**Correlation Tests of mRNA Expression and Copy-Number Alterations for FAT1 and EGFR in Different Cancer Types**

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**Statistical Methods**

The correlation between mRNA expression and copy-number alterations of two genes (FAT1 and EGFR) were calculated in three different cancer types. Cancer types were Head and Neck Squamous Cell Carcinoma (HNSCC), Lung Squamous Cell Carcinoma (Lung SCC) and Cervical Squamous Cell Carcinoma (Cervical SCC).

Pearson, Spearman and Kendall correlations were calculated for each gene of each cancer type. Additionally, one-way ANOVA was performed to compare means of mRNA expression among all the copy-number alteration categories. Copy-number alterations were treated as numeric when calculated for Pearson, Spearman and Kendall correlations. However, Spearman correlation was not recommended in this case, as its p-values were not accurate with ties. In one-way ANOVA, it was considered as categorical. Scatter point plots with linear regression lines were presented with 95% confidence intervals.

The significance level was set at 0.05. R software version 4.0.3 was used for data analysis and management.

**Results**

1. HNSCC
2. Correlation between mRNA expression and copy-number alterations

**Table 1.1 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.3098303 | 1.202e-08 |
| EGFR | 0.5140695 | < 2.2e-16 |

**Table 1.2 Spearman correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2543987 | 1.202e-08 |
| EGFR | 0.4689638 | < 2.2e-16 |

**Table 1.3 Kendall correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2017809 | 9.106e-09 |
| EGFR | 0.3796417 | < 2.2e-16 |

1. One-way ANOVA

**Table 1.4 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 19.64 | 9.106e-09 |
| EGFR | 68.95 | <2e-16 |

1. Lung SCC
2. Correlation between mRNA expression and copy-number alterations

**Table 2.1 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2489197 | 5.182e-08 |
| EGFR | 0.4383278 | < 2.2e-16 |

**Table 2.2 Spearman correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2576931 | 1.666e-08 |
| EGFR | 0.411743 | < 2.2e-16 |

**Table 2.3 Kendall correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2054728 | 1.513e-08 |
| EGFR | 0.3296223 | < 2.2e-16 |

1. One-way ANOVA

**Table 2.4 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 8.13 | 2.43e-06 |
| EGFR | 44.2 | <2e-16 |

1. Cervical SCC
2. Correlation between mRNA expression and copy-number alterations

**Table 3.1 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2864389 | 1.365e-06 |
| EGFR | 0.3358416 | 1.125e-08 |

**Table 3.2 Spearman correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2131006 | 0.0003726 |
| EGFR | 0.2797567 | 2.446e-06 |

**Table 3.3 Kendall correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.1695754 | 0.0003446 |
| EGFR | 0.225934 | 2.328e-06 |

1. One-way ANOVA

**Table 3.4 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 16.86 | 4.55e-10 |
| EGFR | 16.16 | 1.07e-09 |

1. Scatter point plots with linear regression line and 95% confidence interval

**Figure 1. Scatter point plots with linear regression line for FAT1 and EGFR**

Graphical user interface

Description automatically generated

**Conclusions**

From the results, we could see that mRNA and copy-number alterations were positively and significantly correlated for FAT1 and EGFR in all these three cancer types. One-way ANOVA results also indicated that the means of mRNA expression in each copy-number alteration category were significantly different in these three cancer types.