Supplementary Material

# Supplementary Tables

**Supplementary Table S****1** Differentially expressed KEGG genes which correspond to functional groups of protein metabolism and biogenesis of mitochondria and ribosomes shared by sporophytes of the Helgoland selfing and both reciprocal crosses among Helgoland and Spitsbergen *Laminaria digitata* at 20.5°C in comparison to 10°C.

|  |  |  |
| --- | --- | --- |
| **Putative function** | **KEGG gene** | **Description** |
|  |  |  |
| **Down-regulated** |  |  |
|  |  |  |
| Protein degradation | *BB* | E3 ubiquitin-protein ligase BIG BROTHER and related proteins |
|  | *HERC4* | E3 ubiquitin-protein ligase HERC4 |
| Protein modification | *AURKX* | aurora kinase, other |
|  | *ANKRD52* | serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C |
| Transcription | *CSTF2, RNA15* | cleavage stimulation factor subunit 2 |
|  | *CTDNEP1, DULLARD, NEM1* | CTD nuclear envelope phosphatase 1 |
|  | *CTDSPL2* | CTD small phosphatase-like protein 2 |
|  | *ELAVL2\_3\_4* | ELAV like protein 2/3/4 |
|  | *PKNOX* | homeobox protein PKNOX |
|  | *PARN, PNLDC1* | poly(A)-specific ribonuclease |
|  | *CTDP1, FCP1* | RNA polymerase II subunit A C-terminal domain phosphatase |
|  | *E2F7\_8* | transcription factor E2F7/8 |
|  | *YAP1, Yki* | transcriptional coactivator YAP1 |
| Translation | *dapB* | 4-hydroxy-tetrahydrodipicolinate reductase |
|  | *efp* | elongation factor P |
|  | *EEF2KMT* | protein-lysine N-methyltransferase EEF2KMT |
|  |  |  |
| **Up-regulated** |  |  |
|  |  |  |
| Amino acid synthesis | *argAB* | amino-acid N-acetyltransferase |
|  | *OTC, argF, argI* | ornithine carbamoyltransferase |
| Mitochondrial biogenesis | *FDXR* | adrenodoxin-NADP+ reductase |
|  | *COX10, ctaB, cyoE* | heme o synthase |
|  | *BCS1* | mitochondrial chaperone BCS1 |
|  | *ERV1, GFER, ALR* | mitochondrial FAD-linked sulfhydryl oxidase |
|  | *ATP23, XRCC6BP1* | mitochondrial inner membrane protease ATP23 |
|  | *GRPE* | molecular chaperone GrpE |
|  | *hscB, HSCB, HSC20* | molecular chaperone HscB |
|  | *NAA20, NAT3* | N-terminal acetyltransferase B complex catalytic subunit |
| **Table S1** continued | |  |
| **Putative function** | **KEGG gene** | **Description** |
|  | *NDUFAF3* | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 |
|  | *NDUFAF6* | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 6 |
|  | *SIL1, SLS1* | nucleotide exchange factor SIL1 |
| Protein degradation | *COPS3, CSN3* | COP9 signalosome complex subunit 3 |
|  | *PSMD14, RPN11, POH1* | 26S proteasome regulatory subunit N11 |
|  | *PSMC5, RPT6* | 26S proteasome regulatory subunit T6 |
|  | *SENP8, NEDP1, DEN1* | sentrin-specific protease 8 |
|  | *UCHL3, YUH1* | ubiquitin carboxyl-terminal hydrolase L3 |
| Protein modification | *PIGP, GPI19, DSCR5* | phosphatidylinositol N-acetylglucosaminyltransferase subunit P |
|  | *GAA1* | GPI-anchor transamidase subunit GAA1 |
|  | *TP53RK, PRPK, BUD32* | TP53 regulating kinase and related kinases |
| Ribosome synthesis | *RP-L10e, RPL10* | large subunit ribosomal protein L10e |
|  | *RP-L11e, RPL11* | large subunit ribosomal protein L11e |
|  | *RP-L13, MRPL13, rplM* | large subunit ribosomal protein L13 |
|  | *RP-L14e, RPL14* | large subunit ribosomal protein L14e |
|  | *RP-L18Ae, RPL18A* | large subunit ribosomal protein L18Ae |
|  | *RP-L19e, RPL19* | large subunit ribosomal protein L19e |
|  | *RP-L20, MRPL20, rplT* | large subunit ribosomal protein L20 |
|  | *RP-L22e, RPL22* | large subunit ribosomal protein L22e |
|  | *RP-L27Ae, RPL27A* | large subunit ribosomal protein L27Ae |
|  | *RP-L27e, RPL27* | large subunit ribosomal protein L27e |
|  | *RP-L29e, RPL29* | large subunit ribosomal protein L29e |
|  | *RP-L32e, RPL32* | large subunit ribosomal protein L32e |
|  | *RP-L34e, RPL34* | large subunit ribosomal protein L34e |
|  | *RP-L35Ae, RPL35A* | large subunit ribosomal protein L35Ae |
|  | *RP-L36e, RPL36* | large subunit ribosomal protein L36e |
|  | *RP-L6e, RPL6* | large subunit ribosomal protein L6e |
|  | *RP-L7e, RPL7* | large subunit ribosomal protein L7e |
|  | *NSA2* | ribosome biogenesis protein NSA2 |
|  | *RP-S10e, RPS10* | small subunit ribosomal protein S10e |
|  | *RP-S11e, RPS11* | small subunit ribosomal protein S11e |
|  | *RP-S14e, RPS14* | small subunit ribosomal protein S14e |
|  | *RP-S16e, RPS16* | small subunit ribosomal protein S16e |
|  | *RP-S17e, RPS17* | small subunit ribosomal protein S17e |
|  | *RP-S23e, RPS23* | small subunit ribosomal protein S23e |
|  | *RP-S24e, RPS24* | small subunit ribosomal protein S24e |
|  | *RP-S3e, RPS3* | small subunit ribosomal protein S3e |
|  | *RP-S7e, RPS7* | small subunit ribosomal protein S7e |
|  | *RP-S8e, RPS8* | small subunit ribosomal protein S8e |
| **Table S1** continued | |  |
| **Putative function** | **KEGG gene** | **Description** |
|  | *RP-S27Ae, RPS27A, UBA80* | ubiquitin-small subunit ribosomal protein S27Ae |
| Transcription | *RPB9, POLR2I* | DNA-directed RNA polymerase II subunit RPB9 |
|  | *TAF9B, TAF9* | transcription initiation factor TFIID subunit 9B |
|  | *SUPT4H1, SPT4* | transcription elongation factor SPT4 |
| Translation | *dtd, DTD* | D-aminoacyl-tRNA deacylase |
|  | *EEF1B* | elongation factor 1-beta |
|  | *EEF1G* | elongation factor 1-gamma |
|  | *METTL6* | methyltransferase-like protein 6 |

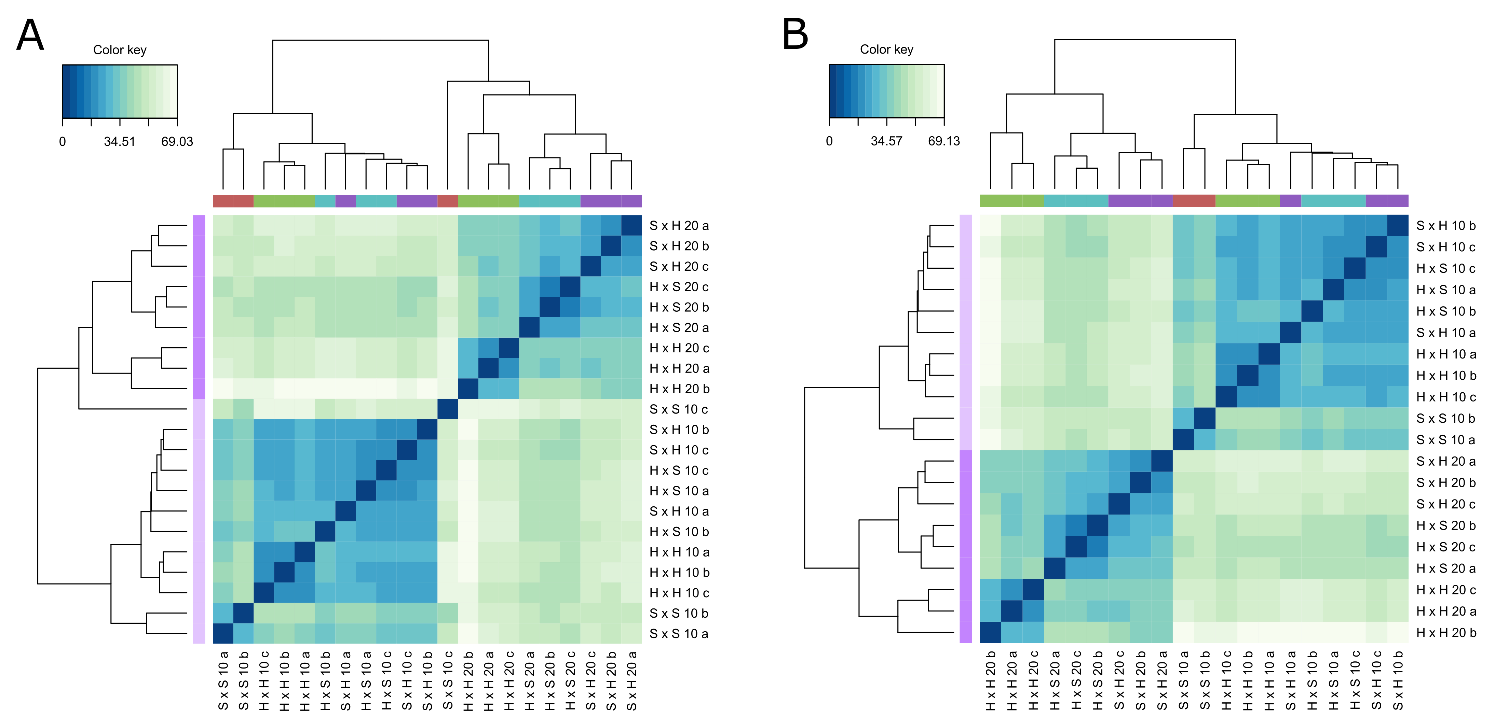
**Supplementary Table S2** Differentially expressed KEGG genes common to the comparisons of both reciprocal crosses and one selfing against the remaining selfing at 10°C, which indicates lineage-specific regulation patterns.

|  |  |  |
| --- | --- | --- |
| **KEGG KO** | **KEGG gene** | **Description** |
|  |  |  |
| **Down-regulated in the reciprocal crosses and SxS vs. HxH at 10°C** | | |
|  |  |  |
| K05643 | *ABCA3* | ATP-binding cassette, subfamily A (ABC1), member 3 |
| K07098 | *K07098* | uncharacterized protein |
|  |  |  |
| **Up-regulated in the reciprocal crosses and SxS vs. HxH at 10°C** | | |
|  |  |  |
| K12460 | *KIDINS220, ARMS* | ankyrin repeat-rich membrane spanning protein |
| K00698 | *CHS1* | chitin synthase |
| K08844 | *LRRK2* | leucine-rich repeat kinase 2 |
| K09597 | *SPPL2B* | signal peptide peptidase-like 2B |
| K14716 | *SLC39A10, ZIP10* | solute carrier family 39 (zinc transporter), member 10 |
|  |  |  |
| **Down-regulated in the reciprocal crosses and HxH vs. SxS at 10°C** | | |
|  |  |  |
| K12460 | *KIDINS220, ARMS* | ankyrin repeat-rich membrane spanning protein |
| K10712 | *ADO* | cysteamine dioxygenase |
| K24835 | *GLIPR2* | glioma pathogenesis-related protein 2 |
|  | | |
| **Up-regulated in the reciprocal crosses and HxH vs. SxS at 10°C** | | |
|  |  |  |
| K11793 | *CRBN* | cereblon |
| K13993 | *HSP20* | HSP20 family protein |
| K04419 | *MAP3K11, MLK3* | mitogen-activated protein kinase kinase kinase 11 |
| K04441 | *P38* | p38 MAP kinase |
| K04716 | *SGPP1* | sphingosine-1-phosphate phosphatase 1 |
| K19673 | *TTC21B, IFT139B* | tetratricopeptide repeat protein 21B |

**Supplementary Table S3** Differentially expressed KEGG genes shared by both reciprocal crosses at 20.5°C in comparison to the Helgoland selfing at 20.5°C, which indicates regulation patterns specific for the Spitsbergen lineage.

|  |  |  |
| --- | --- | --- |
| **KEGG KO** | **KEGG gene** | **Description** |
|  |  |  |
| **Down-regulated in the reciprocal crosses vs. HxH at 20.5°C** | | |
|  |  |  |
| K22200 | *E3.1.3.63* | 2-carboxy-D-arabinitol-1-phosphatase |
| K14652 | *ribBA* | 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II |
| K00549 | *metE* | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase |
| K16339 | *THEM4, CTMP* | acyl-coenzyme A thioesterase THEM4 |
| K21407 | *APMAP* | adipocyte plasma membrane-associated protein |
| K15303 | *AKR7* | aflatoxin B1 aldehyde reductase |
| K01480 | *speB* | agmatinase |
| K00496 | *alkB1\_2, alkM* | alkane 1-monooxygenase |
| K03844 | *ALG11* | alpha-1,2-mannosyltransferase |
| K24611 | *AMMECR1, AMMECR1L* | AMME syndrome candidate gene 1 protein |
| K05643 | *ABCA3* | ATP-binding cassette, subfamily A (ABC1), member 3 |
| K24139 | *PILS, ECM3* | auxin efflux carrier family protein |
| K05869 | *CAMK4* | calcium/calmodulin-dependent protein kinase IV |
| K01672 | *CA* | carbonic anhydrase |
| K06628 | *CDC45* | cell division control protein 45 |
| K12192 | *CHMP2B* | charged multivesicular body protein 2B |
| K07213 | *ATOX1, ATX1, copZ, golB* | copper chaperone |
| K22544 | *SAMHD1* | deoxynucleoside triphosphate triphosphohydrolase SAMHD1 |
| K11754 | *folC* | dihydrofolate synthase / folylpolyglutamate synthase |
| K02685 | *PRI2* | DNA primase large subunit |
| K10950 | *ERO1L* | ERO1-like protein alpha |
| K07192 | *FLOT* | flotillin |
| K00471 | *BBOX1* | gamma-butyrobetaine dioxygenase |
| K00804 | *GGPS1* | geranylgeranyl diphosphate synthase, type III |
| K24835 | *GLIPR2* | glioma pathogenesis-related protein 2 |
| K00717 | *FUT8* | glycoprotein 6-alpha-L-fucosyltransferase |
| K00463 | *IDO, INDO* | indoleamine 2,3-dioxygenase |
| K17256 | *IGFALS, ALS* | insulin-like growth factor-binding protein complex acid labile subunit |
| K01637 | *E4.1.3.1, aceA* | isocitrate lyase |
| K01424 | *E3.5.1.1, ansA, ansB* | L-asparaginase |
| K00140 | *mmsA, iolA, ALDH6A1* | malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase |
| K00045 | *E1.1.1.67, mtlK* | mannitol 2-dehydrogenase |
| K03406 | *mcp* | methyl-accepting chemotaxis protein |
| K19304 | *mepM* | murein DD-endopeptidase |
| K03434 | *PIGL* | N-acetylglucosaminylphosphatidylinositol deacetylase |
| **Table S3** continued | |  |
| **KEGG KO** | **KEGG gene** | **Description** |
| K12385 | *NPC1* | Niemann-Pick C1 protein |
| K14001 | *SIL1, SLS1* | nucleotide exchange factor SIL1 |
| K10798 | *PARP2\_3\_4* | poly [ADP-ribose] polymerase 2/3/4 |
| K19704 | *PTC1* | protein phosphatase PTC1 |
| K22895 | *cruH* | renierapurpurin 18,18'-hydroxylase |
| K03537 | *POP5* | ribonuclease P/MRP protein subunit POP5 |
| K14686 | *SLC31A1, CTR1* | solute carrier family 31 (copper transporter), member 1 |
| K00235 | *SDHB, SDH2* | succinate dehydrogenase (ubiquinone) iron-sulfur subunit |
| K03133 | *TAF9B, TAF9* | transcription initiation factor TFIID subunit 9B |
| K12624 | *LSM5* | U6 snRNA-associated Sm-like protein LSm5 |
| K07098 | *K07098* | uncharacterized protein |
| K23887 | *UAPA\_C* | uric acid-xanthine permease |
| K20241 | *WDR44, RAB11BP* | WD repeat-containing protein 44 |
|  |  |  |
| **Up-regulated in the reciprocal crosses vs. HxH at 20.5°C** | | |
|  |  |  |
| K03715 | *MGD* | 1,2-diacylglycerol 3-beta-galactosyltransferase |
| K02551 | *menD* | 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase |
| K21737 | *ACET6, DES6* | acyl-lipid Delta6-acetylenase / acyl-lipid (9-3)-desaturase |
| K11996 | *MOCS3, UBA4* | adenylyltransferase and sulfurtransferase |
| K01785 | *galM, GALM* | aldose 1-epimerase |
| K12460 | *KIDINS220, ARMS* | ankyrin repeat-rich membrane spanning protein |
| K05674 | *ABCC10* | ATP-binding cassette, subfamily C (CFTR/MRP), member 10 |
| K08766 | *CPT2* | carnitine O-palmitoyltransferase 2 |
| K23882 | *CISD2* | CDGSH iron-sulfur domain-containing protein 2 |
| K08818 | *CDC2L* | cell division cycle 2-like |
| K06238 | *COL6A* | collagen type VI alpha |
| K08803 | *DAPK* | death-associated protein kinase |
| K22848 | *DGAT2* | diacylglycerol O-acyltransferase 2, plant |
| K03164 | *TOP2* | DNA topoisomerase II |
| K00366 | *nirA* | ferredoxin-nitrite reductase |
| K01845 | *hemL* | glutamate-1-semialdehyde 2,1-aminomutase |
| K11275 | *H1\_5* | histone H1/5 |
| K00913 | *ITPK1* | inositol-1,3,4-trisphosphate 5/6-kinase / inositol-tetrakisphosphate 1-kinase |
| K08844 | *LRRK2* | leucine-rich repeat kinase 2 |
| K03428 | *bchM, chlM* | magnesium-protoporphyrin O-methyltransferase |
| K12613 | *DCP2* | mRNA-decapping enzyme subunit 2 |
| K00855 | *PRK, prkB* | phosphoribulokinase |
| K22686 | *NMA111* | pro-apoptotic serine protease NMA111 |
| K14662 | *NTAN1* | protein N-terminal asparagine amidohydrolase |
| K11699 | *RDR, RDRP* | RNA-dependent RNA polymerase |
| K14823 | *EBP2, EBNA1BP2* | rRNA-processing protein EBP2 |
| K19833 | *CLA4* | serine/threonine-protein kinase CLA4 |
| K09597 | *SPPL2B* | signal peptide peptidase-like 2B |
| K14716 | *SLC39A10, ZIP10* | solute carrier family 39 (zinc transporter), member 10 |
| K07748 | *NSDHL, ERG26* | sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating) |
| **Table S3** continued | |  |
| **KEGG KO** | **KEGG gene** | **Description** |
| K11650 | *SMARCD* | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D |
| K09649 | *PRSS16* | thymus-specific serine protease |
| K07137 | *K07137* | uncharacterized protein |
| K11807 | *WDTC1, DCAF9* | WD and tetratricopeptide repeats protein 1 |

# Supplementary Figures



**Supplementary Figure S1** Cluster heatmaps based on a distance matrix of KEGG gene expression in replicates (a–c) of *Laminaria digitata* sporophytes produced by crossing females x males from Helgoland (H) and Spitsbergen (S) in experiment 2 at 10 and 20.5°C (**A**) including and (**B**) excluding the outlier replicate S x S 10 c.