

## **PRMT7 methylation controls *trans*-regulator function in *Leishmania* protozoa**

### **Supplemental Information**

#### **Supplemental Figure Legends**

**Supplemental Fig S1.** Multiple sequence alignment of all the annotated PRMTs in *L. major* (*Lmj*PRMTs) and *Homo sapiens* (*Hs*PRMTs). The double E loop is part of the catalytic domain of the PRMTs and is important for S-adenosyl-methionine (SAM) and protein substrate binding. The asterisk depicts the *Lmj*PRMT7 E202 residue mutated to generate catalytically inactive E202K and E202Q mutants *in vitro*.

**Supplemental Fig S2.** Endogenous FLAG-HA-tagging of *L. major* RBPs (A) Plasmid map of pFLAG\_HA plasmid, synthesized by GenScript for this work, with Alba3 5' flank region (5'FLR) and Alba3<sup>wgg</sup> mutant sequence in the "RBP-CDS" region. *Sfi*I enzyme sites used (A,B,C,D) produce different overhangs allowing the ligation of four different synthesized DNA sequences at the same time in a specific order (Fulwiler *et al.* 2011). Homologous sequences required for gene replacement are the 5'FLR (500bp) and the protein coding sequence (RBP-CDS, variable). (B) Primers that bind to the 5'FLR region of the gene and 3'FLR immediately downstream of the RBP-CDS but absent in the plasmid sequence were used to verify correct replacement of at least one allele by the HA-tagged gene. Expected PCR band sizes are shown for each tagged gene. (C) Positive clones were analyzed by PCR amplification of the modified HA-RBP allele (upper bands) and the original unmodified RBP allele (lower bands). DNA marker used was Gene Ruler 1kb (Thermo Fisher).

**Supplemental Fig S3.** (A) qPCR showing relative concentrations of transcript targets immunoprecipitated with HA-Alba3 in the presence or absence of PRMT7 levels relative to endogenous transcript levels. Alba3 transcript target nmt levels remain unchanged in the presence or absence of PRMT7 levels or the mutation of Alba3 RGG motifs to WGG. (B) Alba3 protein levels and stability are unaltered in the presence or absence of PRMT7 levels in log- or stat- stage promastigote cells. (C) Cytoplasmic HA-RBP16 levels display a reduced

half-life specifically in stat-stage human-infective promastigotes in the absence of PRMT7 expression.

**Supplemental Fig S4.** (A) Western blot examining endogenous levels of *Lmj*RBP16 using anti-*Tb*RBP16 (kind gift of L.Read). *Lmj*RBP16 protein levels are constant in the presence and absence of PRMT7 levels. (B-D) Immunofluorescence of Log and Stat stage promastigotes: DAPI (Blue), Mitotracker (Green), RBP (Red), line = 5 $\mu$ m. (B) Subcellular localisation of endogenous *Lmj*RBP16 using anti-*Tb*RBP16 shows mitochondrial localisation constant in promastigote lifecycle stages examined. (C) Subcellular localisation of endogenously-tagged HA-*Lmj*RBP16 using anti-HA shows cytoplasmic localisation that is destabilized specifically in the absence of PRMT7 levels in stationary (stat) stage promastigote cells. (D) Subcellular localisation of endogenously-tagged HA-*Lmj*Alba3 using anti-HA shows cytoplasmic localisation constant in promastigote lifecycle stages examined.

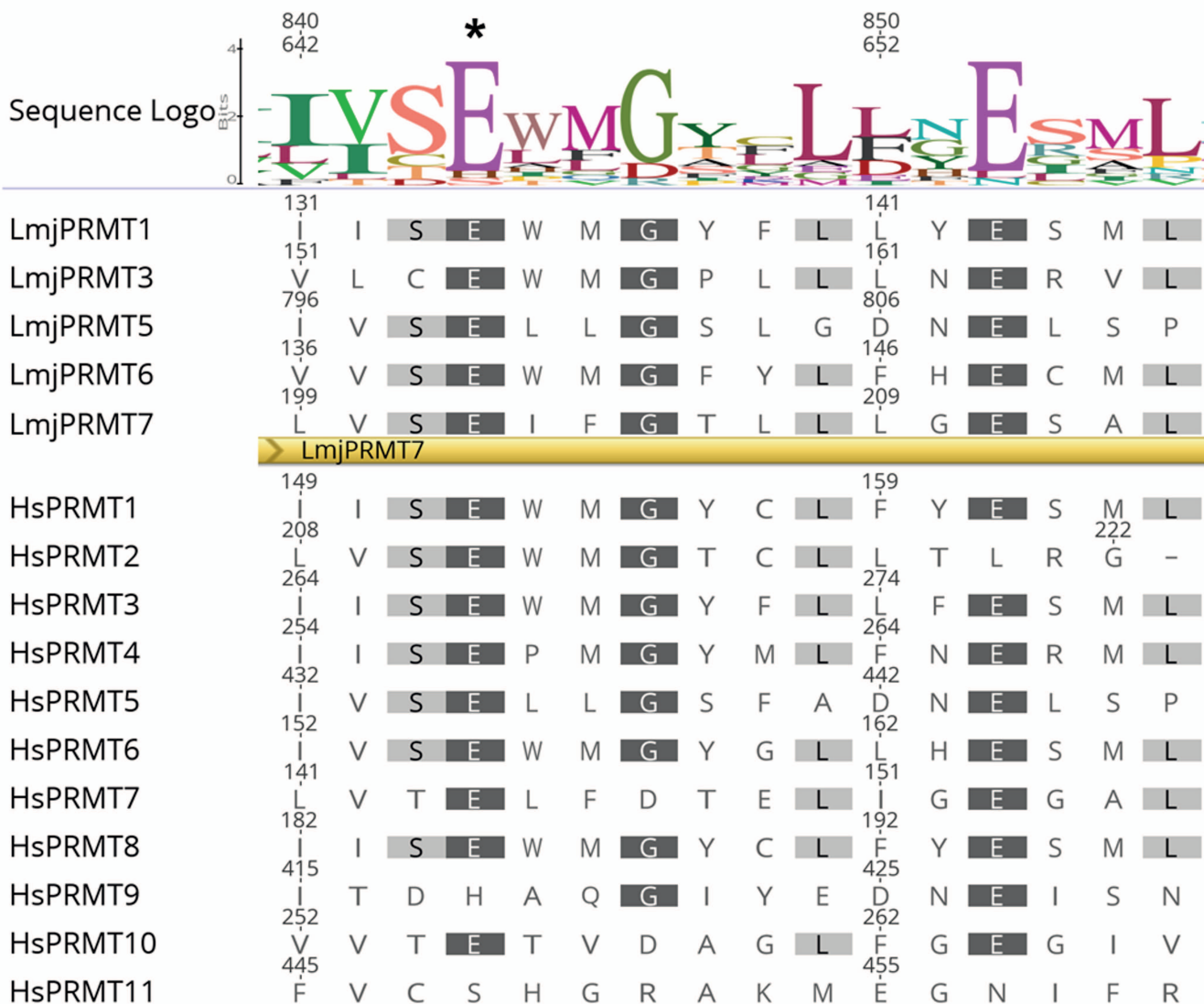
#### **Supplemental Table Legends**

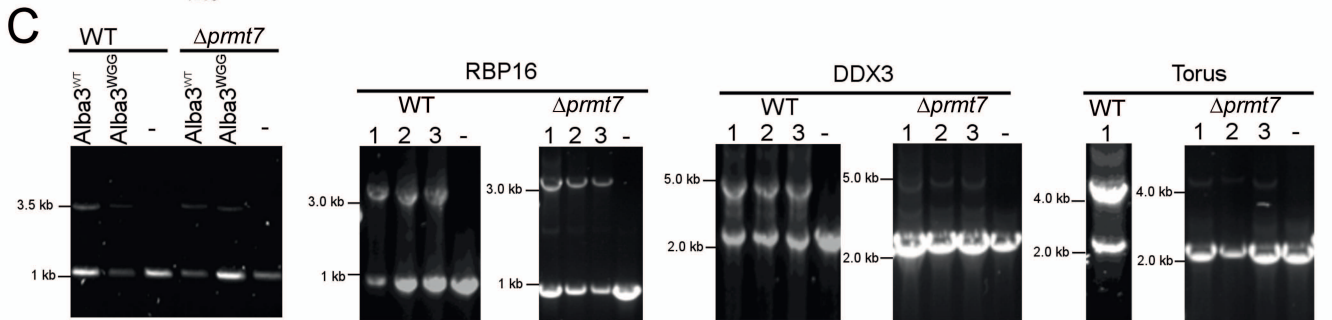
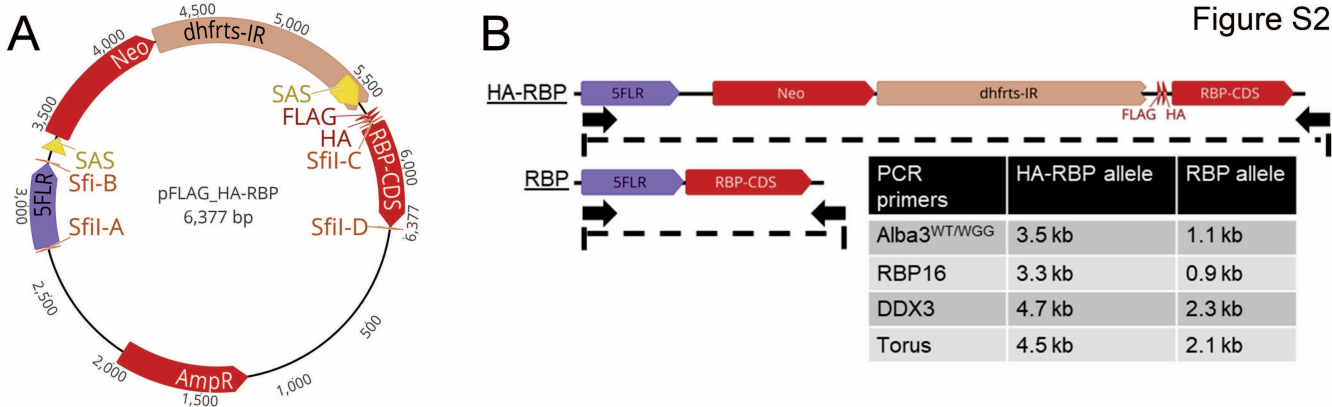
**Supplemental Table S1.** Global monomethyl arginine peptides identified and quantified by heavy methyl SILAC analysis in WT and  $\Delta$ *prmt7* *Leishmania major*.

**Supplemental Table S2.** Methylpeptides from RNA-binding proteins (RBPs) that are differentially methylated between WT and  $\Delta$ *prmt7* *Leishmania major*. Proteins were considered RBPs if they present an RNA-binding domain or if they are orthologs of a validated *Trypanosoma brucei* RBP.

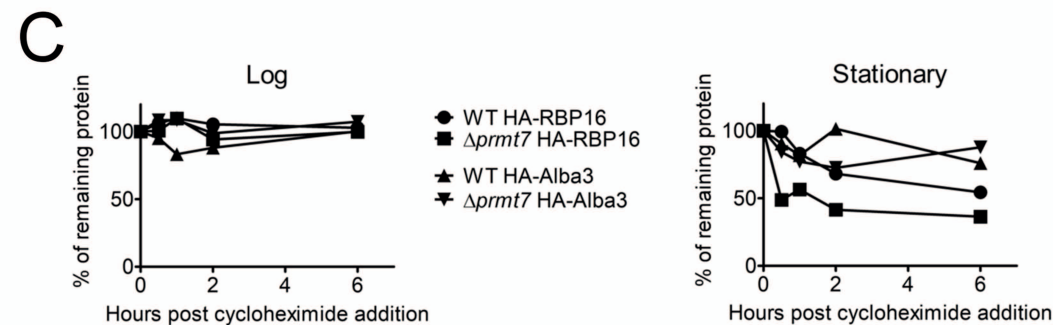
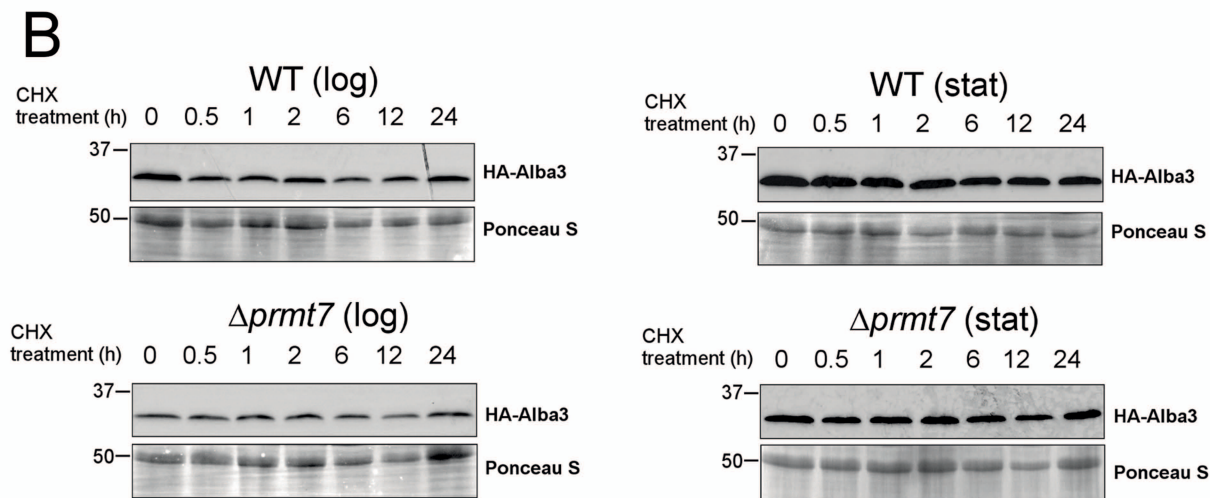
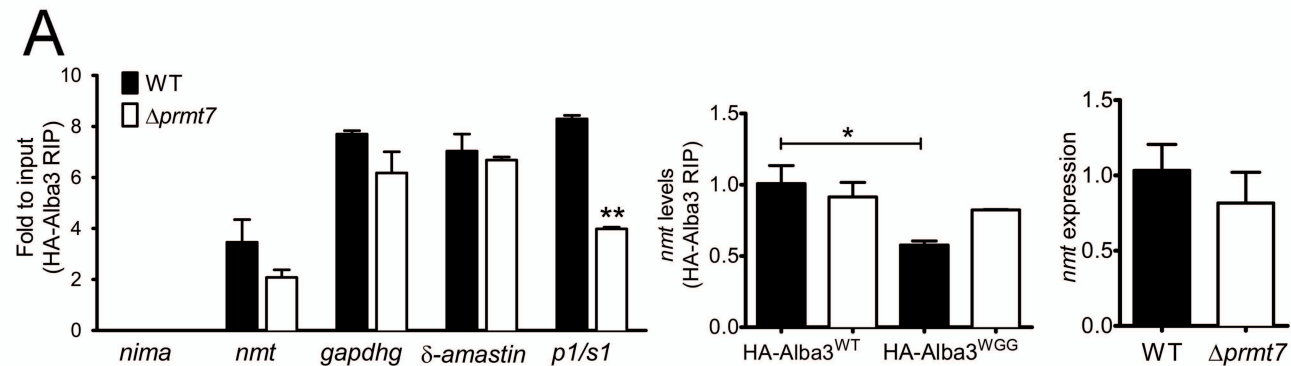
**Supplemental Table S3.** List of oligonucleotides used in this study for PCR or qRT-PCR.

## Double E loop in SAM binding domain

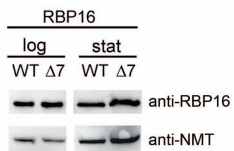




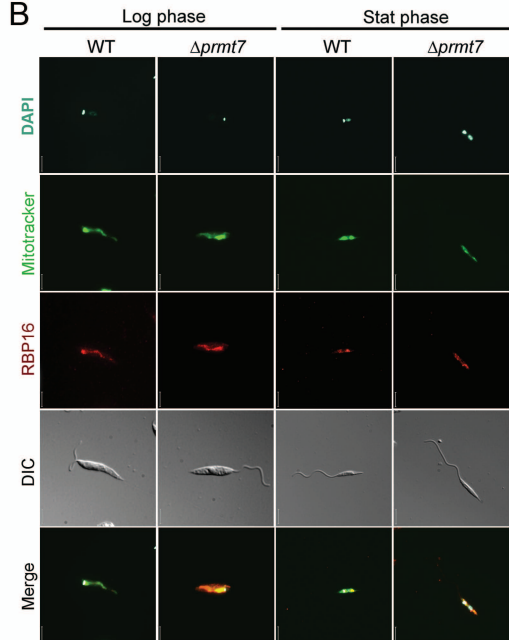
# Figure S3



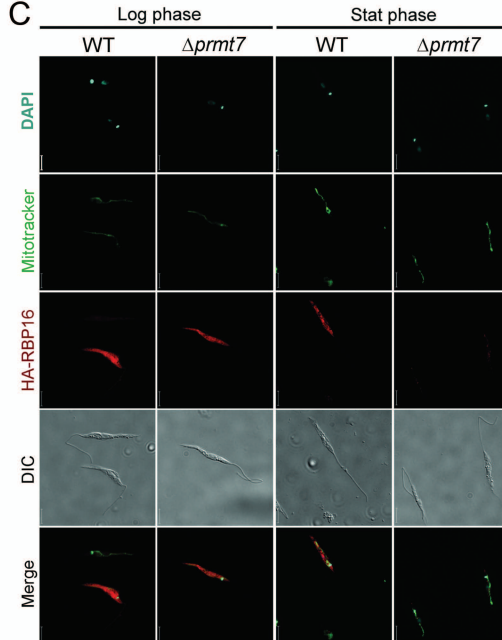
A



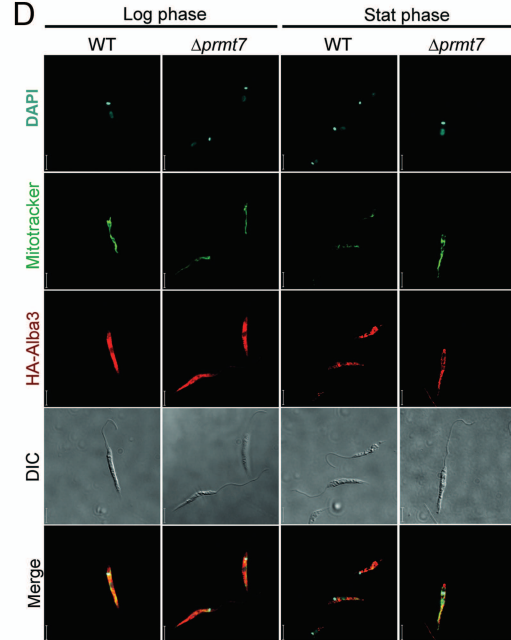
B



C



D



**Supplemental Table S1.** Global monomethyl arginine peptides identified and quantified by heavy methyl SILAC analysis in WT and  $\Delta$ prmt7 *Leishmania major*.

Gene ID	Product description	log2FC WT/Δ7 (methylpeptides)	q-value (H&B test)	Methyl/peptide sequence*	Modification site <sup>†</sup>
LmjF.27.1680	hypothetical protein, conserved (NXF1)	41.28	0.00E+00	SGPSSGGVGLGNNGSRGGGR +3 Methyl x 2	R26 Methyl M3 Oxidation, R10 Methyl, M24 Oxidation
LmjF.35.2200	RNA-binding protein, putative	39.62	0.00E+00	HNMAGSAYGRGAPYQVGAESTEMNGTEPLKPR +5 Methyl x	
LmjF.16.0730	ubiquitin hydrolase, putative	38.04	0.00E+00	SGGRRGGGAGATNAPSVPSPSEVTEASAPPEPQTELEGR +methyl:2H(3)13C(1), R9 Methyl:2H(3)13	
LmjF.10.0880	hypothetical protein, conserved	37.47	0.00E+00	GRGGAEDAGPSAARGAGIPAVLR +4 Methyl x 2	methyl:2H(3)13C(1), R15 Methyl:2H(3)13
LmjF.16.0730	ubiquitin hydrolase, putative	35.85	0.00E+00	SGGRRGGGAGATNAPSVPSPSEVTEASAPPEPQTELEGR +methyl:2H(3)13C(1), R9 Methyl:2H(3)13	M3 Oxidation, R10 Methyl, M24 Oxidation
LmjF.35.2200	RNA-binding protein, putative	35.33	0.00E+00	HNMAGSAYGRGAPYQVGAESTEMNGTEPLKPR +4 Methyl x	
LmjF.34.1110	Shwachman-Bodian-Diamond syndrome (SBDS) protein/SBDS protein C-terminal domain cont	35.19	0.00E+00	LGLDPSHLQDDSDDDGGRGRGR +3 Methyl x 2 Phos x 1	S13 Phospho, R21 Methyl R2 Methyl:2H(3)13C(1), R5
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	35.17	0.00E+00	GRGRRAAAAAASATAAASAATR +4 Methyl x 2	Methyl:2H(3)13C(1), R5 R2 Methyl:2H(3)13C(1), R5
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	34.51	0.00E+00	GRGRRAAAAAASATAAASAATR +3 Methyl x 2	Methyl:2H(3)13C(1)
LmjF.19.0380	hypothetical protein, conserved	34.32	0.00E+00	RVPDSGASMASSGAGRGRGR +4 Methyl x 2	R17 Methyl, R21 Methyl, R23 Methyl
LmjF.01.0260	Calmodulin-binding, putative	34.10	0.00E+00	AQYDHSVSHGVRAGSAAAPSGSR +3 Methyl x 1	R13 Methyl
LmjF.14.0570	WD domain, G-beta repeat, putative	7.33	1.80E-18	GGSSVGRGHATSGR +3 Methyl x 1	R7 Methyl:2H(3)13C(1)
LmjF.34.2580	ALBA-domain protein 3 (Alba3)	7.15	1.15E-02	GGRGVAAIDRR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.25.0290	RNA-binding protein, putative	6.70	4.96E-16	SVARPPPPPPRIGR +4 Methyl x 2	R14 Methyl, R16 Methyl
LmjF.27.1680	hypothetical protein, conserved (NXF1)	6.70	1.94E-16	SGPSSGGVGLGNNGSRGRGR +2 Methyl x 1	R22 Methyl
LmjF.27.0130	WW domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative (ZFP3)	6.58	2.15E-07	THWSIPPTAYEPYNNRGR +3 Methyl x 1	R19 Methyl
LmjF.32.2410	hypothetical protein, conserved	6.54	3.79E-03	TSTGRAGSAAAGPDLHR +3 Methyl x 1	R5 Methyl:2H(3)13C(1) R3 Methyl:2H(3)13C(1), R7
LmjF.32.1800	hypothetical protein, conserved	6.28	2.88E-16	SGRSGARGSSSHNR +3 Methyl x 2	Methyl:2H(3)13C(1)
LmjF.10.0280	hypothetical protein, conserved	5.80	8.74E-14	GGRRGSLSR +3 Methyl x 1	R4 Methyl:2H(3)13C(1), R21 R19 Methyl:2H(3)13C(1), R21
LmjF.27.0130	WW domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative (ZFP3)	5.38	3.17E-05	THWSIPPTAYEPYNNRGR +4 Methyl x 2	Methyl:2H(3)13C(1)
LmjF.18.1420	pumilio protein 2, putative (PUF2)	4.89	3.54E-13	DNRPGGVSSSGNGSGRGRGR +3 Methyl x 1	R22 Methyl
LmjF.26.0730	hypothetical protein, conserved	4.63	4.23E-12	TSSRGGGSRENDVQPAEQQR +3 Methyl x 1 Phos x 1	R5 Methyl
LmjF.10.1110	PAB1-binding protein, putative (PBP1)	4.53	4.97E-09	KEAAATSAAAPAAATPAATATAGRGAAR +4 Methyl x 1	R27 Methyl
LmjF.34.1110	Shwachman-Bodian-Diamond syndrome (SBDS) protein/SBDS protein C-terminal domain cont	4.44	4.14E-11	LGLDPSHLQDDSDDDGGRGR +3 Methyl x 1 Phos x 1	S13 Phospho, R19 Methyl:2H(3)13C(1)
LmjF.19.0190	multi-protein-bridging factor 1, putative (MBF1)	4.39	5.24E-11	PRGAIPTGDDWEEQR +3 Methyl x 1	R2 Methyl
LmjF.19.0190	multi-protein-bridging factor 1, putative (MBF1)	4.03	1.81E-05	PRGAIPTGDDWEEQRNFQQR +4 Methyl x 1	R2 Methyl
LmjF.25.0290	RNA-binding protein, putative	3.92	1.67E-12	SVARPPPPPPRIGR +3 Methyl x 1	R14 Methyl:2H(3)13C(1) R4 Methyl:2H(3)13C(1), M12
LmjF.04.0570	DENN (AEX-3) domain containing protein, putative	3.88	6.80E-06	AYRGLGIESEMFDPVAR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.27.1300	KH domain containing protein, putative	3.69	2.41E-13	GRRGGGAGAPNDDAAR +3 Methyl x 2	R3 Methyl, R7 Methyl
LmjF.15.0620	hypothetical protein, conserved	3.64	3.24E-12	ASSHONGSNGAVIRGGGNAR +3 Methyl x 1	R16 Methyl
LmjF.22.0930	mitochondrial chaperone, putative	3.45	7.96E-12	SDGAPAVRGGGGTGR +2 Methyl x 1	R18 Methyl
LmjF.24.0820	inositol polyphosphate phosphatase, putative	3.22	9.58E-08	GRGGAAMHMTSAAGPSAR +3 Methyl x 1	R2 Methyl
LmjF.10.1110	PAB1-binding protein, putative (PBP1)	2.97	5.67E-08	EAATAASAAPAAATPAATATAGRGAAR +3 Methyl x 1	R26 Methyl
LmjF.24.1180	Surfeit locus protein 6, putative (SURF6)	2.77	2.44E-07	GARFPAPQRGGGASSR +3 Methyl x 1	IN/A
LmjF.26.0730	hypothetical protein, conserved	2.61	7.62E-07	TSSRGGGSRENDVQPAEQQR +3 Methyl x 1	R5 Methyl
LmjF.24.0710	Protein of unknown function (DUF523), putative	2.60	1.29E-04	RPAASAAQR +3 Methyl x 1	IN/A
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	2.34	2.94E-06	SSGGRRGSSSFPVSGHGTGSGFNPR +3 Methyl x 1	R6 Methyl:2H(3)13C(1) R15 Methyl:2H(3)13C(1), M19
LmjF.21.1350	PB1 domain containing protein, putative	2.15	2.28E-03	QASVSLTTSAGRRGAMAAR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.22.0930	mitochondrial chaperone, putative	2.05	3.87E-07	SDGAPAVRGGGGTGR +3 Methyl x 1	R18 Methyl
LmjF.36.5100	hypothetical protein, conserved (PUF11)	1.99	1.16E-03	GGYVGGGAGGAGIQQVYGAAPISR +3 Methyl x 1	R28 Methyl
LmjF.19.0190	multi-protein-bridging factor 1, putative (MBF1)	1.79	5.55E-03	FNQQRGGSSQAQR +3 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	1.75	1.15E-03	SSGGRRGSSSFPVSGHGTGSGFNPR +4 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.22.0930	mitochondrial chaperone, putative	1.74	1.83E-11	SDGAPAVRGGGGTGR +3 Methyl x 1	R9 Methyl
LmjF.05.0850	zinc-finger of a C2HC-type, putative	1.59	1.16E-03	CGSSGGGRRPAAWNSDVEVR +4 Methyl x 1	R13 Methyl
LmjF.14.0570	WD domain, G-beta repeat, putative	1.56	6.34E-04	GGSSVGRGHATSGR +2 Methyl x 1	R7 Methyl:2H(3)13C(1)
LmjF.33.1150	pumilio protein 6, putative (PUF6)	1.49	2.34E-04	GSYEGMAGVTVYRGTGPTAK +3 Methyl x 1	R15 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	1.44	1.49E-03	AAAAAASATAAASAATRGRSR +3 Methyl x 1	R19 Methyl M11 Label:13C(1)2H(3), M15 Label:13C(1)2H(3), R16 Methyl:2H(3)13C(1)
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	1.33	4.90E-03	KADTETGPEMVSRRGRF +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.32.1800	hypothetical protein, conserved	1.26	1.19E-04	RGASWAANTDTPPGGK +3 Methyl x 1	R1 Methyl
LmjF.33.0260	RGG-containing protein 2, putative (RGG2)	1.25	1.52E-04	DSSDGGGRRGGHSGGGGDKDAPTGR +5 Methyl x 1	R10 Methyl:2H(3)13C(1)
LmjF.08.0520	hypothetical protein, conserved	1.19	2.37E-02	SSRGGAAQAR +2 Methyl x 1	R3 Methyl
LmjF.30.0090	hypothetical protein, conserved	1.12	3.00E-04	IEGFRGGTVQSR +3 Methyl x 1	R6 Methyl
LmjF.15.1310	MGT1 magnesium transporter	0.91	1.18E-03	LVRPLSRGGAVVFGSR +3 Methyl x 1 Phos x 1	S4 Phospho, R9 Methyl
LmjF.13.0580	hypothetical protein, conserved	0.82	1.33E-03	SGAARGGGIVSAPSK +3 Methyl x 1	R5 Methyl:2H(3)13C(1) S3 Phospho, M8 Label:13C(1)2H(3), R27 Methyl:2H(3)13C(1)
LmjF.36.5850	flagellum targeting protein kharon1, putative	0.81	2.88E-03	RASLHNLMYASGDAYVASRGGQASR +4 Methyl x 1 Phos x 1	R27 Methyl:2H(3)13C(1)
LmjF.31.2360	hypothetical protein, conserved	0.73	1.85E-02	NYPNLDPPTEEALGSRGGTGGAYGR +3 Methyl x 1	R28 Methyl
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	0.67	2.34E-02	LPSGRPPGSPSGR +3 Methyl x 1	IN/A
LmjF.33.1150	pumilio protein 6, putative (PUF6)	0.64	2.02E-02	YNNNSAGGGVGGGRVGR +3 Methyl x 1	R15 Methyl
LmjF.05.0850	zinc-finger of a C2HC-type, putative	0.63	5.07E-03	CGSSGGGRRPAAWNSDVEVR +3 Methyl x 1	R13 Methyl
LmjF.24.1430	kinesin, putative	0.80	1.29E-03	NGGAAAGRRGCNAPALLDAPR +3 Methyl x 1	R10 Methyl:2H(3)13C(1)
LmjF.35.3100	ATP-dependent RNA helicase, putative (DED1)	0.475378065	2.33E-02	NYDDGGGEGYSRNSYGGGGYR +3 Methyl x 1	R14 Methyl
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DXD3)	0.398086975	3.12E-03	KPNVQNPQR +2 Methyl x 1	R9 Methyl
LmjF.36.4590	PHD-like zinc-binding domain containing protein, putative	0.38904051	3.98E-02	NSGGDTDSALGSSPTARGGAVGGGHAR +3 Methyl x 1	R31 Methyl:2H(3)13C(1)
LmjF.21.1030	hypothetical protein, conserved	0.352663399	4.92E-02	GAGGPRPFAVDNDDANYSDDGGRRGR +3 Methyl x 1 Phos x 1	R27 Methyl:2H(3)13C(1)
LmjF.04.0920	hypothetical protein	0.319371052	8.31E-03	SRDAGCPSQALGRR +3 Methyl x 1	R12 Methyl
LmjF.17.1030	hypothetical protein, conserved	0.232130541	5.40E-03	SSRGGVPPQGSAAVAGGSPQLNR +3 Methyl x 1	R4 Methyl
LmjF.34.1360	Nucleoporin NUP225	0.212786983	2.26E-04	SGSAVNRGSSAAALEAYYQQQR +3 Methyl x 1	R7 Methyl
LmjF.31.2360	hypothetical protein, conserved	0.161499462	3.61E-03	LQRGGYQALQGR +2 Methyl x 1	R3 Methyl
LmjF.35.1510	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	0.126983206	2.20E-03	ANNNDHQHRGGGAR +3 Methyl x 1	R11 Methyl R4 Methyl:2H(3)13C(1), M10 Label:13C(1)2H(3)+Oxidation
LmjF.36.0490	zinc-finger of a C2HC-type, putative	-0.60	2.30E-03	FSSRGGGGMGGGGGGR +2 Methyl x 1	R2 Methyl
LmjF.32.0850	polypyrimidine tract-binding protein, putative (DRBD4)	-0.75	9.35E-03	DRGGGAGSDCAKSDPAVQR +3 Methyl x 1	R9 Methyl
LmjF.23.0080	hypothetical protein, conserved	-0.79	2.91E-03	AVSAQVQARGR +2 Methyl x 1	R2 Methyl M3 Label:13C(1)2H(3), R5 Methyl:2H(3)13C(1)
LmjF.36.4260	hypothetical protein, conserved	-0.81	9.04E-03	SSMARGGASPR +3 Methyl x 1	R9 Methyl
LmjF.07.0340	ATP-dependent RNA helicase DBP2B, putative	-1.05	4.65E-03	SGGGYGGRYGGYGGGR +2 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.05.0850	zinc-finger of a C2HC-type, putative	-1.70	1.99E-07	GAGGGGGGGGADAAAGAAK +3 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.05.0850	zinc-finger of a C2HC-type, putative	-1.83	2.01E-06	GAGGGGGGGGADAAAGAAK +2 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.30.0760	hypothetical protein, conserved	-2.50	9.72E-07	RRGGGDDVAAGGNEGR +3 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.15.0800	hypothetical protein, conserved	-2.50	6.17E-03	RRGGGDSGAVDR +3 Methyl x 1	R1 Methyl
LmjF.32.0840	hypothetical protein, conserved (DRBD18)	-3.01	4.02E-04	GRRGGSGFGSQPTNTSIR +3 Methyl x 1	R3 Methyl
LmjF.07.0340	ATP-dependent RNA helicase DBP2B, putative	-3.57	7.25E-09	DGGYGGYGGRRGGR +3 Methyl x 1	R12 Methyl:2H(3)13C(1) R2 Methyl:2H(3)13C(1), M5 Label:13C(1)2H(3)
LmjF.36.6980	eukaryotic translation initiation factor 3 subunit c	-3.62	1.35E-08	GRGMAAGR +2 Methyl x 1	R14 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-3.65	7.62E-08	DPAIEVHAPARGR +3 Methyl x 1	R14 Methyl
LmjF.32.1800	hypothetical protein, conserved	-3.83	1.17E-03	GGQIRGGHSAQR +3 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.27.1300	KH domain containing protein, putative	-3.96	5.52E-11	GGRRGAGAPNDDAAR +2 Methyl x 1	R4 Methyl:2H(3)13C(1)
LmjF.34.4290	nucleolar protein family a, putative	-4.11	1.44E-10	LTFEPKPR +3 Methyl x 1	R9 Methyl:2H(3)13C(1)
LmjF.27.1680	hypothetical protein, conserved (NXF1)	-4.66	4.15E-10	SGPSSGGVGLGNNGSRGGGR +3 Methyl x 1	R22 Methyl
LmjF.36.5100	hypothetical protein, conserved (PUF11)	-5.37	8.50E-14	GGPGLQRGR +2 Methyl x 1	R8 Methyl:2H(3)13C(1) M16 Label:13C(1)2H(3), R17
LmjF.31.0080	hypothetical protein, conserved (ZC3H34) CUE domain/Domain of unknown function (DUF1771)/Smr domain containing protein, putative	-5.82	6.18E-07	GGWYPSAGSGYNNMR +2 Methyl x 1	R1 Methyl
LmjF.01.0210	CUE domain/Domain of unknown function (DUF1771)/Smr domain containing protein, putative	-3.88	3.32E-01	RGGSQQDNVAR +2 Methyl x 1	R1 Methyl
LmjF.01.0210	CUE domain/Domain of unknown function (DUF1771)/Smr domain containing protein, putative	0.00	1.00E+00	RGGSQQDNVAR +3 Methyl x 1	R1 Methyl
LmjF.01.0260	Calmodulin-binding, putative	0.00	1.00E+00	LGSPCAPGASASGGGGTSDASGAASCVGAPNR +3 Methyl	R36 Methyl
LmjF.01.0260	Calmodulin-binding, putative	0.00	1.00E+00	LGSPCAPGASASGGGGTSDASGAASCVGAPNR +3 Met	R36 Methyl:2H(3)13C(1)
LmjF.01.0540	hypothetical protein, conserved	-0.42	6.83E-01	RGVYVPHLDFCEPLPR +4 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.01.0620	hypothetical protein, conserved	2.69	8.39E-01	QARGLNTSGASAIR +3 Methyl x 1	R3 Methyl
LmjF.01.0680	hypothetical protein, unknown function	0.35	1.00E+00	ARGGCTVQR +2 Methyl x 1	R2 Methyl:2H(3)13C(1)

LmjF.01.0740	hypothetical protein, conserved	0.00	1.00E+00 RSRGGAALR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.01.0740	hypothetical protein, conserved	0.06	1.07E+00 SRGGAALR +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.02.0530	hypothetical protein, conserved	0.00	1.00E+00 IAANGRRGPNDR +3 Methyl x 1	R6 Methyl:2H(3)13C(1), M17 R9 Methyl:2H(3)13C(1), M17
LmjF.02.0560	hypothetical protein, unknown function	-0.73	8.39E-01 GVDGVSRTGGGGQPIPIR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.02.0660	Nop14-like family, putative	0.99	1.00E+00 SGHRGAGGYTASEMEVR +3 Methyl x 1	R5 Methyl
LmjF.03.0260	hypothetical protein, conserved	-1.00	1.09E+00 YGSPKAGVDGR +2 Methyl x 1	#N/A
LmjF.03.0350	protein kinase, putative	1.85	1.00E+00 EVVAASSAGAVAGRANMSR +3 Methyl x 1	#N/A
LmjF.03.0560	hypothetical protein	-1.28	8.55E-01 AVYTGVAATSPAARGGACGTMLSTK +3 Methyl x 1	R16 Methyl:2H(3)13C(1), M23
LmjF.03.0600	arginine N-methyltransferase, putative (PRMT3)	-0.11	9.43E-01 TGAPTQGRSE +2 Methyl x 1	Label:13C(1)2H(3)
LmjF.03.0800	6-phosphofructo-2-kinase 1	-1.13	5.01E-01 VGRGGATGGAVASDSEEEALLR +3 Methyl x 1 Phos x 1	R7 Methyl
LmjF.03.0800	6-phosphofructo-2-kinase 1	-0.63	2.08E-01 VGRGGATGGAVASDSEEEALLR +3 Methyl x 1	R3 Methyl
LmjF.03.0800	6-phosphofructo-2-kinase 1	-0.34	1.06E+00 SRGTSLVSAASQLATHAR +4 Methyl x 1	R2 Methyl
LmjF.03.0800	6-phosphofructo-2-kinase 1	0.00	1.00E+00 RVRGGGATGGAVASDSEEEALLR +4 Methyl x 1	R4 Methyl
LmjF.03.0800	6-phosphofructo-2-kinase 1	0.00	1.00E+00 SRGTSLVSAASQLATHAR +3 Methyl x 1	R2 Methyl
LmjF.03.0820	hypothetical protein, conserved	-0.15	1.00E+00 ARGGGVAVQQQR +2 Methyl x 1	R2 Methyl
LmjF.04.0830	hypothetical protein, conserved	0.66	1.05E+00 GRGGLTQPR +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.04.0920	hypothetical protein	0.66	1.20E-01 DAGSQPQLRGGIR +3 Methyl x 1	R10 Methyl
LmjF.05.0140	nucleolar RNA helicase II, putative	-2.30	1.68E-01 GGFNYGGGGRRGPGVGNR +3 Methyl x 1	R9 Methyl:2H(3)13C(1)
LmjF.05.0140	nucleolar RNA helicase II, putative	-0.62	8.17E-01 GGRGFNYGGGR +2 Methyl x 1	#N/A
LmjF.05.0300	hypothetical protein, conserved	-1.01	1.03E+00 GSAPDNSAVGRRGR +3 Methyl x 1	#N/A
LmjF.05.0370	hypothetical protein, conserved	0.25	8.21E-01 RGGAAATCAQGFIFEDPAVTMAR +3 Methyl x 1	R1 Methyl
LmjF.05.0640	Ankyrin repeats (many copies)/Ankyrin repeats (3 copies), putative	0.00	1.00E+00 HQQAPSYAADVMDGDPGVNYPLGGTGGSSSARGR +4 Methyl	R34 Methyl
LmjF.05.0720	phosphatase-like protein	-0.48	1.00E+00 QQLNALIPVMSPSYTFAGPAPTRGGAK +3 Methyl x 1 Phos x 1	#N/A
LmjF.05.0850	zinc-finger of a C2HC-type, putative	2.27	8.68E-02 GSGGGGGRRRPAWNSDVEVR +2 Methyl x 1	R13 Methyl
LmjF.05.0850	zinc-finger of a C2HC-type, putative	0.01	3.46E-01 GPAASSPAAGASGLVTSAGRGYGSNDEEAGNAYMPQQPS!	S5 Phospho, R23 Methyl
LmjF.05.0850	zinc-finger of a C2HC-type, putative	8.42	4.62E-01 SGGGGGGAGGGGGGGGADAAAGAAK +4 Methyl x 2	R8 Methyl, R16 Methyl
LmjF.05.0850	zinc-finger of a C2HC-type, putative	8.04	1.06E+00 SGGGGGGAGGGGGGGGADAAAGAAK +3 Methyl x 2	R8 Methyl, R16 Methyl
LmjF.05.1190	hypothetical protein, conserved	0.85	4.19E-01 RGGGNSAAAPR +3 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.05.1190	hypothetical protein, conserved	0.04	2.19E-01 RGGGNSAAAPR +2 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.06.0460	ATP-NAD kinase-like protein	-0.07	1.07E+00 SPLRGGVDTTR +2 Methyl x 1	R5 Methyl:2H(3)13C(1)
LmjF.06.0550	hypothetical protein, conserved	-0.35	9.78E-01 QLRGGSPR +2 Methyl x 1	R3, R12
LmjF.06.0640	STE/STE11 serine/threonine-protein kinase, putative	0.62	1.17E-01 RGGAGASTPAPPLVPLDAVDVK +3 Methyl x 1 Phos x 1	R1 Methyl, S12 Phospho
LmjF.06.0810	hypothetical protein, unknown function	-0.39	9.25E-01 GARGGGGSSSSASPTSR +2 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.06.0810	hypothetical protein, unknown function	-0.18	8.59E-01 GARGGGGSSSSASPTSR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.06.0940	STE/STE11 serine/threonine-protein kinase, putative	-0.74	1.04E+00 AAVSSSNAAMSVSHGADIVVPSRGR +4 Methyl x 1	M12 Label:13C(1)2H(3), R27 Methyl:2H(3)13C(1)
LmjF.06.0970	Domain of unknown function (DUF3883), putative	-0.13	1.09E+00 SGTASALRGGGGGAER +3 Methyl x 1	#N/A
LmjF.07.0340	ATP-dependent RNA helicase DBP2B, putative	-0.67	2.61E-01 SGGVGGGGYGGYGGGR +3 Methyl x 1	R9 Methyl
LmjF.07.0340	ATP-dependent RNA helicase DBP2B, putative	-0.90	8.65E-01 SGGVGGGGYGGYGGGR +3 Methyl x 2	R9 Methyl
LmjF.07.0490	hypothetical protein, conserved	-0.42	2.15E-01 VVSSSIHGGRGRTN +2 Methyl x 1	R11 Methyl:2H(3)13C(1)
LmjF.07.0490	hypothetical protein, conserved	-0.21	1.09E+00 VVSSSIHGGRGRTN +3 Methyl x 1	R11 Methyl:2H(3)13C(1)
LmjF.07.0740	hypothetical protein, conserved	2.49	7.84E-01 AVTAAGRGTVDHEGAFTSMR +3 Methyl x 1	#N/A
LmjF.07.0870	splicing factor ptrs1-like protein	1.19	8.54E-01 RGGYGSDR +2 Methyl x 1	R1 Methyl
LmjF.07.0940	Domain of unknown function (DUF3437), putative	-0.46	1.00E+00 LLPATTAAVESPGYNGRAGQPLVLPSTPAVIGVAPSATLR +4 Me!	R19 Methyl:2H(3)13C(1)
LmjF.08.0110	hypothetical protein, unknown function	-1.72	1.00E+00 MGSGLRGLSPSPAAQPIYNDIASR +3 Methyl x 1	M1 Label:13C(1)2H(3), R6 Methyl:2H(3)13C(1)
LmjF.08.0620	hypothetical protein, conserved	-0.67	4.36E-01 SGAAVVRGGPSLAVLSAQSPPLSVLGGAAEAASSSNR +3	R8 Methyl, R43 Methyl:2H(3)13C(1)
LmjF.08.0620	hypothetical protein, conserved	0.98	1.06E+00 SGAAVVRGGPSLAVLSAQSPPLSVLGGAAEAASSSNR +5	R8 Methyl, R43 Methyl:2H(3)13C(1)
LmjF.08.0620	hypothetical protein, conserved	1.43	3.78E-01 SPGAVGGGGGRTTSSSAAASANTAGANR +3 Methyl x 1	R11 Methyl
LmjF.08.0620	hypothetical protein, conserved	-0.58	8.47E-01 SGAAVVRGGPSLAVLSAQSPPLSVLGGAAEAASSSNR +4	R8 Methyl, R43 Methyl:2H(3)13C(1)
LmjF.08.0620	hypothetical protein, conserved	0.32	1.21E-01 SGAAVVRGGPSLAVLSAQSPPLSVLGGAAEAASSSNR +4	R8 Methyl, R43 Methyl:2H(3)13C(1)
LmjF.08.0880	SET domain containing protein, putative	0.66	1.04E+00 HMGIDLSNQAAGTHASGCIHRGGNSDGV +5 Methyl x 1	#N/A
LmjF.08.1000	AAA domain (dynein-related subfamily)/von Willebrand factor type A domain containing prote	-0.40	4.70E-01 NSASAAPACRGR +2 Methyl x 1	R11 Methyl
LmjF.08.1250	hypothetical protein, conserved	0.00	1.00E+00 DADGSCWIGVSPATQPPQFAPRGGAGTCDR +3 Methyl x	R25 Methyl:2H(3)13C(1) R1 Methyl:2H(3)13C(1), M33 Label:13C(1)2H(3)
LmjF.09.0390	hypothetical protein, conserved	1.26	1.06E+00 RGGGGGGGNSGGTVDVDPDPSNTQTPTSSMNGGGGR +4	R10 Methyl
LmjF.09.0520	Flagellum attachment zone protein 3	-1.02	7.70E-01 ASRGGAAATPRPSTAPPSPENNAADILADENMR +4 Methyl x 1	R10 Methyl
LmjF.09.0520	Flagellum attachment zone protein 3	0.05	1.00E+00 ASRGGAAATPRPSTAPPSPENNAADILADENMR +4 Methyl x 1 Ph	R10 Methyl
LmjF.09.0530	leucine-rich repeat protein, putative	-0.48	1.00E+00 QRGGGGGGDALASMR +3 Methyl x 1	#N/A
LmjF.09.0540	hypothetical protein, unknown function	-0.18	9.25E-01 VRGSSGFGGR +2 Methyl x 1	R2 Methyl
LmjF.09.0540	hypothetical protein, unknown function	0.26	1.09E+00 VRGSSGFGGR +3 Methyl x 1	R2 Methyl
LmjF.09.0620	hypothetical protein, conserved	-0.12	3.44E-01 AQTSPNGRGGAVEPNPDLQR +3 Methyl x 1	R10 Methyl
LmjF.09.0750	acyl-CoA binding protein, putative	1.23	1.00E+00 LPTVRRGGPHAAVPSVSSPGIESALAGGCHSTGIAGVEDALVQN	R6 Methyl:2H(3)13C(1)
LmjF.09.1180	hypothetical protein, conserved	2.29	1.06E+00 NLGDEGLDSEVSSSESMSPPCPANTTTVPNGRAR +4 Me!	#N/A
LmjF.09.1440	Dnal domain containing protein, putative	-0.08	1.07E+00 NHRGGPNK +2 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.10.1110	PAB1-binding protein, putative (PBP1)	0.00	1.00E+00 RGGMATAAR +2 Methyl x 1	R1 Methyl
LmjF.10.1110	PAB1-binding protein, putative (PBP1)	-0.35	1.00E+00 KEAAATSAAPAAPATPAATATAGRGAAR +3 Methyl x 1	R27 Methyl
LmjF.10.1130	hypothetical protein, conserved	-1.23	1.05E+00 MAAALSFTR +3 Methyl x 1	#N/A
LmjF.11.0600	hypothetical protein, conserved	0.00	1.00E+00 YSEGHGGGSRGGGQR +3 Methyl x 1	R12 Methyl
LmjF.11.0820	hypothetical protein, conserved	-1.84	2.71E-01 QQQMDMNFGR +2 Methyl x 1	R11 Methyl
LmjF.11.0820	hypothetical protein, conserved	-1.08	4.74E-01 MQMPPPPQQYSR +2 Methyl x 1	R13 Methyl
LmjF.11.0820	hypothetical protein, conserved	-0.54	4.80E-01 QQQMDMNFGRSQSQYNPAPNTGYPQR +3 Methyl x 1	M4 Label:13C(1)2H(3), M6 Label:13C(1)2H(3), R11 Methyl:2H(3)13C(1)
LmjF.11.0830	hypothetical protein, conserved	0.97	1.03E+00 SIGYARGGGGGAGDK +2 Methyl x 1	#N/A
LmjF.11.1330	Flagellar-associated PapD-like, putative	-0.24	1.21E-01 GRGGGAGAAASSSSASK +3 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.11.1330	Flagellar-associated PapD-like, putative	0.40	1.04E+00 GRGGGAGAAASSSSASK +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.12.0320	Myotubularin-related protein, putative	0.00	1.00E+00 CCLGRGGAPVSGEAE +3 Methyl x 1	#N/A
LmjF.12.1110	Dnal domain containing protein, putative	0.65	1.01E+00 GARGGGVPPSSMASPVDPAAPAAGAA +3 Methyl x 1	#N/A
LmjF.12.1180	hypothetical protein, conserved	0.82	1.00E+00 SAQRGGTNAANGSGGGGPTSYR +3 Methyl x 1	R4 Methyl:2H(3)13C(1)
LmjF.13.0580	hypothetical protein, conserved	-2.64	8.73E-01 WGPSALSATATPPSNRAGAVNNR +3 Methyl x 1	R18 Methyl
LmjF.13.0580	hypothetical protein, conserved	0.28	3.33E-01 SGAARGGGVSPASK +2 Methyl x 1	R5 Methyl:2H(3)13C(1)
LmjF.13.0700	kinesin, putative	0.00	1.00E+00 QRGGGGAPPLAAALVQR +3 Methyl x 1	#N/A
LmjF.13.0810	hypothetical protein, conserved	-0.02	1.69E-01 GAAAVFGSASRGGAVNR +3 Methyl x 1	#N/A
LmjF.13.0880	hypothetical protein, conserved	0.10	2.77E-01 RGMGSHSQSQSQR +2 Methyl x 1	R1 Methyl
LmjF.13.0880	hypothetical protein, conserved	-0.14	1.09E+00 RGMGSHSQSQSQR +3 Methyl x 1	R1 Methyl
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	-0.93	1.00E+00 HSYRGGGNAASGYRSDSLATANCSVALLSR +4 Methyl x 1 PI	R4 Methyl, S13 Phospho
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	-0.46	1.00E+00 DNLEDDAALLALSDVDVGGVGRGR +3 Methyl x 1	S15 Phospho, R28 Methyl
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	-0.45	7.60E-01 HSYRGGGNAASGYR +3 Methyl x 1	R4 Methyl
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	-0.39	8.18E-01 SLAPKDNLEDDAALLALSDVDVGGVGRGR +4 Methyl x 1 S21 Phospho, R34 Methyl:2H(3)13C(1)	
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	-0.25	9.31E-01 HSYRGGGNAASGYR +2 Methyl x 1	R4 Methyl
LmjF.13.1130	Uncharacterised ACR, YagE family COG1723, putative	0.00	1.00E+00 SLAPKDNLEDDAALLALSDVDVGGVGRGR +3 Methyl x 1 S21 Phospho, R34 Methyl:2H(3)13C(1)	
LmjF.14.0570	WD domain, G-beta repeat, putative	0.00	1.00E+00 GSRGSSYGR +2 Methyl x 1	R3 Methyl
LmjF.15.0290	hypothetical protein, conserved	0.50	8.73E-01 LADTLSCFNRRGGGGGAR +3 Methyl x 1	R1 Methyl
LmjF.15.0360	RNA pseudouridylate synthase, putative	-0.53	1.00E+00 QLTRGGGASLLAWAALQPVSGVGAAPAR +3 Methyl x 1	R4 Methyl
LmjF.15.0860	hypothetical protein, conserved	-0.82	4.20E-01 SDGPRGGVAGPPSGADLFHGSAPQLQLR +4 Methyl x 1	R6 Methyl
LmjF.15.0920	protein phosphatase 2A regulatory subunit, putative	0.00	1.00E+00 QAAVQHVALSGAGGSGAAHWSSNSRSGASR +4 Methyl x 1	R27 Methyl:2H(3)13C(1)
LmjF.15.0920	protein phosphatase 2A regulatory subunit, putative	0.00	1.00E+00 QAAVQASASAHSGCYK +3 Methyl x 1	R12 Methyl
LmjF.15.1200	STE group serine/threonine-protein kinase, putative	0.00	1.00E+00 HVAGGGGGVGGGNASNIHLTAPPNSNEGSVYLMMADEHQGDGI	#N/A
LmjF.15.1310	MGT1 magnesium transporter	-0.08	8.50E-02 PLLRGGAVVGFGR +3 Methyl x 1 Phos x 1	S1 Phospho, R6 Methyl
LmjF.15.1380	nucleolar RNA binding protein, putative	0.38	3.32E-01 MNTSGFNDRRGR +3 Methyl x 1	M1 Label:13C(1)2H(3)+Oxidation, R10 Methyl:2H(3)13C(1)
LmjF.15.1380	nucleolar RNA binding protein, putative	1.16	7.76E-01 GRRGGGGFK +2 Methyl x 1	R3 Methyl:2H(3)13C(1) M1 Label:13C(1)2H(3), R10 Methyl:2H(3)13C(1), R13 Methyl:2H(3)13C(1)
LmjF.15.1380	nucleolar RNA binding protein, putative	2.07	1.05E+00 MNTSGFNDRRGGGGGGFK +3 Methyl x 2	#N/A
LmjF.16.0660	hypothetical protein, conserved	0.52	3.95E-01 CDMTNPSSGARGGTGASSATSSLR +3 Methyl x 1	R6 Methyl:2H(3)13C(1), R10 Methyl:2H(3)13C(1), R10
LmjF.16.0730	ubiquitin hydrolase, putative	1.16	1.00E+00 RSGGGRSGRGGAGATNAPSVPAPSPSETVTEASAPPEPQLEGR	R6 Methyl:2H(3)13C(1), R10 Methyl:2H(3)13C(1), R10
LmjF.16.0730	ubiquitin hydrolase, putative	0.00	1.00E+00 RSGGGRSGRGGAGATNAPSVPAPSPSETVTEASAPPEPQLEGR	R6 Methyl:2H(3)13C(1), R10 Methyl:2H(3)13C(1), R10
LmjF.16.1230	hypothetical protein, conserved	0.10	3.95E-01 GSRPASPSGASVSGRGR +4 Methyl x 1	R15 Methyl
LmjF.16.1230	hypothetical protein, conserved	-0.40	9.47E-01 GKSRRPASPSGASVSGRGR +3 Methyl x 1	R17 Methyl:2H(3)13C(1)
LmjF.16.1230	hypothetical protein, conserved	0.12	1.09E+00 GSRPASPSGASVSGRGR +3 Methyl x 1	R15 Methyl



LmjF.16.1270	hypothetical protein, conserved	-0.15	8.42E-01	VALSQPMPCSPRGGGLGR +3 Methyl x 1	M7 Label:13C(1)2H(3), R12
LmjF.16.1340	hypothetical protein, conserved	-0.57	1.03E+00	ESQTSARGGANGVSSAR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.17.0380	Qa-SNARE protein, putative	-1.31	1.00E+00	APHQPATAGVSSSSSTGRGGGNNVSSAR +4 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.17.0380	Qa-SNARE protein, putative	-0.29	8.53E-01	APHQPATAGVSSSSSTGRGGGNNVSSAR +3 Methyl x 1	R20 Methyl
LmjF.17.0510	hypothetical protein, unknown function	-0.35	8.14E-01	SAALEGPGASCEISAPRGR +3 Methyl x 1	R20 Methyl
LmjF.17.0550	RNA-binding protein, putative	0.36	8.57E-02	GMSRGNNSRAGGNHR +3 Methyl x 2	R4 Methyl, R11 Methyl
LmjF.17.0550	RNA-binding protein, putative	4.31	1.20E-01	EGRGMSRGNNNR +3 Methyl x 2	R3 Methyl:2H(3)13C(1), M5
LmjF.17.0550	RNA-binding protein, putative	0.00	1.00E+00	GRGGAHLQPCQNFQQPQQYQLHPLPPPPP +5 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.18.0390	hypothetical protein, conserved	0.00	1.00E+00	AIAGRGGVVGAPP +3 Methyl x 1	R2 Methyl
LmjF.18.0650	PA26 p53-induced protein (sestrin), putative	0.00	1.00E+00	GVHRRGGVSAAGR +3 Methyl x 1	#N/A
LmjF.18.0800	Ribosomal protein S8, putative	0.01	4.20E-01	VYGGATTAFVPGSSSSSSSTASVGDYLRGR +3 Methyl x 1	R4 Methyl
LmjF.18.0840	hypothetical protein, conserved	-0.71	1.03E+00	GSFGTGRGGASTK +2 Methyl x 1	R3 Methyl
LmjF.18.1240	pre-RNA processing PIH1/Nop17, putative	1.12	8.42E-01	DRNSAAAASGRGGGGEAAAR +4 Methyl x 1	R7 Methyl
LmjF.18.1240	pre-RNA processing PIH1/Nop17, putative	1.03	8.32E-01	LNSAAAASGRGGGGEAAAR +3 Methyl x 1	R13 Methyl:2H(3)13C(1)
LmjF.18.1420	pumilio protein 2, putative (PUF2)	0.51	8.63E-01	DNRPGGVGSSSSGNNNGSGRAGRGR +4 Methyl x 2	R11 Methyl:2H(3)13C(1)
LmjF.18.1420	pumilio protein 2, putative (PUF2)	10.97	1.00E+00	AGRGGRRNNNNSSNNQHSQDK +3 Methyl x 2	R22 Methyl:2H(3)13C(1), R25
LmjF.18.1420	pumilio protein 2, putative (PUF2)	10.97	1.00E+00	DNRPGGVGSSSSGNNNGSGRAGRGR +3 Methyl x 2	R3 Methyl:2H(3)13C(1), R6
LmjF.18.1420	pumilio protein 2, putative (PUF2)	10.97	1.00E+00	DNRPGGVGSSSSGNNNGSGRAGRGR +4 Methyl x 3	R22 Methyl:2H(3)13C(1), R25
LmjF.18.1420	pumilio protein 2, putative (PUF2)	0.00	1.00E+00	DNRPGGVGSSSSGNNNGSGRAGRGR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.18.1420	pumilio protein 2, putative (PUF2)	0.00	1.00E+00	DNRPGGVGSSSSGNNNGSGRAGRGR +3 Methyl x 2	R22 Methyl
LmjF.18.1420	pumilio protein 2, putative (PUF2)	0.00	1.00E+00	GRRGNNNNSSNNQHSQDKNNAMR +4 Methyl x 1	R3 Methyl
LmjF.18.1420	pumilio protein 2, putative (PUF2)	0.00	1.03E+00	DNRPGGVGSSSSGNNNGSGRAGRGR +4 Methyl x 1	R22 Methyl
LmjF.19.0060	40S ribosomal protein S2	0.15	1.00E+00	GRGGPEEKVEWPTK +3 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.19.0270	hypothetical protein, conserved	-0.32	1.00E+00	YGHAPDAVIAIAGRGGSGNGGAAADNSPAPFHTNGCGSN	R14 Methyl:2H(3)13C(1)
LmjF.19.0270	hypothetical protein, conserved	0.00	1.00E+00	KYGHAPDAVIAIAGRGGSGNGGAAADNSPAPFHTNGCGSN	R15 Methyl:2H(3)13C(1)
LmjF.19.0380	hypothetical protein, conserved	10.97	1.00E+00	RVPDSGAMASSGAGRAGRGR +4 Methyl x 3	R17 Methyl, R21 Methyl, R23 Methyl
LmjF.19.0430	hypothetical protein, conserved	-0.92	5.59E-02	DGRGGAAPLCSSSSSGGK +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.19.0800	ABC transport system ATP-binding protein, putative	-1.34	5.82E-02	MTRGGLTDAVVKDSR +3 Methyl x 1	R3 Methyl
LmjF.19.1020	tRNA pseudouridine synthase A-like protein	-2.13	4.55E-01	AAASSTGRRGPPVSSAYSAEHLTSHLGR +5 Methyl x 1	R10 Methyl
LmjF.19.1020	tRNA pseudouridine synthase A-like protein	0.32	8.22E-01	AAASSTGRRGPPVSSAYSAEHLTSHLGR +4 Methyl x 1	R10 Methyl
LmjF.19.1090	hypothetical protein, unknown function	-0.60	1.08E+00	TARGRGAAGGAAR +3 Methyl x 2	R3 Methyl:2H(3)13C(1), R5
LmjF.19.1130	hypothetical protein, conserved	-0.64	4.81E-01	ALLFEQVAQQLVLSAR +2 Methyl x 1	Phos x 1
LmjF.20.0360	Protein of unknown function (DUF2946), putative	-0.50	9.44E-01	TLRGGP +2 Methyl x 1	#N/A
LmjF.20.1080	WD40 repeat-containing protein	-1.18	9.25E-01	LTGSSDMVNLGRGWLR +3 Methyl x 1	M7 Label:13C(1)2H(3), R13
LmjF.20.1240	Raptor N-terminal CASPase like domain containing protein, putative	-0.20	8.61E-01	TGARGTSSATTR +2 Methyl x 1	R4 Methyl
LmjF.21.0270	STE group serine/threonine-protein kinase, putative	0.02	4.09E-01	EVGRGGSAVLR +3 Methyl x 1	#N/A
LmjF.21.0270	STE group serine/threonine-protein kinase, putative	0.45	7.73E-02	SLTVVNPGRGGGELNSTYDK +3 Methyl x 1	R12 Methyl
LmjF.21.0490	DnaI protein, putative	0.96	1.00E+00	GRQAHAEEDEFVDDDDQEQYFR +4 Methyl x 1	Phos x 1
LmjF.21.0490	DnaI protein, putative	0.32	1.00E+00	GRQAHAEEDEFVDDDDQEQYFR +3 Methyl x 1	Phos x 1
LmjF.21.1030	hypothetical protein, conserved	-0.70	8.60E-01	GAGGSRPPFAVDDDANYSDDGGRRGR +4 Methyl x 1	R27 Methyl:2H(3)13C(1)
LmjF.21.1030	hypothetical protein, conserved	0.00	1.00E+00	GAGGSRPPFAVDDDANYSDDGGRRGR +3 Methyl x 1	R27 Methyl:2H(3)13C(1)
LmjF.21.1850	hypothetical protein, conserved	0.46	1.18E-01	GRGGAEPPEER +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.22.1320	hypothetical protein, unknown function	-1.09	1.00E+00	GGNALLSSGEPVGRGSLVWGGGGDSSGALAPLR +3 Methyl x 1	R16 Methyl:2H(3)13C(1)
LmjF.23.0080	hypothetical protein, conserved	-0.59	1.09E+00	AVSAQVQAR +2 Methyl x 1	R9 Methyl
LmjF.23.0090	Domain of unknown function (DUF1767), putative (TDRD3)	5.72	4.57E-01	NGGGGRRQAQGDNYEGR +3 Methyl x 1	R7 Methyl:2H(3)13C(1)
LmjF.23.0090	Domain of unknown function (DUF1767), putative (TDRD3)	0.02	8.95E-01	NGGGGRRQAQGDNYEGR +2 Methyl x 1	R7 Methyl:2H(3)13C(1)
LmjF.23.1010	hypothetical protein, conserved	0.60	8.13E-01	QHQRRGGGKPEVSPAPNSGGSSNNR +4 Methyl x 1	R5 Methyl:2H(3)13C(1), M6
LmjF.23.1290	hypothetical protein, unknown function	-0.23	4.74E-01	RGGGMASEAFR +2 Methyl x 1	Label:13C(1)2H(3)
LmjF.23.1290	hypothetical protein, unknown function	0.35	8.75E-01	RGGGMASEAFR +3 Methyl x 1	R1 Methyl:2H(3)13C(1), M6
LmjF.23.1620	hypothetical protein	-1.95	1.00E+00	DQGRPRGGGSSAAATFGHGSVTDYDQVTSAAELR +5 Methyl x 1	Label:13C(1)2H(3)
LmjF.23.1620	hypothetical protein	0.00	1.00E+00	DQGRPRGGGSSAAATFGHGSVTDYDQVTSAAELR +4 Methyl x 1	R4 Methyl
LmjF.23.1730	RING-H2 zinc finger, putative	-0.78	1.07E+00	SRGDDLHQQGR +3 Methyl x 1	R2 Methyl
LmjF.23.1730	RING-H2 zinc finger, putative	10.97	1.00E+00	GGDGLHQQGRSGQR +3 Methyl x 1	R10 Methyl:2H(3)13C(1)
LmjF.23.1730	RING-H2 zinc finger, putative	0.00	1.00E+00	SRGDDLHQQGR +4 Methyl x 1	R2 Methyl
LmjF.24.1070	hypothetical protein, conserved	-0.85	3.46E-01	SAAGSPTAAGAATSRGGGPGKPPR +3 Methyl x 1	#N/A
LmjF.24.1070	hypothetical protein, conserved	-0.52	1.02E-01	SAAGSPTAAGAATSRGGGPGK +3 Methyl x 1	R15 Methyl
LmjF.24.1470	hypothetical protein, conserved	-3.13	8.25E-01	GGGGRRGALLMNESSLQR +3 Methyl x 1	Phos x 1
LmjF.24.1470	hypothetical protein, conserved	-1.19	1.00E+00	TEFVDSYRGGGRRGALLMNESSLQR +4 Methyl x 1	R15 Methyl
LmjF.24.1470	hypothetical protein, conserved	-0.34	8.04E-01	GGGGRRGALLMNESSLQR +3 Methyl x 1	R6 Methyl:2H(3)13C(1), M13
LmjF.24.1580	hypothetical protein, conserved	-0.03	2.78E-01	HGAQPQQGSRGVAAGAAQAR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.24.1580	hypothetical protein, conserved	0.12	3.48E-01	HGAQPQQGSRGVAAGAAQAR +4 Methyl x 1	R11 Methyl
LmjF.24.1880	cyclin 11, putative	0.34	1.10E+00	SGVRGGSSGGVR +2 Methyl x 1	R1 Methyl
LmjF.25.0290	RNA-binding protein, putative	-0.12	4.32E-01	GRGVGCMNPPAPISDGLAIPVPSAR +3 Methyl x 1	R4 Methyl:2H(3)13C(1), M7
LmjF.25.0290	RNA-binding protein, putative	10.97	1.00E+00	SVARPPPPPPPIRGR +3 Methyl x 2	Label:13C(1)2H(3)
LmjF.25.0290	RNA-binding protein, putative	10.97	1.00E+00	SVARPPPPPPPIRGRGVCMTNPPAPISDGLAIPVPSAR +5 Methyl x 1	R14 Methyl, R16 Methyl
LmjF.25.0290	RNA-binding protein, putative	1.25	1.00E+00	SVARPPPPPPPIRGRGVCMTNPPAPISDGLAIPVPSAR +5 Methyl x 1	#N/A
LmjF.25.0290	RNA-binding protein, putative	0.00	1.00E+00	AEQVFPSPPTGPIPLR +2 Methyl x 1	Phos x 1
LmjF.25.0290	RNA-binding protein, putative	-4.36	1.00E+00	AEQVFPSPPTGPIPLR +2 Methyl x 1	R18 Methyl:2H(3)13C(1)
LmjF.25.0290	RNA-binding protein, putative	0.13	1.03E+00	AEQVFPSPPTGPIPLRGR +3 Methyl x 1	R20 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	0.83	1.19E-01	ADTETFGPEMVMRGRFR +3 Methyl x 1	R15 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-0.70	1.36E-01	DPAIVEVHAPARGRGR +3 Methyl x 3	R14 Methyl:2H(3)13C(1), R17
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	0.32	2.71E-01	KADTFEGPEMVMRGR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-0.09	3.88E-01	DSSSPQARDPAIVEVHAPARGRGR +4 Methyl x 2	Phos x 1
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-0.98	4.39E-01	DSSSPQARDPAIVEVHAPARGRGR +4 Methyl x 3	R20 Methyl, R22 Methyl, R25 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	0.15	4.63E-01	DSSSPQARDPAIVEVHAPARGRGR +4 Methyl x 2	R20 Methyl, R22 Methyl, R25 Methyl
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	1.36	8.22E-01	DPAIVEVHAPARGRGR +3 Methyl x 2	R14 Methyl:2H(3)13C(1), R17
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-1.32	8.32E-01	GGRAAAAPASATASAAATR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-4.77	8.35E-01	NHRGGYGR +2 Methyl x 1	#N/A
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	1.13	8.43E-01	KADTFEGPEMVMRGRFR +4 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	10.97	1.00E+00	DPAIVEVHAPARGRGGRAAAAAPASATASAAATR +5 Methyl x 1	M11 Label:13C(1)2H(3), M15
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-0.49	1.03E+00	SYDEAQPYSRGGGGR +3 Methyl x 1	Label:13C(1)2H(3), R16
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-1.18	1.07E+00	GGYGRGGSGNYR +2 Methyl x 1	Label:13C(1)2H(3), R16
LmjF.25.0540	hypothetical protein SCD6.10 (SCD6)	-1.04	1.09E+00	GGYGRGGSGNYR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.25.1080	hypothetical protein, conserved	-1.63	8.23E-01	GGSRGGGASCCER +3 Methyl x 2	R4 Methyl, R7 Methyl
LmjF.25.1430	Putative intraflagellar transport protein A1	0.00	1.00E+00	RRGGGLSLPMSDEDNGENAPR +3 Methyl x 1	Phos x 1
LmjF.25.1540	mitochondrial RNA binding complex 1 subunit, putative	1.26	4.56E-01	AIAAQSVRGGGVLVESAPATSFAFR +3 Methyl x 1	#N/A
LmjF.25.1540	mitochondrial RNA binding complex 1 subunit, putative	4.03	1.00E+00	RGRSYADAVSDGNMNR +3 Methyl x 2	R9 Methyl
LmjF.25.1540	mitochondrial RNA binding complex 1 subunit, putative	-0.38	1.00E+00	AIAAQSVRGGGVLVESAPATSFAFR +4 Methyl x 1	R1 Methyl, R3 Methyl
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	-0.11	3.17E-01	HGVGNNGSRGGDGAPR +2 Methyl x 1	R9 Methyl
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	-1.10	3.43E-01	HGVGNNGSRGGDGAPR +3 Methyl x 1	R10 Methyl
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	0.04	4.03E-01	RGGPMGR +2 Methyl x 1	R1 Methyl
LmjF.25.1740	mitochondrial RNA binding complex 1 subunit, putative	-0.06	1.03E+00	HGVGNNGSRGGDGAPR +4 Methyl x 1	R10 Methyl
LmjF.25.1830	Histone RNA hairpin-binding protein RNA-binding domain containing protein, putative	0.53	1.00E+00	MRSNVSSGAR +2 Methyl x 1	M1 Label:13C(1)2H(3), R2
LmjF.25.2000	hypothetical protein, conserved	-0.50	8.26E-01	GRGGCAGGAGTLHWQR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.25.2070	Rieske [2Fe-2S] domain containing protein, putative	-0.47	6.28E-01	ERPMSPVLDGGGLR +3 Methyl x 1	R2 Methyl:2H(3)13C(1)
LmjF.26.0920	hypothetical protein, conserved	-1.56	1.00E+00	TGAALDCAOPLNPLSPSDFELRGR +3 Methyl x 1	M4 Label:13C(1)2H(3), R13
LmjF.26.1110	TROVE domain containing protein, putative	0.47	8.54E-01	RGASVAVSAPPAQATTFVEAPR +3 Methyl x 1	Methyl:2H(3)13C(1)

LmjF.26.1530	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative	-0.16	5.14E-01 SHSNQYSQDSGVSSGGAGMQRGMR +4 Methyl x 1	M20 Label:13C(1)2H(3), M24
LmjF.26.1820	hypothetical protein, conserved	-0.54	1.03E+00 SSRGGTFLVQSEEDAR +2 Methyl x 1	Label:13C(1)2H(3), R25
LmjF.26.1820	hypothetical protein, conserved	0.12	1.36E-01 SSRGGTFLVQSEEDAR +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.26.2120	hypothetical protein, conserved	2.12	5.86E-01 GASSPLLPPEFVGRGVR +3 Methyl x 1	R3 Methyl
LmjF.26.2170	Cornifin (SPRR) family, putative	0.52	8.74E-01 SCRGGGSCFAAHTTSTR +3 Methyl x 1	R20 Methyl
LmjF.26.2380	Fibronectin type III domain containing protein, putative	-0.52	4.11E-01 RGGASTSPAATLTEMANR +3 Methyl x 1	R3 Methyl
LmjF.26.2420	hypothetical protein, conserved	-0.12	5.30E-01 RGGGTPLGR +2 Methyl x 1	R1 Methyl, T5 Phospho
LmjF.27.0130	WW domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative (ZFP3)	0.87	7.48E-02 TTHWSIPPTAYEPYNNRGRGAGYR +5 Methyl x 2	#N/A
LmjF.27.0130	WW domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative (ZFP3)	-7.63	1.00E+00 TTHWSIPPTAYEPYNNRGRG +4 Methyl x 1	R19 Methyl:2H(3)13C(1), R21
LmjF.27.0270	hypothetical protein, conserved	-1.16	1.03E+00 TKVPGNNAQDQPSNEVASDLDNHTALRGK +4 Methyl x 1 Phi	Methyl:2H(3)13C(1)
LmjF.27.0700	hypothetical protein, conserved	-1.35	8.55E-01 RGGGGAASQGGSDVDDMSQTASGDVR +3 Methyl x 1	S19 Phospho, R29 Methyl
LmjF.27.1300	KH domain containing protein, putative	-2.35	1.17E-01 GGGRGAGAPGNDDAAR +3 Methyl x 1	R1 Methyl:2H(3)13C(1), M17
LmjF.27.1300	KH domain containing protein, putative	-1.53	3.34E-01 GGNDEGRGGYVPR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.27.1300	KH domain containing protein, putative	0.01	6.82E-01 RAGPPAGQHPHPR +3 Methyl x 1	R4 Methyl:2H(3)13C(1)
LmjF.27.1300	KH domain containing protein, putative	0.07	1.01E+00 GGNDEGRGGYVPR +2 Methyl x 1	R7 Methyl
LmjF.27.2170	hypothetical protein, conserved	-0.62	1.21E-01 SVQLSSSEVDTRGGTGTR +3 Methyl x 1	R1 Methyl
LmjF.27.2170	hypothetical protein, conserved	0.38	8.93E-01 RGGTGSAGORPVTPQSEIENR +4 Methyl x 1	R7 Methyl
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	1.24	9.75E-01 AENVTPAGGKLPSPRPPEGSPGR +4 Methyl x 1	R13 Methyl:2H(3)13C(1)
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	10.97	1.00E+00 VYSWMSGRGFGIEDNADKK +3 Methyl x 1	R11 Methyl:2H(3)13C(1)
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	10.81	1.00E+00 VYSWMSGRGFGIEDNADKK +4 Methyl x 1	R26 Methyl
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	10.81	1.00E+00 VYSWMSGRGFGIEDNADKK +3 Methyl x 1	R8 Methyl
LmjF.28.0825	RNA binding protein rbp16, putative (RBP16)	0.41	1.00E+00 VYSWMSGRGFGIEDNADKK +3 Methyl x 1	R8 Methyl
LmjF.28.1060	hypothetical protein, conserved	0.00	1.07E+00 VYSWMSGR +2 Methyl x 1	#N/A
LmjF.28.1080	hypothetical protein, conserved	-1.50	1.00E+00 RGQAATPTGNR +2 Methyl x 1	#N/A
LmjF.28.2780	heat-shock protein hsp70, putative	-0.44	1.36E-01 EVADTQDVEVPAASRRGR +3 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.29.0290	zinc-finger of a CZHC-type, putative	-0.51	1.07E+00 TTPSYVAFDSE +2 Methyl x 1	R19 Methyl
LmjF.29.0290	zinc-finger of a CZHC-type, putative	-0.40	1.04E+00 QGRGGISAVNPVSTAAGR +2 Methyl x 1	R13 Methyl
LmjF.29.0370	protein kinase-like protein	-0.63	7.74E-01 QGRGGISAVNPVSTAAGR +3 Methyl x 1	R3 Methyl
LmjF.29.0370	protein kinase-like protein	0.00	1.00E+00 SPPLSNLNEANGTGRGFSFPCPSPLK +3 Methyl x 1	R3 Methyl
LmjF.29.0680	Triple RNA binding domain protein 3 (TRRM3)	-0.53	1.00E+00 SPPLSNLNEANGTGRGFSFPCPSPLK +3 Methyl x 1	R15 Methyl:2H(3)13C(1)
LmjF.29.0680	Triple RNA binding domain protein 3 (TRRM3)	-0.43	1.55E-01 HAGGNGHWRGGAATAA +4 Methyl x 1	R15 Methyl:2H(3)13C(1)
LmjF.29.0680	Triple RNA binding domain protein 3 (TRRM3)	-0.43	3.16E-01 HAGGNGHWRGGAATAA +3 Methyl x 1	R9 Methyl
LmjF.29.0680	Triple RNA binding domain protein 3 (TRRM3)	0.00	1.00E+00 GGASASSAFSSR +2 Methyl x 1	R9 Methyl
LmjF.29.0680	Triple RNA binding domain protein 3 (TRRM3)	-0.15	1.00E+00 RGHDSASHHDEEHDDEAGLDSNAAK +3 Methyl x 1 Phos	#N/A
LmjF.29.0770	hypothetical protein, conserved	0.14	1.04E+00 RGHDSASHHDEEHDDEAGLDSNAAK +4 Methyl x 1 Phos	R1 Methyl, S18 Phospho
LmjF.29.1090	ribosomal protein L1a, putative	-0.13	8.43E-01 ATDSVQGLLR +2 Methyl x 1	R11 Methyl:2H(3)13C(1)
LmjF.29.1090	ribosomal protein L1a, putative	-1.94	8.52E-01 ISGGTSTSGAGAFGNMCRGR +3 Methyl x 1	M17 Oxidation, R19 Methyl
LmjF.29.1110	hypothetical protein, conserved	10.97	1.04E+00 ISGGTSTSGAGAFGNMCR +2 Methyl x 1	M17 Label:13C(1)2H(3), R19
LmjF.29.1230	COPII coat assembly protein sec16, putative	-0.35	1.00E+00 AAGRGDAAGLSQHASFGDVL +4 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.29.2330	hypothetical protein, conserved	0.03	1.16E-01 VDLTTSRGR +3 Methyl x 1	R4 Methyl:2H(3)13C(1)
LmjF.30.0090	hypothetical protein, conserved	1.19	4.99E-01 VSPPTGPRGSVNLDDLH +3 Methyl x 1 Phos x 1	#N/A
LmjF.30.0260	mitochondrial RNA binding protein 1, putative	-3.64	9.28E-01 TRIEGRGRTQVSR +3 Methyl x 1	S3 Phospho, R10 Methyl
LmjF.30.0320	Sad1 / UNC-like C-terminal, putative	10.97	6.16E-01 QQRGGAGCVGAASNSHAAEGDVAVPVR +4 Methyl x 1	R8 Methyl
LmjF.30.0760	hypothetical protein, conserved	-2.97	1.00E+00 YNIRGGSGVAVGGNGPPLWPR +3 Methyl x 1	#N/A
LmjF.30.0760	hypothetical protein, conserved	4.25	3.18E-01 RGGSGDVAVAGGNEGR +2 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.30.0760	hypothetical protein, conserved	-0.27	4.60E-01 RGGSGDVAVAGGNEGRGR +3 Methyl x 2	R1 Methyl:2H(3)13C(1), R17
LmjF.30.0760	hypothetical protein, conserved	0.00	1.02E+00 GRGGGGHEDAMEK +3 Methyl x 1	Methyl:2H(3)13C(1)
LmjF.30.0760	hypothetical protein, conserved	0.00	1.00E+00 GRGGGGHEDAMEK +2 Methyl x 1	R2 Methyl
LmjF.30.0760	hypothetical protein, conserved	0.00	1.00E+00 RGGPPT +2 Methyl x 1	R2 Methyl
LmjF.30.0780	mitochondrial oligo_U binding protein TBRGG1, putative	-0.39	1.02E+00 GGYEGRGGPR +2 Methyl x 1	#N/A
LmjF.30.0900	hypothetical protein, conserved	-1.05	1.23E-01 RGNIRPGRSAPSQAQASVVDQPR +4 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.30.1810	Zeta toxin, putative	-0.96	8.59E-01 AGTSSSSTAGSRRGNAGGNYAHTSK +4 Methyl x 1	#N/A
LmjF.30.1810	Zeta toxin, putative	0.00	1.00E+00 AGTSSSSTAGSRRGNAGGNYAHTSK +3 Methyl x 1	R14 Methyl:2H(3)13C(1)
LmjF.30.2710	hypothetical protein, conserved	-0.32	8.55E-01 SSSGAGRGASGGPGGSDGQR +3 Methyl x 1	R14 Methyl:2H(3)13C(1)
LmjF.30.2710	hypothetical protein, conserved	0.00	1.00E+00 SSSGAGRGASGGPGGSDGQR +3 Methyl x 1 Phos x 1	S2 Phospho, R8 Methyl
LmjF.31.0080	hypothetical protein, conserved (ZC3H34)	-1.99	9.73E-01 GRGGWYPPSAGSGYNNMR +3 Methyl x 1	R8 Methyl
LmjF.31.0080	hypothetical protein, conserved (ZC3H34)	0.00	1.00E+00 HMDGIPPHAYQPPVYQPPVYPMGNPMYVNPQGYPPAMF	R45 Methyl
LmjF.31.0560	mevalonate kinase, putative	-0.68	8.51E-01 LSGTRGGIYALAASSDQR +3 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.31.1050	hypothetical protein, unknown function	-2.19	9.29E-01 SHAVPYEGTVHPSSRGR +4 Methyl x 1	#N/A
LmjF.31.1260	Microtubule-binding stalk of dynein motor, putative	-0.69	4.76E-01 VSPAPSPRGSAGK +2 Methyl x 1	R8 Methyl
LmjF.31.1380	hypothetical protein, unknown function	-0.38	6.28E-01 TARGGAACQLQR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.31.1750	nucleosome assembly protein-like protein	-2.78	1.02E+00 GRRGGAASQPPQEQEK +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.31.1750	nucleosome assembly protein-like protein	-1.92	4.37E-01 QRGGATPGGR +2 Methyl x 1	R2 Methyl
LmjF.31.2360	hypothetical protein, conserved	0.95	6.36E-01 LQRGGYQALQGR +3 Methyl x 1	R3 Methyl
LmjF.31.2590	TerD domain containing protein, putative	0.00	1.00E+00 RGGREVTQATR +3 Methyl x 1	R1 Methyl
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	0.34	1.07E+00 LATPPYEGVQLPGAASAEER +4 Methyl x 1 Phos x 1	#N/A
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	-0.16	5.30E-01 NGGGGFRGGFGGGGGR +3 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	0.02	8.53E-01 QYGGNRFNDQAQTYGGGFNR +3 Methyl x 1	R7 Methyl
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	0.32	1.00E+00 QYGGNRFNDQAQTYGGGFNR +2 Methyl x 1	R7 Methyl
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	-0.74	1.03E+00 SGFGGFRGGFGGGGGRGVR +3 Methyl x 1	R19 Methyl
LmjF.32.0400	ATP-dependent RNA helicase HEL67 (DDX3)	0.07	1.05E+00 NGGGGFRGGFGGGGGR +2 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.32.0620	hypothetical protein, conserved	-0.31	2.77E-01 GPSVERGAGAR +3 Methyl x 1	#N/A
LmjF.32.0620	hypothetical protein, conserved	6.24	1.00E+00 GGMGRAGSR +2 Methyl x 1	R5 Methyl
LmjF.32.0840	hypothetical protein, conserved (DRBD18)	0.51	1.00E+00 GRGGRRGCLDTMGMAQYMPFPQVGGMAR +4 Methyl x 2	R2 Methyl:2H(3)13C(1), M13
LmjF.32.0840	hypothetical protein, conserved (DRBD18)	-7.25	1.00E+00 GRGGRRGCLDTMGMAQYMPFPQVGGMAR +3 Methyl x 1	Label:13C(1)2H(3), M15
LmjF.32.0850	polypyrimidine tract-binding protein, putative (DRBD4)	0.66	1.18E-01 GGGIRGGSGTGLGAATGFSFPFSGTTPARGGASVGR +4 Methyl	Label:13C(1)2H(3), M20
LmjF.32.0850	polypyrimidine tract-binding protein, putative (DRBD4)	-0.42	8.29E-01 GGGIRGGSGTGLGAATGFSFPFSGTTPAR +3 Methyl x 1	Label:13C(1)2H(3), M28
LmjF.32.0880	60S ribosomal protein L18a, putative	0.74	7.75E-01 HYQVGR +2 Methyl x 1	Label:13C(1)2H(3)
LmjF.32.1130	hypothetical protein, conserved	-0.66	9.70E-02 QSAPRGGGSAVAR +3 Methyl x 1	R3 Methyl
LmjF.32.1650	hypothetical protein, conserved	-0.89	2.88E-01 SIRAGGPGSAGK +3 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.32.1800	hypothetical protein, conserved	-0.71	7.77E-01 GGGAGRGGQGR +2 Methyl x 1	R6 Methyl:2H(3)13C(1)
LmjF.32.1970	ribosome biogenesis protein TSR3, putative	-0.18	8.36E-01 GRGGSGGVCTSGFHNEPPAHPCSVPLAMWDFEQCDPNACS	#N/A
LmjF.32.2130	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative	0.01	2.93E-01 EPPYLSNRPPYGGPGMRRGGMR +4 Methyl x 1	#N/A
LmjF.32.2490	hypothetical protein, conserved	-0.14	8.61E-01 GYQYAGRGAK +2 Methyl x 1	R8 Methyl
LmjF.32.2520	hypothetical protein, unknown function	0.74	8.24E-01 GHPSYGERGGR +3 Methyl x 1	R9 Methyl
LmjF.32.2520	hypothetical protein, unknown function	1.31	1.00E+00 SAPPRGGYGAAPMSLSPAPALMSK +3 Methyl x 1	#N/A
LmjF.32.2580	hypothetical protein, conserved	-0.82	1.05E+00 MHEEDQSGRRGGR +3 Methyl x 1	M1 Label:13C(1)2H(3), R11
LmjF.32.2830	hypothetical protein, conserved	0.71	8.45E-01 QNVTSSGRGSAVAQDGDADVGEESTAPR +3 Methyl x 1 Phos	Methyl:2H(3)13C(1)
LmjF.32.2830	hypothetical protein, conserved	0.00	1.00E+00 QNVTSSGRGSAVAQDGDADVGEESTAPR +3 Methyl x 1	R8 Methyl:2H(3)13C(1)
LmjF.32.3090	hypothetical protein, conserved	-0.31	1.06E+00 SPALVTPSSASRGR +3 Methyl x 1	R14 Methyl
LmjF.32.3090	hypothetical protein, conserved	0.00	1.00E+00 AELPASGTSAPLGAARRGK +3 Methyl x 1	R19 Methyl:2H(3)13C(1)
LmjF.32.3690	hypothetical protein, conserved	6.81	8.57E-01 RGEVSGAGAAEGR +2 Methyl x 1	R1 Methyl:2H(3)13C(1)
LmjF.33.0260	RGG-containing protein 2, putative (RGG2)	-0.18	4.53E-01 DSSDHWGGRRGGHSGWGGDQKADPTGDR +4 Methyl x :	R10 Methyl:2H(3)13C(1)
LmjF.33.0260	RGG-containing protein 2, putative (RGG2)	-1.16	8.61E-01 RRRGGSGGVWGPAAEDAWNAAPPSPQPPVR +4 Methyl	#N/A
LmjF.33.0260	RGG-containing protein 2, putative (RGG2)	0.21	9.74E-01 DSSDHWGGRRGGHSGWGGDQKADPTGDR +3 Methyl x :	R10 Methyl:2H(3)13C(1)
LmjF.33.0260	RGG-containing protein 2, putative (RGG2)	-2.14	1.00E+00 GRGGSGGVWGPAAEDAWNAAPPSPQPPVR +3 Methyl x	R2 Methyl:2H(3)13C(1)
LmjF.33.0940	hypothetical protein, conserved	-1.17	1.00E+00 QASRRGGNVAAMSLTGSATNLR +3 Methyl x 1	R5 Methyl:2H(3)13C(1), M13
LmjF.33.1080	YEATS family, putative	0.14	8.08E-02 VQAGEVRGAPSPSPSR +3 Methyl x 1	Label:13C(1)2H(3)
LmjF.33.1150	pumilio protein 6, putative (PUF6)	-0.58	6.84E-01 FARGGGIGNPNSGR +2 Methyl x 1	#N/A
LmjF.33.1150	pumilio protein 6, putative (PUF6)	0.07	8.55E-01 GRRGAGGMSMESGSPNSHR +4 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.33.1150	pumilio protein 6, putative (PUF6)	-0.59	8.71E-01 FARGGGIGNPNSGR +3 Methyl x 1	R3 Methyl
LmjF.33.1150	pumilio protein 6, putative (PUF6)	-0.25	8.77E-01 GRRGAGGMSMESGSPNSHR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
LmjF.33.1150	pumilio protein 6, putative (PUF6)	-0.29	9.75E-01 RYNNNSAGGVGGGRVGR +3 Methyl x 1	R3 Methyl
LmjF.33.1150	pumilio protein 6, putative (PUF6)	0.29	1.00E+00 NNVRGGAGGMSMESGSPNSHR +4 Methyl x 2	R16 Methyl
				R4 Methyl, R7 Methyl

Lmjf.33.1220	hypothetical protein, conserved	-1.34	8.07E-01	EVVTTDNPDWASPLIARGGR +3 Methyl x 1	R20 Methyl
Lmjf.33.2130	hypothetical protein, conserved	0.76	1.00E+00	ESSGSGTRHGGGAGGGAASGGGHR +3 Methyl x 1	R8 Methyl:2H(3)13C(1)
Lmjf.33.2130	hypothetical protein, conserved	-0.07	1.04E+00	ESSGSGTRHGGGAGGGAASGGGHR +4 Methyl x 1	R8 Methyl:2H(3)13C(1)
Lmjf.33.2210	hypothetical protein, conserved	-1.36	1.04E+00	HLRGGAAAAR +3 Methyl x 1	R3 Methyl:2H(3)13C(1)
Lmjf.33.2360	ATP synthase regulation protein NCA2, putative	0.00	1.00E+00	GGVVGWCDFNANQSMFWSPIAAGVGRGR +3 Methyl x 1	R29 Methyl
Lmjf.33.2450	hypothetical protein, conserved	-0.51	8.50E-01	AGSVALGGGPNHAPPARGGGGGSGGR +3 Methyl x 1	R29 Methyl
Lmjf.33.2640	hypothetical protein, conserved	-0.44	6.45E-01	QAVSCACRAGYEHVWR +4 Methyl x 1	R10 Methyl
Lmjf.34.1110	Shwachman-Bodian-Diamond syndrome (SBDS) protein/SBDS protein C-terminal domain cont	0.82	1.00E+00	LGDPSPHLDQDDSDDDGRRGRSR +4 Methyl x 1 Phos x 1	S13 Phospho, R21 Methyl
Lmjf.34.1260	mitochondrial DNA polymerase I protein A, putative	0.33	8.34E-01	KRGGDAILPGLGALVSCATPAPR +4 Methyl x 1	R2 Methyl
Lmjf.34.1470	EAP30/Vps36 family, putative	-1.95	8.58E-01	VTTAGARGGSPAK +2 Methyl x 1	R7 Methyl:2H(3)13C(1)
Lmjf.34.2430	DNAJ-like protein	-0.38	4.75E-01	AGGFNSSTYSGGNANDYYRGR +3 Methyl x 1	R20 Methyl
Lmjf.34.2473	hypothetical protein, conserved	-0.15	1.80E-01	QSVAGRGGGGGGYGFY +2 Methyl x 1	R6 Methyl:2H(3)13C(1)
Lmjf.34.3815	ribosomal protein L14, putative	0.13	1.01E+00	FKRGGGGGEVSR +3 Methyl x 1	R4 Methyl:2H(3)13C(1)
Lmjf.34.4290	nucleolar protein family a, putative	2.10	7.26E-01	GGRGGGGFGGR +2 Methyl x 1	R3 Methyl
Lmjf.34.4290	nucleolar protein family a, putative	-5.12	8.20E-01	GGRGGGGFGGR +3 Methyl x 1	R3 Methyl
Lmjf.34.4290	nucleolar protein family a, putative	-0.65	1.00E+00	GGRRGGHMEPPPEVEVTFMNAEGLVYK +3 Methyl x	R4 Methyl
Lmjf.34.4290	nucleolar protein family a, putative	-4.18	1.00E+00	GGRRGGHMEPPPEVEVTFMNAEGLVYK +4 Methyl x	R4 Methyl
Lmjf.35.0610	hypothetical protein, conserved	0.00	1.00E+00	ANGPAPSGRSGK +2 Methyl x 1	R10 Methyl:2H(3)13C(1)
Lmjf.35.0630	Nucleoporin NUP65, putative	-0.90	8.30E-01	RGGLLESPQANVPDSADATESILR +3 Methyl x 1	R1 Methyl:2H(3)13C(1)
Lmjf.35.0630	Nucleoporin NUP65, putative	-0.00	1.00E+00	RRGGLLESPQANVPDSADATESILR +4 Methyl x 1	#N/A
Lmjf.35.0740	hypothetical protein, conserved	0.01	9.26E-01	ARGGGASGTSGLGTAK +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
Lmjf.35.0740	hypothetical protein, conserved	0.43	1.07E+00	ARGGGASGTSGLGTAK +3 Methyl x 1	R2 Methyl:2H(3)13C(1)
Lmjf.35.1510	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	0.26	7.31E-02	RANNSNDHQHRRGGAR +3 Methyl x 1	#N/A
Lmjf.35.1510	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	-2.24	4.74E-01	RANNSNDHQHRRGGAR +4 Methyl x 1	#N/A
Lmjf.35.1620	Concanavalin A-like lectin/glucanases superfamily, putative	0.37	8.46E-01	NNGSSNRNQHVASSITIGASSAAR +3 Methyl x 2 Phos x 1	#N/A
Lmjf.35.2090	kinesin, putative	0.44	5.68E-02	RRGGPSAAQAQLEWEMPFQGTVFR +3 Methyl x 1	R1 Methyl
Lmjf.35.2200	RNA-binding protein, putative	2.45	8.29E-01	HNMGASAYGR +2 Methyl x 1	M3 Oxidation, R10 Methyl, M24 Oxidation
Lmjf.35.2200	RNA-binding protein, putative	10.97	1.00E+00	HNMGASAYGRGAPYQVGAESTEMNGTEPLPKPR +4 Methyl x	M3 Oxidation, R10 Methyl, M24 Oxidation
Lmjf.35.2200	RNA-binding protein, putative	0.00	1.00E+00	HNMGASAYGRGAPYQVGAESTEMNGTEPLPKPR +3 Methyl x	M3 Oxidation, R10 Methyl, M24 Oxidation
Lmjf.35.3100	ATP-dependent RNA helicase, putative (DED1)	0.03	8.06E-02	SGGPGRRGGGGGGGSDRSPASGGGR +4 Methyl x 1	R7 Methyl
Lmjf.35.3100	ATP-dependent RNA helicase, putative (DED1)	0.14	6.16E-01	SGGPGRRGGGGGGGSDRSPASGGGR +3 Methyl x 1	R7 Methyl
Lmjf.35.3100	ATP-dependent RNA helicase, putative (DED1)	0.22	8.48E-01	RRGGGGGGGGHHR +3 Methyl x 3	#N/A
Lmjf.35.3100	ATP-dependent RNA helicase, putative (DED1)	0.00	1.00E+00	RYDDDEDYEGGDRAGGTGNETDDYEDGGYDAYR +4 Methyl	R1 Methyl
Lmjf.35.3100	ATP-dependent RNA helicase, putative (DED1)	-0.36	1.03E+00	RRGGVDDGGF +2 Methyl x 1	R1 Methyl:2H(3)13C(1)
Lmjf.35.3310	Leucine Rich repeats (2 copies), putative	-1.13	1.00E+00	KATSSVSGFGGNNVNRGGSGASGNPTIHK +4 Methyl x 1	R17 Methyl:2H(3)13C(1)
Lmjf.35.3310	Leucine Rich repeats (2 copies), putative	-0.97	8.21E-01	ATSSVSGFGGNNVNRGGSGASGNPTIHK +3 Methyl x 1	R17 Methyl:2H(3)13C(1)
Lmjf.35.3310	Leucine Rich repeats (2 copies), putative	0.63	2.82E-01	ATSSVSGFGGNNVNRGGSGASGNPTIHK +4 Methyl x 1	R17 Methyl:2H(3)13C(1)
Lmjf.35.3310	Leucine Rich repeats (2 copies), putative	-0.13	2.14E-01	KATSSVSGFGGNNVNRGGSGASGNPTIHK +4 Methyl x 1 Phos	#N/A
Lmjf.35.3980	4E-interacting protein, putative	0.48	2.09E-01	RRGGGGGGGRDSSNSNSVR +4 Methyl x 1	R1 Methyl, S15 Phospho
Lmjf.35.3980	4E-interacting protein, putative	1.47	2.15E-01	GGHNSMGNGSSNSNSVRSSSTPYVSGGGRRGDNR +4 Meth	M7 Oxidation, R13 Methyl
Lmjf.35.3980	4E-interacting protein, putative	-0.23	8.05E-01	RRGGGGGGGRDSSNSNSVR +3 Methyl x 1	R1 Methyl, S15 Phospho
Lmjf.35.3980	4E-interacting protein, putative	-0.11	8.42E-01	QGRGVGTGNGMSTVPPSPQFQPPPPR +3 Methyl x 1	R3 Methyl
Lmjf.35.3980	4E-interacting protein, putative	10.97	1.00E+00	GGHNSMGNGSSNSNSVRSSSTPYVSGGGRRGDNR +5 Met	Methyl:2H(3)13C(1), R37
Lmjf.35.4125	hypothetical protein, conserved	-0.26	3.75E-01	SARGGASNGHSPASACTATR +3 Methyl x 1	R4 Methyl
Lmjf.35.4140	hypothetical protein, unknown function	2.02	1.00E+00	ERGGFSAR +2 Methyl x 1	R2 Methyl:2H(3)13C(1)
Lmjf.35.4380	hypothetical protein, conserved	0.00	1.00E+00	GGRGGAPQGLSTPLNTR +3 Methyl x 1	#N/A
Lmjf.35.4950	zinc finger protein family member, putative	-0.42	3.85E-01	SPPATSASTSPAPPRLGLGR +3 Methyl x 1	R22 Methyl:2H(3)13C(1)
Lmjf.35.4950	zinc finger protein family member, putative	0.27	4.72E-01	LSSMERGGMTGVPQHLLPR +4 Methyl x 1	R6 Methyl
Lmjf.35.4950	zinc finger protein family member, putative	0.65	8.14E-01	GAQQHHGVRGVEGNGSSR +3 Methyl x 1	#N/A
Lmjf.35.4950	zinc finger protein family member, putative	-4.78	8.52E-01	SPPATSASTSPAPPRL +2 Methyl x 1	R18 Methyl:2H(3)13C(1)
Lmjf.35.4950	zinc finger protein family member, putative	-1.07	8.56E-01	LSSMERGGMTGVPQHLLPR +4 Methyl x 2	R6 Methyl
Lmjf.35.4950	zinc finger protein family member, putative	0.70	1.00E+00	GTEGVGNSYRGAQHHGYR +4 Methyl x 1	#N/A
Lmjf.35.4950	zinc finger protein family member, putative	-0.65	1.00E+00	GATVTVGGHDSVVRGGAAPMSMGAGAASR +4 Methyl x 1	R17 Methyl
Lmjf.35.4950	zinc finger protein family member, putative	-0.25	1.03E+00	LSSMERGGMTGVPQHLLPRASPPASQR +4 Methyl x 1 Phos	#N/A
Lmjf.35.4950	zinc finger protein family member, putative	-0.05	1.03E+00	LSSMERGGMTGVPQHLLPR +3 Methyl x 1	R6 Methyl
Lmjf.35.5040	polyadenylate-binding protein 1 (PABP1)	10.97	1.00E+00	QLLGGRAQGHMPMPSPQQAQAQPAQGFATPSAVFVQATP	R6 Methyl
Lmjf.36.0450	hypothetical protein, conserved	0.53	9.34E-01	SFTSAGIGEGGAGRRGAR +3 Methyl x 1	R16 Methyl
Lmjf.36.0490	zinc-finger of a C2HC-type, putative	-0.41	4.17E-01	GPARGGLGATPSYGGDAGMSAR +3 Methyl x 1	R4 Methyl:2H(3)13C(1), M21
Lmjf.36.0490	zinc-finger of a C2HC-type, putative	-0.56	6.04E-01	GPARGGLGATPSYGGDAGMSAR +3 Methyl x 1 Phos x 1	Label:13C(1)2H(3)-Oxidation
Lmjf.36.0490	zinc-finger of a C2HC-type, putative	-0.56	8.08E-01	FSSRGGGGMMGGGGGGGR +3 Methyl x 1	R4 Methyl:2H(3)13C(1), M21
Lmjf.36.1240	hypothetical protein, conserved	-1.38	1.07E+00	VSPVPTPLPRGR +3 Methyl x 1	Label:13C(1)2H(3)-Oxidation
Lmjf.36.1640	universal minicircle sequence binding protein, putative	0.73	1.22E-01	CGQEGHLSRDCPSQGSRRGGYQK +3 Methyl x 1	R19 Methyl
Lmjf.36.1640	universal minicircle sequence binding protein, putative	-0.15	8.55E-01	DCPSQGSRRGGYQK +4 Methyl x 1	R10 Methyl:2H(3)13C(1)
Lmjf.36.1640	universal minicircle sequence binding protein, putative	-0.25	8.81E-01	DCPSQGSRRGGYQK +3 Methyl x 1	R10 Methyl:2H(3)13C(1)
Lmjf.36.1640	universal minicircle sequence binding protein, putative	-0.28	9.26E-01	DCPSQGSRRGGYQK +2 Methyl x 1	R10 Methyl:2H(3)13C(1)
Lmjf.36.1640	universal minicircle sequence binding protein, putative	-0.26	1.01E+00	DCPSQGSRRGGYQK +3 Methyl x 1	R10 Methyl:2H(3)13C(1)
Lmjf.36.1925	60S ribosomal protein L37a	-0.19	1.08E+00	TVAGGAYLSTPNNTVTR +2 Methyl x 1	#N/A
Lmjf.36.2130	ATP-dependent RNA helicase DBP2A, putative	-0.68	2.91E-01	NYSFSGFSTSRGGGGGAHR +3 Methyl x 1	R13 Methyl:2H(3)13C(1)
Lmjf.36.2130	ATP-dependent RNA helicase DBP2A, putative	0.58	8.50E-01	NYSFSGFSTSR +2 Methyl x 1	#N/A
Lmjf.36.2130	ATP-dependent RNA helicase DBP2A, putative	-0.02	1.06E+00	NYSFSGFSTSRGGGGGAHR +4 Methyl x 1	R13 Methyl:2H(3)13C(1)
Lmjf.36.2580	related to multifunctional cyclin-dependent kinase pho85-like protein	0.67	8.90E-01	VMRGSSSSQNDMCGSSAR +3 Methyl x 1	R3 Methyl
Lmjf.36.2670	hypothetical protein, conserved	-2.47	1.04E+00	IATRRGGGQPEGVVR +3 Methyl x 1	R4 Methyl
Lmjf.36.3200	DNA topoisomerase III, putative	0.00	1.00E+00	GRRGGDAAAATPSGGVDPVCGCGTPAK +3 Methyl x 1	#N/A
Lmjf.36.3280	Enoyl-CoA hydratase/isomerase family/2-enoyl-CoA Hydratase C-terminal region, putative	0.19	1.00E+00	WFIQGHNPNSGLLR +3 Methyl x 1	#N/A
Lmjf.36.3280	Enoyl-CoA hydratase/isomerase family/2-enoyl-CoA Hydratase C-terminal region, putative	0.27	1.00E+00	WFIQGHNPNSGLLR +4 Methyl x 1	#N/A
Lmjf.36.4330	predicted C2 domain protein	10.97	1.00E+00	YECDHVGTTEAPPAGRRGSHGR +3 Methyl x 1	#N/A
Lmjf.36.4590	PHD-like zinc-binding domain containing protein, putative	-0.91	1.05E+00	NSGGGTDSDALSSPTARGGAVGGGHR +4 Methyl x 1	R31 Methyl:2H(3)13C(1)
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-0.86	2.61E-01	GGYPTPPQQQLQQQYASRGGYGGGAYGAGIQQYYPG	R21 Methyl
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-0.85	4.72E-01	GYPPODGMQYPPQAGR +2 Methyl x 1	M8 Label:13C(1)2H(3), R17
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-0.26	5.02E-01	GYSAQYNSYAAR +2 Methyl x 1	Label:13C(1)2H(3)13C(1)
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-0.83	8.03E-01	GYSAQYNSYAARGYPTPPQQQLQQQYASR +4 Methyl x	R13 Methyl
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	0.46	8.50E-01	GYSAQYNSYAARGYPTPPQQQLQQQYASR +3 Methyl x	R13 Methyl:2H(3)13C(1)
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-0.39	1.00E+00	GGYPTPPQQQLQQQYASRGGYGGGAYGAGIQQYYPG	R21 Methyl
Lmjf.36.5100	hypothetical protein, conserved (PUF11)	-1.32	1.02E+00	GGYGPYGPYVQQQQGYNQYQNPNTYPAAR +3 Meth	R36 Methyl:2H(3)13C(1)
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-3.12	1.00E+00	TRGSGVNGATAPFR +2 Methyl x 2 Phos x 1	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-2.21	8.03E-01	TRGSGVNGATAPFR +3 Methyl x 2	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-1.72	8.15E-01	TRGSGVNGATAPFR +2 Methyl x 1	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-0.84	8.47E-01	TRGSGVNGATAPFR +2 Methyl x 1 Phos x 1	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-0.72	8.61E-01	TRGSGVNGATAPFR +3 Methyl x 1 Phos x 1	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-0.43	2.80E-01	TRGSGVNGATAPFR +3 Methyl x 1	R2 Methyl
Lmjf.36.5850	flagellum targeting protein kharon1, putative	-0.35	5.67E-01	ASHLNLMYASGDYAVASRGGASR +4 Methyl x 1	R20 Methyl
Lmjf.36.6030	hypothetical protein, conserved	-3.27	8.49E-01	FRGMR +2 Methyl x 1	#N/A
Lmjf.36.6060	eukaryotic translation initiation factor 4 gamma 4	-0.09	1.18E-01	GPIHSSNAGNRRGTRPPSMADR +4 Methyl x 1	#N/A
Lmjf.36.6060	eukaryotic translation initiation factor 4 gamma 4	0.23	1.09E+00	YRGGGPGGLR +2 Methyl x 1	R3 Methyl:2H(3)13C(1)
Lmjf.36.6525	hypothetical protein, conserved	0.13	1.00E+00	SRGGAFVSVFASHDR +4 Methyl x 1	R2 Methyl
Lmjf.36.6980	eukaryotic translation initiation factor 3 subunit c	-2.11	4.70E-01	GRGGMAGRRGAGVR +3 Methyl x 2	R2 Methyl, R9 Methyl
Lmjf.36.6980	eukaryotic translation initiation factor 3 subunit c	10.97	1.00E+00	GRGGMAGRR +2 Methyl x 2	R2 Methyl:2H(3)13C(1), M5 Label:13C(1)2H(3)

\*some peptides have the same sequence but different charges or additional post-translational modifications (e.g. Phosphorylation)

Localization score of PTMs was not possible to calculate for some peptides identified by the Proteome Discoverer software

red values: hypomethylated in  $\Delta$ prmt7,  $\log_2(WT/\Delta T) > 0.6$ ; q-value < 0.05

blue values: hypermethylated in  $\Delta$ prmt7,  $\log_2(WT/\Delta T) < -0.6$ ; q-value < 0.05



LmjF33.0280	RGG-containing protein 2, putative (RGG2)	0.21	9.74E-01	RGRGGGGVWGPAAADEAWNAAPSFQPPVR +4 Methyl x 1
LmjF33.0280	RGG-containing protein 2, putative (RGG2)	-2.14	1.00E+00	GRGGGGVWGPAAADEAWNAAPSFQPPVR +3 Methyl x 1
LmjF33.1150	pumilio protein 6, putative (PUF6)	-0.58	6.84E-01	NNVRRGGGAGGMSGSGPNSHR +4 Methyl x 2
LmjF33.1150	pumilio protein 6, putative (PUF6)	0.07	8.65E-01	GRRGAGGMSGSGPNSHR +4 Methyl x 1
LmjF33.1150	pumilio protein 6, putative (PUF6)	-0.59	8.71E-01	GRRGAGGMSGSGPNSHR +3 Methyl x 1
LmjF33.1150	pumilio protein 6, putative (PUF6)	-0.25	8.77E-01	RNNNSAGGVGGGRGR +3 Methyl x 1
LmjF33.1150	pumilio protein 6, putative (PUF6)	-0.29	9.75E-01	FARRGGGINNSGR +2 Methyl x 1
LmjF33.1150	pumilio protein 6, putative (PUF6)	0.29	1.00E+00	FARRGGGINNSGR +3 Methyl x 1
LmjF34.1110	Shwachman-Bodian-Diamond syndrome (SBDS) protein/SBDS protein C-terminal domain contai	0.82	1.00E+00	LGLDPSHLDDDDDDGGGRGRGR +4 Methyl x 1 Phos x 1
LmjF34.3515	ribosomal protein L14, putative	0.31	1.01E+00	FKGRGGGGVSR +3 Methyl x 1
LmjF34.4290	nucleolar protein family a, putative	2.10	7.26E-01	GRRGGGGVGGGR +2 Methyl x 1
LmjF34.4290	nucleolar protein family a, putative	-5.12	8.20E-01	GGRGGHMSPEPPENVEVGTFMNAEGLVYK +3 Methyl x 1
LmjF34.4290	nucleolar protein family a, putative	-0.65	1.00E+00	GGRGGHMSPEPPENVEVGTFMNAEGLVYK +4 Methyl x 1
LmjF34.4290	nucleolar protein family a, putative	-4.18	1.00E+00	GRRGGGGVGGGR +3 Methyl x 1
LmjF35.0630	Nucleoporin NUP65, putative	-0.90	8.30E-01	RRGLLESQANVPSADATESILR +4 Methyl x 1
LmjF35.0630	Nucleoporin NUP65, putative	0.00	1.00E+00	RRGLLESQANVPSADATESILR +3 Methyl x 1
LmjF35.1510	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	0.26	7.31E-02	RANNSNDHQRGGGR +4 Methyl x 1
LmjF35.1510	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	2.24	4.74E-01	RANNSNDHQRGGGR +3 Methyl x 1
LmjF35.2200	RNA-binding protein, putative (DRB2)	2.45	8.29E-01	HNMAAGYRGAPYVGAESTEMNGTEPLPKPR +4 Methyl x 1
LmjF35.2200	RNA-binding protein, putative (DRB2)	10.97	1.00E+00	HNMAAGYRGAPYVGAESTEMNGTEPLPKPR +3 Methyl x 1
LmjF35.2200	RNA-binding protein, putative (DRB2)	0.00	1.00E+00	HNMAAGYRGAPYVGAESTEMNGTEPLPKPR +3 Methyl x 1 Phos x 1
LmjF35.3100	ATP-dependent RNA helicase, putative (DED1)	0.03	8.08E-02	RRGGGGGGGGGR +3 Methyl x 3
LmjF35.3100	ATP-dependent RNA helicase, putative (DED1)	0.14	6.18E-01	SGPGGRGGGGGGGSDRSPAPSGGR +3 Methyl x 1
LmjF35.3100	ATP-dependent RNA helicase, putative (DED1)	0.22	8.48E-01	SGPGGRGGGGGGGSDRSPAPSGGR +4 Methyl x 1
LmjF35.3100	ATP-dependent RNA helicase, putative (DED1)	0.00	1.00E+00	RYVDEDDYEGGDRAGTGNEDDDYEDGGYDAYR +4 Methyl x 1
LmjF35.3100	ATP-dependent RNA helicase, putative (DED1)	-0.36	1.03E+00	RRGGVDDGGF +2 Methyl x 1
LmjF35.3980	4E-interacting protein, putative	0.48	2.09E-01	GGHNSGNGGSSNHPGSSTPVYSGGGRRGDNR +5 Methyl x 1
LmjF35.3980	4E-interacting protein, putative	1.47	2.15E-01	GGHNSGNGGSSNHPGSSTPVYSGGGRRGDNR +4 Methyl x 1
LmjF35.3980	4E-interacting protein, putative	-0.23	8.05E-01	RRGGGGGNGRRDSSNSVR +4 Methyl x 1
LmjF35.3980	4E-interacting protein, putative	-0.11	8.42E-01	GGRVGTGNGMSTVPPSPQFQPPPPR +3 Methyl x 1
LmjF35.3980	4E-interacting protein, putative	10.97	1.00E+00	RRGGGGGNGRRDSSNSVR +3 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	-0.42	3.85E-01	GTEGVNSYRGAQGHYGR +4 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	0.27	4.72E-01	GAQQHHYRGVGGSSR +3 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	0.65	8.14E-01	LSSMERGMTVGPQHLLPPR +4 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	-4.78	8.52E-01	LSSMERGMTVGPQHLLPPR +3 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	-1.07	8.56E-01	LSSMERGMTVGPQHLLPPR +4 Methyl x 1 Phos x 1
LmjF35.4950	zinc finger protein family member, putative	0.70	1.00E+00	SPPATSASTSAPPALRLGR +3 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	-0.65	1.00E+00	GATVTVGVIDSSVGRGGAAPMSGMGAASR +4 Methyl x 1
LmjF35.4950	zinc finger protein family member, putative	-0.25	1.03E+00	LSSMERGMTVGPQHLLPPR +4 Methyl x 2
LmjF35.4950	zinc finger protein family member, putative	-0.05	1.03E+00	SPPATSASTSAPPALRL +2 Methyl x 1
LmjF35.5040	polyadenylate-binding protein 1 (PABP1)	10.97	1.00E+00	QLLGRAGHPMPSPQOPQAPQGFATPSAVGFVQATPK +4 Methyl x 1
LmjF36.0490	zinc-finger of a C2HC-type, putative	-0.41	4.17E-01	GPARGGLFATPSGYGDGAGMSAR +3 Methyl x 1
LmjF36.0490	zinc-finger of a C2HC-type, putative	-0.56	6.04E-01	GPARGGLFATPSGYGDGAGMSAR +3 Methyl x 1 Phos x 1
LmjF36.0490	zinc-finger of a C2HC-type, putative	-0.56	8.08E-01	FSSRGGGGGGGGGGGR +3 Methyl x 1
LmjF36.1640	universal minicircle sequence binding protein, putative	0.73	1.22E-01	CGQEGHLSRDCSSQGGRRGQK +3 Methyl x 1
LmjF36.1640	universal minicircle sequence binding protein, putative	-0.15	8.55E-01	DCPSSQGGRRGQK +4 Methyl x 1
LmjF36.1640	universal minicircle sequence binding protein, putative	-0.25	8.51E-01	DCPSSQGGRRGQK +3 Methyl x 1
LmjF36.1640	universal minicircle sequence binding protein, putative	-0.28	9.26E-01	DCPSSQGGRRGQK +3 Methyl x 1
LmjF36.1640	universal minicircle sequence binding protein, putative	-0.26	1.01E+00	DCPSSQGGRRGQK +2 Methyl x 1
LmjF36.1925	60S ribosomal protein L37a	-0.19	1.08E+00	TVAGGYLSTFNNSTR +2 Methyl x 1
LmjF36.2130	ATP-dependent RNA helicase DBP2A, putative	-0.88	2.81E-01	NYSFSGSTTSRGGGSAHR +4 Methyl x 1
LmjF36.2130	ATP-dependent RNA helicase DBP2A, putative	-0.08	8.50E-01	NYSFSGSTTSR +2 Methyl x 1
LmjF36.2130	ATP-dependent RNA helicase DBP2A, putative	0.52	1.08E+00	NYSFSGSTTSRGGGSAHR +3 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-0.86	2.61E-01	GYSDAYNGSYAARGGYQTPPQQQAQLQGGYASR +3 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-0.85	4.72E-01	GYSDAYNGSYAARGGYQTPPQQQAQLQGGYASR +2 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-0.26	5.02E-01	GGYQTPPQQQAQLQGGYASRGGYQGGGAYGGAGIOQGYPGAAPISR +5 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-0.83	8.03E-01	GYSDAYNGSYAARGGYQTPPQQQAQLQGGYASR +4 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	0.46	8.50E-01	GYPPQDGMGYQDAGR +2 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-0.39	1.08E+00	GGYQTPPQQQAQLQGGYASRGGYQGGGAYGGAGIOQGYPGAAPISR +4 Methyl x 1
LmjF36.5100	hypothetical protein, conserved (PUF11)	-1.32	1.02E+00	GGYQTPPQQQAQLQGGYASRGGYQGGGAYGGAGIOQGYPGAAPISR +3 Methyl x 1
LmjF36.6060	eukaryotic translation initiation factor 4 gamma 4	-0.09	1.18E-01	YRGGGPGCLR +2 Methyl x 1
LmjF36.6060	eukaryotic translation initiation factor 4 gamma 4	0.23	1.09E+00	GRHSSNAGNRRGSTRPPSMADR +4 Methyl x 1
LmjF36.6080	eukaryotic translation initiation factor 3 subunit c	-2.11	4.70E-01	GRGGMAGGR +2 Methyl x 2
LmjF36.6080	eukaryotic translation initiation factor 3 subunit c	10.97	1.00E+00	GRGGMAGGRGAGVR +3 Methyl x 2

\*some peptides have the same sequence but different charges or additional post-translational modifications (e.g. Phosphorylation)  
 Socalization score of PTMs was not possible to calculate for some peptides identified by the Proteome Discoverer software

red values: hypomethylated in  $\Delta$ prmt7,  $\log_2(WT/\Delta) > 0.6$ ; q-value < 0.05  
 blue values: hypermethylated in  $\Delta$ prmt7,  $\log_2(WT/\Delta) < -0.6$ ; q-value < 0.05

**Supplemental Table S3.** List of oligonucleotides used in this study for PCR or qRT-PCR.

Oligo	Oligo sequence	Strategy
914.RT-NIMA-R	GCA CAA TCT GGT AGA AGA GA	RIP-qRT-PCR
913.RT-NIMA-F	GAC AAG CTG TTG CTT ATT AT	RIP-qRT-PCR
910.RT-p1s1-301530-R	CCA TCG CGT CAA GCT TTT CC	RIP-qRT-PCR
909.RT-p1s1-301530-F	TGT GCG TGA CTG AGG TTC TC	RIP-qRT-PCR
908.RT-GAPDHcyto-R	TGT CAT GAG GCC CTC GAC TA	RIP-qRT-PCR
907.RT-GAPDHcyto-F	ACG GGC AGC CCA TTA TAT CG	RIP-qRT-PCR
906.RT-amastin340500-R	ACC TTC TCT CCA TGC TGT GC	RIP-qRT-PCR
905.RT-amastin340500-F	TGC CAG AAC AGA GGG CTT TC	RIP-qRT-PCR
B3-18S-2	TCC TTG AAG AAT GCC TTC GC	RIP-qRT-PCR
F3-18S-2	AAC CTC GGT TCG GTG TGT	RIP-qRT-PCR
Lmex NMT qPCR For	GCCAAAGACGGTGGCCGATA	RIP-qRT-PCR
Lmex NMT qPCR Rev	GGCGTCCACCACTCAAATGT	RIP-qRT-PCR
800.5FLR-Alba20-F	ACA TCC TTC CTG TTC CCC CA	Confirm HA-Alba3 integration
787.3FLR-CCCH0740-R	GCC GGT AGA CCC TCT TCC AT	Confirm HA-Torus integration
786.3FLR-Alba20-R	AAA TAG CCA GCC CCT CCC C	Confirm HA-Alba3 integration
784.3FLR-HEL67-R	ACG TGT TCC CTC CTG CCT TA	Confirm HA-DDX3 integration
783.3FLR-RBP16-R	GCC CTC TCA CTC GTC CTC TT	Confirm HA-RBP16 integration
799.Alba20-HindIII-R	TGA AAG CTT CTA GTT CTC GCG GTC ATC HA-tagging - Alba3	
798.Alba20-noATG-NheI-BamHI-F	TGA GCT AGC GGA TCC CCT CCA CGT CCC HA-tagging - Alba3	
5'FLR-CCCH0740-SfiIA-F	TGA GGCCACCTAGGCC GTTCGACGTAGCC HA-tagging - Torus	
5'FLR-CCCH0740-SfiIB-R	TGA GGCCACGCAGGCC CGTCGTCTTCGTT HA-tagging - Torus	
CCCH0740-noATG-SfiIC-F	TGA GGCCGCTGGGGCC TTCCCCATGGAT HA-tagging - Torus	
821.CCCH0740-SfiID-OK-R	TGA GGC CTG ACT GGC CCT ACT CGA TCC HA-tagging - Torus	
5'FLR-Hel67-SfiIA-F	TGA GGCCACCTAGGCC GGGGAGGAAAAA HA-tagging - DDX3	
5'FLR-Hel67-SfiIB-R	TGA GGCCACGCAGGCC GATTCGTGCTTAC HA-tagging - DDX3	
Hel67-noATG-SfiIC-F	TGA GGCCGCTGGGGCC TATAAGAATCAG HA-tagging - DDX3	
Hel67-SfiID-R	TGA GGCTCAGTGGCC CTA CTGACCAAAC HA-tagging - DDX3	
5'FLR-RBP16-SfiIA-F	TGA GGCCACCTAGGCC CATTCTCTCGGT HA-tagging - RBP16	
5'FLR-RBP16-SfiIB-R	TGA GGCCACGCAGGCC GACTGCTTGAAA HA-tagging - RBP16	
RBP16-noATG-SfiIC-F	TGA GGCCGCTGGGGCC TTCCGTGTTTCCT HA-tagging - RBP16	
RBP16-SfiID-R	TGA GGCTCAGTGGCC CTAGAACTCATCG HA-tagging - RBP16	