

**FIGURE 2.** PCA and AA using the 1320 biopsy population. PCA and AA representing injury was done with 10 injury-associated transcript set scores as input variables. (A) Correlations between the input variables and PCs 1 and 2. Transcript set scores: AMAT, cIRITs, DAMP, HT1, HT2, IGT, IRITD3, IRITD5, IRRAT, and QCMAT. (B) Principal component scores from the same analysis. Each small triangle is a biopsy, colored by its injury archetype group. AA, archetypal analysis; AMAT, alternative macrophage-associated transcripts; cIRIT, cardiac injury and repair induced transcript; DAMP, damage-associated molecular pattern transcripts; 1, heart transcripts set 1; HT2, heart transcripts set 2; IGT, immunoglobulin transcripts; IRITD3, injury and rejection-induced transcripts (intermediate); IRITD5, injury and rejection-induced transcripts (late); IRRAT, injury/repair-associated transcripts (acute kidney injury); LVEF, left cular ejection fraction; PCA, principal component analysis; QCMAT, quantitative constitutive macrophage-associated transcripts.