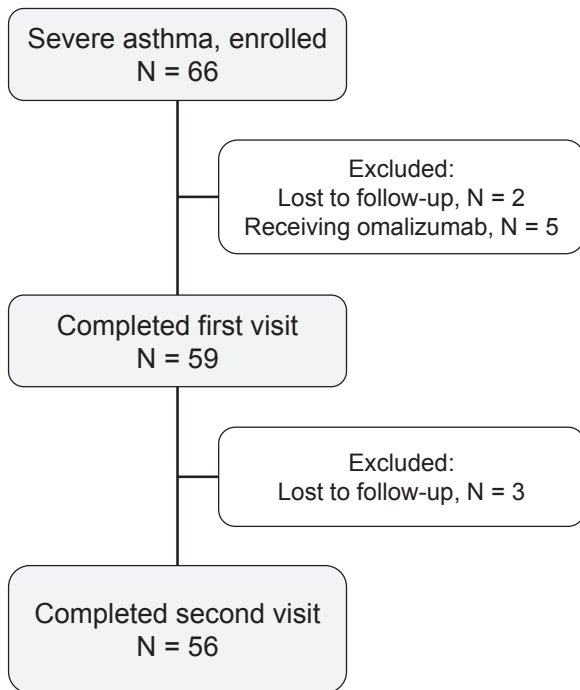**APPENDIX**



**FIGURE E1.** Flowchart of participant inclusion.

**TABLE E1.** Genes included in the mRNA gene expression array

| Gene symbol | Gene name | GeneBank no. |
|---|---|---|
| *AIMP1* | Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 | NM_004757 |
| *BMP2* | Bone morphogenetic protein 2 | NM_001200 |
| *C5* | Complement component 5 | NM_001735 |
| *CCL1* | Chemokine (C-C motif) ligand 1 | NM_002981 |
| *CCL2* | Chemokine (C-C motif) ligand 2 | NM_002982 |
| *CCL3* | Chemokine (C-C motif) ligand 3 | NM_002983 |
| *CCL4* | Chemokine (C-C motif) ligand 4 | NM_002984 |
| *CCL5* | Chemokine (C-C motif) ligand 5 | NM_002985 |
| *CCL7* | Chemokine (C-C motif) ligand 7 | NM_006273 |
| *CCL8* | Chemokine (C-C motif) ligand 8 | NM_005623 |
| *CCL11* | Chemokine (C-C motif) ligand 11 | NM_002986 |
| *CCL13* | Chemokine (C-C motif) ligand 13 | NM_005408 |
| *CCL15* | Chemokine (C-C motif) ligand 15 | NM_032965 |
| *CCL16* | Chemokine (C-C motif) ligand 16 | NM_004590 |
| *CCL17* | Chemokine (C-C motif) ligand 17 | NM_002987 |
| *CCL20* | Chemokine (C-C motif) ligand 20 | NM_004591 |
| *CCL22* | Chemokine (C-C motif) ligand 22 | NM_002990 |
| *CCL23* | Chemokine (C-C motif) ligand 23 | NM_005064 |
| *CCL24* | Chemokine (C-C motif) ligand 24 | NM_002991 |
| *CCL26* | Chemokine (C-C motif) ligand 26 | NM_006072 |
| *CCR1* | Chemokine (C-C motif) receptor 1 | NM_001295 |
| *CCR2* | Chemokine (C-C motif) receptor 2 | NM_001123396 |
| *CCR3* | Chemokine (C-C motif) receptor 3 | NM_001837 |
| *CCR4* | Chemokine (C-C motif) receptor 4 | NM_005508 |
| *CCR5* | Chemokine (C-C motif) receptor 5 | NM_000579 |
| *CCR6* | Chemokine (C-C motif) receptor 6 | NM_004367 |
| *CCR8* | Chemokine (C-C motif) receptor 8 | NM_005201 |
| *CD40LG* | CD40 ligand | NM_000074 |
| *CSF1* | Colony-stimulating factor 1 (macrophage) | NM_000757 |
| *CSF2* | Colony-stimulating factor 2 (granulocyte-macrophage) | NM_000758 |
| *CSF3* | Colony-stimulating factor 3 (granulocyte) | NM_000759 |
| *CX3CL1* | Chemokine (C-X3-C motif) ligand 1 | NM_002996 |
| *CX3CR1* | Chemokine (C-X3-C motif) receptor 1 | NM_001337 |
| *CXCL1* | Chemokine (C-X-C motif) ligand 1 (melanoma growth- stimulating activity, alpha) | NM_001511 |
| *CXCL2* | Chemokine (C-X-C motif) ligand 2 | NM_002089 |
| *CXCL3* | Chemokine (C-X-C motif) ligand 3 | NM_002090 |
| *CXCL5* | Chemokine (C-X-C motif) ligand 5 | NM_002994 |
| *CXCL6* | Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) | NM_002993 |
| *CXCL9* | Chemokine (C-X-C motif) ligand 9 | NM_002416 |
| *CXCL10* | Chemokine (C-X-C motif) ligand 10 | NM_001565 |
| *CXCL11* | Chemokine (C-X-C motif) ligand 11 | NM_005409 |
| *CXCL12* | Chemokine (C-X-C motif) ligand 12 | NM_000609 |
| *CXCL13* | Chemokine (C-X-C motif) ligand 13 | NM_006419 |
| *CXCR1* | Chemokine (C-X-C motif) receptor 1 | NM_000634 |
| *CXCR2* | Chemokine (C-X-C motif) receptor 2 | NM_001557 |
| *FASLG* | Fas ligand (TNF superfamily, member 6) | NM_000639 |
| *IFNA2* | Interferon, alpha 2 | NM_000605 |
| *IFNG* | Interferon, gamma | NM_000619 |
| *IL1A* | Interleukin 1, alpha | NM_000575 |
| *IL1B* | Interleukin 1, beta | NM_000576 |
| *IL1R1* | Interleukin 1 receptor, type I | NM_000877 |
| *IL1RN* | Interleukin 1 receptor antagonist | NM_000577 |
| *IL3* | Interleukin 3 (colony-stimulating factor, multiple) | NM_000588 |
| *IL5* | Interleukin 5 (colony-stimulating factor, eosinophil) | NM_000879 |

**TABLE E1.** *(Continued)*

| Gene symbol | Gene name | GeneBank no. |
|---|---|---|
| *IL5RA* | Interleukin 5 receptor, alpha | NM_000564 |
| *IL7* | Interleukin 7 | NM_000880 |
| *IL8* | Interleukin 8 | NM_000584 |
| *IL9* | Interleukin 9 | NM_000590 |
| *IL9R* | Interleukin 9 receptor | NM_002186 |
| *IL10RA* | Interleukin 10 receptor, alpha | NM_001558 |
| *IL10RB* | Interleukin 10 receptor, beta | NM_000628 |
| *IL13* | Interleukin 13 | NM_002188 |
| *IL15* | Interleukin 15 | NM_000585 |
| *IL16* | Interleukin 16 | NM_004513 |
| *IL17A* | Interleukin 17A | NM_002190 |
| *IL17C* | Interleukin 17C | NM_013278 |
| *IL17F* | Interleukin 17F | NM_052872 |
| *IL21* | Interleukin 21 | NM_021803 |
| *IL27* | Interleukin 27 | NM_145659 |
| *IL33* | Interleukin 33 | NM_033439 |
| *LTA* | Lymphotoxin alpha (TNF superfamily, member 1) | NM_000595 |
| *LTB* | Lymphotoxin beta (TNF superfamily, member 3) | NM_002341 |
| *MIF* | Macrophage migration inhibitory factor (glycosylation-inhibiting factor) | NM_002415 |
| *NAMPT* | Nicotinamide phosphoribosyltransferase | NM_005746 |
| *OSM* | Oncostatin M | NM_020530 |
| *SPP1* | Secreted phosphoprotein 1 | NM_000582 |
| *TNF* | Tumor necrosis factor | NM_000594 |
| *TNFRSF11B* | Tumor necrosis factor receptor superfamily, member 11b | NM_002546 |
| *TNFSF10* | Tumor necrosis factor (ligand) superfamily, member 10 | NM_003810 |
| *TNFSF11* | Tumor necrosis factor (ligand) superfamily, member 11 | NM_003701 |
| *TNFSF13* | Tumor necrosis factor (ligand) superfamily, member 13 | NM_003808 |
| *TNFSF13B* | Tumor necrosis factor (ligand) superfamily, member 13b | NM_006573 |
| *TNFSF4* | Tumor necrosis factor (ligand) superfamily, member 4 | NM_003326 |
| *VEGFA* | Vascular endothelial growth factor A | NM_003376 |

**TABLE E2.** Associations between the ACQ score and other outcome variables after triamcinolone injection

| Variable | AQLQ score | Exhaled nitric oxide (ppb)* | Blood eosinophils (%)* | FEV$_1$ (% predicted value) |
|---|---|---|---|---|
| ACQ | $r = -0.759$<br>$P < .001$ | $r = 0.284$<br>$P = 0.034$ | $r = 0.103$<br>$P = 0.602$ | $r = -0.439$<br>$P = .001$ |
| AQLQ | | $r = -0.150$<br>$P = .268$ | $r = -0.164$<br>$P = .405$ | $r = 0.383$<br>$P = .004$ |
| Exhaled nitric oxide (ppb)* | | | $r = 0.234$<br>$P = .230$ | $r = -0.396$<br>$P = .003$ |
| Blood eosinophils (%)* | | | | $r = -0.272$<br>$P = .162$ |

Higher ACQ scores represent poorer asthma control. Higher AQLQ scores represent better asthma-related quality of life.
*Data were logarithmically transformed before statistical analyses.

**TABLE E3.** Associations between mRNA delta CT values and other biomarkers

| Variable | Exhaled nitric oxide (ppb)* | Blood eosinophils (%)* | FEV$_1$ (% predicted) |
|---|---|---|---|
| AIMP1 | $r = -0.287$ $P = .059$ | $r = 0.009$ $P = .952$ | $r = 0.098$ $P = .528$ |
| C5 | $r = -0.038$ $P = .807$ | $r = 0.204$ $P = .184$ | $r = -0.034$ $P = .826$ |
| CCL3 | $r = -0.070$ $P = .650$ | $r = -0.027$ $P = .863$ | $r = 0.213$ $P = .166$ |
| CCR2 | $r = -0.328$ $P = 0.030$ | $r = 0.152$ $P = 0.324$ | $r = 0.037$ $P = 0.813$ |
| CCR5 | $r = 0.391$ $P = .088$ | $r = 0.026$ $P = .869$ | $r = 0.135$ $P = .383$ |
| CCR6 | $r = 0.035$ $P = .822$ | $r = 0.261$ $P = .087$ | $r = 0.012$ $P = .939$ |
| IFNG | $r = -0.434$ $P = .003$ | $r = 0.095$ $P = .540$ | $r = 0.326$ $P = .031$ |
| IL10RB | $r = -0.053$ $P = .734$ | $r = 0.049$ $P = .752$ | $r = -0.069$ $P = .656$ |
| IL17C | $r = -0.160$ $P = .299$ | $r = -0.263$ $P = .085$ | $r = 0.187$ $P = .225$ |
| IL1A | $r = -0.225$ $P = .152$ | $r = -0.031$ $P = .845$ | $r = 0.383$ $P = .012$ |
| IL1RN | $r = 0.028$ $P = .856$ | $r = 0.021$ $P = .891$ | $r = 0.109$ $P = .479$ |
| IL5 | $r = -0.206$ $P = .181$ | $r = 0.167$ $P = .277$ | $r = 0.188$ $P = .222$ |
| TNFSF13B | $r = 0.107$ $P = .489$ | $r = 0.023$ $P = .881$ | $r = -0.026$ $P = .866$ |
| VEGFA | $r = 0.055$ $P = .721$ | $r = 0.187$ $P = .223$ | $r = 0.049$ $P = .751$ |

CT, Cycle threshold.

Delta CT values were obtained by subtracting the mean CT of the housekeeping genes from the CT of the gene of interest. Higher delta CT values reflect lower expression of the gene.

*Data were logarithmically transformed before statistical analyses.

**TABLE E4.** Clinical predictors of uncontrolled asthma after triamcinolone injection

| Predictor | Odds ratio* | 95% CI |
|---|---|---|
| Black race | 5.33 | 0.58-49.18 |
| Obesity | 3.38 | 0.90-12.72 |
| Prior hospitalization for asthma (lifetime) | 0.80 | 0.20-3.22 |
| Near-fatal asthma exacerbation (lifetime) | 0.33 | 0.09-1.19 |
| Tobacco smoke exposure | 0.12 | 0.01-1.05 |
| Tree, grass, or pollen sensitization | 1.07 | 0.25-4.59 |
| Mold sensitization | 0.40 | 0.09-1.76 |
| Dog or cat sensitization | 1.44 | 0.34-6.04 |
| Dust mite sensitization | 3.20 | 0.32-32.53 |
| Cockroach sensitization† | 15.40 | 2.50-95.05 |
| FEV$_1$ <80% of predicted value | 1.17 | 0.33-4.16 |
| Exhaled nitric oxide >35 ppb | 1.58 | 0.45-5.50 |
| Eosinophils >4% | 1.00 | 0.23-4.31 |

Asthma control was determined using a cut-point of 1.5 on the ACQ.

*Versus children who achieved control with triamcinolone.

†$P = .003$.