

Additional File 10

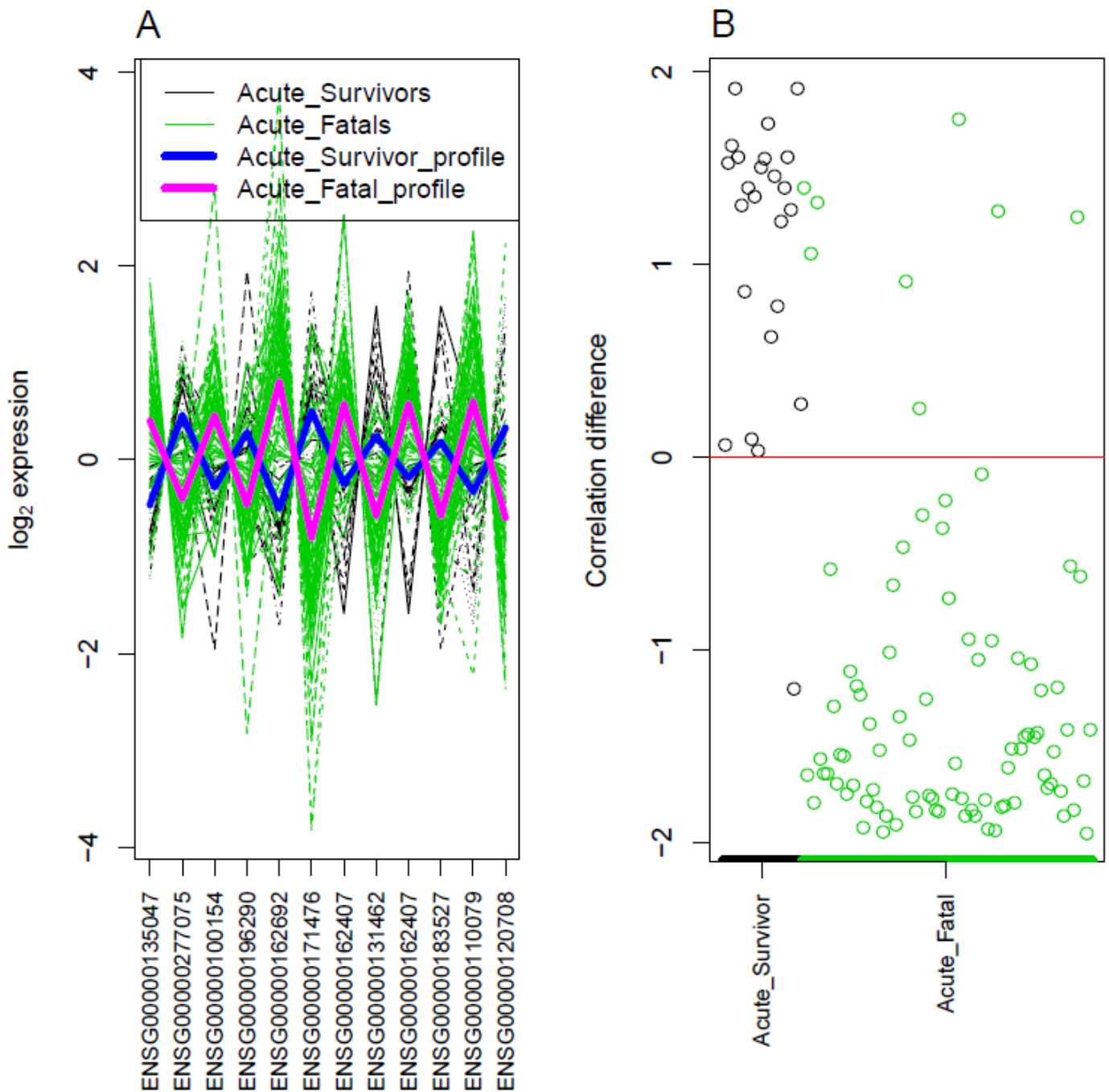


Figure Legend

The *paired gene profiling method* for outcome prediction. Gene pairs were selected by an algorithm searching through the gene space for those gene pairs displaying maximal discrimination between treatment groups. In this case 6 gene pairs were selected to provide a profile (left hand panel) from which the correlation coefficient (CC) of the training set for each of the two grouped profiles (heavy lines) was calculated. The CC difference for acute-fatal and acute-survivor patients were then displayed in order on the right hand panel. The red horizontal line separates the two domains, from which % prediction accuracy was calculated. Thus, the acute_survivor symbols (24) lie above the line with one exception, whilst for the 88 acute_fatal symbols 80 lay below the line and only 8 above.