YMTHE, Volume 28

Supplemental Information

BEON: A Functional Fluorescence Reporter

for Quantification and Enrichment

of Adenine Base-Editing Activity

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Supplementary Information

Supplementary Table I. Oligos for PCR and construction of gRNAs and reporters

Purpose	Name	Sequences (5' \rightarrow 3')
	S1gRNA-F	ACCGATGACAGGCAGGGGCACCG
	S1gRNA-R	AAACCGGTGCCCTGCCTGTCAT
	DYSF_Q605X_gF	ACCGATCCTACAGCATGGTGGCTG
	DYSF_Q605X_gR	AAACCAGCCACCATGCTGTAGGAT
gRNAs	DYSF_R377X_gF	ACCGCCTCACAGGGCTACGCCTGT
	DYSF_R377X_gR	AAACACAGGCGTAGCCCTGTGAGG
	DYSF_Q1278X_gF	ACCGTCTCTAGATGAGCTCAAAAG
	DYSF_Q1278X_gR	AAACCTTTTGAGCTCATCTAGAGA
	CAR-gF	ACCGCTTTAATGCGCTGACTTGTG
	CAR-gR	AAACCACAAGTCAGCGCATTAAAG
	mTmem5-gF	ACCGACTTACGTTGCTACACCTAA
	mTmem5-gR	AAACTTAGGTGTAGCAACGTAAGT
	S1-F	TTCCAGTGGTTCAATGGTCA
	S1-R	CTTTCAACCCGAACGGAGAC
	puro-F	AGTGGTCTCCGGAAACCTCCGCGCCCCGCAAC
	EGFP_R	GTAGGTCAGGGTGGTCACGA
PCK	CAR-F	CCCTCTGTTATGCCACCAGT
	CAR-R	ACTCAGGAGGCTGAAGTGGA
	mTmem5-F	GAAGAGGGCAAAATCCAACA
	mTmem5-R	TTGCTTGGAAATGAGCACTG
	S1-repF	AATTCGGATGACAGGCAGGGGCACCGCGGAGTG
	S1-repR	GATCCACTCCGCGGTGCCCCTGCCTGTCATCCG
	S1NNG-F	AATTCGGATGACAGGCAGGGGCACCGAAGTTTG
	S1NNG-R	GATCCAAACTTCGGTGCCCCTGCCTGTCATCCG
	S1NNG2-F	AATTCGGATGACAGGCAGGGGCACCGCAGTTTG
	S1NNG2-R	GATCCAAACTGCGGTGCCCCTGCCTGTCATCCG
	S1NNG3-F	AATTCGGATGACAGGCAGGGGCACCGGAGTTTG
	S1NNG3-R	GATCCAAACTCCGGTGCCCCTGCCTGTCATCCG
	S1NNG4-F	AATTCGGATGACAGGCAGGGGCACCGATGTTTG
	S1NNG4-R	GATCCAAACATCGGTGCCCCTGCCTGTCATCCG
Reporters	S1NNG5-F	AATTCGGATGACAGGCAGGGGGCACCGCTGTTTG
	S1NNG5-R	GATCCAAACAGCGGTGCCCCTGCCTGTCATCCG
	S1NNG6-F	AATTCGGATGACAGGCAGGGGCACCGGTGTTTG
	S1NNG6-R	GATCCAAACACCGGTGCCCTGCCTGTCATCCG
	S1NNG7-F	AATTCGGATGACAGGCAGGGGCACCGTTGTTTG
	S1NNG7-R	GATCCAAACAACGGTGCCCCTGCCTGTCATCCG
	S1NNG8-F	AATTCGGATGACAGGCAGGGGCACCGACGTTTG
	S1NNG8-R	GATCCAAACGTCGGTGCCCCTGCCTGTCATCCG
	S1NNG9-F	AATTCGGATGACAGGCAGGGGCACCGCCGTTTG
	S1NNG9-R	GATCCAAACGGCGGTGCCCCTGCCTGTCATCCG
	S1NNG10-F	AATTCGGATGACAGGCAGGGGCACCGGCGTTTG

S1NNG10-R	GATCCAAACGCCGGTGCCCCTGCCTGTCATCCG
S1NNG11-F	AATTCGGATGACAGGCAGGGGCACCGTCGTTTG
S1NNG11-R	GATCCAAACGACGGTGCCCCTGCCTGTCATCCG
DYSF_Q605X_repF	AATTCTACTCAGCCACCATGCTGTAGGATGTGG
DYSF_Q605X_repR	GATCCCACATCCTACAGCATGGTGGCTGAGTAG
DYSF_R377X_repF	AATTCCGGCCCACAGGCGTAGCCCTGTGAGGAGCCG
DYSF_R377X_repR	GATCCGGCTCCTCACAGGGCTACGCCTGTGGGCCGG
DYSF Q1278X repF	AATTCCTGGCCTCTTTTGAGCTCATCTAGAGAGAGG
DYSF Q1278X repR	GATCCCTCTCTAGATGAGCTCAAAAGAGGCCAGG
CAR-rep-F	AATTCCTTTAATGCGCTGACTTGTGTGGGG
CAR-rep-R	GATCCCCCACACAAGTCAGCGCATTAAAGG
mTmem5-rep-F	AATTCTGGCCTTTAGGTGTAGCAACGTAAGTACAAG
mTmem5-rep-R	GATCCTTGTACTTACGTTGCTACACCTAAAGGCCAG

Purpose	Name	Information
gRNAs	pLenti-S1-ogRNA	S1 optimized gRNA
	pLenti-Q605X-ogRNA	Q605X optimized gRNA
	pLenti-R377X-ogRNA	R377X optimized gRNA
	pLenti-Q1278X-ogRNA	Q1278X optimized gRNA
	pLenti-CAR-ogRNA	CAR optimized gRNA
	pLenti-mTmem5-ogRNA	mTmem5 optimized gRNA
ABEs	ABE7.10	ABE based on SpCas9
	ABEmax	ABE based on codon optimized SpCas9
	xABE	ABE based on xCas9(3.7)
	ScCas9-ABE	ABE based on codon optimized ScCas9
		ABE based on codon optimized SpCas9-
		NG
Reporters	pLKO-puro-E2A-GFP	Empty reporter
	pLKO-puro-S1-E2A-EGFP	S1 reporter
	pLKO-puro-Q605X-E2A-EGFP	Dysferlin Q605X reporter
	pLKO-puro-R377X-E2A-EGFP	Dysferlin R377X reporter
	pLKO-puro-Q1278X-E2A- EGFP	Dysferlin Q1278X reporter
	pLKO-puro-S1NNG(1-11)-E2A-	S1NNG (1-11) reporters
	pLKO-puro-CAR-E2A-EGFP	CAR reporter
	pLKO-puro-mTmem5-E2A- EGFP	mTmem5 reporter

Supplementary Table II. List of plasmids used in this study



Supplementary Figure S1. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG3 (GAG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG3 reporter. The PAM sequences are listed in yellow. Scale bar: 100 µm.



Supplementary Figure S2. (A) Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG4 (ATG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG4 reporter. The PAM sequences are listed in yellow. Scale bar: 100 μ m. (B) FACS quantification of GFP⁺ cells for S1NNG4 reporter with or without ScCas9-ABE editing. **p*<0.05. (C) FACS quantification of the geometric mean of GFP fluorescence intensity in GFP⁺ cells (out of a total 1x10⁵ cells) for S1NNG4 reporter with or without ScCas9-ABE editing. **p*<0.01.



Supplementary Figure S3. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG5 (CTG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG5 reporter. The PAM sequences are listed in yellow. Scale bar: 100 µm.



Supplementary Figure S4. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG6 (GTG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG6 reporter. The PAM sequences are listed in yellow. Scale bar: 100 μ m.



Supplementary Figure S5. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG7 (TTG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG7 reporter. The PAM sequences are listed in yellow. Scale bar: 100 μ m.



Supplementary Figure S6. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG8 (ACG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG8 reporter. The PAM sequences are listed in yellow. Scale bar: 100 µm.



Supplementary Figure S7. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG9 (CCG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG9 reporter. The PAM sequences are listed in yellow. Scale bar: 100 µm.



Supplementary Figure S8. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG10 (GCG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG10 reporter. The PAM sequences are listed in yellow. Scale bar: 100 µm.



Supplementary Figure S9. Representative fluorescence and bright-field (merged) images of HEK293 cells transfected with the S1NNG11 (TCG)-reporter alone, or co-transfected with S1-gRNA, ScCas9-ABE and S1NNG11 reporter. The PAM sequences are listed in yellow. Scale bar: 100 μ m.