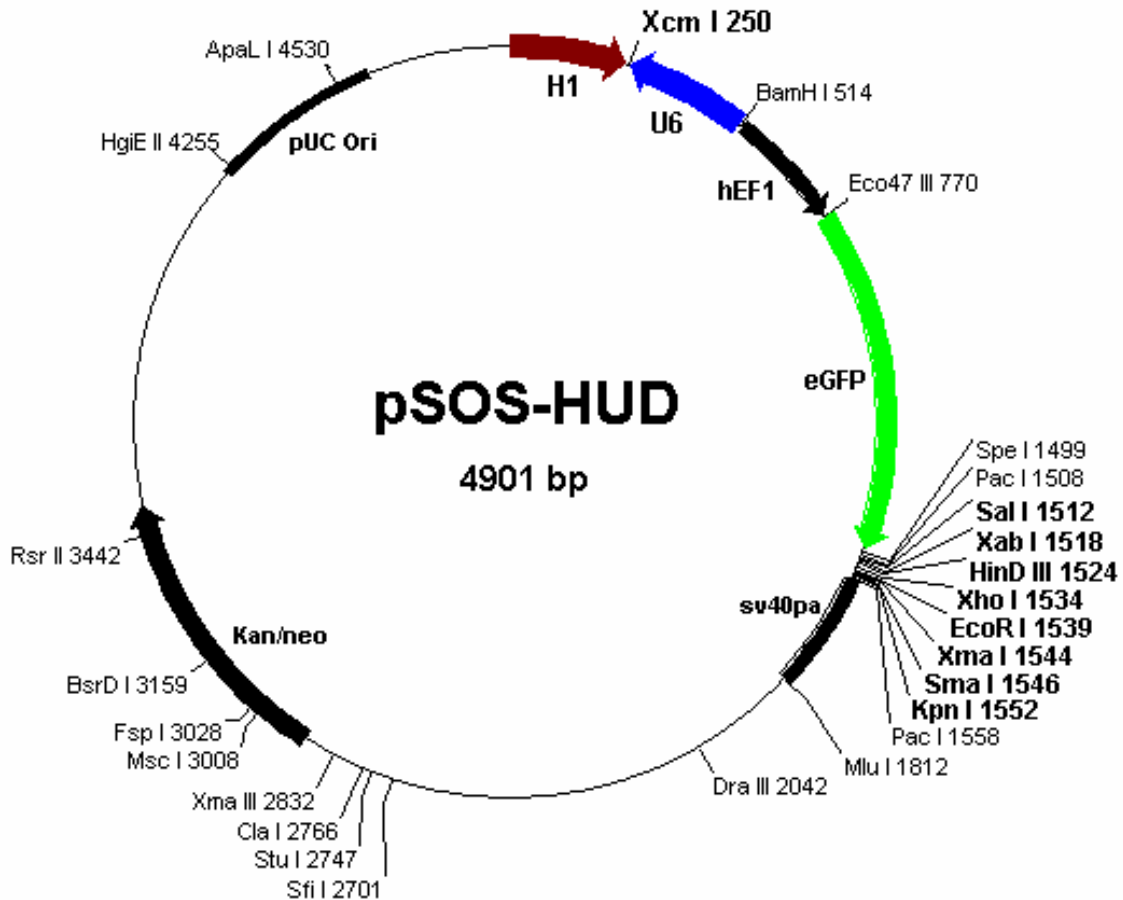


**Vector:** pSOS-HUD

**Antibiotic Selection:** Kan

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

**Date of Construction:** September and December, 2005



### Xcm I Site and siRNA Cassette Design:

**H1 promoter >>>** tct **cca**aaaaat tttt **tgg**gtc **<<< U6 promoter**  
3'-aga **ggt**tttttaaaa **acc**cag-5'

Xcm I Digestion

**H1 promoter >>>** tct **cca**aaaaa **NNN---NNNA** tttt **tgg**gtc **<<< U6 promoter**  
3'-aga **ggt**tttt **TNNN---NNN** taaaa **acc**cag-5'

**pSOS-HUD Sequence (Xcm I site, hEF $\alpha$ 1 promoter)**  
(by Qing Luo, 9/15/05)

TAGTTATTACagcttaattcgaacgctgacgtcatcaaccgctccaaggaatcgcgggccagtgctactagggcgggaaca  
cccagcgcgctgcccctggcaggaagatggctgtgagggacaggggagtgggcgcctgcaatatttgcagtgctgctatgt  
gttctgggaaatcaccataaacgtgaaatgtctttggatttgggaatcttataagttctgtatgagaccacagatctccaaa  
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AACGCCAGCAACGCGGCCCTTTTTACGGTTCCTGGCCCTTTTGCTGGCCCTTTTGCTCACATGTTCTTTTCCTGCGTTATCCCCTG  
 ATTCTGTGGATAACCGTATTACCGCCATGCAT

H1 promoter >>> tct ccaaaaaatttttggggtc <<< U6 promoter  
 3'-aga ggttttttaaaaacc cag-5'

Xcm I Digestion

H1 promoter >>> tct ccaaaaaa NNN---NNNA tttt tgg gtc <<< U6 promoter  
 3'-aga ggtttttt TNNN---NNN taaaa acc cag-5'

Unique enzymes in pSOS-HUD:

Aat II	G,ACGT`C	33
Bsp120 I	G`GGCC,C	58
Apa I	G,GGCC`C	62
BssH II	G`CGCG,C	88
Xcm I	CCANNNN,N`NNNNTGG250	
PpuM I	RG`GWC,CY	257
Nde I	CA`TA,TG	317
Ase I	AT`TA,AT	425
Vsp I	AT`TA,AT	425
BamH I	G`GATC,C	514
BspM II	T`CCGG,A	517
Pvu I	CG,AT`CG	530
EcoN I	CCTNN`N,NNAGG	620
Psp1406 I	AA`CG,TT	724
Eco47 III	AGC GCT	770
Spe I	A`CTAG,T	1499
Sal I	G`TCGA,C	1512
Acc I	GT`MK,AC	1513
HinD III	A`AGCT,T	1524
Paer7 I	C`TCGA,G	1534
Xho I	C`TCGA,G	1534
EcoR I	G`AATT,C	1539
PspA I	C`CCGG,G	1544
Xma I	C`CCGG,G	1544
Sma I	CCC GGG	1546
Acc65 I	G`GTAC,C	1548
Asp718	G`GTAC,C	1548
Kpn I	G,GTAC`C	1552
Bcl I	T`GATC,A	1583
Hpa I	GTT AAC	1689
Mlu I	A`CGCG,T	1812
Dra III	CAC,NNN`GTG	2042
Sfi I	GGCCN,NNN`NGGCC	2701
Bgl I	GCCN,NNN`NGGC	2701
Stu I	AGG CCT	2747
Cla I	AT`CG,AT	2766
Eag I	C`GGCC,G	2832
Xma III	C`GGCC,G	2832
Msc I	TGG CCA	3008
Fsp I	TGC GCA	3028
Tth111 I	GACN`N,NGTC	3044
BsrD I	GCAATG, 8	3159
Rsr II	CG`GWC,CG	3442
HgiE II	ACCNNNNNGGTT -1/134255	
ApaL I	G`TGCA,C	4530
Number of enzymes = 45		

The following enzymes do not cut in pSOS-HUD:

Afl II	Ahd I	Asc I	Bbs I	Bbv II
Blp I	BsiW I	BsmB I	BsrG I	Bst1107 I

BstE II	BstX I	Eco72 I	EcoR V	Esp I
Fse I	Nhe I	Not I	Nru I	PflM I
Pme I	Pml I	Pst I	Sac I	Sac II
Sca I	SnaB I	Spl I	Srf I	Xca I

pSOS-HUD: sites sorted by name:

Aat II	(1)	33			
Acc I	(1)	1513			
Acc65 I	(1)	1548			
Aci I	(58)	41	56	75	631
		668	748	1005	1046
		1113	1152	1290	1403
		1463	1466	2186	2213
		2241	2244	2258	2301
		2348	2411	2596	2608
		2617	2629	2639	2650
		2696	2835	2898	2992
		3056	3157	3160	3400
		3440	3445	3495	3511
		3537	3593	3662	3665
		3731	3813	3878	3945
		4018	4252	4261	4396
		4506	4627	4646	4773
		4801	4892		
Afl III	(2)	1812	4844		
Age I	(2)	609	774		
Aha II	(5)	30	136	2926	3628
		3707			
Alu I	(22)	13	761	807	840
		912	945	1161	1209
		1320	1494	1526	1705
		1872	2129	2424	2712
		3032	3490	4287	4544
		4590	4680		
Alw I	(18)	510	521	527	1282
		1479	1557	1577	2793
		3104	3171	3350	3715
		3742	4101	4102	4199
		4199	4285		
		4027	4435		
AlwN I	(2)	4027	4435		
Apa I	(1)	62			
ApaL I	(1)	4530			
Apo I	(5)	248	1539	1740	1844
		1855			
Ase I	(1)	425			
Asp718	(1)	1548			
Ava I	(4)	576	678	1534	1544
Ava II	(4)	257	1443	3442	3887
Avr II	(2)	2748	3763		
BamH I	(1)	514			
Ban I	(8)	135	537	612	822
		1548	2079	2925	2960
Ban II	(4)	62	2117	3291	4001
Bbe I	(2)	139	2929		
Bbv I	(9)	1038	1322	1329	1714
		2999	3041	3562	4015
		4515			
Bcl I	(1)	1583			
Bcn I	(8)	817	1471	1546	1547
		2931	3091	3704	4468
Bfa I	(12)	71	617	766	1500
		1519	1574	1775	2193
		2749	3764	4098	4351
Bgl I	(1)	2701			
Bgl II	(2)	237	1530		
Bpm I	(4)	1231	1471	3709	3766
Bsa I	(2)	223	3915		
BsaA I	(3)	388	2042	3230	

BsaB I	(3)	519	1588	2785		Eco57 I	(6)	939	985	1182	3071
BsaH I	(5)	30	136	2926	3628			3503	4303		
BsaJ I	(25)	3707				EcoN I	(1)	620			
		46	99	510	679	EcoO109 I	(3)	257	492	4024	
		785	815	955	1118	EcoR I	(1)	1539			
		1142	1197	1544	2460	EcoR II	(15)	99	830	955	1067
		2532	2655	2690	2699			1142	1196	2460	2515
		2748	3089	3358	3763			2532	3311	3890	3993
		3890	3891	3993	3994			4683	4696	4817	
		4684				Ehe I	(2)	137	2927		
BsaW I	(9)	517	534	609	774	Fnu4H I	(37)	748	946	1005	1027
		1567	2957	3801	4491			1311	1318	1369	1372
		4638						1466	1703	2222	2244
BseR I	(2)	817	2744					2258	2696	2835	2887
Bsg I	(4)	727	915	1012	1336			2898	2988	2993	3030
BsiC I	(2)	20	3608					3071	3158	3161	3164
BsiE I	(4)	530	779	2835	4510			3400	3496	3537	3551
BsiHKA I	(4)	1396	3039	3229	4534			3665	4004	4019	4230
Bsm I	(2)	1677	1770					4436	4439	4504	4647
BsmA I	(5)	224	2351	2769	3788			4802			
		3916				Fok I	(7)	814	1180	2599	2793
BsmF I	(9)	136	558	2442	2514			3250	3275	3729	
		2578	3077	3609	3718	Fsp I	(1)	3028			
		3873				Gdi II	(6)	859	1246	2831	2833
BsoF I	(37)	748	946	1005	1027			3396	3423		
		1311	1318	1369	1372	Gsu I	(4)	1230	1470	3710	3765
		1466	1703	2222	2244	Hae I	(5)	2747	3008	4370	4822
		2258	2696	2835	2887			4833			
		2898	2988	2993	3030	Hae II	(6)	139	772	2193	2201
		3071	3158	3161	3164			2929	4604		
		3400	3496	3537	3551	Hae III	(23)	60	493	860	960
		3665	4004	4019	4230			1249	1361	1892	2034
		4436	4439	4504	4647			2689	2695	2704	2747
		4802						2834	3008	3399	3426
Bsp120 I	(1)	58						3935	3992	4025	4370
Bsp1286 I	(2)	1396	3229					4804	4822	4833	
BspH I	(2)	2352	4124			Hga I	(5)	2260	3635	3714	4155
BspM I	(3)	2813	3194	3644				4733			
BspM II	(1)	517				HgiA I	(4)	1396	3039	3229	4534
Bsr I	(11)	63	644	665	1399	HgiE II	(1)	4255			
		1956	2634	2869	3070	Hha I	(30)	90	92	98	138
		4316	4430	4443				559	631	771	1076
BsrB I	(5)	43	2186	2350	3539			1117	1433	2192	2200
		3593						2226	2248	2257	2270
BsrD I	(1)	3159						2301	2920	2928	2992
BssH II	(1)	88						3029	3295	3555	3731
BssS I	(4)	967	3518	3644	4671			3817	4220	4329	4503
BstB I	(2)	20	3608					4603	4670		
BstN I	(15)	101	832	957	1069	HinC II	(2)	1514	1689		
		1144	1198	2462	2517	Hind II	(2)	1514	1689		
		2534	3313	3892	3995	Hind III	(1)	1524			
		4685	4698	4819		Hinf I	(14)	51	209	477	1515
BstU I	(20)	56	90	92	631			1969	1991	2401	3411
		1115	1433	1814	1850			3545	3597	3655	3692
		2226	2246	2270	2301			4474	4870		
		2992	3293	3731	3815	HinI I	(5)	30	136	2926	3628
		3878	3947	4220	4801			3707			
BstY I	(14)	237	514	520	1286	HinP I	(30)	88	90	96	136
		1530	1561	1570	3097			557	629	769	1074
		3343	3735	4094	4106			1115	1431	2190	2198
		4192	4203					2224	2246	2255	2268
Bsu36 I	(2)	2406	4038					2299	2918	2926	2990
Cac8 I	(33)	58	90	94	910			3027	3293	3553	3729
		943	991	1315	1322			3815	4218	4327	4501
		2145	2188	2202	2475	Hpa I	(1)	1689	4668		
		2494	2547	2566	2820	Hpa II	(26)	518	535	610	775
		3006	3225	3291	3297			815	878	938	1469
		3325	3329	3370	3374			1545	1568	2144	2831
		3428	3711	3898	3945			2908	2930	2958	3089
		4001	4023	4234	4794			3179	3246	3427	3702
		4831						3710	3802	4276	4466
Cfr10 I	(7)	609	774	937	2143			4492	4639		
		3245	3426	3709		Hph I	(10)	170	800	805	1133
Cla I	(1)	2766						1157	1286	2044	3105
Csp6 I	(6)	396	659	1215	1497			3996	4112		
		1549	3231			Kas I	(2)	135	2925		
Dde I	(9)	1390	1408	1527	2406	Kpn I	(1)	1552			
		2708	3589	4038	4161	Mae I	(12)	71	617	766	1500
		4570						1519	1574	1775	2193
Dpn I	(27)	239	516	522	529			2749	3764	4098	4351
		1288	1436	1474	1532			30	186	382	387
		1563	1572	1585	2765	Mae II	(16)	30	186	382	387
		2769	2788	3099	3177			724	851	1064	1235
		3258	3267	3345	3721			1986	1998	2041	2151
		3737	4096	4108	4186			3042	3229	4010	4143
		4194	4205	4280		Mae III	(14)	66	304	383	969
DpnII	(27)	237	514	520	527			1458	1714	2215	2227
		1286	1434	1472	1530			3046	3352	4042	4308
		1561	1570	1583	2763			4424	4487		
		2767	2786	3097	3175	Mbo I	(27)	237	514	520	527
		3256	3265	3343	3719			1286	1434	1472	1530
		3735	4094	4106	4184			1561	1570	1583	2763
		4192	4203	4278				2767	2786	3097	3175
Dra I	(5)	333	346	1628	4070			3256	3265	3343	3719
		4089						3735	4094	4106	4184
Dra III	(1)	2042						4192	4203	4278	
Drd I	(3)	1997	2953	4742				119	490	1030	1075
Dsa I	(3)	785	2655	3358		Mbo II	(15)	1078	1271	2181	2409
Eae I	(6)	858	1247	2832	3006			3286	3496	3578	3745
		3397	3424					3945	4115	4188	
Eag I	(1)	2832				Mlu I	(1)	1812			
Ear I	(4)	502	2393	3270	3480	Mme I	(3)	2018	4452	4636	
Eco47 III	(1)	770				Mnl I	(35)	113	504	585	674



NspB II	CMG CKG	5	NspH I	R,CATG`Y	5	SfaN I	GCATC 9/13	14	Sfc I	C`TRYA,G	3
Pac I	TTA,AT`TAA	2	Paer7 I	C`TCGA,G	1	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	1
Pal I	GG CC	23	Pf1M I	CCAN,NNN`NTGG	-	SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	-	Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	1	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	3
Psp1406 I	AA`CG,TT	1	PspA I	C`CCGG,G	1	Stu I	AGG CCT	1	Sty I	C`CWWG,G	7
Pst I	C,TGCA`G	-	Pvu I	CG,AT`CG	1	Taq I	T`CG,A	20	Tfi I	G`AWT,C	8
Pvu II	CAG CTG	3	Rsa I	GT AC	6	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	1
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	27	Xcm I	CCANNNN,N`NNNTGG1	-	Xho I	C`TCGA,G	1
Sau96 I	G`GNC,C	13	Sca I	AGT ACT	-	Xho II	R`GATC,Y	14	Xma I	C`CCGG,G	1
ScrF I	CC`N,GG	23	Sec I	C`CNNG,G	25	Xma III	C`GGCC,G	1	Xmn I	GAANN NNITC	-