Figure S1: A model of 3D niche space. (A) (1.) An initial track (of two steps in length) provides a skeleton around which (2.) points are sampled on spheres of radius 4μm and 2μm. (3.) Cylindrical sampling is used to connect spheres with separation > 4 μm. (4.) Rendering of the resultant α-shape. (B) Curvature is quantified by the following procedure: (1.) for each vertex (grey dot) in the α-shape, (2.) find its neighbours, and (3.) sum the angles formed by each pair of connections, for all sets of connections that do not form a triangle on the surface of the shape. (C) The corresponding convex hull for the trajectory shown in (A).

Figure S2: Characteristics of cell tracks. (A) Projection of 3D tracks into the xy-domain. (B) Comparison of the variance in each dimension demonstrates that the z-direction is not significantly different from x or y. (C) Histogram of the cell track lengths for control and infected groups.

Table S1: Stem cell migration statistics for ctl. tracks. Description of the cell migration statistics used to quantify tracks in 3D for control (ctl.) cells. SA, surface area.

Table S2: Stem cell migration statistics for inf. tracks. Description of the cell migration statistics used to quantify tracks in 3D for infected (inf.) cells. SA, surface area.