Supplementary data for article:

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Supplemental Fig. S1. A schematic overview of the screening method used to find improved tyrosinase variants based on melanin production.

Supplemental Fig. S2. SDS-PAGE of purified tyrosinase from the wild type (WT) and selected tyrosinase variants: molecular weight standard (M): WT tyrosinase (lane 1), random mutation variant RVC10 (lane 2), and random mutation variant RV145 (lane 3). Proteins were stained with Instant*Blue*^{TM}, (Expedeon, UK).

Supplemental Fig. S3. Protein alignment of tyrosinase WT and random mutation variants with the amino acid mutations marked in grey boxes. The six conserved H residues directly involved in copper binding are marked in ovals. Continuous ovals denote H in CuA binding region (continuous arrow) and dashed ovals denote H in CuB binding region (dashed arrow arrow).

Supplemental Fig. S4. Side chain structures of the amino acids at A) positions 183 and 322 in the WT, random mutation variant RVC10, and single mutation variants of tyrosinase and B) side chain structures of the amino acids at positions 119 and 153 in the WT, random mutation variant RV145, and new single mutation variants of tyrosinase.