Supporting Information

Morphology, Migration and Transcriptome Analysis of Schwann Cell Culture on Butterfly Wings with Different Surface Architectures

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Methods

Butterfly wing surface chemical composition analysis

Butterfly wing surface chemical composition was analyzed by Fourier transform infrared spectrophotometry (FTIR, Thermo Scientific, Nicolet iS10, USA), solid state nuclear magnetic resonance spectroscopy (NMR, Bruker, Avance Ⅲ 400 MHz, Germany) and X-ray Photoelectron Spectroscopy (XPS, Shimadzu, AXIS-Ultra DLD, Japan).
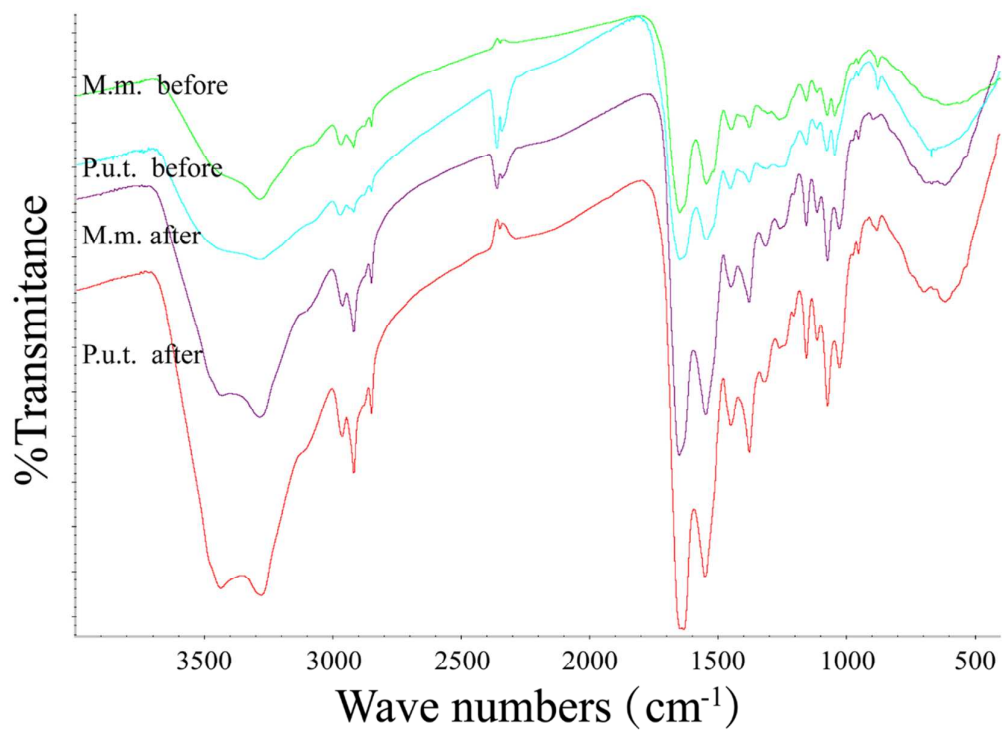
Figure S1. The FTIR spectra of M.m. and P.u.t. butterfly wings before or after the acid-base treatment.
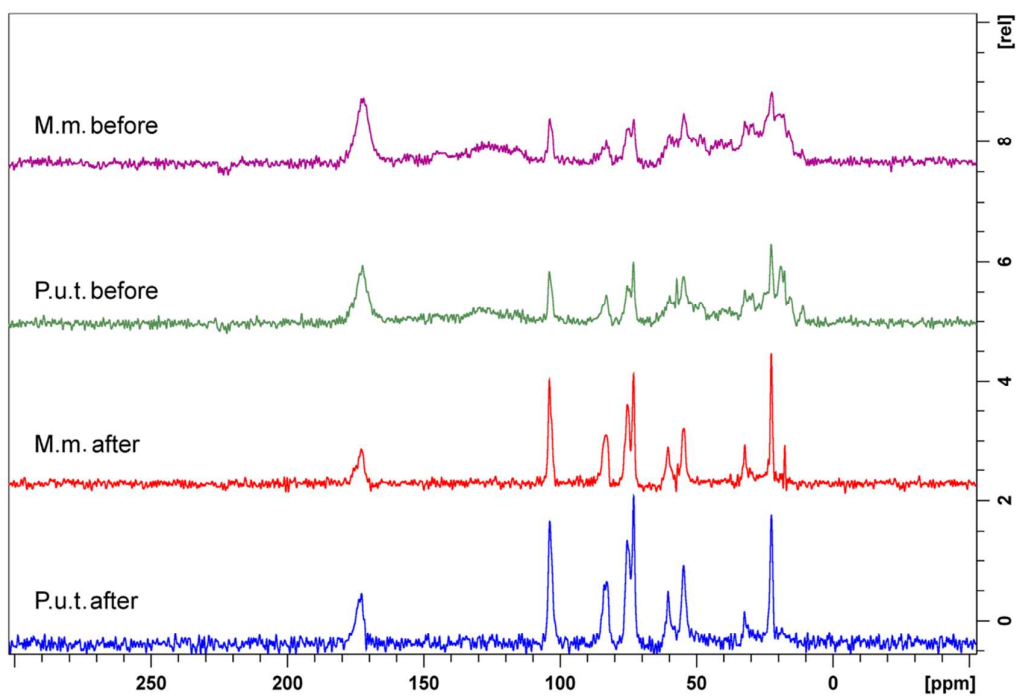
Figure S2. The solid state NMR ^{13}C analysis of M.m. and P.u.t. butterfly wings before or after the acid-base treatment.
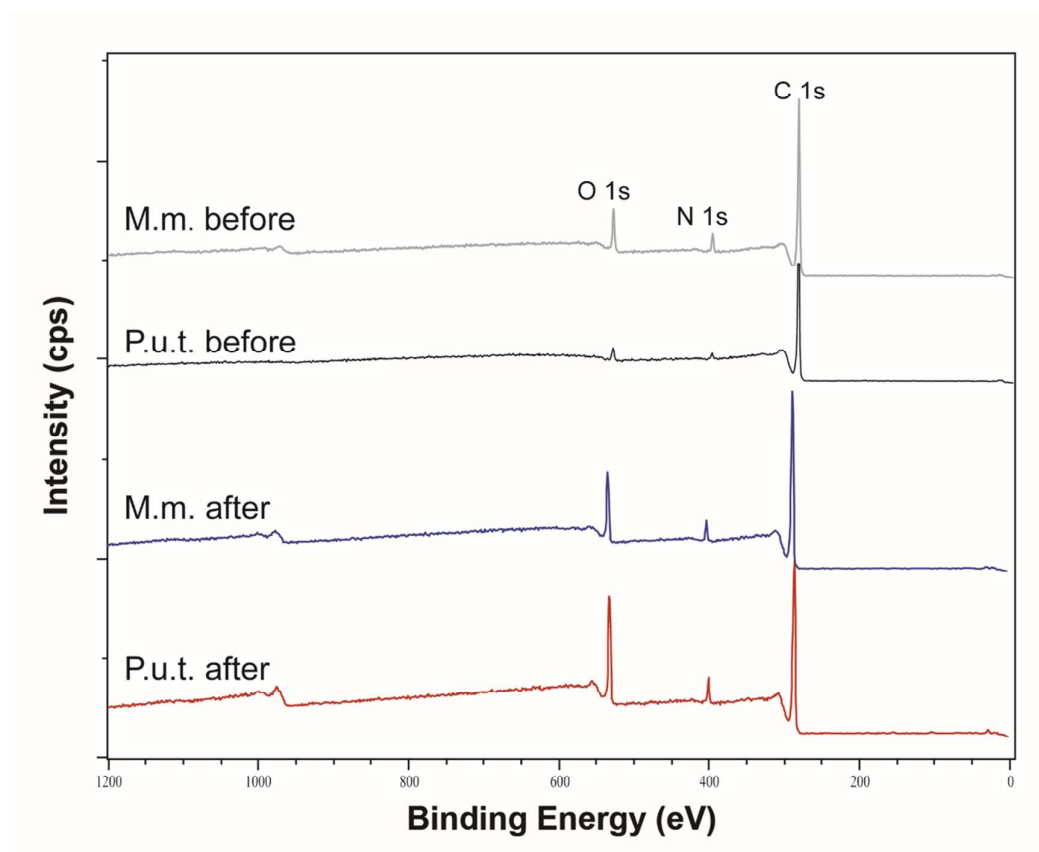
Figure S3. The surface element analysis of M.m. and P.u.t. butterfly wings before or after the acid-base treatment.
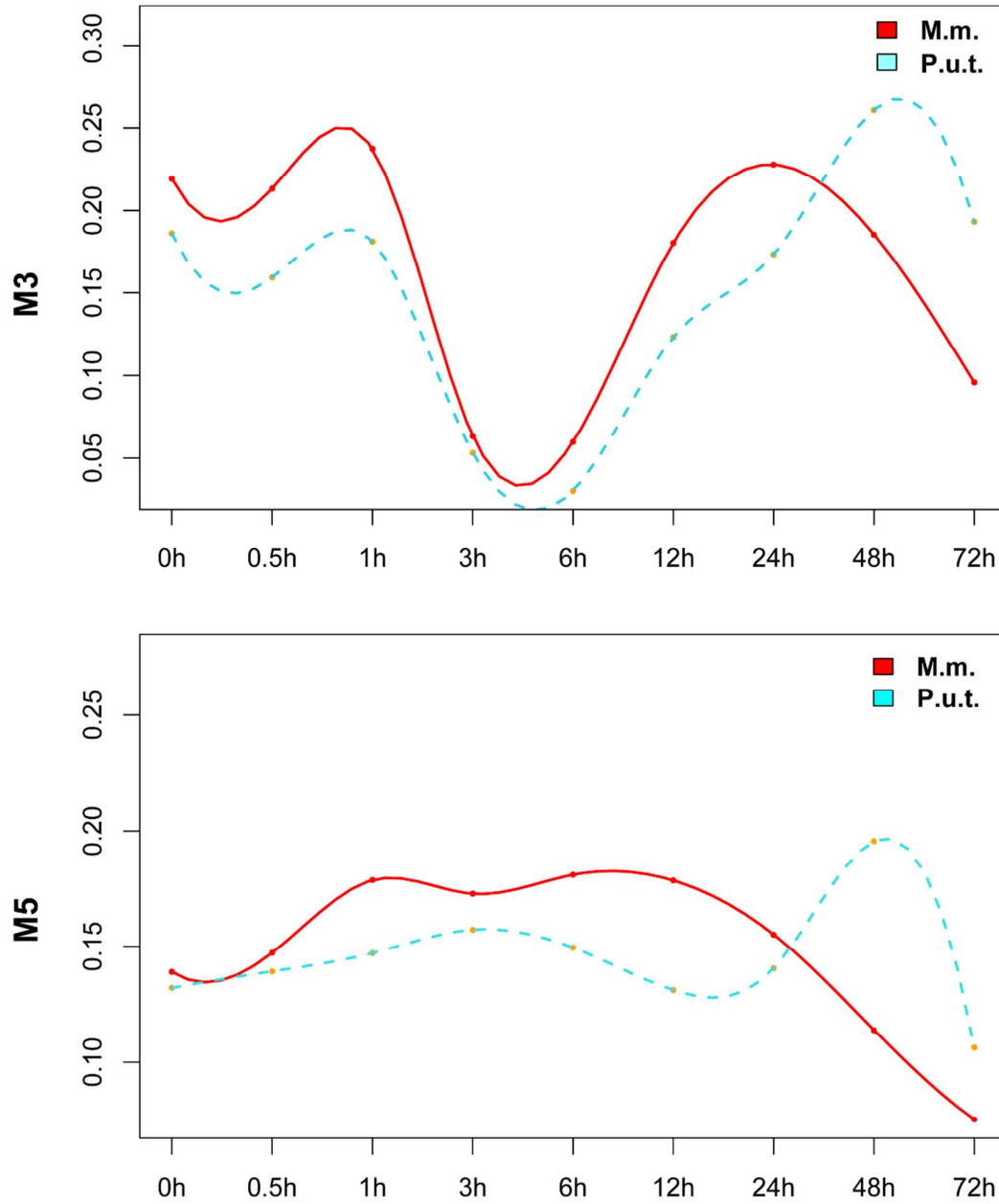
Figure S4. Expression trajectory of specific modules. Expression trajectory of module 3 (main function: lysosome, nucleotide binding, transport) and module 5 (main function: cell migration, ion binding) based on ME (module eigengene).
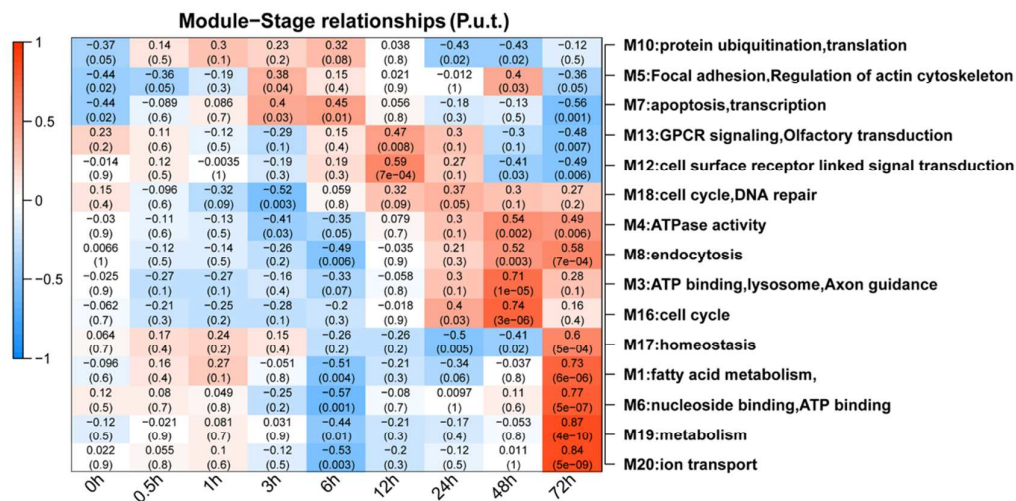
Module−Stage relationships (P.u.t.)

Module	0h	0.5h	1h	3h	6h	12h	24h	48h	72h
M10: protein ubiquitination, translation	-0.37 (0.05)	0.14 (0.5)	0.3 (0.1)	0.23 (0.2)	0.32 (0.08)	0.038 (0.8)	-0.43 (0.02)	-0.43 (0.02)	-0.12 (0.5)
M5: Focal adhesion, Regulation of actin cytoskeleton	-0.44 (0.02)	-0.36 (0.05)	-0.19 (0.3)	0.38 (0.04)	0.15 (0.4)	0.021 (0.9)	-0.012 (1)	0.4 (0.03)	-0.36 (0.05)
M7: apoptosis, transcription	-0.44 (0.02)	-0.089 (0.6)	0.086 (0.7)	0.4 (0.03)	0.45 (0.01)	0.056 (0.8)	-0.18 (0.3)	-0.13 (0.5)	-0.56 (0.001)
M13: GPCR signaling, Olfactory transduction	0.23 (0.2)	0.11 (0.6)	-0.12 (0.5)	-0.29 (0.1)	0.15 (0.4)	0.47 (0.008)	0.3 (0.1)	-0.3 (0.1)	-0.48 (0.007)
M12: cell surface receptor linked signal transduction	-0.014 (0.9)	0.12 (0.5)	-0.0035 (1)	-0.19 (0.3)	0.19 (0.3)	0.59 (7e-04)	0.27 (0.1)	-0.41 (0.03)	-0.49 (0.006)
M18: cell cycle, DNA repair	0.15 (0.4)	-0.096 (0.6)	-0.32 (0.09)	-0.52 (0.003)	0.059 (0.8)	0.32 (0.09)	0.37 (0.05)	0.3 (0.1)	0.27 (0.2)
M4: ATPase activity	-0.03 (0.9)	-0.11 (0.6)	-0.13 (0.5)	-0.41 (0.03)	-0.35 (0.05)	0.079 (0.7)	0.3 (0.1)	0.54 (0.002)	0.49 (0.006)
M8: endocytosis	0.0066 (1)	-0.12 (0.5)	-0.14 (0.5)	-0.26 (0.2)	-0.49 (0.006)	-0.035 (0.9)	0.21 (0.3)	0.52 (0.003)	0.58 (7e-04)
M3: ATP binding, lysosome, Axon guidance	-0.025 (0.9)	-0.27 (0.1)	-0.27 (0.1)	-0.16 (0.4)	-0.33 (0.07)	-0.058 (0.8)	0.3 (0.1)	0.71 (1e-05)	0.28 (0.1)
M16: cell cycle	-0.062 (0.7)	-0.21 (0.2)	-0.25 (0.2)	-0.28 (0.1)	-0.2 (0.3)	-0.018 (0.9)	0.4 (0.03)	0.74 (3e-06)	0.16 (0.4)
M17: homeostasis	0.064 (0.7)	0.17 (0.4)	0.24 (0.2)	0.15 (0.4)	-0.26 (0.2)	-0.26 (0.2)	-0.5 (0.005)	-0.41 (0.02)	0.6 (5e-04)
M1: fatty acid metabolism,	-0.096 (0.6)	0.16 (0.4)	0.27 (0.1)	-0.051 (0.8)	-0.51 (0.004)	-0.21 (0.3)	-0.34 (0.06)	-0.037 (0.8)	0.73 (6e-06)
M6: nucleoside binding, ATP binding	0.12 (0.5)	0.08 (0.7)	0.049 (0.8)	-0.25 (0.2)	-0.57 (0.001)	-0.08 (0.7)	0.0097 (1)	0.11 (0.6)	0.77 (5e-07)
M19: metabolism	-0.12 (0.5)	-0.021 (0.9)	0.081 (0.7)	0.031 (0.9)	-0.44 (0.01)	-0.21 (0.3)	-0.17 (0.4)	-0.053 (0.8)	0.87 (4e-10)
M20: ion transport	0.022 (0.9)	0.055 (0.8)	0.1 (0.6)	-0.12 (0.5)	-0.53 (0.003)	-0.2 (0.3)	-0.12 (0.5)	0.011 (1)	0.84 (5e-09)

Figure S5. Network analysis of cell growth on P.u.t. butterfly wings. Based on the co-expression modules defined by the WGCNA, matrix with the Module-trait relationships association with time variables on the x-axis. The top number in each cell corresponds to correlation and the bottom number is the p-value: red is a strong positive correlation, while blue is a strong negative correlation. Corresponding functional annotation is superimposed on the right frame.
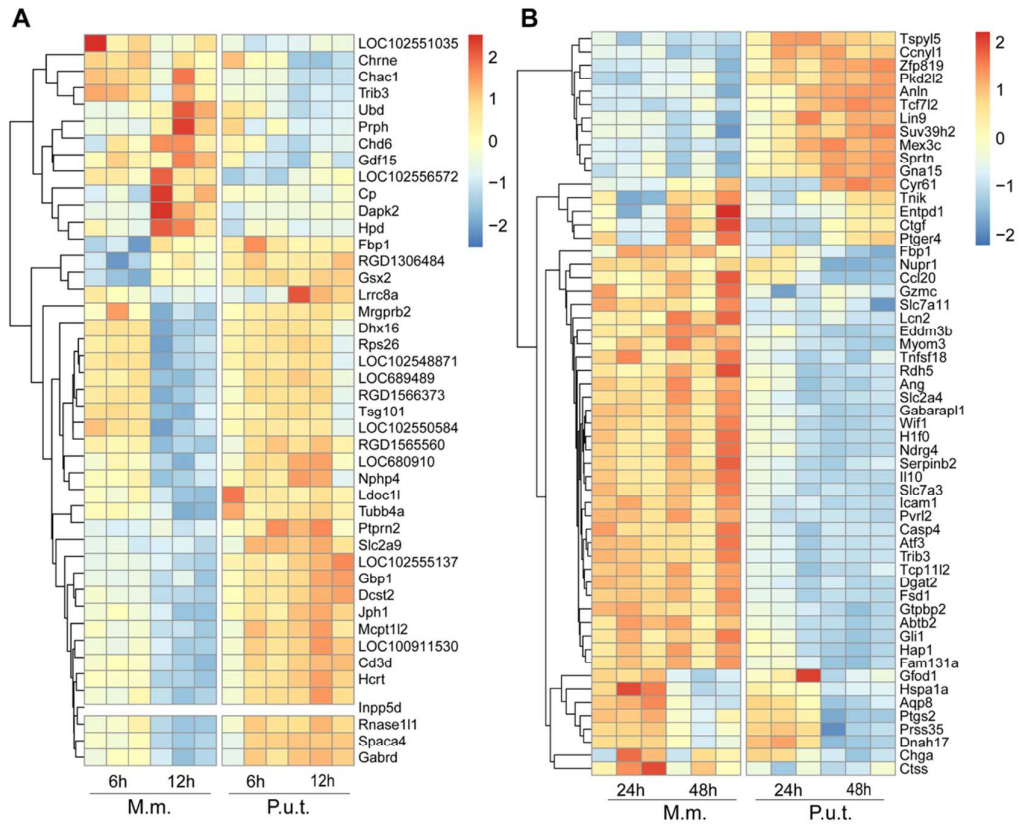
Figure S6. Differential expressed gene analysis of stage 2 and stage 3. Heatmap showing relative expression patterns of DEGs at stage 2 (6 h to 12 h) (A) and stage 3 (24 h to 48 h) (B).