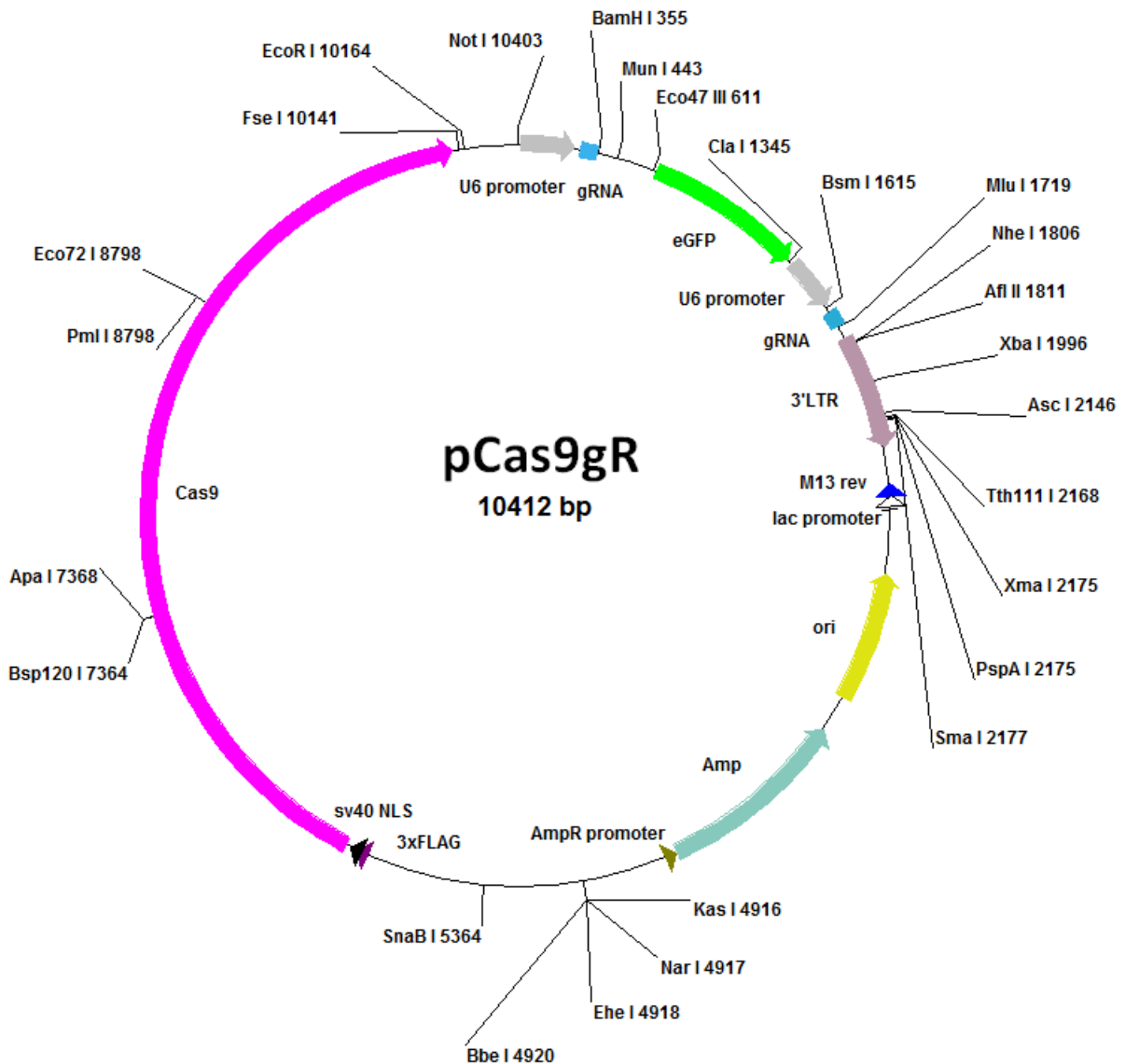


Vector: pCas9gR (Cas9 and sgRNA vector; eGFP w/o PA signal)

Antibiotic Selection: Amp

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

Date of Construction: March, 2016



pCas9gR Full-Length Sequence

aaacGAGGGCCTATTTCCCATGATTCCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAATTGGAATTAATTTGACTGTAAAC
ACAAAGATATTAGTACAAAATACGTGACGTAGAAAAGTAATAATTTCTTGGGTAGTTTGCAGTTTTAAAATATGTTTTAAAATGGACTATC
ATATGCTTACCGTAACTTGAAAGTATTTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGAcgaaacaccggGTCTTCgaGAAGACctGT
TTTAGAGCTAGAAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTggatccggatc
tgcgatCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACCGGTG
CCTAGAGAAGGTGGCGCGGGTAAACTGGGAAAGTGTATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCGGTGAACGTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGtCTAGCGCTACCGGTGCCACCatggtgagcaa
ggcgaggagctgttcaccggggtggtgcccatacctggtcgagctggacggcgacgtaaacggccacaagttcagcgtgtccggcgagggc
gagggcgatgccacctacggcaagctgacctgaagttcatctgcaccaccggcaagctgcccgtgccctggcccaccctcgtagaccacc
tgacctacggcgtgcagtgcttcagccgctaccccgaccacatgaagcagcagcacttctcaagtccgcatgcccgaaggctacgtcca
ggagcgcaccatcttcttcaaggacgacggcaactacaagaccgcgcccaggtgaagttcgagggcgacaccctggtgaaccgcatcgag
ctgaagggcatcgacttcaaggaggacggcaacatcctggggcacaagctggagtacaactacaacagccacaacgtctatatcatggccg
acaagcagaagaacggcatcaaggtgaactcaagatccgccacaacatcgaggacggcagcgtgcagctcgccgaccactaccagcagaa
caccatcgccgacggccccgtgctgctgcccgaacaaccactacctgagcaccagctccgcccgtgagcaagaccccaacgagaagcgc
gatcacatggtcctgctggagttcgtgaccgcccgggatcactctcgcatggacgagctgtaactaatcgatttaattaaatgatctGAG
GGCCTATTTCCCATGATTCCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAATTGGAATTAATTTGACTGTAAACACAAAGA
TATTAGTACAAAATACGTGACGTAGAAAAGTAATAATTTCTTGGGTAGTTTGCAGTTTTAAAATATGTTTTAAAATGGACTATCATATGCT
TACCGTAACTTGAAAGTATTTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGAcgaaaGAATGCGACTGGAGTTGCAGATCACCGGTT
TTAGAGCTAGAAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTaccggtttaa
aaCGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACG
CCATTTTGC AAGGCATGAAAATACATAACTGAGAATAGAGAAGTTTCAGATCAAGGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAC
AGGATATCTGTGGTAAGCAGTTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCC GCCCTCAGCAGTTTCTAGAGA
ACCATCAGATGTTTCCAGGTTGCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTT
GCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCCACAACCCCTCACTCGGCGCGCCAGTCTCCGATAGACTGCGTCCGCCGGGTACCC
GTGTATCCAATAAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCA
GCGGGGTCTTTCATGGGTAAACAGTTTCTTGAAGTTGGAGAACAACATTTCTGAGGGTAGGAGTTCGAATATTAAGTAATCCTGACTCAATTA
GCCACTGTTTTGAATCCACATACTCCAATACTCCTGAAATAGTTTCATTATGGACAGCGCAGAAGAGCTGGGGAGAATTAATTCGTAATCAT
GGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATCCACACAACATACGAGCCGGAAGCATAAAAGTGTAAAGCCTGGGGTGC
CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCATTAATGAATC
GGCCAACGCGCGGGGAGAGCGGTTTGCATTTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGCTTCCGGTGC
GAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCA
AAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC
TTACCGGATACCTGTCCGCTTCTCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCT
TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCGCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTA
AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT
GGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG
ATCCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT
TTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTACCT
AGATCCTTTTAAATAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTGGTCTGACAGTTACCAATGCTTAATCAGTGA
GGCACCTATCTCAGCGATCTGCTATTTCTGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCA
TCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGC
GCAGAAGTGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTT
GCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTACGCTCCGTTCCCAACGATCAAGG
CGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCTCCGATCGTTGTGCAAGTAAGTTGGCCGAGTGTAT
CACTCATGGTTATGGCAGCACTGCATAATCTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTC
ATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAATTTAAAAGTG
CTCATCATTTGAAAAACGTTCTTCCGGGGCGAAAACCTCAAGGATCTTACCCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCA
ACTGATCTTACGATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAAATAAGGGCGAC
ACGAAATGTTGAATACTCATACTCTTCTTTTCAATATTAATGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAA
TGTATTTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGCTAAGAAACCATTATTAATCATGACAT
TAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCGCTCTCGCGCTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGA
GACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCTCAGCGGGTGTGGCGGGTGTGGGGCTGGCTT
AACTATGCCGCATCAGAGCAGATTGACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCA
GGCGCCATTCGCCATTACGGTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATG
TGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAAAACGACGGCGAAGGAATGGTGCATGcACTAGAG

		5501	6594	7248	8151					5087	5128	5303	5572
		9327								5635	5642	5658	5704
BsiE I	(11)	371	620	2717	3141					5746	6617	6844	7088
		4064	4213	4960	6125					7109	7267	7545	7618
		9635	10004	10406						7635	7989	8166	8192
BsiHKA I	(11)	1237	2116	3119	4280					8265	8750	9084	9273
		4365	4862	5849	6991					9649	9659	9725	9922
		8176	8248	10177						10120	10139	10177	10211
Bsm I	(1)	1615								10388	10392		
BsmA I	(13)	1761	1884	2231	2252	Cfr10 I	(16)	450	615	778	3774		
		3756	4530	4683	4727					5880	6124	7086	7977
		5909	8757	9193	10072					8190	8263	8500	8748
		10098								9657	10065	10118	10137
BsmB I	(2)	4684	4726			Cla I	(1)	1345					
BsmF I	(10)	399	1950	1963	5199	Csp6 I	(34)	105	500	1056	1338		
		5350	5764	5985	8034					1463	2180	4173	4849
		8338	9399							5098	5242	5267	5322
BsoF I	(86)	589	787	846	868					5355	6020	6080	6401
		1152	1159	1210	1213					6863	7046	7550	7556
		1307	2626	2707	2725					8441	8447	8474	8834
		2728	2846	3001	3144					9008	9035	9053	9113
		3209	3212	3418	3746					9398	9608	9716	9983
		4085	4112	4207	4436					10013	10073		
		4723	4832	4936	5009	Dde I	(34)	1231	1249	1362	1851		
		5483	5549	5552	5555					1945	1986	2255	2326
		5568	5602	5605	5608					3076	3485	3651	4191
		5611	5614	5638	5654					4617	4852	5782	6420
		5661	5687	5690	5700					6654	6738	6804	6912
		6007	6173	6351	6462					6924	6957	7039	7626
		6620	6693	6801	6883					7992	8536	8730	8830
		7026	7029	7032	7035					9013	9267	9391	9604
		7203	7212	7232	7263					10096	10313		
		7278	7281	7530	7631	Dpn I	(65)	357	363	370	1129		
		7695	7956	7965	8091					1277	1315	1360	1629
		8195	8339	8384	8424					1871	3369	3444	3455
		8658	8661	8664	8726					3463	3541	3553	3658
		9186	9317	9404	9495					3999	4017	4063	4321
		9524	9600	9973	10123					4338	4374	4959	5926
		10403	10406							6069	6150	6243	6261
Bsp120 I	(1)	7364								6468	6492	6516	6684
Bsp1286 I	(4)	1237	5849	6991	8176					6852	6942	6972	7248
BspH I	(5)	3521	4529	4634	5927					7326	7335	7762	7795
		9133								7902	8007	8097	8289
BspM I	(7)	5858	6466	6847	7207					8358	8391	8787	8808
		7519	7666	8461						8856	8874	8940	9000
BspM II	(3)	358	8905	9178						9072	9177	9195	9222
Bsr I	(25)	485	506	1240	1620					9366	9504	9591	9813
		2152	2602	3208	3221					9825	9849	10050	10086
		3335	3741	3859	3902					10183			
		4169	4341	5047	5320	DpnII	(65)	355	361	368	1127		
		6312	6435	6861	8493					1275	1313	1358	1627
		8657	8742	8919	9386					1869	3367	3442	3453
		9687								3461	3539	3551	3656
BsrB I	(10)	2493	2734	4535	5567					3997	4015	4061	4319
		5681	5744	6350	7487					4336	4372	4957	5924
		7630	10402							6067	6148	6241	6259
BsrD I	(3)	3755	3929	8176						6466	6490	6514	6682
BssH II	(5)	2095	2146	5570	5633					6850	6940	6970	7246
		5656								7324	7333	7760	7793
BssS I	(10)	808	2974	4358	4665					7900	8005	8095	8287
		6345	6393	7020	7176					8356	8389	8785	8806
		8169	8247							8854	8872	8938	8998
BstN I	(40)	673	798	910	985					9070	9175	9193	9220
		1039	2019	2541	2829					9364	9502	9589	9811
		2950	2963	5036	5132					9823	9847	10048	10084
		5307	5842	6033	6324					10181			
		6480	6744	6780	6831	Dra I	(8)	157	170	1515	1528		
		6996	7113	7146	7254					3560	3579	4271	8120
		7376	7397	7433	7779	Dra III	(3)	7946	8408	9875			
		7827	8046	8142	8154	Drd I	(2)	2909	4778				
		8484	8811	9162	9720	Dsa I	(7)	626	5384	5890	5993		
		9804	9852	10143	10253					7738	8407	9421	
BstU I	(27)	472	956	1274	1634	Eae I	(19)	699	1088	2640	4082		
		1721	2095	2097	2148					6277	6781	6880	7372
		2648	2650	2848	3429					8150	8188	8296	9163
		3759	4252	4584	4684					9445	9632	9721	9853
		4686	4789	5572	5635					10123	10139	10403	
		5637	5658	5697	5725	Eag I	(2)	9632	10403				
		8341	8935	10408		Ear I	(14)	2423	2685	4489	4977		
BstX I	(2)	6053	6623							6195	6307	6325	7111
BstY I	(17)	355	361	1127	1358					8356	8620	9474	9633
		3442	3453	3539	3551					10002	10371		
		4319	4336	6241	6259	Eco47 III	(1)	611					
		7246	7333	8389	8806	Eco57 I	(15)	780	826	1023	3348		
		9175								4362	6218	6249	7325
Cac8 I	(54)	751	784	832	1156					7979	8075	8567	8900
		1163	1804	1808	2097					9306	9497	9761	
		2148	2594	2623	2732	Eco72 I	(1)	8798					
		2818	2855	3415	3806	EcoN I	(3)	461	6516	6783			
		4819	4967	4987	4991	EcoO109 I	(10)	8	1366	2032	4670		

		6950	6998	7196	7365					4686	4789	4919	4940
		9386	9584							5073	5572	5574	5635
EcoR I	(1)	10164								5637	5658	5660	5699
EcoR II	(40)	671	796	908	983					6963	7464	8935	
		1037	2017	2539	2827			Hinf I	(21)	23	339	1381	1703
		2948	2961	5034	5130					2336	2358	2379	2636
		5305	5840	6031	6322					2701	2776	3172	3689
		6478	6742	6778	6829					5648	5998	6315	7390
		6994	7111	7144	7252					7734	8556	8814	9330
		7374	7395	7431	7777					9536			
		7825	8044	8140	8152			HinI I	(10)	4231	4613	4917	5164
		8482	8809	9160	9718					5199	5282	6628	6901
		9802	9850	10141	10251					8965	10039		
EcoR V	(2)	1917	7862					HinP I	(39)	398	470	610	915
Ehe I	(1)	4918								956	1272	2095	2097
Esp I	(5)	5782	6804	6912	7992					2146	2148	2423	2583
		9267								2648	2676	2709	2979
Fnu4H I	(86)	589	787	846	868					3046	3146	3320	3429
		1152	1159	1210	1213					3822	3915	4252	4584
		1307	2626	2707	2725					4684	4787	4917	4938
		2728	2846	3001	3144					5071	5570	5572	5633
		3209	3212	3418	3746					5635	5656	5658	5697
		4085	4112	4207	4436					6961	7462	8933	
		4723	4832	4936	5009			Hpa II	(59)	253	359	376	451
		5483	5549	5552	5555					616	656	719	779
		5568	5602	5605	5608					1310	1941	2176	2519
		5611	5614	5638	5654					3008	3155	3181	3371
		5661	5687	5690	5700					3775	3809	3876	3986
		6007	6173	6351	6462					4228	4729	4763	5709
		6620	6693	6801	6883					5767	5881	6125	6194
		7026	7029	7032	7035					6239	6500	6697	7087
		7203	7212	7232	7263					7316	7676	7750	7978
		7278	7281	7530	7631					7997	8018	8032	8149
		7695	7956	7965	8091					8191	8264	8501	8597
		8195	8339	8384	8424					8749	8780	8819	8858
		8658	8661	8664	8726					8906	9179	9214	9239
		9186	9317	9404	9495					9635	9658	9899	10004
		9524	9600	9973	10123					10066	10119	10138	
		10403	10406					Hph I	(21)	641	646	974	998
Fok I	(25)	655	1021	2200	3660					1127	3538	3765	4179
		3841	4128	4771	5015					4387	4420	4704	4713
		5819	6549	6624	6801					5405	5750	6063	6936
		6891	6906	7128	7221					7419	7554	8868	9498
		7335	7412	7502	8001					10056			
		8115	8202	8834	9656			Kas I	(1)	4916			
		9921						Kpn I	(2)	2183	5101		
Fse I	(1)	10141						Mae I	(14)	282	307	458	607
Fsp I	(2)	3916	4939							1646	1671	1807	1997
Gdi II	(15)	700	1087	2641	4081					3296	3549	3884	5092
		6780	6879	8151	8187					10170	10203		
		9631	9633	9852	10124			Mae II	(25)	114	119	565	692
		10140	10402	10404						905	1076	1472	1477
Gsu I	(6)	1071	1311	1637	1745					3504	3920	4293	4613
		3765	5862							5055	5164	5199	5282
Hae I	(16)	2816	2827	3279	6189					5363	5404	6547	7360
		6279	6387	6636	6715					7594	8476	8614	8797
		7374	7647	8298	9165					9058			
		9426	9447	9651	9723			Mae III	(24)	115	194	810	1299
Hae II	(6)	613	2679	3049	4920					1473	1552	1815	2293
		6964	7465							3157	3220	3336	3619
Hae III	(66)	10	701	801	1090					3950	4008	4161	4349
		1202	1368	1906	1951					4737	5028	5048	5103
		2642	2816	2827	2845					5172	5726	7595	7682
		3279	3737	3817	4084			Mbo I	(65)	355	361	368	1127
		4671	4969	5126	5301					1275	1313	1358	1627
		5616	5756	5964	6031					1869	3367	3442	3453
		6063	6189	6279	6387					3461	3539	3551	3656
		6453	6477	6483	6505					3997	4015	4061	4319
		6636	6715	6748	6783					4336	4372	4957	5924
		6846	6882	6951	7366					6067	6148	6241	6259
		7374	7647	8152	8190					6466	6490	6514	6682
		8263	8298	8715	8728					6850	6940	6970	7246
		8748	9165	9188	9238					7324	7333	7760	7793
		9426	9447	9634	9651					7900	8005	8095	8287
		9687	9723	9855	9924					8356	8389	8785	8806
		10069	10118	10125	10137					8854	8872	8938	8998
		10141	10405							9070	9175	9193	9220
Hga I	(10)	2159	2911	3489	4221					9364	9502	9589	9811
		4779	6635	6908	8972					9823	9847	10048	10084
		9866	10046							10181			
HgiA I	(11)	1237	2116	3119	4280			Mbo II	(46)	251	276	871	916
		4365	4862	5849	6991					919	1112	2439	2673
		8176	8248	10177						3462	3535	4290	4368
HgiE II	(4)	3380	4860	10001	10248					4477	4965	5983	6151
Hha I	(39)	400	472	612	917					6211	6225	6228	6244
		958	1274	2097	2099					6255	6291	6323	6341
		2148	2150	2425	2585					6354	6715	6718	7053
		2650	2678	2711	2981					7127	7298	7342	7769
		3048	3148	3322	3431					7868	8341	8372	8636
		3824	3917	4254	4586					8647	8650	8656	9076

		9111	9490	9544	9649			7366	8990	9387	9388
		10018	10387					9749	9965	10261	
Mlu I	(1)	1719				Not I	(1)	10403			
Mme I	(8)	2240	2292	3015	3199	Nsp7524 I	(5)	2801	4718	5085	9271
		5857	6921	8085	8532			10390			
Mnl I	(80)	-1	426	515	636	NspB II	(24)	602	2277	2625	3143
		717	723	816	954			3388	4329	4795	4989
		966	1017	1137	1357			6172	6569	6590	6619
		1994	2146	2165	2210			6692	6803	7034	7214
		2237	2261	2321	2650			7697	7958	8093	8423
		2699	2909	2982	3233			8663	8768	9776	10100
		3633	3714	3860	4066	NspH I	(5)	2805	4722	5089	9275
		4661	4719	4979	5088			10394			
		5385	5444	5511	5528	Pal I	(66)	10	701	801	1090
		5536	5591	5702	5773			1202	1368	1906	1951
		5783	6179	6326	6374			2642	2816	2827	2845
		6512	6590	6779	6973			3279	3737	3817	4084
		7160	7187	7377	7409			4671	4969	5126	5301
		7436	7595	7697	7783			5616	5756	5964	6031
		7829	7838	7880	7898			6063	6189	6279	6387
		8117	8357	8544	8621			6453	6477	6483	6505
		8629	8715	9198	9296			6636	6715	6748	6783
		9340	9634	9661	9703			6846	6882	6951	7366
		9749	10003	10022	10098			7374	7647	8152	8190
		10197	10239	10285	10360			8263	8298	8715	8728
Msc I	(6)	6279	7374	8298	9165			8748	9165	9188	9238
		9447	9723					9426	9447	9634	9651
Mse I	(35)	76	156	169	296			9687	9723	9855	9924
		1350	1354	1434	1514			10069	10118	10125	10137
		1527	1660	1725	1729			10141	10405		
		1812	2346	2444	2572	PflM I	(2)	6308	8489		
		2631	3507	3559	3564	Ple I	(8)	347	1711	2344	3180
		3578	3631	3866	3905			5656	6006	6323	9338
		4270	4642	4823	5020	Pml I	(1)	8798			
		5469	5801	5827	5834	PpuM I	(5)	2032	6998	7196	9386
		8119	8206	10412				9584			
Msl I	(4)	1114	3946	4105	7680	Psp1406 I	(3)	565	3920	4293	
Msp I	(59)	253	359	376	451	PspA I	(1)	2175			
		616	656	719	779	Pst I	(5)	6802	8224	8428	8458
		1310	1941	2176	2519			9670			
		3008	3155	3181	3371	Pvu I	(3)	371	4064	4960	
		3775	3809	3876	3986	Pvu II	(16)	602	2625	4989	6569
		4228	4729	4763	5709			6590	6692	6803	7034
		5767	5881	6125	6194			7697	7958	8093	8423
		6239	6500	6697	7087			8663	8768	9776	10100
		7316	7676	7750	7978	Rsa I	(34)	106	501	1057	1339
		7997	8018	8032	8149			1464	2181	4174	4850
		8191	8264	8501	8597			5099	5243	5268	5323
		8749	8780	8819	8858			5356	6021	6081	6402
		8906	9179	9214	9239			6864	7047	7551	7557
		9635	9658	9899	10004			8442	8448	8475	8835
		10066	10119	10138				9009	9036	9054	9114
MspA1 I	(24)	602	2277	2625	3143			9399	9609	9717	9984
		3388	4329	4795	4989			10014	10074		
		6172	6569	6590	6619	Sac I	(3)	2116	8248	10177	
		6692	6803	7034	7214	Sap I	(2)	2423	2685		
		7697	7958	8093	8423	Sau3A I	(65)	355	361	368	1127
		8663	8768	9776	10100			1275	1313	1358	1627
Mun I	(1)	443						1869	3367	3442	3453
Nae I	(7)	7088	8192	8265	8750			3461	3539	3551	3656
		9659	10120	10139				3997	4015	4061	4319
Nar I	(1)	4917						4336	4372	4957	5924
Nci I	(25)	254	657	1311	1941			6067	6148	6241	6259
		2176	2177	3181	3877			6466	6490	6514	6682
		4228	4729	4764	5709			6850	6940	6970	7246
		5768	6194	6501	6697			7324	7333	7760	7793
		7317	8019	8598	8780			7900	8005	8095	8287
		8819	8859	9215	9240			8356	8389	8785	8806
		9900						8854	8872	8938	8998
Nco I	(3)	626	5384	5890				9070	9175	9193	9220
Nde I	(4)	184	1542	4865	5258			9364	9502	9589	9811
NgoM I	(7)	7086	8190	8263	8748			9823	9847	10048	10084
		9657	10118	10137				10181			
Nhe I	(1)	1806				Sau96 I	(43)	8	800	1201	1284
Nla III	(31)	23	630	864	894			1366	1904	1949	1964
		1089	1284	1329	1381			1977	2032	3736	3815
		1838	2292	2459	2805			3832	4054	4670	4967
		3525	4016	4026	4104			5125	5300	5615	5755
		4140	4533	4638	4722			5878	5903	5963	6061
		5089	5328	5388	5894			6476	6482	6503	6746
		5931	6491	8090	9137			6845	6950	6998	7196
		9275	9515	10394				7216	7364	7365	7655
Nla IV	(39)	335	357	380	455			8261	8480	8522	9236
		507	665	1203	1699			9386	9584	9686	
		1966	1979	2024	2181	Sca I	(5)	4174	7557	9114	9609
		2547	2833	2872	3644			9984			
		3738	3779	3990	4580	ScrF I	(65)	254	657	673	798
		4918	5099	5885	5965			910	985	1039	1311
		6044	6088	6155	6354			1941	2019	2176	2177
		6504	6952	7106	7163			2541	2829	2950	2963

	3181	3877	4228	4729	Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	9	
	4764	5036	5132	5307	Ebe I	G,GC`C	1	Bbs I	GAAGAC 8/12	2	
	5709	5768	5842	6033	Bbv I	GCAGC 13/17	23	Bbv II	GAAGAC 7/11	2	
	6194	6324	6480	6501	Bcl I	T`GATC,A	8	Bcn I	CC,S`GG	25	
	6697	6744	6780	6831	Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7	
	6996	7113	7146	7254	Bgl II	A`GATC,T	2	Blp I	GC`TNA,GC	5	
	7317	7376	7397	7433	Bpm I	CTGGAG 22/20	6	Bsa I	GGTCTC 7/11	3	
	7779	7827	8019	8046	BsaA I	YAC GTR	7	BsaB I	GATNN NNATC	2	
	8142	8154	8484	8598	BsaH I	GR`CG,YC	10	BsaJ I	C`CNNG,G	47	
	8780	8811	8819	8859	BsaW I	W`CCGG,W	13	BseR I	GAGGAG 16/14	3	
	9162	9215	9240	9720	Bsg I	GTGCAG 22/20	9	BsiC I	TT`CG,AA	-	
	9804	9852	9900	10143	BsiE I	CG,RY`CG	11	BsiHKA I	G,WGCW`C	11	
	10253				BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1	
Sec I	(47)	520	626	656	796	BsmA I	GTCTC`/9	13	BsmB I	CGTCTC 7/11	2
	959	983	1038	1939	BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	86	
	2018	2028	2175	2238	Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	4	
	2540	2961	5035	5384	BspH I	T`CATG,A	5	BspM I	ACCTGC 10/14	7	
	5707	5890	5993	6184	BspM II	T`CCGG,A	3	Bsr I	ACT,GG`	25	
	6280	6478	6500	6631	BsrB I	GAG CGG	10	BsrD I	GCAATG, 8	3	
	6743	6784	6946	7165	BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	5	
	7253	7375	7431	7600	BssS I	C`TCGT,G	10	Bst1107 I	GTA TAC	-	
	7738	7777	7778	8140	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	-	
	8153	8407	8597	8710	BstN I	CC`W,GG	40	BstU I	CG CG	27	
	9160	9214	9301	9421	BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	17	
	9559	9754	10251		Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	54	
SfaN I	(25)	727	1003	1018	1117	Cfr10 I	R`CCGG,Y	16	Cla I	AT`CG,AT	1
	1963	2221	2897	3949	Csp6 I	G`TA,C	34	Dde I	C`TNA,G	34	
	4142	4389	4750	4842	Dpn I	GA TC	65	DpnII	`GATC,	65	
	4880	4918	6033	6141	Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	3	
	6780	7242	7356	8022	Drd I	GACNN,NN`NNGTC	2	Dsa I	C`CRYG,G	7	
	8223	8376	9635	10068	Eae I	Y`GGCC,R	19	Eag I	C`GGCC,G	2	
	10309				Ear I	CTCTTC 7/10	14	Eco47 III	AGC GCT	1	
Sfc I	(10)	1791	3066	3257	3935	Eco57 I	CTGAAG 21/19	15	Eco72 I	CAC GTG	1
	6798	8220	8424	8454	EcoN I	CCTNN`N,NNAGG	3	Eco109 I	RG`GNC,CY	10	
	9122	9666			EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	40	
Sma I	(1)	2177			EcoR V	GAT ATC	2	Ehe I	GGC GCC	1	
SnaB I	(1)	5364			Esp I	GC`TNA,GC	5	Fnu4H I	GC`N,GC	86	
Sph I	(3)	5089	9275	10394	Fok I	GGATG 14/18	25	Fse I	GG,CCGG`CC	1	
Ssp I	(2)	2344	4498		Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	15	
Sty I	(10)	626	2028	2238	5384	Gsu I	CTGGAG 21/19	6	Hae I	WGG CCW	16
	5890	6280	6631	6946	Hae II	R,GC`G`Y	6	Hae III	GG CC	66	
	8710	9559			Hga I	GACGC 9/14	10	HgiA I	G,WGCW`C	11	
Taq I	(40)	211	261	677	971	HgiE II	ACNNNNNNNGGT -1/134	Hha I	G,CG`C	39	
	998	1013	1142	1345	HinC II	GTY RAC	-	Hind II	GTY RAC	-	
	1569	2339	2901	4345	Hind III	A`AGCT,T	-	Hinf I	G`ANT,C	21	
	5390	6166	6517	6595	HinI I	GR`CG,YC	10	HinP I	G`CG,C	39	
	6775	7063	7222	7327	Hpa I	GTT AAC	-	Hpa II	C`CG,G	59	
	7441	7483	7501	7723	Hph I	GGTGA 12/11	21	Kas I	G`GCGC,C	1	
	7732	7903	7936	8290	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	14	
	8359	8563	8698	9196	Mae II	A`CG,T	25	Mae III	`GTNAC,	24	
	9409	9529	9544	9619	Mbo I	`GATC,	65	Mbo II	GAAGA 12/11	46	
	9817	10000	10087	10190	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	8	
Tfi I	(7)	23	1381	2379	2636	Mnl I	CCTC 10/10	80	Msc I	TGG CCA	6
	2776	7390	9536		Mse I	T`TA,A	35	Msl I	CAYNN NNRTG	4	
Tsp45 I	(10)	115	810	1299	1473	Msp I	C`CG,G	59	MspA1 I	CMG CKG	24
	3950	4161	4737	5048	Mun I	C`AATT,G	1	Nae I	GCC GGC	7	
	7595	7682			Nar I	GG`CG,CC	1	Nci I	CC`s,GG	25	
Tth111 I	(1)	2168			Nco I	C`CATG,G	3	Nde I	CA`TA,TG	4	
Tth111 II	(12)	1110	1923	3390	3399	NgoM I	G`CCGG,C	7	Nhe I	G`CTAG,C	1
	3429	7550	7873	8039	Nla III	,CATG`	31	Nla IV	GCN NCC	39	
	9769	9809	9908	10213	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-	
Vsp I	(7)	76	1434	2444	2572	Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	5
	2631	3866	5827		NspB II	CMG CKG	24	NspH I	R,CATG`Y	5	
Xba I	(1)	1996			PaeR7 I	C`TCGA,G	-	Pal I	GG CC	66	
Xcm I	(2)	9548	10031		PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	8	
Xho II	(17)	355	361	1127	1358	Pme I	CTTT AAAC	-	Pml I	CAC GTG	1
	3442	3453	3539	3551	PpuM I	RG`GWC,CY	5	Psp1406 I	AA`CG,TT	3	
	4319	4336	6241	6259	PspA I	C`CCGG,G	1	Pst I	C,TGCA`G	5	
	7246	7333	8389	8806	Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	16	
	9175				Rsa I	GT AC	34	Rsr II	CG`GWC,CG	-	
Xma I	(1)	2175			Sac I	G,AGCT`C	3	Sac II	CC,GC`GG	-	
Xma III	(2)	9632	10403		Sal I	G`TCGA,C	-	Sap I	GCTCTTC 8/11	2	
Xmn I	(5)	2407	2445	4293	8913	Sau3A I	`GATC,	65	Sau96 I	G`GNC,C	43
	9141				Sca I	AGT ACT	5	SerF 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	-	Srf I	GCCC GGGC	-	
					Ssp I	AAT ATT	2	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`NNNNTGG2	-	
					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	Acc 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						