**Supplementary Table 3. Mammalian functions of the MIGs identified in the majority essentialome.** Column three (“Core Essential.”=core essentialome) indicates whether that MIG is found in the core essentialome, while column four (“Ancient Essent.”=ancient essentialome) notes whether that MIG traces back to the last eukaryotic common ancestor (LECA) or earlier (Y=yes, N=no). Based on the findings of literature curation, listed in the Function Description column, MIGs were classified into different functional categories (sixth column). Syn=synonyms.

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| --- | --- | --- | --- | --- | --- |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *ACTL6A* | *BAF53A* | N | Y | part of chromatin remodeling complex (Lessard et al., 2007; Bao et al., 2013); necessary and sufficient for neural progenitor proliferation (Lessard et al., 2007); constitutive knockout is early embryonic lethal (Krasteva et al., 2012) | transcription; cell cycle (proliferation); development (central nervous system) |
| *AHCTF1* | *ELYS* | N | N | in HeLa cells, localizes to nuclear pore and kinetochores, and RNAi-mediated knockdown causes cytokinesis defects (Rasala et al., 2006); required for nuclear pore assembly (Rasala et al., 2006); siRNA-mediated knockdown in HeLa cells results in mislocalization of LBR, which is important for reforming nuclear envelope post-mitosis (Clever et al., 2012); mouse knockout results in early embryonic lethality (Okita et al., 2004) | cell cycle (mitosis/cytokinesis) |
| *ARL2* | *ARFL2* | N | Y | centrosomal protein that regulates microtubule nucleation and organization (Zhou et al., 2006); a fraction of ARL2 protein localizes to the mitochondria, where it regulates ATP levels and mitochondrial integrity (Newman et al., 2014); based on work in non-mammalian model systems, mutations in ARF2 may cause shortening of microtubules, aberrant microtubule and spindle organization, cell division and cytokinesis defects (Antoshechkin and Han, 2002; Price et al., 2010) | metabolism; cell cycle (mitosis/cytokinesis) |
| *ATP6V1A* | *ATP6V1A1* | N | Y | acidifying vacuolar ATPase (vATPase) subunit A (van Hille et al., 1993) | ion transport |
| *BRF1* | *CFDS, GTF3B, TAF3C, TAF3B2, TAFIII90, TIS11b* | N | Y | the 90 kDa beta subunit of RNA polymerase III (Wang and Roeder, 1995); regulates degradation of a subset of mRNAs with AU-rich elements (AREs) in their 3'-untranslated region (Stoecklin et al., 2002; Raineri et al., 2004); via its role in ARE-dependent mRNA turnover, regulates degree of proliferation in mouse embryonic stem cells (Tan and Elowitz, 2014) | transcription; non-coding RNA biogenesis; cell cycle (proliferation) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *C1orf109* |  | N | N | functions in cancer cell proliferation, based on misexpression and knockdown studies (Liu et al., 2012) | cell cycle (proliferation) |
| *C3orf17* | *NEPRO, NET17* | N | N | involved in maintenance of neocortex neural progenitor cells downstream of Notch and plays a role in repression of proneural gene expression; misexpression causes inhibition of neuronal differentiation in the early neocortex, while knockdown drives neuron differentiation (Muroyama and Saito, 2009); localized to the nucleolus, and knockout in mice causes impaired blastocyst formation and apoptosis (Hashimoto et al., 2015) | cell cycle (proliferation/progenitor cell identity); development (central nervous system) |
| *CDC45* | *CDC45L* | Y | Y | initiation of DNA replication (Gerhardt et al., 2015); recruits DNA polymerase α-primase (see *PRIM1* below) to the DNA replication complex (Kukimoto et al., 1999) | cell cycle (DNA replication/S phase) |
| *CHD4* | *Mi-2β* | N | Y | a catalytic subunit of the nucleosome remodeling and deacetylase (NuRD) complex (Xue et al., 1998; Zhang et al., 1998); controls chromatin relaxation prior to repair of double-stranded DNA breaks (Larsen et al., 2010; Polo et al., 2010; Urquhart et al., 2011; Pan et al., 2012); via roles in chromatin remodeling and p53 deacetylation, regulates self-renewel of embryonic stem cells and cell cycle progression (Larsen et al., 2010; Zhao et al., 2017) | transcription regulation; genome integrity (DNA repair); cell cycle (progression) |
| *CNIH4* | *CNIH2* | N | Y | encodes a GPCR-interacting protein that functions in GPCR export from the endoplasmic reticulum (ER) in the early secretory pathway (Sauvageau et al., 2014) | transport (ER to Golgi) |
| *CRNKL1* | *CLF*, *CRN, HCRN, SYF3* | Y | Y | encodes a protein component of the spliceosome (Chung et al., 2002; Bertram et al., 2017b) | RNA processing (mRNA splicing) |
| *DCTN6* | *WS3,* p27 | N | Y | encodes a subunit of dynactin, located in the pointed end complex (Eckley et al., 1999); via its role as a binding partner for PLK1, regulates the spindle assembly checkpoint and mitotic progression (Yeh et al., 2013) | transport (organelles), cell cycle (mitosis) |
| *DDB1* | *XPE, DDBA* | Y | Y | large subunit of DNA damage-binding complex (Yeh et al., 2012); nucleotide excision repair (Li et al., 2006); involved in ubiquitin…  | genome integrity (DNA repair) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *DDB1* | *XPE, DDBA, XAP1, XPCE* | Y | Y | … complex via interaction with the MIG CUL4A (Leung-Pineda et al., 2009); constitutive ablation is embryonically lethal in mice, and brain-specific ablation leads to accumulation of cell cycle regulators, genomic instability, and apoptosis of proliferating NPCs (Cang et al., 2006) | genome integrity (DNA repair) |
| *DDX54* | *DP97* | ~~N~~ | Y | RNA helicase that localizes to the nucleolus; in the DNA damage response, increases splicing efficiency of pre-mRNA transcripts generated in response to DNA damage (Milek et al., 2017); interacts with constitutive androstane nuclear receptor (response to xeno-chemical stimuli) and acts as co-activator to upregulate expression of downstream genes involved in drug metabolism (Kanno et al., 2012); estrogen-dependent interaction with nuclear estrogen receptors results in inhibition of transcriptional activity (Rajendran et al., 2003); constitutive ablation is early embryonically lethal (Dickinson et al., 2016); binds to myelin basic protein (MBP) in oligodendrocytes, and knockdown causes depletion of MBP (Zhan et al., 2013) | transcription regulation; RNA processing (splicing); stress response; neuron function (myelination) |
| *DONSON* | *MIMIS, B17, MSSLA, C24orf60* | Y | Y | a replisome protein that functions in stabilization of the replication fork and the intra-S phase checkpoint (Reynolds et al., 2017); mutation causes microcephalic dwarfism (Evrony et al., 2017; Reynolds et al., 2017); constitutive ablation is early embryonic lethal in mice (Evrony et al., 2017) | genome integrity (DNA repair); cell cycle (checkpoint control); development |
| *EIF3I* | *TRIP1, EIF3S2, PRO2242, eIF3-beta* | Y | Y | translation initiation factor, but not required for translation initiation (Masutani et al., 2007); in intestinal epithelial cells, ectopic overexpression triggers oncogenesis (Qi et al., 2014); mTOR directly interacts with eIF3 (all Eif3s, not just the product of this gene) to increase association to eIF4G (Harris et al., 2006); regulates osteoblast differentiation and proliferation, and knockdown decreases the number of cells in S-phase while increasing cells in G2/M phase (Metz-Estrella et al., 2012); in vitro overexpression triggers increased cell size, increased proliferation, and cell cycle progression (Ahlemann et al., 2006) | translation; cell cycle; development |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *ELP3* | *KAT9* | N | Y | encodes a 58 kDa histone acetyltransferase that functions as the catalytic subunit of the Elongator complex, which interacts with RNA polymerase II to facilitate transcription through chromatin, although this role has been questioned in recent years (Hawkes et al., 2002; Kim et al., 2002; Dalwadi and Yip, 2018); plays a conserved role in translation regulation via wobble uridine tRNA modification (Huang et al., 2005; Mehlgarten et al., 2010; Selvadurai et al., 2014; Yoo et al., 2016) | transcription regulation; non-coding RNA biogenesis (tRNA); translation regulation |
| *EXOSC2* | *RRP4, p7, Rrp4p* | N | Y | exosome component; high affinity for binding to phosphorylated Upf1 (involv-ed in nonsense mediated decay pathway; considered signal to recruit mRNA degradation factors to transcript) (Lejeune et al., 2003; Isken et al., 2008); in HEp-2 cells, required for exosome stability, with knockdown inhibiting cell growth (van Dijk et al., 2007); in yeast, required for processing of 7S pre-rRNA to 5.8S rRNA (Mitchell et al., 1996) | RNA metabolism |
| *FAM96B* | *CIAO2B, CIA2B, MIP18* | N | Y | component of the MMXD complex; possibly required for Aurora B localization; localized to mitotic spindle, and knockdown results in abnormal mitotic spindle formation, chromosome missegregation, and multi-nucleation (Ito et al., 2010); interacts with and downregulates E2-2 (role in endothelial cell quiescence) while also enhancing endothelial migration, proliferation, and tube formation (Yang et al., 2011); knockdown experiments indicate target specificity of its Fe-S assembly activity (necessary for maturation of nucleotide metabolism proteins DPYD and GPAT; interacts with the MIG *DNA2*); involved in the regulation of iron homeostasis by decreasing IRE-binding activity and protein levels of IRP2 (Stehling et al., 2013) | cell cycle (mitosis); iron homeostasis |
| *GARS* | *HMN5, CMT2D, DSMAV, SMAD1* | N | Y | glycyl-tRNA synthetase, which covalently links glycine with corresponding tRNAs (Motley et al., 2010); mutations are linked to Charcot-Marie-Tooth (CMT) disease, which specifically affects neurons (Motley et al., 2010); constitutive genetic disruption in mice is embryonically lethal (Seburn et al., 2006) | translation |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *GPN1* | *XAB1, MBDIN, NTPBP, RPAP4* | Y | Y | a GTPase that, along with GPN3, is required for the nuclear translocation of RNA polymerase II subunits (Forget et al., 2010; Carre and Shiekhattar, 2011); also regulates the nuclear translocation of XPA, a powerful regulator of nucleotide excision repair (Dong et al., 2010) | transport (nucleocytoplasmic); transcription regulation; genome integrity (DNA repair) |
| *GPN2* | *ATPBD1B* | Y | Y | a GTPase that, in yeast, is required for the nuclear translocation of RNA polymerase II and III subunits and regulates the assembly of RNA polymerase II (Minaker et al., 2013; Zeng et al., 2018) | transport (nucleocytoplasmic); transcription regulation |
| *GPN3* | *ATPBD1C* | Y | Y | a GTPase that, along with GPN1, is required for the nuclear translocation of RNA polymerase II subunits (Calera et al., 2011; Carre and Shiekhattar, 2011); in yeast, regulates the nuclear translocation of RNA polymerase III subunits (Minaker et al., 2013) | transport (nucleocytoplasmic); transcription regulation |
| *HARS* | *HARS1, USH3B* | Y | Y | encodes histidyl-tRNA synthetase (Wasmuth and Carlock, 1986) | translation |
| *IK* | *RED, RER, CSA2* | Y | Y | initially identified as a cytokine that inhibits IFN-gamma-mediated upregulation of MHC class II antigens (Krief et al., 1994); plays multiple roles in mitotic progression, such as the localization of the spindle assembly checkpoint protein MAD1 and the recruitment PP2A to dephosphorylate Aurora B (Yeh et al., 2012; Lee et al., 2014; Lee et al., 2016); found in the spliceosomal B complex, linking the U2 and U5 snRNPs (Bertram et al., 2017a) | cell cycle (mitosis); RNA processing (mRNA splicing) |
| *INTS4* | *INT4* | N | Y | one of 12 subunits of the Integrator complex, which regulates the 3'-end processing of snRNAs (Baillat et al., 2005); required for snRNA export from the nucleus and for proper formation of the Cajal bodies, the site of snRNP and snoRNP maturation (Takata et al., 2012) | non-coding RNA biogenesis (snRNA); RNA processing (mRNA splicing) |
| *LSM8* | *NAA38* | N | Y | one of 7 Sm-like proteins that, together, function in the maturation of rRNAs, tRNAs and the U6 spliceosomal snRNA (Achsel et al., 1999; Kufel et al., 2002; Kufel et al., 2003); found in the spliceosomal B complex, in the U4/U6.U5 tri-snRNP (Bertram et al., 2017a); knockdown results in upregulation of processing…  | non-coding RNA biogenesis; RNA processing (mRNA splicing) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *LSM8* | *NAA38* | N | Y | … bodies, formed of LSM1-7, which mediate mRNA degradation (Novotny et al., 2012) | non-coding RNA biogenesis; RNA processing (mRNA splicing) |
| *MTBP* | *MDM2BP* | Y | N | an MDM2-binding protein that enhances MDM2-mediated p53 degradation (Boyd et al., 2000; Brady et al., 2005); knockdown reduces MAD1 and MAD2 kinetochore localization and triggers chromosome missegregation (Agarwal et al., 2011); via interaction with the DNA replication factor TICRR, regulates DNA replication initiation (Boos et al., 2013) | cell cycle (DNA replication/S phase, mitosis) |
| *NAA15* | *NATH, TBDN, NAT1P* | N | Y | an auxillary component of the N-terminal acetyltransferase A complex, which associates with the ribosome (Arnesen et al., 2005) | protein modification |
| *NAT10* | *ALP, NET43* | N | Y | N-acetyltransferase (Shen et al., 2009); direct role in decondensation of chromosomes at mitosis exit; knockdown results in prolonged chromosome condensation (Chi et al., 2007); DNA damage triggers increased amount of Nat10 in mitotic midbody, and results in enhanced acetylation of alpha-tubulin of midbody (Shen et al., 2009); knockdown results in abnormal nucleolus size, lengthened G2/M transition, multi-nucleated cells, and defects in cytokinesis, sometimes resulting in cell death (Shen et al., 2009); associates with U3 snoRNA and is required for 18S rRNA processing; knockdown results in decreased levels of 47S pre-rRNA, indicating that Nat10 is a transcriptional UTP (participates in pre-rRNA transcription) by targeting UBF for acetylation to facilitate association with RNA pol I-associated factor (Kong et al., 2011); 18S rRNA processing (Ito et al., 2014) | non-coding RNA biogenesis (rRNA); transcription (rRNA); cell cycle (mitosis/cytokinesis) |
| *NCBP1* | *CBP80, NCBP* | Y | Y | one of two proteins in the mRNA cap binding protein complex (other = CBP20), which regulates mRNA splicing (Izaurralde et al., 1994); nonsense mutation-containing transcripts are bound to Ncbp1 during nonsense-mediated decay (NMD) (Ishigaki et al., 2001); through interaction with TREX component Aly, allows…  | RNA metabolism; RNA processing (mRNA splicing); RNA transport; translation (pioneer round) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *NCBP1* | *CBP80, NCBP* | Y | Y | … for proper mRNA export (Cheng et al., 2006); required for poly(A) RNA export (Gebhardt et al., 2015); as CBC, mediates translation initially for pioneer round, then replaced by eIF4E, which controls steady-state translation (Maquat et al., 2010); associates with Upf1 to promote nonsense-mediated decay (Hosoda et al., 2005; Hwang et al., 2010) | RNA metabolism; RNA processing (mRNA splicing); RNA transport; translation (pioneer round) |
| *NCBP2* | *CBP20, CBC2, NIP1, PIG55* | Y | Y | one of two proteins in the mRNA cap binding protein complex (other being NCBP1), which affects RNA stability, splicing, export (specifically U RNA export), and translation initiation by binding 5' end (Izaurralde et al., 1995); NCBP2 specifically binds the cap (Calero et al., 2002); also involved in processing of 3' end of the mRNA transcript (Flaherty et al., 1997); nonsense mutation-containing transcripts are bound to NCBP2 during NMB (Ishigaki et al., 2001); as CBC, mediated translation initially, then replaced by eIF4E, which controls steady-state translation (Kim et al., 2009) | RNA metabolism; RNA processing (mRNA splicing); RNA transport (snRNA); translation (pioneer round) |
| *NEDD1* | *TUBGCP7* | Y | Y | centrosomal protein that is required for γ-tubulin ring complex localization to the centrosome, with knockdown causing defects in centrosomal microtubule nucleation, aberrant mitotic spindles, and inhibition of centriole duplication (Haren et al., 2006) | cell cycle (mitosis) |
| *NOP2* | *P120, NOL1* | Y | Y | initially discovered as proliferation-associated based on expression, with moderately strong ribosome RNA methyl transferase activity (Freeman et al., 1988); introduction of antisense RNA limited proliferation in NIH 3T3 cells (Valdez et al., 1992); proliferation marker of neural stem cells, and is expressed in the adult brain (Kosi et al., 2015); potential role in neutrophil maturation (Khanna-Gupta et al., 2006) | cell cycle (proliferation) |
| *NUP205* | *NPHS13, C7orf14* | N | Y | a 205 kDa component of the nuclear pore complex that is required for long-term nuclear pore complex maintenance (Grandi et al., 1997; Krull et al., 2004); based on work in *C. elegans*, may inform nuclear pore complex permeability and distribution (Galy et al., 2003) | transport (nucleocytoplasmic) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *PDCD11* | *ALG4, NFBP, RRP5* | N | Y | interacts with the U3 snoRNA (involved in rRNA maturation/ biogenesis), and knockdown represses 18S rRNA maturation (Sweet et al., 2008); part of SSU processome, where it likely recruits U3 to sites of rRNA maturation (Turner et al., 2009)  | non-coding RNA biogenesis (rRNA) |
| *POLA2* |  | N | Y | indirectly, regulates DNA replication by increasing protein synthesis and nuclear translocation of catalytic alpha subunit (p180) (Mizuno et al., 1999); hyperphosphorylated by cyclin-dependent kinases in G2 phase, which enhances activation of pol-alpha enzyme (DNA replication) by phosphorylated Rb (Takemura et al., 2006); constitutive knockout is embryonically lethal in mice (Dickinson et al., 2016) | cell cycle (DNA replication/S phase) |
| *POLE2* | *DPE2* | Y | Y | DNA polymerase accessory subunit (epsilon), 55 kDa subunit (Li et al., 1997); possible stabilizing role for DNA polymerase epsilon complex (Li et al., 1997); role in chromatin regulation, based on reporter plasmid assays (Wada et al., 2002) | cell cycle (DNA replication/S phase); transcription regulation |
| *POLR2E* | *RPB5, RPABC1, XAP4* | Y | Y | subunit shared by all RNA polymerases (Cheong et al., 1995); role in transcription activation, according to work in yeast (Miyao and Woychik, 1998); in COS1 cells, directly binds RAP30, component of the general transcription factor IIF (TFIIF) complex; this complex is assembled within the initiation complex and is known to associate with RNA pol II, inhibiting the association of TFIIF and pol II (Wei et al. 2001; Wei et al., 2003)  | transcription |
| *POLR2K* | *RPB12, RPABC4, RPB10α, ABC10α* | N | Y | a small subunit of all three DNA-directed RNA polymerases (Shpakovski et al., 1995) | transcription; non-coding RNA biogenesis |
| *POLR3H* | *RPC8* | Y | Y | subunit of RNA polymerase III, acting paralogously to Rpb7 in pol II (Hu et al., 2002) | transcription; non-coding RNA biogenesis |
| *PPIL4* |  | N | Y | a member of the cyclophilin family of peptidyl-prolyl isomerases (Zeng et al., 2001; Wang and Heitman, 2005) | protein folding |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *PRIM1* | p49 | Y | Y | catalytic primase subunit of DNA polymerase α-primase (Urban et al., 2010); generates an RNA primer, followed by primer extension to produce RNA-DNA primer, to initiate DNA replication (reviewed by Waga and Stillman, 1998) | cell cycle (DNA replication/S phase) |
| *PSMA1* | *PROS30* | Y | Y | component of 20S proteasome (Cron et al., 2013) | protein metabolism |
| *RABGGTA* | *PTAR3* | N | Y | geranylgeranyl transferase; mutation in splice acceptor site results in gunmetal mouse, which has platelet and megakaryocyte defects (prolonged bleeding), macrothrombocytopenia (Detter et al., 2000) | protein modification; hemostasis |
| *RNPC3* | *IGHD5, RBM40, RNP, SNRNP65* | Y | Y | the minor spliceosome-specific U11/U12 65k protein; when bound to the U11/U12 di-snRNP, it bridges the U12 snRNA and U11-59K protein, stabilizing the di-snRNP and thereby regulating minor splicing (Benecke et al., 2005); germline deletion in mice results in embryonic lethality (Doggett et al., 2018); constitutive deletion in adult mice results in lower levels of lymphocytes, monocytes, erythrocytes, and thrombocytes; decreased thymus size; gastrointestinal mucosa degeneration; and death within 8 days of induction (Doggett et al., 2018); in humans, mutation is linked to isolated familial growth hormone deficiency (Argente et al., 2014) | RNA processing (splicing); development |
| *RPL4* |  | Y | Y | ribosomal protein component of the 60S subunit (Chan et al., 1995) | translation |
| *RPP30* | *TSG15* | N | Y | 30 kDa subunit of the ribonuclease P/MRP complex, which processes tRNA (Jarrous et al., 1998) | non-coding RNA biogenesis |
| *SACM1L* | *SAC1* | N | Y | phosphoinositide phosphatase integral membrane protein localized to endoplasmic reticulum and Golgi apparatus (Nemoto et al., 2000; Rohde et al., 2003); mouse KO is early embryonic lethal (Liu et al., 2008); knockdown causes Golgi apparatus disorganization, delayed G2/M transition, and aberrant mitotic spindle formation (Liu et al., 2008) | cell cycle (mitosis); Golgi-mediated transport |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *SBNO1* | *MOP3* | Y | Y | a putative member of the SF2-type DExD/H helicases that regulates transcription (Watanabe et al., 2017); in mice, required for preimplantation development (Watanabe et al., 2017) | transcription regulation |
| *SMC3* | *BAM, HCAP, CSPG6* | N | Y | an ATPase component of cohesin, mediating sister chromatid cohesion and metaphase progression (Schmiesing et al., 1998); mirroring cohesin's role in DNA repair and the DNA damage-induced intra-S and G2/M phase checkpoints, SMC3 is phosphorylated upon DNA damage (Watrin and Peters, 2009); also a subunit of the RC-1 complex, which functions in DNA recombination and repair (Stursberg et al., 1999) | cell cycle (mitosis); genome integrity (DNA repair) |
| *SNRPE* | *SME, Sm-E, HYPT11* | Y | Y | the "E" subunit of the Sm complex, which functions in snRNP maturation; associates with U snRNPs, including those involved in RNA splicing and histone mRNA processing (Pillai et al., 2001; Urlaub et al., 2001; Chari et al., 2008; Pasternack et al., 2013); in cancer cells, misexpression prevents DNA synthesis and arrests cells in G2, while knockdown drives cells through these phases (Li and Putzer, 2008) | RNA processing (splicing); transcription; cell cycle |
| *SPC24* | *SPBC24* | Y | N | NDC80 kinetochore complex component; required to establish and maintain kinetochore-microtubule attachment in mitosis (McCleland et al., 2004) | cell cycle (mitosis) |
| *SRP72* | *BMFF, BMFS1* | N | Y | the 72 kDa subunit of the signal recognition particle, which mediates co-translational protein targeting to the endoplasmic reticulum (Lutcke et al., 1993) | transport (protein, to ER); translation |
| *SSU72* | *HSPC182* | N | Y | phosphatase associated with CTD of RNA pol II (TFIIB) (St-Pierre et al., 2005); regulates RNA pol II activity via CTD phosphatase activity in yeast (Krishnamurthy et al., 2004); phosphorylated by Aurora B to regulate sister chromatid cohesion during mitosis (Kim et al., 2013) | transcription; cell cycle (mitosis) |
| *TAF1C* | *SL1, TAFI110, TAFI95* | N | N | TATA box-binding protein associated factor (TAF) for RNA pol I; part of SL1 complex, which directs pol I transcription and can independently interaction with rDNA promoters (Friedrich et al., 2005) | non-coding RNA biogenesis (rRNA) |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *TCP1* | *CCT1, CCT-alpha, CCTa* | Y | Y | cytosolic chaperonin responsible for stabilizing folding of numerous proteins, including actin (Neal and Joyce, 1992) and tubulin (Yaffe et al., 1992; Yam et al., 2008); involved in ciliogenesis and biogenesis of rod outer segment (Sinha et al., 2014); via chaperone function for Tcab1, controls scaRNA localization and telomerase function (Freund et al., 2014) | protein folding |
| *TRAPPC8* | *GSG1, TRS85* | N | Y | a component of the TRAPP III complex, which functions in ER-to-Golgi transport in the early secretory pathway and in autophagy (Choi et al., 2011; Scrivens et al., 2011; Lamb et al., 2016) | transport (ER to Golgi); autophagy |
| *UBL5* | *HUB1* | Y | Y | ubiquitin-like protein; knock-down experiments indicate a role in stabilization of the spliceosome and in mitotic progression to anaphase (Oka et al., 2014); via this role, important for the proper splicing of the cohesin factor sororin, thereby indirectly promoting sister chromatid cohesion (Oka et al., 2014) | RNA processing (splicing); cell cycle (mitosis) |
| *UFD1L* | *UFD1* | N | Y | an adaptor protein component of the AAA-ATPase Cdc48/p97 complex that functions in endoplasmic reticulum-associated degradation (ERAD) (Chen et al., 2011); required for proper chromosome segregation and mitotic progression, due to role in Aurora B regulation (Dobrynin et al., 2011); mediates the G2/M checkpoint by targeting CDC25A upon DNA damage (Riemer et al., 2014); required for proper localization of the ESCRT-III complex to the nuclear envelope during nuclear envelope reformation during late mitosis (Olmos et al., 2015) | protein turnover; cell cycle (mitosis) |
| *UPF1* | *RENT1* | N | Y | functions in nonsense-mediated mRNA decay (Sun et al., 1998) and genome integrity (Azzalin and Lingner, 2006); constitutive knockout is embryonically lethal (Medghalchi et al., 2001) | RNA metabolism; genome integrity |
| *VPS25* | *DERP9, EAP20, FAP20* | Y | Y | part of ESCRT (endosomal sorting complex required for transport)-II (Yorikawa et al., 2005); role in cargo sorting, especially sorting of ubiquitinated cargo (Im et al., 2009); by regulating receptor number, affects FGF signaling in limbs, indicative of a role in skeletal/limb development (Handschuh et al., 2014); constitutive knockout is embryonically lethal (Dickinson et al., 2016) | transport; limb/skeletal development |
| **MIG** | **Syn** | **Core****Essent.?** | **Ancient****Essent.?** | **Function Description** | **Functional Categories** |
| *ZPR1* | *ZNF259, ZFP259* | N | Y | depletion disrupts nucleolar function, including pre-ribosomal RNA expression (Galcheva-Gargova et al., 1998); interacts with the Smn protein and colocalizes in Geminins and Cajal bodies; depletion analysis indicates Zfp259 regulates localization of Smn in nuclear bodies (Gangwani et al., 2001); in conditonal knockout mouse, loss of Zfp259 disrupts the subcellular localization of Smn and the spliceosomal snRNPs; early embryonic lethality is observed, showing reduced proliferation and increased apoptosis [378]; depletion blocks S-phase progression, triggers G1 and G2 arrest, and causes mislocalization of Smn and NPAT (Gangwani et al., 2001); in Zfp259-deficient mice, observe axonal pathology and neurodegeneration (Doran et al., 2006); in spinal muscular atrophy, loss of Zpr1 increases motor neuron loss and severity and depleted SMN-containing subnuclear bodies (Ahmad et al., 2012) | RNA processing (splicing); neuron function (survival) |

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