

Supplementary Information 2

Relationship between somatic mosaicism of *Pax6* mutation and variable developmental eye abnormalities—an analysis of CRISPR genome-edited mouse embryos

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Supplementary Table S8. List of off-target sites located in exonic regions

T1	GGAGGATCACCTGCAGAATT CCG				
OT1	CGAGGCTCACCTGCAGATG AGG	0.2	4	chr1:-36556408	cyclin M4 (Cnrm4)
OT2	GGAGGATCACCTTCGGAAACC GGG	0	4	chr1:-75249699	protein tyrosine phosphatase, receptor type, N (Ptpn)
OT3	AGAGGATCCTCTGCAGAAATG CAG	0.4	4	chr1:+155584967	RIKEN cDNA C230024C17 gene (C230024C17Rik), long non-coding RNA
OT4	GGAGGAACAACAGCAGAATA AGG	0.2	4	chr10:+121005198	TANK-binding kinase 1 (Tbk1)
OT5	GGATCATCACATGGAGAATT GAG	0.1	4	chr10:+126440482	advinil (Avil)
OT6	CGAGCATCACCTACGCAATT GAG	0.2	4	chr11:-55109664	FAT atypical cadherin 2 (Fat2)
OT7	GGAGCTCACCTGCAGCATG GAG	0.2	4	chr11:-79498870	RAB11 family interacting protein 4 (class II) (Rab11fp4)
OT8	GGAGGATCACCTGCAGCCGA TGG	0	4	chr11:+118344242	endo-beta-N-acetylglucosaminidase (Engase)
OT9	GGAGACTCACCTGCATATT TGG	0.1	4	chr12:-57591978	RIKEN cDNA E030019B13 gene (E030019B13Rik), long non-coding RNA
OT10	GATGAGCACCTGCAGATG GGG	0.4	4	chr12:-113104690	protein phosphatase 1, regulatory (inhibitor) subunit 13B (Ppp1r13b)
OT11	CTCGGATCACCTGCAGATT GGG	0.6	4	chr15:+82990588	cytochrome b5 reductase 3 (Cyb5r3)
OT12	GGAGGACCACTCTAGAAAT TAG	0	4	chr15:+89119580	SET binding factor 1 (Sbf1)
OT13	AGAGTATCACTTCAGAATT CAG	0.5	4	chr18:-60754220	synaptopodin (Synpo)
OT14	GGAGGATCCCTGCAGTCTT AAG	0.1	3	chr2:-157021534	retinoblastoma-like 1 (p107) (Rb1)
OT15	GAAGGCTCAGCTGCAGAAATG AGG	0.4	4	chr4:+115131400	cytochrome P450, family 4, subfamily a, polypeptide 30b (Cyp4a30b)
OT16	GGATCATCACCTGCAGATG CAG	1.4	3	chr5:+69969380	glucosamine-6-phosphate deaminase 2 (Gnpd2)
OT17	GGTGTTCACCTGCAGAAAT AGG	1.4	3	chr6:+72582151	transcription factor 7 like 1 (T cell specific, HMG box) (Tcf7l1)
OT18	GAAGAACACCTGCAGATA AAG	1	3	chr7:-20613786	NLR family, pyrin domain containing 9B (Nlrp9b)
OT19	GAAGAACACCTGCAGATA AAG	0.2	4	chr7:+27165589	NLR family, pyrin domain containing 9C (Nlrp9c)
OT20	GAAGAACACCTGCAGATA AAG	0.2	4	chr7:-27347447	NLR family, pyrin domain containing 9A (Nlrp9a)
T2	GGTTGTGTGAGTAAAATCT GGG				
OT1	GCATGTGTGAAATAAATCT TAG	0.3	4	chr1:-14871933	transient receptor potential cation channel, subfamily A, member 1 (Trpa1)
OT2	GGTTGTTAGTAAAATTA AGG	0.2	4	chr1:-58580968	family with sequence similarity 126, member B (Fam126b),
OT3	CTTTGTGTGAGTAAAATCT TGG	0.2	4	chr10:+82951250	aldehyde dehydrogenase 1 family, member L2 (Aldh1l2)
OT4	GGAGGTGTGTGTTAAAATCT AGG	0.5	4	chr11:-69171183	chromodomain helicase DNA binding protein 3 (Chd3)
OT5	GTTTTCTGAAATAAATCT TGG	0.5	4	chr11:-77505213	nuclear fragile X mental retardation protein interacting protein 2 (Nufip2)
OT6	GGTTGTGTGAGAAAATCTA TGG	0	4	chr14:-65212409	Mir124-1 host gene (non-protein coding) (Mir124a-1hg)
OT7	GATTTGTGTGAGTAAATTTT AAG	0.2	3	chr15:-36530293	poly(A) binding protein, cytoplasmic 1 (Pabpc1)
OT8	GTTTGTGTGAGTAAATCT TGG	0.1	4	chr17:-55764005	vomer nasal 2, receptor 118 (Vmn2r118),
OT9	GGTCTGTGTGAGTAAACCA GGG	0	4	chr19:-41726099	slit homolog 1 (Drosophila) (Slit1)
OT10	GGCTGTGTGAGAAAATCT GGG	0.1	4	chr19:+44835506	paired box 2 (Pax2)
OT11	GTTTCTGTAGTAAAATTT TGG	0.3	4	chr2:-37288374	zinc finger and BTB domain containing 26 (Zbtb26)
OT12	GGTTGCTTAGTAAACTCT TAG	0.1	4	chr2:+120686417	ubiquitin protein ligase E3 component n-recognin 1 (Ubr1)
OT13	GGATGTCTGAGGAAATCT GAG	0.1	4	chr2:-180969533	helicase with zinc finger 2, transcriptional coactivator (Helz2)
OT14	GCTTCTGTAAATAAATCT GGG	0.5	4	chr3:-98102948	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2)
OT15	GGTTGTGTGAGAAAATCT TGG	1.7	2	chr4:-44710392	paired box 5 (Pax5)
OT16	GGCTGTGTGAGCAAGATCT AGG	0	4	chr6:-28396312	paired box 4 (Pax4), transcript variant 3

Predicted each for T1 and T2 gRNAs using the Zhang laboratory CRISPR design tool. Red bases indicate sequence differences from target sequence.