

**Table S1.** List of genome editing (GE) studies among the nine major crop species using tissue culture. The genotypes, explants, SDNs, delivery systems and gene targets, mutation rates and study references are listed in separate columns. If nothing else is stated under the mutation rates, they are based on the rate of regenerated plants. The list is based on GE studies from January 2011 until June 2022.

Species	Genotype	Explant	SDN	Delivery systems	Target gene(s)	Mutation rate (%)	References
Barley	Compass, Flinders, Scope, Spartacus, Golden Promise	Anther culture	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvPDS</i>	53	[1]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvPM19-1, HvPM19-3</i>	10-23	[2]
	Igri	Microspore	TALENs	<i>Agrobacterium</i>	<i>GFP</i>	22	[3]
	Golden Promise	Immature embryo	TALENs	<i>Agrobacterium</i>	<i>HvPAPhy_a</i>	16-31	[4]
	Igri	Immature embryo	TALENs-HDR	Biolistic	<i>YFP, GFP</i>	2-3	[5]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvCMF7</i>	nd	[6]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i> Biolistic	<i>ENGase</i>	78	[7]
	Golden Promise	Immature embryo	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	<i>HORVU4Hr1G061310</i>	50-89	[8]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvMPK6</i>	0.14	[9]
	Igri	Microspore	CRISPR/Cas9	<i>Agrobacterium</i>	<i>EIF4E</i>	nd	[10]
	Igri	Microspore	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PDIL5-1, EIF4E, QSD1</i>	nd	[11]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvCKX1, HvCKX3</i>	21-88	[12]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvCsIF6, HvCsIH1, HvCsIF3, HvCsIF9</i>	4.7-35.3	[13]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvHPT, HvHGGT</i>	50-65	[14]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvCOMT1</i>	42	[15]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>WDV1, WDV2</i>	nd	[16]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>D hordein</i>	0.39	[17]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>B-1,3-glucanases</i>	nd	[18]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PTST1, GBSS1a</i>	1.74-3.33	[19]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvITPK1</i>	46	[20]

	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>EGT2</i>	nd	[21]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MORC1, MORC6a</i>	80-90 58	[22]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvCKX1</i>	92.8	[23]
	Golden Promise	Immature embryo	CRISPR/Cas9	Biolistic	<i>HvMORC1</i>	70-100	[24]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvLFY</i>	nd	[25]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvAP2, HvMADS29</i>	nd	[26]
	Golden Promise, and 5 commercial barley cultivars	nd	CRISPR/Cas9	nd	<i>elF4E</i>	nd	[27]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>D-hordein</i>	14-25	[28]
	Golden Promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Qsd1, Qsd2</i>	30-42.9	[29]
	Golden promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CRT, PDI, IPI, GST, HSP70, HSP26, HSP16.9</i>	nd	[30]
	Golden Promise, Spartacus, Vlamingh, Compass	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvARE1</i>	50-90	[31]
	Golden promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HvTB2</i>	nd	[32]
	Golden promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HVP10</i>	nd	[33]
	Golden promise	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SSIIa</i>	5.6-15.4	[34]
	Golden Promise	Embryogenic callus	CRISPR/Cas9	Biolistic	<i>HvPIN9</i>	86.7	[35]
	Golden promise	Immature embryo	CRISPR/Cas9 TALENs	<i>Agrobacterium</i>	<i>HvPAPhy_a</i>	44 43	[36]
Wheat	Kenong199 Bobwhite	Immature embryo	TALENs	Biolistic	<i>TaMLO-A1, TaMLO-B1, TaMLO-D1</i>	3.4-6	[37]
	Kenong 199	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaEDR1</i>	nd	[38]
	Kenong 199	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaGW2, TaGASR7</i>	2.2-4.4	[39]
	BW208,THA53, Don Pedro	Immature scutella	CRISPR/Cas9	Biolistic	<i>α-gliadin</i>	5.18	[40]
	Kenong199, Bobwhite	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaGASR7, TaDEP1, TaNAC2, TaPIN1, TaLOX2, TdGASR7, TaGW2</i>	1.1-9.5	[41]

	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaQsd1</i>	0.88	[42]
	Zhengmai7698	Callus	CRISPR/Cas9	Biolistic	<i>TaGASR7</i>	nd	[43]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPDS</i>	11-17	[44]
	Bobwhite	Immature embryo	Nickases	Biolistic	<i>TaMLO</i>	nd	[45]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaCKX2-1, TaGLW7, TaGW2, TaGW8</i>	10	[46]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPDS</i>	83	[47]
	Kenong199, YZ814	Immature embryo	CRISPR/Cas9 IVTs	Biolistic	<i>GASR7, LOX2 and CER9</i>	1.8	[48]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PINB, WAXY, DA1</i>	6.8-54.17	[49]
	Zhengmai, Bobwhite	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaSBEIIa</i>	nd	[50]
	Fielder	Immature embryo	CRISPR/Cas9	Biolistic <i>Agrobacterium</i>	<i>TaQsd1</i> <i>TraesCS4A02G110300</i> <i>TaLOX2</i>	3-38.5 3.8-6.7 6.9	[51]
	CB037	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaNP-A1, TaNP-B1, TaNP-D1</i>	5.83-6.56	[52]
	Bobwhite	Immature embryo	CRISPR/Cas9 replicons	Biolistic	<i>TaUbi, MLO</i>	10-fold	[53]
	Fielder, Gladius	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Ms1</i>	70	[54]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaDA1, TaPDS, TaNCED1</i>	37.04	[55]
	H29, Fielder Ningchun4	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaWaxy, TaMTL</i>	80.5	[56]
	Bobwhite	Mature embryo SAM	CRISPR/Cas9	Biolistic	<i>TaGASR7-A1, TaGASR7-B1, TaGASR7-D1</i>	5.2	[57]
	Svevo	Immature embryo	CRISPR/Cas9	Biolistic	<i>CM3</i> <i>CM16</i>	13 7.4	[58]
	Borlaug 2016	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaIPK1.A, TaIPK1.B, TaIPK1.D</i>	10.8-12.7	[59]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>pinb-47</i> <i>waxy-2</i> <i>ppo-7</i> <i>psy-13</i>	6.82-38.72 46.73-100 6.02-37.27 5.81-16.7	[60]

	Cadenza, Cezanne, Goncourt, Prevert	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaBAK1-2, Ta-elf4E, Ta-elf(iso)4E</i>	nd	[61]
	Cadenza	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaASN2</i>	64	[62]
	DMSW	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Ms2</i>	9	[63]
	Bobwhite	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaGW7</i>	1.1-8.3	[64]
	Bobwhite	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaGW2, TaLpx-1, TaMLO</i>	20	[65]
	Fielder	Immature embryo	CRISPR/dCas9	<i>Agrobacterium</i>	<i>TaPDS</i>	nd	[66]
	Fielder	Immature embryo	CRISPR/dCas9	<i>Agrobacterium</i>	$\alpha$ -gliadin, $\gamma$ -gliadin	nd	[67]
	Fielder, SBC0456D	Immature embryo	CRISPR/dCas9	<i>Agrobacterium</i>	<i>Ms45</i>	nd	[68]
	Fielder	Immature embryo	CRISPR/dCas9	<i>Agrobacterium</i>	<i>TaNFXL1</i>	nd	[69]
	Reeder	Immature embryo	CRISPR/Cas9 CRISPR/AsCpf1 CRISPR/LbCpf1	Biolistic	<i>TaPDS</i>	nd	[70]
	Desert King, Fielder Hahn, Cadenza	Immature embryo	CRISPR/dCas9	<i>Agrobacterium</i>	<i>AP2L-A5</i>	97	[71]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaHAG1</i>	nd	[72]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>YGL1</i>	nd	[73]
	Kenong199	Immature embryo	CRISPR/MAD7	Biolistic	<i>TaDEP1, TaDME-T1</i>	65.6	[74]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaZIP4-B2</i>	4.9	[75]
	Yumehikara Haruyokoi Kitanokaori	Embryonic shoot apical meristem (SAM)	CRISPR/Cas9	Biolistic	<i>TaQsd1</i>	2.51	[76]
	Fielder	Embryonic shoot apical meristem (SAM)	CRISPR/Cas9	Biolistic	<i>TaLOX2</i> <i>TaGASR7</i>	8-11	[77]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPLA</i>	nd	[78]
	Fielder	Immature embryo	Base editing-ABE	<i>Agrobacterium</i>	<i>Tubulins</i>	78.3	[79]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPHT1;9-4B</i>	nd	[80]
	Kenong199	Immature embryos	Base editing-ABE	Biolistic	<i>TaDEP1</i> <i>TaGW2</i>	1.1 0.4	[81]

	Kenong199	Immature embryo	Base editing-CBE	<i>Agrobacterium</i>	<i>TamIR396 and TaGASR6</i>	2.0-3.5	[82]
	Kenong199	Immature embryo	TALEN	Biolistic	<i>TaGW2</i>	1.77	[83]
	NIL-Ne2, RIL-66	Immature embryo	CRISPR/Cas9	Biolistic	<i>Ne2</i>	nd	[84]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>WFZP-A/D, TaDL-A/B/D</i>	nd	[85]
	nd	Maize sperm cell	CRISPR/Cas9	Pollination	<i>TaBRI1, TaSD1</i>	nd	[86]
	Bobwhite, Zhengmai 7698, Fielder	Seedlings	CRISPR/Cas9	BSMV-Virus	<i>TaPDS, TaGW2, TaGASR7,</i>	12.9-100	[87]
	Fielder	Immature embryo	CRISPRa and CRISPRi	<i>Agrobacterium</i>	<i>TaPDS</i>	nd	[66]
	nd	Mature embryos SAMs	CRISPR/Cas9 RNPs	Biolistic	<i>TaQsd1, TaOr_t0, TaOr_t1 TaHRGP-like1_t2, TaSD1</i>	1-8.3	[88]
	CB037B	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPDI</i>	65.6	[89]
	CB037	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaMBF1c</i>	nd	[90]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TaPGS1</i>	nd	[89]
	CB037	Immature embryo	CRISPR/Cas9	Biolistic	<i>FT-1</i>	nd	[91]
	Bobwhite	Immature embryo	CRISPR/Cas9	Biolistic	<i>TaPDS, TaHRC</i>	49-58	[92]
	Fielder	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MTL</i>	nd	[93]
Rice <i>Japonica</i>	Kitaake	Callus	TALENs	<i>Agrobacterium</i>	<i>Os11N3</i>	T <sub>1</sub> (48/63)	[94]
<i>Japonica</i>	Nipponbare	Callus	TALENs	<i>Agrobacterium</i>	<i>OsDEP1 OsBADH2 OsCKX2 OsSD1</i>	31.3 26.9 61.7 3.8	[95]
Rice <i>(Indica)</i>	Kasalath	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SPP ROC5 YSA</i>	5 26 75	[96]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsCAO1 OsLAZY1</i>	83.3 (T <sub>1</sub> ) 91.6 (T <sub>1</sub> )	[97]
	Nipponbare	Callus	CRISPR/Cas9	Biolistics	<i>OsPDS OsBADH2</i>	9.7 7.1	[98]

	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSWEET11</i> <i>OsSWEET13</i> <i>OsSWEET1a</i> <i>OsSWEET1b</i> <i>Chr. 2 cluster (245 kb)</i> <i>Chr. 4 cluster (170 kb)</i>	12.5 100 70 20 16.6 25	[99]
	Nipponbare	Callus	CRISPR/Cas9	Biolistic	<i>OsPDS</i> <i>OsMPK2</i>	9.4 4	[100]
<i>Indica</i>	Nipponbare Kasalath	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsMYB1</i> <i>OsYSA-gRNA 1</i> <i>OsROC5</i> <i>OsDERF1</i> <i>OsYSA – gRNA 2</i> <i>OsPDS</i> <i>OsMSH1</i> <i>OsMYB5</i> <i>OsSPP</i> <i>OsPMS3</i> <i>OsEPSPS</i> <i>OsMSH1+OsDERF1</i> <i>OsMSH1+OsPDS</i> <i>OsPDS+OsPMS3</i> <i>OsPDS+OsDERF1</i>	66.7 66.7 65.1 50.9 51.4 41.9 37 31.9 28.9 26.3 21.1 33.3 32.7 8.6 5.7	[101]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>BEL</i>	2-16	[102]
	Nipponbare Kitaake	Callus	TALENs	<i>Agrobacterium</i>	<i>OsSWEET14</i>	nd	[103]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsDL</i>	77.8	[104]
	Nipponbare	Callus	TALENs Base substitution	Biolistic	<i>OsEPSPS</i>	21 1.2	[105]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPDS</i> <i>Os02g23823</i> <i>OsMPK2</i> <i>OsPDS+Os02g23823+OsMPK2</i>	68.2 66.4 81 60	[106]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSWEET13</i>	nd	[107]
	Nipponbare	Callus	TALENs TALENs	<i>Agrobacterium</i> Biolistic	<i>OsBADH2</i> <i>OsBADH2+ OsCKX2+ OsDEP1</i>	30 1.9	[108]
	Nipponbare	Callus	TALENs	<i>Agrobacterium</i>	<i>OsLOX3</i>	4	[109]

	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsYSA-g1+OsROC5+OsYSA-g2</i>	33.3+53.3+46.7	[110]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsAOX1a</i> <i>OsAOX1b</i> <i>OsAOX1c</i> <i>OsBEL</i>	50 57 75 86	[111]
	Taichung 65	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	Os 1 (8 FTL targets) Os 2 (3 FTL targets) Os 3 (3 targets) Os 4 (3x Waxy targets) Os 5 (Os05g0591600) Os 6 (Os03g0126800+Os03g0126800) Os 7 (Os07g0409500+Os07g0409500) Os 8 (Os07g0625500+Os07g0625500) Os 9 (Os07g0261200+Os07g0261200) Os 10 (3x targets) Os 11 (3x targets) Os 12 (Os07g0411300+Os10g0484800) Os 13 (Os04g0595000) Os 14 (Os12g0242700) Os 15 (Os03g0216800) Os 16 (Os02g0459600+Os01g0891000) Os 17 (Os10g0413900+Os10g0413900) Os 18 (Os06g0142000+Os06g0142100) Os 19 (Os03g0247300) Os 20 (Os06g0275000+Os06g0275000)	Average 85.4	[112]
	Kitaake  Nipponbare	Callus	CRISPR/Cas9  CRISPR/Cas9	<i>Agrobacterium</i>	<i>sgRNA1</i> <i>sgRNA2</i> <i>PTG6</i> <i>PTG7</i> <i>PTG9</i>	44 60 100 47 86	[113]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PDS-1</i> <i>PDS-2</i> <i>PDS-3</i> <i>PDS-4</i>	46 3 93 87	[114]

					DL-1 DL-2 DL-3 DL-4 LigIV-1 LigIV-2 LigIV-3 LigIV-4 ALS-1 ALS-2 ALS-3 ALS-4	68 94 93 76 62 90 96 88 5 73 69 26	
	LH422	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	GW2+ TGW6+ GW5	95 (triple mutant)	[115]
	Nipponbare	Callus	CRISPR/FnCas12a	<i>Agrobacterium</i>	OsDL OsALS	85.7 90	[116]
	Kuiku131	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	OsERF922	42	[117]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	OsGn1a OsDEP1 OsGS3 OsIPA1	42.5 67.5 57.5 27.5	[118]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	OsPDS OsYSA OsDEP1 OsPDS (2 sgRNA) OsYSA (2 sgRNA)	85.2 100 72.2 86.2 66.7	[119]
	Nipponbare	Callus	TALENs	<i>Agrobacterium</i>	OsCSA OsPMS3 OsDERF1 OsGN1a OsTAD1 OsMST7 OsMST8 OsPMS3 OsPMS3	2.3 3.8 2.8 0 0 6.6 5.3 25 21.7	[120]
	Kitaake	Callus	TALENs-HDR	Biolistic	OsALS	6.3	[121]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	gRNA guides 1-21	Average 82.2	[122]



	Nipponbare/ Zhonghua11	Callus	CRISPR/Cas9-VQR  CRISPR/Cas9-VRER	<i>Agrobacterium</i>	NAL1-Q1 NAL1-Q2 LPA1 LG1 GL1-1 LPA1+LG1 LG1+GL1-1 NAL1 LG1 GL1-1	0 13.3 2.1 23.4 17 2.1 8.5 3.9 1.6 36.5	[123]
	Nipponbare	Callus	CRISPR/Cas9 CRISPR/Cas9n CRISPR/Cas9 CRISPR/Cas9n	<i>Agrobacterium</i>	<i>OsCDKB2</i>  <i>OsDMC1A</i>	41.6 22.7 84 0	[124]
	Nakdong	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>JAZ9</i>	69	[125]
	Nipponbare	Callus	CRISPR/Cas9-HDR	Biolistic <i>Agrobacterium</i>	<i>OsALS</i>	92 75	[126]
	Nipponbare	Callus	CRISPR/Cas9-HDR	Biolistic	<i>OsEPSPS</i> (gene replacement – 2 targets) <i>OsEPSPS</i> (gene insertion – 1 target)	2 2.2	[127]
<i>japonica</i> <i>Indica</i>	Zhonghua11 Zhenshan97B ZhongzheB TianfengB YixiangB ReB HuahuiB HuanongB Yuejingsimiao Yuenongsimiao Wushansimiao GAZ	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TMS5a-j</i> (paired) <i>TMS5ab</i>	69.2-94.1 88.89 83.33 92.86 100 88.23 84.62 72.72 100 11.11 85.71 92.86	[128]
<i>Japonica</i> <i>Japonica</i> <i>Indica</i> <i>Hybrid</i> <i>Japonica</i>	Nipponbare Koshihikari IR64[129] NERICA1 Curinga	immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPDS</i>	84.9 64.7 100 90.7 79.8	[130]
	Xiushui11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsTCD10</i>	nd	[131]

	Nipponbare	Callus	CRISPR/Cas9	Biolistic	<i>OsBEI1b</i>	5	[132]
<i>Japonica</i>	9522 Kongyu131 Jiaoyou5B	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CSA</i>	50 6.8 69.2	[133]
	Kitaake	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsSERK1</i> <i>OsSERK2</i> <i>ipa1</i> <i>pi-ta</i>	17 10.5 22.2 18.2	[134]
	Nipponbare	Callus	CRISPR/LbCas12a	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsDEP1</i> <i>OsROC5</i>	100 100 100	[135]
	Zhonghua11	callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsNRT1.1B</i> <i>OsSLR1</i>	2.7 13.3	[136]
	nd	Embryonic cells	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSAPK2</i>	10	[137]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSBEI</i> <i>OsSBEI1b</i>	80 70	[138]
<i>Indica</i>	Huazhan Longke638S	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsNramp5</i>	82.4 80	[139]
	Nipponbare	Immature embryos or callus	TALENs	<i>Agrobacterium</i>	<i>Os09g29100</i>	4.1 (T <sub>1</sub> )	[140]
<i>Japonica</i>	Longdao16 Longdao18 Daohuaxiang2 Songjing19 Dongnong430	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsHD2-1+OsHD4-1+OsHD4-2+OsHD5+OsHD2-2</i>	77.8 (sum of all cultivars)	[141]
	Taipei309	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsAnn3</i>	31.6	[142]
	Nipponbare	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsALS</i>	3.41	[143]
	Kitaake	Callus	TALENs	<i>Agrobacterium</i>	<i>SWEET14-AvrXa7</i> <i>SWEET14- TalC</i>	51 30	[144]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MPK1</i> <i>MPK2</i> <i>MPK6</i> <i>MPK5</i> <i>MPK5+1</i> <i>MPK6+2</i> <i>MPK5+1+6+2</i>	100 100 100 100 89 67 86	[145]

	Xidao #1 nd	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsLCT1</i> <i>OsBADH2</i>	100 100	[146]
	Nipponbare	Mature embryo	CRISPR/Cas12a	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsBEL</i>	21.4, 41.2	[147]
	Nipponbare	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsCDC48</i>	43.48	[148]
	Kitaake	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsSBEIIb</i>	2.3 20	[149]
	Kitaake	Callus	CRISPR/FnCas12a-HDR CRISPR/LbCas12a-HDR  CRISPR/FnCas12a CRISPR/LbCas12a	Biolistic	CAO1 site #1 CAO1 site #1 CAO1 site #2 CAO1 site #1 CAO1 site #1 CAO1 site #2	8 0 3 24 1 10	[150]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TMS10L</i>	nd	[151]
<i>Indica</i>	IR64	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsEPFL9</i>	4-10	[152]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsMIR408</i> <i>OsMIR528</i> <i>OsMIR815(a/b/c)</i> <i>OsMIR820(a/b/c)</i>	47.6 88.9 10 61.1	[153]
	Nipponbare	Callus	CRISPR/FnCas12a       CRISPR/LbCas12a	<i>Agrobacterium</i>	<i>OsRLK</i> (4 sites) <i>OsEPSPS-1</i> <i>OsEPSPS-2</i> <i>OsBEL-1</i> <i>OsBEL-2</i> <i>OsPDS-1</i> <i>OsPDS-2</i> <i>OsBEL</i> (4 sites) <i>OsEPSPS-1</i> <i>OsEPSPS-2</i> <i>OsBEL-1</i> <i>OsBEL-2</i> <i>OsPDS-1</i> <i>OsPDS-2</i>	34.4 0 16.7 19.4 12.5 8.3 0 40 5.6 20.8 62.5 20 73.5 1.8	[154]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>BADH2+DEP1+Gn1a+GS3+GW2</i> <i>+Hd1+EP3+LPA1</i>	25	[155]
	Nipponbare	Callus	CRISPR/SpCas9-HDR	<i>Agrobacterium</i>	<i>OsALS</i>	2.1	[156]

	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsCYP97A4</i> <i>OsDSM2</i> <i>OsCCD4a</i> <i>OsCCD4b</i> <i>OsCCD7</i>	37.5 50 37.5 93.7 20	[157]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	Library (12,802 genes)	Nd	[158]
<i>Japonica</i>	Kuiku 131	Callus	TALENs	<i>Agrobacterium</i>	<i>OsERF922</i>	2.7	[159]
	E4	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SaF</i> <i>SaM</i>	Nd nd	[160]
	Nipponbare	Callus	CRISPR/Cas9  CRISPR/Cas12a	<i>Agrobacterium</i>	<i>OsDEP1</i> <i>OsSPL14</i> <i>OsTB1</i> <i>OsLAC</i> <i>OsmiR398a</i> <i>Os02circ25329</i> (2x) <i>Os03circ00204</i> (2x) <i>OsPDS</i> <i>OsDEP1</i> <i>OsROC5</i>	75 63.6 15.4 58.8-100 71.4 66.7-80 18.8-43.8 100 100 100	[161]
	Nipponbare	Immature embryo or callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>RAD51A</i> -NGG <i>RAD51A</i> -NAG <i>DMC1</i> -NGG <i>DMC1</i> -NAG <i>NAL1+LPA1+LG1+GL1-1</i> (NAG) <i>NAL1+LPA1+LG1+LG1</i> (NAG)	87.5 67.9 74.3 34.3 15.5-44.8 21.4+82.1	[162]
<i>Japonica</i>	Nanjing 9108 Wuyunjing 27 Yangjing 4227 Zhejiang 22 Zhejiang 88	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGS3+OsGn1a</i>	nd	[163]
	Zhonghua11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPDS</i> (multiplex)	50-85	[164]
	Kitaake	Callus	CRISPR/LbCas12a-RR	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsSBEIIb</i> <i>OsPDS+OsSBEIIb</i>	22.2 31.1 9.3	[165]
	Nipponbare	Callus	CRISPR/Cas9  CRISPR/Cas9-VQR	<i>Agrobacterium</i>	<i>OsMOC3</i> <i>OsGW2</i> <i>OsMOC3+OsGW2</i> <i>3x targets</i>	65.9 56.5 29.35	[166]

						13.9 (double mutant) Approx.. 5 Approx. 10	
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsGn1a</i> <i>OsDEP1</i>	28 49 39	[167]
	Zhonghua11	Callus	CRISPR/LbCas12a-HDR	biolistic	ALS-gene replacement	2.1-2.8	[168]
	Zhonghua11	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsCDC48</i> <i>OsNRT1.1B-T1</i>	82.9 44.1	[169]
	Dongjin	Germinating rice seed	ZFN	<i>Agrobacterium</i>	<i>SSIVa</i>	57.1	[170]
	Nipponbare	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>OsALS</i> <i>OsALS+OsFTIP1e</i>	64.1 43.2	[171]
	Zhonghua11	Callus	Base editing-ABE	<i>Agrobacterium</i>	<i>OsACC</i> <i>OsALS</i> <i>OsCDC48</i> <i>OsDEP1-T1</i> <i>OsDEP1-T2</i> <i>OsNRT.1B</i>	20.6 21.4 33.3 46.5 15.8 59.1	[81]
	Nipponbare	Immature embryo or callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CCD7</i>	36.4-100	[172]
	Nipponbare	Callus	CRISPR/FnCas12a  CRISPR/LbCas12a-RR  CRISPR/FnCas12a-RR  CRISPR/LbCas12a-RVR  CRISPR/FnCas12a-RVR	<i>Agrobacterium</i>	<i>OsDEP1-TTV</i> <i>OsEPFL9-TTV</i> <i>OsDPS-TTV</i> <i>OsDEP1-TTTV</i> <i>OsEPFL9-TTTV</i> <i>OsROC5-CCCC</i> <i>OsPDS-TCCG</i> <i>OsROC5-TCCG</i> <i>OsPDS-TTCC</i> <i>OsROC5-TTCC</i> <i>OsDEP1-CCCC</i> <i>OsDEP1-TTCC</i> <i>OsPDS-TATC</i> <i>OsROC5-TATG</i> <i>OsDEP1-TATG</i>	46.7 57.1 0 87.1 89.3 47.5 0 40 93.3 100 0 13.3 0 60 0	[173]
	Nipponbare	Callus	CRISPR/FnCas12a	<i>Agrobacterium</i>	<i>LEA_1+LEA_2</i> (8 targets)	0-70.8 0-70.8	[174]

			CRISPR/LbCas12a		<i>LEA_Dehydrins</i> (9 targets)	4.2-54.2	
			CRISPR/Cas9		<i>CYP81A</i> (3 targets)	4.2-58.3 70.8-79.2 50-86.4	
	Kitaake	Callus	Base editing-CBE	<i>Agrobacterium</i>	<i>Pi-d2</i> <i>OsFLS2</i> <i>OsAOS1</i> <i>OsJAR1</i> <i>OsJAR2</i> <i>OsCOI2</i>	30.8 57 23.3 21.7 11.8 69.4	[175]
	Nipponbare	Callus	TALENs	<i>Agrobacterium</i>	<i>Os01g0833500</i>	16.8-60.4	[176]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PYL1–PYL6+ PYL12</i> <i>PYL7–PYL11+PYL13</i>	nd	[177]
	Nipponbare	Scutellum	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsFAD2-1</i>	8.7	[178]
	Nipponbare	Callus	Base editing-ABE	<i>Agrobacterium</i>	<i>OsSPL14</i> <i>SLR1</i> <i>OsSPL16+OsSPL18</i> <i>OsSPL14+OsSPL17</i> <i>OsSPL16+OsSPL18</i>	26 12.5 9.5 41.9 14.6	[179]
	Kitaake	Callus	Base editing-ABE	<i>Agrobacterium</i>	<i>OsSERK2</i> <i>OsWRKY45</i>	32 62.3	[180]
<i>Indica</i>	IR64	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>eIF4G</i>	59.7	[181]
<i>Indica</i>	ASD16	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPFT1</i>	nd	[182]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsBBM1</i> <i>OsBBM2</i> <i>OsBBM3</i>	Nd Nd Nd	[183]
	IR64	Immature embryos	CRISPR/Cas12a	<i>Agrobacterium</i>	<i>OsEPFL9</i>	nd	[184]
Rice hybrid	Chunyou 84	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsREC8+OsPAIR1+OsOSD1</i> <i>OsMTL</i> <i>OsREC8+OsPAIR1+OsOSD1+OsMTL</i>	21.9 34.4 13.6	[185]
	Nipponbare	Callus	CRISPR/Cas-directed evolution (CDE)	<i>Agrobacterium</i>	<i>OsSF3B1</i>	0.14	[186]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsMYB108</i>	14.3-100	[187]
	nd	nd	Base editing-ABE	nd	<i>Wx</i> <i>GL2/OsGRF4</i>	15.1 13.3	[188]

					<i>OsGRF3</i>	16.7	
<i>indica</i>	Kitaake  IR64 Ciherang-Sub1	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSWEET11+OsSWEET13+OsSWEET14</i>	25  Nd Nd	[189]
	Xidao 1	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsITPK6</i>	30.4	[190]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsDEP1</i> <i>OsPDS</i> <i>OsDEP1</i> <i>OsPDS</i> <i>OsDEP1</i>	20.7 52.9 77.1 86.6 75.9 93.3	[191]
	Nipponbare	Callus	CRISPR/xCas9  CRISPR/Cas9-NG CRISPR/Cas9-NGv1 CRISPR/Cas9-NG CRISPR/Cas9-NGv1 CRISPR/Cas9-NG CRISPR/Cas9-NGv1 CRISPR/Cas9-NG CRISPR/Cas9-NGv1 Cas9-NG(base editing)	<i>Agrobacterium</i>	<i>OsGS3</i> -CGA <i>DEP1</i> -CGT <i>DEP1</i> -TGC <i>DEP1</i> -CGC <i>DEP1</i> -CGC  <i>PDS</i> -AGG  <i>PDS</i> -CGT  <i>DEP1</i> -GGT  <i>OsDEP1</i> site 1 <i>OsDEP1</i> site 2	11.1 6.7 21.1 0 56.3 18.2 33.3 8 22.2 3.5 38.5 13.6 45 30.4	[192]
	Kitaake	Callus	CRISPR/Cas9-NG  Base editing-CBE Base editing-ABE	<i>Agrobacterium</i>	<i>OsMPK11</i> <i>OsMPK7</i> <i>OsMPK10</i> <i>OsMPK8</i> <i>OsSERK1+OsSERK2</i> <i>OsGSK4+OsETR2</i> <i>OsBZR1</i> <i>OsSERK2</i> <i>OsSERK2</i> <i>OsSERK2</i>	38.2 25 21.4 4.5 93.3 12.8 35.3 54.2 40.4 upregulation	[193]

	Nipponbare	Callus	Base editing-ABE  Base editing-CBE CRISPR/pSaKKH-Cas9 Base editing-ABE+CBE	<i>Agrobacterium</i>  <i>Agrobacterium</i> Bombardment Bombardment	<i>OsSPL14+OsSPL17</i> <i>OsSPL16+OsSPL18</i> <i>SNB</i> <i>PMS3</i> <i>PMS1</i> <i>OsSPL14+OsSPL17+SNB</i>	66.7+74.3 30+66.7 6.5 71.4 35.7 9.8	[194]
	Nipponbare	Callus	CRISPR/Cas9          CRISPR/Cas12a	<i>Agrobacterium</i>	<i>OsPDS</i>          <i>OsPDS+OsDEP1</i>          <i>OsPDS+OsPDS-sgRNA02+OsDEP1</i>          <i>OsPDS-sgRNA01+OsPDS-sgRNA02+OsDEP1-sgRNA01+OsDEP1-sgRNA02+OsYSA-sgRNA01+OsYSA-sgRNA02 (6x)</i> <i>OsDEP1-crRNA01</i> <i>OsDEP1-crRNA02</i> <i>OsROC5-crRNA01</i> <i>OsROC5-crRNA02</i> <i>OsDEP1-crRNA01+OsDEP1-crRNA02+OsROC5-crRNA01+OsROC5-crRNA02</i>	74.5 88.2 81 76.9 90.6 86.7 58.3 60.6 67.6 47.4          61.1 82.4 53.8 54.5 16.7	[195]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OslAMT</i>	nd	[196]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsCALd5H1</i>	0-100	[197]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Tos17<sup>chr7</sup></i>	10-90	[198]
	nd	nd	CRISPR/SaCas9  CRISPR/SaKKH   CRISPR/Sa-BE3 (CBE) CRISPR/Sa-eBE3 (CBE) CRISPR/Sa-BE3 (CBE) CRISPR/Sa-eBE3 (CBE)	<i>Agrobacterium</i>	<i>PDS</i> <i>DL</i> <i>PDS</i> <i>DL</i> <i>NAL1</i> <i>SLR1</i>    <i>IPA1</i>	64.2 77.8 90.6 41.7 66.7 10 71.9 8.3 15	[199]



			CRISPR/Sa-BE3 (CBE) CRISPR/SaKKH-BE3 (CBE)  CRISPR/SaKKH-eBE3 (CBE)  CRISPR/Sa-CDA (CBE)  CRISPR/SaKKH-CDA (CBE)  CRISPR/Sa-ABE  CRISPR/SaKKH-ABE		<i>TAC1</i> <i>Ehd1</i> <i>Pi-d2</i> <i>Ehd1</i> <i>Pi-d2</i> <i>IPA1</i> <i>OsMKK6</i> <i>OsMPK3</i> <i>Pi-ta</i> <i>IPA1</i> <i>OsSPL17</i> <i>GL2</i> <i>OsGRF</i> <i>Wx</i> <i>Pi-d3</i>	15.6 20.5 6.3 25 5.4 8.5 2.1 6.3 0 41.2 63.2 6.5 16.1 9.4 0	
	WPB106	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsRR22</i>	64.3	[200]
<i>Indica</i>	93-11 Huazhan	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PTGMS2-1</i>	nd	[201]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsOr</i>	nd	[202]
	Nipponbare	Callus	CRISPR/Cas9 CRISPR/xCas9 3.6 CRISPR/xCas9 3.7 CRISPR/SpCas9-NG CRISPR/xCas9 3.6 CRISPR/xCas9 3.7 CRISPR/SpCas9-NG CRISPR/xCas9 3.6 CRISPR/xCas9 3.7 CRISPR/SpCas9-NG CRISPR/xCas9 3.6 CRISPR/xCas9 3.7 CRISPR/xCas9 3.6 CRISPR/xCas9 3.7 Base editing-ABE	<i>Agrobacterium</i>	<i>OsSPL14</i> -CGG    <i>LF</i> -AGC   <i>OsSPL7</i> -CGT   <i>OsSPL4</i> -GAT  <i>OsMADS57</i> -GAA  <i>OsSPL14</i>    <i>LF1</i>	87.9 85.3 89.3 65.7 23.8 3.2 81.8 84 85.7 74.2 11.1 3.3 0 0 0 0 2.6 2.9 0	[203]



	Zhonghua11		CRISPR/LbCas12a-RR  CRISPR/LbCas12a-RVR		NAL Gn1a+GS3+IPA1 LCD+OsNrAMP5+LCT1+OsNrAMP1 OsDL-CCCC  OsPDS-TTCA  OsDL-TATC  OsPDS-TATG	92.9 35.7 66.7 17.8 56.3 41.7 69.4  8.3 45 2 13.9	
	Zhonghua 11	Callus	CRISPR/Cas9	Agrobacterium	OsSPCH1 OsSPCH2 OsMUTE OsFAMA OsICE1 OsICE2 OsSCR1 OsSCR2 OsSHR1 OsSHR2	nd	[205]
	Xidao 1	Callus	CRISPR/Cas9	Agrobacterium	OsLCT1 OsNramp5	21.7 16.7-100	[206]
	nd	Callus	CRISPR/xCas9  CRISPR/Cas9 CRISPR/xCas9  CRISPR/Cas9 CRISPR/xCas9 CRISPR/Cas9	Agrobacterium	GAA PAM sites  AGA, TGT and CGC PAM sites  GGG PAM site	0-4.2 2.1-12.5 0 2.1-8 4.2-18.4 0 4.2-10.4 75-77.1	[207]
	Pinzhan	Callus	CRISPR/Cas9	Agrobacterium	TMS5+Pi21+Xa13	nd	[208]
	Nipponbare	nd	CRISPR/Cas9	Agrobacterium	OsLHT1	nd	[209]
Japonica	Sasanishiki	Callus	CRISPR/Cas9	Agrobacterium	Se13 PHYB Se14	60 45 35	[210]

					<i>Hd3a</i> <i>Ef7</i> <i>RFT1</i> <i>Ehd1</i> <i>Hd1</i> <i>Ghd7</i> <i>Dth8</i>	40 50 55 45 40 70 60 50	
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>LAZY1</i>	44.5-52.5	[211]
	Nipponbare	Callus	CRISPR/AsCas12a	<i>Agrobacterium</i>	<i>OsDEP1</i> <i>OsROC5</i>	77.8 92.8	[212]
landraces	Kasalath	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SD1</i>	44-68	[213]
	TTP (TeTePu)				<i>SD1+SE5</i>	21-28	
	BTA	Callus	mitoTALENs	<i>Agrobacterium</i>	<i>orf79</i>	33.3	[214]
	nd	Callus	Base editing-ABE	<i>Agrobacterium</i>	chr04_33074491–33074510	30.3	[215]
<i>japonica</i>	Nipponbare and Yuhikihikari	Zygotes	CRISPR/Cas9-RNP  CRISPR/Cas9	PEG	gDsRed2 gDL-2 gDL-3 gGW7 gGCS1 gDL-2 gPRR37-1 gPRR37-2	25 14.3 13.6 21.4 64.3 16.7 16 4	[216]
	Zhonghua 11	Callus	CRISPR/LbCpf1-HDR	Biolistics	<i>OsALS</i>	4.6	[217]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	Multiple targets (open- and closed chromatin regions)	Up to 100	[218]
	EYI	Mature embryos	CRISPR/Cas9 CRISPR/Cas9d	biolistics	<i>Wx</i>	nd	[219]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsACS1</i> <i>OsACS2</i>	nd	[220]
<i>Indica</i>	Jingxi Glutinous Rice	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGA20ox2</i>	73.5	[221]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Os8N3</i>	25	[222]
	Nipponbare	Mature seeds derived embryos	CRISPR/Cas9-RNP CRISPR/Cas9	Biolistics	<i>OsPDS1</i>	62.8 62	[223]

		Callus	CRISPR/Cas9	<i>Agrobacterium</i>		100	
	GXU16 GXU20 GXU28	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SRL1 or SRL2</i>	68.1 56.8 71.6	[224]
<i>Indica</i>	209B	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsWaxy</i>	68.2	[225]
<i>Japonica</i>	Jijing809 Liaojing237	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGS3+OsGW2+OsGN1a</i>	80 33.3	[226]
	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	LOC_Os09g26999	nd	[227]
	Dongjin	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsVP1</i>	60	[228]
	Heugseonchal  Sinmyungheugchal	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsF3'H</i> <i>OsDFR</i> <i>OsLDOX</i>	60 52.9 57.1	[229]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsBIG</i>	nd	[230]
	Zhonghua 11	Callus	CRISPR/ScCas9	<i>Agrobacterium</i>	NAG (PAM) NTG (PAM) NCG (PAM) NGG (PAM)	41.67 79.19 4.65 32.56	[231]
	Nipponbare	Callus	Base editor-CBE	<i>Agrobacterium</i>	<i>ALS-T1</i> <i>CHL9</i> <i>IPA</i> <i>NRT1.1</i> <i>SLR1</i> <i>ALS-T2</i> <i>Pi-d2</i>	Approx. 66 Approx. 71 Approx. 61 Approx. 52 Approx. 89 Approx. 75 Approx. 86	[232]
	Zhonghua11	Callus	CRISPR/Cas9-HDR	Biolistic	<i>DRO1</i> -dsADHE <i>DRO1</i> -ssADHE <i>DRO1</i> -ADHE <i>SKC1</i> -ADHE <i>SLR1</i> -ADHE <i>SOS1</i> -ADHE <i>WRKY71</i> -AMVE <i>DEP1</i> -AMVE <i>BZR1</i> -AMVE <i>bZIP5</i> -AMVE  <i>OsPAP10a</i> - P1BS	4.2 0 45.5 31.7 26.5 35.7 25 43 47.3 23.5  26.1	[233]





[illegible]



					ALS-T1 ALS-T2 ALS-T3 DEP1 Waxy NRT1.1B-T1 NRT1.1B-T2 NRT1.1B-T3 CDC48-T1 CDC48-T2 ALS-T1 ALS-T2 ALS-T3 DEP1 Waxy NRT1.1B-T1 NRT1.1B-T2 NRT1.1B-T3 CDC48-T1 CDC48-T2 ALS-T4 CDC48-T3 AAT DEP1-T2 ACC NRT1.1B-T4 SPL14 WRKY45 DELLA ALS-T4 CDC48-T3 AAT DEP1-T2 ACC NRT1.1B-T4 SPL14 WRKY45 DELLA	66.7 63.3 47.8 60 13.3 58.6 56.6 31 53.3 33.3 67.8 63.3 69.2 76.9 30 73.3 76.9 36 76.9 61.5 34.1 18.2 12.2 68.2 54.2 0 40.6 66.7 26.5 93.2 82.9 79.5 96 88 13 60 92.6 65.2	
	TianFengB	nd	Base editor-ABE	CRISPR/Cas9	Agrobacterium	pWx <sup>a</sup> pWxa-5'UISS	nd [249]

					<i>Wx<sup>a</sup></i>		
<i>Indica</i>	MTU1010[250] (modified)	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>DST</i>	30-33.3	[251]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>FWL1-8</i>	81.6 (avg.)	[252]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsbZIP11+ OsbZIP41 OsRLI1</i>	nd	[253]
<i>Indica</i>	Super Basmati	Callus	CRISPR/Cas9	Biolistic	<i>OsSWEET14</i> -gRNA1 <i>OsSWEET14</i> -gRNA2 <i>OsSWEET14</i> -gRNA3	4.4 0 5.3	[254]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGAD3</i>	nd	[255]
	Zhonghua11	Callus	CRISPR/Cas9  CRISPR/AFID-3	<i>Agrobacterium</i>	<i>OsCDC48-T2 OsSPL14 OsSWEET14 OsCDC48-T2 OsSPL14 OsSWEET14</i>	93.6 50 64.2 93.5 65.9 66.2	[82]
	Kitaake	Callus	Cas9p-HDR	Biolistic	Carotenoid cassette (5.2 kb)	6.2	[256]
	nd	nd	CRISPR/Cas9  CRISPR/xCas9  CRISPR/Cas9-NG  CRISPR/eCas9-NG  Cas9n-NG-CBE eCas9n-NG-CBE Cas9n-ABE	nd	<i>OsWaxy</i> -TGG <i>OsWaxy</i> -TGA <i>OsWaxy</i> -TGT <i>OsWaxy</i> -TGC <i>OsWaxy</i> -TGG <i>OsWaxy</i> -TGA <i>OsWaxy</i> -TGT <i>OsWaxy</i> -TGC <i>OsWaxy</i> -TGG <i>OsWaxy</i> -TGA <i>OsWaxy</i> -TGT <i>OsWaxy</i> -TGC <i>OsWaxy</i> -TGG <i>OsWaxy</i> -TGA <i>OsWaxy</i> -TGT <i>OsWaxy</i> -TGC  GGG (PAM) TGG (PAM)	76.5 5.8 0 0 27.3 0 0 0 27.3 22.7 9.1 45.5 0 5.5 0 8.3 13.3 22.7 55.6 11.1	[257]

			Cas9n-NG-ABE		GGG (PAM)	6.5	
	Nipponbare Kitaake	Callus	Base editor-ABE	<i>Agrobacterium</i>	<i>OsSPL14</i> <i>SLR1</i> <i>OsSERK2</i> <i>Tms9-1</i> <i>OsNRT1.1B</i> <i>OsACC1</i> <i>OsDEP1</i> <i>SPX-MSF2</i> <i>OsSPL14+OsSPL17</i> <i>OsSPL16+OsSPL18</i> <i>OsSPL13</i> <i>SNB</i>	37.5 70.6 17.5 35 66.7 77.8 4.5 11.1 72.9 96.3 69.4 73.8 80 71.4 9.8 15.9 39.3 41.7 15.1 2.2 6.1 9.1 33.9	[258]
	Nipponbare	Callus	Base editor-ABE	<i>Agrobacterium</i>	<i>OsNRT1.1B</i> <i>OsSPL14</i> <i>OsWRKY45</i> <i>OsSLR1</i> <i>OsACC</i> <i>OsNRT1.1B</i> <i>OsSPL14</i> <i>OsWRKY45</i> <i>OsSLR1</i> <i>OsACC</i> <i>OsNRT1.1B</i> <i>OsSPL14</i> <i>OsWRKY45</i> <i>OsSLR1</i> <i>OsACC</i>	75 70.8 75 12.5 66.7 77.3 54.5 63.6 26.1 78.3 83.3 66.7 54.2 38.1 61.9	[259]

			Base editor-CBE		<i>OsNRT1.1B</i> <i>OsSPL14</i> <i>OsWRKY45</i> <i>OsSLR1</i> <i>OsACC</i> <i>OsWaxy-1+OsWaxy-2+OsCDC48+OsSNB</i>	66.7 41.7 30.4 34.8 52.2 0+3.1+0+43.8 0+17.4+0+52.4 3.2+25.8+0+67.7	
	Nipponbare	Callus	Prime editor	<i>Agrobacterium</i>	<i>HPT</i> <i>OsPDS</i> <i>OsACC1</i> <i>OsWx</i> <i>OsACC1</i> <i>OsACC1</i>	100 31.3 14.6 0 18 6.3	[260]
	nd	Callus	Prime editor	<i>Agrobacterium</i>	<i>OsIPA</i> <i>OsTB1</i> <i>OsALS</i>	nd nd approx. 1.8 approx. 2.2	[261]
	Zhonghua11	Callus	Prime editor	<i>Agrobacterium</i>	<i>OsCDC48 (deletion)</i> <i>OsALS</i> <i>OsCDC48 (substitution)</i>	21.8 14.3 2.6	[262]
	Zhonghua11	Callus	Prime editor	Biolistic	<i>OsEPSPS</i>	2.2	[263]
	Nipponbare	Callus	CRISPR/Cas9-NG  CRISPR/Cas9  CRISPR/xCas9	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsLAZY</i> <i>IPA1</i> <i>DL</i> <i>BADH2</i> <i>OsPDS</i> <i>OsLAZY</i> <i>OsPDS</i> <i>OsLAZY</i>	95.8 62.5 93.8 89.6 12.5 82.3 50 10.4 64.6	[264]
	Nipponbare	Callus	CRISPR/AacCas12b CRISPR/AaCas12b CRISPR/AacCas12b CRISPR/AaCas12b CRISPR/dAaCas12b-TV	<i>Agrobacterium</i>	<i>OsEPFL9</i>  <i>OsEPFL9</i>  <i>OsROC5+OsEPFL9+OsGS3</i>  <i>OsROC5+OsEPFL9+OsGS3</i>	36.4  54.2  16.7 (double mutants) 66.7 (double mutants)	[265]

	Kitaake	Callus (cells)	Base editor-ABE+CBE	Biolistic <i>Agrobacterium</i>	<i>OsALS1</i>	28 24	[266]
	Nangeng 46	Callus	Base editor-CBE	<i>Agrobacterium</i>		10	
	Yandao 8	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSUN1+OsSUN2</i>	nd	[267]
	Nipponbare	Callus	CRISPR/Cas9-HDR	Biolistic	<i>OsALS</i> <i>OsCCD7</i>	1.58-9.87 1.5-8.8	[268]
	Nipponbare	Callus	SaKKHn-Base editor-CBE	<i>Agrobacterium</i>	16 target sites 3x multiplex O + 3 bp	6.3-75 (12 sites) 2.5-45.9 10-86.4	[269]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>GS3+ GL3.1</i>	100+72.2	[270]
	Nipponbare	Callus	CRISPR/xCas9  xCas9-CBE	<i>Agrobacterium</i>	GAA (PAM) GAT (PAM) GAG (PAM) GAC (PAM) NGG (PAM) NGA (PAM) NGT (PAM) NGC (PAM) GAA (PAM) GAT (PAM) GAG (PAM) NGG (PAM) NGA (PAM) NGT (PAM) NGC (PAM) GAC (PAM)	0-29.4 5-75 5-65 0 45-95 26.3-70 68.4-94.7 0-30 0-33.3 0-47.4 10-70 25-68.4 5.3-65 50-66.7 0-51.9 0-10.5	[271]
	Nipponbare	Callus	CRISPR/Cas9  CRISPR/Cas12a	<i>Agrobacterium</i>	<i>pOsXa13</i>  <i>OsPDS</i>	85.7 91.3 16.4 28.7	[272]
	VP 1636	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Pi21</i>	66	[273]
	CWA  Taichung T65	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PPR2</i> <i>pPPR2</i> <i>RMS</i> <i>RMS</i>	28.6 14.3 T <sub>1</sub> T <sub>1</sub>	[274]

	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>pWx<sup>b</sup></i> (1 or 2 targets)	42.6	[275]
	Chao2-10	Callus	CRISPR/Cas9-AAC	<i>Agrobacterium</i>	<i>LAZY1</i>	Approx. 80	[276]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsmiR535</i>	nd	[277]
	3-8 line	nd	CRISPR/Cas9	nd	<i>SAW1</i>	nd	[278]
	ASD16	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>eIF4G</i>	46	[279]
	Kitaake	Callus	Base editor-ABE	<i>Agrobacterium</i>	<i>OsWSL5+OsZEBRA3</i>	1.34+38.92 2.81+14	[280]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Dof1-30</i>	5-26.3 (homo)	[281]
	Nipponbare	Callus	CRISPR/FnCas12a	<i>Agrobacterium</i>	<i>DL</i> <i>ALS</i> <i>AAO2</i> <i>NCED1</i>	0-95.6 20-93.5 32.8-75.8 18.8-25	[282]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsCNGC14</i> <i>OsCNGC16</i>	nd	[283]
	nd	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsBHY+</i> <i>OsEHY+</i> <i>OsWaxy</i> (5 sgRNA)	nd	[284]
	Nipponbare	Callus	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	<i>OsALS</i>  <i>OsCly1</i>	0-0.26 (calli) 0.24-1.31 (calli) 0-0.52 (calli)	[285]
	nd	Callus	CRISPR/ SpG  CRISPR/SpCas9 CRISPR/SpRY	<i>Agrobacterium</i>	NGA (PAM) NGT (PAM) NGC (PAM) NGG (PAM) NGG (PAM) NAA (PAM) NAC (PAM) NAG (PAM) NTA (PAM) NTT (PAM) NTC (PAM) NTG (PAM) NCA (PAM) NCT (PAM) NCC (PAM) NCG (PAM) NGA (PAM)	100 66.7 4.2-95.8 0-93.7 35.4-100 1.7-95.6 0-40 0-67.8 0 2.1 2.1-2.4 0-2.1 0 0 0-2.1 0-20.8 2.1-16.67	[286]

			ABE-nSpCas9 ABE-nSpG ABE-nSpRY		NGT (PAM) NGC (PAM) NGG (PAM) NGG (PAM) NGG (PAM) NGG (PAM)	0-6.8 6.2-12.5 0-45.8 4.3 (calli) 4.3 (calli) 2.1 (calli)	
	Xidao #1	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsIPK1</i>	38.1	[287]
	Zhonghua11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGSK1+OsGSK2+OsGSK3+OsGSK4</i> <i>OsBZR1+OsBZR2+OsBZR3+OsBZR4</i> <i>OsPPKL1+ OsPPKL2+ OsPPKL3</i>	14.3 0 0 (lethal?)	[288]
	Kitaake	Callus	CRISPR/SpyMacCas9 CRISPR/iSpyMacCas9  iSpymac-zCas9-CBE  iSpymac-zCas9-ABE	<i>Agrobacterium</i>	<i>OsPDS-GAAG</i> <i>OsPDS-GAAG</i> <i>OsPDS-GAAA</i> <i>OsROC5-AAAG</i> <i>OsROC5- TAAA</i> <i>OsROC5- CAAA</i> <i>OsROC5- TAAA</i>	20 57.1 37.5 88.9 18.8 38.9 12.5	[289]
<i>Japonica</i>	Songjing	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsHd2-uORF1</i> <i>OsHd2-uORF2</i> <i>OsHd2-uORF3</i>	nd	[290]
	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>elF4G</i>	50	[291]
<i>Japonica</i>	Presidio	Callus	CRISPR/Cas9	<i>Agrobacterium</i> Biolistic	<i>OsPDS</i> <i>OsPDS</i>	61.2 59.4	[292]
<i>Japonica</i>	TP309	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGS3</i>	80	[293]
	Zhonghua 11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsOPR7</i>	100	[294]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsHOL1</i> <i>OsHOL2</i>	63 83.3	[295]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsTIR1</i> <i>OsAFB2</i> <i>OsTIR1+ OsAFB2</i> <i>OsAFB3</i> <i>OsAFB4</i> <i>OsAFB5</i>	Nd Nd Nd Nd Nd Nd	[296]
	Chunyou84 (CY84)	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZEP1</i>	73.3	[297]
	nd	nd	CRISPR/ScCas9 (Sc <sup>++</sup> )	<i>Agrobacterium</i>	NAG (PAM) NTG (PAM)	5.6-73.8 0-19	[298]

			CRISPR/ScCas9  Base editor-CBE  Base editor-ABE		NCG (PAM) NGG (PAM) NAG (PAM) NTG (PAM) NCG (PAM) NGG (PAM) NAG (PAM) NGG (PAM) NCG (PAM) NTG (PAM) NAG (PAM) NGG (PAM) NCG (PAM) NTG (PAM) NAG (PAM) NGG (PAM) NCG (PAM) NTG (PAM) NAG (PAM) NGG (PAM) NCG (PAM) NTG (PAM)	3.6-59 9.2-51.3 0-82.3 0-7.1 0-46.7 0-97.9 0-39.1 0-7.4 0-4.6 0 0-37 0 0 0 31.2-52.6 61.4-95.7 50 0 0-68.7 0-20.8 10.4 0	
	Kitaake	Callus	CRISPR/SpCas9-NG and CRISPR/SpG  CRISPR/SpRY Base editor-CBE Base editor-ABE	<i>Agrobacterium</i>	<i>OsPAL5</i> <i>OsGSK4</i> <i>OsCERK1</i> <i>OsETR2</i> <i>OsRLCK185</i> Multiple targets and PAMs <i>OsCOI2</i> <i>BSR-K1</i> <i>OsMPK13</i> <i>OsGS1</i> <i>BSR-D1</i> <i>OsGSK4</i>	62.5 and 30 52.6 and 36.2 46.3 and 11.1 5.2 and 2.2 2.6 and 2 2.13 to 73.9 34.1 4.3 29.8 93.7 0 51.3	[299]
	Nipponbare	Callus	SpCas9-NRRH  SpCas9-NRCH	<i>Agrobacterium</i>	PDS LAZY1 DL BADH2 PDS LAZY1	33.3 75 20.8 2 0 14.6	[300]



			CRISPR/Cas9	DL	12.5	
				BADH2	6.25	
				PDS	75	
				LAZY1	20.8	
				DL	79.2	
			NRRH-Base editor-CBE	BADH2	8.3	
				IPA1-CAGC	33.3	
				Pikh-GAGC	75	
				WX-GAAA	64.6	
				IPA1-CAGC	25	
				Pikh-GAGC	43.7	
				WX-GAAA	29.2	
			NRRH-Base editor-ABE	IPA1-GAGT	100	
				ACC1-CAGA	100	
				Pi37-TAAA	52	
			NRCH-Base editor-CBE	Pita-GACT	100	
				IPA1-AACC	0	
				ALS-CACC	2	
				Pita-GACT	35.4	
				IPA1-AACC	4.2	
				ALS-CACC	20.8	
			NRCH-Base editor-ABE	Hd6-GACC	100	
				NAL1-GACT	89.6	
				PSS2-TACC	87.5	
			NRTH-Base editor-CBE	IPA1-GATA	72.9	
				D2-CATC	75	
				GS5-AATT	0	
			NRTH-Base editor-ABE	Pi36-TATT	100	
				Pi37-CATC	100	
				SPL18-AATC	100	
			SpG-Base editor-CBE	Pita-TGA	87.5	
				D2-CGC	79.2	
				ACC1-AGC	47.9	
				SLR1-GGT	37.5	
				Pita-TGA	77	
				D2-CGC	33.3	
				ACC1-AGC	29.2	
				SLR1-GGT	33.3	
			SpG-Base editor-ABE	Hd6-GGA	100	
				IPA1-AGT	100	

			SpRY-Base editor-CBE		ACC1-TGC NAL1-TGA TAC1-GAA IPA1-CAG ACC1-AAC SLR1-TCG TT1-CTT TAC1-GAA IPA1-CAG ACC1-AAC SLR1-TCG TT1-CTT SPL13-TAG ACC1-CGA IPA1-GCT NAL1-ACT WX-TTC	85.4 79.2 52 16.7 8.3 0 0 12.5 6.2 14.6 0 0 47.9 22.9 6.2 0 0	
			SpRY-Base editor-ABE				
	nd	Callus	CRISPR/LbCas12a CRISPR/Lb5Cas12a CRISPR/BsCas12a CRISPR/Mb2Cas12a CRISPR/TsCas12a CRISPR/MICas12a CRISPR/BoCas12a CRISPR/MbCas12a CRISPR/ErCas12a CRISPR/LbCas12a CRISPR/Lb5Cas12a CRISPR/BsCas12a CRISPR/Mb2Cas12a CRISPR/TsCas12a CRISPR/MICas12a CRISPR/BoCas12a CRISPR/MbCas12a CRISPR/ErCas12a CRISPR/MbCas12a  CRISPR/LbCas12a	<i>Agrobacterium</i>	<i>OsDEP1</i> -TTTC          <i>OsEPFL9</i> -TTTG          <i>Os09g37860</i> -CTTC <i>Os12g24050</i> -GTTG 16 targets	90 54.5 37.5 68.4 100 0 29.2 70.6 44.4 91.7 68.4 88.2 83.3 85 40.9 14.3 58.6 89.3 80 20 Avg. 89.3 (16x 4.8)	[301]

	Zhonghua11	Callus	Base editor-CBE	<i>Agrobacterium</i>	<i>OsALS-P171</i> <i>OsALS-G628</i> <i>OsALS-P171+OsALS-G628</i>	35 50 19.2	[302]
<i>Indica</i>	Longke638S	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Bsr-d1</i> <i>Pi21</i> <i>ERF922</i> <i>Bsr-d1/Pi21/ERF922</i>	82 68 73 71	[303]
<i>O. alta</i> (CCDD)	polyploid rice 1	Callus	CRISPR/Cas9  Base editor-CBE CRISPR/Cas9	<i>Agrobacterium</i>	<i>OaQSH1-CC+OaQSH1-DD</i> <i>OaAn-1-CC+OaAn-1-DD</i> <i>OaAn-1-DD</i> <i>OaSD1-CC+OaSD1-DD</i> <i>OaGS3-CC+OaGS3-DD</i> <i>OaIPA1-CC+OaIPA1-DD</i> <i>OaGhd7-CC+OaGhd7-DD+OaDTH7-CC+OaDTH7-DD</i>	nd	[304]
<i>indica</i>	IR58025B	Callus	CRISPR/ LbCas12a	<i>Agrobacterium</i>	<i>xa13</i> –transgene-free enrichment-1 <i>xa13</i> –transgene-free enrichment-2	39.6 56.4	[305]
<i>Oryza alta</i>	PPR1	Callus	CRISPR/Cas9-de novo domestication  Base editor-CBE	<i>Agrobacterium</i>	<i>OaQSH1-CC+OaQSH1-DD</i> (1 guide) <i>OaAn-1-CC+OaAn-1-DD</i> (1 guide) <i>OaSD1-CC+OaSD1-DD</i> (1 guide) <i>OaGS3</i> (1 guide) <i>OaGhd7-CC+OaGhd7-DD+OaDTH7-CC+ OaDTH7-DD</i> (3 guides) <i>OaIPA1-DD</i> (1 guide)	Nd Nd Nd Nd Nd 75 Nd	[306]
	Nipponbare	Callus	CRISPR/SpRY  SpRY-Base editor-CBE SpRY-Base editor-ABE	<i>Agrobacterium</i>	<i>OsPDS</i> <i>OsDEP1</i> <i>OsDEP1</i> <i>OsALS</i> <i>OsPDS</i>	Up to 95.7 Up to 100 Up to 42.1 72.2 Up to 79	[307]
<i>Japonica</i>	Nanjing46	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPHYC</i>	nd	[308]
	IPB3S	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSD1</i>	nd	[309]
<i>Japonica</i>	Nipponbare	Callus	iSpyMacCas9-CBE Base editor-CBE	<i>Agrobacterium</i>	<i>OsROC5</i> <i>OsCGRS55</i> <i>OsCGRS56</i> <i>OsCGRS57</i> <i>OsCGRS58</i> <i>OsCGRS55</i> <i>OsCGRS56</i>	68.8 18.8 9.5 30 16.7 10 22.7	[310]



			ScCas9n++-base editor-CBE		<i>CHALK5-3</i> <i>Wx-6</i> <i>Sd1</i> <i>ALS</i> <i>IPA1</i> <i>GS3</i> <i>TB1</i> <i>MADS26</i> <i>Wx-1</i> <i>Wx-2</i> <i>Wx-3</i> <i>Euil-4</i> <i>Euil-5</i> Intergenic-1 <i>Os03g0163600</i> <i>Os01g0101150</i> <i>Os01g0101200</i> Intergenic-2 <i>Wx-1+Wx-2+Wx-3+Euil-4+Euil-5</i>	0 78.6 51.8 0 11.1 0 0 0 8.7 60.9 60.9 21.7 60.9 75 80.6 13.9 86.1 8.3 nd	
<i>Indica</i>	TianFengB						
<i>Japonica</i>	Guihong1 Zhonghua11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSWEET11</i> <i>OsSWEET14</i> <i>OsSULTR3;6</i>	nd	[312]
	Zhonghua11	Callus	CRISPR-MAD7	<i>Agrobacterium</i>	<i>OsALS</i> <i>OsEPSPS</i> <i>OsNRAMP5</i>	49 65.6 56.9	[74]
	Nipponbare	Callus	Nm1-base editor-ABE  CRISPR/Nm1Cas9	<i>Agrobacterium</i>	<i>PDS-1</i> <i>NAL1-4</i> <i>WX-3</i> <i>OsPDS-1</i> <i>NAL1-4</i> <i>WX-3</i> <i>ACC-1</i> <i>GS5-1</i> <i>Hd6-1</i> <i>ACC-1</i> <i>GS5-1</i> <i>Hd6-1</i> <i>ALS-1</i> <i>PDS-1</i> <i>PDS-2</i>	0 0 1 4.2 87.5 12.5 0 0 2 25 0 33.3 Approx. 60 Approx. 62 Approx. 63	[313]



	Nangeng 46		ScCas9n-Base editor-ABE  Base editor-ABE		<i>OsMPK13</i> site 2 <i>OsGS1</i> site 3 <i>OsGS1</i> site 4 <i>OsSERK2</i> site 2 <i>Wx</i> <i>OsCPK6</i> <i>OsMPK9</i> <i>OsALS1+OsGS1</i> site 3 <i>OsTubA2+OsACC</i> site 2 <i>OsALS1+OsGS1</i> site 3+ <i>OsTubA2+OsACC</i> site 2	33.3 95.8 41.7 66.7 68.7 10.4 0 72.9 (plants) 73.8 56.2	
	nd	nd	CRISPR/Cas9-TKC	nd	4 genes 4 genes 5 genes	61.5 19 0 (lethal gene)	[320]
	Nipponbare	nd	CRISPR/Cas9	nd	<i>CAO1</i>	nd	[321]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsPLT8</i> <i>OsPLT9</i> <i>OsPLT7</i> <i>OsAP2</i> <i>OsAD5</i>	Nd Nd Nd Nd Nd	[322]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>pOsREM20</i> <i>OsREM20</i>	Nd Nd	[323]
	Nipponbare	Callus	eCDAL-base editor-CBE  pDuBE1-base editor-ABE	<i>Agrobacterium</i>	<i>ALS</i> <i>BADH2</i> <i>LAZY1</i> <i>PDS</i> <i>BADH2</i> <i>FSD2</i> <i>LAZY1</i> <i>PDS</i> <i>ALS</i> (dual C-to-T and A-to-G conversion)	81.3 95.8 68.8 87.5 89.6 (dual) 68.7 (dual) 72.9 (dual) 58.3 (dual) 100	[324]
	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsVQ4</i>	nd	[325]
<i>Japonica</i>	Jingeng 818	Callus	CRISPR/Cas9 knock-up	<i>Agrobacterium</i>	911 kb inversion 338 kb duplication	3 0.1	[326]
<i>Indica</i>	CO51	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSWEET14</i>	83.3	[327]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Os02circ25329</i>	14	[328]

					<i>Os06circ02797</i> <i>Os03circ00204</i> <i>Os05circ02465</i>	8.8 10.9 13.6	
<i>Indica</i>	MTU1010	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGW2</i>	62.5	[329]
	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Oscmt2</i> <i>Oscmt3a</i> <i>Oscmt3b</i> <i>Osdrm1a</i> <i>Osdrm1b</i> <i>Osdrm2</i> <i>Osdrm3</i> <i>Osmet1a</i> <i>OsMET1b</i> <i>Oscmt2/3a</i> <i>Osdrm1a/1b</i> <i>Osdrm2/3</i> <i>Osdrm2/cmt2</i> <i>Osdrm2/cmt3a</i> <i>Osdrm2/cmt2/3a</i> <i>Osdrm2/3/cmt2/3a</i> <i>Osdrm2/3/cmt2/3a/3b</i>	nd	[330]
	Pusa Basmati1 (PB1)	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGA20ox2</i>	8.75	[331]
<i>Indica</i>	Ciherang-Sub1	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SUB1A</i>	100	[332]
	Nipponbare	Callus	CRISPR/Cas9	nd	<i>OsOR</i>	nd	[333]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>LHW</i> <i>ARF15</i> <i>OSH6</i>	nd	[334]
	RT102A	Callus	mitoTALEN	<i>Agrobacterium</i>	<i>orf352</i>	nd	[335]
	Kitaake	Callus	Base editor-CBE SpRY-base editor-CBE	<i>Agrobacterium</i>	<i>OsALS</i>	47.6-94.1 47.6-75	[336]
	NIL- <i>HL6</i>	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsSPL10</i>	nd	[337]
	Zhonghua 11	nd	CRISPR/Cas9	nd	<i>SWEET2a</i>	nd	[338]
	Dongjin	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OFF</i>	nd	[339]
<i>Indica</i>	ASD16	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>eIF4G</i>	32.3-62.5	[340]



<i>Oryza rufipogon</i> Griff	CLCWR	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OrNCED3</i> <i>OrNCED5</i> <i>OrNCED1-OrNCED3</i>	50-70 60-70 20-30	[341]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsXLG1</i> <i>OsXLG2</i> <i>OsXLG4</i> <i>Osxlg1&amp;2</i> <i>Osxlg1&amp;4</i> <i>Osxlg2&amp;4</i> <i>Osxlg1,2&amp;4</i>	nd	[342]
	Taipei-309	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsLip1</i>	nd	[343]
	Kitaake	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CYP76M7+CYP76M8</i>	nd	[344]
	Dongjin	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsMORE1a</i>	40	[345]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsGA3ox1</i>	nd	[346]
	Kitaake	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>RLK</i> family (1,072 members)	89	[347]
	Zhonghua11	Callus	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	Marker gene excision	73.3	[348]
	Nipponbare	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>TAS3a</i> <i>TAS3b</i> <i>TAS3c</i>	nd	[349]
	Nipponbare	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>OsAP47</i>	nd	[350]
	Zhonghua11	Callus	Prime editor	<i>Agrobacterium</i>	<i>OsALS</i>	11.3 2.1	[351]
	Zhonghua11	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CDC20.1+CDC20.2+CDC20.3</i>	nd	[352]
Sorghum	nd	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>mDsRED2</i>	33	[353]
	Tx430	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Sb-CENH3</i>	37-40	[354]
	Tx430	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>k1C</i> gene family	92.4	[355]
	P898012	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SbFT</i> <i>SbGA2ox5</i>	33.3 83.3	[356]
	Tx430	Immature embryo	CRISPR/Cas9	Biolistic	<i>SbLG1</i>	33.3	[357]

	Wheatlan	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SbBADH2</i>	38.9	[358]
	nd	Embryogenic callus	CRISPR/Cas9	Biolistic	<i>GHD7, ̢-kafrin, ̣-kafrin, IDS1, SID1</i>	55.6-90.1	[35]
	RTx430, BTx623, BTx642, SC187	Immature embryos	CRISPR/Cas9	<i>Agrobacterium</i>	<i>pds</i>	16.7	[359]
Soybean	Bert	Cotyledons	ZFN	<i>A. rhizogenes</i>	<i>DCL1a, DCL1b</i> <i>DCL2a, DCL2b</i> <i>DCL4a+ DCL4b</i> <i>RDR6a, RDR6b, HEN1a</i> <i>DCL4a+ DCL4b</i>	0-100%  66.7%	[360]
	Bert	Half-seed	TALENs	<i>A. rhizogenes</i>	<i>FAD2-1A + FAD2-1B</i>	21%	[361]
	Jack	cotyledons	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>Glyma07g14530</i> <i>Glyma01g38150+ Glyma11g07220</i> <i>miR1509, and miR1514</i>	95 % of transgenic roots	[362]
		Somatic embryos		Biolistic	<i>Glyma07g14530, 01g, 11gDDM1</i>	nd	
	Bert	cotyledons	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>GS1, CHI20</i>	100 % of transgenic roots	[363]
	Williams	Cotyledonary node	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>Glyma06g14180, Glyma08g02290, Glyma12g37050</i>	3-20 % of transgenic roots	[364]
	93B86	Embryogenic callus	CRISPR/Cas9-HDR	Biolistic	DD20 Genomic location  DD43 Genomic locations	Callus: OK; plants: not HDR: nd Callus ok Plants ok HDR: nd	[365]
	Bert Mutated in FAD2-1A, FAD2-1B	Half-seed	TALENs	Biolistic	<i>FAD3</i>	22%	[366]
	Hill	Cotyledonary node	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>Rj4</i> <i>Glyma.01G165800,</i> <i>Glyma.01G165800-D</i>	nd	[367]
	Bert	Half-seed	ZFN	<i>A. rhizogenes</i>	<i>DCL1a + DCL1b</i>	17%	[368]

	Jack	Cotyledon  Cotyledonary node	TALENs CRISPR/Cas9 CRISPR/Cas9	<i>A. rhizogenes</i>  <i>Agrobacterium</i>	<i>PDS11, PDS18</i>  <i>PDS11+PDS18</i>  <i>PDS11+PDS18</i>	18-21 % of hairy roots 12-48% of hairy roots nd	[369]
	Williams 82	Cotyledonary node	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>Rj4</i>	nd	[370]
	Bert	Half-seed	TALENs CRISPR/Cas9	<i>A. rhizogenes</i>	<i>Dcl2a, Dcl2b, Dcl3a</i> <i>Drb2a+Drb2</i>	0-75% 75%	[371]
	Kariyutaka	Cotyledonary node	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PPD1+PPD2</i>	nd	[372]
	Jack	Half-seed	CRISPR/Cas9	<i>Agrobacterium</i>	<i>FT2, GmFT5a</i>	36%-72%	[373]
	Jinong 38	Half-seed	CRISPR/Cas9	<i>Agrobacterium</i>	<i>FAD2-2</i>	21 %	[374]
	Tianlong 1	Cotyledonary node	CRISPR/Cas9	<i>Agrobacterium.</i>	<i>Hsp90A2</i>	nd	[375]
	Williams 82	Cotyledonary node	CRISPR/Cas9	<i>Agrobatcerium</i>	<i>SPL9a+SPL9b+SPL9c+SPL9d</i>	nd	[376]
	Harosoy	Cotyledonary node	CRISPR/Cas9	<i>Agrobatcerium</i>	<i>LHY1a+ LHY1b+ LHY2a+HY2b</i>	5%	[377]
	Maverick	Cotyledonary node	CRISPR/Cas9	<i>Agrobatcerium</i>	<i>GmFAD2-1A + GmFAD2-1B.</i>	100 %	[378]
	Jack	Cotyledonary node	CRISPR/Cas9	<i>Agrobacterium</i>	<i>E1</i>	75%	[379]
	Harosoy 63	Cotyledonary node	CRISPR/Cas9	<i>A. rhizogenes</i>	Glyma.20g148400, Glyma.20g146200, Glyma.10g246300, Glyma.20g148200, Glyma.10g037100, Glyma.03g163500, Glyma.19g164900, Glyma.13g123500, Glyma.19g164800	4-44% of hairy root	[380]
	X5  Westag 97  Maverick	Embryogenic callus   Immature embryos	ZFN	Biolistic	Targeted insertions of large fragments into the FAD2-1a gene via HDR Targeted insertions of large fragments into the FAD2-1a gene via NHEJ Targeted insertions of large fragments into the FAD2-1a gene via NHEJ	Callus: Via HDR: 0-9%. Callus: Via NHEJ: 8-27% Targeted insertion in regenerated plants via NHEJ: 0.04%	[381]
	Jack	Somatic embryos	CRISPR/Cas9	Biolistic	<i>CPR5</i>	100%	[382]
	Williams 82	Cotyledonary node	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SWEET15a+SWEET15b</i>	Nd	[383]

	Williams 82	Cotyledonary node	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>LCLa1+ LCLa2+ LCLb1+ LCLb2</i>	Nd	[384]
	Jack	nd	Base editing-CBE	<i>Agrobacterium</i>	<i>FT2a</i> <i>FT4</i>	18% 6%	[385]
	Zigongdongdou Jack	Half-seed	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PRR37</i>	nd nd	[386]
	Huachun 6	Cotyledonary node	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Lox1+ Lox2+ Lox</i>	37%	[387]
	Jinong 38	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>FAD2-1A +FAD2-2A</i>	66.67%.	[388]
	Jack	Cotyledons Cotyledonary nodes	CRISPR/Cas9	<i>A. rhizogenes</i> <i>Agrobacterium</i>	<i>F3H1+F3H2+FNSII-1</i> <i>F3H1 + F3H2 + FNSII-1</i>	6-13% 44 %	[389]
	Tianlong no 1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Nac8</i>	nd	[390]
	Hx3	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>APa1a+ APa1b + APa1c+ APa1d</i>	20%	[391]
	Tianlong 1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PRR3b</i>	nd	[392]
	Jack	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>NMHC5</i>	25%	[393]
	DongNong50	Embryonic tips of mature seeds.	CRISPR/Cas9	Biolistic	<i>LMM2</i>	nd	[394]
	Tianlong1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>DCL2a + DCL2b</i>	nd	[395]
	Bert	Cotyledonary nodes	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>KASII</i>	100%	[396]
	Maverick DT26 Maverick DT26	Cotyledons  Cotyledonary nodes	CRISPR/Cas9	<i>A. rhizogenes</i>  <i>Agrobacterium</i>	<i>GOLS1A + GOLS1B</i> <i>GOLS1A + GOLS1B</i> <i>GOLS1A + GOLS1B</i> <i>GOLS1A + GmGOLS1B</i>	100% of roots 100% of roots 100% 100%	[397]
	Enrei Kariyutaka	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>m Bd 28 K + m Bd 30 K</i>	nd	[398]
	Jack	Embryogenic callus	CRISPR/Cas9	Biolistic	<i>m Bd 30K</i>	100%	[399]

	Williams 82	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MS1</i>	nd	[400]
	Williams 82	hypocotyl	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>lncRNA77580</i>	nd	[401]
	N8855	Half-seeds	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PPR576</i>	33%	[402]
	Tianlong 1	Half-seeds	CRISPR/Cas9	<i>A. rhizogenes</i> <i>Agrobacterium</i>	<i>PLA-IIε, PLA-IIζ</i>	nd	[403]
	Williams 82	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>LNK2a + LNK2b + LNK2c + LNK2d</i>	nd	[404]
	Williams 82	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>FATB1a+FATB1b</i>	nd	[405]
	nd	nd	CRISPR/Cas9	nd	<i>Glyma.13G114200</i>	nd	[406]
	Huachun 6	nd	CRISPR/Cas9	nd	<i>GmJAG1+ GmJAG2</i>	nd	[407]
	Williams 82	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>GmAMS1, GmAMS2</i>	14-25%	[408]
	ZP661	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Glyma.13G114200</i>	nd	[409]
	Jack	nd	CRISPR/Cas9	nd	<i>NMHC5</i>	nd	[410]
	nd	nd	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>DRR1</i>	nd	[411]
	93Y21	embryonic axes	CRISPR/Cas9-HDR	<i>Ochrobactrum haywardense</i> Oh H1-8	DD38 genomic sites DD51 genomic sites	HDR:3.4% HDR:2 %	[412]
	Tianlong1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>E1</i>	nd	[413]
	Williams 82	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>HSP17.9</i>	nd	[414]
	DS-9712	Leaf disks	CRISPR/Cas9	<i>Agrobacterium</i> -mediated Disc Assay for Transient Expression <i>Agrobacterium</i>	<i>IPK2</i>	60%	[415]
		Cotyledonary nodes				nd	
	Tian Long 1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>BIC1a+ BIC1b + BIC2a + BIC2b</i>	nd	[416]

	Huachun6	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PDH1</i>	43%	[417]
	Tianlong No. 1	Cotyledonary nodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>UGT</i>	nd	[418]
Maize	nd	Immature embryo	CRISPR/Cas9 (HDR)	Biolistic <i>Agrobacterium</i>	<i>LIG1, Ms26, Ms45, ALS1, ALS2</i>	1.3-3.9	[419]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PSY1</i>	10.67	[420]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Zmzb7</i>	19-31	[421]
	nd	Immature embryo	CRISPR/Cas9 CRISPR/Cas9-HDR	Biolistic	<i>ARGOS8</i>	60-98 1	[422]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPDS, ZmIPK1A, ZmIPK, ZmMRP4</i>	13.1-19.1	[423]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmLG1, UB2, and UB3</i>	4.1	[424]
	B73-329	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmTMS5</i>	nd	[43]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmMS26</i>	27.8	[425]
	NP2222	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MATL</i>	nd	[426]
	Z31	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmLTPg11, ZmLTPx2</i>	21.5-26.7	[427]
	Hi-II, B104	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmAgo18a, ZmAgo18b, a1, a4</i>	16-35	[428]
	PH1V69	Immature embryo	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	<i>NptII</i>	4.7	[429]
	B104	Immature embryo	CRISPR/Cas9 CRISPR/Cas12a	<i>Agrobacterium</i>	<i>gl2</i>	90.3-100 0-60	[430]
	ND73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CDPK10</i>	69-93	[431]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MS8</i>	nd	[432]
	Hi-II	Immature embryo	CRISPR/Cas9–gRNA RNP	Biolistic	<i>LIG, ALS2, MS26, MS45</i>	2.4-9.7	[433]
	A188	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>20 maize kernel development genes</i>	53	[434]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>zb7</i>	66	[435]
	Hi-II	Immature embryo	CRISPR/Cas9 CRISPR/Cas12a	<i>Agrobacterium</i>	<i>Opaque2</i>	nd	[436]

	355, LN005M, XCW175	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmBADH2a, ZmBADH2b</i>	nd	[437]
	Cal	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>GA20ox3</i>	nd	[438]
	PH1V5T	Immature embryo	CRISPR/Cas9-RNP	<i>Agrobacterium</i>	<i>pericentric inversion in chromosome</i>	nd	[439]
	KN5585	Immature embryo	CRISPR/Cas9-RNP	<i>Agrobacterium</i>	<i>Zm00001d040611, Zm00001d033267</i>	nd	[440]
	B104	Immature embryo	CRISPR/Cas9 CRISPR/Cas12a	<i>Agrobacterium</i>	<i>A842B-2-2, A842B-5-1</i>	51.4-100	[441]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>14 TF genes</i>	nd	[442]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPRO1, ZmPRO3</i>	0-90	[443]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>1244 candidate genes</i>	51-91	[444]
	nd	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>br2</i>	nd	[445]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MADS, MYBR, AP2, RPL, PPR, lncRNA, lncRNA2</i>	57.1-100	[446]
	NP2222	Immature embryo	CRISPR-Cas12a-RNP	Biolistic	<i>Bx9</i>	60-100	[447]
	PH184C, PHH5G, PH1CJB, PH1V69, PH25KM, PH2DNP, PH1D84, PH1V5T, PH2DYM, PH17JT, PH1W4R, PH4257	Immature embryo	CRISPR/Cas9	Biolistic	<i>Wx1</i>	4-19	[448]
	B73	Immature embryo	CRISPR/Cas9-Prime	<i>Agrobacterium</i>	<i>ZmALS1, ZmALS2</i>	15.2-71.4	[449]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPHYC1, ZmPHYC2</i>	nd	[450]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>stiff1</i>	nd	[451]
	PH184C, PH1V5T	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>CXE-20</i>	8.3	[452]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmGAMYB, ZmGAMYB-2</i>	nd	[453]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>dek42</i>	nd	[454]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmCCT9</i>	nd	[455]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmGB1</i>	nd	[456]

	ZC01	Immature embryo	CRISPR/Cas9-APOBEC1	<i>Agrobacterium</i>	<i>ZmALS1, ZmALS2</i>	nd	[457]
	B104	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmCLCg</i>	10-70	[458]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPT7</i>	nd	[459]
	32990700	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmHKT2</i>	nd	[460]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ct2</i>	nd	[461]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Zmpif3, Zmpif4, Zmpif5</i>	nd	[462]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmACD6</i>	nd	[463]
	PHFFB	Immature embryo	CRISPR/Cas9-HDR	Biolistic	<i>Rf4</i>	nd	[464]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>nrpc2, smk7</i>	nd	[465]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>coi1a, jaz15</i>	nd	[466]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmMs33</i>	nd	[467]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Zmsmc3</i>	25-100	[468]
	B73-329	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmCEP1</i>	nd	[469]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>gl2</i>	80	[470]
	B104	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmSIP</i>	nd	[471]
	B73-329	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmNL4</i>	nd	[472]
	W22	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmbZIP22</i>	nd	[473]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>wx</i>	80-100	[474]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>Zmabcg, zmfar1</i>	nd	[475]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmGRP1</i>	nd	[476]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>AGAP, KNR6</i>	nd	[477]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmMs25</i>	nd	[478]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>srl5</i>	nd	[479]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>lox3</i>	62.8	[480]



	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>dcl5</i>	nd	[481]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPEPR1, ZmPEPR2</i>	nd	[482]
	Hi-II B104	Immature embryo	TALEN	<i>Agrobacterium</i>	<i>gl2</i>	3.7 10	[483]
	LH244	Immature embryo	CRISPR/Cas12a	<i>Agrobacterium</i>	<i>180 kb chromosomal region</i>	30–100	[484]
	Zheng 58, Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmTGA9-1/-2/-3, ZmDFR1, ZmDFR2, ZmACOS5-1, ZmACOS5-2</i>	80-84	[485]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>YIGE1</i>	nd	[486]
	ZC01	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmGDIα</i>	41	[487]
	KN5585	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmPAT7</i>	nd	[488]
	B73	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmMI, ZmNTN2</i>	nd	[489]
	B104	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmCOI2a, ZmCOI2b</i>	nd	[490]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmFCP1, ZmCLE7, ZmCLE1E5</i>	nd	[491]
	Hi-II	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>mms21</i>	nd	[492]
	LH244	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>zmpld3, mtl, zmdmp</i>	nd	[493]
	Q319	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>ZmThx20</i>	nd	[494]
	B104	Immature embryo	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SAMBA-1, samba-2, samba-3</i>	nd	[495]
	Hi-II	nd	CRISPR/Cas9	nd	<i>GRX</i>	nd	[496]
Potato <i>Solanum tuberosum</i> L.	double-haploid DM	stem segments	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StIAA2</i>	83.3	[497]
	Désirée MSX914-10	leaf[498]	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StALS1</i>	5-60 3-55	[499]
	Ranger Russet	Protoplast	TALEN	PEG	<i>VInv</i> (4 alleles)	11-33	[500]
	Ranger Russet	explant	TALEN-knock-in	<i>Agrobacterium</i>	<i>mStALS</i>	7	[501]
	D52	leaf	pLSLm+CRISPR	<i>Agrobacterium</i>	<i>ALS1</i>	32.2	[502]

			pLSLm+TALEN pLSLm+TALEN/RT2			33.3 34.5	
	Désirée	protoplast	TALEN	PEG	ALS	10	[503]
	Sassy	nd	TALEN	<i>Agrobacterium</i>	<i>StSSR2</i>	6.9	[504]
	Kuras (tetraploid)	protoplast	CRISPR/Cas9	PEG	<i>GBSS</i>	10.3	[505]
	Désirée	internode	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StMYB44</i>	81.8	[506]
	Kuras (tetraploid)	protoplast	CRISPR/Cas9-RNP	PEG	<i>GBSS</i>	9	[507]
	Sayaka	Stem internodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>GBSSI</i> (2x gRNA) <i>GBSSI</i> (3x gRNA)	54 (>1 allele) 28 (all 4 alleles)	[508]
	Mayqueen	Shoot	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>St16DOX</i>	nd	[509]
	Phureja S15-65	internodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>S-RNase</i>	5.2	[510]
	Désirée	Stem and petiole	CRISPR/CBE	<i>Agrobacterium</i>	<i>StALS1</i>	25	[511]
	Sassy	Internodes	TALEN	<i>Agrobacterium</i>	<i>SSR2</i>	nd	[512]
	Xuan Shu 2	Stem segments	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StPDS</i>	46.7	[513]
	DRH 195 DRH 310	Leaf	CRISPR/Cas9	<i>Agrobacterium</i>	<i>S-RNase</i>	4.3 3.8	[514]
	Désirée	protoplast	CRISPR/Cas9	PEG	<i>GBSS</i>	35	[515]
	Désirée	Stem protoplast	CRISPR/Cas9	<i>Agrobacterium</i> PEG	<i>SBE1+SBE2</i>	6 (large del.) 1.5	[516]
	Désirée	protoplast	Base editing-ABE	PEG	<i>StGBSS</i>	6.5	[169]
	Désirée	Stem, petiole protoplast	CRISPR/Cas9 Base editing-CBE CRISPR/Cas9 (transient)	<i>Agrobacterium</i> PEG	<i>StGBSSI</i> <i>StGBSSI</i> (2x) <i>StGBSSI</i> (2x) <i>StGBSSI</i>	71 86.6-89.6 0.7-8.6 16	[517]
<i>Solanum chacoense</i>	DMF1	Stem	CRISPR/Cas9	<i>A. rhizogenes</i>	<i>StPDS</i> (2x)	25-100	[518]
	Sassy	Stem	TALEN	<i>Agrobacterium</i>	<i>SSR2</i>	5.1	[519]
	Désirée	Protoplast	CRISPR/Cas9-RNP	PEG	<i>StPPO2</i>	24-68	[520]
	Désirée	Stem, petiole	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StSS6</i>	50	[521]

	Désirée	Stem, petiole	CRISPR/SaCas9 CRISPR/SaCas9-CBE	<i>Agrobacterium</i>	<i>StGBSSI + StDMR6-1</i> <i>StDMR6-1</i>	0+33 8	[522]
	Désirée	Stem, petiole	CRISPR/SpCas9-NG CRISPR/SpCas9-NG-CBE CRISPR/SpCas9-NG-ABE	<i>Agrobacterium</i>	<i>StDMR6-1+ StGBSSI</i>	0+10 9+64 8+48	[523]
	Désirée	Tuber Leaf	CRISPR/Cas9	<i>Agrobacterium</i>	<i>PDS</i>	47-88 64-78	[524]
	Chicago	meristem	CRISPR/Cas9-RNP	Biolistics Vacuum infiltration	Coilin	nd	[525]
	Désirée	Protoplast internodes	CRISPR/Cas9-RNP CRISPR/Cas9 CRISPR/Cas9	PEG <i>Agrobacterium</i>	<i>StPPO2</i>	18.4 31.9 9.6	[526]
	Désirée  King Edward	Leaf	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StMLO1</i> <i>StHDS</i> <i>StTTM2</i> <i>StCHL1</i> <i>StDMR6-2</i>  <i>StDND1</i> <i>StDMR6-1</i>	33 14 16.1 76 23.9 14.2 3.9 11.7	[527]
	Atlantic	Stem segmenst	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StSSR2</i>	46	[528]
	Sayaka	Stem internodes	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SBE3</i>	71 (8 all 4 alleles)	[529]
	Désirée	Protoplast	CRISPR/Cas9-RNP	PEG	<i>Sbe1</i> <i>Sbe1+Sbe2</i>	52 72	[530]
	Yagana-INIA	Internode, leaves	CRISPR/Cas9	<i>Agrobacterium</i>	<i>StPPO1</i> <i>StPPO2</i> <i>StvacINV1</i> <i>StBAM1</i>	1 0 0 4.7	[531]
	CE3027	nd	CRISPR/Cas9	<i>Agrobacterium</i>	<i>pStFLORE</i>	2	[532]
	Russet Burbank	Internodal stem	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	<i>StCCoAOMT</i>	6.2	[533]
	Désirée	Leaf disc	CRISPR/Cas9	<i>Agrobacterium</i>	<i>VInv</i>	nd	[534]
Cassava ( <i>Manihot</i> )	60444 TME 204	Friable embryogenic callus (FEC)	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MePDS-1/MePDS-2</i>	47 22	[535]

<i>esculenta</i> Crantz)							
	60444	Friable embryogenic callus (FEC)	CRISPR/Cas9	<i>Agrobacterium</i>	<i>MeGBSS</i> <i>MePTST1</i>	86 100	[536]
	60444	Friable embryogenic callus (FEC)	CRISPR/Cas9	<i>Agrobacterium</i>	<i>nCBP-1</i> <i>nCBP-2</i> <i>nCBP-1/2</i>	Avg. 91	[537]
	TME 419	Friable embryogenic callus (FEC)	CRISPR/Cas9-HDR-based gene tagging	<i>Agrobacterium</i>	<i>MeSWEET10a(GFP-tag)</i>	2	[538]
	TME 419 TME 204	Friable embryogenic callus (FEC)	CRISPR/Cas9-HDR	<i>Agrobacterium</i>	EPSPS (TIPA) (3.2 kb)	0.13 events per cm <sup>3</sup> settled cell volume	[539]
	60444	Friable embryogenic callus (FEC)	CRISPR/Cas9	<i>Agrobacterium</i>	SBE2	93.02	[540]
Foxtail millet ( <i>Setaria italica</i> L.)	Ci846	Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SiNP1</i>	nd	[541]
<i>S. viridis</i> (green foxtail)		Callus	CRISPR/Cas9	<i>Agrobacterium</i>	<i>SvLes1</i> (2 targets)	nd	[542]
Foxtail millet ( <i>Setaria italica</i> )	Yugu1  Xiaomi	Callus	CRISPR/Cas9  Base editing-CBE Base editing-ABE CRISPR/SpCas9 multiplex (MCTU)	<i>Agrobacterium</i>	<i>FMBP</i> <i>Dof4</i> <i>BADH2</i> <i>GBSS1</i> <i>Dof4</i> <i>ALS</i> <i>ACC</i> <i>Dof4, BADH2, GBSS1, and IPK1</i>	100 100 83.3 100 100 50 30.8 80 (quadruple)	[543]

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