

Table S1

<i>D. rerio</i> Gene Name ^a	Ensembl Identifier ^b	Chromosomal Location ^c	Zebrafish Gene Percent Identity with Homolog in ^d :			
			Human	Fugu	Medaka	Mouse
<i>aldoaa</i>	ENSDARG00000011665	Chr. 3: 39.56	84	92	93	85
<i>aldoab</i>	ENSDARG00000034470	Chr. 12: 4.75Rev	84	ND	ND	82
<i>asphd1</i>	ENSDARG00000075813	Chr. 3: 14.87	52	ND	72	50
<i>c16orf53</i>	ENSDARG00000076966	Chr. 12: 4.31	50	54	60	48
<i>cdipt</i>	ENSDARG00000070686	Chr. 3: 21.35	69	70	76	60
<i>coro1a</i>	ENSDARG00000054610	Chr. 3: 31.09Rev	69	85	84	69
<i>doc2a</i>	ENSDARG00000078736	Chr. 3: 15.15	63	81	48	63
<i>fam57ba</i>	ENSDARG00000026875	Chr. 3: 21.15	58	ND	73	58
<i>fam57bb</i>	ENSDARG00000074564	Chr. 12: 4.34Rev	60	ND	74	55
<i>gdpd3</i>	ENSDARG00000074466	Chr. 3: 23.47Rev	46	67	66	44
<i>gdpd3</i> (incomplete) ^e	ENSDARG00000006944	Chr. 12: 4.58Rev	48	61	60	47
<i>hirip3</i>	ENSDARG00000027749	Chr. 3: 14.81Rev	32	ND	37	30
<i>ino80e</i>	ENSDARG00000022939	Chr. 16: 12.02	48	70	74	49
<i>kctd13</i>	ENSDARG00000044769	Chr. 3: 14.83Rev	62	80	80	62
<i>kif22</i>	ENSDARG00000077375	Chr. 12: 5.80Rev	52	70	69	51
<i>mapk3</i>	ENSDARG00000070573	Chr. 3: 26.81	81	83	83	81
<i>maz</i>	ENSDARG00000087330	Chr. 3: 21.33Rev	45	ND	44	36
<i>mvp</i>	ENSDARG00000021242	Chr. 3: 15.33Rev	68	83	46	68
<i>ppp4ca</i>	ENSDARG00000070570	Chr. 3: 26.79	93	95	94	93
<i>ppp4cb</i>	ENSDARG00000076439	Chr. 12: 4.65Rev	98	98	98	98
<i>prrt2</i>	ENSDARG00000089367	Chr. 12: 5.77Rev	36	15	9	24
<i>sez6l2</i>	ENSDARG00000076052	Chr. 3: 14.86Rev	56	80	78	56
<i>taok2a</i>	ENSDARG00000074899	Chr. 3: 21.37Rev	70	89	87	69
<i>taok2b</i>	ENSDARG00000079261	Chr. 12: 4.50Rev	62	70	85	62
<i>tbx24</i>	ENSDARG00000011785	Chr.12: 4.59	19	18	19	20
<i>ypel3</i>	ENSDARG00000055510	Chr. 3: 26.84	89	ND	98	89

Table S1. Gene Assignment and Conservation.

^a *D. rerio* gene names, which correspond to homologs indicated in Fig. 1.

^b Ensembl identifiers (Release 62, April 2011).

^c Chromosomal location (Release 62, April 2011). Chromosomal orientation of the zebrafish gene is on the plus strand unless the location number is followed by “Rev”.

^d Zebrafish percent identity with human, fugu, medaka, and mouse homologs of human 16p11.2 genes is shown.

^e As the *gdpd3* gene on chromosome 12 is incomplete, the *gdpd3* gene on chromosome 3 was used for all phenotypic assays performed.

D. rerio, *Danio rerio*; Chr., chromosome; ND, not determined.

Table S2

Gene Name ^a	Antisense Morpholino Oligonucleotide ^b		Primer Sequences (5' to 3') ^c	
	MO Sequence (5' to 3')	Splice or Translation Blocking	Forward	Reverse
<i>aldoa</i>	CCATGCTGAGGAGGAATGCAAGATT	Splice Site	GACACTGGTTCATGGCATTG	GCATCAAAGTGGACAAGGGT
			AGATGCATGGCATCGTTCCAATCG#	GGCCCTTGACACAGCAGCCA#
<i>asphd1</i>	GAGAGCTTCCCATGTCTGACCTGAT	Splice Site	AGCAGCTCAGGCCGTTCTCAT	GAGTGGGAACACAGTCTGGCCCTTT
			GCAATCAGGCCAGGATCAAT#	ATAGCTGGCCTCCAGAACCT#
<i>c16orf53</i>	GGAGTGTGTAAGCTCATACTGTT	Splice Site	CGCTGGAGTGGTGAACGG	CTCCTGCGTGTGTTCTGCG
			CGACGGAGGACAACACTGCAGAAAG#	CTCCTCATCACTGTAAGGGATCATCC#
<i>cdipt</i>	TTGTACCTAAGGACGAGGCACGAAT	Splice Site	GCCAGACTTCAGCAGACACA	TTTAATCGGATATGCCGATCTGTAC
			GTGCGCTCAATCAAGGTACAAAATTTGGTGC#	ACGGGTACAGCAGTGCAGGT#
<i>coro1a</i>	TGGTTTCTGATGTGGTTTACCTGCA	Splice Site	GAGGAGCCTTCATTGTCTGTG	ACGTTCCAGAGGATCACACC
			TGTAGTGTATGATCTGGGAGA#	TCACAGCCTGCACCTATTAG#
	ATGAAGTCTTGTCACTCACCATGA	Splice Site	ATCTGGGAGATCCAGAGGG^	ATTATCAGCAGCTGCACAT^
<i>doc2a</i>	CCGAGCTACACAATCACAGGAATGA	Splice Site	ACTGCGCTGGGAGCCTAGA	AATCCCTCGCCGGGACTC
			GCACCATCATCAGAGCAAGGGTTTG#	TTGGCCTTGCATGCTCTGGTAGA#
<i>fam57ba</i>	ATGCTGGAAGGAAAATGGAAGAGA	Splice Site	ATCTGACGCTGCTCAACCT	ATAATCCCCTTTGGCCCTGT
			CTTGTAAAGACATCATCGAGGCCAGC#	GTACCAGTACACAGAAACATGGCA#
<i>dtdp3</i>	GCTCGCCATATTTCCAAAACAATT	Translation Start Site	NA	NA
			TGTTTTCCGCAAAATTTCTC*	CAGCGCTTTTCTCATTTGCA*
<i>hirp3</i>	TTATCGCGTCTTTCTTTGGCCAT	Translation Start Site	NA	NA
			CITTTCACTCACTGTTTACCTGCA	Splice Site
<i>ino80e</i>	CCTCTACTTCTGCTTCCCGTTTCAT	Translation Start Site	NA	NA
			AACGGGCAAGCAGAAGTAGA*^	GGAGAGAGTGGACCAACCA*^
	AGATGGTAACGTACTTACATACACC	Splice Site		
<i>kctd13</i>	CCAGCCTTCAATACAATGACACA	Splice Site	GTAATCCCTGATGCTGCC	CTCTGCGTTTCTGTAATGTGT
			AGCATCGACTCTGAAGGCTGGGTG#	CTCCTCCAGCTCCCTCGTGT#
<i>kif22</i>	CTTTCTGAGGTGAAGAAAGAAT	Splice Site	GTGTTGCTGTGAACGATGGA	GGAGCGCTGGTTGATTTAG
			CAGGCCGTTGTACTCCATT*	CAAAGTGTAGATCGCTGA*
			GTTTTCTGACCTCGTCAAGC#	TCCAACAGATTGAAGACTC#
<i>mapk3</i>	GCTACTGCCGATCCGCCATCGTT	Translation Start Site	NA	NA
			CCTGAACATGACCACACTGG*	GGAGGTAGTCTCTGGCTTC*^
	GTACGATATAGCTGAAACGCGGTTA	Splice Site	CATCATCGGGATCAATGACA^	
<i>maz</i>	ACTGGTTTTACTGGGAAAGAGAAGA	Splice Site	ATGCAGCTGGAGCAATTTT	CCTGTTCCCAAAGTATGC
			ACCCTCAATCAGATCTTCTC*#	GATTTCTCTGACCGGATTG*#
				GTTTACCGGCGGATGG#
<i>mvp</i>	TGCAGTCTTTCAGATTACCTCTCAT ¹	Splice Site	CCCACCTCACCTACATCC^	AATGTATCCCGGCACAAAG
			GAGGGACCAGGACTACAT*	TCTGCAACTGAGGGAATGTG*^
	TCCATGTTTCTCTACGGGCATTCT ²	Translation Start Site	NA	NA
	GGTCCCTGCCGGATTAAACACAG ³	Splice Site		
<i>ppp4ca</i>	GTGGAGTAAAAGAGTTACCTTGCT	Splice Site	GCGACTTCACTGACCTGGAC	CTGGCCATGATGTCACCAC
			CAAAGCAAGGGAGATTCTGG*#^	CTGTCAAGGATATCGCACCTT*
				GTTTGTTCGGGACTTCAC#
	CCGACCTAAAGACAATCATCAGAGA	Splice Site		GCAGAGCGTATTTCTGATG^
<i>prrt2</i>	ACGCCTGATGGTACTCTGTTCCAT	Translation Start Site	NA	NA
			GGAAGGTCATCGTGTGGT*^	GCTCCAGACTGTTCTCGAC*^
<i>sez6l2</i>	TCACAGCAAAAAGTGTGGACACCAT	Translation Start Site	NA	NA
			TTTCTAGTCCCCGCCCTGG*^	AGGTGCACTCCAGTGGGAA*^
<i>taok2a</i>	TAATGTTGTGGCTGCTCACAAGT	Splice Site	CCGTGTGTTGATTGAAACG	GCCCTGAAGTGCACCTGGG
			GGAAGCAGTGTACTTTGCTCACGAT#	GGGGTGTCTGAGCTCTGCAAGA#
<i>taok2b</i>	CCATCTGAAAAACAGCACAACCT	Splice Site	AAAGCTCGGGCACCCCAACA	GCAGGTGTGCCGAGTGACCA
			GTGGGCACACCTTACTGGATGGC#	TGCCAGTGAACCACTGCA#
<i>tbx24</i>	CATTCCACACCCAGCATGCTCGG	Translation Start Site	ACATGTGAGATGGCAGCTGGC*	TGAGTTTGGCCGTTGGAAGGA*
<i>ypel3</i>	CCTACGTTACCCCTAAAACACAAA	Splice Site	AGCAGCAAGGCCAAAAC	TCAGTCCCAGCCATTATCT
			GCAAGTCAAGGACGAGCCTAC*	
			TCAAGGACGAGCCTACTGT#	CAGTGTGTTGGCAATTCT#

Table S2. Primer and MO sequences.

^a Gene names corresponding with zebrafish genes included in Table S1 that were targeted for loss of function (LOF) by antisense morpholino oligonucleotides (MOs).

^b MO sequences and primer sequences are listed 5'-3'. Splice site MOs are designed to either the donor or acceptor side of the intron - exon boundary. Where multiple MOs are shown for one gene, the top-most MO was used for phenotypes reported.

^c The first set of primers listed for each gene was used to monitor changes in splicing after MO injection, except for translation-blocking MOs (NA).

^{1, 2, 3} *mvp* MOs are included in this order in Tables 1, 2, and S3. *mvp* MO¹ is included in Figs. 2A and 3.

* Indicates primers used for the developmental expression timing RT-PCR if different from those used to monitor changes in splicing.

Represents primers used for qPCR.

^ Indicates primers used to monitor changes in splicing for second or third MOs (see Table 1), whose phenotypes are otherwise not reported (aside from reporting for *mvp* MOs in Tables 2 and S3).

NA, not applicable.

Table S3

Gene Name ^a	Brain Phenotypes ^b			Tail & Muscle Phenotypes ^c			Movement Phenotypes ^d		
	Total Embryos	Affected Embryos	Abnormal Brain %	Total Embryos	Affected Embryos	Abnormal Tail %	Total Embryos	Affected Embryos	Abnormal Movement %
<i>aldoaa</i>	152	141	93	152	140	92	104	88	85
<i>asphd1</i>	198	193	97	115	115	100	115	0	0
<i>c16orf53</i>	90	66	73	90	66	73	90	0	0
<i>cdipt</i>	117	104	89	117	0	0	117	0	0
<i>coro1a</i>	106	94	89	106	92	87	91	87	96
<i>doc2a</i>	140	83	59	140	0	0	140	0	0
<i>fam57ba</i>	169	162	96	169	162	96	71	65	92
<i>gdpd3</i>	88	65	74	100	83	83	99	89	90
<i>hirip3</i>	102	102	100	150	131	87	150	123	82
<i>ino80e</i>	103	100	97	103	97	94	68	68	100
<i>kctd13</i>	165	149	90	115	107	93	75	65	87
<i>kif22</i>	351	308	88	351	313	89	242	238	98
<i>mapk3</i>	158	154	97	158	156	99	124	123	99
<i>maz</i>	202	170	84	201	149	74	46	44	96
<i>mvp</i> ¹	167	145	87	167	145	87	67	65	97
<i>mvp</i> ²	28	18	64	28	18	64	ND	ND	ND
<i>mvp</i> ³	50	50	100	50	50	100	40	40	100
<i>ppp4ca</i>	101	96	95	101	83	82	97	71	73
<i>prrt2</i>	64	5	8	64	5	8	64	1	2
<i>sez6l2</i>	47	42	89	109	99	91	109	0	0
<i>taok2a</i>	71	62	87	71	0	0	21	10	48
<i>taok2b</i>	74	67	91	78	65	83	78	0	0
<i>tbx24</i>	95	0	0	95	95	100	95	95	100
<i>ypel3</i>	49	47	96	49	38	78	47	42	89

Table S3. Quantification of brain, tail, and movement phenotypes. Data was gathered in 2-7 experiments for each LOF condition and includes 24 - 48 hpf experimental timepoints. Data is summarized in Fig. 3 and representative images are shown in Fig. 2.

^a Genes indicated in Table S1 were targeted in LOF experiments by MOs included in Table S2, using MO mass tabulated in Table 2. Where multiple MOs were designed, this table represents data obtained using the first MO listed in Table S2, aside from *mvp*, where three genes are listed.

^b Brain phenotypes, including abnormally shaped ventricle neuroepithelium were observed in 24 hpf LOF embryos using criteria described in Methods and shown in Figs. 2 and 3. Phenotypes observed for forebrain, midbrain, and hindbrain were included as a group in the number of abnormally affected embryos that is indicated.

^c Summation of major categories of tail and muscle phenotypes (including tail length, extension, and shape and muscle segment chevron abnormalities) were observed in 24 hpf LOF embryos using criteria described in Methods and data shown in Figs. 2 and 3. The number of abnormally affected embryos is indicated.

^d Movement abnormalities (which may arise from motor neuron or muscular defects) include grouping of spontaneous movement and touch response defects, which are assays described in Methods. The number of abnormally affected embryos are indicated.

^{1, 2, 3} The *mvp* MOs are included in the same order as Tables 2 and S2.

¹ Indicates the *mvp* MO that is included in Figs. 2 and 3.

ND, not determined.

Table S4

Gene Name ^a	Human or Fish Gene ^b	GenBank Accession No. ^c	Parent Vector ^d	Cloning into pCS2+ ^e (primers 5' to 3' or restriction enzymes)	in situ sense probe preparation ^f	in situ antisense probe preparation ^f	mMessage rescue mRNA ^g
<i>ALDOA</i>	human	NM_184043.1	pINCY	EcoRI/SalI			SP6 Pol, NotI RE
<i>aldoa</i>	zebrafish	BC065320	pCMV-SPORT6.1	NA ^h	SP6 Pol, NotI RE	T7 Pol, KpnI RE	
<i>ASPHD1</i>	human	BC126319	pCR4-TOPO	EcoRI/XbaI			SP6 Pol, NotI RE
<i>asphd1</i>	zebrafish	NA	NA	GATCGGATCCTGATCCTCCATCCCACTC	SP6 Pol, NotI RE	T7 Pol, HindIII RE	
<i>C16ORF53</i>	human	BC003640	pOTB7	AAGAATTCCTGCCCTAGTGGCCTATGTCCC			SP6 Pol, NotI RE
<i>c16orf53</i>	zebrafish	NA	NA	AACTCGAGTCAGTATTTCGCTGCCGAGGG			
				AAGAATTCTTAATCACCCCGCGGGCTC	SP6 Pol, XhoI RE	T7 Pol, EcoRI RE	
				AACTCGAGCCCTCTGAAGACTGAGCTGTCC			
<i>CDIPT</i>	human	BC001444.2	pOTB7	EcoRI/BglIII (blunt) to StuI site in pcs2+			SP6 Pol, NotI RE
<i>cdipt</i>	zebrafish	BC066511	pCMV-SPORT6.1	NA ^h	SP6 Pol, NotI RE	T7 Pol, SpeI RE	
<i>CORO1A</i>	human	BC110374	pCMV-SPORT6	ATTAGGATCCCAGAATGAGCCGGCAGGTGGT			SP6 Pol, NotI RE
				GCATCTCGAGGGCTCACTTGGCCTGGACTG			
<i>coro1a</i>	zebrafish	BC055237.1	pME18SFL3	EcoRI/XbaI	SP6 Pol, XbaI RE	T7 Pol, EcoRI RE	
<i>DOC2A</i>	human	BC041769	pBluescriptR	AAGAATTCGCCAGGGGTGCTGATGAGG			SP6 Pol, NotI RE
				AATCTAGATGTGCCGGGACACTGCTGTC			
<i>doc2a</i>	zebrafish	NA	NA	GATCGGATCCCCCTGCTTCTCCACTGTCTC	SP6 Pol, NotI RE	T7 Pol, HindIII RE	
				GATCCTCGAGACTGTGACCTCAGCGCTT			
<i>FAM57B</i>	human	BC007892	pOTB7	EcoRI/XhoI			SP6 Pol, NotI RE
<i>fam57b</i>	zebrafish	BC059567	pBluecript SK(-)	NA ^h	T3 Pol, XhoI RE	T7 Pol, EcoRI RE	na
<i>GDPD3</i>	human	BC002714	pOTB7	EcoRI/XhoI (Removes 3'UTR)			SP6 Pol, NotI RE
<i>gdpd3</i>	zebrafish	BC064306	pExpress-1	NA ^h	SP6 Pol, NotI RE	T7 Pol, EcoRV RE	
<i>HIRIP3</i>	human	NM_003609	pCMV6-AC	AAGAATTCGAGCCGTCAATCCCGGGTTG			SP6 Pol, NotI RE
				AACTCGAGTGGGGGTGGCAGAGCTCAGT			
<i>hirip3</i>	zebrafish	BC055674	pME18SFL3	XhoI	SP6 Pol, NotI RE	T7 Pol, HindIII RE	
<i>INO80E</i>	human	BC047712.2	pCMV-SPORT6	ATTAGGATCCGGTCATGAACGGGCGCGGACG			SP6 Pol, NotI RE
				GCATCTCGAGCAGGCTCACTCCGGGATGTCGAT			
<i>ino80e</i>	zebrafish	BC065338	pCMV-SPORT6	NA ^h	SP6 Pol, XhoI RE	T7 Pol, StuI RE	
<i>KCTD13</i>	human	BI548684.1	pBluescriptR				
<i>kctd13</i>	zebrafish	BC122284	pME18SFL3	XhoI	SP6 Pol, BglII RE	T7 Pol, EcoRI RE	SP6 Pol, NotI RE
<i>KIF22</i>	human	BC028155	pCMV-SPORT6	EcoRI/XhoI (114 n.t. of 3' UTR remains)			SP6 Pol, NotI RE
<i>kif22</i>	zebrafish	BC154464	pME18SFL3	XhoI	SP6 Pol, XbaI RE	T7 Pol, EcoRI RE	
<i>MAPK3</i>	human	BC013992	pOTB7	TGTA AAAACGACGGCCAGTAA			SP6 Pol, NotI RE
				GGTG CAGAGATGTCTGTCTGG			
<i>mapk3</i>	zebrafish	BC097073	pCMV-SPORT6	NA ^h	SP6 Pol, XhoI RE	T7 Pol, EcoRV RE	
<i>maz</i>	zebrafish	NA	NA	ACGTCATGATGGATGCAGCTTGG	SP6 Pol, NotI RE	T7 Pol, EcoRI RE	SP6 Pol, NotI RE
				CCTCTCTCTGTTGGTTAGCTG			
<i>MVP</i>	human	BC015623	pOTB7	EcoRI/XhoI (93 n.t. of 3' UTR remains)			SP6 Pol, NotI RE
<i>mvp</i>	zebrafish	BC063949.1	pExpress-1	NA ^h	SP6 Pol, NotI RE	T7 Pol, EcoRI RE	
<i>mvp</i>	zebrafish	BC063949.2	pExpress-1	EcoRI/NsiI			SP6 Pol, NotI RE
<i>PPP4C</i>	human	BC001416	pOTB7	EcoRI/XhoI (301 n.t. of 3' UTR remains)			SP6 Pol, NotI RE
<i>ppp4ca</i>	zebrafish	BC049430	pME18SFL3	EcoRI/XbaI	SP6 Pol, XbaI RE	T7 Pol, EcoRI RE	
<i>ppp4cb</i>	zebrafish	BC155609	pExpress-1	NA ^h	SP6 Pol, NotI RE	T7 Pol, EcoRV RE	
<i>prrt2</i>	zebrafish	BC053594	pCMV-SPORT6	NA	NA	NA	NA
<i>SEZ6L2</i>	human	BC000567	pOTB7	AAGAATTCAGATCGGGGTGAGTCGCCA			SP6 Pol, NotI RE
				AACTAGTTGCAGCTGTAGTCTTGGGGTTCA			
<i>sez6l2</i>	zebrafish	NA	NA	GATCGGATCCCATACGCCCAATGACGTTC	SP6 Pol, NotI RE	T7 Pol, HindIII RE	
				GATCCTAGACTCCAAGTGAATGGGGCTGT			
<i>TAOK2</i>	human	BC142663	pCMV-SPORT6	AAGAATTCACAGCCAGGCCCACTC			SP6 Pol, NotI RE
				AACTAGTCAGCTaCCTCCAGGGGGGCAG			
<i>taok2a</i>	zebrafish		pGEM-T Easy	AGCGGGGAGCAGGTACAC	T7 Pol, SpeI RE	SP6 Pol, SacII RE	
				ATGGGGGCGCTCTCGGCATAA			
<i>taok2b</i>	zebrafish		pGEM-T Easy	CCTTCAAAAAGCTGCGGCACCC	T7 Pol, SpeI RE	SP6 Pol, SacII RE	
				TGATTCAGTGCTTTGTGCAGCAGC			
<i>TBX6</i>	human	BC026031	pOTB7				
<i>YPEL3</i>	human	BC050664	pCMV-SPORT6	EcoRI/XhoI (48 n.t. of 3' UTR remains)			SP6 Pol, SacII RE
<i>ypel3</i>	zebrafish	BC067578	pCMV-SPORT6	NA ^h	SP6 Pol, XhoI RE	T7 Pol, KpnI RE	