Supplementary

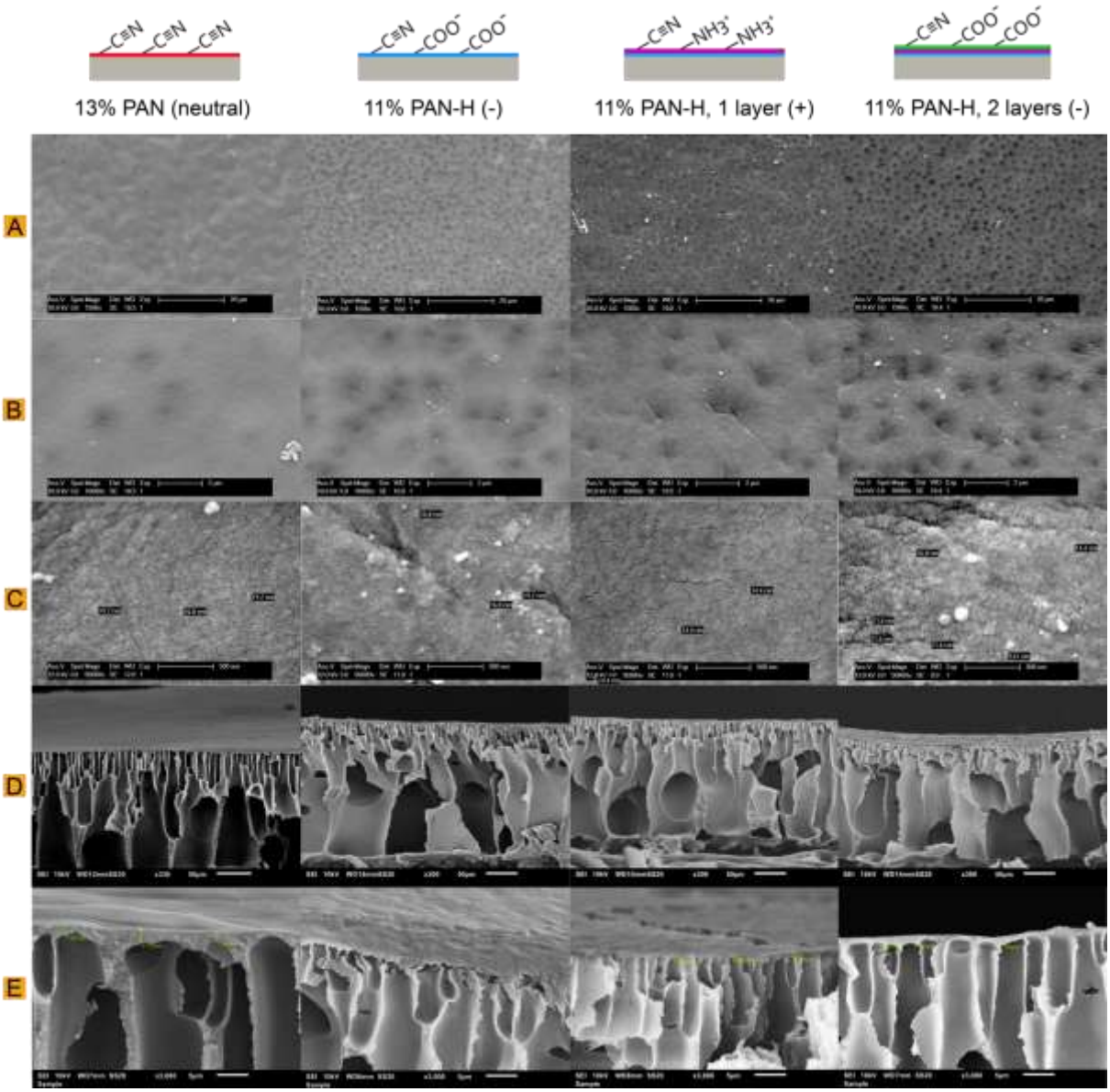

Figure S 1 SEM surface [A-C] and cross-sectional [D-E] visualization of the four membrane types at different magnifications.

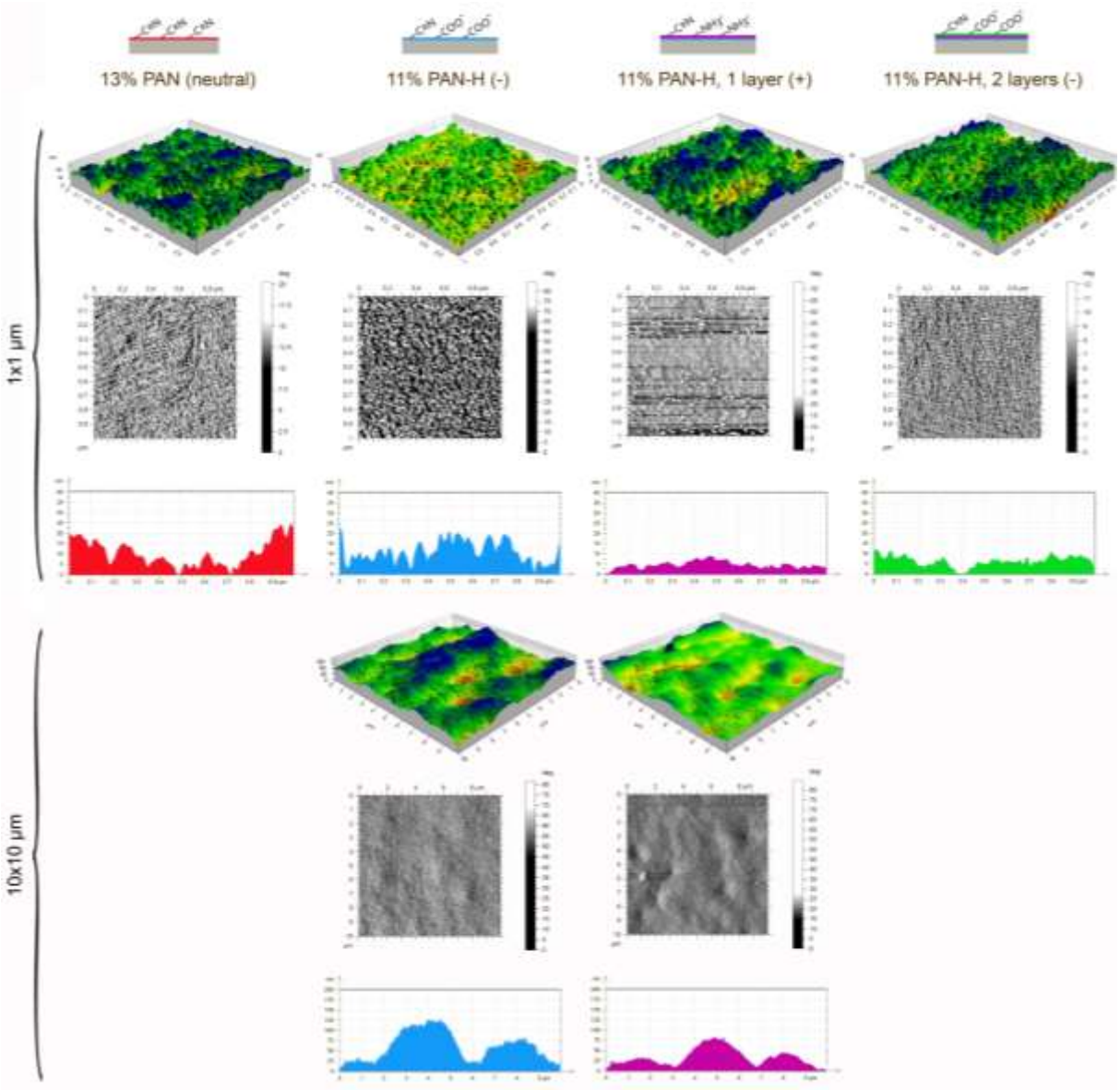

Figure S 2 Atomic Force Microscopy observations (2D and 3D) of the four membrane types at 1x1 µm and of two membrane types at 10x10 µm surface areas. The first and second row of images within each series (1x1 µm or 10x10 µm) represent the 3D and the 2D surface structure respectively. The third row of images within each series represents the profile structure of the upper surface region of the membranes.

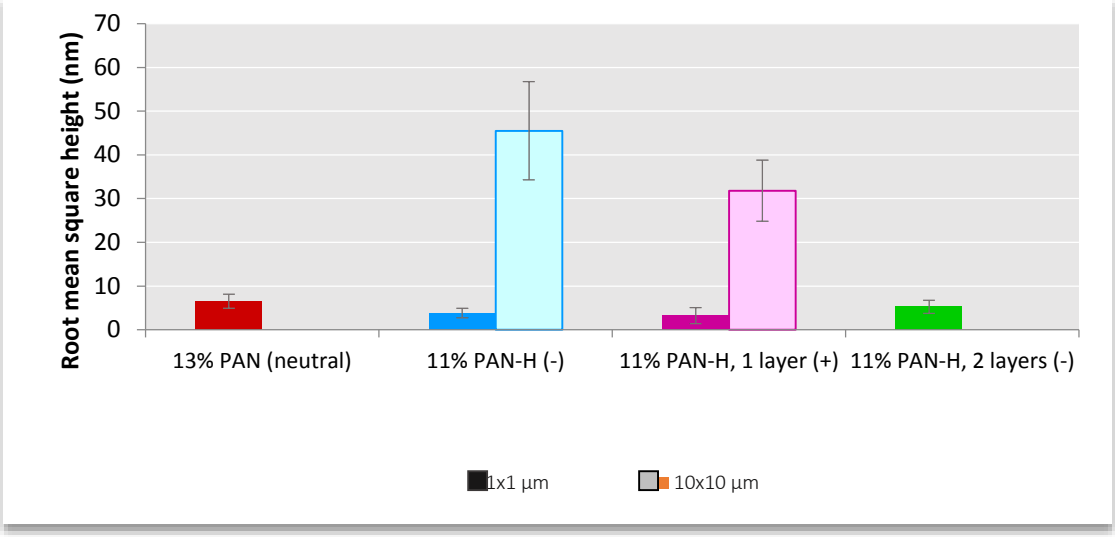

Figure S 3 Membrane surface roughness expressed as root mean square height (nm) for the four membrane types at 1x1 µm and for two membrane types 10x10 µm surface areas. Error bars represent standard deviations from the mean value (n = 3).

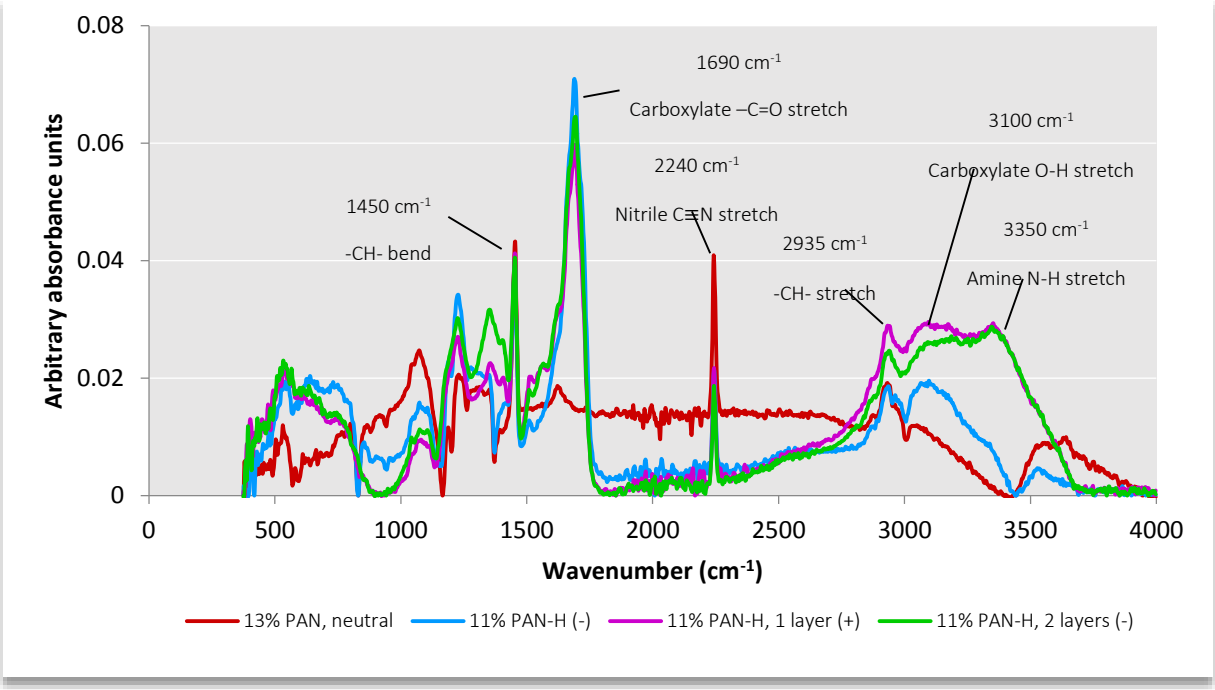

Figure S 4 ATR-FTIR spectra of the four membrane types

Appendix 1

Adapted CTAB-lysozyme method for genomic DNA extraction (Based on (Larsen et al., 2007))

A. Transfer the sample suspension in 450 µl GTE buffer to a sterile 2-ml microcentrifuge tube containing 50 µl of a 10 mg ml^{-1} lysozyme solution.

EDTA binds heavy metals and forms complexes with bivalent cations, thus destabilizing the cell membrane. It inhibits deoxyribonuclease thus prevents DNA to be broken up. Glucose increases the osmotic pressure and enhances cell lysis. The lysozyme solution was prepared in MQ instead of 25 mM Tris.Cl. Lysozyme weakens the peptidoglycan cell wall and permits water to enter the cell, thus causing lysis.

B. Mix gently and incubate 1 h at 37 °C at 900 rpm shaking speed (MB-102, ThermocCell Mixing Block, Bioer).

C. Make a 2:1 solution (v/v) of 10% SDS solution and 10 mg ml^{-1} proteinase K in MQ. Add 150 µl of this solution to the cells and mix gently. Incubate 40 min at 55 °C at 900 rpm shaking speed.

SDS is an anionic detergent destroying de cytoplasmatic membrane of the cells. Proteinase K destroys proteins. Plasmids and chromosomal DNA are released from the cells.

D. Add 1 µl RNAase A.

Destruction of the RNA released from the cell.

E. Add 200 µl of 5 M NaCl and mix gently.

NaCl blocks the binding of DNA to cetrimide.

F. Preheat CTAB solution to 65 °C in a water bath (RTE-101, Neslab), add 160 µl, and mix gently. Incubate 10 min at 65 °C in a water bath.

G. Add an equal volume (~1 ml) 25:24:1 (v/v) phenol/chloroform/isoamyl alcohol, shake vigorously to mix, and microcentrifuge for 5 min at 12 000 rcf and 4 °C (Centrifuge 5424, Eppendorf or Mikro 200R, Hettich Zentrifugen).

The aqueous (upper) layer (isoamyl alcohol) contains the DNA. The apolar (bottom) layer (phenol/chloroform) contains the undesirable organic compounds (lipids, proteins, polysaccharides, etc.).

H. Transfer 900 µl aqueous layer to a fresh sterile 2-ml microcentrifuge tube.

I. Repeat extraction with 25:24:1 (v/v) phenol/chloroform/isoamyl alcohol, shake vigorously to mix, and spin in microcentrifuge for 5 min at 12 000 rcf and 4 °C..

J. Transfer 800 µl to fresh sterile 1.5-ml microcentrifuge tube.

CAUTION: For BSL3 organisms, dip tube in a disinfectant such as Vesphene IIse to disinfect outer surface. From this point on, the supernatant can be processed in a BSL-2 laboratory (see Strategic Planning).

K. To 800 µl aqueous layer, add 560 µl (0.7 vol) isopropanol, mix gently by inversion until the DNA has precipitated out of solution.

Precipitation of DNA.

L. Incubate 30 min at room temperature. Microcentrifuge for 15 min at 12 000 rcf, room temperature.

M. Aspirate supernatant and add 1 ml of 70% ethanol in MQ to wash DNA pellet. Mix gently by inversion and microcentrifuge 5 min at 12 000 rcf at room temperature.

DNA is washed in order to remove precipitated salts.

N. Carefully aspirate supernatant, avoiding the pellet, and air-dry DNA pellet for 2 min. Do not overdry.

O. Add 30, 50 or 100 µl TE buffer (10 mM Tris.HCl, 0.1 mM EDTA in MQ, *pH* 8.23), depending on size of DNA pellet, to dried DNA pellet and store overnight at 4 °C to allow pellet to dissolve. Store up to 1 year at −20 °C.

RNase A can be added to TE (1 µg/ml) to reduce RNA contamination.