**Supplementary Material**

Table S1. Glossary of biomarkers of system HDF3CGF used in the study

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| **Readout** | **Description** |
| **CCL2/MCP-1** | MCP-1 system is a chemokine that mediates recruitment of monocytes and T cells into sites of inflammation. MCP-1 is categorized as an inflammation-related activity in the HDF3CGF system modeling Th1 inflammation involved in wound healing and matrix remodeling. |
| **CD106/VCAM-1** | VCAM-1 is a cell adhesion molecule that mediates adhesion of monocytes and T cells to endothelial cells. VCAM-1 is categorized as an inflammation-related activity. |
| **CD54/ICAM-1** | ICAM-1 is a cell adhesion molecule that mediates leukocyte-endothelial cell adhesion and leukocyte recruitment. ICAM-1 is categorized as an inflammation-related activity. |
| **Collagen I** | Collagen I is involved in tissue remodeling and fibrosis, and is the most common fibrillar collagen that is found in skin, bone, tendons and other connective tissues. Collagen I is categorized as a tissue remodeling-related activity. |
| **Collagen III** | Collagen III is an extracellular matrix protein and fibrillar collagen found in extensible connective tissues (skin, lung and vascular system) and is involved in cell adhesion, cell migration, tissue remodeling. Collagen III is categorized as a tissue remodeling-related activity. |
| **CXCL10/IP-10**  | IP-10 is a chemokine that mediates T cell, monocyte and dendritic cell chemotaxis. IP-10 is categorized as an inflammation-related activity. |
| **CXCL11/I-TAC**  | I-TAC is a chemokine that mediates T cell and monocyte chemotaxis. I-TAC is categorized as an inflammation-related activity. |
| **CXCL8/IL-8**  | IL-8 is a chemokine that mediates neutrophil recruitment into acute inflammatory sites. IL-8 is categorized as an inflammation-related activity. |
| **CXCL9/MIG** | MIG is a chemokine that mediates T cell recruitment. MIG is categorized as an inflammation-related activity. |
| **EGFR** | EGFR is a cell surface receptor for epidermal growth factor involved in cell proliferation during development as well as tumor growth. EGFR is involved in Epithelial cell proliferation, epithelial cell differentiation keratinocyte proliferation, tissue remodeling. EGFR is categorized as a tissue remodeling-related activity. |
| **M-CSF**  | M-CSF is a secreted and cell surface cytokine that mediates macrophage differentiation. M-CSF is categorized as an immune modulation-related activity. |
| **MMP-1**  | MMP-1 is an interstitial collagenase that degrades collagens I, II and III and is involved in the process of tissue remodeling. MMP-1 is categorized as a tissue remodeling-related activity. |
| **PAI-I** | PAI-I is a serine proteinase inhibitor and inhibitor of tissue plasminogen activator (tPA) and urokinase (uPA) and is involved in tissue remodeling and fibrinolysis. PAI-I is categorized as a tissue remodeling-related activity. |
| **Proliferation\_72hr** | Proliferation\_72hr in the HDF3CGF system is a measure of dermal fibroblast proliferation which is important to the process of wound healing and fibrosis. |
| **SRB** | SRB is a measure of the total protein content of dermal fibroblasts. Cell viability of adherent cells is measured by Sulforhodamine B (SRB) staining, a method that determines cell density by measuring total protein content of test wells.  |
| **TIMP-1** | TIMP-1 is a tissue inhibitor of matrix metalloprotease-7 (MMP-7) and other MMPs, and is involved in tissue remodeling, angiogenesis and fibrosis. TIMP-1 is categorized as a tissue remodeling-related activity. |
| **TIMP-2**  | TIMP-2 is a tissue inhibitor of matrix metalloproteases and is involved in tissue remodeling, angiogenesis and fibrosis. TIMP-2 is categorized as a tissue remodeling-related activity. |

Table S2. The 49 genes most-impacted by cardamom essential oil (CEO) 0.011% (v/v)

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| **Illumina Gene ID** | **Fold Change in Log2 form** | **Definition** |
| TFRC | 2.09 | Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. |
| ANGPTL4 | 1.81 | Homo sapiens angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA. |
| OAZ2 | 1.77 | Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2), mRNA. |
| EZH2 | 1.76 | Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), transcript variant 1, mRNA. |
| KRTAP5-5 | 1.69 | Homo sapiens keratin associated protein 5-5 (KRTAP5-5), mRNA. |
| CNTNAP2 | 1.69 | Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. |
| SNORD78 | 1.65 | Homo sapiens small nucleolar RNA, C/D box 78 (SNORD78), small nucleolar RNA. |
| C19ORF26 | 1.64 | Homo sapiens chromosome 19 open reading frame 26 (C19orf26), mRNA. |
| KLF6 | 1.63 | Homo sapiens Kruppel-like factor 6 (KLF6), transcript variant 1, mRNA. |
| LOC653994 | 1.63 | PREDICTED: Homo sapiens similar to Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosome region 1 protein homolog), transcript variant 2 (LOC653994), mRNA. |
| HNRPH1 | 1.62 | Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA. |
| LOC644466 | 1.61 | PREDICTED: Homo sapiens hypothetical protein LOC644466 (LOC644466), mRNA. |
| PRKAA2 | 1.58 | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA. |
| LOC644330 | 1.58 | PREDICTED: Homo sapiens similar to tropomyosin 3 isoform 2 (LOC644330), mRNA. |
| HLA-A | 1.57 | Homo sapiens major histocompatibility complex, class I, A (HLA-A), mRNA. |
| LOC442459 | 1.55 | Homo sapiens X-ray repair complementing defective repair pseudogene (LOC442459), non-coding RNA. |
| REXO4 | 1.55 | Homo sapiens REX4, RNA exonuclease 4 homolog (S. cerevisiae) (REXO4), mRNA. |
| OBP2B | 1.55 | Homo sapiens odorant binding protein 2B (OBP2B), mRNA. |
| LDB3 | 1.53 | Homo sapiens LIM domain binding 3 (LDB3), transcript variant 1, mRNA. |
| TMPRSS12 | 1.53 | Homo sapiens transmembrane protease, serine 12 (TMPRSS12), mRNA. |
| LOC100128892 | 1.53 | PREDICTED: Homo sapiens hypothetical protein LOC100128892 (LOC100128892), mRNA. |
| TAKR | 1.52 | PREDICTED: Homo sapiens aldo-keto reductase, truncated (tAKR), mRNA. |
| NCOA2 | 1.51 | Homo sapiens nuclear receptor coactivator 2 (NCOA2), mRNA. |
| MIR651 | 1.51 | Homo sapiens microRNA 651 (MIR651), microRNA. |
| C14ORF65 | 1.51 | PREDICTED: Homo sapiens misc\_RNA (C14orf65), miscRNA. |
| LEFTY1 | 1.50 | Homo sapiens left-right determination factor 1 (LEFTY1), mRNA. |
| LOC100130880 | 1.50 | PREDICTED: Homo sapiens hypothetical LOC100130880 (LOC100130880), mRNA. |
| MRO | -1.50 | Homo sapiens maestro (MRO), mRNA. |
| C18ORF25 | -1.50 | Homo sapiens chromosome 18 open reading frame 25 (C18orf25), transcript variant 1, mRNA. |
| TTTY16 | -1.52 | Homo sapiens testis-specific transcript, Y-linked 16 (non-protein coding) (TTTY16), non-coding RNA. |
| DNER | -1.52 | Homo sapiens delta/notch-like EGF repeat containing (DNER), mRNA. |
| LOC100127988 | -1.52 | PREDICTED: Homo sapiens hypothetical protein LOC100127988 (LOC100127988), mRNA. |
| LOC730415 | -1.53 | PREDICTED: Homo sapiens hypothetical LOC730415, transcript variant 2 (LOC730415), mRNA. |
| MYH11 | -1.53 | Homo sapiens myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SM1A, mRNA. |
| SYNC1 | -1.54 | Homo sapiens syncoilin, intermediate filament 1 (SYNC1), mRNA. |
| HS.569199 | -1.54 | CR747253 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGp998J216211 ; IMAGE:2495732 5, mRNA sequence |
| CRYBA2 | -1.54 | Homo sapiens crystallin, beta A2 (CRYBA2), transcript variant 1, mRNA. |
| SULF1 | -1.55 | Homo sapiens sulfatase 1 (SULF1), mRNA. |
| FLJ42709 | -1.57 | PREDICTED: Homo sapiens hypothetical gene supported by AK124699 (FLJ42709), mRNA. |
| LOC100133797 | -1.57 | PREDICTED: Homo sapiens hypothetical protein LOC100133797 (LOC100133797), mRNA. |
| CFB | -1.60 | Homo sapiens complement factor B (CFB), mRNA. |
| VCAM1 | -1.63 | Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA. |
| CCL5 | -1.64 | Homo sapiens chemokine (C-C motif) ligand 5 (CCL5), mRNA. |
| MS4A13 | -1.66 | Homo sapiens membrane-spanning 4-domains, subfamily A, member 13 (MS4A13), mRNA. |
| HAS3 | -1.70 | Homo sapiens hyaluronan synthase 3 (HAS3), transcript variant 1, mRNA. |
| LOC643449 | -1.71 | PREDICTED: Homo sapiens similar to hCG2041756 (LOC643449), mRNA. |
| ZNF354A | -1.72 | Homo sapiens zinc finger protein 354A (ZNF354A), mRNA. |
| MT1H | -1.78 | Homo sapiens metallothionein 1H (MT1H), mRNA. |
| MT1JP | -1.95 | Homo sapiens metallothionein 1J (pseudogene) (MT1JP), mRNA. |