

File name: Supplementary Information

Description: Supplementary tables.

File name: Peer review file

Description:

Supplementary Table 1. Target sites in this study. Red colors means PAM sequences.

Gene name	Target sites
<i>twist2-1</i>	gGCTCCAGAACCAAGCGCGTCC TGG
<i>twist2-2</i>	gGCCGCTCGCGTACGTT CGCCAGG
<i>twist2-3</i>	GCGTCCTGGCGAACGTACG CGA
<i>gdf6</i>	GGTCGATCAGAGAGGCCA CTGG
<i>ntl</i>	GGAACCAGCCACCGACTGT TGG
<i>tyr</i>	GGCAATCCCGGGGACCA CGACCGG
<i>urod-1</i>	GAGATCGTGAGGAGGATGTT GGA
<i>urod-2</i>	GTTCCCTGAAGCTTGCTG TGA
<i>tial1</i>	GGCCTCCGTAA CATCCCTGGAGA

Supplementary Table 2. Primers used in this study.

Name	Sequence of the primer (5'-3')
<i>twist2-1</i> gRNA	TAATACGACTCACTATAgGCTCCAGAACCAAGCGCGTCC GTTTTAGAGCTA
<i>twist2-2</i> gRNA	TAATACGACTCACTATAgGCCGCTCGCGTACGTT CGCC GTTTTAGAGCTA
<i>gdf6</i> gRNA	TAATACGACTCACTATAgGTCGATCAGAGAGGCCACGTTTTAGAGCTA
<i>ntl</i> gRNA	TAATACGACTCACTATAGGAACCAGCCACCGACTGT GTTTTAGAGCTA
<i>tyr</i> gRNA	TAATACGACTCACTATAgGCAATCCCGGGGACCA CGAC GTTTTAGAGCTA
<i>twist2-3</i> gRNA	TAATACGACTCACTATAgGCGTCCTGGCGAACGTACGTTTTAGAGCTA
<i>urod-1</i> gRNA	TAATACGACTCACTATAgGAGATCGTGAGGAGGATGTT GTTTTAGAGCTA
<i>urod-2</i> gRNA	TAATACGACTCACTATAgGTTCCCTGAAGCTTGCTG GTTTTAGAGCTA
<i>tial1</i> gRNA	TAATACGACTCACTATAGGCCTCCGTAA CATCCCTGG GTTTTAGAGCTA
tracr rev	AAAAAAAAAGCACCGACTCGGTGCCAC
<i>twist2</i> detect	F: AAGTGGAGATCGTATTTTCTC
	R: GTTCGGCATTATCAGGACGCG
<i>gdf6</i> detect	F: GCTCTCTCCTTTGCGAA GAC
	R: AATCCCCCAAACG TCCAGAA
<i>ntl</i> detect	F: GCCAAAGCTTTCCTCGATGC
	R: TTGCTCTTACTGGTGGTAGTGC
<i>tyr</i> detect	F: TGAAAGTTACAACCTCCGCGA
	R: AGTCAGTGAAAGTCA GGGAACA
<i>urod-1</i> detect	F: CAAATTTAGGCCCTGCTGG
	R: TTAGCGTTTGA GAA GCTGGC
<i>urod-2</i> detect	F: GACTCCACAAGTCACATG TTC

	R: AATGTAATGACACAGCCGT
<i>tial1</i> detect	F: CCAGGGATGTTACGGA GGCC
	R: GGCCTCCGTAACATCCCTGG
genotyping for <i>tyr</i> locus	F: GCGTCTCACTCTCCTCGACTCTTC
	R: GTAGTTTCCGGCGCACTGGCA G
VQR SpCas9 R1335Q,T1337R double mutation	F: GATAGAAAGcaGTACAgaTCCACTAAGGA GGTGCTGGACGCTACA CTGA
	R: CCTTAGTGGAtcTGTA CtgCTTTCTATCGATTGTA GTGT CGAA GTACTTG
VQR SpCas9 D1135V	F: GGAGGCTTTGtCTCTCCCA CTGTGGCATACTCCGTCCTGGTG
	R: AGTGGGA GA GaCAAAGCCTCCATACTTCTTA GGGTCCCA GTC
H840A mutation	F: CGACGTGGATgcTATCGTCCCCA GA GTTTCATCAAAGATGAC
	R: GGGGACGATAgcATCCACGT CGTAATCAGACA GCCTGTTAATA