

**P038** Microarray Analysis of Multiple Sclerosis brain tissue.  
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Multiple Sclerosis is a primary demyelinating disease of the central nervous system. The cause of MS is unknown and pathological hallmarks include plaque formation with immune cell infiltration. A comprehensive analysis of genes whose expression levels are over or under expressed in areas of MS plaque and normal appearing white matter has been completed. Pathological analyses of samples include Oil Red O staining, gliosis markers, lymphocyte infiltration, immune activation and tight junction protein status. Microarray analysis of tissue samples from three MS cases and two non-neurological controls was performed using the Affymetrix U133A GeneChip, containing 23,000 characterised human genes. Data was interrogated using GeneSpring software where a minimum fold change of 2 required for significance. Increased transcripts of genes encoding immune related molecules, including, chemokine(C-X-C motif)ligand 14, with a fold change of(3.3), complement component 1q (2.35) and major histocompatibility complex, class 1 A, B, C, E and F, molecules involved in signal transduction include, CD53 (2.68), MAP3K7 (2.0) and interleukin 13 receptor A1(2.2). These genes play important roles in immune activation within the CNS. This large-scale analysis of transcripts in MS illuminates new aspects of pathogenesis of the disease.