**Table 2: Gene expressions, median fold change and statistical analyses of GWAS identified genes and MTORC1-associated genes in the discovery cohort**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | Post Hoc tests | | | | |
| Marker | **Group** | **Mean ΔCT ±SD** | **Median Fold Change** | **Multiple comparison**† | Post hoc  KC vs. HC‡ | Post hoc  KC vs. DG‡ | Post hoc  DG vs HC‡ | Post hoc  HC vs. KC+DG† | Post hoc  KC vs. HC+DG† |
| *FOXO1* | HC  DG  KC | 43.26 ± 23.00  60.52 ± 77.74  50.96 ± 34.58 | *0.000*  *0.000*  *0.000* | *0.783* | *-* | *-* | *-* | *-* | *-* |
| *FNDC3B* | HC  DG  KC | 12.79 ± 15.24  22.75 ± 18.66  39.32 ± 29.19 | *0.009*  *0.000*  *0.000* | *0.021\** | *0.150* | *0.220* | *0.766* | *0.011\** | *0.044* |
| *PDGFRA* | HC  DG  KC | 50.89 ± 76.23  39.64 ± 62.21  336.99 ± 464.68 | *0.000*  *0.000*  *0.000* | *0.001\*\** | *0.304* | *0.086* | *0.998* | *< 0.001\*\** | *0.143* |
| *FRAP1/ MTOR* | HC  DG  KC | 4.299 ± 0.637  2.754 ± 0.970  1.813 ± 0.966 | *0.048*  *0.148*  *0.313* | *0.005\** | *0.004\** | *0.182* | *0.081* | *0.005\** | *0.013\** |
|  |  |  |  |  |  |  |  |  |  |
| *AKT1* | HC  DG  KC | 2.130 ± 0.926  -1.713 ± 0.514  -1.901 ± 0.738 | *0.159*  *3.638*  *3.950* | *< 0.001\*\** | *< 0.001\*\** | *0.843* | *< 0.001\*\** | *< 0.001\*\** | *0.047* |
| *DEPTOR* | HC  DG  KC | 5.971 ± 0.732  2.308 ± 0.883  3.751 ± 0.635 | *0.015*  *0.190*  *0.074* | *< 0.001\*\** | *0.006\** | *0.026* | *< 0.001\*\** | *0.001\*\** | *0.815* |
| *IGF1* | HC  DG  KC | 9.513 ± 2.257  2.815 ± 1.308  4.887 ± 0.472 | *0.002*  *0.084*  *0.033* | *< 0.001\*\** | *0.005\** | *0.124* | *< 0.001\*\** | *< 0.001\*\** | *0.826* |
| *IGF1R* | HC  DG  KC | 0.681 ± 1.040  -3.704 ± 0.737  -3.952 ± 0.956 | *0.621*  *14.470*  *12.676* | *< 0.001\*\** | *< 0.001\** | *0.837* | *< 0.001\*\** | *< 0.001\*\** | *0.049* |
| *RAPTOR* | HC  DG  KC | 6.565 ± 0.346  3.699 ± 1.729  3.955 ± 0.308 | *0.012*  *0.075*  *0.058* | *0.010\** | *0.018\** | *0.927* | *0.014\** | *0.002\*\** | *0.306* |
| *RICTOR* | HC  DG  KC | 2.755 ± 0.580  4.363 ± 0.596  3.732 ± 1.241 | *0.169*  *0.044*  *0.069* | *0.109* | *-* | *-* | *-* | *-* | *-* |
| GWAS: Genome Wide Association Study, see references 7,8,9. MTORC1: Mammalian Target Of Rapamycin Complex 1. ΔCT: delta cycle threshold. SD: standard deviation. HC: healthy control. DG: decompensated graft/diseased control. KC: keratoconus. \*: significance < 0.05, \*\*: significance <0.002 (corrected for multiple testing). †: One-way ANOVA in normal distributions and Kruskal-Wallis for non-normal distribution. ‡: post-hoc Tukey.V-Akt Murine Thymoma Viral Oncogene Homolog 1 *(AKT1),* DEP domain containing MTOR-interacting protein *(DEPTOR),* fibronectin type III domain containing 3B *(FNDC3B),* Forkhead Box O1 *(FOXO1),* Insulin-Like Growth Factor 1 *(IGF1),* Insulin-Like Growth Factor 1 Receptor *(IGF1R),* Mammalian Target Of Rapamycin *(MTOR),* Platelet Derived Growth Factor Receptor Alpha *(PDGFRA),* Rapamycin-Insensitive Companion Of MTOR *(RICTOR),* Regulatory Associated Protein Of MTOR *(RAPTOR).* | | | | | | | | | |