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| **Table S5. Negative univariate associations between T cell related genes and genes involved in muscle catabolic pathways of rectus abdominis muscle of secondary female cohort (n=64)** |
| **T cell category** | **Gene name** | **Muscle catabolic pathway** | **Gene name** | **r** | **p** |
| T cell function | CD3G | Ubiquitin proteasome | UBR2 | -0.30 | 1.76E-02 |
| Ubiquitin proteasome | FOXO4 | -0.28 | 2.47E-02 |
| HAVCR2 | Apoptosis | BECN1 | -0.30 | 1.80E-02 |
| Ubiquitin proteasome | UBE2L3 | -0.32 | 1.02E-02 |
| Ubiquitin proteasome | TRIM63 | -0.30 | 1.55E-02 |
| Ubiquitin proteasome | UBR2 | -0.28 | 2.40E-02 |
| PDCD1 | Ubiquitin proteasome | UBAP2 | -0.61 | 1.04E-07 |
| Ubiquitin proteasome | UBR3 | -0.50 | 2.31E-05 |
| Ubiquitin proteasome | FOXO4 | -0.42 | 4.93E-04 |
| Ubiquitin proteasome | UBR2 | -0.35 | 4.02E-03 |
| Ubiquitin proteasome | FOXO4 | -0.32 | 1.05E-02 |
| Ubiquitin proteasome | USP25 | -0.31 | 1.21E-02 |
| Ubiquitin proteasome | UBE2R2 | -0.31 | 1.38E-02 |
| Ubiquitin proteasome | UBE2V1 | -0.30 | 1.68E-02 |
| Ubiquitin proteasome | UBE2V1 | -0.25 | 4.93E-02 |
| CD28 | Apoptosis | SIVA1 | -0.37 | 2.32E-03 |
| Apoptosis | BECN1 | -0.36 | 3.91E-03 |
| Signaling | ACVR2B | -0.39 | 1.42E-03 |
| Signaling | ACVR1B | -0.27 | 2.79E-02 |
| Ubiquitin proteasome | UBC | -0.37 | 2.59E-03 |
| Ubiquitin proteasome | PSMA7 | -0.36 | 3.67E-03 |
| Ubiquitin proteasome | UBE2V1 | -0.35 | 4.15E-03 |
| Ubiquitin proteasome | FOXO4 | -0.33 | 8.25E-03 |
| Ubiquitin proteasome | UBC | -0.29 | 1.80E-02 |
| Ubiquitin proteasome | UBE2B | -0.29 | 1.88E-02 |
| Ubiquitin proteasome | UBA52 | -0.29 | 2.07E-02 |
| Ubiquitin proteasome | UBB | -0.27 | 2.82E-02 |
| Ubiquitin proteasome | TRIM63 | -0.26 | 4.03E-02 |
| Ubiquitin proteasome | UBR2 | -0.25 | 4.28E-02 |
| Ubiquitin proteasome | UBC | -0.25 | 4.75E-02 |
| STAT4 | Ubiquitin proteasome | PSMA7 | -0.28 | 2.56E-02 |
| CD2 | Ubiquitin proteasome | USP2 | -0.37 | 2.38E-03 |
| Ubiquitin proteasome | STUB1 | -0.33 | 7.25E-03 |
| Ubiquitin proteasome | UBE2V1 | -0.32 | 1.09E-02 |
| Ubiquitin proteasome | UBE2V1 | -0.28 | 2.55E-02 |
| Ubiquitin proteasome | FOXO4 | -0.28 | 2.78E-02 |
| CD6 | Ubiquitin proteasome | FOXO4 | -0.29 | 1.88E-02 |
| PTPRC (CD45) | Apoptosis | BECN1 | -0.30 | 1.65E-02 |
|  |  |  |  |
| Apoptosis | SIVA1 | -0.27 | 3.07E-02 |
| Signaling | ACVR2B | -0.47 | 9.17E-05 |
| Signaling | ACVR1B | -0.41 | 7.61E-04 |
| Ubiquitin proteasome | STUB1 | -0.55 | 2.10E-06 |
| Ubiquitin proteasome | UBB | -0.51 | 2.00E-05 |
| Ubiquitin proteasome | UBA52 | -0.50 | 3.16E-05 |
| Ubiquitin proteasome | UBC | -0.49 | 3.62E-05 |
| Ubiquitin proteasome | UBC | -0.48 | 5.33E-05 |
| Ubiquitin proteasome | UBB | -0.48 | 5.70E-05 |
| Ubiquitin proteasome | UBC | -0.45 | 2.25E-04 |
| Ubiquitin proteasome | UBC | -0.44 | 2.34E-04 |
| Ubiquitin proteasome | UBA52 | -0.41 | 8.11E-04 |
| Ubiquitin proteasome | UBE2R2 | -0.37 | 2.48E-03 |
| Ubiquitin proteasome | UBA52 | -0.36 | 3.60E-03 |
| Ubiquitin proteasome | PSMA7 | -0.35 | 4.17E-03 |
| Ubiquitin proteasome | USP2 | -0.32 | 9.14E-03 |
| Ubiquitin proteasome | DNAJC11 | -0.30 | 1.49E-02 |
| Ubiquitin proteasome | TRIM63 | -0.26 | 3.67E-02 |
| Ubiquitin proteasome | MUL1 | -0.27 | 3.29E-02 |
| Ubiquitin proteasome | FOXO4 | -0.26 | 3.68E-02 |
| Ubiquitin proteasome | UBE2V1 | -0.26 | 4.09E-02 |
| IL2RB | Apoptosis | BECN1 | -0.31 | 1.39E-02 |
| IL2RB | Signaling | ACVR2B | -0.33 | 8.24E-03 |
| IL2RB | Ubiquitin proteasome | UBC | -0.46 | 1.36E-04 |
| IL2RB | Ubiquitin proteasome | UBC | -0.44 | 2.58E-04 |
| IL2RB | Ubiquitin proteasome | UBC | -0.40 | 9.27E-04 |
| IL2RB | Ubiquitin proteasome | FOXO4 | -0.32 | 9.18E-03 |
| CD8 T cell specific function | FASLG | Ubiquitin proteasome | USP2 | -0.40 | 1.09E-03 |
| FASLG | Ubiquitin proteasome | FOXO4 | -0.30 | 1.50E-02 |
| GZMA | Ubiquitin proteasome | USP2 | -0.35 | 4.75E-03 |
| GZMK | Ubiquitin proteasome | USP2 | -0.33 | 6.89E-03 |
| GZMK | Ubiquitin proteasome | STUB1 | -0.27 | 3.32E-02 |
| r= Pearson's correlation coefficient. p = <0.05: statistical significance. Genes analyzed in the preset table are based on the univariate negative gene correlations from the secondary male cohort (a 46 gene list). No significant or negative correlations where observed for LCK, CASP8, ATG13, FBXO32, UBE2L3 and USP4. |