Genomic Coordinates	Locus Type	Nearest Gene Name	# of Mismatches	Target Sequence at Locus (mismatches in red)	Result of Off-Target Analysis
chrX:74283651-74283673	Exon	*Taz*	0	TCCTAAAACTCCGCCACATC	Two deviant alleles detected in TAZ-KO; 81 bp deletion and single-base deletion near end of *Taz* exon 3
chr5:116193392-116193414	Intron	*Ccdc60*	4	T**G**CT**TC**A**G**CTCCGCCACATC	No differences detected between WT and TAZ-KO
chrX:99228578-99228600	Intergenic	*Efnb1*	4	TCCT**TTTC**CTCCGCCACATC	No differences detected between WT and TAZ-KO
chr7:17982183-17982205	Intergenic	*Ceacam11*	4	**A**CC**C**AAA**C**CTC**A**GCCACATC	No differences detected between WT and TAZ-KO
chr4:141881515-141881537	Intergenic	*Fhad1os2*	4	T**T**CT**C**AA**C**CTC**T**GCCACATC	No differences detected between WT and TAZ-KO
chr13:40369162-40369184	Intergenic	*Ofcc1*	4	**GG**CTA**T**AACTCCG**G**CACATC	No differences detected between WT and TAZ-KO
chr15:79038802-79038824	Intron	*Gcat*	4	TCCT**T**A**T**AC**C**C**T**GCCACATC	No differences detected between WT and TAZ-KO
chr16:57507735-57507757	Intron	*Filip1l*	4	T**T**CTAAA**TG**TCC**A**CCACATC	No differences detected between WT and TAZ-KO
chr5:24422964-24422986	Intron	*Cdk5*	4	TC**AC**AAAACT**A**C**T**CCACATC	No differences detected between WT and TAZ-KO
chr2:31561027-31561049	Intergenic	*Gm13426*	4	TCC**C**AAA**GA**TCC**T**CCACATC	No differences detected between WT and TAZ-KO
chr6:89519351-89519373	Intron	*RP24-69A18.1*	4	TCCT**GT**AACT**G**C**A**CCACATC	No differences detected between WT and TAZ-KO

Supplementary Table 1. Off-target CRISPR/Cas9 effects were not detected in TAZ-KO cells. The top ten predicted off-target sites were identified using the CCTop-CRISPR/Cas9 target predictor tool based on the *Mus musculus* GRCm38 reference genome and the gRNA sequence utilized to create the TAZ-KO cell line (46,65). None of the predicted sites were located in an exonic region of the genome, and all off-target sites contained at least four mismatched bases relative to the gRNA sequence. To determine whether any of these sites were altered by Cas9 in the TAZ-KO line, whole-genome sequencing was performed on wild type (WT) and TAZ-KO cells, and differential variant analysis was run to identify deviations between the WT and TAZ-KO genomes. This analysis indicated that none of the predicted off-target sites differed between the two genomes, and also confirmed the presence of two deviant alleles at the primary gRNA target of tafazzin exon 3 (46).