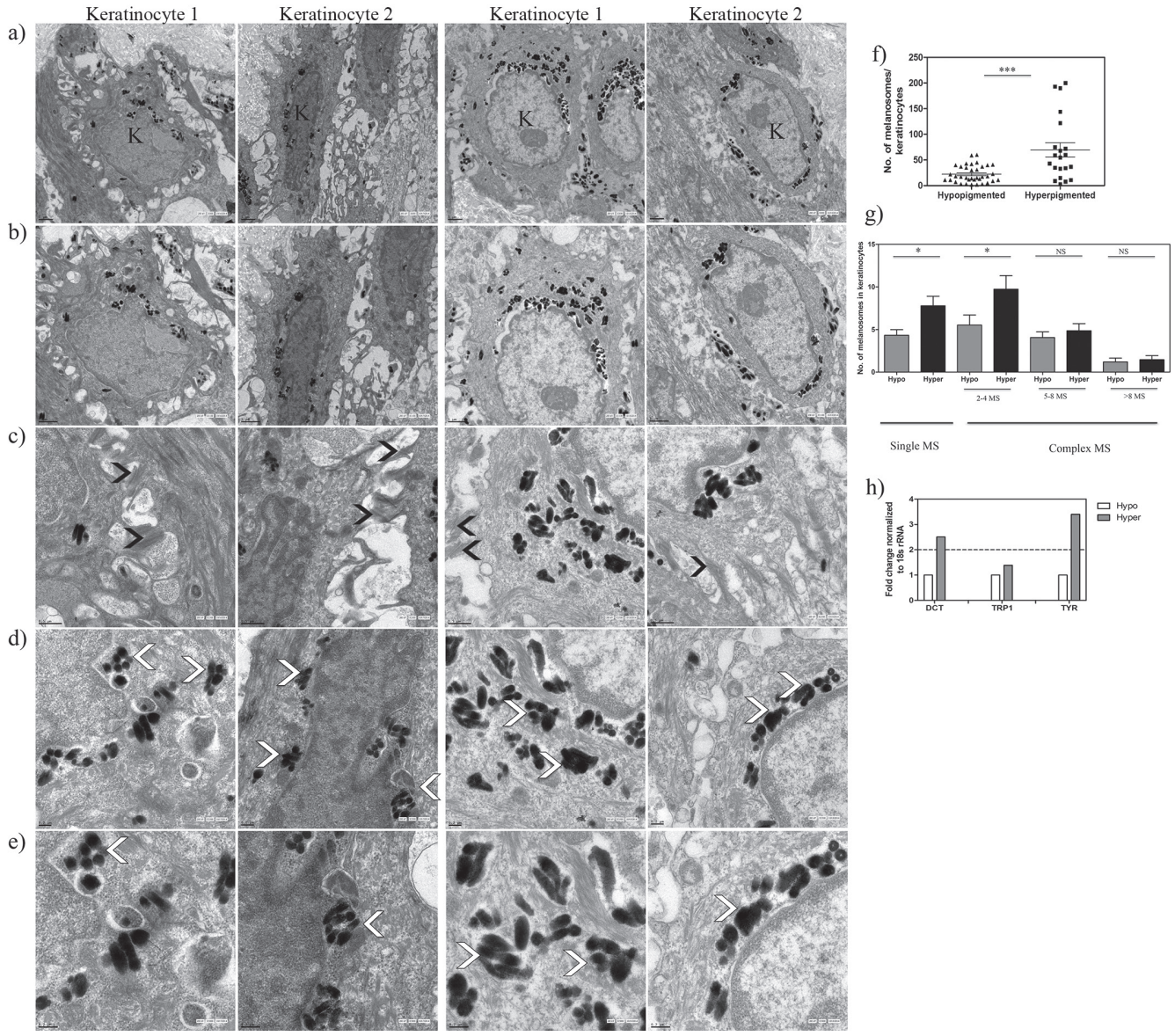

Fig. S3. Altered melanosome numbers in keratinocytes of hypopigmented vs hyperpigmented lesions: Presence of melanosomes in 2 representative keratinocytes (K) in hypopigmented (vertical panel 1 and 2) and hyperpigmented lesion (vertical panel 3 and 4). Micrographs in a) and b) horizontal panels show keratinocytes at lower magnifications (scale bar 1 μm). Horizontal panel c) shows presence of prominent desmosomal connections in cell-cell junction (black arrowheads) between neighbouring keratinocytes (scale bar 0.5 μm). Magnified images in d) and e) reveal presence of melanosomes in clusters (white arrowheads) in keratinocytes of both hypo- and hyperpigmented lesions (scale bar 0.2 μm). f) Number of melanosomes in keratinocytes of hypo- and hyperpigmented skin plotted as column bar graph. Keratinocytes in hyperpigmented epidermis show significantly higher number of melanosomes per keratinocytes compared to hypopigmented skin ($n = 36$ keratinocytes counted in hypopigmented, $n = 21$ keratinocytes counted in hyperpigmented skin). *** indicates p-value < 0.0001 using unpaired t test. g) Distribution pattern of melanosomes in keratinocytes plotted as present as single, and in clusters of 2–4, 5–8 and greater than 8 ($n = 15$ each for hypo- and hyperpigmented skin). The melanosome numbers are significantly lower in hypopigmented skin in both single as well as in 2–4 clusters. * indicates p-value < 0.05 using unpaired t test. There was no significant difference in number of melanosomes in clusters of 5–8 and >8 melanosomes per cluster. h) Real-time PCR analyses of DCT, TRP1 and TRP2 carried out using Taqman duplex assays were normalised to 18S ribosomal RNA (rRNA) and represented as fold change with respect to corresponding hypopigmented lesion plotted in a bar graph. Fold change was calculated using $2^{-\Delta\Delta Ct}$, where $\Delta\Delta Ct$ represents ΔCt of hyperpigmented–ΔCt of hypopigmented skin. DCT- Dopachrome tautomerase, TRP1-Tyrosinase related protein 1, TYR- Tyrosinase. Horizontal line represents fold change greater than 2-fold.