

Table S6. Primers Used in the Current Work

Gene	Sequence	Amplified fragment length (bp)
QRT-PCR analysis		
<i>CMT3</i>	5' - TTACCAAGTCCGAATGGGAATGAT 5' - TCATCCGTGTTGAGTTGAAGTGG	421
<i>DRM1/2</i>	5' - CATCCCTCTTATCGCTGCCTTCC 5' - AAGCAGACCTTACTTCTCGTGGG	352
<i>DCL3</i>	5' - TTGGTAGGAGAGGGGTTTGATAG 5' - ACTGGGGTGGCAGGCGTAG	245
<i>ROS1</i>	5' - CAACAGTTACAAGCCGCATCCAC 5' - AAGGTACTIONTGCACGGGTCGTCAG	334
<i>DME</i>	5' - ATGCTGCTTCTATCCCTACTCCA 5' - GATCATCAGGTTCCCGCTTTT	126
<i>UBQ7</i>	5' - GAAGGCATTCCACCTGACCAAC 5' - CTTGACCTTCTTCTTCTTGTGCTTG	198
<i>UBQF</i>	5' - GCCAGATGCTTCTCAGTTGACTC 5' - GCTGGGATAGAAGTGATTGCTGT	246
<i>TUA3</i>	5' - GAGGTTTTCTCCCGAATCGAC 5' - CATTGACTGCGACTGCTGATTT	231
<i>TUA8</i>	5' - AGGTGCAGCGAGCTGTTTGT 5' - CCTCACAGGGTGAACCCATC	295
<i>TUB2</i>	5' - CTGGTGAGGGAATGGATGAGAT 5' - ACAAAGGAACGAACAGAGCAGAA	282
<i>TUB10</i>	5' - ACTGGTGAAGGGATGGATGAAA 5' - CAAGGCTGGAATGCAAACATAA	296
<i>TUB18</i>	5' - TGGCAAATGAGCACTAAGGAA 5' - CCTAATCCTCGTACTCCGCTTC	383
<i>RPL8C</i>	5' - CGTCGTCTTCCGTCATCCA 5' - GAGGTTTCTCGGTCCTTCCA	356
<i>RPL19B</i>	5' - ATCCACAAGTCCAAGGCTGAG 5' - CACAAACATCTTCCATCTTCCATT	347
<i>RPS4A</i>	5' - AAGATGCTGCTGGGCACGAA 5' - TCTATGACATCACCCACAACACAA	269
<i>RPSA</i>	5' - ACAAACCCCTGGTGCTCCTA 5' - TTCCATTGTTTCGACATAGCTCATA	132
<i>RPS9C</i>	5' - ATTAGGGTTGGTAGGCAAGTGG	262

	5' - CAATGGAGGTGATGGCAAAGT	
<i>eIF2A</i>	5' - GTGAGCGAACGGGATGATAAA	238
	5' - TCCATGAGATGAGGCCAATTG	
<i>eIF2B</i>	5' - TAGGTGTGCTTACTCCTTCCGTC	261
	5' - TGGCAATCTTTGCATTCTTCAA	
<i>eIF3B</i>	5' - GCTTGAAACAATGGCAACTGC	363
	5' - CCATTCGCTTATCCATTTTTCC	
<i>eIF4A</i>	5' - TGGTCGTTTCAGGTCGCTTTG	239
	5' - TGCCTTCAGTTTCCACGGTG	
<i>GAPDH</i>	5' - TTGTTGGCGATTCCAGGTCT	270
	5' - TCACTGATTTATGTCCCGTGCA	
<i>COX</i>	5' - GCTCCTGCTGTTGTCAAGTCCT	196
	5' - GATCATCATCGCCATGTCCG	
<i>ACT7</i>	5' - AGAATGAGCAAGGAAATCACAGC	255
	5' - CGAAACCCAAGCCAAACCA	
<i>FBA</i>	5' - CAAAGTGAGGAGGAGGCTACCC	329
	5' - CCCCCAAAATCATCAATACAGAA	
<i>KCS13</i>	5' - AAGCGTTTGAACACTTCTGTATCCA	287
	5' - TGGTCCATCTTTTGGTGTTTTG	
<i>SUR4</i>	5' - TAATGGCGATGCTTGACTIONTCTA	150
	5' - ATTGTTGACCTTTGGGGGAGT	
<i>ERF6</i>	5' - CCCACCAAAAATCAAGCAGC	211
	5' - ATTCCAGGCTCCAGATTTGTTC	

Bisulfite sequencing analysis

<i>KCS13</i>	5' - TTATTGATGAAAGYAAGGGTTTA	299
	5' - AATTAATCCCTTTATRTTAAATCA	
<i>SUR4</i>	5' - TTTTAATTGTTTGGGGGTGTTT	366
	5' - TCCCATTCTATCTTTTRTRAAA	
<i>ERF6</i>	5' - GGGTGGYGGATTATGTTA	391
	5' - TTATTATTRTCATTRATCCCTAART	
<i>TUB3</i>	5' - TATAYTTTTYGAATTTTAAAATTT	362
	5' - AAARRAAAATACCTTAATTTAACA	
<i>EIF2A</i>	5' - TGTATTYGTYAGGAGYAAGGTA	450
	5' - TTRATAATTATCCTTCTCCCTRT	

Methylation-sensitive Southern blotting

<i>KCS13 -466 ~ -178</i>	5' - TGTCTGGTTATTCCGTGAGCC	289
	5' - GCAGTCAGGCAGATGAGAGGAT	
<i>SRU4 -1155 ~ -856</i>	5' - GATAAGAGCTTCTAAATAGGTTTATGGTTG	300

	5' - CAATACTTAATACTTGTTAATGTAGTTCCGG	
<i>ERF6</i> -263 ~ -21	5' - CACCGGGCACAATTTTTCACA	243
	5' - CTCATAACACAAGGTATTATTTCTGGG	
<i>ERF6</i> -173 ~ -14	5' - ACCTCCAAAATGTCCCTCACTT	187
	5' - GCACCTCCACACATAGACCAAGA	
Methylation-sensitive PCR		
<i>KCS13</i> -770 ~ -447	5' - GAAGCCTGAGACCAACCGATAT	324
	5' - GCTCACGGAATAACCAGACAAT	
<i>SUR4</i> -1014 ~ -346	5' - GAGTTTGACTTCGGGGTTGC	669
	5' - CCACCCTACCATCTACTCTGTTTT	
<i>ERF6</i> -594 ~ -96	5' - CACCGGGCACAATTTTTCACA	499
	5' - CTCATAACACAAGGTATTATTTCTGGG	
<i>ERF6</i> -496 ~ -90	5' - GCGTCCAACATTCTACATTCCTAC	407
	5' - TCAGAAGGTGTGTAGCCGAGAG	
RNAi line vector		
<i>ROS1 pos</i>	5' - GAGCTGGTGGGATGAATAATGTGCTTGCTC	549
	5' - CCCGGGCAGATGTTCCATTTTCAGTAGCAC	
<i>ROS1 neg</i>	5' - CTCGAGGTGGGATGAATAATGTGCTTGCTC	549
	5' - GTCGACCAGATGTTCCATTTTCAGTAGCAC	
<i>NPTII</i>	5' - GCGATACCGTAAAGCACGAGGAA	417
	5' - TCCTGCCGAGAAAGTATCCATCA	