APPENDIX

Control of NAD⁺ homeostasis by autophagic flux modulates cardiac function

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Appendix Figure S1. cAtg3-KO does not alter autophagic flux in non-cardiomyocyte tissues and does not influence MTOR and AMPK signaling in hearts, Related to Figure 1.

- A Protein levels of ATG3, LC3 (MAP1LC3A), SQSTM1, and GAPDH in liver, skeletal muscle, white adipose tissue, and kidney of WT and cAtg3-KO mice. Representative blots are shown, n=2 per group.
- B Quantification of MTOR S2448 and AMPK α T172 phosphorylation. Mice were randomly fed. n=6 per group. Data are mean \pm SEM.



Appendix Figure S2. cAtg3-KO does not alter protein expression of NADK, NAMPT or NAMNAT1-3 in hearts, Related to Figure 5.

Protein levels of NADK, NAMPT, and NAMNAT1-3, TUBA4A (alpha-tubulin) in WT and cAtg3 KO mouse hearts. Mice were randomly fed, n=4 to 5 per group. Data are mean \pm SEM. Representative section images are shown.



Appendix Figure S3. cAtg3-KO inhibited Sirt1 activities and increased protein acetylation in hearts, Related to Figure 5.

- A Protein levels of SIRT1 to 7 and GAPDH in WT and cAtg3 KO mouse hearts. Mice were randomly fed, n=4 to 5 per group. Data are mean ± SEM.
- B SIRT1 enzymatic activity measurement in 4-week-old WT and Atg3 KO mouse hearts, without or with the addition of 10 mM exogenous NAD⁺, n=4 to 6 per group. Data are mean±SEM. Unpaired t-tests were used to determine statistical significance between two groups. *p<0.05.</p>
- C Levels of Ac-lysine and TUBA4A (alpha-tubulin) in 4-week-old WT and cAtg3 KO mouse hearts. Mice were randomly fed, n=3 per group. Data are mean ± SEM. An unpaired t-test was used to determine statistical significance between two groups. *p<0.05.
- D Protein levels of Ac-FOXO1, FOXO1, and TUBA4A in 4-week-old WT and cAtg3 KO mouse hearts. Mice were randomly fed, n=3 per group. Data are mean ± SEM. An unpaired t-test was used to determine statistical significance between two groups. **p<0.01.
- E Ac-FOXO1 expression levels in hearts from mice that were injected with PBS or NMN, n=3 to 6 per group. Data are mean ± SEM. One-way ANOVA followed by Bonferroni's multiple comparison tests was used to determine statistical significance. *p<0.05.



Appendix Figure S4. cAtg3-KO does not alter PARP1/2 protein expression, PARP1/2 activities, or abundance of CD38 and BST1 (CD157) in hearts, Related to Figure 5.

- A PARP1/2 protein expression in 4-week-old WT and cAtg3 KO mouse hearts, n=4 to 5 per group. Data are mean ± SEM.
- B PARP1/2 enzymatic activity measurement in 4-week-old WT and cAtg3 KO mouse hearts, n=5 per group. Data are mean ± SEM.
- C Abundance of PAR in 16-week-old WT and cAtg3 KO mouse hearts, n=4 per group. Data are mean \pm SEM.
- D Protein levels of CD38 and BST1, and GAPDH in WT and cAtg3 KO mouse hearts. Mice were randomly fed, n-4 to 5 per group. Data are mean ± SEM. An unpaired t-test was used to determine statistical significance between two groups. *p<0.05. Representative section images are shown.</p>



Appendix Figure S5. Oxygen consumption in response to increasing concentrations of Me-NAM in H9c2 cardiomyocytes, Related to Figure 6.

Oxygen consumption rate (OCR) in H9c2 cells treated with PBS (Veh) or concentrations of MeNAM as indicated, n=3 to 4 per group. Data are mean \pm SEM. Step 1 to 4: 20 µM glucose medium, step 5 to 7: oligomycin (1µg/ml), step 8 to 10: FCCP (0.5µg/ml), step 11 to 13: rotenone (1µg/ml).



Appendix Figure S6. Autophagosomes do not engulf NNMT protein or mRNA in H9c2 cardiomyocytes, Related to Figure 7. H9c2 cardiomyocytes were first transfected with adenovirus encoding either GFP or GFPtagged LC3 (MAP1LC3A), and then cells encoding GFP-LC3 were treated with either vehicle (Veh) or chloroquine (CQ) at 20 uM for 16 h. under nutrient replete conditions.

- A The protein levels of ULK1, SQSTM1, GFP, GFP-LC3, LC3, NNMT, and GAPDH in isolated autophagosomes. GFP-LC3 were probed with antibodies against GFP and LC3, and the images of immunoblots were acquired using LI-COR Odyssey DXL system at two independent laser channels, respectively. Therefore, GFP antibody detects GFP and GFP-LC3, and LC3 antibody detects GFP-LC3 only. The experiments were repeated three times. Representative blots are shown. NC indicates the separation buffer with GFP antibody. Input is cytosolic fractions.
- B *NNMT* mRNA levels in isolated autophagosomes. n=3 per group. Data are mean±SEM.

Sex	Genotype	Ν.	%
N/	WT	89	25.72
IVI	cAtg3 KO	85	24.57
	WT	81	23.41
Г	cAtg3 KO	91	26.30

Table S1. Percentage of cAtg3 KO mice

Table S2. Primer Sequences

GAPDH (M)GCAACAATCTCCACTTTGCCAC AATGGTGAAGGTCGGTCGACTGCAC GCTCTCTGCTCCCCTGTTC GAGGCTGGCACTGCACAAGAPDH (R)GCTCTCTGCTCTCCCCTGTTC GAGGCTGGCACTGCACAARP16STCTTTGATCTCCTTCTTAGAACTB (M)TGGATGCCCAGGGATTCCAACTB (R)GAGACCTTCAACACCCCAGCC TCGGGGCATCGGAACCGCTCARPL13A (M)CCCCCTATGACAGGAACAGTTC18S (R)CTTCTGGCCTTATGACAACCGTTT18S (R)CCTTCCTGGTCCTTCCCATCA CCTTCGCTCTGGACAGGTGAAATCTTA18S (R)CCTCTCTGGACAGGGCAAAGGCAAAGCC ACTBCTCCTGAAGGTGCGTCCTTC18S (R)CCTCCTGGACAGGTGCAGTTCC CCTGCTCCTGAGGCGTGCCGTCCTNPPA (M)CCAGCCTCAGAGGTGCTGTT CCCATCAGGCTGGCTGTTNPPA (M)CCCATCATGCACTTGGAAAC CCCATCAGGCTGGCTGTNPPB (M)TTCTTTTGTGAGGCCTTGGT TCTTTTGTGAGGCCTTGGTPLN (M)CCAAGCTGAGACACGATGGA CCCAGCTAAGGTGAAAGCGATGAT CCCAGCTAAGCTCCCATAAGNNMT (R)GAATGCAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Gene	Sequences		
GAPDH (M)AATGGTGAAGGTCGGTGTGAACGAPDH (R)GCTCTCTGCTCCTCCCTGTTCGAPTH6STCTTTGATCTCCTTCTTAGARP16STCTTTGATCTCCTTCTTAGAACTB (M)TGGATGCCACAGGATTCCAACTB (R)CGAGACCTTCAACACCCCAGCCCCGAGGCATCGGAACCGGCTCACTCTGGCCTTTCCTTTTGRPL13A (M)CTCTGGCCTTTCCCTTTTGRPL13A (R)CCCACCCTATGACAACACCGGTCARPL13A (R)CCCACCCTATGACAAGAAAAAGCACTB (R)CCCACCCTATGACAAGAAAAAAGCACTB (R)CCCACCCTATGACAAGAAAAAAGCRPL13A (R)CCCCTCTGGCCGTCTTRNU6-1 (R)GCCACTAGGGTGAAATTCTTA18S (R)CCTGCTTCCTCAGTCGGTCCNPPA (M)CCTGCTTCCTCAGTCGTGCTCNPPA (M)CCGTCCTCCTCAGGCTGCTNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACATTGGAACCCCCAGGCTAGGCTGAGGTGGATAACAGGCAGCCAAATGTGAMVHT (R)GCAGCCTGAGAGACACGATGGANNMT (R)GCAGCCGAGAGAGAGAGCGATGATNNMT (M)GAACCAGGAGCCAACGATGGANRF1 (M)CTTCAGAACTGCCAACCACANRF2 (M)TCTGCCATGGGGAGAAGTTNMNAT1 (M)GCAAAGGATGATTCGGCTCNMNAT2 (M)CAGAGCACCACAGGGAAGTNMAPT (M)CCAGAGCCCACAGGGATTCNMAPT (M)CCGAGAGCCACACAGGGATTCNMAPT (M)CCGCCCATTCAAACATNMAPT (M)CCGCCCAGGCCTTACCACANMAPT (M)CCGCCCAGGCCACACGGGATTCNMAPT (M)CCGCCCAGGCCACACAGGGATTCNMAPT (M)CCGCCCAGGCCAACTAGCCNMRK1 (M)CTTGAAGCCTTGCTCCCGCACNMRK2 (M)GCGTGCAACTTGGTGGTGGAT </td <th></th> <td colspan="3">GCAACAATCTCCACTTTGCCAC</td>		GCAACAATCTCCACTTTGCCAC		
GAPDH (R)GCTCTCTGCTCCTCCTGTTC GAGGCTGGCACTGCACAGARP16SGATTTGCTGGTGGGATATCACTB (M)CGATGCCCTGAGGCTCTT T TGGATGCCACAGGATTCCAACTB (R)TCGGGGCATCGAACCCCCAGCCACTB (R)TCGGGGCATCGGAACCGCTCARPL13A (M)CTCTGGCCTTTTCTTTTTG CCGAAGAAGGGAGAACAGTTCRPL13A (R)CCCACCCTATGACACCCCAGCAACTB (R)CCCACCCTATGACAACGCTCARPL13A (R)CCCACCCTATGACAAGAAAAAGCRPL13A (R)GCCGCTAGAGGTGAAATTCTTA18S (R)GCCGCTAGAGGTGAAATTCTTA18S (R)CTTTCGCTCTGGTCGTCTNPPA (M)CCTGCTTCCTCAGTCTGCTCNPPA (M)GCACTCATGCACTTTGGAAACCCCATGAGGTAGGCTGTTTCTTTTGTGAGGCCTTGTNPPB (M)TTCTTTTGTGAGGCCTGTGTMYH7 (M)CCCATGAGCTGAGACGCAAATGTGAMYH7 (M)CCCATGAGCTGAGACACGATGGAMNMT (R)GAAGCAGACAAACGAGCGAAAGCGAAGANNMT (R)GAACCAGGAGCAGAGAGAAGCTGATNNMT (M)GAACCAGGAGCCAAATGTGGANRF1 (M)CTTCACGGCCTCAACTCCNRF2 (M)TCTGTCAGTGGGCTTTGGTFAM (M)TCACGGCATTCAAAGGAAGCTNMNAT1 (M)AGGACCACAGAGGCGTTTGGNMAAT2 (M)CAGAAGCCAACACACAGGAGACCANMAAT3 (M)CCAGAAGCCGAGTTCAAAGTAGGANMAPT (M)CCTGCAGTCCTCCACCACACAGGAACTNMARK1 (M)CTTGAAGCTTGCTCTGCGACNMRK2 (M)GCAGAACCTGGTCTGGTGGGAAATAGCAGCCCCAGGACCAAATAGCAAGCCCCAGGACCAAATAGCNMRK2 (M)GCAGAACTTGGTGGGATTCAGAGCCCAGAGCTAAATAGCAAGCCCCAGGACCAAATAGCCAGAACCTGCCAGACCAAATAGCAAGCCCCAGGACC	GAPDH (M)	AATGGTGAAGGTCGGTGTGAAC		
GAPDH (R)GAGGCTGGCACTGCACAARP16STCTTTGATCTCCTGCGGATATCACTB (M)TGGATGCCCTGAGGCTCTTTGGATGCCACAGGATTCCAACTB (R)GAGACCTTCAACACCCCAGCCRPL13A (M)CTCTGGCCTTTTCCTTTTGCCGAAGAAGGAGACAGTTCRPL13A (R)CCCACCCTATGACAAGAAAAAGCACTB (R)GCCGCTAGAGGTGAAATTCTTA18S (R)CTTTCGCTCTGGTCCGTCTT18S (R)CTTTCGCTCTGGTCCGTCTRNU6-1 (R)GCAATTCGTGAAGCGTGCCNPPA (M)CCTGCTTCCTCAGTCTGCTCNPPA (M)CCTGCTTCCTGAGGCTGTTNPPA (M)CCCATGAGGTAGCCTTGGTNPPB (M)TTCTTTTGTGAGGCTGATTTGTACAGGCAGCAAAGAAGCCCCATGAGGTAGCTGATTGTNNMT (R)CCCATGAGCTAGACCACGATGGANNMT (R)GCAGCCAGAGACACGATGGAMRF1 (M)CTTCAGGACTGCCAACTTCNRF2 (M)TCTTCTCCATGGGGGAGAAGTTCCNMNAT1 (M)GCAAAGGATGATTCGGCTCTFAM (M)CAGAGCCCAAGGGAGAAGTTCAACNMNAT2 (M)CAGAGCCCACACAGGAGAAGTTCAACTCCAATAAANMAT2 (M)CAGAGCCCACACAGGAGATCCNMAPT (M)CAGAGCACCACAGGAGATTCNMAPT (M)CAGAGCACCACAGGAGATCNMAPT (M)CAGAAGCACCACAGGAGTTCAACATNMAPT (M)CAGAAGCACCACAGGGATTCNMAPT (M)CAGAAGCACCACAGGGATTCNMAPT (M)CAGAAGCCCACAGGGATTCNMRK1 (M)CTTGAAGCTTGCTTCCCAACCACACANMRK2 (M)CTTGAAGCTTGCTTGGTGGGATNMRK2 (M)CAGACCAAGCTTGAAACTTGGTGGAT		GCTCTCTGCTCCTCCTGTTC		
RP16SGATTIGCTGGTGTGGATATC TCTTIGATCTCCTTTTAGAACTB (M)CGATGCCCTGAGGCTCTT TGGATGCCACAGGATTCCAACTB (R)GAGACCTTCAACACCCCAGCC TCGGGGCATCGGAACCGCTCARPL13A (M)CTCTGGCCTTITCCTTTTTG CCGAAGAAGGAGACAGTTCRPL13A (R)CCCACCCTATGACAAGAAAAGC ACATTCTTTTCTGCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCTGGTCCGTCTRNU6-1 (R)GCAATTCGTGAAGCGTCC CCTGCTTCCTCAGTCTGCTCNPPA (M)CCTGCTTCCTCAGAGGTGCTGT CCTGCTTCCTCAGTCTGCTCNPPB (M)TTCTTTTTGTGAGGCCTTGGT TTCTTTTGTGAGGCCTGGTNPPB (M)GCATCATGCACTTTGGAAAC CCCATGAGGTAGGTGAATTGTA CCCATGAGGTAGGCCAATGTGANNMT (R)CACAGCCAGAGAGACACGATGGA GCAGCAGAGAGAGAGCTGATTGGNNMT (R)CACAGCCAGAGAGAGAGCTGAT GATTCACAGCCCTCAACTTCT GAACCAGGAGCAGAGAGAGCTGATTGGGNRF1 (M)CTTCAGAACTGCCAACCACA GCTAGGGCGTTTGGCTNRF2 (M)TCTGTCACTGGCGCTCTCACT TCTGCCATGGGGAGAAGTTC AGGTCTCATCACACACANMNAT1 (M)GCAAAGGATGATTCGGCTC TCAGGCACCACAGGAGACACCACAGGAGATGATTCA AGGACCACGCATTCAAAGTAGGANMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGAGATTCAAGTCC CCTGCAGCACCACAGGAGATTCAAGTAGGA NMAPT (M)MMAPT (M)CAGAAGCCCAAGGAGTTCAACAT CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGAGTTCAACAT CCTGCAGCACCACAGGGATTC AGGCACCACAGGAGCCAATAAA GCAGAAGCCGAGTTCAACAT NMAPT (M)CAGAAGCCCAGGGACTCAACAT AGGCCCAAGCCAAATAGC AAGCCCCAGGACCAAATAGC ACGCCCAGGACCAAATAGC CCTGCAGAACTTGCTTGCCGCAC ACAGACCCAGGACCAAATAGC AAGCCCCAGGACCAAATAGC AAGCCCAGGACCAAATAGCNMRK2 (M)CTGCAGACCTGCTGCGACAACTTGGTGGGAT CCTGCAGAACTTGGTGGGATT	GAPDH (R)	GAGGCTGGCACTGCACAA		
RP16STCTTTGATCTCCTTCTTAGAACTB (M)CGATGCCCTGAGGCTCTT TTGGATGCCACAGGATTCCAGAGACCTTCAACACCCCAGCCACTB (R)TCGGGGCATCGGAACCGCCTCACRL13A (M)CTCTGGCCTTTTCCTTTTTGCCGAAGAAGGGAGAACAGTTCCCGAAGAAGGGAGACAGTTC18S (R)GCCGCTAGAGGTGAAATCTTA18S (R)GCCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGGGTGCCTTNPPA (M)CCTGCTTCCTCAGTCTGGTCNPPB (M)TTCTTTTGTGAGGGCCTTGGTNPPB (M)TTCTTTTGTGAGGGCCTGGTNPPB (M)TCCTAGCCAAAGCAAAAAAGCMYH7 (M)GCCATCATGCACTTTGGAAACCCCAGGGAGGCAGAGGGTGGAMYH7 (M)CCCAGGCTAAGCTCCCATAAGNNMT (R)GATTGCACGCCTCAACTTCTGAACCAGGAGCAGGAGAAGCTGATNNMT (M)GATTGCACGCCTCAACCACANRF1 (M)CTTCAGAGGTGGGCTGATTCGNRF2 (M)TCTGCCAGTGAGACACGAGGCTTCACNRF2 (M)TCTGCCCCCTCAACCACANMNAT1 (M)GATCCCCATGGGGAGAAAGTTAMNAT2 (M)CAGAGCACCACAGGAGCTTTGGNMNAT2 (M)CAGAGCACCACAGGAGCTCAGAAGCACCACAGGGATTCCCGCACACACACAGGATTCNMAPT (M)CAGAAGCACCACAGGGATTCNMAPT (M)CAGAAGCCCACAGGGATTCNMAPT (M)CAGAAGCCCACAGGGATTCNMAPT (M)CAGAAGCCCACAGGGATTCNMRK1 (M)CTTGAAGCTTGCTCCCACACACACACACACACACACACAC		GATTTGCTGGTGTGGATATC		
ACTB (M)CGATGCCTGAGGCTCTT T TGGATGCCACAGGATTCCAACTB (R)GAGACCTTCAACACCCCAGCCRPL13A (M)CTCTGGCCTTTTCCTTTTTGCCACCCTATGACAAGAACGGCACAGTTCCCACCCTATGACAAGAAAAAGCRPL13A (R)CCCCCCTATGACAAGAAAAAGCACATTCTTTTCGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTACTTTCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGCGTGCCNPPA (M)CTGCTTCTCAGTCTGCTCCNPPB (M)TTCTTTTGGAGGCTGCTTTRNU6-1 (R)GCATCTCCTGAAGGTGCTGTNPPB (M)GGATCTCCTGAAGGTGCTGTNPPB (M)GCCATCATGCACTTTGGAAACCCCATGAGGTAGGCTGGATTTGTACAGGCAGCCAAATGTGACCCAGGTAAGCTCCCATAAGNMHT (R)CCAGAGCTGAGACACGATGGACCTCTGCCAGGAGAGAGAGCTGATNMMT (M)GATTGCACGCCTCAACTTCTGAACCAGGAAGCGCTTTGACTGGNRF1 (M)CTTCAGCACGCCTCAACTGCACTCTGCCAGTGAGGCTGATTCGGCTCTFAM (M)TCAGCTCTCCCCAAGACTTCANMNAT1 (M)GAGCTCACGGGAGAAGCTGATAGGACTAGGGCCGATTGGNMNAT2 (M)CCTGCACACCACAGGAGTTCAATCCCATCACATAAANMAT3 (M)CCTGCAGCACCACAGGGATTCAATAAANMAPT (M)CCTGCAGCACCACAGGGATTCAACATNMART1 (M)CAGAAGCCCCAAGGAGATCCCACACANMAPT (M)CCTGCAGCACCACAGGGATTCAACATNMRK1 (M)CTTGAAGCTTGCCTTGCGACNMRK2 (M)CTGCACACCACACAATAGCQCGTGCAAACTTGTGTGGATCAGGACCCAAATAGCNMRK2 (M)CAGGACCCAAATAGCCCGTGCAAACTTGTGTGGATCAGAAGCCCAAATAGCNMRK2 (M)CCTGCACACTTGTGTGGAT	RP16S	TCTTTGATCTCCTTCTTAGA		
ACTB (M)TGGATGCCACAGGATTCCAACTB (R)GAGACCTTCAACACCCCAGCCTCGGGGCATCGGAACCGCTCACTCTGGCCTTTTCCTTTTGRPL13A (M)CTCTGGCCTTTTCCTTTTGCCACCCTATGACAAGAAAAGCACATTCTTTCGCCTGTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA18S (R)CTTCGTCTGGTCCGTCTNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)CTGCTTCTCATCATCTGCTCNPPB (M)GGATCTCCTGAAGGTGCTGTTTCTTTTGTGAGGCCTTGGTCNPPB (M)CCCACGCTAGAGGTAGGTGCTGTNPPB (M)GGATCTCCTGAAGGTGCTGTTTCTTTTGTGAGGCCTTGGTCNPPB (M)CCCATCATGCACTTTGGAAACMYH7 (M)CCCATGAGGTAGGCTGATTTGTPLN (M)CCCAGGCAAAGGTGGACCAGGCCGAAAGGTGGANIMT (R)GCAGGCCGAAAGGTGGAGCAGGCAGAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCCCAACAGGAGAMRF1 (M)GCTTCTGCCAGGAGAGAGCTGATNRF2 (M)TCGCTCTTCCCAAGGACTCACAMNAT1 (M)GAGTCTCCCGCAATCACAATAAAMNAT1 (M)GAGCCCGCGAATCACAATAAAMNAT2 (M)CCAGGACCACAGGGATTCCNMNAT3 (M)CCAGGACCCACAGGGATTCNMAPT (M)CCTGCAGCACATCACAATAAAMMAPT (M)CCTGCAGCACCACAGGGATTCNMAPT (M)CCTGCAGCACACAGGGATTCNMAPT (M)CCTGCAGCACCACAGGGATTCNMRK1 (M)CTTGAAGCTTGCTCGCGACNMRK2 (M)CTGCAGGCCAAATAGCQCGTGCAAACTTGTGTGGAACCCGTGCAAACTGGTGGAT		CGATGCCCTGAGGCTCTT T		
ACTB (R)GAGACCTTCAACACCCCAGCC TCGGGGCATCGGAACCGCTCARPL13A (M)CTCTGGCCTTTTCCTTTTG CCACCCTATGACAAGAAAAAGC ACATTCTTTCTGCCTGTTTCCRPL13A (RCCACCCTATGACAAGAAAAAGC ACATTCTTTCTGCCTGTTTCC18S (R)GCCGCTAGAGGTGAATTCTTA CTTTCGCTCGGTCCGTCT18S (R)GCCACCTTCTCCAGTCTGCC CTCCCCAGTCTGGTCCGTCCNPPA (M)CTGGCTCCTTGAAGCGTCC CTCCTCAGTCTGGTNPPA (M)GGATCTCCTGAAGGTGCTGT CCTGCTTCCTCAGTCTGGTNPPB (M)TTCTTTTGTGAGGCCTTGGT GGATCTCCTGAAGGTGGTGTNPPB (M)TCCTTTTGGAAAC CCCATGAGGTAGGCTGGTNPPB (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTNMMT (M)GCCATCATGCACCATGGA CCAGAGCAGAGAGAGCTGATNMMT (R)CAGAGCTGAGACACGATGGA CCAGAGCAGAGAGAGCTGATNNMT (M)GATTGCACGCCCTCAACTTCT GAACCAGGAGGAGAGCTGATNRF1 (M)CTTCAGAACTGCCAACCACA CCTCTCACTGCCAGTGAGCTCCNRF2 (M)TCTGTCATGGGGAGAGAGCTGGT TCAGCTCATGGGGAGAGAGCTCC TFAM (M)TCACGCCAATCACAATAAA GCAAGGCTCAATCCCAATCACAATAAA MMNAT1 (M)GCAGAGGCGCGTTGG AGCTCCAATCCCAATCACAATAAA AGCCCCAGGACACACAGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATCC CCTGCAGCACCACAGGGATCC CCTGCAGCACCACAGGGATCC NMART3 (M)CTGCGCAATCACAATAAA CCTGCAGACCACAAGGAGA CCCGTTGCACCACCA MMRK1 (M)CTTGAAGCTTGCTCTGCGAC CCCGTGGAAACTTGTGTGGAC CCCGTGCAAACTGGTGGACCACACA CCCGTGCAAACTGGTGGACCAAATAGC GCGTGCAAACTGGTGGAATTGGCATGGAT	ACTB (M)	TGGATGCCACAGGATTCCA		
ACTB (R)TCGGGGCATCGGAACCGCTCARPL13A (M)CTCTGGCCTTTTCCTTTTGCCGAAGAAGGGAGACAGTTCCCACCCTATGACAAGAAAAAGCACATTCTTTTCTGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA18S (R)GCCGCTAGAGGTGAAATTCTTACTTTCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)CCTGCTTCCTCAGTCTGGTCNPPB (M)TCTTTTGGAGGCCTTGGTMYH7 (M)GCATCATGCACTTGGAGGCTGGTMYH7 (M)GCCATCATGCACTTTGGAAACCCCAGGCAGGCAGACCGAATGTGACCCAGGCAGAGGAGGCTGATTTGTPLN (M)CACAGGCAGCAAATGTGACCCAGGCAGAGGAGAGCTGATTGTGCATTGCACGCCCCATAAGNNMT (R)GCAGGCAGAGAGAGAGCTGATMNMT (M)GATCGCCACGCCAACGACGAGCTTCTGCCAGGAGAGAGCTGATCTTCAGAACTGCCAACCACANRF1 (M)CTTCAGAACTGCCAACCACACTCTGCCAGTGATGTGGCTCTCGGTFAM (M)TCGCTCTCCCCAGGATGCTACCCGCAAGGAGGACTTCANMNAT1 (M)GCAAAGGATGATTCGGCTCAGCCCAGGAGCACCACAGGAAGTTAGCCCCAGGACACCACAGGAATTCNMNAT2 (M)CCTGCAGTCACCACACAGGAATTCCAGAAGCACCACAGGGATTCAACATCAGAAGCCCCACAGGGATTCAACATNMART1 (M)CTTGAAGCTTCAAGGCACCACAGGAATTCNMAPT (M)CCTGCAGCACCACAGGGATTCAGCCCCAGGACCACAAGGAGACCGCGCATTCAAAGTAGGANMART1 (M)CTTGAAGCTTGCCTTGCGACNMRK1 (M)CTTGAAGCTTGCTCTGCGACCACACANMRK2 (M)CCTGCAAACTTGTGTGGGAT		GAGACCTTCAACACCCCAGCC		
RPL13A (M)CTCTGGCCTTTTCTTTTG CCGAAGAAGGGAGACAGTTCRPL13A (R)CCACCCTATGACAAGAAAAAGC ACATTCTTTTCGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCA CCTGCTTCCTCAGTCTGCTNPPB (M)GGATCTCCTGAAGGTGCTGT TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)CCCAGCAAGGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)GATTGCACGCCTCAACTTCT GAACCAGGAGACACGATGGANNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCAACTGCAACTGCNRF1 (M)CTTCTGCCAGTGAGGCTCC CTTCAGAACTGCCAACCACCANRF2 (M)TCTGTCACTGCCCCTCATC TCTGCCATGGGGGAGAAGTTAAA MNAT1 (M)AGCCTCCAGCAATGAGGACCGATGGA ACGCCTCAATCCACACCACANMNAT2 (M)CAGAGCTCCATCAGGGCAGAGAAGTT ACGCCTCAACCACCACANMNAT3 (M)CAGAAGCACCACAGAGGATTC CCTGCAGCACCACACACANMAPT (M)CAGAAGCATCCAACAGAGA CCTGCAGCACCACACACANMAPT (M)CAGAAGCATCACAAAGAAGATTC CCTGCAGCACCACACACATNMRK1 (M)CTTGAAGCCCCAACACACAT CTCCGTTTGCACACCACCANMRK2 (M)CAGCCCCAGGAACTTGTGTGACACACACA GCGTGCAAACTTGTGGGAT	ACTB (R)	TCGGGGCATCGGAACCGCTCA		
RPL13A (M)CCGAAGAAGGGAGACAGTTCRPL13A (RCCACCCTATGACAAGAAAAAGC ACATTCTTTTCTGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCA CCTGCTTCCTCAGTCGGTNPPA (M)GGATCTCCTGAAGGTGCTGT TTCTTTTGTGAGGCCTGGTNPPB (M)TTCTTTTGTGAGGCCTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)CCCAGCTAAGCTCCCATAAG CCCAGCTAAGCTCCCATAAGNMMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)TCTGTCAGTGGGGCTTCTGG TFAM (M)TGAGTCCATGGGGAGAAGCTGAT MNAT1 (M)GCAAAGGATGATTCGGCTC TCTGCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAGGGATCA CCTGCAGCACTCACATCACAT NMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACTCACACACACANMRK1 (M)CTTGAAGCTGCTCTGCGCAC CTCCGTTTGTCACACCACCA AAGCCCCAGGACCAATAAC AAGCCCCAGGACCAATAACNMRK1 (M)CTTGAAGCTGCTCTGCGAC CCCGGTTGACCAACAATAAC GCGTGCAAACTTGTGTGACACCACCACACA				
RPL13A (RCCACCCTATGACAAGAAAAAGC ACATTCTTTTCTGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCTGGTCCGTCTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCA CCTGCTCCTCAGTCGCTCNPPA (M)GGATCTCCTGAAGGTGCTGT TTCTTTTGTGAGGCCTTGGTNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACCTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GACCAGGAGCCTCAACTTCT NNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTACCNRF1 (M)GCTTCTGCCAGTGATGCTAC NRF2 (M)AGTCTTCACTGCCCACACCACA GCAGGCAGAGAGAGTGATTCGGCTC TFAM (M)TGAGTCCATGGGGAGAAGCTGATT MNAT1 (M)AGGCCTAGGGCAGAGAAGCTGAT AGGCCTCAACTCCAACTTCA TCTGCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAGGGATC CCTGCAGCATCACAATAAA GCAGGCTCAACCACCACA NMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCATCACAATAAA MCAT3 (M)CAGAAGCTGCCAACACACA CCTCGCAGTTCAACATCACAT NMRK1 (M)NMRK1 (M)CTTGAAGCTTGCTCTGCGAC CCCGCCAATAACCACACA AAGCCCCAGGACCAATAGC GCGTGCAAACTTGTGTGACACACACACACACANMRK2 (M)CAGCCCCAGGAACTTGTGTGACACACACACACACACACAC	<i>RPL13A</i> (M)			
RPL13A (ROCNOCINATION CONTRICT ACATTCTTTTCTGCCTGTTTCC18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCGGTCCGTCTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCA CCTGCTTCCTCAGTCTGCTGNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)CCCAGGTAAGCCCAAATGTGA CCCAGCTAAGCCCCCCATAAGNNMT (R)GCAGCGCAGAGAGAAGCTGAT GAACCAGGAGCCAACTGCAACCACA MRF1 (M)GCTTCTGCCAGGAGCCACACCACA CTCAGACTGCCACCACCACNRF1 (M)GCTTCTGCCAGTGATGCACCACCACA GCAAAGGATGATTCGGCTC TCTGCCAGTGGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCCCATGGGGAGAAGTT AGGCTCCATGGGGCAGAGAAGATTCA GCAAAGGACCACACACACACACACACACACACACACACA				
ACKITCUTTICISCUTATION18S (R)GCCGCTAGAGGTGAAATTCTTA CTTTCGCTCTGGTCCGTCTTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCA CCTGCTTCCTCAGTCTGCTCNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)CCCATGAGGCAGCCAAATGTGA CCCAGGCAGCCAAATGTGANNMT (R)CAGAGCTGAGACCCATAAG CCAGGCAGAGAGAAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCAACTGCAACCACA CTTCAGAACTGCCAACCACA NRF1 (M)CTTCAGAACTGCCAACCACA CTTCAGTAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTCCCAAGACTTCA TCTGCTCTCCCAAGACTTCA NMNAT1 (M)AGCCCCAGGCAGCATTCAAAG CCAGGACCACCACACACTNMNAT1 (M)CAGAACCAGGAGCACAATAAA GCAGCTTCAATCCCATCACT CCTGCAGGCAGATTCAATCCCATCACTNMNAT2 (M)CCTGCAGCACCACAGGATTC CCTGCAGCACCTTCAACTC CTTGCAGCACCACAGGATTCAAAGTAGGA MMNAT3 (M)CAGAAGCACCACAGGGATTCAAAGTAGGA CCTCGCTTGCCACCACCACA NMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTGCCACCACAAATAGC GCGTGCAAACTTGTGTGGGATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTGCCACCACAATAACGC GCGTGCAAACTTGTGTGGGAT	<i>RPL13A</i> (R			
18S (R)CCCGCTAGAGCGTAGAGCGTACAGTAGAGCGTTCTRNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCAACACCTGCTTCCTCAGTCTGCTCCCGGTTCCTGAGGTGGTGTNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAACCCCAGGCTAGGGCAGCCAAATGTGACCCAGGCTAGGCCGAATGTGAPLN (M)AACAGGCAGCCAAATGTGACCCAGCTAAGCTCCCATAAGNNMT (R)GCAGGCAGAGAGAGACACGATGGANNMT (M)GATTGCACGCCTCAACTTCTNNMT (M)GATTGCACGCCTCAACTTCTORF1 (M)CTTCAGAACTGCCAACCACACTTCAGAACTGCCAACCACANRF2 (M)TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTCTCTGCCATGGGGAGAAGCTTCANMNAT1 (M)AGGCTCCATGGGGAGAAGTTAGGCTCCAACCACACACACANMNAT2 (M)CCAGAAGCACCACAGGGATTCNMAT3 (M)CAGAAGCACCACAGGGATCCNMAPT (M)TCACCGGCATTCAAAGTAGGANMAPT (M)CTTGAAGCTTGCTCTGCGACNMAPT (M)CCTGCAGGCCGTTTACAGTCNMAPT (M)CCTGCAGCACCACAGGGATTCNMAPT (M)CCTGCAGCACCACAGGGATCNMAPT (M)CCTGCAGCACCACAGGGATCNMRK1 (M)CTTGAAGCTTGCTCTGCGACNMRK1 (M)CTTGAAGCTCCACCACAATAGCNMRK2 (M)AAGCCCCAGGACCAAATAGCGCGTGCAAACTTGTGTGGGAT				
RNU6-1 (R)GCAAATTCGTGAAGCGTTCCNPPA (M)ATGGGCTCCTTCTCCATCACCTGCTTCCTCAGTCTGCTCGGATCTCCTGAAGGTGCTGTNPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAACCCCATGAGGTAGGCTGATTTGTAACAGGCAGCCAAATGTGAPLN (M)CACAGGCAGCCAAATGTGACCCAGCTAAGCTCCCATAAGCCCAGGCTAAGCTCCCATAAGNNMT (R)GACAGGCAGCAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCTNNMT (M)GATTGCACGCCTCAACTGCARF1 (M)CTTCAGAACTGCCAACCACANRF1 (M)GCAAGGATGATTCGGCTCTCTGTCAGTGTGGGGTGCTCTCTGTCAGTGTGGGCTTCTGGNRF2 (M)TGAGTCCATGGCGAGAGAGTTNMNAT1 (M)GGACAAGGACCATCACAATAAANMNAT1 (M)AGCCTCAGCCATCACAATAAANMNAT2 (M)CAGAAGCACCACAGGGATTCNMNAT3 (M)CAGAAGCACCACAGGGATTCNMAPT (M)TCACGGCATTCAAAGTAGGANMRK1 (M)CTTGAAGCTTGCTCTGCGACNMRK1 (M)CTTGAAGCTTGCTCTGCGACNMRK2 (M)AGCCCCAGGACCAAATAGCAGCCCCAGGACCAAATAGCGCGTGCAAACTTGTGTGGAT	<i>18</i> S (R)	CTTTCCCTCTCCCTCTCT		
NN00-7 (N)GCAAATTEGIGAAGGSTICCNPPA (M)ATGGGCTCCTTCCAGTCGATCACCTGCTTCCTCAGTCTGCTCGGATCTCCTGAGGTGGTGTTTCTTTTGTGAGGCCTTGGTTTCTTTTGTGAGGCCTGGTMYH7 (M)GCCATCATGCACTTTGGAAACCCCATGAGGTAGGCTGATTTGTAACAGGCAGCCAAATGTGAPLN (M)AACAGGCAGCCAAATGTGACCCAGCTAAGCTCCCATAAGCCCAGGCAGAGAGAGACGCGATGANNMT (R)GATTGCACGCCTCAACTTCTNNMT (M)GATTGCACGCCTCAACTGCARF1 (M)GATTGCACGCCTCAACTGCNRF1 (M)CTTCAGAACTGCCAACCACANRF2 (M)TCTGTCAGTGTGGCTTCTGGTFAM (M)TCAGATCATGGGGAGAAGTTNMNAT1 (M)AGGCTCATGGGGAGAAGTTAGGACTAGGGCCGTTTGGNMNAT2 (M)CCTGCAGCACACACAGGAATCCNMAT3 (M)CAGAAGCACCACAGGGATTCNMAPT (M)TCACGGCATTCAAAGTAGGANMAPT (M)CCTGCAGCACTTCAACATAAAMAPT (M)CCTGCAGCACCACAGGGATTCNMAPT (M)CCTGCAGCACCACAGGAATTNMAPT (M)CCTGCAGCACCACAGGAATTCNMRK1 (M)CTTGAAGCTTGCTCTGCGACNMRK2 (M)AAGCCCCAAGGACCAAATAGCGCAGTGCAAACTTGTGTGGATGCAGGTGCAAATAGCNMRK2 (M)CAGCACCACAACTGTGTGGAT	DNI 16 1 (D)			
NPPA (M)ATGGGCTCCTTCTCAGTCTCAGTNPPB (M)GGATCTCCTGAGGCTGGTTTCTTTTGTGAGGCCTTGGTTTCTTTTGTGAGGCCTGGTMYH7 (M)GCCATCATGCACTTTGGAAACCCCATGAGGTAGGCTGATTTGTAACAGGCAGCCAAATGTGAPLN (M)CACAGGCAGACACGATGGANNMT (R)CAGAGCTGAGACACGATGGAGATTGCACGCCTCAACTTCTGAACCAGGAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCTNNMT (M)GATTGCACGCCTCAACTTCTNRF1 (M)CTTCAGAACTGCCAACCACANRF2 (M)CTTCAGAACTGCCAACCACANRF2 (M)TCTGTCAGTGTGGCTTCAGGTFAM (M)GCAAAGGATGATTCGGCTCNMNAT1 (M)AGGCTCATGGGGAGAAGTTAGGACTAGGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAGGGATTCCCTGCAGCACCACAGGGATTCNMNAT3 (M)CAGAAGCACCACAGGGATTCNMAPT (M)CTTGAAGCTTCAAAGTAGGANMRK1 (M)CTTGAAGCTTGCTCTGCGACNMRK2 (M)AGCCCCAAGGACCAAATAACNMRK2 (M)GCAGGTGCAACTTGTGTGGAT	KN00-1 (K)	ATCCCCTCCTTCTCCATCA		
NPPB (M)GGATCTCCTGAAGGCTGGTGT TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)GATTGCACGGCCTCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)TCTGTCAGTGTGGCTTCTGG TCTGCTCTTCCCAAGACTTCANRF2 (M)TCTGCTCTTCCCAAGACTTCA TCTGCTCTTCCCAAGACTTCANMNAT1 (M)GCAAAGGATGATTCGGCTC TCTGCCATCATCATCANMNAT1 (M)AGCCTCGCCACACACACACA GCAGCTTCAATCCCATCACATAAA GCAGCTTCAATCCCATCACTNMNAT2 (M)CAGAAGCACCACAAGGATTC CCTGCAGCACTCAAGTTCANMAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACTTCAAAGTAGGA MAPT (M)CTCGCGCATTCAAAGTAGGA CCTGCAGCACTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CCTCGCAACCACACACANMRK2 (M)AGCCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NPPA (M)			
NPPB (M)TTCTTTTGTGAGGCCTTGGTMYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)GATTGCACGCCTCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCAGAACTGCCAACCACA GCAGGCCTTTCCCAAGACTTCT TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCCATGGGGAGAGAGTT AGGCTCCATGGGGAGAGAGTT AGGACTAGGGCCGTTTGGNMNAT1 (M)AGACCAGGGACCAACAAAAA GCAGCTTCAATCCCATCACTNMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGGATCCNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACTTCAAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCCACAGGACTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCACA AAGCCCCAGGACCAATAGC GCGTGCAAACTTGTGTGGAT				
MYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCAGTAGTGTGGCTTCTGG TCTGCCAGTGTGGCTCTCGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCCATGGGGAGAGACTTCANMNAT1 (M)AGCTCTCATGCGCAATCACAATAAA GCAGCTTCAATCCCATCATCATCCAATCCCATCATCAATCCCATCACTNMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMNAT3 (M)CAGAAGCACCACAGGGATCC CTCGCAGCACGTTCAACATNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGGTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTGCAACACACACACACA AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NPPB (M)	GGATCTCCTGAAGGTGCTGT		
MYH7 (M)GCCATCATGCACTTTGGAAAC CCCATGAGGTAGGCTGATTTGTPLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)GATTGCACGCCTCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCAGAACTGCCAACCACA GCAAAGGATGATTCGGCTCTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTCCCAAGGACTTCANMNAT1 (M)AGGCTCAGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAGGGATCC CCTGCAGCACCATCACATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTACAGGCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGGAT				
PLN (M)AACAGGCAGCCAAATGTGA CCCAGCTAAGCTCCCATAAGPLN (M)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGAGAGAGAGAGAGAGA GCAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	<i>MYH7</i> (M)	GCCATCATGCACTTTGGAAAC		
PLN (M)AACAGGCAGCCAAATGTGA CCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCCATGGGGAGAAGTT AGGCTCCTTCCCAAGGGCCGTTTGGNMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT1 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGATTC CCTGCAGCACCATCACATTAAA GCAGAAGCCCGAGTTCAACATNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCTTCAACAT CCTGCAGCACCTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT				
NNMT (R)CCCAGCTAAGCTCCCATAAGNNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCAGTAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT1 (M)ATCCCGCCAATCACAATAAA GCAGAGCACCACAGGGATTC CCTGCAGCACCATCACATCACATAAA GCAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCTTCAAGTAGGA GCAGAAGCCGAGTTCAACATNMNAT3 (M)CCAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCTTCAACAT AGCAGCTTCAACAT CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCA AGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGGAT	PLN (M)	AACAGGCAGCCAAAIGIGA		
NNMT (R)CAGAGCTGAGACACGATGGA GCAGGCAGAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)CTTCAGTAGTGGCCTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT1 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCATCNMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCGTTTACAGTCNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTCAACATNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGGAT		CCCAGCTAAGCTCCCATAAG		
NNMT (N)GCAGGCAGAGAGAGAGCTGATNNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)GGAGGCCGTTTGG GCAGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGGATTC CCTGCAGCACCACAGGATTCAATAANMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACCGACTTCAACATNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCACAGGATTGCNMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NNMT (R)	CAGAGCTGAGACACGATGGA		
NNMT (M)GATTGCACGCCTCAACTTCT GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)CAGAAGCACCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCACAGGATTG AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		GCAGGCAGAGAGAAGCTGAT		
NRF1 (M)GAACCAGGAGCCTTTGACTGNRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NNMT (M)	GATTGCACGCCTCAACTTCT		
NRF1 (M)CTTCAGAACTGCCAACCACA GCTTCTGCCAGTGATGCTACNRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		GAACCAGGAGCCTTTGACTG		
NRT F (M)GCTTCTGCCAGTGATGCTACNRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NRE1 (M)	CTTCAGAACTGCCAACCACA		
NRF2 (M)AGTCTTCACTGCCCCTCATC TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACACANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		GCTTCTGCCAGTGATGCTAC		
MKF2 (M)TCTGTCAGTGTGGCTTCTGGTFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACACAGGATTG GCGTGCAAACTTGTGTGGAT		AGTCTTCACTGCCCCTCATC		
TFAM (M)GCAAAGGATGATTCGGCTC TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACACACACACACACACACACACAC	///// Z (W)	TCTGTCAGTGTGGCTTCTGG		
ITTAM (M)TCTGCTCTTCCCAAGACTTCANMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACACA GCGTGCAAACTTGTGTGGAT		GCAAAGGATGATTCGGCTC		
NMNAT1 (M)TGAGTCCATGGGGAGAAGTT AGGACTAGGGCCGTTTGGNMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACACACACACACACACACACACAC		TCTGCTCTTCCCAAGACTTCA		
NMINATY (M) AGGACTAGGGCCGTTTGG NMNAT2 (M) ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACT NMNAT3 (M) CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTC NMAPT (M) TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACAT NMAPT (M) CTTGAAGCCGAGTTCAACAT NMRK1 (M) CTTGAAGCTTGCTCTGCGAC NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGGAT	$\Lambda \Lambda \Lambda \Lambda \Lambda T 1 (\Lambda \Lambda)$	TGAGTCCATGGGGAGAAGTT		
NMNAT2 (M)ATCCCGCCAATCACAATAAA GCAGCTTCAATCCCATCACTNMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		AGGACTAGGGCCGTTTGG		
INMINAT2 (M) GCAGCTTCAATCCCATCACT NMNAT3 (M) CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTC NMAPT (M) TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACAT NMRK1 (M) CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCA NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		ATCCCGCCAATCACAATAAA		
NMNAT3 (M)CAGAAGCACCACAGGGATTC CCTGCAGCACGTTTACAGTCNMAPT (M)TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACATNMRK1 (M)CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCANMRK2 (M)AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NMNATZ(M)	GCAGCTTCAATCCCATCACT		
NMNAT3 (M) CCTGCAGCACGTTTACAGTC NMAPT (M) TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACAT GCAGAAGCCGAGTTCAACAT NMRK1 (M) CTTGAAGCTTGCTCTGCGAC NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGGAT		CAGAAGCACCACAGGGATTC		
NMAPT (M) TCACGGCATTCAAAGTAGGA GCAGAAGCCGAGTTCAACAT NMRK1 (M) CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCA NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NIMINA I 3 (M)	CCTGCAGCACGTTTACAGTC		
NMAPT (M) GCAGAAGCCGAGTTCAACAT NMRK1 (M) CTTGAAGCTTGCTCTGCGAC NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		TCACGGCATTCAAAGTAGGA		
NMRK1 (M) CTTGAAGCTTGCTCTGCGAC CTCCGTTTGTCACACCACCA NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NMAPI (M)	GCAGAAGCCGAGTTCAACAT		
NMRK1 (M) CTCCGTTTGTCACACCACCA NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT		CTTGAAGCTTGCTCTGCGAC		
NMRK2 (M) AAGCCCCAGGACCAAATAGC GCGTGCAAACTTGTGTGGAT	NMRK1 (M)	CTCCGTTTGTCACACCACCA		
NMRK2 (M) GCGTGCAAACTTGTGTGGAT		AAGCCCCAGGACCAAATAGC		
	NMRK2 (M)	GCGTGCAAACTTGTGTGGAT		

	CACCTTCCAGAAGCAGGAGA
FARF I (IVI)	GCAGCGAGAGTATTCCCAAG
	GCAACAGAAGACGACTCTCCT
PARF2 (W)	CAGCCATAGGCCCTTTTCTCT
	ACATCGGTTATGGGAGCAAC
RFL32	GGGATTGGTGACTCTGATGG
$mtDN(A_{1}(M))$	CCTATCACCCTTGCCATCAT
	GAGGCTGTTGCTTGTGTGAC
	ATGGAAAGCCTGCCATCATG
	TCCTTGTTGTTCAGCATCAC
DDA Do	GAGAATCCACGAAGCCTACC
FFARa	AATCGGACCTCTGCCTCTTT
	AGGCAGTTCTGGACAAGCCA
VECAD	TTCCTCAAAGAACCGGGCCA
	GCATTGGTGGGGACTTGCTC
LCAD	TGTCATGGCTATGGCACCGA
MCAD	ACTGACGCCGTGCAGATTTT
WICAD	GCTTAGTTACACGAGGGTGATG

Table S3. Antibodies

Name	Company	Catalog Number
ATG3	Sigma-Aldrich	A3231
	Sigma-Aldrich	1 8918
TUBA4A	Sigma-Aldrich	T5168
ACTB	Cell Signaling	3700
SQSTM1	Cell Signaling	5114
Acetylated-Lysine	Cell Signaling	9441
ATG7	Cell Signaling	8858
FOX01	Cell Signaling	2880
RELA S536	Cell Signaling	3036
RELA	Cell Signaling	6956
MTOR S2448	Cell Signaling	4517
MTOR	Cell Signaling	2971
P70S6K T389	Cell Signaling	9206
p70S6K	Cell Signaling	2708
ΑΜΡΚα Τ172	Cell Signaling	2531
ΑΜΡΚα	Cell Signaling	2793
ULK1	Cell Signaling	8054
GFP	Cell Signaling	55494
Sirtuin antibody sampler kit	Cell Signaling	9787
SIRT4	Cell Signaling	69786
PARP1	Cell Signaling	9532
NADK	Cell Signaling	89833
NRF1	Cell Signaling	69432
GAPDH	Cell Signaling	2118
PRKN	Cell Signaling	4211
CASP3	Cell Signaling	9665
CD38	Proteintech	60006-1-lg
BST1	Proteintech	16337-1-AP
NMNAT1	Proteintech	11399-1-AP
NMNAT3	Proteintech	13236-1-AP
PARP2	Proteintech	20555-1-AP
NMNAT2	ThermoFisher Scientific	PA5-115662
NNMT	Proteintech	15123-1-AP
PINK1	Proteintech	23274-1-AP
NAMPT	Proteintech	11776-1-AP
GAPDH	SCBT	SC-32233
TFAM	SCBT	SC-166965
NRF2	SCBT	SC-722
Ac-FKHR	SCBT	SC-49437
PARGC1A	SCBT	SC-13067
SIRT1	SCBT	SC-74504
TOMM20	SCBT	SC-17764
SDHA	abcam	ab14715

Table S4. siRNA sequence

Name	Sequences/Company with catalog number	
Control ai BNA	5'-UAAGGCUAUGAAGAGAUAC-3'	
Control SIRNA	5'-GUAUCUCUUCAUAGCCUUA-3'	
	5'-CCCAGAAGAGUUUGUGGCAGCUGGA-3'	
ATG5 SIRNA	5'-UCCAGCUGCCACAAACUCUUCUGGG-3'	
ON-TARGETplus SMARTpool NNMT siRNA	GE Dharmacon (L-101014-02-0005)	
SignalSilence SQSTM1/p62 siRNA II	Cell Signaling Technology (6399)	
SOSTM1/262	5'-CCUGUGGUGGGAACUCGCUAUAAGU-3'	
3Q3111/p02	5'-ACUUAUAGCGAGUUCCCACCACAGG-3'	
SignalSilence® <i>NF-кВ p65</i> (<i>RELA</i>) siRNA I	Cell Signaling Technology (6261S)	

	Name	Company/Institute	Catalog Number/Provider
	HA-FLAG	Addgene	10792
Plasmids	HA-SQSTM1	Addgene	28027
	ATG7	Addgene	24921
	GFP	Beth Israel Deaconess Medical Center, Boston, MA	Dr. Pavlos Pissios
Adenovirus	GFP-LC3	Cedars Sinai, Los Angeles,	CA Dr. Roberta A. Gottlieb
-	NNMT	Beth Israel Deaconess Medical Center, Boston, MA	Dr. Pavlos Pissios

Table S5. Plasmids and adenovirus