Despite the advent of antiretroviral therapy, HIV-infected individuals continue to succumb to greater cardiovascular, neurological, renal, and metabolic co-morbidities in comparison to uninfected subjects. Studies have linked chronic immune activation to these co-morbidities, though the etiology of elevated immune activation in treated HIV infection remains poorly understood. Persistent impairments in gut barrier function have been observed in HIV and SIV infection, and studies have implicated traslocation of bacterial products from the gut lumen into systemic circulation as a potential driver of HIV-associated chronic immune activation. While numerous studies have found that the gut microbiota of treated HIV-infected subjects differs from uninfected subjects, whether specific gut bacteria contribute to HIV-associated inflammation and the identities of such bacteria remains unknown. Using the endogenous immunoglobulin repertoire of HIV-infected subjects and uninfected controls as well as SIV-infected non-human primates, we have identified previously uncultured gut microbiota members of the *Erisypelotrichaceae* family that are consistently targeted by the systemic immune system uniquely in progressive HIV and SIV disease. Using murine models in conjunction with isolates obtained from HIV-infected subject stool, we have found that these gut microbiota members can elicit systemic innate immune activation and T cell activation, suggesting a putative causal role for the gut microbiome in HIV-associated chronic inflammation and disease progression.