| **Statistical Analyses** | **IV(s)** | **IV type(s)** | **DV(s)** | **DV type(s)** | **Control Var** | **Control Var type** | **Question to be answered** | ***H0*** | **alpha** | **link to paper \*\*** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-square** | **celldivision** | **Cell**  **Divisionper intervals** | **Rate of mutation Family patternIndividual development** | **Family patternIndividual development** | **Fixed family size** | **Multiplefamily sizes** | **Estimate biological mutation rates** | ***Mutation of of the family is same*** | **1%and3%**  **\*See table-4** | [**http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0135398**](http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0135398) |
| **T test** | differentially expressed genes | complex human background at concentrations | **Hybridzations of Spike in genes** | differentially expressed genes | **Group Replicates** |  | **Compute false positiva rate** | that the expected values of expression for a given gene are equal between two groups of interest | **5%** | **http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0012336** |