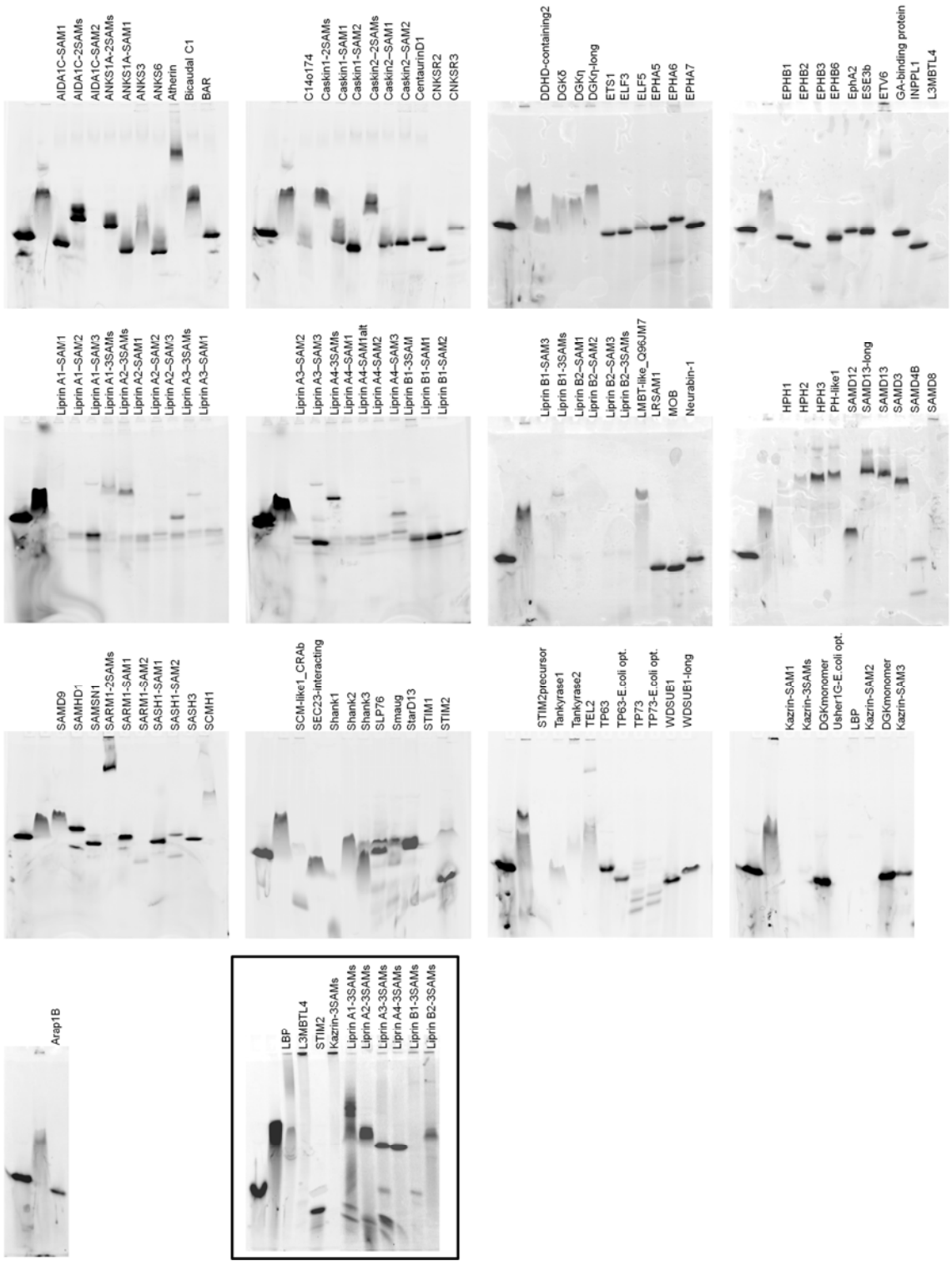

Supplemental Figure 1. Native gel analysis of negGFP-hSAM fusions. The soluble fraction of cell lystaes containing negGFP-hSAM fusion proteins were run on native gels and the bands visualized by fluorescence. Samples that were purified, concentrated, and rerun are shown in the boxed gel. All gels include a DGK-SAM monomeric mutant and a DGK-SAM polymer in the first two lanes as controls.

Protein	Gene ID#	Gel Result	EM Result	Function
AIDA1C/ANKS1B / cajalin2-2SAMs	56899	NP/WP		Acts as a neuronal scaffolding protein in the postsynaptic density. Tandem SAM NMR structure solved (PDB ID#2KIV) and shows head-to-tail dimer that occludes nuclear import signal.[1]
AIDA1C/ANKS1B/ cajalin2-SAM2	*fragment*	*E*		
AIDA1C/ANKS1B/ cajalin2-SAM1	*fragment*	*NP/WP*		*NMR srtucture solved. (PDB ID#2KE7)*
ANKS1A/ odin-2SAMs	23294	BO		Odin (ANKS1A) is a Src family kinase target in colorectal cancer cells.[2]
ANKS1A /odinSAM1	*fragment*	*BO*		
ANKS3	124401	PP	Likely Polymer	Unknowen
ANKS6/ SAMD6	203286	BO		The polycystic kidney disease-related proteins Bicc1 (BicaudalC1) and SamCystin (ANKS6) interact although not necessarily through their respective SAM domains. ANKS6 self-associates (co-immunoprecipitation) in a manner that requires both the SAM domain and the ankyrin repeats. Mutations in either gene cause renal cysts in rodents.[3]
Atherin/ SAMD1	90378	PP	Likely Polymer	A lesion-specific, LDL-binding protein in human atherosclerosis.[4]
BAR	51283	NP/WP		Involved in the regulation of neuronal survival.[5]; Appears as a monomer at high concentration (unpublished result)
BicaudalC1	80114	PP		Controls cilia orientation and leftward flow.[6]
C14orf174	161394	PP		UNK
Caskin-1-2SAMs	57524	PP	Likely Polymer	Binds CASK, a scaffolding protein at neuronal synapses in the vertebrate brain; may couple CAST to downstream effectors.[7]
Caskin-1-SAM1	*fragment*	*BO*		
Caskin-1-SAM2	*fragment*	*NP/WP*		
Caskin2/ANKS5B–2SAMs	57513	PP	Likely Polymer	See Caskin 1
Caskin2–SAM1	*fragment*	*NP/WP*		
Caskin2–SAM2	*fragment*	*NP/WP*		
CentaurinD1/ ARAP1	116985	NP/WP		In vitro, displays RHO-GAP and phosphatidylinositol (3,4,5) trisphosphate (PIP3)-dependent ARF-GAP activity; Associates with the Golgi, and mediates changes in the Golgi and the formation of filopodia; Thought to regulate the cell-specific trafficking of a receptor protein involved in apoptosis. [provided by RefSeq]

Protein	Gene ID#	Gel Result	EM Result	Function
CNKSR2	22866	NP/WP		Functions as a scaffold protein to mediate the mitogen-activated protein kinase pathways downstream from Ras; Induced by vitamin D and inhibits apoptosis in certain cancer cells; May play a role in complex assembly of synaptic proteins at the postsynaptic membrane and coupling of signal transduction to membrane/cytoskeletal remodeling. [provided by RefSeq]
CNKSR3	154043	BO		CNKSR3, a homologue of scaffold proteins involved in MAPK pathway regulation, is a direct target of MR and is required for the maintenance of transepithelial sodium transport in the kidney.[8]
DDHD-containing2	23259	BO		Locallized in golgi; regulates golgi-to-plasma membrane trafficking.[9]
DGKd	8527	PP		Involved in lipid signalling - converts diacylglycerol to phosphatidic acid. Plays inhibitory role in CopII vesicle formation. Required for efficient uptake of cargo into clathrin-coated vesicles. Involved in diabetes.[10-14]
DGKh	160851	PP		Involved in lipid signalling - converts diacylglycerol to phosphatidic acid. Linked to bipolar depression.[15,16]
DGKh-long	*repeat*	*PP*		
DKFZp686D0662, ETS1	2113	NP/WP		Regulates numerous genes and is involved in stem cell development, cell senescence and death, and tumorigenesis. Regulates protein tyrosine kinases in cancer cells.[17-20]
ELF3/ESE-1	1999	NP/WP		ETS transcription factor implicated in a variety of cancers and a potential role in airway inflammation[21-23]
Elf-5	2001	NP/WP		Member of an epithelium-specific subclass of the Ets transcritpion factor family; Regulates the later stages of terminal differentiation of keratinocytes and epithelium-specific genes found in tissues containing glandular epithelium such as salivary gland and prostate. [provided by RefSeq]
EPHA2	1969	NP/WP		EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system; Involved in many forms of cancer and is an effector of chemotherapeutic agents; Kinase activity required for regulation of cell adhesion and cytoskeletal rearrangement
EPHA5	2044	NP/WP		EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system. [provided by RefSeq]

Protein	Gene ID#	Gel Result	EM Result	Function
EPHA6	285220	NP/WP		EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system; Involved in neural circuits underlying aspects of learning and memory. [provided by RefSeq]
EPHA7	13841	NP/WP		EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system. Implicated in hepato-, prostate and lung cancers.[24-26]
EPHB1	2047	NP/WP		EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system; Loss of expression of EphB1 protein in gastric carcinoma is associated with invasion and metastasis; Regulate the proliferation and migration of neural progenitors in the hippocampus; Involved in bone cancer pain. Regulates NMDA-receptors[27-30]
EPHB2	2048	NP/WP		Ephrin receptors and their ligands, the ephrins, mediate numerous developmental processes, particularly in the nervous system. EphB2 enhances proliferation through a kinase-dependent pathway and inhibits migration independent of its kinase activity.[31]
EPHB3	2049	E, X		May have roles in squamous cell carcinoma of the lung; EphB3-ephrin-B interaction promotes mesenchymal-to-epithelial transition (MET) by re-establishing epithelial cell-cell junctions and such an MET-promoting effect contributes to EphB3-mediated tumor suppression.[32,33]
EPHB6	2051	NP/WP		EphB6 receptor significantly alters invasiveness and other phenotypic characteristics of human breast carcinoma cells; May play an important role in regulating thymocyte differentiation and modulating responses of mature T cells; Both positively and negatively regulates cell adhesion and migration.[34,35]
ESE3	26298	NP/WP		Belongs to an ETS transcription factor subfamily characterized by epithelial-specific expression (ESEs); Acts as a transcriptional repressor and may be associated with asthma susceptibility; May be involved in epithelial differentiation and carcinogenesis. [provided by RefSeq]
GA-binding protein/GABP	2551	NP/WP		Transcription factor subunits which functions as a DNA-binding subunit; Likely involved in activation of cytochrome oxidase expression and nuclear control of mitochondrial function; May play a role in the Down Syndrome phenotype. [provided by RefSeq]

Protein	Gene ID#	Gel Result	EM Result	Function
INPPL1	3636	NP/WP		An SH2-containing 5'-inositol phosphatase that is involved in the regulation of insulin function; Plays a role in the regulation of epidermal growth factor receptor turnover and actin remodelling; Supports metastatic growth in breast cancer and is a valuable biomarker for breast cancer. [provided by RefSeq]
Kazrin-3SAMs, purified	23254	PP	Likely Polymer	KazrinE is a desmosome-associated liprin that colocalises with acetylated microtubules[36]
Kazrin-S1	*fragment*	*E*		
Kazrin-S2	*fragment*	*E*		
Kazrin-S3	*fragment*	*E*		
L3MBTL4, purified	91133	PP		LMBT proteins are polycomb group proteins, involved in the maintenance of transcriptional repression. Homozygous mutations in the l(3)mbt gene cause brain tumors in Drosophila, identifying l(3)mbt as a tumor suppressor gene. Maps to a chromosomal region deleted in myeloid hematopoietic malignancies. Implicated in breast cancers.[37]
LBP-1, purified	7342	PP	Likely Polymer	LBP-1 proteins form dimers and act as transcription factors that activate a number of genes related to cell growth and differentiation. Shown to self-associate via SAMs[38]
Liprin A1–SAM1	*fragment*	*E*		
Liprin A1–SAM2	*fragment*	*E*		
Liprin A1–SAM3	*fragment*	*E*		
LiprinA1-3SAMs, purified	8500	NP/WP		Binds to tyrosine phosphatase LAR (important for axon guidance and mammary gland development), and appears to localize LAR to cell focal adhesions; May regulate the disassembly of focal adhesion and thus help orchestrate cell-matrix interactions. [provided by RefSeq]
LiprinA2–3SAMs, purified	8499	NP/WP		This protein is most closely related to PPFIA1, a liprin family member known to interact with the protein phosphatase LAR. The expression of this gene is found to be downregulated by androgens in a prostate cancer cell line. [provided by RefSeq]
LiprinA2-SAM1	*fragment*	*E*		
LiprinA2–SAM2	*fragment*	*E*		
LiprinA2–SAM3	*fragment*	*E*		
LiprinA3–3SAMs, purified	8541	NP/WP		See Liprin A1
LiprinA3–SAM1	*fragment*	*E*		
LiprinA3–SAM2	*fragment*	*E*		
LiprinA3–SAM3	*fragment*	*X*		
LiprinA4-3SAMs, purified	8497	NP/WP		See LiprinA1

Protein	Gene ID#	Gel Result	EM Result	Function
LiprinA4-SAM1	*fragment*	*E*		
LiprinA4–SAM1-insertion	*fragment*	*E*		*Sequence contains a small insertion not found in the NCBI database*
LiprinA4-SAM2	*fragment*	*E, X*		
LiprinA4–SAM3	*fragment*	*E, X*		
LiprinB1-3SAM	8496	PP	Likely Polymer	Binds to tyrosine phosphatase LAR (important for axon guidance and mammary gland development); Found to interact with S100A4, a calcium-binding protein related to tumor invasiveness and metastasis. [provided by RefSeq]
LiprinB1-3SAMs, rerun	*8496*	*PP*		
LiprinB1-SAM1	*fragment*	*BO*		
LiprinB1-SAM2	*fragment*	*E*		
LiprinB1-SAM3	*fragment*	*E, X*		
LiprinB2–3SAMs	8495	PP		See other liprin entries
LiprinB2–SAM1	*fragment*	*E*		
LiprinB2–SAM2	*fragment*	*E, X*		
LiprinB2–SAM3	*fragment*	*E*		
LMBT-like_Q96JM7_L3MBTL3	84456	PP		Polycomb group (PcG) proteins participate in DNA-binding complexes with gene-repressing activity, many of which have been highlighted for their involvement in hematopoiesis; Deletion is predicted to be responsible for myeloid hematopoietic malignancies. H-L(3)MBT directly interacts with TEL.[39,40]
LRSAM1	90678	NP/WP		Multifunctional RING finger protein that selectively regulates cell adhesion molecules, has ubiquitin ligase activity, and plays a role in receptor endocytosis and viral budding. Mutations found in patients with Charcot-Marie-Tooth disease. [41-43]
MOB	259230	NP/WP		The protein encoded by this gene is predicted to be a five-pass transmembrane protein. Regulates subcellular pools of diacylglycerol-binding proteins in the Golgi apparatus; Regulates, lipid messengers; Influences apoptosis.[44-46]
Neurabin-1	55607	NP/WP		Acts as regulatory subunit of protein phosphatase I, and controls actin cytoskeleton reorganization. [provided by RefSeq]
Ph1	1911	PP		Drosophila 'Polycomb' group of genes responsible for the stable inheritance of gene activity; Form a multimeric, chromatin-associated protein complex. Homologous to Drosophila 'polyhomeotic' (Ph); The specific function in human cells has not yet been determined. [provided by RefSeq]
PH2	1912	PP		Drosophila 'Polycomb' group of genes responsible for the stable inheritance of gene activity; Form a multimeric, chromatin-associated protein complex. Homologous to Drosophila 'polyhomeotic' (Ph); The specific function in human cells has not yet been determined. [provided by RefSeq]

Protein	Gene ID#	Gel Result	EM Result	Function
PHC3	80012	PP		Loss of PHC3 may favor tumorigenesis by potentially disrupting the ability of cells to remain in G(0)
SAMD12	401474	BO		Unknown
SAMD13-long	148418	PP		Unknown
SAMD13-short	*Repeat*	*PP*		*Repeat*
SAMD3	154075	PP		Unknown
SAMD4B	55095	NP/WP		Inhibits AP-1-, p53- and p21-mediated transcriptional activity.[47]
SAMD8	142891	PP		Homology to sphingomyelin synthases [RefSeq]
SAMD9	54809	PP	Likely Polymer	SAMD9 could be a key molecule to control cancer cell death by inactivated Sendai virus particle or IFN-beta treatment; Deficient in normophosphatemic familial tumoral calcinosis; Interacts with RGL2 to diminish the expression of EGR1.[48,49]
SAMHD1	25939	M/BO		This gene may play a role in regulation of the innate immune response. The encoded protein is upregulated in response to viral infection and may be involved in mediation of tumor necrosis factor-alpha proinflammatory responses. Mutations in this gene have been associated with Aicardi-Goutieres syndrome. [provided by RefSeq]
SAMSN1	64092	NP/WP		SAMSN1 is a member of a novel gene family of putative adaptors and scaffold proteins containing SH3 and SAM (sterile alpha motif) domains.[50]
SARM1-2SAMs	23098	PP		TIR adaptor SARM is a negative regulator of Toll-like receptor signaling; Also a candidate gene in the onset of hereditary infectious/inflammatory diseases; Regulates neuronal response to stress.[51-53]
SARM1-SAM1	*fragment*	*NP/WP*		
SARM1-SAM2	*fragment*	*E*		
SASH1-SAM1	23328	NP/WP		Downregulated expression of the candidate tumour suppressor gene SASH1 is associated with colon cancer. Tumor suppressor gene possibly involved in tumorigenesis of breast and other solid cancers.[54,55]
SASH1-SAM2	*fragment*	*NP/WP*		
SASH3	54440	NP/WP		The protein encoded by this gene contains a Src homology-3 (SH3) domain and a sterile alpha motif (SAM), both of which are found in proteins involved in cell signaling. This protein may function as a signaling adapter protein in lymphocytes.[56]
SCMH1	22955	PP		A polycomb group protein involved in transcriptional repression; A crystal structure of the SAM of a homologue shows it forms helical polymers; Forms co-polymers with PH.[57,58]
SCM-like1/CRAb/SFMBT1	51460	PP		This gene shares high similarity with the Drosophila Scm (sex comb on midleg) gene. It encodes a protein which contains four malignant brain tumor repeat (mbt) domains and may be involved in antigen recognition. Several alternative splice variants have been characterized. [provided by RefSeq]

Protein	Gene ID#	Gel Results	EM Results	Function
SEC23-interacting protein/SEC23IP	11196	BO		COPII-coated vesicles are involved in protein transport from the endoplasmic reticulum to the Golgi apparatus. The protein encoded by this gene was identified by its interaction with a mouse protein similar to yeast Sec23p, an essential component of the COPII. Overexpression of this protein has been shown to cause disorganization of the endoplasmic reticulum-Golgi intermediate compartment and Golgi apparatus, which suggests its role in the early secretory pathway. [provided by RefSeq]
Shank1	50944	X		Plays scaffolding role in post synaptic density.[59]
Shank2	22941	PP		Plays scaffolding role in post synaptic density; Mutations linked to autism and mental retardation; Regulates Na+/H+ exchanger 3.[59-61]
Shank3	85358	PP		Plays scaffolding role in post synaptic density; Crystal structure and EM results show that Shank3-SAM can form sheets made of aligned polymers.[59,62]
SLP76/LCP2	3937	NP/WP		SLP-76 was originally identified as a substrate of the ZAP-70 protein tyrosine kinase following T cell receptor (TCR) ligation in the leukemic T cell line Jurkat. Functions as an adaptor or scaffold protein. Studies using SLP-76 deficient T cell lines or mice have provided strong evidence that SLP-76 plays a positive role in promoting T cell development and activation as well as mast cell and platelet function. [provided by RefSeq]
Smaug_SAMD4A	23034	NP/WP		Sterile alpha motifs (SAMs) in proteins such as SAMD4A are part of an RNA-binding domain that functions as a posttranscriptional regulator by binding to an RNA sequence motif known as the Smaug recognition element, which was named after the Drosophila Smaug protein.[63-65]
StarD13-deletion	90627	BO		The gene is located in a region of chromosome 13 that has loss of heterozygosity in hepatic cancer. [provided by RefSeq] has GAP activity specific for RhoA and Cdc42; inhibits the Rho mediated assembly of actin stress fibers in cultured cells and is underexpressed in hepatocellular carcinoma tissues
STIM1	6786	E		Monomeric in the calcium-bound state. In the apo state the protein has a tendency to aggregate. Transmembrane protein that mediates Ca2+ influx after depletion of intracellular Ca2+ stores by gating of store-operated Ca2+ influx channels (SOCs).[66-69] May be associated with the Beckwith-Wiedemann syndrome, Wilms tumor, rhabdomyosarcoma, adrenocrotical carcinoma, and lung, ovarian, and breast cancer.

Protein	Gene ID#	Gel Results	EM Results	Function
STIM2, purified	57620	PP		Regulates calcium concentrations in the cytosol and endoplasmic reticulum, and is involved in the activation of plasma membrane Orai Ca(2+) entry channels. This gene initiates translation from a non-AUG (UUG) start site. [provided by RefSeq]
STIM2-long	*repeat*	*E*		*repeat*
Tankyrase1	8658	PP		Spindle aberration associated gene. May play structural scaffolding role; Regulates telomere elongation (inhibited by SAM multimerization). Shown to form polymers via EM; Aberrantly expressed in colon tumors and contain multiple epitopes that induce humoral and cellular immune responses in cancer patients.[70-73]
Tankyrase-2	80351	PP		See Tankyrase 1
TEL/ETV6	2120	PP		This gene encodes an ETS family transcription factor. Required for hematopoiesis and maintenance of the developing vascular network. This gene is known to be involved in a large number of chromosomal rearrangements associated with leukemia and congenital fibrosarcoma. [provided by RefSeq]
TEL2	51513	PP		Transcriptional regulator that plays an important role in a variety of cellular processes throughout development and differentiation, and are involved in oncogenesis as well; Cooperates with Myc in B lymphomagenesis (Potter et al., 2000 [PubMed 10828014]).[supplied by OMIM] [74-77]
TP63	8626	NP/WP		This gene encodes a member of the p53 family of transcription factors. Involved in development and maintenance of stratified epithelial tissues. Mutations associated with ectodermal dysplasia, and cleft lip/palate syndrome 3 (EEC3); split-hand/foot malformation 4 (SHFM4); ankyloblepharon-ectodermal defects-cleft lip/palate; ADULT syndrome (acro-dermato-ungual-lacrimal-tooth); limb-mammary syndrome; Rap-Hodgkin syndrome (RHS); and orofacial cleft 8. [provided by RefSeq]
TP63-optimized	*repeat*	*NP/WP*		*Repeat*
TP73	7161	X		This gene encodes tumor protein p73, which is a member of the p53 family of transcription factors involved in cellular responses to stress and development. [provided by RefSeq]
TP73-optimized	*repeat*	*X*		*Repeat*

Protein	Gene ID#	Gel Results	EM Results	Function
Usher1G-optimized	124590	E		Interacts with harmonin, which is associated with Usher syndrome type 1C; Plays a role in the development and maintenance of the auditory and visual systems and functions in the cohesion of hair bundles formed by inner ear sensory cells; Mutations in this gene are associated with Usher syndrome type 1G (USH1G). [provided by RefSeq]
WDSUB1	151525	NP/WP		Unknown
WDSUB1-long	*repeat*	*NP/WP*		

PP = Possible Polymer, BO = Borderline Oligomer, NP/WP = Non-polymer/Weak polymer, X = Proteolyzed, E = Low expression

YELLOW – SAM previously shown to form polymer, GREEN – Homologous SAM shown to form polymer, BLUE – SAM shown to be monomeric

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