**Onco-Wiki Healthy Dataset**

1. **Healthy Dataset**

The Healthy dataset is a sequenced putatively ‘healthy’ dataset which can be manually adjusted to simulate a cancer patient. Fold changes are measure of how many times bigger the expression value of one sample is over the other. This effective mean gene expression level has been calculated using real RNA-Sequenced data from five human patients undergoing reduction mammoplasty surgeries who are believed to have no known cancer. 57,773 spliced gene variants have measured fold change levels and are exported in an .xlsx file below.

1. **Download Dataset**

The Healthy Dataset can be downloaded from:

[**http://oncowiki.co.uk/support/healthy.xlsx**](http://oncowiki.co.uk/support/healthy.xlsx)

1. **Fold Change Calculation**

Fold change means between the experiments are balanced by a repeated measures ANOVA test. Through testing the equality of means, this test helps to account for differences in mean scores, particularly important with 'in-vivo' human tissue genomic data as read counts are extremely variable. Given this high level of variance, each patient is assigned as a unique conditional group. An overall fold change is calculated for each gene spliced variant (57,773) across each sample in fulfilling a critical assumption of the repeated measures ANOVA test, termed sphericity.

For a fold change to be calculated, there must be discrete expression values of read counts in all 5 samples. A lack of gene expression in at least 1 sample results in an inconclusive overall measurement of gene expression, characterised as an infinity (∞) fold change. As a result, this test suffers from a high probability of Type II errors (false negatives).

1. **Advanced Dataset**

For those interested in the raw values in the calculation of these fold changes, a full raw exported version of this dataset can be downloaded from:

[**http://oncowiki.co.uk/support/healthyraw.xlsx**](http://oncowiki.co.uk/support/healthyraw.xlsx)

NKC – denotes ‘No Known Cancer’ patient samples.