diagnosis of SLE, and had active disease involving skin or joints. RNA isolated from whole blood at baseline and weeks 2, 4, 12, and 24 was analyzed using Affymetrix HTA2.0 array.

**Results** Gene expression profiling demonstrated a statistically significant elevation of STAT1 and STAT2 gene expression at baseline in SLE patients. There was a significant association between the overexpression of STAT1 and STAT2 at baseline. Baricitinib 4-mg treatment resulted in modest reduction in STAT1, STAT2, and STAT4 expression, and a statistically significant reduction in multiple genes downstream of STAT1, STAT2, and STAT4. The reduction in expression of STAT-associated genes with baricitinib treatment correlated with clinical improvement in SLE patients using SLEDAI-2K measurements (table 1).

**Conclusions** Baricitinib may partially mediate its effect in SLE through changes in STAT-related gene expression, with changes associated with clinical improvement in SLE.

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