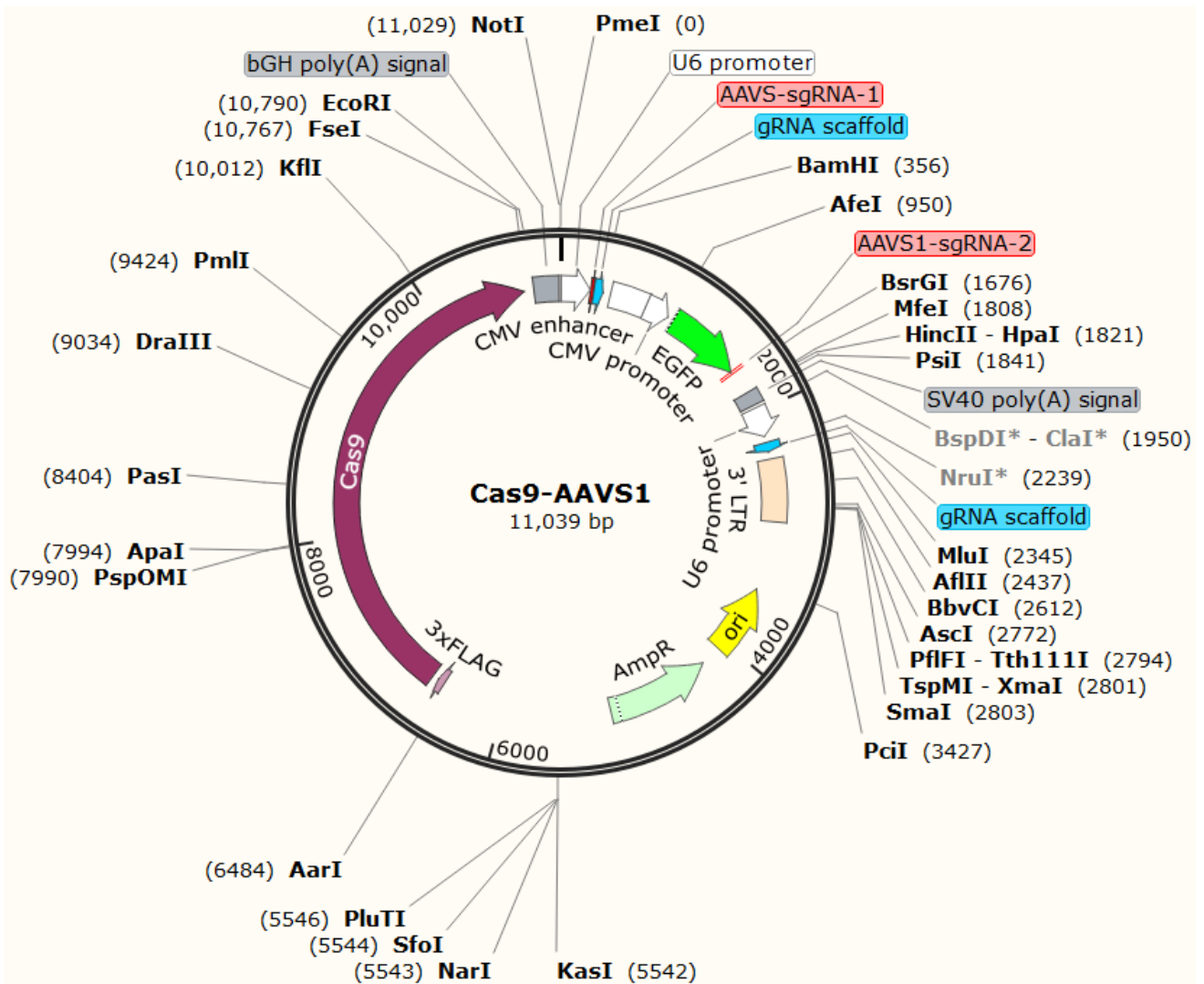


Vector: pCas9gG-AAVS1

Antibiotic Selection: Amp

Creator(s): Li Li, Xue Hu, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: May, 2016



pCas9G-AAVS1 Vector Sequence

aaacGAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAAATTGGAATTAATTTGACTGTAAACACAAA
GATATTAGTACAAAATACGTGACGTAGAAAGTAATAATTTCTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATATGCTTAC
CGTAACTTGAAAGTATTCGATTTCTGGCTTTATATACTTGTGGAAAGGAcgaaa**CACCGTCCCTCCACCCCAAGTGGTTTTAGAGCTAGAA**
ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCAGTCCGGTCTTTTTT**ggatccTAATAGTAATCAATTACGGGGTC**
ATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAAATTACGGTAAATGGCCCCCTGGCTGACCGCCAACGACCCCGCCATTGACGTC
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TCCTACTGGCAGTACATCTACGTATTAGTCATCGTATTACCATGCTGATGCGGTTTTGGCAGTACATCAATGGCCGTGGATAGCGGTTTGCATC
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CCCATTGACGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTAGTGAACCGTCAGATCCGCTAGCGCTACCGGTC
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cgaaaGAATGGGGCCACTAGGGACAGGATCGC**ACTGGAGTTGCAGATCACGGC****GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG**
TTATCAACTTGAAAAGTGGCACCGAGTCGGTGTCTTTTT**acgcgttaataa****CGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAGGGGG**
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CATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTCTGAAGGACGACTCCATCGACAACAAGGTGTGACCAGAAAGCGA
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AGGTGTCATTCTATTTGGGGGTTGGGGTGGGGAGGACAGCAAGGGGAGGATTGGGAAGAGAATAGCAGCATGTGGGAGCGCCCGCgttt

Unique enzymes in pCas9gG-AAVS1:

BamH I	G`GATC,C	355
Mun I	C`AATT,G	443
Eco47 III	AGC GCT	611
Cla I	AT`CG,AT	1345
Bsm I	GAATG,C 7	1615
Mlu I	A`CGCG,T	1719
Nhe I	G`CTAG,C	1806
Afl II	C`TTAA,G	1811
Xba I	T`CTAG,A	1996
Asc I	GG`CGCG,CC	2146
Tth111 I	GACN`N,NGTC	2168
PspA I	C`CCGG,G	2175
Xma I	C`CCGG,G	2175
Sma I	CCC GGG	2177
Kas I	G`GCGC,C	4916
Nar I	GG`CG,CC	4917
Ehe I	GGC GCC	4918
Bbe I	G,GCGC`C	4920
SnaB I	TAC GTA	5364
Bsp120 I	G`GGCC,C	7364
Apa I	G,GGCC`C	7368
Eco72 I	CAC GTG	8798
Pml I	CAC GTG	8798
Fse I	GG,CCGG`CC	10141
EcoR I	G`AATT,C	10164
Not I	GC`GGCC,GC	10403

Number of enzymes = 26

pCas9gG: sites sorted by name:

Aat II	(4)	4616	5167	5202	5285
Acc65 I	(2)	2179	5097		
Aci I	(116)	472	509	589	846
		887	954	993	1131
		1244	1304	1307	1634
		1975	1981	2277	2491
		2594	2650	2660	2684
		2727	2734	2755	2846
		2874	3001	3020	3141
		3251	3386	3395	3757
		3848	4039	4085	4206
		4250	4327	4436	4535
		4582	4756	4795	4805
		4831	4869	4882	4908
		4965	5128	5140	5154
		5303	5494	5511	5523
		5528	5538	5548	5551
		5567	5601	5604	5607
		5610	5613	5637	5640
		5644	5679	5684	5687
		5690	5700	5704	5723
		5744	5748	5978	6172
		6208	6350	6461	6619
		6883	7025	7102	7205
		7214	7277	7280	7346
		7468	7487	7618	7630
		7964	7967	8200	8339
		8354	8465	8657	8725
		8992	9062	9106	9185
		9257	9316	9403	9883
		9973	10122	10402	10406
Afl II	(1)	1811			
Afl III	(2)	1719	2801		
Age I	(3)	450	615	5880	
Aha II	(10)	4231	4613	4917	5164

The following enzymes do not cut in pCas9gG:

Acc I	Avr II	BsiC I	BsiW I	BsrG I
Bst1107 I	BstB I	BstE II	Bsu36 I	HinC II
Hind II	Hind III	Hpa I	Nru I	Nsi I
Paer7 I	Pme I	Rsr II	Sac II	Sal I
Sfi I	Spe I	Spl I	Srf I	Stu I

		5199	5282	6628	6901			5199	5282	6628	6901
		8965	10039					8965	10039		
Ahd I	(4)	2224	2270	3694	8027	BsaJ I	(47)	520	626	656	796
Alu I	(66)	281	602	648	681			959	983	1038	1939
		753	786	1002	1050			2018	2028	2175	2238
		1161	1335	1645	1806			2540	2961	5035	5384
		1810	2114	2433	2466			5707	5890	5993	6184
		2561	2625	2743	2969			6280	6478	6500	6631
		3059	3105	3362	3883			6743	6784	6946	7165
		3983	4046	4725	4744			7253	7375	7431	7600
		4989	5781	6295	6557			7738	7777	7778	8140
		6569	6590	6692	6803			8153	8407	8597	8710
		7017	7034	7184	7262			9160	9214	9301	9421
		7477	7577	7697	7958			9559	9754	10251	
		8003	8093	8246	8378	BsaW I	(13)	358	375	450	615
		8423	8438	8542	8663			3007	3154	3985	5880
		8678	8768	8852	8891			6238	7675	8905	9178
		9017	9362	9494	9526			10003			
		9599	9623	9740	9776	BseR I	(3)	658	2241	5753	
		10100	10175			Bsg I	(9)	568	756	853	1177
Alw I	(27)	351	362	368	1123			5501	6594	7248	8151
		1320	3363	3449	3449			9327			
		3546	3547	4011	4326	BsiE I	(11)	371	620	2717	3141
		4332	5931	6248	7242			4064	4213	4960	6125
		7329	8091	8363	8385			9635	10004	10406	
		8802	8850	9171	9509	BsiHKA I	(11)	1237	2116	3119	4280
		9843	10044	10091				4365	4862	5849	6991
AlwN I	(8)	1935	3217	7001	7034			8176	8248	10177	
		8393	8489	8666	8810	Bsm I	(1)	1615			
Apa I	(1)	7368				BsmA I	(13)	1761	1884	2231	2252
ApaL I	(3)	3115	4361	4858				3756	4530	4683	4727
Apo I	(2)	6099	10164					5909	8757	9193	10072
Asc I	(1)	2146						10098			
Ase I	(7)	76	1434	2444	2572	BsmB I	(2)	4684	4726		
		2631	3866	5827		BsmF I	(10)	399	1950	1963	5199
Asp718	(2)	2179	5097					5350	5764	5985	8034
Ava I	(6)	417	519	2109	2175			8338	9399		
		8274	9753			BsoF I	(86)	589	787	846	868
Ava II	(16)	1284	1964	1977	2032			1152	1159	1210	1213
		3832	4054	5878	5903			1307	2626	2707	2725
		6998	7196	7216	7655			2728	2846	3001	3144
		8480	8522	9386	9584			3209	3212	3418	3746
BamH I	(1)	355						4085	4112	4207	4436
Ban I	(17)	333	378	453	663			4723	4832	4936	5009
		1697	2022	2179	2545			5483	5549	5552	5555
		3642	4916	5097	5883			5568	5602	5605	5608
		6042	6086	6352	7161			5611	5614	5638	5654
		10259						5661	5687	5690	5700
Ban II	(9)	2116	2129	5401	6158			6007	6173	6351	6462
		7368	8248	9750	9968			6620	6693	6801	6883
		10177						7026	7029	7032	7035
Bbe I	(1)	4920						7203	7212	7232	7263
Bbs I	(2)	250	272					7278	7281	7530	7631
Bbv I	(23)	879	1163	1170	3220			7695	7956	7965	8091
		3223	3429	4123	4734			8195	8339	8384	8424
		5494	5566	6018	6812			8658	8661	8664	8726
		7040	7043	7223	7243			9186	9317	9404	9495
		7706	7967	8102	8206			9524	9600	9973	10123
		8395	8672	9535				10403	10406		
Bbv II	(2)	251	271			Bsp120 I	(1)	7364			
Bcl I	(8)	6067	6490	6970	8005	Bsp1286 I	(4)	1237	5849	6991	8176
		8872	8998	9589	10181	BspH I	(5)	3521	4529	4634	5927
Bcn I	(25)	255	658	1312	1942			9133			
		2177	2178	3182	3878	BspM I	(7)	5858	6466	6847	7207
		4229	4730	4765	5710			7519	7666	8461	
		5769	6195	6502	6698	BspM II	(3)	358	8905	9178	
		7318	8020	8599	8781	Bsr I	(25)	485	506	1240	1620
		8820	8860	9216	9241			2152	2602	3208	3221
		9901						3335	3741	3859	3902
Bfa I	(14)	282	307	458	607			4169	4341	5047	5320
		1646	1671	1807	1997			6312	6435	6861	8493
		3296	3549	3884	5092			8657	8742	8919	9386
		10170	10203					9687			
Bgl I	(7)	3814	4932	5132	5236	BsrB I	(10)	2493	2734	4535	5567
		5307	8187	10143				5681	5744	6350	7487
Bgl II	(2)	1358	6259					7630	10402		
Blp I	(5)	5782	6804	6912	7992	BsrD I	(3)	3755	3929	8176	
		9267				BssH II	(5)	2095	2146	5570	5633
Bpm I	(6)	1072	1312	1638	1744			5656			
		3764	5863			BssS I	(10)	808	2974	4358	4665
Bsa I	(3)	2232	2253	3755				6345	6393	7020	7176
BsaA I	(7)	115	1473	5364	7361			8169	8247		
		7595	8477	8798		BstN I	(40)	673	798	910	985
BsaB I	(2)	360	9507					1039	2019	2541	2829
BsaH I	(10)	4231	4613	4917	5164			2950	2963	5036	5132

		5307	5842	6033	6324			8356	8389	8785	8806
		6480	6744	6780	6831			8854	8872	8938	8998
		6996	7113	7146	7254			9070	9175	9193	9220
		7376	7397	7433	7779			9364	9502	9589	9811
		7827	8046	8142	8154			9823	9847	10048	10084
		8484	8811	9162	9720			10181			
		9804	9852	10143	10253						
BstU I	(27)	472	956	1274	1634	Dra I	(8)	157	170	1515	1528
		1721	2095	2097	2148			3560	3579	4271	8120
		2648	2650	2848	3429	Dra III	(3)	7946	8408	9875	
		3759	4252	4584	4684	Drd I	(2)	2909	4778		
		4686	4789	5572	5635	Dsa I	(7)	626	5384	5890	5993
		5637	5658	5697	5725			7738	8407	9421	
		8341	8935	10408		Eae I	(19)	699	1088	2640	4082
BstX I	(2)	6053	6623					6277	6781	6880	7372
BstY I	(17)	355	361	1127	1358			8150	8188	8296	9163
		3442	3453	3539	3551			9445	9632	9721	9853
		4319	4336	6241	6259			10123	10139	10403	
		7246	7333	8389	8806	Eag I	(2)	9632	10403		
		9175				Ear I	(14)	2423	2685	4489	4977
Cac8 I	(54)	751	784	832	1156			6195	6307	6325	7111
		1163	1804	1808	2097			8356	8620	9474	9633
		2148	2594	2623	2732			10002	10371		
		2818	2855	3415	3806	Eco47 III	(1)	611			
		4819	4967	4987	4991	Eco57 I	(15)	780	826	1023	3348
		5087	5128	5303	5572			4362	6218	6249	7325
		5635	5642	5658	5704			7979	8075	8567	8900
		5746	6617	6844	7088			9306	9497	9761	
		7109	7267	7545	7618	Eco72 I	(1)	8798			
		7635	7989	8166	8192	EcoN I	(3)	461	6516	6783	
		8265	8750	9084	9273	EcoO109 I	(10)	8	1366	2032	4670
		9649	9659	9725	9922			6950	6998	7196	7365
		10120	10139	10177	10211			9386	9584		
		10388	10392			EcoR I	(1)	10164			
Cfr10 I	(16)	450	615	778	3774	EcoR II	(40)	671	796	908	983
		5880	6124	7086	7977			1037	2017	2539	2827
		8190	8263	8500	8748			2948	2961	5034	5130
		9657	10065	10118	10137			5305	5840	6031	6322
Cla I	(1)	1345						6478	6742	6778	6829
Csp6 I	(34)	105	500	1056	1338			6994	7111	7144	7252
		1463	2180	4173	4849			7374	7395	7431	7777
		5098	5242	5267	5322			7825	8044	8140	8152
		5355	6020	6080	6401			8482	8809	9160	9718
		6863	7046	7550	7556			9802	9850	10141	10251
		8441	8447	8474	8834	EcoR V	(2)	1917	7862		
		9008	9035	9053	9113	Ehe I	(1)	4918			
		9398	9608	9716	9983	Esp I	(5)	5782	6804	6912	7992
		10013	10073					9267			
Dde I	(34)	1231	1249	1362	1851	Fnu4H I	(86)	589	787	846	868
		1945	1986	2255	2326			1152	1159	1210	1213
		3076	3485	3651	4191			1307	2626	2707	2725
		4617	4852	5782	6420			2728	2846	3001	3144
		6654	6738	6804	6912			3209	3212	3418	3746
		6924	6957	7039	7626			4085	4112	4207	4436
		7992	8536	8730	8830			4723	4832	4936	5009
		9013	9267	9391	9604			5483	5549	5552	5555
		10096	10313					5568	5602	5605	5608
Dpn I	(65)	357	363	370	1129			5611	5614	5638	5654
		1277	1315	1360	1629			5661	5687	5690	5700
		1871	3369	3444	3455			6007	6173	6351	6462
		3463	3541	3553	3658			6620	6693	6801	6883
		3999	4017	4063	4321			7026	7029	7032	7035
		4338	4374	4959	5926			7203	7212	7232	7263
		6069	6150	6243	6261			7278	7281	7530	7631
		6468	6492	6516	6684			7695	7956	7965	8091
		6852	6942	6972	7248			8195	8339	8384	8424
		7326	7335	7762	7795			8658	8661	8664	8726
		7902	8007	8097	8289			9186	9317	9404	9495
		8358	8391	8787	8808			9524	9600	9973	10123
		8856	8874	8940	9000			10403	10406		
		9072	9177	9195	9222	Fok I	(25)	655	1021	2200	3660
		9366	9504	9591	9813			3841	4128	4771	5015
		9825	9849	10050	10086			5819	6549	6624	6801
		10183						6891	6906	7128	7221
DpnII	(65)	355	361	368	1127			7335	7412	7502	8001
		1275	1313	1358	1627			8115	8202	8834	9656
		1869	3367	3442	3453			9921			
		3461	3539	3551	3656	Fse I	(1)	10141			
		3997	4015	4061	4319	Fsp I	(2)	3916	4939		
		4336	4372	4957	5924	Gdi II	(15)	700	1087	2641	4081
		6067	6148	6241	6259			6780	6879	8151	8187
		6466	6490	6514	6682			9631	9633	9852	10124
		6850	6940	6970	7246			10140	10402	10404	
		7324	7333	7760	7793	Gsu I	(6)	1071	1311	1637	1745
		7900	8005	8095	8287			3765	5862		
						Hae I	(16)	2816	2827	3279	6189

		7316	7676	7750	7978					Pvu I	(3)	371	4064	4960		
		7997	8018	8032	8149					Pvu II	(16)	602	2625	4989	6569	
		8191	8264	8501	8597							6590	6692	6803	7034	
		8749	8780	8819	8858							7697	7958	8093	8423	
		8906	9179	9214	9239							8663	8768	9776	10100	
		9635	9658	9899	10004					Rsa I	(34)	106	501	1057	1339	
		10066	10119	10138								1464	2181	4174	4850	
MspA1 I	(24)	602	2277	2625	3143							5099	5243	5268	5323	
		3388	4329	4795	4989							5356	6021	6081	6402	
		6172	6569	6590	6619							6864	7047	7551	7557	
		6692	6803	7034	7214							8442	8448	8475	8835	
		7697	7958	8093	8423							9009	9036	9054	9114	
		8663	8768	9776	10100							9399	9609	9717	9984	
Mun I	(1)	443										10014	10074			
Nae I	(7)	7088	8192	8265	8750					Sac I	(3)	2116	8248	10177		
		9659	10120	10139						Sap I	(2)	2423	2685			
Nar I	(1)	4917								Sau3A I	(65)	355	361	368	1127	
Nci I	(25)	254	657	1311	1941							1275	1313	1358	1627	
		2176	2177	3181	3877							1869	3367	3442	3453	
		4228	4729	4764	5709							3461	3539	3551	3656	
		5768	6194	6501	6697							3997	4015	4061	4319	
		7317	8019	8598	8780							4336	4372	4957	5924	
		8819	8859	9215	9240							6067	6148	6241	6259	
		9900										6466	6490	6514	6682	
Nco I	(3)	626	5384	5890								6850	6940	6970	7246	
Nde I	(4)	184	1542	4865	5258							7324	7333	7760	7793	
NgoM I	(7)	7086	8190	8263	8748							7900	8005	8095	8287	
		9657	10118	10137								8356	8389	8785	8806	
Nhe I	(1)	1806										8854	8872	8938	8998	
Nla III	(31)	23	630	864	894							9070	9175	9193	9220	
		1089	1284	1329	1381							9364	9502	9589	9811	
		1838	2292	2459	2805							9823	9847	10048	10084	
		3525	4016	4026	4104							10181				
		4140	4533	4638	4722					Sau96 I	(43)	8	800	1201	1284	
		5089	5328	5388	5894							1366	1904	1949	1964	
		5931	6491	8090	9137							1977	2032	3736	3815	
		9275	9515	10394								3832	4054	4670	4967	
Nla IV	(39)	335	357	380	455							5125	5300	5615	5755	
		507	665	1203	1699							5878	5903	5963	6061	
		1966	1979	2024	2181							6476	6482	6503	6746	
		2547	2833	2872	3644							6845	6950	6998	7196	
		3738	3779	3990	4580							7216	7364	7365	7655	
		4918	5099	5885	5965							8261	8480	8522	9236	
		6044	6088	6155	6354							9386	9584	9686		
		6504	6952	7106	7163					Sca I	(5)	4174	7557	9114	9609	
		7366	8990	9387	9388							9984				
		9749	9965	10261						ScrF I	(65)	254	657	673	798	
Not I	(1)	10403										910	985	1039	1311	
Nsp7524 I	(5)	2801	4718	5085	9271							1941	2019	2176	2177	
		10390										2541	2829	2950	2963	
NspB II	(24)	602	2277	2625	3143							3181	3877	4228	4729	
		3388	4329	4795	4989							4764	5036	5132	5307	
		6172	6569	6590	6619							5709	5768	5842	6033	
		6692	6803	7034	7214							6194	6324	6480	6501	
		7697	7958	8093	8423							6697	6744	6780	6831	
		8663	8768	9776	10100							6996	7113	7146	7254	
NspH I	(5)	2805	4722	5089	9275							7317	7376	7397	7433	
		10394										7779	7827	8019	8046	
Pal I	(66)	10	701	801	1090							8142	8154	8484	8598	
		1202	1368	1906	1951							8780	8811	8819	8859	
		2642	2816	2827	2845							9162	9215	9240	9720	
		3279	3737	3817	4084							9804	9852	9900	10143	
		4671	4969	5126	5301							10253				
		5616	5756	5964	6031					Sec I	(47)	520	626	656	796	
		6063	6189	6279	6387							959	983	1038	1939	
		6453	6477	6483	6505							2018	2028	2175	2238	
		6636	6715	6748	6783							2540	2961	5035	5384	
		6846	6882	6951	7366							5707	5890	5993	6184	
		7374	7647	8152	8190							6280	6478	6500	6631	
		8263	8298	8715	8728							6743	6784	6946	7165	
		8748	9165	9188	9238							7253	7375	7431	7600	
		9426	9447	9634	9651							7738	7777	7778	8140	
		9687	9723	9855	9924							8153	8407	8597	8710	
		10069	10118	10125	10137							9160	9214	9301	9421	
		10141	10405									9559	9754	10251		
PflM I	(2)	6308	8489							SfaN I	(25)	727	1003	1018	1117	
Ple I	(8)	347	1711	2344	3180							1963	2221	2897	3949	
		5656	6006	6323	9338							4142	4389	4750	4842	
Pml I	(1)	8798										4880	4918	6033	6141	
PpuM I	(5)	2032	6998	7196	9386							6780	7242	7356	8022	
		9584										8223	8376	9635	10068	
Psp1406 I	(3)	565	3920	4293								10309				
PspA I	(1)	2175								Sfc I	(10)	1791	3066	3257	3935	
Pst I	(5)	6802	8224	8428	8458							6798	8220	8424	8454	
		9670										9122	9666			

Sma I	(1)	2177				BspM II	T`CCGG,A	3	Bsr I	ACT,GG`	25
SnaB I	(1)	5364				BsrB I	GAG CGG	10	BsrD I	GCAATG, 8	3
Sph I	(3)	5089	9275	10394		BsrG I	T`GTAC,A	-	BSSH II	G`CGCG,C	5
Ssp I	(2)	2344	4498			BssS I	C`TCGT,G	10	Bst1107 I	GTA TAC	-
Sty I	(10)	626	2028	2238	5384	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	-
		5890	6280	6631	6946	BstN I	CC`W,GG	40	BstU I	CG CG	27
		8710	9559			BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	17
Taq I	(40)	211	261	677	971	Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	54
		998	1013	1142	1345	Cfr10 I	R`CCGG,Y	16	Cla I	AT`CG,AT	1
		1569	2339	2901	4345	Csp6 I	G`TA,C	34	Dde I	C`TNA,G	34
		5390	6166	6517	6595	Dpn I	GATC	65	DpnII	`GATC,	65
		6775	7063	7222	7327	Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	3
		7441	7483	7501	7723	Drd I	GACNN,NN`NNGTC	2	Dsa I	C`CRYG,G	7
		7732	7903	7936	8290	Eae I	Y`GGCC,R	19	Eag I	C`GGCC,G	2
		8359	8563	8698	9196	Ear I	CTCTTC 7/10	14	Eco47 III	AGC GCT	1
		9409	9529	9544	9619	Eco57 I	CTGAAG 21/19	15	Eco72 I	CAC GTG	1
		9817	10000	10087	10190	EcoN I	CCTNN`N,NNAGG	3	Eco109 I	RG`GNC,CY	10
Tfi I	(7)	23	1381	2379	2636	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	40
		2776	7390	9536		EcoR V	GAT ATC	2	Ehe I	GGC GCC	1
Tsp45 I	(10)	115	810	1299	1473	Esp I	GC`TNA,GC	5	Fnu4H I	GC`N,GC	86
		3950	4161	4737	5048	Fok I	GGATG 14/18	25	Fse I	GG,CCGG`CC	1
		7595	7682			Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	15
Tth111 I	(1)	2168				Gsu I	CTGGAG 21/19	6	Hae I	WGG CCW	16
Tth111 II	(12)	1110	1923	3390	3399	Hae II	R,GCGC`Y	6	Hae III	GG CC	66
		3429	7550	7873	8039	Hga I	GACGC 9/14	10	HgiA I	G,WGCW`C	11
		9769	9809	9908	10213	HgiE II	ACCNNNNNNGGT -1/134		Hha I	G,CG`C	39
Vsp I	(7)	76	1434	2444	2572	Hinc II	GTY RAC	-	Hind II	GTY RAC	-
		2631	3866	5827		Hind III	A`AGCT,T	-	Hinf I	G`ANT,C	21
Xba I	(1)	1996				HinI I	GR`CG,YC	10	HinP I	G`CG,C	39
Xcm I	(2)	9548	10031			Hpa I	GTT AAC	-	Hpa II	C`CG,G	59
Xho II	(17)	355	361	1127	1358	Hph I	GGTGA 12/11	21	Kas I	G`GCGC,C	1
		3442	3453	3539	3551	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	14
		4319	4336	6241	6259	Mae II	A`CG,T	25	Mae III	`GTNAC,	24
		7246	7333	8389	8806	Mbo I	`GATC,	65	Mbo II	GAAGA 12/11	46
		9175				Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	8
Xma I	(1)	2175				Mnl I	CCTC 10/10	80	Msc I	TGG CCA	6
Xma III	(2)	9632	10403			Mse I	T`TA,A	35	Msl I	CAYNN NNRTG	4
Xmn I	(5)	2407	2445	4293	8913	Msp I	C`CG,G	59	MspAl I	CMG CKG	24
		9141				Mun I	C`AATT,G	1	Nae I	GCC GGC	7
						Nar I	GG`CG,CC	1	Nci I	CC`s,GG	25
						Nco I	C`CATG,G	3	Nde I	CA`TA,TG	4
						NgoM I	G`CCGG,C	7	Nhe I	G`CTAG,C	1
						Nla III	,CATG`	31	Nla IV	GN NCC	39
						Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
						Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	5
						NspB II	CMG CKG	24	NspH I	R,CATG`Y	5
						PaeR7 I	C`TCGA,G	-	Pal I	GG CC	66
						PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	8
						Pme I	CTTT AAAC	-	Pml I	CAC GTG	1
						PpuM I	RG`GWC,CY	5	Psp1406 I	AA`CG,TT	3
						PspA I	C`CCGG,G	1	Pst I	C,TGCA`G	5
						Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	16
						Rsa I	GT AC	34	Rsr II	CG`GWC,CG	-
						Sac I	G,AGCT`C	3	Sac II	GC,GC`GG	-
						Sal I	G`TCGA,C	-	Sap I	GGTCTTC 8/11	2
						Sau3A I	`GATC,	65	Sau96 I	G`GNC,C	43
						Sca I	AGT ACT	5	ScrF I	CC`N,GG	65
						Sec I	C`CNNG,G	47	SfaN I	GCATC 9/13	25
						Sfc I	C`TRYA,G	10	Sfi I	GGCCN,NNN`NGGCC	-
						Sma I	CCC GGG	1	SnaB I	TAC GTA	1
						Spe I	A`CTAG,T	-	Sph I	G,CATG`C	3
						Spl I	C`GTAC,G	2	Srf I	GCCC GGGC	-
						Ssp I	AAT ATT	-	Stu I	AGG CCT	-
						Sty I	C`CWWG,G	10	Taq I	T`CG,A	40
						Tfi I	G`AWT,C	7	Tsp45 I	`GTSAC,	10
						Tth111 I	GACN`N,NGTC	1	Tth111 II	CAARCA 16/14	12
						Vsp I	AT`TA,AT	7	Xba I	T`CTAG,A	1
						Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNTGG2	-
						Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	17
						Xma I	C`CCGG,G	1	Xma III	C`GGCC,G	2

Site usage in pCas9gG:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	-
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	116
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	3	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	66
Alw I	GGATC 8/9	27	AlwN I	CAG,NNN`CTG	8
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	7	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	6	Ava II	G`GWC,C	16
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RGCY`C	9
Bbe I	G,CGGC`C	1	Bbs I	GAAGAC 8/12	2
Bbv I	GCAGC 13/17	23	Bbv II	GAAGAC 7/11	2
Bcl I	T`GATC,A	8	Bcn I	CC,S`GG	25
Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7
Bgl II	A`GATC,T	2	Blp I	GC`TNA,GC	5
Bpm I	CTGGAG 22/20	6	Bsa I	GGTCTC 7/11	3
BsaA I	YAC GTR	7	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	10	BsaJ I	C`CNNG,G	47
BsaW I	W`CCGG,W	13	BseR I	GAGGAG 16/14	3
Bsg I	GTGCAG 22/20	9	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	11	BsiHKA I	G,WGCW`C	11
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1
BsmA I	GTCTC`/9	13	BsmB I	CGTCTC 7/11	2
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	86
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	4
BspH I	T`CATG,A	5	BspM I	ACCTGC 10/14	7