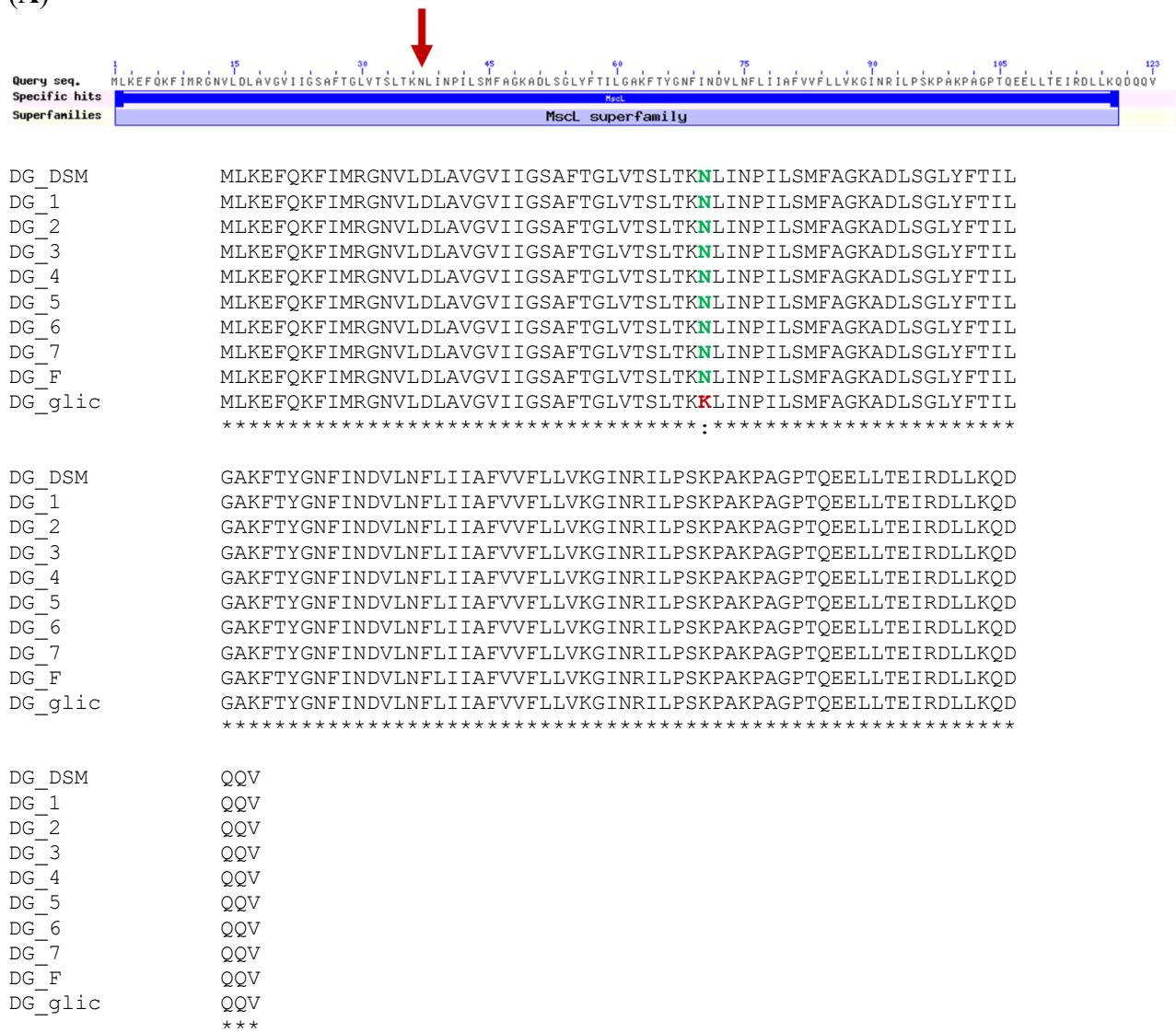


Supplementary Figure 1. ClustalW multiple sequence alignment of the aminoacidic sequence translated from the three putative genes where non-conservative mutations have been identified. **(A)** Large-conductance mechanosensitive channel protein MscL. **(B)** Ndh, NADH dehydrogenase, FAD-containing subunit; DocX, Uncharacterized membrane protein YphA, DoxX/SURF4 family. **(C)** FoF1-type ATP synthase, alpha subunit. The pictures before the alignments derive from the output of the NCBI Conserved Domain Database search (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>). The vertical red arrows indicate the position of the mutation. ClustalW symbols: "*" means that the residues or nucleotides in that column are identical in all sequences in the alignment; ":" means conserved substitutions.

(A)



(B)



DG_6	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_5	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_4	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_3	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_2	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_1	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY
DG_DSM	GDVSLVDQDGTGKGQPQIVQGAEATALTALTNIEAKLENKQQVEYKANYSGFMVSLGSKY *****
DG_glic	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_F	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_7	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_6	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_5	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_4	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_3	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_2	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_1	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS
DG_DSM	GVANIMGWLHLSGFFAMLMKHLVNMLYFIQVYSGYYLFQYFMHEFFRTRNGRNMFRGHLS *****
DG_glic	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_F	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_7	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_6	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_5	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_4	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_3	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_2	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_1	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA
DG_DSM	RQGNVLWTL P ARLTLGAMWLIDCWPKIQGKESWFIDKLRLPFTWLQPAATSGASAAGADA *****
DG_glic	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_F	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_7	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_6	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_5	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_4	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_3	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_2	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_1	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA
DG_DSM	TSAATGAAAGAAKATKTVFSLSYQYGNPMMVFEKMPNWYYSITKALIPNQQVAFFMQKA *****
DG_glic	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_F	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_7	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_6	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_5	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_4	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_3	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_2	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_1	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF
DG_DSM	MTIMEILIGLALVAGLFTWLTSAAITAFVGVFCLSGMFYWVNIWMIPMAFACMNGSGRAF *****
DG_glic	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_F	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_7	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_6	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_5	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_4	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_3	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_2	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_1	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK
DG_DSM	GLDKWVVPYLQKVFGKWRYGTPRSLYGTDTLK *****

(C)



DG_glic	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_F	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_7	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_6	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_5	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_4	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_3	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_2	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_DSMZ	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI
DG_1	LERAAKLSDKLGGGSMTALPVIETQAGDISAYIPTNVISITDGQIFLQSDLFYAGTRPAI

DG_glic	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_F	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_7	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_6	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_5	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_4	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_3	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_2	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_DSMZ	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV
DG_1	DAGASVSRVGGDAQVKAMKKVAGTLRLDLASFRELEAFTQFGSDLDAATQAKLNRGRRTV

DG_glic	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_F	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_7	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_6	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_5	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_4	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_3	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_2	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_DSMZ	EVLKQPVHKPLPVEKQVILIYALTHGFLDP I PIEDITRFQDELDFDFDSNAADLLKQIRD
DG_1	EVLKQPVHKPLPVEKQVILIYALTHGFLDP V PIEDITRFQDELDFDFDSNAADLLKQIRD
	*****:*****
DG_glic	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_F	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_7	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_6	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_5	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_4	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_3	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_2	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_DSMZ	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
DG_1	TGNLPDTDKLDAQIKAFAGGFQTSKQLAAAKD
