

Supplementary Material 5. Functional characterization of HOGs including differentially expressed genes from *O.nungara* (ONUN) and *S. mediterranea* (SMED) shared between different experiments. A) Comparisons between experiments and between species in different experiments. Blue: comparison between species in the same experiment and the same regulation do not share HOGs. expA has been used to represent all experimental conditions. Green: comparisons sharing a high number of HOGs. Pink: comparisons sharing a low number of HOGs. B) Functional characterization of shared HOGs. Up: a simplified treemap of the enriched functions in all shared HOGs. Only the most general GOs in the squares are indicated. Some enriched GOs that can be related to adaptation to life on land are indicated out of the treemap. Down (left): Identified pathways were these genes are involved. Down (right): General functions of HOGs that can act as regulatory elements

A

expA_UP_ONUN-expA_UP_SMED	0
expA_Down_ONUN-expA_Down_SMED	0
ONUN_Hyperoxia-SMED_Osmo	122
ONUN_Hypoxia-SMED_Osmo	102
ONUN_VL-SMED_Osmo	80
ONUN_Osmo-SMED_Osmo	13
ONUN_Hyperoxia-SMED_chemoDeath	4
ONUN_Hyperoxia-SMED_chemoFood	3
ONUN_Hyperoxia-SMED_UV24D	3
ONUN_Hypoxia-SMED_chemoDeath	3
ONUN_Hypoxia-SMED_UV24D	3
ONUN_chemoFood-SMED_Osmo	2
ONUN_Hyperoxia-SMED_Hypoxia	2
ONUN_Hyperoxia-SMED_VL	2
ONUN_chemoDeath-SMED_Osmo	1
ONUN_Hypoxia-SMED_chemoFood	1

