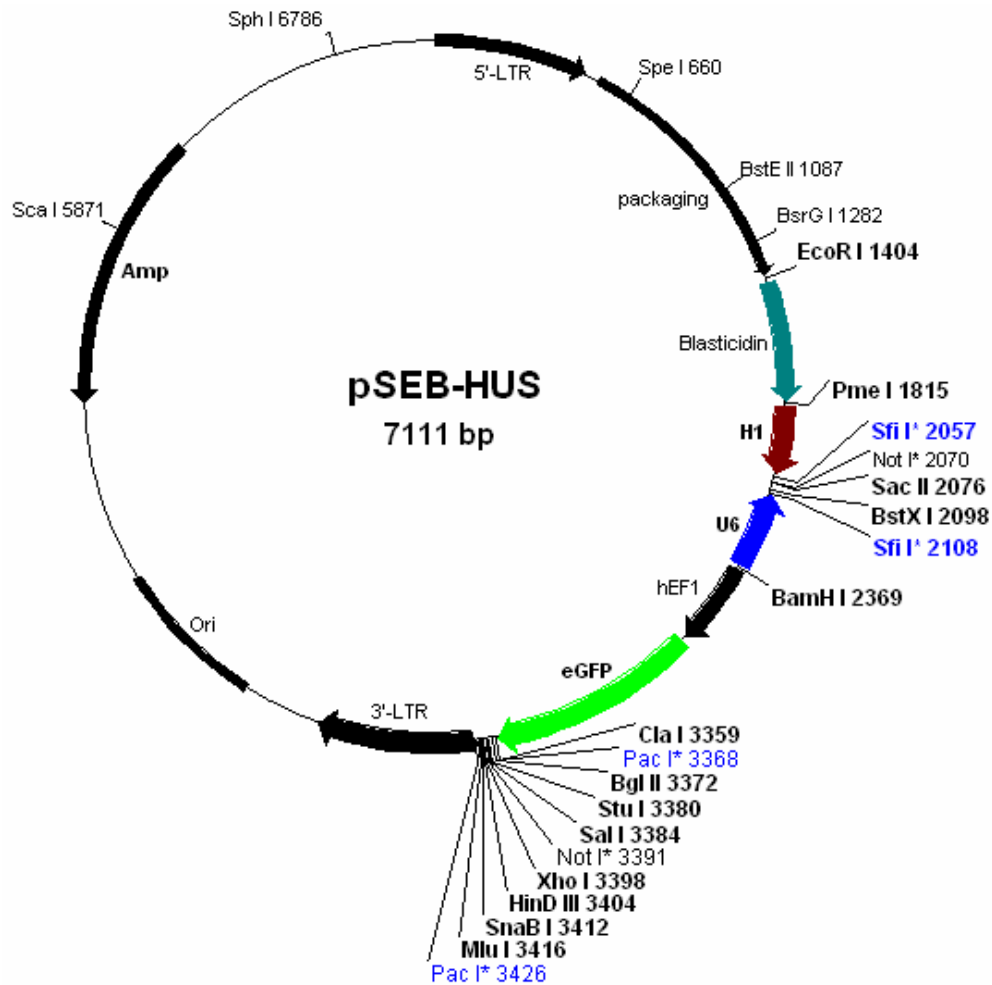


**Vector:** pSEB-HUS (a. k. a. **pSOS**)

**Antibiotic Selection:** Amp

**Creator(s):** Qing Luo & Hong Yin, Molecular Oncology Lab of The University of Chicago

**Date of Construction:** Jan, 2006



**Sfi I Site Stuffer and siRNA Cassette Design:**

```
                    EcoRV  Not I      M13Rev      BstX I
H1>>>  ggccaaaacGGCCgatatacGCGGCCGCggaaacagctatgaCCAtgacgcTGGCCgttttgcc
        ccggttttgCCGGctatagcgccggcgctttgtcgatactggtactgcgaccggcaaaaaccgg <<<U6
```

Sfi I Digestion

5' -GGCCAAAA	A(n19-27nt)TTTT	TGGCC-3'
3' -CCGGT	TTTT(n19-27nt)A	AAAACCGG-5'

## pSEB-HUS (aka, pSOS) Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG  
TTAGGAACAGAGACAGCAGAAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAGAACAGATGGTCCCAGATGCGGTCCC  
CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCCAGGACCTGAAATGACCTTGTGCCCTATTGAACTAACCAATCAGTTCGCTTCTCGCTTCT  
GTTCCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATTTCCCAAT  
AAAGCCTCTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG  
GTTCCACCAG GATTTGGAGACCCCTGCCCA GGGACCACCGACCCCCCGC CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGCTTTTGTG  
CGTGTTTGTGCCGGCATCTAATGTTTGCCTGCTGCTGCTACTAGTGTAGCTAAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGAAACACCCG  
GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT  
CTGGTAGGAGACGAGAACCCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTTCGGTT TGGAAACCGAAGCCGCGCTG TTGTCTGCTG CAGCGCTGA  
GCATCGTTCT GTTGTGTCTC TGCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTC CACTCCCTTAAGTTTACCTTAGTCTACTG  
GAAAGATGTCGAGCGGATCG CTCACAACCA GTCGGTAGAT GTCAAGAAAGAGACGTTGGGT TACCTTCTGC TCTGCAGAAAT GGCCAACCTTTAACGTCGGA  
TGGCCGCGAGACGGCACCT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACTGGCCGATGGACA CCCAGACCAGGTCCCCTACA  
TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT  
CCCCCTGAACTCCTCGTTTCGACCCCGCTCGATCCTCCTTTATCCAGCCCTCACTCCTTCTTAGGCGCCGGAATTCACCAATGCCAAAGCCTTTGTCTCAAGA  
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GCCGACGGCAGTTGGGATTCTGTAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTaa**gtttaaacagctt**aat t cgaacgctgacgt cat caaccg  
ctccaaggaatcgcgggccagtgctactaggcgggaacacccagcgcgctgcccctggcaggaagatggctgtgagggacag  
gggagtgggcgcctgcaatattgcatgtcgctatgtgttctgggaaatcaccataaacgtgaaatgtcttggatttgggaatc  
ttataagttctgtatgagaccacagatc**ggccaaaacggcc** gatatcGCGGCCG**gaaacagctatgaCCAtgacgcT**  
**ggcggtttggcc**tcctttccacaagatatataaagccaagaaatcgaataactttcaagttacggttaagcatatgatagtcct  
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cctgcccagcctt**ggatcc**gga tct gcgat**CGTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGTC**  
**CCGAGAAGTTGGGGGGAGGGGTCCGCAATTGAACCGGTGCTAGAGAAGGTGGCGGGGTAAACTGGGAAAGTGATGTCTGT**  
**ACTGGTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCCCGTGAACGTTCTTTTTCGCAACGGGT**  
**TGCCCGAGAACACAGTGTCTAGCGTACCGGTGCCACCatggtgagcaagggcgaggagctgttaccggggtggtgccc**  
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accctgaagttcatctgcaccaccggcaagctgcccgtgcccactcgtgaccacctgacctacggcctgagctgct  
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gagaagcgcgatcacatggtcctgctggagttcgtgaccgcccgggatcactctcgcatggacgagc**tgtaclaa**tcgat tt  
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GAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTCAAGGCATGAAAATAACATAACTGAGAATAGAGAAGTTTACAGTCAAGGTTA  
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GGCAGCGGT ATCAGCTCAC TCAAAGCGG TAATACGGTTATCCACAGAA TCAGGGGATAACCGAGGAAA GAACATGTGAGCAAAAGCC AGCAAAAAGC  
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CGGG AAGCCTGGCCTTTCTCATA GCTCACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTTCCAGCTGGGCTGTGTGCACGAACCCCGCTTACGCC  
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CGAGTATGT AGGCGGTGCT ACAGAGTCTTGAAGTGGTG GCCTAACTACGGCTACACTA GAAGGACAGT ATTTGGTATC TGCCTCTGCTGAAGCCAGT  
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 TCACCAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAA

**Unique enzymes in pSEB-HUS:**

Spe I	A`CTAG,T	660	Ban II	(8)	338	351	1677	1870
BstE II	G`GTNAC,C	1087	Bbe I	(6)	3813	3826	6863	6877
BsrG I	T`GTAC,A	1282			1401	1947	6617	6800
EcoR I	G`AATT,C	1404			6914	6935		
Bbv II	GAAGAC 7/11	1497	Bbs I	(1)	1498			
Bbs I	GAAGAC 8/12	1498	Bbv I	(12)	931	939	1524	1629
Nru I	TCG CGA	1644			2893	3177	3184	4917
Pme I	CTTT AAC	1815	Bbv II	(1)	1497			
BsiC I	TT`CG,AA	1828	Bcn I	(16)	164	399	400	571
BstB I	TT`CG,AA	1828			724	2672	3326	3639
Bsp120 I	G`GGCC,C	1866	Bfa I	(16)	31	219	661	673
Apa I	G,GGCC`C	1870			1394	1522	1879	2472
Sac II	CC,GC`GG	2076			2621	3376	3504	3694
BstX I	CCAN,NNNN`NTGG	2098			4993	5246	5581	7016
BamH I	G`GATC,C	2369	Bgl I	(4)	2057	2108	5511	6629
BspM II	T`CCGG,A	2372	Bgl II	(1)	3372			
Mun I	C`AATT,G	2457	Bpm I	(5)	3086	3326	3441	5461
Bsp1286 I	G,DGCH`C	3251			7079			
Cla I	AT`CG,AT	3359	Bsa I	(7)	476	530	1149	2031
Bgl II	A`GATC,T	3372			3929	3950	5452	
Stu I	AGG CCT	3380	BsaA I	(2)	2243	3412		
Sal I	G`TCGA,C	3384	BsaB I	(2)	1711	2374		
Acc I	GT`MK,AC	3385	BsaH I	(10)	742	1398	1838	1944
HinC II	GTY RAC	3386			5928	6310	6614	6797
Hind II	GTY RAC	3386			6911	6932		
Paer7 I	C`TCGA,G	3398	BsaJ I	(41)	161	240	250	397
Xho I	C`TCGA,G	3398			461	497	546	547
Hind III	A`AGCT,T	3404			694	733	734	746
SnaB I	TAC GTA	3412			747	1167	1236	1245
Mlu I	A`CGCG,T	3416			1265	1266	1411	1716
Sca I	AGT ACT	5871			1854	1907	2073	2365
Sph I	G,CATG`C	6786			2534	2640	2670	2810
Number of enzymes = 32					2973	2997	3052	3636
					3715	3725	3872	3935
					4237	4658	6732	6810
					6816			

**The following enzymes do not cut in pSEB-HUS:**

Avr II	Bcl I	Blp I	BsiW I	Bsm I	BsaW I	(7)	2372	2389	2464	2629
BspM I	Bst1107 I	Dra III	Eco72 I	Esp I	BseR I	(5)	4704	4851	5682	
Fse I	Hpa I	Nsi I	PflM I	Pml I	Bsg I	(5)	464	1293	1332	2672
Rsr II	Spl I	Srf I	Xca I	Xcm I			3938			
					BsiC I	(1)	1600	2582	2770	2867
					BsiE I	(14)	3191			
							1828			
					BsiHKA I	(7)	592	727	1532	1648
							2061	2073	2385	2634
							3394	4414	4838	5761
							5910	6657	3813	4816
					BsmA I	(22)	5977	6062	6559	
							107	475	531	609
							734	832	949	1073
					BsmB I	(7)	1132	1150	1328	1431
							2032	3458	3581	3928
					BsmF I	(12)	3949	5453	6227	6380
							6424	7096		
					BsoP I	(47)	733	831	1072	1131
							1329	6381	6423	
							172	185	564	729
							764	1205	1585	1944
							2413	3647	3660	6792
							727	901	917	920
							925	928	1133	1513
							1532	1606	1609	1612
							1615	1618	1782	2070
							2073	2603	2801	2860
							2882	3166	3173	3224
							3227	3321	3391	3394
							4323	4404	4422	4425
							4543	4698	4841	4906
							4909	5115	5443	5782
							5809	5904	6133	6420
							6529	6633	6706	
					Bsp120 I	(1)	1866			
					Bsp1286 I	(1)	3251			
					BspH I	(4)	5218	6226	6331	6855
					BspM II	(1)	2372			
					Bsr I	(20)	374	1030	1058	1546
							1570	1871	2499	2520
							3254	3849	4299	4905
							4918	5032	5438	5556
					BsrB I	(5)	5599	5866	6038	6744
							1042	1851	4190	4431
							6232			
					BsrD I	(2)	5452	5626		
					BsrG I	(1)	1282			
					BssH II	(5)	317	368	1896	3792
							3843			
					BssS I	(5)	1587	2822	4671	6055
							6362			
					BstB I	(1)	1828			
					BstE II	(1)	1087			
					BstN I	(23)	241	548	735	748
							1169	1194	1217	1237
							1267	1717	1909	2687
							2812	2924	2999	3053
							3716	4238	4526	4647
							4660	6733	7010	
					BstU I	(30)	317	319	370	903
							905	1135	1644	1864
							1898	1900	2069	2075
							2486	2970	3288	3390
							3418	3792	3794	3845
							4345	4347	4545	5126
							5456	5949	6281	6381
							6383	6486		
					BstX I	(1)	2098			
					BstY I	(10)	2369	2375	3141	3372
							5139	5150	5236	5248
							6016	6033		
					Bsu36 I	(2)	781	1018		
					Cac8 I	(40)	28	32	319	370

**pSEB-HUS: sites sorted by name:**

Aat II	(3)	745	1841	6313					
Acc I	(1)	3385							
Acc65 I	(2)	401	3876						
Aci I	(74)	197	203	566	588				
		688	727	860	901				
		1042	1133	1199	1298				
		1317	1355	1532	1614				
		1681	1849	1864	1883				
		2069	2073	2075	2486				
		2523	2603	2860	2901				
		2968	3007	3145	3258				
		3318	3321	3390	3394				
		3672	3678	3974	4188				
		4291	4347	4357	4381				
		4424	4431	4452	4543				
		4571	4698	4717	4838				
		4948	5083	5092	5454				
		5545	5736	5782	5903				
		5947	6024	6133	6232				
		6279	6453	6492	6502				
		6528	6566	6579	6605				
		6662	6921						
Afl II	(3)	35	1006	3508					
Afl III	(2)	3416	4498						
Age I	(2)	2464	2629						
Aha II	(10)	742	1398	1838	1944				
		5928	6310	6614	6797				
		6911	6932						
Ahd I	(4)	1020	3921	3967	5391				
Alu I	(39)	30	34	336	580				
		668	676	1515	1620				
		1821	2084	2616	2662				
		2695	2767	2800	3016				
		3064	3175	3349	3406				
		3503	3507	3811	4130				
		4163	4258	4322	4440				
		4666	4756	4802	5059				
		5580	5680	5743	6422			</	

		582	586	631	650	HinC II	(1)	3386				
		1199	1508	1622	1866	HinD II	(1)	3386				
		1898	1902	2100	2765	HinD III	(1)	3404				
		2798	2846	3170	3177	Hinf I	(18)	442	450	791	802	
		3501	3505	3794	3845			1437	1769		1859	2017
		4291	4320	4429	4515			2332	4033		4055	4076
		4552	5112	5503	6516			4333	4398		4473	4869
		6664	6684	6688	6784			5386	7024			
		6825	6873	6915	6945	HinI I	(10)	742	1398		1838	1944
Cfr10 I	(7)	629	2464	2629	2792			5928	6310		6614	6797
		5471	6934	6943				6911	6932			
		3359						317	319		368	370
Cla I	(11)	402	658	1283	2251	HinP I	(46)	646	903		922	1398
Csp6 I	(11)	2514	3070	3352	3877			1510	1896		1898	1904
		5870	6546	7057				1944	2412		2484	2624
Dde I	(21)	75	167	208	476			2929	2970		3286	3792
		781	1018	1290	1808			3794	3843		3845	4120
		3245	3263	3548	3642			4280	4345		4373	4406
		3683	3952	4023	4773			4676	4743		4843	5017
		5182	5348	5888	6314			5126	5519		5612	5949
		6549						6281	6381		6484	6614
Dpn I	(32)	94	459	1046	1178			6635	6768		6797	6851
		1363	1647	1708	1722			6911	6932			
		2047	2371	2377	2384	Hpa II	(32)	163	398		569	630
		3143	3291	3329	3374			723	1401		2373	2390
		3568	5066	5141	5152			2465	2630		2670	2733
		5160	5238	5250	5355			2793	3324		3638	3873
		5696	5714	5760	6018			4216	4705		4852	4878
		6035	6071	6656	6880			5068	5472		5506	5573
		92	457	1044	1176			5683	5925		6426	6460
DpnII	(32)	1361	1645	1706	1720			6812	6935		6944	6959
		2045	2369	2375	2382			1157	1183		1401	1978
		3141	3289	3327	3372	Hph I	(19)	2655	2660		2988	3012
		3566	5064	5139	5150			3141	5235		5462	5876
		5158	5236	5248	5353			6084	6117		6401	6410
		5694	5712	5758	6016			6903	6948		7029	
		6033	6069	6654	6878	Kas I	(6)	1397	1943		6613	6796
		1815	2188	2201	5257			6910	6931			
Dra I	(6)	5276	5968			Kpn I	(2)	405	3880			
Drd I	(3)	1500	4606	6475		Mae I	(16)	31	219		661	673
Dsa I	(5)	694	1411	2073	2640			1394	1522		1879	2472
		6816						2621	3376		3504	3694
Eae I	(17)	582	724	1109	1130			4993	5246		5581	7016
		1414	1529	2049	2058			742	1081		1122	1838
		2070	2100	2713	3102	Mae II	(17)	1994	2237		2242	2579
		3391	4337	5779	6813			2706	2919		3090	3411
		6945						5201	5617		5990	6310
Eag I	(5)	724	1529	2058	2070			6752				
		3391				Mae III	(24)	39	994		1022	1087
Ear I	(7)	1070	1311	2357	4120			1231	1874		2159	2238
		4382	6186	6674				2824	3313		3412	3512
Eco47 III	(3)	923	2625	6852				3990	4854		4917	5033
Eco57 I	(7)	1509	2794	2840	3037			5316	5647		5705	5858
		5045	6059	7063				6046	6434		6725	6745
EcoN I	(3)	784	1392	2475				92	457		1044	1176
EcoO109 I	(7)	254	1219	1572	2347	Mbo I	(32)	1361	1645		1706	1720
		3729	6367	6821				2045	2369		2375	2382
EcoR I	(1)	1404						3141	3289		3327	3372
EcoR II	(23)	239	546	733	746			3566	5064		5139	5150
		1167	1192	1215	1235			5158	5236		5248	5353
		1265	1715	1907	2685			5694	5712		5758	6016
		2810	2922	2997	3051			6033	6069		6654	6878
		3714	4236	4524	4645	Mbo II	(20)	1086	1299		1445	1502
		4658	6731	7008				1530	1927		2345	2885
EcoR V	(4)	140	2065	3614	6999			2930	2933		3126	4136
Ehe I	(6)	1399	1945	6615	6798			4370	5159		5232	5987
		6912	6933					6065	6174		6662	6874
Fnu4H I	(47)	727	901	917	920	Mlu I	(1)	3416				
		925	928	1133	1513	Mme I	(6)	829	1106		3937	3989
		1532	1606	1609	1612			4712	4896			
		1615	1618	1782	2070	Mnl I	(60)	167	216		368	387
		2073	2603	2801	2860			432	460		484	506
		2882	3166	3173	3224			510	566		776	872
		3227	3321	3391	3394			1168	1271		1304	1310
		4323	4404	4422	4425			1313	1319		1349	1352
		4543	4698	4841	4906			1367	1374		1390	1454
		4909	5115	5443	5782			1795	1796		1921	2121
		5809	5904	6133	6420			2359	2440		2529	2650
		6529	6633	6706				2731	2737		2830	2968
Fok I	(13)	423	1140	1300	1464			2980	3031		3151	3406
		1699	2669	3035	3897			3691	3843		3862	3907
		5357	5538	5825	6468			3934	3958		4018	4347
		6712						4396	4606		4679	4930
Fsp I	(2)	5613	6636					5330	5411		5557	5763
Gdi II	(19)	723	725	1129	1528			6358	6416		6676	6960
		1530	2050	2057	2059	Msc I	(3)	584	1111		1416	
		2069	2071	2099	2714	Mse I	(31)	36	1007		1119	1149
		3101	3390	3392	4338			1173	1814		1823	2187
		5778	6814	6946				2200	2280		3364	3368
Gsu I	(5)	3085	3325	3442	5462			3422	3426		3509	4043
		7080						4141	4269		4328	5204
Hae I	(8)	584	1111	1416	2111			5256	5261		5275	5328
		3380	4513	4524	4976			5563	5602		5967	6339
Hae II	(11)	925	1401	1947	2627			6520	6717		6987	
		4376	4746	6617	6800	Msl I	(4)	1993	3128		5643	5802
		6854	6914	6935		Msp I	(32)	163	398		569	630
Hae III	(40)	129	173	584	726			723	1401		2373	2390
		762	774	987	1111			2465	2630		2670	2733
		1132	1197	1416	1531			2793	3324		3638	3873
		1868	2051	2060	2072			4216	4705		4852	4878
		2102	2111	2348	2715			5068	5472		5506	5573
		2815	3104	3216	3380			5683	5925		6426	6460
		3393	3603	3648	4339			6812	6935		6944	6959
		4513	4524	4542	4976			588	1620		2075	2616
		5434	5514	5781	6368	MspAl I	(12)	3974	4322		4840	5085
		6666	6815	6823	6947			6026	6492		6686	7042
		381	642	895	1491	Mun I	(1)	2457				
Hga I	(12)	2103	3395	3856	4608	Nae I	(2)	631	6945			
		5186	5918	6476	6945	Nar I	(6)	1398	1944		6614	6797
HgiA I	(7)	338	3251	3813	4816			6911	6932			
		5977	6062	6559		Nci I	(16)	163	398		399	570
HgiE II	(2)	5077	6557					723	2671		3325	3638
Hha I	(46)	319	321	370	372			3873	3874		4878	5574
		648	905	924	1400			5925	6426		6461	6812
		1512	1898	1900	1906	Nco I	(2)	1411	2640			
		1946	2414	2486	2626	Nde I	(2)	2172	6562			
		2931	2972	3288	3794	NgoM I	(2)	629	6943			
		3796	3845	3847	4122	Nhe I	(2)	30	3503			
		4282	4347	4375	4408	Nla III	(26)	62	1205		1415	1964
		4678	4745	4845	5019			2095	2339		2644	2878
		5128	5521	5614	5951			2908	3103		3298	3343
		6283	6383	6486	6616			3535	3989		4156	4502
		6637	6770	6799	6853			5222	5713		5723	5801
		6913	6934					5837	6230		6335	6419

Nla IV	(39)	6786	6859		
		188	201	246	403
		521	552	692	761
		893	1144	1221	1399
		1573	1689	1868	1945
		2371	2394	2469	2521
		2679	3217	3663	3676
		3721	3878	4244	4530
		4569	5341	5435	5476
		5687	6277	6615	6798
		6822	6912	6933	
		2070	3391		
Not I	(2)				
Nru I	(1)				
Nsp7524 I	(4)	1960	4498	6415	6782
NspB II	(12)	588	1620	2075	2616
		3974	4322	4840	5085
		6026	6492	6686	7042
NspH I	(4)	1964	4502	6419	6786
Pac I	(2)	3368	3426		
PaeR7 I	(1)	3398			
Pal I	(40)	129	173	584	726
		762	774	987	1111
		1132	1197	1416	1531
		1868	2051	2060	2072
		2102	2111	2348	2715
		2815	3104	3216	3380
		3393	3603	3648	4339
		4513	4524	4542	4976
		5434	5514	5781	6368
		6666	6815	6823	6947
Ple I	(3)	799	4041	4877	
Pme I	(1)	1815			
PpuM I	(4)	254	1219	1572	3729
Psp1406 I	(3)	2579	5617	5990	
PspA I	(2)	397	3872		
Pst I	(3)	921	929	1105	
Pvu I	(4)	1648	2385	5761	6657
Pvu II	(5)	1620	2616	4322	6686
		7042			
Rsa I	(11)	403	659	1284	2252
		2515	3071	3353	3878
		5871	6547	7058	
Sac I	(2)	338	3813		
Sac II	(1)	2076			
Sal I	(1)	3384			
Sap I	(2)	4120			
Sau3A I	(32)	1361	1645	1706	1720
		2045	2369	2375	2382
		3141	3289	3327	3372
		3566	5064	5139	5150
		5158	5236	5248	5353
		5694	5712	5758	6016
		6033	6069	6654	6878
Sau96 I	(32)	127	171	186	199
		254	551	690	760
		773	985	1196	1219
		1572	1866	1867	2347
		2814	3215	3298	3601
		3646	3661	3674	3729
		5433	5512	5529	5751
		6367	6664	6821	7006
Sca I	(1)	5871			
ScrF I	(39)	163	241	398	399
		548	570	723	735
		748	1169	1194	1217
		1237	1267	1717	1909
		2671	2687	2812	2924
		2999	3053	3325	3638
		3716	3873	3874	4238
		4526	4647	4660	4878
		5574	5925	6426	6461
		6733	6812	7010	
Sec I	(41)	161	240	250	397
		461	497	546	547
		694	733	734	746
		747	1167	1236	1245
		1265	1266	1411	1716
		1854	1907	2073	2365
		2534	2640	2670	2810
		2973	2997	3052	3636
		3715	3725	3872	3935
		4237	4658	6732	6810
		6816			
SfaN I	(24)	185	444	641	938
		1485	1542	1674	1720
		2741	3017	3032	3131
		3660	3918	4594	5646
		5839	6086	6447	6539
		6577	6615	6931	6943
Sfc I	(10)	15	917	925	1101
		1496	3488	4763	4954
		5632	7050		
Sfi I	(2)	2057	2108		
Sma I	(2)	399	3874		
SnaB I	(1)	3412			
Spe I	(1)	660			
Sph I	(1)	6786			
Ssp I	(3)	1955	4041	6195	
Stu I	(1)	3380			
Sty I	(9)	250	461	1245	1411
		1854	2365	2640	3725
		3935			
Taq I	(18)	794	1038	1349	1360
		1705	1828	2145	2691
		2985	3012	3027	3156
		3359	3385	3399	4036
		4598	6042		
Tfi I	(10)	442	802	1437	1769
		1859	2017	2332	4076
		4333	4473		
Tsp45 I	(10)	1022	1231	1874	2238
		2824	3313	5647	5858
		6434	6745		
Tth111 I	(4)	390	811	1217	3865
Tth111 II	(9)	146	422	613	632
		3124	3620	5087	5096
		5126			
Vsp I	(5)	2280	4141	4269	4328
		5563			
Xba I	(2)	218	3693		
Xho I	(1)	3398			
Xho II	(10)	2369	2375	3141	3372
		5139	5150	5236	5248

Xma I	(2)	6016	6033		
Xma III	(5)	397	3872		
		724	1529	2058	2070
		3391			
Xmn I	(3)	4104	4142	5990	

## Site usage in pSEB-HUS:

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	74
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	2	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	39
Alw I	GGATC 8/9	17	AlwN I	CAG,NNN`CTG	2
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	5	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	-	BamH I	G`GTAC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	8
Bbe I	G,CGCC`C	6	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	12	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	16
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	4
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	2	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	10	BsaJ I	C`CNGG,G	41
BsaW I	W`CCGG,W	7	BseR I	GAGGAG 16/14	5
Bsg I	GTGCAG 22/20	5	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	14	BsiHKA I	G,WGCW`C	7
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	47
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	20
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	5
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	23	BstU I	CG CG	30
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	10
Bsu36 I	CC`TNA,GA	2	Cac8 I	GCN NGC	40
Cfr10 I	R`CCGG,Y	7	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	11	Dde I	C`TNA,G	31
Dpn I	GA TC	32	DpnII	`GATC,	22
Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	5
Eae I	Y`GGCC,R	17	Eag I	G`GGCC,C	5
Ear I	CTCTTC 7/10	7	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	7	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	3	Eco109 I	RG`GNC,CY	7
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	23
EcoR V	GAT ATC	4	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	47
Fok I	GGATG 14/18	13	Fse I	GG,CCGG`CC	-
Psp I	TGC GCA	2	Gdi II	`YGGC,CG	19
Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	8
Hae II	R,CGCC`Y	11	Hae III	GG CC	40
Hga I	GACGG 9/14	12	HgaI I	G,WGCW`C	7
HglE II	ACCCNNNNNGGT -1/132	1	Hha I	G,CG`C	46
Hinc II	GTY RAC	1	Hind I	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	18
HinI I	GR`CG,YC	10	HinP I	G`CG,C	46
Hpa I	GTT AAC	-	Hpa II	C`CG,G	32
Hph I	GGTGA 12/11	19	Kas I	G`GGCC,C	6
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Mae II	A`CG,T	17	Mae III	`GTNAC,	24
Mbo I	`GATC,	32	Mbo II	GAAGA 12/11	20
Mlu I	A`CGCG,T	1	Mne I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	60	Msc I	TGG CCA	3
Mse I	T`TA,A	31	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	32	MspAl I	CMG CKG	12
Mun I	C`AATT,G	1	Nae I	GCC GGC	2
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	16
Nco I	C`CATG,C	2	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
Nla III	,CATG`	26	Nla IV	GGN NCC	39
Not I	GC`GGCC,GC	2	Nru I	TCG CGA	1
Nsi I	A,TCGA`T	-	Nsp7524 I	R`CATG,Y	4
NspB II	CMG CKG	12	NspH I	R,`CATG,Y	4
Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	1
Pal I	GG CC	40	Pf1M I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	4
Pvu II	CAG CTG	5	Rsa I	GT AC	11
Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	32
Sau96 I	G`GNC,C	32	Sca I	AGT ACT	1
ScrF I	CC`N,GG	39	Sec I	C`CNGG,G	41
SfaN I	GCATC 9/13	24	Sfc I	C`TRYA,G	10
Sfi I	GGCCN,NNN`NGGCC	2	Sma I	CCC GGG	2
SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	1	Sp1 I	C`GTAC,G	-
Srf I	GGCC GGGC	-	Ssp I	AAT ATT	3
Stu I	AGG CCT	1	Sty I	C`CWGG,G	9
Taq I	T`CG,A	18	Tfi I	G`ANT,C	10
Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	4
Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	5
Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNNTGG-	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	10	Xma I	C`CCGG,G	2
Xma III	C`GGCC,G	5	Xmn I	GAANN NNFTC	3