Supplementary information, Table S4. sgRNA sequences and primers

sgRNA sequences

Locus	Sequence (5'-3')	Figure
GFP-A	AAGGGCGAGGAGCTGTTCACCGG	1
GFP-B	CTGAAGTTCATCTGCACCACCGG	1
GFP-C	GGAGCGCACCATCTTCTTCAAGG	1
GFP-D	GGTGAACCGCATCGAGCTGAAGG	1
Tyr-A	GGGAAGGGTTACTCAGAGTCAGG	2
Tyr-B	GCGAAGGCACCGCCCTCTTTTGG	2
Tyr-C	CCAGAAGCCAATGCACCTATCGG	2
Tyr-D	CTTCATAACATCCAAGGATCTGG	2
Tyr-E	TACAGCTACCTCCAAGAGTCAGG	2
Tyr-F	CAATGTGGGTAACCTCTTTGGGG	2
Tet1-A	GGCATGCTGGACTTCATTCTCGG	3
Tet1-B	GATGTCCATGCCGGTTACACAGG	3
Tet1-C	GAAGCCAGAGGCCACCTCACAGG	3
Tet2-A	CAGGGAGCAAGAGATTCCGAAGG	3
Tet2-B	TCAGTCCTCCACTCTCAGACCGG	3
Tet2-C	GTGAACCAAGGACCGTCTCCAGG	3
Tet3-A	CCCTACTTCCACAGAGCCTCAGG	3
Tet3-B	GCCTGTTAGGCAGATTGTTCTGG	3
Tet3-C	ACAAGCTGGAGGAGCTCATCCGG	3
Zfy1-A	GGATAGTGACCAGATTGTTGTGG	4
Zfy1-B	CCTGAGCAAGTTCTCAATTTAGG	4
Ubey1y-A	GAAACCCCTACTTGCCTCGCTGG	4
Ubey1y-B	CTCAGCACAGCAGGCCTCCTCGG	4
Kdm5d-A	GATGGTACCTACAGAAGTTGTGG	4
Kdm5d-B	GGACTTATCTCCTGAAGAAAAGG	4
Eif2s3y-A	ACAATTGGTCATGTTGCTCATGG	4
Eif2s3y-B	AGGAATATTACCATAAAACTTGG	4
Ddx3y-A	GTCTGTGATAAGGACAGTTCAGG	4
Ddx3y-B	GTGATCGTGGAAGTGGATCCAGG	4
Usp9y-A	ACTCTGGCTCTGTGTTTCCCAGG	4
Usp9y-B	AGGATTAGACTACCTTTGGAAGG	4
Sry-A	GCATTTATGGTGTGGTCCCGTGG	4
Sry-B	CGAAAAAAGGCCCTTTTTCCAGG	4
Erdr1-A	ACGGACGGACTCCACAAGGTAGG	4
Erdr1-B	TGGCACATACATCTTGACCGCGG	4
Prrt2-A	GATGGCAGCCAGCAGCTCTGAGG	5
Prrt2-B	GGCCAAGCTCTTAAGCATCGTGG	5
Prrt2-C	GCCTCCTGCGTCATCAACTTAGG	5
Prrt2-D	CAGGCAGGGGAGGAATGGAACGG	5

ArntL-A	GCTGGCCACCCACAAAGATGGGG	5
ArntL-B	GCAGTCGTCCAATTGCAACGAGG	5
ArntL-C	GTTTCTCGGCACGCGATAGATGG	5

Primer sequences used to generate the templates for sgRNA *in vitro* transcriptions.

Locus	Sequence (5'-3')	Figure
GFP-A	TAATACGACTCACTATAGGGAAGGGCGAGGAGCTGTTCACGTTTTAGAGCTAGAAATAG	1
GFP-B	TAATACGACTCACTATAGGGCTGAAGTTCATCTGCACCACGTTTTAGAGCTAGAAATAG	1
GFP-C	TAATACGACTCACTATAGGGGGAGCGCACCATCTTCTTCAGTTTTAGAGCTAGAAATAG	1
GFP-D	TAATACGACTCACTATAGGGGGTGAACCGCATCGAGCTGAGTTTTAGAGCTAGAAATAG	1
Tyr-A	TAATACGACTCACTATAGGGGGGAAGGGTTACTCAGAGTCGTTTTAGAGCTAGAAATAG	2
Tyr-B	TAATACGACTCACTATAGGGGCGAAGGCACCGCCCTCTTTGTTTTAGAGCTAGAAATAG	2
Tyr-C	TAATACGACTCACTATAGGGCCAGAAGCCAATGCACCTATGTTTTAGAGCTAGAAATAG	2
Tyr-D	TAATACGACTCACTATAGGGCTTCATAACATCCAAGGATCGTTTTAGAGCTAGAAATAG	2
Tyr-E	TAATACGACTCACTATAGGGTACAGCTACCTCCAAGAGTCGTTTTAGAGCTAGAAATAG	2
Tyr-F	TAATACGACTCACTATAGGGCAATGTGGGTAACCTCTTTGGTTTTAGAGCTAGAAATAG	2
Tet1-A	TAATACGACTCACTATAGGGGGCATGCTGGACTTCATTCTGTTTTAGAGCTAGAAATAG	3
Tet1-B	TAATACGACTCACTATAGGGGATGTCCATGCCGGTTACACGTTTTAGAGCTAGAAATAG	3
Tet1-C	TAATACGACTCACTATAGGGGAAGCCAGAGGCCACCTCACGTTTTAGAGCTAGAAATAG	3
Tet2-A	TAATACGACTCACTATAGGGCAGGGAGCAAGAGATTCCGAGTTTTAGAGCTAGAAATAG	3
Tet2-B	TAATACGACTCACTATAGGGTCAGTCCTCCACTCTCAGACGTTTTAGAGCTAGAAATAG	3
Tet2-C	TAATACGACTCACTATAGGGGTGAACCAAGGACCGTCTCCGTTTTAGAGCTAGAAATAG	3
Tet3-A	TAATACGACTCACTATAGGGCCCTACTTCCACAGAGCCTCGTTTTAGAGCTAGAAATAG	3
Tet3-B	TAATACGACTCACTATAGGGGCCTGTTAGGCAGATTGTTCGTTTTAGAGCTAGAAATAG	3
Tet3-C	TAATACGACTCACTATAGGGACAAGCTGGAGGAGCTCATCGTTTTAGAGCTAGAAATAG	3
Zfy1-A	TAATACGACTCACTATAGGGGGATAGTGACCAGATTGTTGGTTTTAGAGCTAGAAATAG	4
Zfy1-B	TAATACGACTCACTATAGGGCCTGAGCAAGTTCTCAATTTGTTTTAGAGCTAGAAATAG	4
Ube1y1-A	TAATACGACTCACTATAGGGGAAACCCCTACTTGCCTCGCGTTTTAGAGCTAGAAATAG	4
Ubey1y-B	TAATACGACTCACTATAGGGCTCAGCACAGCAGGCCTCCTGTTTTAGAGCTAGAAATAG	4
Kdm5d-A	TAATACGACTCACTATAGGGGATGGTACCTACAGAAGTTGGTTTTAGAGCTAGAAATAG	4
Kdm5d-B	TAATACGACTCACTATAGGGGGACTTATCTCCTGAAGAAAGTTTTAGAGCTAGAAATAG	4
Eif2s3y-A	TAATACGACTCACTATAGGGACAATTGGTCATGTTGCTCAGTTTTAGAGCTAGAAATAG	4
Eif2s3y-B	TAATACGACTCACTATAGGGAGGAATATTACCATAAAACTGTTTTAGAGCTAGAAATAG	4
Ddx3y-A	TAATACGACTCACTATAGGGGTCTGTGATAAGGACAGTTCGTTTTAGAGCTAGAAATAG	4
Ddx3y-B	TAATACGACTCACTATAGGGGTGATCGTGGAAGTGGATCCGTTTTAGAGCTAGAAATAG	4
Usp9y-A	TAATACGACTCACTATAGGGACTCTGGCTCTGTGTTTCCCGTTTTAGAGCTAGAAATAG	4
Usp9y-B	TAATACGACTCACTATAGGGAGGATTAGACTACCTTTGGAGTTTTAGAGCTAGAAATAG	4
Sry-A	TAATACGACTCACTATAGGGGCATTTATGGTGTGGTCCCGGTTTTAGAGCTAGAAATAG	4
Sry-B	TAATACGACTCACTATAGGGCGAAAAAAGGCCCTTTTTCCGTTTTAGAGCTAGAAATAG	4
Erdr1-A	TAATACGACTCACTATAGGGACGGACGGACTCCACAAGGTGTTTTAGAGCTAGAAATAG	4
Erdr1-B	TAATACGACTCACTATAGGGTGGCACATACATCTTGACCGGTTTTAGAGCTAGAAATAG	4
Prrt2-A	GAAATTAATACGACTCACTATAGGGCTGCAGCAGCTGGTTGAGGGTTTTAGAGCTAGAAATAGC	5

Prrt2-B	GAAATTAATACGACTCACTATAGGGGCCAAGCTCTTAAGCATCGGTTTTAGAGCTAGAAATAGC	5
Prrt2-C	GAAATTAATACGACTCACTATAGGGCCTCCTGCGTCATCAACTTGTTTTAGAGCTAGAAATAGC	5
Prrt2-D	GAAATTAATACGACTCACTATAGGCAGGCAGGGGAGGAATGGAAGTTTTAGAGCTAGAAATAGC	5
ArntL-A	TAATACGACTCACTATAGGGGCTGGCCACCCACAAAGATGGTTTTAGAGCTAGAAATAG	5
ArntL-B	TAATACGACTCACTATAGGGGCAGTCGTCCAATTGCAACGGTTTTAGAGCTAGAAATAG	5
ArntL-C	TAATACGACTCACTATAGGGGTTTCTCGGCACGCGATAGAGTTTTAGAGCTAGAAATAG	5
sgRNA-R	AAAAGCACCGACTCGGTGCC	

Cas9 mRNA	F	TAATACGACTCACTATAGGGAGATTTCAGGTTGGACCGGTG
	R	GACGTCAGCGTTCGAATTGC

Primers used for genotyping.

Locus	Sequence (5’-3’)	Product (bp)	Figure
Tyr	Outer F: GTTATCCTCACACTACTTCTG	807	2
	Outer R: GTAATCCTACCAAGAGTCTCA		
	Inner F: TCCTCACACTACTTCTGATG	788	2
	Inner R: GTCTCAAGATGGAAGATCAC		
Eif2s3y	Outer F: ATCACAGGAATCTGGAAGC	834	4
	Outer R: CTACTAAGCAACTGTCACATC		
	Inner F: CAGGCTCACAGAGGTCTA	514	4
	Inner R: ACTCATCAGGTGTACTACTTC		
Zfy1	Outer F: CACAATAAGAAATATATGC	799	4
	Outer R: CAGATAATCCTCACAGTTGATTTTGT		
	Inner F: GTTACATAACCTAAAAGTAGAC	575	4
	Inner R: TATAGGATCAGTGATGACTTCTG		
Ube1y1	Outer F: GCAAAGGCACAGATTAGAC	769	4
	Outer R: GGTTGTCAGTAGCAGGAG		
	Inner F: TGGAGGCATTGTCAGTCA	625	4
	Inner R: ATGGCATCAGAAGCACAC		
Kdm5d	Outer F: GCAGGCTACACAGGAGTA	491	4
	Outer R: AGGGACAGTAACAGGCATA		
	Inner F: TTGGTGAGATGGCTGACT	457	4
	Inner R: GGACAGTAACAGGCATATGA		
Ddx3y	Outer F: CACTATACTACCAAGCCACAT	684	4
	Outer R: CCAAGACATCCAATCTCATAAG		
	Inner F: TTCTCACAATGTAGCTCAGT	512	4
	Inner R: AGGTAAGTAGGTAGACAGATTC		
Usp9y	Outer F: AGATGTAAGTTCAGCTAGGT	875	4
	Outer R: CACACTTTCTACTAACAGTCAC		
	Inner F: GTTGGGTATGTCTTTAGGTT	702	4

	Inner R: CATGAAGGACAACAGGTAA		
Sry	Outer F: GCACATTTTGGTCAGTGGCT	632	4
	Outer R: GCTCTACTCCAGTCTTGCCT		
	Inner F: GTTCAGCCCTACAGCCACATG	355	4
	Inner R: GCAGGCTGTAAAATGCCACTC		
Prrt2-Exon3	Outer F: GGAGGGATATGGAAACACAT	937	5
	Outer R: GATGCCAAGACAATGGAAGT		
	Inner F: TTTCCACCTGATCCCTTCTG	776	5
	Inner R: GAGGTCCAGAGAATTTGGGA		
ArntL-Exon 13	Outer F: CCAGTACCTCCAATTTCACTTC	1117	5
	Outer R: CAGAGACTCACATCACTTGTC		
	Inner F: ATACATTCTAGTCCCTCAGC	950	5
	Inner R: GGTACAATCACAGCTTACTG		

Primers used for off-target analysis.

sgRNA	Locus	Sequence	Product (bp)
sgRNA-*Tyr*-B	chr17:57065718	F: CCATTTACCTCATAGGACCT	617
		R: GTTGCTGATCTGAAGAAGTG	
	chr6:138140489	F: GGTATTCACAGCAATAGAGC	777
		R: GCAGTGACTTCTCATCTTGT	
	chr4:138750107	F: TTCTCTATCTGAGGCATCTG	701
		R: GACTCTACTGTTGTAGGACC	
	chr2:32395585	F:AACTCCTGCCCTACTTAGAAG	748
		R:CAATGATGACCTGTAACTCGTG	
	chr9:23096850	F:AAGATGCCTCCTGTTCTGAAG	671
		R:CAATCCATCATGCCTCTGAAG	
	chr17:24453551	F:CTGTCCTGGAACTCACTCTAT	764
		R:GACATTGGTTCTCAGACTTCC	
	chr9:96832929	F:GCTAATGCTAAGCCCTAACTG	633
		R:CATTCTCTGTGTCTGACTCTG	
	chr15:79169441	F:GTATATGTGTATGCCTGCGTC	1075
		R:ACAGAGTGAGTTCTAGGACAG	
	chr4:86233378	F:AGTGCGATACCTTACTGTCTC	659
		R:CATGTAGCAGCCTAGTTCTTC	
	chr6:115975395	F:GATACTTCTGGTCTTCAGCAG	625
		R:CATCCACAGCAGATACTAAGG	
sgRNA-*Tyr*-C	chr8:73203311	F: GCCTGTAATGATTGGACTGT	760
		R: GGACCTAACTATTGTGGGAAG	
	chr10:55107975	F: CATAGACTGTAGGACCAAGAC	625
		R: ACCCTTACCACCTGTTTATG	
	chr10:116978236	F: AGGAGCTGCATCATCTTATG	680

		R: ACAATCTGGAAGGCGAATAG	
	chr10:124330321	F:CAACCTCAAGAGTCAGACAAG	731
		R:CCAGCAGTGAATTTCCATCAG	
	chr17:8532910	F:CTGTGTATTTGTGGGACCTATG	748
		R:GATTAGTCCATCAGAAGCAGAG	
	chr16:57712501	F:GTCCTCTACTATTCTGTGTCTG	639
		R:GATTGGTCTCTGTATAGTTGGC	
	chr17:44031368	F:CCAATGACATACTCAGTGCTC	743
		R:AGAGATGAGAGTTGGAGACAG	
	chr3:6828323	F:CTCTACTTCCACTGAGGGTAC	703
		R:GGACAATTCTCTTGGTTCTCC	
	chr11:28415232	F:TAACCTACCTTACCACCATCC	718
		R:GCCTATTGACCAGAGTTAGTG	
	chr1:33799882	F:TAGTGTCACCTAGTAGAGTCC	857
		R:GAGTAGCCAGTATGCTTAACC	
sgRNA-*Tyr*-D	chr15:74536351	F: AGACAGAGGAAGCATTGAG	516
		R: CTCCAGGTCATACACTGAG	
	chr18:43788370	F: CCTGGATATGGCAGTCTCTA	957
		R: CTGATTCTCTGAGAGGTGGTA	
	chr15:61581619	F: GTGAAGGACTCAGGTTACTA	799
		R: ATGATACAGTGGTAGCAGAC	
	chr13:39330053	F:CATGGCTCAGGTACATGCTATGA	998
		R:GGGCTTCCGATGGTGCGTGTC	
	chr14:80206603	F:GTGGGCACAGTTGCTGATGAT	752
		R:GCAGTTCCAACCCAATGCTCAC	
	chr5:36335565	F:ATGAATCAGACCTTGCCCGTCAC	653
		R:CATGCTGGGTGAAGGCAAGATC	
	chr8:85681387	F:TGGACCATTAGACAGTGGGAGA	941
		R:AGGCAGAAGAGGGTGAGTGGT	
	chr3:98944708	F:TACCTTGGGTCCTTATGGTTGTT	766
		R:TTGGCAGTAGTTGATGAGGAGAAGT	
	chr6:42584574	F:TCTGTAAGGACACGAGTTAGGGATC	893
		R:TTTGCTCCTATGACCTGGGTTCC	
	chr10:18410911	F:GTACTACTTGAATTAGCAGCCACTGC	694
		R:AAGTAGCCATGCAAAGCCAAGC	
sgRNA-*Tyr*-E	chr8:108702504	F: GCTTTGATGTACTGGGAATC	757
		R: GCTTAGAATGGAGGTCACTT	
	chrX:130677312	F: GACAGAAGGATGAGGAATGA	700
		R: CCAACCACTATTGAACTCAC	
	chr3:130295069	F: CTTGTCATAGCAGTGTCCTG	643
		R: GCTCCTTGAGAGTCCATTAG	
	chr7:123982528	F:TAGCCCGCAGTGCCTCCCACAG	766
		R:CTAGTCGCGGCGGCACCTGCTC	

	chr3:133082201	F:CCTGCATCCAGCTAAATGGCACA	1045
		R:AGGCTGCCATACCTCCAACAA	
	chrX:147311924	F:CAGCCAAGGTGGGCACAAGGT	830
		R:CAGGCATCCTCACAGGAAATTATGG	
	chr1:168151597	F:TGAGCATGTCTGACTTCCCAGTT	745
		R:AAGGTTACATTATGCCTCAGTTGT	
	chr5:50071052	F:CAGGGACAGCATCCAGGTTTAT	782
		R:GTGCCATCAATCACTAAGGCAAATC	
	chr2:7777791	F:AAGCTGAAAGTGACTGGGAGA	973
		R:CTGGGTGTATTTGTGCCTGTGT	
	chr10:84425609	F:CATTTGTCAAACAGGAGCCACG	807
		R:TGGTAATGAGGTAGGGACAGGC	
sgRNA-*Prrt2*-B	chr16:19639092	F:GGTAGGTATTGCCAGATCCAA	631
		R:CGGGTTCAAGTGATTCTTCTG	
	chr8:8862302	F:GTTGAGGATCACTGTTCTACC	763
		R:CTTGTCCTGTTTGTAGGTTGG	
	chr7:142439417	F:ACAGACCTACAGAAGTGACTC	677
		R:GCACGGAATCTATACAGAGAC	
	chr16:18400530	F:ACAGACCTACAGAAGTGACTC	663
		R:CAGAGACAGGCTAAGATATTGC	
	chr3:1322473581	F:GAGTGTCTTGTATGGGCTAGA	967
		R:CTCTGTGATTCCTGGTATCTG	
	chr7:9980144	F:ACAAGTCTGGAGATTCCTTC	937
		R:GATGTTCCTTGGTGTGATTC	
	chr10:63847987	F:CCCACCATCAACCTAGATTTG	706
		R:GTCCTCACAGAACTCTCATTC	
	chr8:42993888	F:CCAGAGCAGTTACTTCAGAAG	944
		R:GGCTAGTGGTTACAGTATTGG	
	chr13:43492573	F:GCACAGACCTAGCTAATCTCG	806
		R:CTTCCTTCCTTCCTTCCTTCC	
	chr14:3502008	F:GGACATGGATGAAGTTGGAAG	696
		R:TCAGTAATCTACAGAGGAGGTG	
sgRNA-*Prrt2*-C	chr20:61736084	F:ATGACCTAATCCATGCTCCAG	890
		R:GAACTCCTGACCTCAGATGAT	
	chr5:72228276	F:CAATTCAGTGGGAAGTATAGGG	882
		R:GACACAGTTGTTCACCATCTAC	
	chr7:83976766	F:CCTAAACTCCCTTGACTTCTG	958
		R:CCTGTTGTAACTCACTTCCTG	
	chr1:190035638	F:GATACAGACTCAGAGGAATGG	703
		R:CAGGAGGTCTTCATCTTCAAC	
	chr9:69194244	F:GGTAGGCAAGTATGGTAAAGG	605
		R:GGATTGTATCCTGGTGACTTC	
	chr3:19342682	F:GATCACCTGAGGTTAGGAGTT	708

		R:CAGATTCTAGCTGAGTGGATG	
	chr15:40107119	F:CCTCATCATCTTCATGTCGAG	792
		R:CATCTACTCACTTCCTCTAGC	
	chr20:61058621	F:GGGAACTGAATGAACTGATGG	700
		R:CCTGAAGTGAGGCAATAAGAG	
	chr14:112810197	F:GAGAACAGTGTCCTTGATGAG	897
		R:GGAGGTAGAGGTTGTAGTGAG	
	chr10:85811043	F:CAACAGACAAGGCTAACTCAG	637
		R:GACAGAGTGAGACTCCATTAC	
sgRNA-*Prrt2*-D	chr3:88667957	F:GGTAAGTCTGGAACCAATAGG	635
		R:CAGTCAAGCAGTATCTCTGAG	
	chr7:96903885	F:CTCCTTACATCTCATTGGTCAG	970
		R:CTATCCATCCTTCGTGATCTG	
	chr3:10010150	F:CTCATCCTGTTCTACACCAAG	665
		R:GAGTAAGGGAATCCATCTCTC	
	chr2:37733632	F:CCTACTATACACAAGGTACTGG	794
		R:CTAGAGGAAGACTGCTAAGTG	
	chr12:127960318	F:GCTCACCATATCCAACTCATAC	905
		R:CTCCATCCACTCTCCATCTAT	
	chr5:116240088	F:CGGTTCTCTCCACTAACATTC	765
		R:GTTAGAGGCATCAGGGATTTC	
	chr5:151113455	F:CCCACCATCAACCTAGATTTG	706
		R:GTCCTCACAGAACTCTCATTC	
	chr1:62103725	F:GTGTGGACTGAGTTCTATAAGG	746
		R:GATCACTTGAGGTCAGGAGTT	
	chr1:146757199	F:GGCAGCACTTGGCATTTAACC	760
		R:CTAGGCTCGGCTTGGATGTTC	
	chr2:141699162	F:GCAGAGATCAGTTGCTTGTTC	638
		R:CTGGGCTAGTGTTCTTAATGG	

Primers used for validation of the off-target site from whole-genome analysis.

sgRNA-*Prrt2*-C	chr4:146185910	F:AAGGATACAAGGATCTCAGG	999
		R:ACCACTCCGAAGATAATAGC	