PRINT: ISSN 0972-3757 ONLINE: ISSN 2456-6330
International Journal of
HUMAN GENETICS

Int J Hum Genet, 18(2): 162-171 (2018)
DOI: 10.31901/24566330.2018/18.2.699

Subpathway Strategy used to Extract Significant Subpathways Competitively Regulated by lncRNAs in Atopic Dermatitis Treated by Cyclosporine A Based on lncRNA-mRNA Expression Data and Pathway Topologies

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KEYWORDS Atopic Dermatitis. lncRNA Competitively Regulated Signal Pathways. Long Noncoding RNAs. Pearson Correlation Coefficien. Subpathway

ABSTRACT The aim of this study was to extract significant subpathways to further investigate the molecular mechanism of cyclosporine A (CsA) in patients with atopic dermatitis (AD) using subpathway strategy. Candidate lncRNA-mRNA interactions were reweighted using Pearson Correlation Coefficient (PCC). Condition-specific lncRNA competitively regulated signal pathways (LRSP) were established, and then lncRNA-regulated subpathways were dissected. Subsequently, the significance of candidate subpathways was assessed to further identify the significant subpathways. To further detect key AD-relevant lncRNAs, degree analysis was conducted for all nodes of the LRSP. Overall 61 significant lncRNAs competitively regulating subpathways involved in 41 complete pathways were identified in the LRSP. The top three subpathways included apoptosis, MAPK signaling pathway, and HIF-1 signaling pathway. There were 6 hub lncRNAs, including YLPM1, UBXN8, ERVK13-1, TTTY15, C14orf169, and EPB41L4A-AS1. Subpathways of apoptosis, MAPK signaling pathway, and HIF-1 signaling pathway might play crucial roles in AD after treatment with CsA.