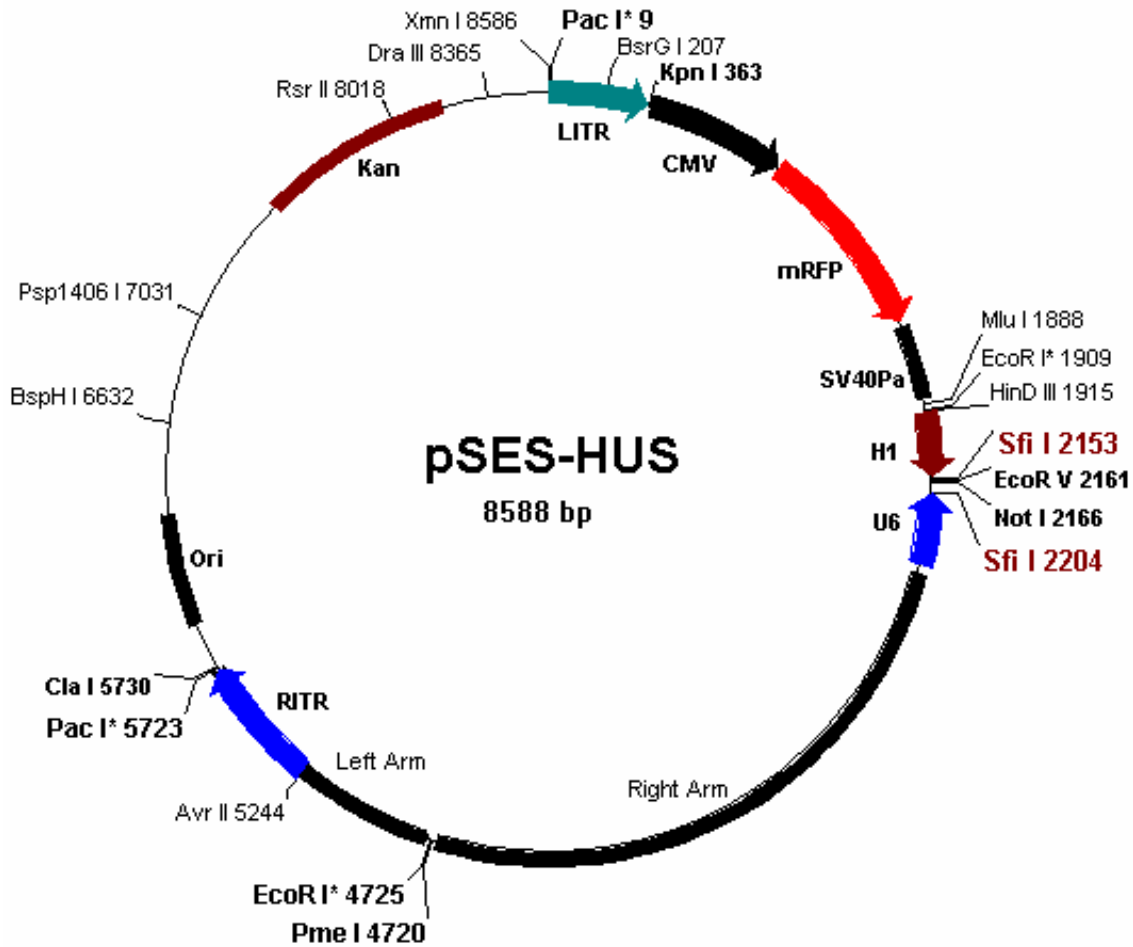


**Vector:** pSES-HUS (adenoviral shuttle vector expressing siRNA)

**Antibiotic Selection:** Kan

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

**Date of Construction:** August, 2005



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

H1>>> **ggccaaaacGGCCgatatacGCGGCCGCggaaacagctatgaCCAtgacgcTGGCCgttttgcc**  
 ccggttttgCCGGctatagcgcggcgccctttgtcgatactggtactgccaacggc<<<U6

**Sfi I Digestion**

5' -GGCCAAAA	<b>A(n19-27nt)TTTT</b>	TGGCC-3'
3' -CCGGT	<b>TTTT(n19-27nt)A</b>	AAAACCGG-5'

# pSES-HUS Full-Length Sequence (formerly known as pASV-HUS) (Adenoviral shuttle vector for siRNA expression)

NNNTTAATTAANNNTCCCTTCCAGCTCTCTGCCCCCTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGTTTGTGACGTGGCGGGGGCGTG  
GGAACGGGGCGGGTGCAGTAGTAGTGTGGCGGAAGTGTGATGTTGCAAGTGTGGCGGAACACATGTAAGCGACGGATGTGGCAAAAGTACGCTTTT  
TGGTGTGCGCCGGGTGACACAGGAAGTACAATTTTCGCGCGGTTTTAGCGGGATGTTGTAGTAAATTTGGCGTAACCGAGTAAGATTTGGCCAT  
TTTCGCGGGAAAACGAATAAGAGGAAGTGAATTCGAATAATTTGTGTACTCATAGCGGTAAANNNGGTaccTAGTTATTAATAGTAATCAATACGGGGTCA  
TTAGTTCATAGCCATATATGGAGTTCGCGTACATAACTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGT  
ATGTTCCCATAGTAACGCCAATAGGGAATTTCCATTGACGTCAAATGGGTGGAGTATTACGGTAAACTGCCACTGGCAGTACATCAAGTGTATCATATGCCAAG  
TACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAGTC  
ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGA  
GTTTTGTTTTGGCACCAAAACCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCAATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAG  
CAGAGCTGGTTTAGTGAACCTCAGATCCGTAGaccATGccctcctccgaggacgctcatcaaggagtcatcgcttcaaggtgcgcatggagggtccggtgaac  
ggccacgagttcgagatcgagggcagggcgagggccgctacgagggcaccagaccgagccggtgaaggtgaaccaagggtgacaaaggcccccctgccttcgctggg  
acatcctgtccctcagttccagtacggctccaaggcctacgtgaagcaccgccgacatccccgactactgaagctgctctcccaggggctcaagtggga  
gcgctgatgaactcgaggacggcggtggtgacgctgaaccaggactcctcctgacggacggcgagttcatctacaaggtgaagctgcgcgccaccaacttc  
cctccgacggccccgtaatgcagaagaagaccatgggctgggagcctccaccgagcggtgtaaccgagggacggcgccctgaagggcgagatcaagatgaggc  
tgaagctgaaggacggcgccgactacgacgcccaggtcaagaccactacatggccaagaagccggtgacgtgcccggcgcccaagaccgacatcaagctgga  
catcactcccacaacgaggactacaccatcgtggaacagtagcagcgccgagggcgccactccaccggcAATCCACCGGATCTAGATAACTGATCATAA  
TCAGCCATACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAACCTCCACACCTCCCGTGAACCTGAAACATAAAATGAATGCAATTTGTTGTTAACTTGT  
TATTGCAGCTTAAATGGTTACAAATAAGCATAGCATCAAAATTTCAAATAAAGCATTTTTTCTACTGCATTCTAGTGTGGTTTTGTCCAACTCATCAAT  
GTATCTTAAACCGTAAactagagctATCCAAATCaagctcaattcgaagcctgacgtcatcaaccgctccaaggaatcgagggccccctgccttcgctggg  
caccagcgcgctgcgccctggcaggaagatggctgtgagggacaggggagtgggcgccctgcaatatttgcagctgcgtatggttctgggaaatcaccataaac  
gtgaatgtccttggatttgggaatcctataagttctgtatgagaccacagatcgcccaaacggc gatatcCGCGCCCGgaacacagctatgaCCatgacgCT  
ggcggTTTTggccctcctttccacaagatataaagccaagaatacgaatacttcaagttacggttaagcatatgatagctcattttaaacaataattttaaacc  
tgc aaactaccaagaataattacttctaogtcagttatgtgataatcttctgtttacagtc aaattaattctctcttaacagctctgta  
cgatatgcaaatatgaaggaatctgggaataagccctctcctgcccacctggactNNNTAAGGGTGGGAAAGAATATATAAGTGGGGTCTTATGTAG  
TTTTGTATCTGTTTTGCAGCAGCCGCCGCCATGAGCACAACCTGTTTGTGGAAGCATTGTGAGCTCATATTTGACAACCGCATGCCCATGGGCCGGG  
TGCCTCAGAATGTGATGGGTCCAGATTGATGGTCGCCCGCTCTGCCGCCAACTCTACTACTTGCCTACGAGACCGTGTCTGGAACGCGCTTGGAGACTGC  
AGCTCCGCGCGCTTCCAGCGTGCAGCCACCGCCCGGGATGTGACTGACTTGTCTTCTGAGCCCGTGAAGCAGTGCAGTCTCCCGT  
ATCCGCCCGCATGACAAGTTGACGGCTCTTTGGCACAATTGGATTCTTTGACCGGAACTTAATGTCTTTCTCAGCAGATTTGGATCTGCG  
CCAGCAGTTTCTGCCCCTGAAGGCTTCTCCCTCCCAATGCGGTTTAAAAATAAATAAAAAACAGACTCTGTTTGGATTTGGATCAAGCAAGT  
GTCTTCTGTCTTTATTTAGGGTTTTGCGCGCGCGGTAGGCCGGGACCAGCGGTCTCGGTCTTGAGGGTCTGTGTATTTTTCCAGGACGTG  
GTAAGGTGACTCTGGATGTTTTCAGATACATGGGCTAAGCCCGTCTGCGGGTGGAGGTAGCACCCTGACAGCTTCATGCTGCGGGGTGGTGT  
GTAGATGATCCAGTCCAGTGAAGGCGCTGGCGTGGTAAAGCTTCTTCAGTAGCAAGCTGATTTGCCAGGAGCTGACCTGCGGTTAGTAAAGT  
GTTTACAAGCGTTAAGTGGGATGGTGCATACGTGGGATATGATGATCTTGGACTGTATTTTTAGGTTGGCTATGTTCCAGCCATATC  
CCTCCGGGATTCATGTTTGCAGAACCCAGCAGAGTGTATCCGGTGCATTTGGGAAATTTGTATGATGCTTGAAGAAATGCGTGAAGAA  
CTTGGAGACGCCCTTGTGACTCCAAGATTTTCCATGCATTCGTCCATAATGATGGCAATGGGCCACGGCGCGGCCCTGGGCGAAGATATTTCT  
GGGATCACTAAGCTGCATGTTGTTTCCAGATGAGTGTGCATAGCCAGTCTTTCAGAAAGCGCGGGCGAGGGTGGCGGTGATGATGTT  
TCCATCCGGCCAGGGCGTAGTTACCCTCACAGATTGCAATTTCCACGCTTTGAGTTCCAGATGGGGGATCATGCTACCTGCGGGCGATGAA  
GAAAACGGTTTTCCGGGTAGGGGAGATCAGCTGGGAAAGAACGAGTTCCTGAGCAGCTGCGACTTACCAGCCGGTGGGCCGTTAAATCACAC  
TATTACCGGGTGCACTGTTAGTAAAGAGAGTGCAGTCCCGTTCATCCCTGACAGGGGGGCACTTCGTTAAGCATGTTCCCTGACTCGCATGTT  
TTCCTGACCAAAATCCGTCAGAGGCGCTCCGCCCGCAGCATAGCAGTCTTGCAGAAAGCAAAGTTTTTCAACGGTTTTGACGGCTTCCGCTG  
AGGCATGCTTTTGAAGCTTTGACCAAGCAGTTCCAGGGGTCACACAGCTCGGTCACTGCTCTACGGCATCTCGATCCAGCATATCTCCTCGTTT  
CGCGGTTGGGGCGGTTTCCGCTGTACGGCAGTAGTCGGTCTGTCAGACGGGCCAGGGTTCATGCTTTCCACGGGCGAGGGTCTCTCGTCAG  
GTAGTCTGGTTCACGGTGAAGGGTGCCTCCGGCTGCGCGTGGCCAGGGTGGCTTGGGCTGGTCTGCTGGTGAAGCGTCCGGCTCT  
TCGCCCTGCGGTCCGCTGACATTTGACCATGTTGACCTGTTGACCTGCTGATAGCCCTCCCGCGCGTGGCCCTTGGCGCGGAGGTTGGGATG  
GCGCCGACGAGGGGCAGTGCAGACTTTTGAAGGCGTAGAGCTTTGGGCGGAGAAATACCGATTCCGGGGAGTAGGCATCCGCGCCGAGGCCCG  
CAGACGGTCTCGCATTCACGAGCCAGGTGAGCTCTGCGGCTTCCGGGTCAA AAAACAGGTTTCCCCCATGCTTTTGTAGCGTTTCTTACCTCTG  
GTTCCATGAGCCGGTGTCCAGCTCGGTGACGAAAAGGCTGCTCGCTGCCGTATACAGACTNNNGTTTAAACGAATCTNNNTATAAAATGCAA  
GGTGTCTGCTCAAAAAATGACGAAAGCCCTCGCGCAAAAAAGGCAAGACATCGTAGTATGCTCATGAGATAAAGCAGGTAACGATTTCCGGAACCA  
CACAGAAAAGACACCATTCTCTCAAAATGTCTGCGGGTTTCTGCATAAAACAAAAATAAATAACAAAAAAATTTAAACATTAGAAGCC  
TGCTTTACAACAGGAAAAACACCCTTATAAGCATAAAGCAGGACTACGGCATTGCCGCTGACCGTA AAAAAACCTGGTCAACCGTATTA AAAAGC  
ACCACCGACAGCTCCCTGGTTCATGTCGGAGTCAATATGTAAGACTCGGTAACACATCAGTTGATTCACTGGTTCAGTCTAAAAGCAGCCGAA  
ATAGCCCGGGGAAATGACATCCCGCAGCGTAGAGCAACATACAGCCCAATGAGGAGGTATAACAAAAATTAATAGGAGCGGTACAGAAATCAAC  
ACCTGAAAAACCCCTCTGCTAGGCAAAATAGCACCTCCCGCTCCAGAACAACATAACAGCGCTTACAGCGGCAGCCCTAACAGTACAGCTTACCA  
GTAAAAAAGAAAACCTATTA AAAA AACACCCTCGACACGGCACCAGCTCAATCAGTACAGTGTAAAAAAGGGC CAAGTGCAGAGCGAGTATATA  
TAGGACTAAAAAATGACGTAACGGTTAAAGTCCACAAAAACACCAGAAAACCGCACGGCAACCTACGCCAGAAAACGAAAGCCAAAAACCCCA  
AACTTCCCAATCGTCACTTCCGTTTTCCCAAGTTACGTAACCTGTTCAATTTTAAAGAAAATCAATTTCCAAACACATCAAGTTACTCCGCCCTA  
AAACCTACGTACCCCGCCCGTTCCACAGCCCGCGCCAGCTCACAACCTCCACCCCTCATATCATATTTGGCTCAATCCAAAATAAGGTATAT  
TATGTGATNNNTAATTAAGGATCCNNNCGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCCTCG  
CTCAGTACTCGTCTCGCTCGGCTCGGCTCGCGCGAGCGGTATCAGCTCCTCAAAGGGGTAATACGGTATACACAGATAACAGGGATAAC  
GCAGGAAAAGACATGTGAGCAAAAAGCCAGCAAAAAGCCAGGAACCGTAAAGAGCGCTTTGCTGGCGTTTTTCCATCCAGCTCCGCCCCCTGAC  
GAGCATCACAAAATCGACGCTCAAGTCAAGGTTGGGAAAACCCGACAGGACTATAAAGATACAGGGCGTTTTCCCGTGGAGCTCCCTCGTGCGC  
TCTCCTGTTCCGACCTTCCGCTTACCGGATACCTGTCCGCTTTCTCCTTCCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTG  
AGTTCGGTGTAGTCTGCTCAAGCTGGGTGTGTGTCAGCAACCCCGCTCAGCCGACCGCTGCGCTTATCCGGTAACTCATCTGCTTGTAG  
TCCAACCGGTAAGACACGACTTATGCCCCTGACGAGCACTGCAACAGGATTTAGCAGAGCGAGGATGTAGGAGCGGTACAGAGTCTTCTT  
AAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCCGAAAAGAGTGGTAGCTCT  
TGATCCGGCAACAACACCAGCTGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGAGATTACCGCGAGAAAAGGATCTCAAGAAGATCCTTTG  
ATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCAGCTTAAGGATTTTGGTCAATGAGATTTTCAAAAGGATCTTCAACCTAGATCTCT  
TTAAATTAATAAGTAAATTAATAAATCAATTAAGATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAACTCAGTGGAGGACCTATCTCA  
GCGATCTGTCTATTTCGTTTCAATCCTAGTTGCTGACTCCCGCTCGTGTAGATAACTACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCA  
ATGATACCGGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCAGCCGGAAGGGCCGAGCGAGAAGTGGTCTGCAACTTTA  
TCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTGCACAACGTTGTTGNNNNNNAAAAAGGA  
CTTTCACCTAGACTTTTTCAGTGAAGCCAGTCCGACAAAGGCTGACAAAGGCTGACTGACCTAGATGTCAGTACTGGCTATCTGGACAAGGGAAA  
ACGCAAGCGCAAGGAAAAGCAGGTAGCTTTCAGTGGCTTACATAGCAGTAGCTACCGCGGTTTTATGGCAGCAAGCCGAAATTC





		2042	2600	2921	3047			1049	1055	1070	1158
		3049	3051	3236	3656			1220	1253	1303	1360
		4004	4249	4293	4305			1385	1405	1412	1444
		4307	4321	4351	4371			1481	1571	1576	1607
		4436	4438	4460	4506			1681	1720	1729	2017
		4541	4778	5287	5645			2217	2455	2738	2957
		5789	5822	6092	6159			2962	3077	3161	3411
		6259	6433	6542	6935			3526	3656	3725	4171
		7028	7158	7256	7327			4265	4318	4423	4445
		7496	7504	7568	7605			4448	4460	4480	4653
		7871	8131	8515	8523			4781	5056	5179	5246
		8549	8568	8570	8579			5270	5528	5675	5810
HinC II	(2)	1765	2846					6020	6093	6344	6744
Hind II	(2)	1765	2846					6825	6971	7267	7353
HinD III	(1)	1915						7417	7553	7910	8102
Hinf I	(22)	774	1290	1955	2113			8393			
		2428	2869	2989	3122	Msc I	(4)	285	1509	4311	7584
		3410	3966	4518	5062	Mse I	(36)	5	9	371	1703
		5076	5098	5812	5887			1764	1885	1919	2283
		6283	6800	7987	8121			2296	2376	2888	2967
		8292	8314					3319	3904	3952	4719
HinI I	(15)	486	539	622	808			4922	5025	5200	5339
		979	1426	1483	1534			5442	5565	5719	5723
		1633	1934	2040	3505			6618	6670	6675	6689
		4458	7254	7502				6742	6977	7016	8175
HinP I	(64)	86	200	231	348			8187	8204	8302	8572
		998	1010	1244	1334	Msl I	(6)	729	2089	3547	3612
		1426	1534	1607	1609			4806	7939		
		1633	1992	1994	2000	Msp I	(39)	203	1531	1630	1644
		2040	2598	2919	3045			2615	2880	3060	3405
		3047	3049	3234	3654			3445	3695	3797	3859
		4002	4247	4291	4303			3887	4296	4355	4522
		4305	4319	4349	4369			4661	4832	4992	5059
		4434	4436	4458	4504			5135	6119	6266	6292
		4539	4776	5285	5643			6482	6886	6920	6987
		5787	5820	6090	6157			7109	7236	7407	7484
		6257	6431	6540	6933			7506	7534	7665	7755
		7026	7156	7254	7325			7822	8003	8467	
		7494	7502	7566	7603	MspAl I	(15)	1526	2171	2749	2765
		7869	8129	8513	8521			2907	3069	3815	3842
		8547	8566	8568	8577			3918	4419	5295	6254
Hpa I	(1)	1765						6499	7248	7608	
Hpa II	(39)	203	1531	1630	1644	Mun I	(2)	1752	2863		
		2615	2880	3060	3405	Nae I	(3)	4993	8004	8468	
		3445	3695	3797	3859	Nar I	(7)	1426	1534	1633	2040
		3887	4296	4355	4522			4458	7254	7502	
		4661	4832	4992	5059	Nci I	(18)	1531	2616	2880	2881
		5135	6119	6266	6292			3060	3061	3406	3798
		6482	6886	6920	6987			3888	4297	4523	5135
		7109	7236	7407	7484			5136	6292	6988	7109
		7506	7534	7665	7755			7506	7666		
		7822	8003	8467		Nco I	(6)	724	961	1381	2608
Hph I	(19)	120	739	1114	1285			4393	7934		
		1336	1557	2074	3130	Nde I	(2)	598	2268		
		4120	4291	4591	4687	NgoM I	(3)	4991	8002	8466	
		5009	5612	6649	6876	Nla III	(40)	162	668	728	965
		7050	7681	8367				998	1016	1385	1508
Kas I	(7)	1425	1533	1632	2039			2060	2191	2435	2550
		4457	7253	7501				2604	2612	3144	3194
Kpn I	(1)	363						3417	3470	3534	3765
Mae I	(13)	364	956	1650	1851			3960	3975	4080	4235
		1898	1975	5245	6407			4397	4624	4658	4805
		6660	6995	7061	7203			4811	4875	4991	5057
		8516						5916	6636	7195	7376
Mae II	(33)	81	113	187	486			7721	7907	7938	7964
		498	539	622	703	Nla IV	(40)	361	831	1022	1082
		808	979	1177	1902			1118	1166	1340	1361
		1934	2090	2333	2338			1427	1535	1634	1964
		3109	3339	3604	5433			2041	2640	3064	3088
		5545	5550	5616	5648			3247	3560	3668	3689
		6615	7031	7074	7618			3832	3866	3942	4114
		7805	8309	8321	8364			4254	4459	4549	4836
		8474						5363	5944	5983	6755
Mae III	(41)	77	109	183	218			6849	6890	7255	7503
		266	337	425	512			7538	8404	8425	8437
		861	1103	1274	1280	Not I	(1)	2166			
		1790	1970	2255	2334	Nsi I	(2)	3358	3536		
		2772	3119	3512	3710	Nsp7524 I	(9)	158	2056	2600	3956
		4125	4274	4676	4996			3971	4076	4871	5912
		5014	5376	5434	5527			7903			
		5546	5551	5595	5617	NspB II	(15)	1526	2171	2749	2765
		5649	6268	6331	6447			2907	3069	3815	3842
		6730	7622	7928	8538			3918	4419	5295	6254
		8550						6499	7248	7608	
Mbo I	(35)	949	1045	1441	1646	NspH I	(9)	162	2060	2604	3960
		1659	2141	2465	2913			3975	4080	4875	5916
		3005	3215	3595	3628			7907			
		3758	3809	4147	5727			9	5723		
		5731	6478	6553	6564	Pac I	(2)	285		641	966
		6572	6650	6662	6767	Pal I	(49)	1033	1066	1117	1173
		7051	7063	7315	7332			1360	1395	1474	1509
		7343	7362	7673	7751			1618	1964	2147	2156
		7832	7841	7919				2168	2198	2207	2444
Mbo II	(17)	1384	1387	2023	2441			2614	3058	3291	3560
		3503	3593	3794	3831			3574	3640	3698	3866
		4352	5784	6573	6646			3943	4224	4311	4377
		7047	7862	8072	8154			4427	4548	4591	4986
		8504						5395	5927	5938	5956
Mlu I	(1)	1888						6390	6848	6928	7410
Mme I	(6)	1377	2697	2892	6126			7584	7975	8002	8215
		6310	8341					8357			
Mnl I	(69)	56	304	905	968	PfI M I	(2)	1387	3110		
		976	979	1010	1043	Ple I	(3)	5070	6291	8300	

Pme I	(1)	4720				Aat II	G,ACGT`C	6	Acc I	GT`MK,AC	2
PpuM I	(2)	3087	4253			Acc65 I	G`GTAC,C	1	Acc I	C`CG,C	114
Psp1406 I	(1)	7031				Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	4
PspA I	(3)	2879	3059	5134		Age I	A`CCGG,T	-	Aha II	GR`CG,YC	15
Pst I	(5)	1303	2727	2754	3184	Ahd I	GACNN,N`NNGTC	3	Alu I	AG CT	45
		3917				Alw I	GGATC 8/9	24	AlwN I	CAG,NNN`CTG	6
Pvu II	(7)	1526	2907	3815	3842	Apa I	G,GGCC`C	3	Apal I	G`TGCA,C	2
		3918	7248	7608		Apo I	R`AATT,Y	7	Asc I	GG`CGCG,CC	-
Rsa I	(14)	209	361	583	608	Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1
		663	696	747	904	Ava I	C`YCGR,G	5	Ava II	G`GNC,C	7
		1161	1413	1602	2348	Avr II	C`CTAG,G	1	BamH I	G`GATC,C	-
		4194	7808			Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	10
Rsr II	(1)	8018				Bbe I	G,CGCC`C	7	Bbs I	GAAGAC 8/12	2
Sac I	(2)	2584	4587			Bbv I	GCAGC 13/17	19	Bbv II	GAAGAC 7/11	2
Sac II	(3)	2172	2766	4420		Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	18
Sap I	(3)	5796	7846	8056		Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	9
Sau3A I	(35)	949	1045	1441	1646	Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-
		1659	2141	2465	2913	Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	6
		3005	3215	3595	3628	BsaA I	YAC GTR	8	BsaB I	GATNN NNATC	3
		3758	3809	4147	5727	BsaH I	GR`CG,YC	15	BsaJ I	C`CNNG,G	46
		5731	6478	6553	6564	BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	5
		6572	6650	6662	6767	Bsg I	GTGCAG 22/20	5	BsiC I	TT`CG,AA	1
		7051	7063	7315	7332	BsiE I	CG,RY`CG	8	BsiHKA I	G,WGCW`C	8
		7343	7362	7673	7751	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	4
		7832	7841	7919		BsmA I	GTCTC`/9	12	BsmB I	CGTCTC 7/11	2
Sau96 I	(32)	447	640	1064	1116	BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	71
		1359	1616	1962	1963	Bsp120 I	G`GGCC,C	3	Bsp1286 I	G,DGCH`C	2
		2443	2612	3057	3063	BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	8
		3087	3290	3558	3559	BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	20
		3697	3864	3865	3941	BsrB I	GAG CGG	6	BsrD I	GCAATG, 8	3
		4112	4222	4253	4331	BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	7
		4426	4547	5393	6847	BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	1
		6926	6943	8018	8356	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	4
ScrF I	(38)	454	647	1133	1287	BstN I	CC`W,GG	20	BstU I	CG NC	41
		1531	2005	2616	2880	BstX I	CCAN,NNNN`NTGG	3	BstY I	R`GATC,Y	13
		2881	3060	3061	3105	Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	53
		3282	3406	3576	3621	Cfr10 I	R`CCGG,Y	10	ClA I	AT`CG,AT	1
		3701	3798	3888	4107	Csp6 I	G`TA,C	14	Dde I	C`TNA,GC	9
		4226	4297	4313	4379	Dpn I	GA TC	35	DpnII	`GATC,	35
		4523	4578	4610	5135	Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	1
		5136	5940	6061	6074	Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	11
		6292	6988	7109	7506	Eae I	Y`GGCC,R	16	Eag I	C`GGCC,C	3
Sec I	(46)	724	961	973	1108	Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	3
		1132	1168	1225	1285	Eco57 I	CTGAAG 21/19	10	Eco72 I	CAC GTG	5
		1381	1417	1486	1612	EcoN I	CCCTN`N,NNAGG	-	EcoO109 I	RG`GNC,CY	-
		1950	2003	2169	2461	EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	20
		2608	2615	2763	2879	EcoR V	GAT ATC	1	Ehe I	GGC GCC	7
		3059	3281	3293	3405	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	71
		3562	3575	3699	3700	Fok I	GGATG 14/18	20	Fse I	GG,CCGG`CC	-
		3797	4225	4241	4312	Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	15
		4393	4417	4429	4447	Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	12
		4522	5047	5134	5135	Hae II	R,CGCC`Y	15	Hae III	GG CC	49
		5244	6072	7107	7311	Hga I	GACGC 9/14	8	HgiA I	G,WGCW`C	8
		7665	7934			HgiE II	ACCNNNNNNGGT -1/132	40	Hha I	G,CG`C	64
SfaN I	(16)	722	1817	3344	3364	Hinc II	GTY RAC	2	Hind II	GTY RAC	2
		4149	4541	4622	5750	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	22
		5788	6008	7461	7716	HinI I	GR`CG,YC	15	HinP I	G`CG,C	64
		7800	7864	7932	8139	Hpa I	GTT AAC	1	Hpa II	C`CG,G	39
Sfc I	(7)	1299	2723	2750	3180	Hph I	GGTGA 12/11	19	Kas I	G`GGCG,C	7
		3913	6177	6368		Kpn I	G,GTAC`C	1	Mae I	C`TA,G	13
Sfi I	(2)	2153	2204			Mae II	A`CG,T	33	Mae III	`GTNAC,	41
Sma I	(3)	2881	3061	5136		Mbo I	`GATC,	35	Mbo II	GAAGA 12/11	17
SnaB I	(2)	704	5551			Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Sph I	(3)	2604	4080	7907		Mnl I	CCTC 10/10	69	Msc I	TGG CCA	4
Ssp I	(1)	2051				Mse I	T`TA,A	36	Msl I	CAYNN NNRTG	6
Stu I	(2)	1173	1395			Msp I	C`CG,G	39	MspAl I	CMG CKG	15
Sty I	(15)	724	961	1108	1168	Mun I	C`AATT,G	2	Nae I	GCC GGC	3
		1381	1950	2461	2608	Nar I	GG`CG,CC	7	Nci I	CC`S,GG	18
		3293	4393	4429	4447	Nco I	C`CATG,G	6	Nde I	CA`TA,TG	2
		5244	7311	7934		NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
Taq I	(16)	1042	1048	1258	1907	Nla III	,CATG`	40	Nla IV	GGN NCC	40
		1924	2241	4146	5354	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	9
		5730	6012	7615	7771	Nsi I	A,TGCA`T	2	Nsp7524 I	R`CATG,Y	-
		7795	7831	7993	8398	NspB II	CMG CKG	15	NspH I	R,CATG`Y	9
Tfi I	(10)	1955	2113	2428	2869	Pac I	TTA,AT`TAA	2	Paer7 I	C`TCGA,C	-
		3410	4518	5098	5887	Pal I	GG CC	49	PflM I	CCAN,NNN`NTGG	2
		7987	8121			Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Tsp45 I	(24)	77	109	183	218	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	2
		1103	1274	1280	1970	Psp1406 I	AA`CG,TT	1	PspA I	C`CCGG,G	3
		2334	2772	3119	3512	Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	-
		4125	4274	4676	4996	Pvu II	CAG CTG	7	Rsa I	GT AC	14
		5014	5376	5527	5617	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
		5649	7622	7928	8538	Sac II	CC,GC`GG	3	Sal I	G`TCGA,C	-
Tth111 I	(2)	2700	7620			Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	35
Tth111 II	(9)	2819	2985	3024	4112	Sau96 I	G`GNC,C	32	Sca I	AGT ACT	-
		4883	6501	6510	6540	ScrF I	CC`N,GG	38	Sec I	C`CNNG,G	46
		7938				SfaN I	GCATC 9/13	16	Sfc I	C`TRYA,G	7
Vsp I	(6)	5	371	2376	5200	Sfi I	GGCCN,NNN`NGGCC	2	Sma I	CCC GGG	3
		5719	6977			SnaB I	TAC GTA	2	Spe I	A`CTAG,T	-
Xba I	(2)	1649	1897			Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Xca I	(1)	4705				Srf I	GCCC GGGC	-	Ssp I	AAT ATT	1
Xcm I	(3)	2993	4584	7318		Stu I	AGG CCT	2	Sty I	C`CWGG,G	15
Xho II	(13)	949	1646	2465	2913	Taq I	T`CG,A	16	Tfi I	G`AWT,C	10
		6553	6564	6650	6662	Tsp45 I	`GTSAC,	24	Tth111 I	GACN`N,NGTC	2
		7051	7063	7315	7673	Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	6
		7919				Xba I	T`CTAG,A	2	Xca I	GTA TAC	1
Xma I	(3)	2879	3059	5134		Xcm I	CCANNNN,N`NNNNTGG3	3	Xho I	C`TCGA,G	-
Xma III	(3)	2154	2166	7408		Xho II	R`GATC,Y	13	Xma I	C`CCGG,G	3
Xmn I	(1)	8586				Xma III	C`GGCC,G	3	Xmn I	GAANN NNNTTC	1

Site usage in pSES-HUS: