

November 24, 2016

**SUPPLEMENTARY INFORMATION**

**to manuscript titled**

**'A ZIP6-ZIP10 heteromer controls GSK3-dependent NCAM1 phosphorylation and integration into focal adhesion complexes during epithelial-to-mesenchymal transition'**

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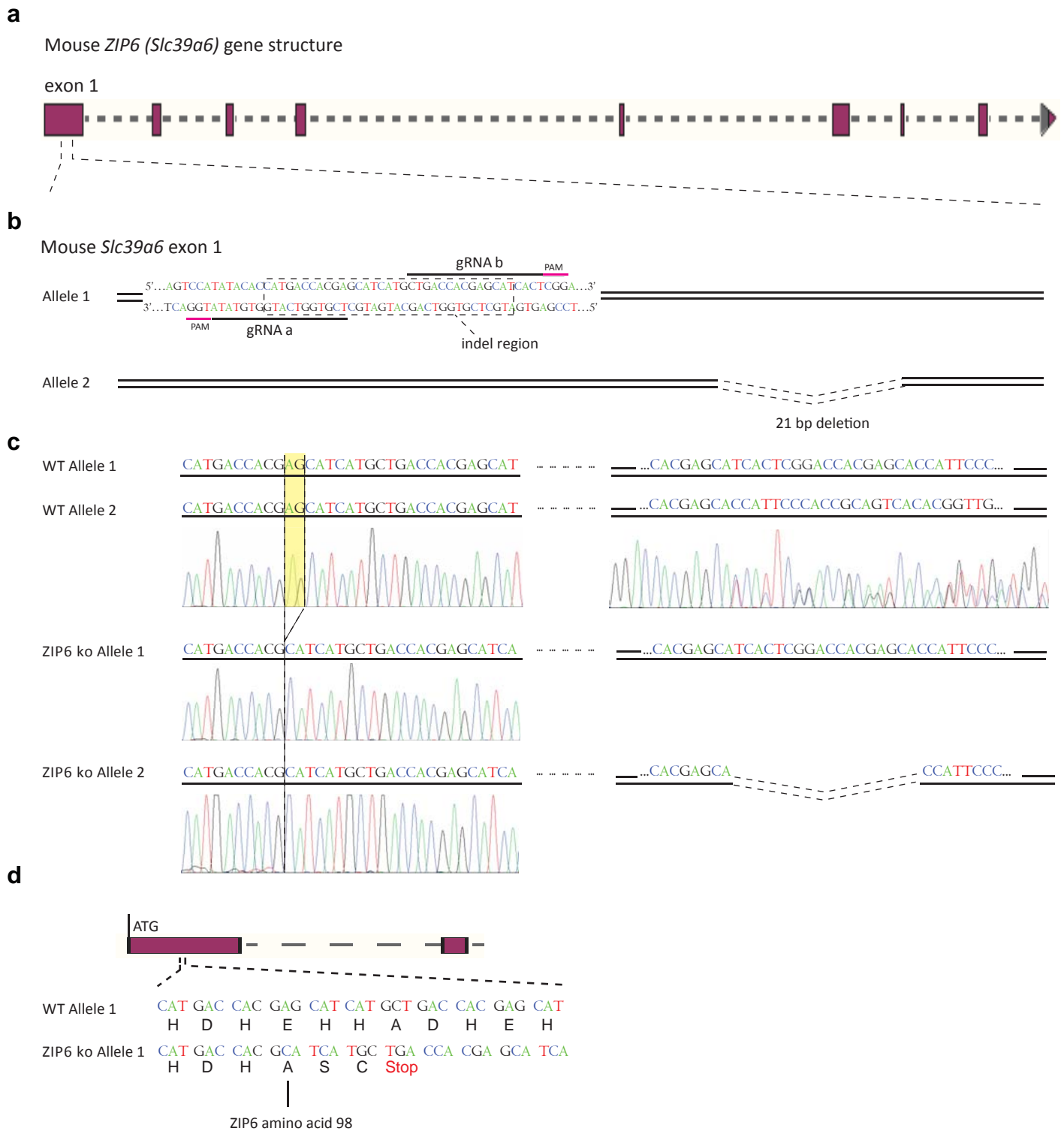
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**Fig S1. Design and genomic validation of CRISPR-Cas9 nickase edited mouse ZIP6 knockout NMuMG cells.**

(a) Exon and intron structure of mouse *Slc39a6*. (b) Targeting the mouse *Slc39a6* Exon 1 locus with a paired CRISPR-Cas9 nickase design using gRNAs 'a' and 'b'. (c) Genomic sequence chromatograms of wt and ZIP6 ko clones with nucleotide residues missing in the ZIP6 ko clone highlighted in yellow. (d) Analysis of genomic PCR sequencing results with revealed that the 2-nucleotide deletion led to the formation of premature STOP codon. Note that due to the presence of additional introns downstream of the translation termination signal , the host-encoded nonsense-mediated decay program is expected to degrade the mutant transcripts, thereby largely precluding the formation of the truncated ZIP6 protein in the ZIP6 ko NMuMG clone.

**Figure S1**



**Table S1: The ZIP6 interactome in mouse NMuMG cells exhibiting a fibroblastoid morphology following 48 hrs of TGFβ1 treatment**

Accession	Description	Description (curated)	Coverage	Proteins	Unique	Total	PSMs	126/131	Var. [%]	127/131	Var. [%]	128/131	Var. [%]	129/131	Var. [%]	130/131	Var. [%]	Count	# AAs	MW [kDa]	calc. pI
IP0046900.4	Zinc transporter ZIP6	Zinc transporter ZIP6	29.28%	2	10	23	101	9,085	427.2	1,000	0.0	7,790	654.8	1,000	0.0	7,976	324.9	27	765	86.3	6.84
IP00989517.1	Uncharacterized protein (Fragment)	Neural Cell Adhesion Molecule 1	42.19%	7	6	21	59	13,952	94.7	1,000	58.1	13,132	75.2	1,000	47.2	10,828	45.8	11	839	92.3	4.88
IP00123639.1	Calreticulin	Calreticulin	10.82%	1	1	6	19	8,139	6.0	0.393	16.7	10,486	11.3	0.863	1.5	7,846	7.6	3	416	48.0	4.49
IP00273801.3	Zinc transporter ZIP10	Zinc transporter ZIP10	18.97%	2	11	16	78	6,653	113.4	1,000	7.0	7,012	219.1	1,000	0.0	5,972	104.3	31	833	94.3	6.71
IP00111218.1	Aldehyde dehydrogenase, mitochondrial	Aldehyde dehydrogenase	42.00%	2	3	15	50	2,452	62.0	1,091	13.0	2,718	206.5	1,023	11.5	2,788	176.4	7	519	56.5	7.62
IP00230108.6	Protein disulfide-isomerase A3	Protein disulfide-isomerase A3	30.30%	2	5	12	37	2,579	83.9	1,000	5.5	3,195	138.5	1,000	19.0	2,096	71.5	13	505	56.6	6.21
IP00463589.2	Uncharacterized protein	ATPase, Ca++ transporting, plasma membrane 4	41.64%	5	6	33	56	3,026	128.1	1,000	0.0	1,971	74.9	1,000	1.8	1,612	19.5	7	1172	129.2	6.73
IP00319994.6	L-lactate dehydrogenase A chain	L-lactate dehydrogenase A chain	44.88%	4	3	12	41	1,951	32.0	1,340	45.5	1,674	89.1	1,261	35.4	2,284	38.5	9	332	36.5	7.74
IP00127841.3	ADP/ATP translocase 2	ADP/ATP translocase 2	42.62%	2	4	9	23	1,578	27.9	0.887	9.6	2,000	40.0	0.985	15.0	1,639	15.0	6	298	32.9	9.73
IP00223060.1	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Phosphoenolpyruvate carboxykinase	18.44%	2	5	10	24	1,475	42.4	1,146	46.9	1,613	72.0	1,134	59.1	1,786	88.6	13	667	73.4	7.74
IP00135130.3	Neutral amino acid transporter A	Neutral amino acid transporter A	40.79%	1	9	16	156	1,541	26.7	0.950	32.2	1,858	37.5	0.896	16.4	1,458	29.4	49	532	56.0	5.87
IP00624175.1	Isoform 1 of Lysophosphatidic acid phosphatase type 6	Lysophosphatidic acid phosphatase type 6	49.28%	4	8	17	58	1,794	38.1	0.991	34.6	1,559	38.0	0.960	26.3	1,496	32.2	20	418	47.6	7.72
IP00122928.1	Tubulin beta-6 chain	Tubulin beta-6 chain	39.82%	2	2	13	38	1,481	20.9	0.882	43.4	1,596	55.3	0.921	27.9	1,575	59.6	6	447	50.1	4.89
IP00554989.3	Peptidyl-prolyl cis-trans isomerase	Peptidyl-prolyl cis-trans isomerase	34.73%	5	3	7	9	1,795	30.6	0.920	16.2	1,551	17.9	0.783	25.2	1,246	31.4	3	167	18.3	7.90
IP00622795.2	Glyceraldehyde-3-phosphate dehydrogenase	Glyceraldehyde-3-phosphate dehydrogenase	36.64%	28	3	13	52	1,389	45.8	0.926	11.4	1,748	20.3	0.889	103.2	1,418	39.2	13	333	35.8	8.03
IP00117348.4	Tubulin alpha-1B chain	Tubulin alpha-1B chain	41.24%	4	1	14	53	1,555	19.0	1,057	13.7	1,520	20.1	1,003	21.9	1,424	30.3	20	451	50.1	5.06
IP00110753.1	Tubulin alpha-1A chain	Tubulin alpha-1A chain	41.24%	5	1	13	53	1,474	19.7	1,048	14.9	1,490	20.2	1,003	21.9	1,378	31.7	20	451	50.1	5.06
IP00117352.1	Tubulin beta-5 chain	Tubulin beta-5 chain	52.70%	6	5	21	57	1,234	32.3	0.977	34.5	1,587	68.6	0.885	38.5	1,493	48.7	13	444	49.6	4.89
IP00874456.1	Dihydropyridyl dehydrogenase, mitochondrial	Dihydropyridyl dehydrogenase	36.94%	2	3	18	43	1,578	69.4	0.975	54.4	1,266	31.1	0.952	62.5	1,463	74.1	6	509	54.2	7.80
IP00118108.1	Tetraspanin-6	Tetraspanin-6	21.22%	1	1	3	8	1,617	4.4	1,065	8.2	1,387	16.0	0.603	57.2	1,228	19.4	4	245	27.3	7.74
IP00895479.1	Uncharacterized protein	KxkL motif-containing protein 1	53.02%	17	3	10	24	1,527	51.4	1,000	0.6	1,469	64.5	1,000	46.6	1,194	13.1	6	232	26.8	9.83
IP00230351.1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Succinate dehydrogenase flavoprotein subunit	44.28%	1	4	24	64	1,399	62.2	1,083	36.8	1,402	48.4	0.949	70.2	1,257	19.7	9	664	72.5	7.37
IP00229517.5	Galectin-1	Galectin-1	53.33%	1	2	6	15	1,658	29.2	1,035	43.1	1,318	30.7	0.980	33.9	1,080	18.2	4	135	14.9	5.49
IP00407130.4	Isoform M2 of Pyruvate kinase isozymes M1/M2	Pyruvate kinase isozymes M1/M2	33.71%	4	5	17	41	1,262	20.0	0.955	61.3	1,362	44.6	1,243	33.5	1,370	31.2	10	531	57.8	7.47
IP00121440.4	Electron transfer flavoprotein subunit beta	Electron transfer flavoprotein subunit beta	37.65%	1	3	9	18	1,173	23.1	0.750	18.2	1,427	1.8	0.949	16.1	1,390	18.6	4	255	27.6	8.10
IP00399958.3	Calumenin isoform 2	Calumenin isoform 2	24.44%	6	3	6	20	1,493	38.5	1,095	15.9	1,208	16.2	0.970	145.1	1,283	56.1	7	315	37.1	4.59
IP00331556.5	Heat shock 70 kDa protein 4	Heat shock 70 kDa protein 4	51.61%	1	10	36	104	1,453	30.5	0.972	14.8	1,279	22.4	0.964	23.3	1,224	30.7	23	841	94.1	5.24
IP00338536.1	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	Succinate dehydrogenase iron-sulfur subunit	60.99%	2	5	20	53	1,287	12.1	1,090	20.8	1,361	26.8	1,089	23.6	1,298	13.9	7	282	31.8	8.68
IP00263863.8	10 kDa heat shock protein, mitochondrial	10 kDa heat shock protein	80.39%	3	6	10	46	1,403	37.2	0.859	22.0	1,233	22.5	0.846	26.9	1,305	16.8	17	102	11.0	8.35
IP00323592.2	Malate dehydrogenase, mitochondrial	Malate dehydrogenase	84.32%	1	11	23	66	1,252	22.8	0.961	13.9	1,322	23.0	0.917	14.3	1,338	16.5	20	338	35.6	8.68
IP00875833.2	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	Monofunctional C1-tetrahydrofolate synthase	43.50%	1	11	38	90	1,064	37.7	1,000	31.5	1,251	35.7	0.903	28.2	1,492	25.3	18	977	105.7	7.02
IP00117083.1	GrpE protein homolog 1, mitochondrial	GrpE protein homolog 1	26.73%	1	6	7	12	1,190	29.3	0.951	33.6	1,318	91.0	0.951	61.0	1,231	21.5	7	217	24.3	8.38
IP00454049.4	Enoyl-CoA hydratase, mitochondrial	Enoyl-CoA hydratase	58.97%	3	13	17	146	1,082	23.1	0.850	22.1	1,384	15.2	0.944	21.6	1,220	22.2	47	290	31.5	8.48
IP00648141.1	Glycogen synthase kinase-3 alpha	Glycogen synthase kinase-3 alpha	50.61%	13	6	19	88	1,056	16.6	1,000	31.3	1,404	28.3	0.979	10.6	1,177	24.5	24	490	51.6	8.61
IP00318614.9	Iso citrate dehydrogenase [NADP], mitochondrial	Iso citrate dehydrogenase [NADP]	31.19%	2	7	13	35	1,156	21.7	0.923	19.4	1,225	14.7	1,000	31.7	1,245	26.8	11	452	50.9	8.69
IP00114209.1	Glutamate dehydrogenase 1, mitochondrial	Glutamate dehydrogenase 1	35.66%	2	11	20	43	1,092	16.6	0.937	9.6	1,125	17.9	0.965	36.6	1,383	35.8	14	558	61.3	8.00
IP00671957.2	Glutaminase isoform 2	Glutaminase isoform 2	52.90%	5	6	18	49	1,196	38.0	1,020	40.6	1,157	50.8	0.884	25.2	1,237	48.1	14	603	66.0	8.12
IP00125319.1	Glycogen synthase kinase-3 beta	Glycogen synthase kinase-3 beta	50.48%	5	6	17	116	1,235	33.5	0.852	29.3	1,220	30.2	1,000	29.3	1,111	24.1	36	420	46.7	8.78
IP00308885.6	Isoform 1 of 60 kDa heat shock protein, mitochondrial	60 kDa heat shock protein	64.75%	4	19	35	193	1,127	16.5	0.950	14.6	1,201	19.9	0.821	23.6	1,219	16.5	60	573	60.9	6.18
IP00111960.2	Lysosomal alpha-glucosidase	Lysosomal alpha-glucosidase	28.23%	5	5	19	46	1,270	7.7	1,079	21.8	1,170	12.5	0.937	12.6	1,103	17.2	9	953	106.2	5.83
IP00113141.1	Citrate synthase, mitochondrial	Citrate synthase	38.36%	1	4	19	52	1,111	23.3	0.920	24.0	1,202	11.7	0.865	15.2	1,229	16.9	12	464	51.7	8.57
IP00116074.1	Aconitate hydratase, mitochondrial	Aconitate hydratase	39.10%	1	13	25	82	1,133	32.3	0.832	26.8	1,216	24.5	0.930	25.5	1,164	26.2	24	780	85.4	7.93
IP00118825.2	Citrate synthase-like protein	Citrate synthase-like protein	43.13%	1	3	18	57	1,174	34.7	1,002	21.4	1,151	20.2	0.916	18.6	1,173	19.2	8	466	52.3	8.79
IP00319992.1	78 kDa glucose-regulated protein	78 kDa glucose-regulated protein	30.38%	1	10	21	109	1,045	27.0	1,000	25.9	1,229	35.3	1,034	29.6	1,167	27.5	30	655	72.4	5.16
IP00117312.1	Aspartate aminotransferase, mitochondrial	Aspartate aminotransferase	43.02%	1	7	14	73	1,160	24.9	1,000	20.5	1,061	23.8	0.895	17.2	1,194	18.1	27	430	47.4	9.00
IP00459725.2	Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Isocitrate dehydrogenase [NAD] subunit alpha	32.51%	2	6	12	36	1,130	45.2	0.873	17.7	1,130	39.5	0.896	15.7	1,116	9.4	10	366	39.6	6.73

