SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1. Abietic acid a structurally similar compound to leelamine without an amine group fails to induce vacuolization and death of melanoma cells. Light microscopic images of UACC 903 cells after leelamine or abietic acid treatments (**left**); Viability of melanoma cell lines after treatment with abietic acid (**right**);

Supplementary Figure 2. Leelamine mediated cell death does not involve de-novo protein synthesis or leakage of proteases from lysosomes. A, Graph showing viability of UACC 903 cells upon leelamine treatment with or without increasing concentrations of protein syntheses inhibitor, cycloheximide; **B,** Viability of UACC 903 cells after 24 hours cotreatment of various protease inhibitors, AEBS, 100μM; Pepstatin A, 50 μM; Leupeptin, 50 μM; ALLM, 25 μM; ALLN, 10 μM with leelamine; **C,** Viability of UACC 903 cells after 24 hours cotreatment of leelamine with various apoptotic signal inhibitors, Bax Inhibiting Peptide V5 (BIP-V5), Bid Inhibitor BI-6C9, apoptosome inhibitor NS3694;

Supplementary Figure 3. Reported targets of leelamine do not play role in leelamine mediated cell death. A and B, Graph showing that neither siRNA mediated knockdown of PDK isoforms nor DCA treatment hinders UACC 903 cell viability indicating that leelamine mediated cell death is not tied to activity of the PDK isoforms; **C,** Graph showing viability of UACC 903 cells following treatment with increasing concentrations of cannabinoid (CB) receptor inverse agonists (AM251 and AM630) in the presence or absence of leelamine; **D,** Viability of UACC 903 cells transfected with siRNA against CB receptors followed treatment with leelamine or DMSO;

Supplementary Figure 4. Statins as cholesterol transport inhibitors are ineffective in inducing death of UACC 903 melanoma cells. Graph showing viability

of UACC 903 cells upon treatment with increasing concentrations of two cholesterol syntheses inhibitors: Pravastatin and Simvastatin.

Supplementary Figure 5. Ingenuity Pathway Analyses. Analyses of the Kinexus protein array data with IPA software's default parameters showing significantly altered signaling pathways.