**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 in HNSCC, Lung SCC and Cervical SCC, respectively. Additionally, one-way ANOVA was performed to compare means of log2 (mRNA expression) among all the copy-number alteration categories. Copy-number alterations were treated as numeric when calculated for Pearson, Spearman and Kendall correlations. In one-way ANOVA, it was considered as categorical. Box plots of mRNA expression for both raw and transformed data were presented. However, Spearman correlation was not recommended in this case, as its p-values were not accurate with ties.

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

**Results**

1. HNSCC
2. Descriptive statistics for mRNA expression and log2 (mRNA expression)

**Table 1.1 Descriptive statistics for FAT1 mRNA expression**

Table

Description automatically generated

**Table 1.2 Descriptive statistics for EGFR mRNA expression**

Table

Description automatically generated

1. Correlation between mRNA expression and copy-number alterations

**Table 1.3 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.3098636 | 2,549e-12 |
| EGFR | 0.5138375 | < 2.2e-16 |

**Table 1.4 Spearman correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2543926 | 1.203e-08 |
| EGFR | 0.4689816 | < 2.2e-16 |

**Table 1.5 Kendall correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2017775 | 9.106e-09 |
| EGFR | 0.3796477 | < 2.2e-16 |

1. One-way ANOVA

**Table 1.6 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 19.66 | 5.28e-15 |
| EGFR | 68.84 | <2e-16 |

1. Lung SCC
2. Descriptive statistics for mRNA expression and log2 (mRNA expression)

**Table 2.1 Descriptive statistics for FAT1 mRNA expression**

Table

Description automatically generated

**Table 2.2 Descriptive statistics for EGFR mRNA expression**

Table

Description automatically generated

1. Correlation between mRNA expression and copy-number alterations

**Table 2.3 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2488554 | 5.225e-08 |
| EGFR | 0.4375131 | < 2.2e-16 |

**Table 2.4 Spearman correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2576738 | 1.671e-08 |
| EGFR | 0.4117305 | < 2.2e-16 |

**Table 2.5 Kendall correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2054575 | 1.516e-08 |
| EGFR | 0.3296031 | < 2.2e-16 |

1. One-way ANOVA

**Table 2.6 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 8.127 | 2.44e-06 |
| EGFR | 43.97 | <2e-16 |

1. Cervical SCC
2. Descriptive statistics for mRNA expression and log2 (mRNA expression)

**Table 3.1 Descriptive statistics for FAT1 mRNA expression**

Table

Description automatically generated

**Table 3.2 Descriptive statistics for EGFR mRNA expression**

Table

Description automatically generated

1. Correlation between mRNA expression and copy-number alterations

**Table 3.3 Pearson correlation**

|  |  |  |
| --- | --- | --- |
| Gene | Sample estimate | P-value |
| FAT1 | 0.2860896 | 1.408e-06 |
| EGFR | 0.3344819 | 1.3e-08 |

**Table 3.4 Spearman correlation**

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

**Table 3.5 Kendall correlation**

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

1. One-way ANOVA

**Table 3.6 One-way ANOVA results**

|  |  |  |
| --- | --- | --- |
| Gene | F-value | P-value |
| FAT1 | 16.83 | 4.71e-10 |
| EGFR | 15.91 | 1.47e-09 |

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

**Figure 1. Box plots of mRNA expression in each of level of copy number**

Diagram, engineering drawing

Description automatically generated

**Figure 1. Box plots of log2 (mRNA expression) in each of level of copy number**

Chart, box and whisker chart

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**Conclusions**

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