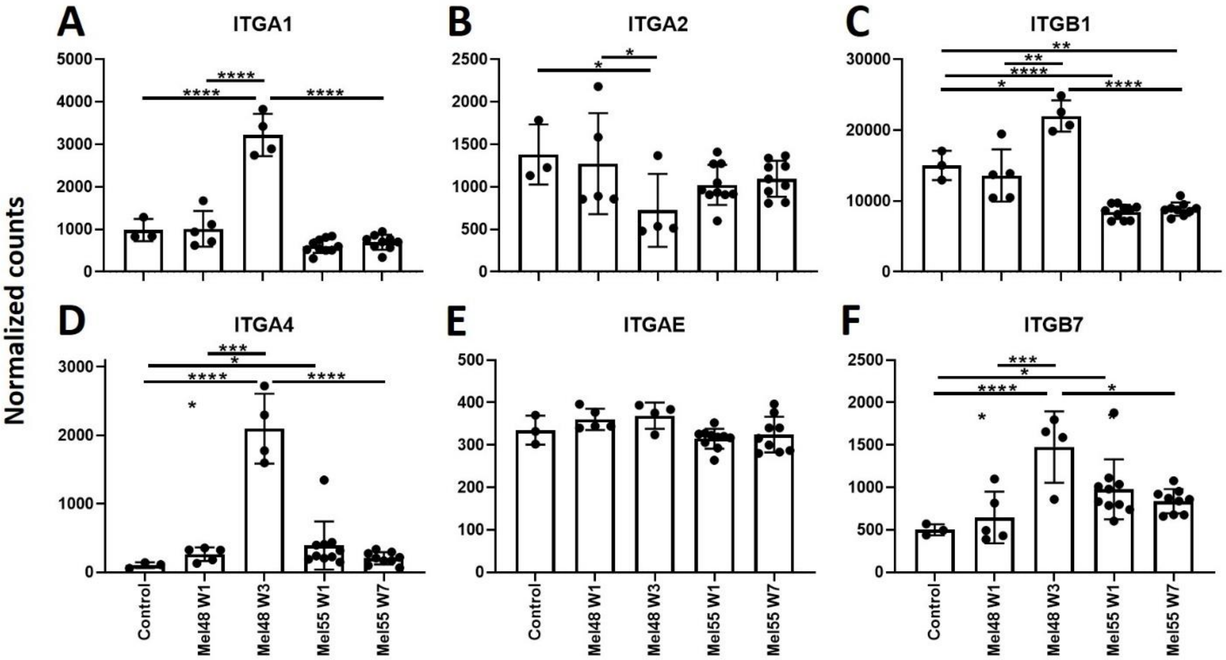
Supplemental Table 1. Overview of patient samples, categorized by trial, week of biopsy, and inclusion in experimental group

Patient ID	TRIAL	STAGE	AGE	SEX	WEEK	IHC	RNAseq
VMM1026	MEL 48	IIIB	59	M	0	Y	X
VMM1032	MEL 48	IIIB	60	M	0	Y	X
VMM1050	MEL 48	IV	59	M	0	Y	X
VMM1007	MEL 48	IIIC	47	M	1	X	X
VMM1021	MEL 48	IIIC	60	M	1	X	X
VMM1029	MEL 48	IIIC	51	M	1	X	X
VMM1033	MEL 48	IIIA	27	M	1	X	X
VMM1055	MEL 48	IIIC	48	F	1	X	X
VMM1036	MEL 48	IV	67	M	1	X	--
VMM1024	MEL 48	IIIB	72	M	1	X	--
VMM1045	MEL 48	IIIB	60	F	1	X	--
VMM1014	MEL 48	IIIB	62	M	1	X	--
VMM1008	MEL 48	IIIC	53	M	3	Y	X
VMM1023	MEL 48	IIIC	72	F	3	Y	X
VMM1034	MEL 48	IIIB	31	F	3	Y	X
VMM1048	MEL 48	IIIC	50	M	3	Y	X
VMM871	MEL 48	IV	37	F	7	X	--
VMM1010	MEL 48	IIB	60	M	7	X	--
VMM1018	MEL 48	IIIA	37	M	7	X	--
VMM1022	MEL 48	IIIC	56	F	7	X	--
VMM1039	MEL 48	IIIA	36	M	7	X	--
VMM1041	MEL 48	IIIB	49	F	7	X	--
VMM1044	MEL 48	IV	58	M	7	X	--
VMM1106	MEL 55	IIIB	51	F	1	X	X
VMM1106	MEL 55				7	X	--
VMM1077	MEL 55	IIIB	69.5	M	1,7	X	X
VMM1078	MEL 55	IIIB	43	M	1,7	X	X
VMM1076	MEL 55	IV	65	M	1,7	X	X
VMM1086	MEL 55	IIIC	51.8	M	1,7	X	X
VMM1089	MEL 55	IV	59.5	M	1,7	X	X
VMM1093	MEL 55	IIIB	54.6	M	1,7	X	X
VMM1095	MEL 55	IV	51.2	F	1,7	X	X
VMM1098	MEL 55	IIIB	40.7	F	1,7	X	X
VMM1112	MEL 55	IIIC	59.2	F	1,7	X	X

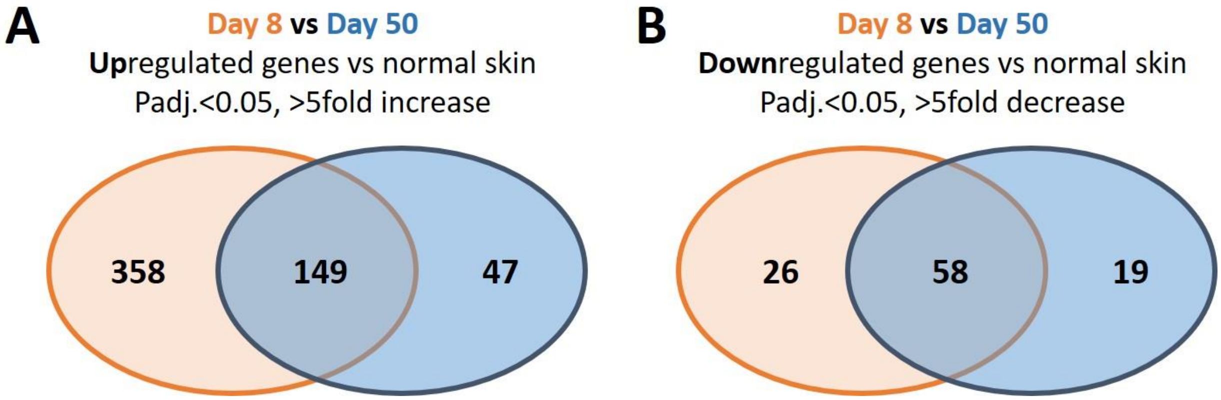
X = done in this study, Y = done in Scheafer et al

Supplemental Table 2. Mean gene expression in normalized counts (± Standard Deviation), categorized by gene, trial, and time point

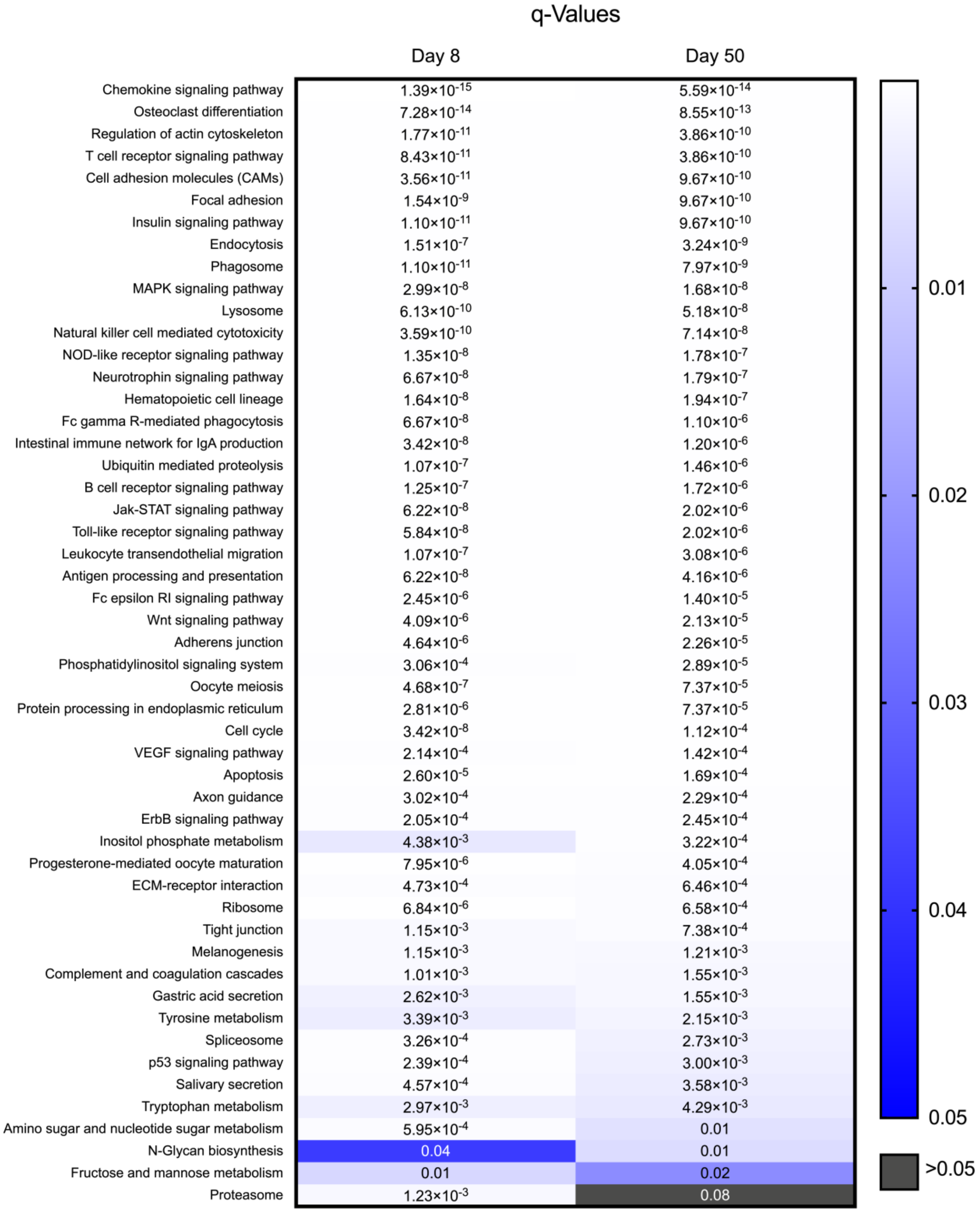
	Control	Mel 48 Week 1	Mel 48 Week 3	Mel 55 Week 1	Mel 55 Week 7
BAFF	146.9 (± 20.15)	644.5 (±210.1)	3756.2 (±679.2)	1359 (±1433)	442.7 (±137.3)
APRIL	279 (±36.49)	483.1 (±148.1)	2222.6 (±392.3)	582.3 (±289.8)	420.1 (±45.04)
LIGHT	28.19 (±10.67)	99.3 (±48.0)	662.3 (130.0)	177.9 (±96.48)	120.3 (±35.49)
LTA	4.719 (±2.15)	12.2 (±3.4)	98.7 (±39.3)	42.48 (±40.79)	20.5 (±7.41)
LTB	51.97 (±7.26)	187.5 (±62.9)	1156.5 (±449.6)	537.8 (±482.5)	239.7 (±106.8)
CD20	14.84 (±12.22)	26.2 (±16.1)	271.0 (±165.5)	58.26 (±58.73)	140.6 (±107)
CCL2	281.2 (±57.84)	1563.5 (±797.9)	52443.5 (±1617.1)	1537 (±2195)	754.1 (±388.8)
CCL3	6.692 (±3.56)	243.8 (±201.6)	1970.6 (±548.0)	50.05 (±35.64)	177.3 (±311.7)
CCL4	5.963 (± 3.759)	154.4 (±112.8)	1821.5 (±554.6)	169.3 (± 250)	82.24 (± 54.76)
CCL5	101.5 (± 42.09)	421.6 (±203.8)	4858.5 (±1958.8)	1372 (± 1586)	668.9 (± 427.1)
CCL8	19.71 (± 11.00)	160.6 (±210.0)	2423.9 (±1179.7)	886.5 (± 1790)	62.04 (± 27.02)
CXCL9	113.5 (± 40.22)	457.4 (±215.4)	25312.3 (±7466.4)	4862 (± 8327)	681.4 (± 425.6)
CXCL10	49.35 (± 20.21)	364.1 (±424.0)	11735.9 (±3120.6)	3718 (± 7170)	225 (± 147.7)
CXCL11	19.46 (± 13.16)	108.3 (±111.9)	1530.5 (±403.6)	68.1 (± 50.13)	1321 (± 2564)
CXCL13	0.5997 (± 1.039)	4.3 (±1.8)	532.7 (±104.3)	14.08 (± 15.29)	39.87 (± 31.64)
CCL18	83.81 (± 38.26)	635.6 (±289.8)	16296.0	517.2 (± 430.1)	483 (± 159.3)
CCL19	296.5 (± 31.35)	930.4 (±247.9)	904.2 (±349.1)	1217 (± 908)	742 (± 292.9)
CCL21	367.1 (± 135.6)	865.4 (±243.9)	284.7 (±87.1)	561.2 (± 171.6)	751.2 (± 248.7)



Supplemental Figure 1. Expression of individual integrin genes ITGA1 (CD49a) **(A),** ITGA2 (CD49b) **(B),** ITGB1 (CD29) **(C),** ITGA4 (CD49d) **(D),** ITGAE (CD103) **(E),** ITGB7 **(F).** Expression data were obtained from vaccine site biopsies of patients treated with IFA (MEL 48) or AS15 (MEL 55), as well as normal tissue obtained pre-vaccination for control purposes (n=3). For patients treated with IFA, gene expression is shown at week (w) 1 (n=3), and week 3 (n=4), following initial vaccination at a site separate from the biopsied tissue. For patients treated with AS15, gene expression is shown at week 1 (n=10) and week 7 (n=9) , following initial vaccination at a distant site. For factors of significance: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$; derived from differential gene expression.



Supplemental Figure 2. Differentially upregulated **(A)** or downregulated **(B)** genes in Mel55 VSME compared to normal skin. Differential expression was determined as adjusted P value of less than 0.05 and at least 5-fold change compared to normal skin.



q-Values

	Day 8	Day 50
Chemokine signaling pathway	1.39×10^{-15}	5.59×10^{-14}
Osteoclast differentiation	7.28×10^{-14}	8.55×10^{-13}
Regulation of actin cytoskeleton	1.77×10^{-11}	3.86×10^{-10}
T cell receptor signaling pathway	8.43×10^{-11}	3.86×10^{-10}
Cell adhesion molecules (CAMs)	3.56×10^{-11}	9.67×10^{-10}
Focal adhesion	1.54×10^{-9}	9.67×10^{-10}
Insulin signaling pathway	1.10×10^{-11}	9.67×10^{-10}
Endocytosis	1.51×10^{-7}	3.24×10^{-9}
Phagosome	1.10×10^{-11}	7.97×10^{-9}
MAPK signaling pathway	2.99×10^{-8}	1.68×10^{-8}
Lysosome	6.13×10^{-10}	5.18×10^{-8}
Natural killer cell mediated cytotoxicity	3.59×10^{-10}	7.14×10^{-8}
NOD-like receptor signaling pathway	1.35×10^{-8}	1.78×10^{-7}
Neurotrophin signaling pathway	6.67×10^{-8}	1.79×10^{-7}
Hematopoietic cell lineage	1.64×10^{-8}	1.94×10^{-7}
Fc gamma R-mediated phagocytosis	6.67×10^{-8}	1.10×10^{-6}
Intestinal immune network for IgA production	3.42×10^{-8}	1.20×10^{-6}
Ubiquitin mediated proteolysis	1.07×10^{-7}	1.46×10^{-6}
B cell receptor signaling pathway	1.25×10^{-7}	1.72×10^{-6}
Jak-STAT signaling pathway	6.22×10^{-8}	2.02×10^{-6}
Toll-like receptor signaling pathway	5.84×10^{-8}	2.02×10^{-6}
Leukocyte transendothelial migration	1.07×10^{-7}	3.08×10^{-6}
Antigen processing and presentation	6.22×10^{-8}	4.16×10^{-6}
Fc epsilon RI signaling pathway	2.45×10^{-6}	1.40×10^{-5}
Wnt signaling pathway	4.09×10^{-6}	2.13×10^{-5}
Adherens junction	4.64×10^{-6}	2.26×10^{-5}
Phosphatidylinositol signaling system	3.06×10^{-4}	2.89×10^{-5}
Oocyte meiosis	4.68×10^{-7}	7.37×10^{-5}
Protein processing in endoplasmic reticulum	2.81×10^{-6}	7.37×10^{-5}
Cell cycle	3.42×10^{-8}	1.12×10^{-4}
VEGF signaling pathway	2.14×10^{-4}	1.42×10^{-4}
Apoptosis	2.60×10^{-5}	1.69×10^{-4}
Axon guidance	3.02×10^{-4}	2.29×10^{-4}
ErbB signaling pathway	2.05×10^{-4}	2.45×10^{-4}
Inositol phosphate metabolism	4.38×10^{-3}	3.22×10^{-4}
Progesterone-mediated oocyte maturation	7.95×10^{-6}	4.05×10^{-4}
ECM-receptor interaction	4.73×10^{-4}	6.46×10^{-4}
Ribosome	6.84×10^{-6}	6.58×10^{-4}
Tight junction	1.15×10^{-3}	7.38×10^{-4}
Melanogenesis	1.15×10^{-3}	1.21×10^{-3}
Complement and coagulation cascades	1.01×10^{-3}	1.55×10^{-3}
Gastric acid secretion	2.62×10^{-3}	1.55×10^{-3}
Tyrosine metabolism	3.39×10^{-3}	2.15×10^{-3}
Spliceosome	3.26×10^{-4}	2.73×10^{-3}
p53 signaling pathway	2.39×10^{-4}	3.00×10^{-3}
Salivary secretion	4.57×10^{-4}	3.58×10^{-3}
Tryptophan metabolism	2.97×10^{-3}	4.29×10^{-3}
Amino sugar and nucleotide sugar metabolism	5.95×10^{-4}	0.01
N-Glycan biosynthesis	0.04	0.01
Fructose and mannose metabolism	0.01	0.02
Proteasome	1.23×10^{-3}	0.08

Supplemental Figure 3. Differentially expressed pathways in VSME of patients vaccinated with AS15 (Mel55) at day 8 or day 50 after the first vaccine, compared to normal skin. Results were obtained through a GAGE pathway analysis. Q-values are provided for enriched pathways at each time point.