Supplementary Information

for the manuscript

CD1a autoreactive T cells recognize natural skin oils that function as headless antigens

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Supplementary Figure 1. Low pH promotes unloading of lipids from CD1a protein.

Plate-bound CD1a protein was treated with citrate buffers of indicated pH. 24h after co-incubation of BC2 T cell line with pH-treated CD1a protein, T cell activation was measured in the supernatant by IFN γ ELISA







Positive mode analysis of MS^2 and MS^3 spectra of (top) m/z= 782.6, detected in CD1a eluates and (bottom) phosphatidylcholine standard, m/z = 812.6



Supplementary Figure 2 Identification of lipids eluted from recombinant CD1a proteins by collision induced dissociation mass spectrometry and comparison with lipid standards (positive mode analysis)



Positive mode analysis of MS^2 spectra of (top) m/z= 1307.8, detected in CD1a eluates and (bottom) monosialoganglioside GM3 standard, m/z = 1307.8



detected in CD1a eluates and (bottom) globotetrahexosylceramide (Gb4) standard, m/z = 1359.9

Supplementary Figure 2 Identification of lipids eluted from recombinant CD1a proteins by collision induced dissociation mass spectrometry and comparison with lipid standards (positive mode analysis)





Negative mode analysis of MS^2 and MS^3 spectra of (top) m/z= 847.3, detected in CD1a eluates and (bottom) sphingomyelin standard, m/z = 737.5

Negative mode analysis of MS^2 and MS^3 spectra of (top) m/z= 870.5, detected in CD1a eluates and (bottom) phosphatidylcholine standard, m/z = 824.4

Supplementary Figure 3 Identification of lipids eluted from recombinant CD1a proteins by collision induced dissociation mass spectrometry and comparison with lipid standards (negative mode analysis)



Negative mode analysis of ${\rm MS}^2$ and ${\rm MS}^3$ spectra of (top) m/z= 834.5, detected in CD1a eluates and (bottom)phosphatidylserine standard, m/z = 834.5



Negative mode analysis of MS^2 spectra of (top) m/z= 885.5, detected in CD1a eluates and (bottom) phosphatidylinositol standard, m/z = 885.5



Negative mode analysis of ${\rm MS}^2$ spectra of (top) m/z= 773.4, detected in CD1a eluates and (bottom) phosphatidylglycerol standard, m/z = 775.5





Negative mode analysis of MS^2 spectra of (top) m/z= 742.4, detected in CD1a eluates and (bottom) phosphatidylethanolamine standard, m/z = 716.5

Supplementary Figure 3 Identification of lipids eluted from recombinant CD1a proteins by collision induced dissociation mass spectrometry and comparison with lipid standards (negative mode analysis)

Negative mode ESI-MS of fraction 2



Fatty acids were major lipids found in fraction 2 of skin epidermal lipids purified by 1D TLC. (Top) Negative mode EIC-MS detected ions at m/z 255.2, 279.2, 281.2, 283.2 etc., correspond to masses of C16:0, C18:2, C18:1, and C18:0 fatty acid, respectively. (Bottom) CID-MS of m/z=281.2 (detected in fraction 2) vs. m/z=281.2 (C18:1 fatty acid standard)

Positive mode ESI-MS of fraction 3-4



Triacylglycerols were major lipids found in fraction 3-4 of skin epidermal lipids purified by 1D TLC. (Top) Positive mode EIC-MS detected ions at m/z 855.7, 879.7, 881.7, 907.7 etc., correspond to homologous series of triacylglycerol. (Bottom) CID-MS of m/z=907.7 (detected in faction 3-4) vs. m/z= 907.7 (triacylglycerol standard)



Triacylglycerols were major lipids found in fraction 3 of skin epidermal lipids purified by 1D TLC. (Top) Positive mode EIC-MS detected ions at m/z 853.7, 879.7, 881.7, 905.7 etc., correspond to homologous series of triacylglycerol. (Bottom) CID-MS of m/z=879.7 (detected in faction 3) vs. m/z= 907.7 (triacylglycerol standard)



Cholesterol esters were major lipids found in fraction 4 of skin epidermal lipids purified by 1D TLC. (Top) Positive mode EIC-MS detected ions at m/z 647.7, 671.6, 673.6, 701.6 etc., correspond to homologous series of cholesterol ester. (Bottom) CID-MS of m/z=673.6 (detected in faction 4) vs. m/z= 647.6 (cholesterol ester standard)

Supplementary Figure 4 Eletron spray Ionization mass spectrometry of lipids eluted from silica fraction of TLC plate. Comparison of collision induced dissociation mass spectrometry profiles with lipid standards

Positive mode ESI-MS of fraction 3

	TRAV	TRAJ	CDR3α	TRBV	TRBD	TRBJ	CDR3β
BC2	26-1	34	CIVPPPDKLIF	29-1	1	1-2	CSVEDIGQGAFDYGYTF
Bgp	21	33	CAVLHSNYQLIW	11-3	1	2-2	CASSLDLGVLDEGTGELFF

Supplementary table 5 T cell receptors of CD1a autoreactive T cell clones

To determine the sequence of the BC2 TCR α and β chains, PCR was performed using the

following primers: TRAV26-1LongF: atgaggctggtggcaagag; TRBV29LongF: catctctcaaaagccaagcagg;

CalphaShortRev: catgtctagcacagttttg; CbetaConstRevForSeq: ggtggcagacaggaccccttgc.

PCR products were sequenced from both sides using the PCR primers.

To determine the sequence of the Bgp TCR α and β chain, a published method was used,

based on circularization of double stranded cDNA and amplification using constant region primers

(Uematsu, Y. A novel and rapid cloning method for the T cell receptor variable region sequences.

1991, Immunogenetics)

Genbank: TCR α and β chain sequences of BC2 and Bgp clones: KF751594, KF751595, KF751596, KF751597