Figure S1. The regulatory regions of CCR9 and Itg-α4 genes and the binding sites for RARα and BATF examined in this study. (A) Putative BATF and RARα binding sites in the 5' upstream region of the CCR9 gene are shown in a VISTA alignment plot. (B) The structure of the Itg-α4 gene and binding sites for BATF and RARα are shown. TSS indicates transcription start sites. The blue bars indicate exons. The ChIP assay results for the binding sites are shown in Fig. 5 (B and C).

Video 1. 3D image of BATF KO T cells migrated into the spleen and PLN. The image was acquired with an SP5 multiphoton system (Leica). Acquisition volume was ~300 × 300 × 100 μm, and z-axis resolution was 0.5 μm.

Video 2. 3D image of BATF KO T cells migrated into a PP and a colonic patch. The image was acquired with an SP5 multiphoton system (Leica). Acquisition volume was ~300 × 300 × 100 μm, and z-axis resolution was 0.5 μm.
Video 3. 3D image of BATF KO T cells migrated into the small intestine and colon. The image was acquired with an SP5 multiphoton system (Leica). Acquisition volume was ~300 x 300 x 100 μm, and z-axis resolution was 0.5 μm.

Table S1. Putative RAR and BATF binding sites on the 5’ regulatory region of the CCR9 gene

| ChIP sites | Binding elements (RARα) | Binding elements (BATF) |
|------------|-------------------------|-------------------------|
| A          | AGGTCA                  | TGACTG                  |
| B          | TGACCT, TGAGTA          | TGACTG                  |
| C          | TGAGTA, TGACCT          | TGACTG                  |
| D          | TGACCT                  | CACTCA                  |
| E          | AGTCTA, TGACCT, CGCTCA, TAGACA | TGAGCTG, TGACTA |
| F          | TGACCT                  | TGAGCTG                 |
| G          | AGTCTA                  | CTCTCA, TGAGAG, TGACTA |
| H          | AGGTCA, TGACCT          | TGAGAG                  |
| I          | GGCTCA                  | TGACTA                  |
| J          | GGCTCA, TGACC           | TGAGCTG, TGAGAG         |
| K          | TGACCT, TGACCT, AGGTCA  | CACTCA                  |
| L          | TAGACA                  | TGAGCTG, CTCTCA         |
| M          | TGACCT, AGGTCA          | TGACTG, CTCTCA          |
| N          | AGGCTA, GGCTA, TGACCT   | TGACTG                  |
| O          | TGACCT, GGCTA, TGACCT   | TGACTG, CTCTCA          |
| P          | TGACCT                  | TGAGAT, CTCTCA          |
| Q          | TGAACC, TGAACCT, GGCTA, TAAACC, TGTCTA | CAGTCA, CACTCA |
| R          | TGACCT                  | TGACTG                  |

Table S2. PCR primers used in this study

| Gene name          | Forward primer                      | Reverse primer                      |
|--------------------|-------------------------------------|-------------------------------------|
| mRARα              | 5’-ACCGAATTCTTGGTCTTTGCCTTC-3’       | 5’-TCTCCAGCATTCTCCTGATCA-3’         |
| mRARβ              | 5’-ACCCATGACTTTCTGTAGG-3’            | 5’-TACACCTGCTGCACCTTCTG-3’          |
| mRARγ              | 5’-GGAGACCGAATGGACCTGGA-3’           | 5’-TGGAGCTCCTGCTCAGAGT-3’           |
| CCR9               | 5’-GATACATCGCATTCTGACAGGG-3’        | 5’-GCACTCAGAATGAGTTGATAG-3’         |
| ltg-α4             | 5’-AGCTGCACCAATACATGCTCCTC-3’        | 5’-GGTACACCAAGACTGATCAAG-3’         |
| ltg-β7             | 5’-TGACGTGAAATGACCTTGAC-3’          | 5’-TGAGTTCTGCTGTCTCTC-3’            |
| 5’ upstream region of ltg-α4 | 5’-ACATTAAGCTCCACGTCTTCTTCAATG-3’ | 5’-ACATTAAGCTTGAGGACTCAACCCC-3’    |
| mBATF1.2           | 5’-TGTCACCGAGATGATCTGAGTTGAGTGGAA-3’ | 5’-AAGAAGCGGCCGCGCAAGGTCAAGGGCTGAGCAGT-3’ |
| mBATF1.1           | 5’-TGTCACCGAGATGAGTGAAGTGACCTGAGAAGA-3’ | 5’-AAGAAGCGGCCGCGAAAGGTCAAGGGCTGAGCAGT-3’ |
| mBATF              | 5’-TGTCACCGGATGAGACCTGACAGGCTC-3’   | 5’-AAGAAGCGGCCGCGAAAGGTCAAGGGCTGAGCAGT-3’ |
| Sites       | Forward primer | Reverse primer |
|------------|----------------|----------------|
| **CCR9 sites** |                |                |
| A          | 5'-CAGAGACATTATTTCCAGTAAGTTG-3' | 5'-CTAAGTCTGCACGCGATCCAC-3' |
| B          | 5'-GCTTCTTTCTGGTCCTGGTCTG-3'   | 5'-CTGAGGAGAAGAATGGGTGGA-3' |
| C          | 5'-CTCTGCAAGTGAGTTTACCATGTA-3' | 5'-CITGTCAGATAAGGTCCTGTC-3' |
| D          | 5'-GCTGTCCTTAAACATAGACAG-3'   | 5'-ACCAGTGAAGAAGATGCACAC-3' |
| E          | 5'-CCACCTAGAACACAGCTGCTA-3'   | 5'-GGAGACATGTCATCTTTCATG-3' |
| F          | 5'-GCAACCTGTCTCAGAAGCTCAG-3'  | 5'-GAACTATCCACCTAGCTGCTA-3' |
| G          | 5'-CATATCCACCTTACAGTGAATACGA-3' | 5'-GCTGGTGAAAGAATTTAATCTGAG-3' |
| H          | 5'-GATTTCCTTCACTGATCGTGAAG-3' | 5'-GACTGTTGGAAGAATTTAATCTGAG-3' |
| I          | 5'-CCTTAGACACAAGCTGCTGATAC-3' | 5'-CCTGGAAGGATACAAAAATTACCAAAC-3' |
| J          | 5'-CATGGTCCACATTCTCGTCTGC-3'  | 5'-CTGCAAGTGCAAGATCAGACTA-3' |
| K          | 5'-CTATCAGCTGTGGTCCTGCTGTC-3' | 5'-CACATTCAGATATCATAGTACGTC-3' |
| L          | 5'-CAGGTAACAGTAGTGTGACCT-3'   | 5'-CAAGAATACAGTGCAAATGCAC-3' |
| M          | 5'-GGACGAGTTCTTCTGATGACAC-3'  | 5'-AATGACTCTTCTCCTCATCAC-3' |
| N          | 5'-GTGAGAGAAGAGAAGGCAGATCTA-3' | 5'-GGACTGTGACAGCATATCAGA-3' |
| O          | 5'-CCTTTTCTCTTAGAAGCAGTATGTG-3' | 5'-GCCACCAGAAAGAAACTTCCAC-3' |
| P          | 5'-CCAGAGCTCGAGCAGGTCCTTTC-3' | 5'-GTCTCTGCAAGATGCTGCTCC-3' |
| Q          | 5'-CGTGTTTGGAAAAGAAGAAGGG-3'  | 5'-TAAGTGGGTTTCTGAAGACCCAGAG-3' |
| R          | 5'-CTGAGAATAAGATGCAAGAAGT-3'  | 5'-GTCCTGCTTAACTACCAAGC-3' |
| **Itg-α4 sites** |               |                |
| A          | 5'-AGCAGTCCAAAGCCCTAAGC-3'    | 5'-CCACTCCCCCCAGTTTGGGAGA-3' |
| B          | 5'-TITGGCAAAACAGGTAAGAGG-3'   | 5'-GTCACCTCCTCATAACTAGTG-3' |