	Age (years)	Sex
CIP	71.5 ± 3.2	25% Male
AD	30.0 ± 14.1	50% Male
Control	72.0 ± 2.1	50% Male

Table S1. Demographics of human skin sample donors. Relates to Figure 5.

Demographics of CIP (N = 4), AD (N = 4), and control skin (N = 4) donors. Age presented as mean ± standard deviation of each group.

GO Accession Number	Name	NES	FDR q-value
GO:0002682	regulation of immune system process	-8.77036	$< 10^{-5}$
GO:0002376	immune system process	-8.66961	$< 10^{-5}$
GO:0080134	regulation of response to stress	-8.02582	$< 10^{-5}$
GO:0050776	regulation of immune response	-7.8129	$< 10^{-5}$
GO:0022613	ribonucleoprotein complex biogenesis	-7.7964	$< 10^{-5}$
GO:0002684	positive regulation of immune system process	-7.77017	$< 10^{-5}$
GO:0006952	defense response	-7.49978	$< 10^{-5}$
GO:0044403	symbiosis, encompassing mutualism through parasitism	-7.30644	$< 10^{-5}$
GO:0050778	positive regulation of immune response	-7.20636	$< 10^{-5}$
GO:0044419	interspecies interaction between organisms	-7.18966	$< 10^{-5}$
GO:0042254	ribosome biogenesis	-7.11062	$< 10^{-5}$
GO:0031347	regulation of defense response	-7.10497	$< 10^{-5}$
GO:0048584	positive regulation of response to stimulus	-7.05507	$< 10^{-5}$
GO:0006396	RNA processing	-7.04048	$< 10^{-5}$
GO:0009607	response to biotic stimulus	-6.93027	$< 10^{-5}$
GO:0043604	amide biosynthetic process	-6.89239	$< 10^{-5}$
GO:0034660	ncRNA metabolic process	-6.8318	$< 10^{-5}$
GO:0006955	immune response	-6.73395	$< 10^{-5}$
GO:0002253	activation of immune response	-6.70878	$< 10^{-5}$
GO:0006518	peptide metabolic process	-6.6791	$< 10^{-5}$
GO:0016072	rRNA metabolic process	-6.56767	$< 10^{-5}$
GO:1901564	organonitrogen compound metabolic process	-6.55732	$< 10^{-5}$
GO:0019058	viral life cycle	-6.53858	$< 10^{-5}$
GO:0031349	positive regulation of defense response	-6.52802	$< 10^{-5}$
GO:0034470	ncRNA processing	-6.35599	$< 10^{-5}$
GO:1901566	organonitrogen compound biosynthetic process	-6.31783	$< 10^{-5}$
GO:0043603	cellular amide metabolic process	-6.24033	$< 10^{-5}$
GO:0061024	membrane organization	-6.19839	$< 10^{-5}$
GO:0032101	regulation of response to external stimulus	-6.11073	$< 10^{-5}$
GO:0045184	establishment of protein localization	-6.09473	$< 10^{-5}$
GO:0071310	cellular response to organic substance	-6.08981	$< 10^{-5}$
GO:0002218	activation of innate immune response	-6.07281	$< 10^{-5}$
GO:0034097	response to cytokine	-6.07209	$< 10^{-5}$
GO:0009057	macromolecule catabolic process	-6.07098	$< 10^{-5}$
GO:0045089	positive regulation of innate immune response	-6.04607	$< 10^{-5}$
GO:0051649	establishment of localization in cell	-6.03101	$< 10^{-5}$
GO:0007005	mitochondrion organization	-6.02195	$< 10^{-5}$
GO:0008104	protein localization	-6.0172	$< 10^{-5}$
GO:0045088	regulation of innate immune response	-5.9712	$< 10^{-5}$
GO:0065003	macromolecular complex assembly	-5.95253	$< 10^{-5}$
GO:0071822	protein complex subunit organization	-5.90784	$< 10^{-5}$
GO:1902580	single-organism cellular localization	-5.87975	$< 10^{-5}$
GO:0070727	cellular macromolecule localization	-5.83766	$< 10^{-5}$
GO:0010941	regulation of cell death	-5.80849	$< 10^{-5}$
GO:0031399	regulation of protein modification process	-5.80517	$< 10^{-5}$
GO:0009617	response to bacterium	-5.7918	$< 10^{-5}$
GO:0006413	translational initiation	-5.75062	$< 10^{-5}$
GO:0051247	positive regulation of protein metabolic process	-5.73842	$< 10^{-5}$
GO:0009605	response to external stimulus	-5.73487	$< 10^{-5}$

Table S2. AD skin demonstrates enrichment of immune activation pathways. Relates to Figure 5.

List of top 50 biological process GO terms enriched in AD in a direct comparison of CIP and AD as determined by gene set enrichment analysis (GSEA). Normalized enrichment score (NES) and false discovery rate (FDR) q-value of individual GO terms are provided.

GO Accession Number	Name	NES	FDR q-value
GO:0032990	cell part morphogenesis	3.093461	0.002029
GO:0044782	cilium organization	2.879501	0.002522
GO:0060271	cilium morphogenesis	2.867324	0.002018
GO:0008589	regulation of smoothened signaling pathway	2.766102	0.003024
GO:0016054	organic acid catabolic process	2.669138	0.006637
GO:0046395	carboxylic acid catabolic process	2.666201	0.005615
GO:0051965	positive regulation of synapse assembly	2.584534	0.010122
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	2.545489	0.011865
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	2.528827	0.012158
GO:0010927	cellular component assembly involved in morphogenesis	2.521315	0.011644
GO:0048667	cell morphogenesis involved in neuron differentiation	2.399559	0.028197
GO:0072329	monocarboxylic acid catabolic process	2.391039	0.027353
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	2.374797	0.027991
GO:0097485	neuron projection guidance	2.356602	0.029745
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	2.32599	0.035653
GO:0051298	centrosome duplication	2.27191	0.048845
GO:0009062	fatty acid catabolic process	2.266665	0.047421
GO:0061512	protein localization to cilium	2.250689	0.050193
GO:0030030	cell projection organization	2.228846	0.055343
GO:0003002	regionalization	2.225651	0.053408
GO:0050807	regulation of synapse organization	2.176872	0.069665
GO:0007224	smoothened signaling pathway	2.16341	0.072499
GO:0048812	neuron projection morphogenesis	2.149574	0.076482
GO:0019228	neuronal action potential	2.135246	0.080783
GO:0071236	cellular response to antibiotic	2.118108	0.08638
GO:0021915	neural tube development	2.111597	0.086502
GO:0021522	spinal cord motor neuron differentiation	2.103877	0.087523
GO:0007600	sensory perception	2.094911	0.089596
GO:0007389	pattern specification process	2.093567	0.087319
GO:0050953	sensory perception of light stimulus	2.082521	0.090076
GO:0021510	spinal cord development	2.050129	0.106422
GO:0000732	strand displacement	2.047653	0.104586
GO:0045494	photoreceptor cell maintenance	2.045306	0.103041
GO:0032989	cellular component morphogenesis	2.042259	0.10153
GO:0021515	cell differentiation in spinal cord	2.028853	0.107171
GO:0019748	secondary metabolic process	2.026103	0.10577
GO:1903825	organic acid transmembrane transport	2.017075	0.108687
GO:0035058	nonmotile primary cilium assembly	2.012586	0.108942
GO:0060401	cytosolic calcium ion transport	1.995952	0.117028
GO:0097553	calcium ion transmembrane import into cytosol	1.986171	0.121127
GO:0031023	microtubule organizing center organization	1.977455	0.124149
GO:0007517	muscle organ development	1.97117	0.125907
GO:1902656	calcium ion import into cytosol	1.970663	0.123353
GO:0007098	centrosome cycle	1.96972	0.121292
GO:0086010	membrane depolarization during action potential	1.964156	0.122664
GO:0098534	centriole assembly	1.960917	0.122407
GO:0070509	calcium ion import	1.959427	0.121073
GO:0009953	dorsal/ventral pattern formation	1.955245	0.121612
GO:0097237	cellular response to toxic substance	1.954725	0.119552

Table S3. CIP skin demonstrates enrichment of transcriptional programs not associated with inflammation. Relates to Figure 5.

List of top 50 biological process GO terms enriched in CIP in a direct comparison of CIP and AD as determined by gene set enrichment analysis (GSEA). Normalized enrichment score (NES) and false discovery rate (FDR) q-value of individual GO terms are provided.

	Age	Sex	History of AD	History of malignancy	Previously failed treatments						
					Topical steroids	Oral steroids	Additional Immuno-suppression[a]	Gabapentin	Anti-histamines	Anti-depressants	Photo-therapy
Patient 1	79	M	None	None	Yes	Yes	Yes	Yes	Yes	Yes	N/A
Patient 2	50	F	None	None	Yes	Yes	N/A	N/A	Yes	N/A	N/A
Patient 3	60	M	None	None	Yes	Yes	N/A	N/A	Yes	N/A	Yes
Patient 4	79	M	None	Yes	Yes	Yes	Yes	Yes	N/A	Yes	N/A
Patient 5	75	F	None	Yes	Yes	Yes	N/A	N/A	N/A	N/A	Yes

[a] azathioprine or cyclosporine

Table S4. Characteristics of CIP patients treated with tofacitinib. Relates to Figure 6.

Demographics and relevant medical history including previously failed treatments of CIP patients given tofacitinib. N/A, not applicable.