Fig. 5. This multilinear HOSVD is reformulated such that it decomposes a data tensor into a linear superposition of all outer products of an eigenarray, an $x$- and a $y$-eigengene, that is, rank-1 subtensors. Raster display of Eq. 2, $T = \sum_{a=1}^{L} \sum_{b=1}^{L} \sum_{c=1}^{M} R_{abc} U_{a:b} \otimes V_{x:b}^{T} \otimes V_{y:c}^{T} \equiv \sum_{a=1}^{L} \sum_{b=1}^{L} \sum_{c=1}^{M} R_{abc} S(a, b, c)$, with overexpression (red), no change in expression (black), and underexpression (green). Explicitly shown are the ninth and tenth subtensors, $S(8 + 2, 4, 3)$ and $S(3 + 7, 2, 3)$, with the corresponding superposition coefficients, that is, higher-order singular values, $R_{8+2,4,3}$ and $R_{3+7,2,3}$. The expression of each array and eigenarray is centered at its gene-invariant level. The expression of each gene and $x$- and $y$-eigengene is centered at its $x$- and $y$-setting-invariant levels, respectively. The genes are sorted by the angular distance $\theta = \arctan(U_{8+2}/U_{3+7})$ between the two superpositions of eigenarrays $U_{8+2}$ and $U_{3+7}$, which define the expression variation across the genes in the ninth and tenth subtensors, respectively.