Dear readers,

Following the publication of this article, we identified 18 duplicate samples from muscle between the datasets GSE3307 and GSE11971. Despite having different GSM accession numbers, these samples contained the same underlying data. We removed the dataset GSE11971 and repeated our analysis for muscle tissue. While there are slight differences, for example, in the number of differentially-expressed genes, the overall main results and conclusions of the paper remain unchanged and robust.

The following summarizes the errors in our original publication and the correct results:

In Supplementary Table 1, GSE11971 should be removed.

In the abstract on p 657, Fig 1, and results section on p 660, instead of six muscle datasets, the text should now read five datasets.

In Fig 1 and in the results section on p 660, instead of 107 total muscle samples with 71 cases and 36 controls, the text should read 84 total muscle samples with 52 cases and 32 controls.

In the abstract on p 657 and the results section p 660, the total number of differentially expressed genes in muscle is 492 instead of 544, with 432 (previously 443) upregulated genes and 60 (previously 101) down-regulated genes.

In the abstract on p 657, the results section p 660, the legend for Figure 3, and the discussion section p 664, the number of shared differentially expressed genes between muscle and skin is 90 rather than 94. In the results section, the significance of this overlap as assessed by the hypergeometric test is $P = 3.0 \times 10^{-73}$ (previously $6.4 \times 10^{-78}$). In Supplementary Table 2, the four genes LAMP3, PLAC8, MNDA, and TRANK1 are no longer significant. These genes nearly below our significance threshold in the original analysis.

Figure 2A should be updated as below. The main interpretation of the figure as stated in the publication is unchanged.

Figures 3 and 4 are unchanged.

In the abstract on p 657 and results section p 662, in the muscle network analysis, the total number of gene modules is six, not eight.
In the results section p 62, “A concentrated cluster of modules highly correlated with DM cases in both muscle and skin networks…” should read “M1, M3 and S1 modules”.

Figure 5A is updated to reflect the WGCNA analysis in muscle and how these networks overlap as below. The interpretation of these modules is unchanged.

The revised Figure 5B shows the same overlapping enriched pathways across modules using the new muscle modules, including the important finding of T cell activation and signaling in both networks. Here, I show the similarities across the top three modules from both tissues, which nicely demonstrates the overlap across the networks with the same conclusions listed in the original manuscript:
Supplementary Table 3 is updated with the network preservation statistics as per the table below. The interpretation of this analysis is unchanged.

| Module Label | Module Color | Module Size (genes) | Correlation | pvalue | adjpvalue | Zsummary score (preservation in skin network) |
|--------------|--------------|---------------------|-------------|--------|----------|---------------------------------------------|
| M1           | MEbrown      | 1000                | -0.8014466  | 5.38E-20 | 3.76E-19 | 22.79995868                                 |
| M2           | MEblue       | 1000                | -0.5658825  | 2.03E-08 | 3.55E-08 | 12.68697834                                 |
| M3           | MEred        | 456                 | -0.5345315  | 1.63E-07 | 2.28E-07 | 50.80011417                                 |
| M4           | MEyellow     | 583                 | 0.45919866  | 1.12E-05 | 1.30E-05 | 6.392592098                                 |
| M5           | METurquoise  | 1000                | 0.60860217  | 8.18E-10 | 1.91E-09 | 8.569047311                                 |
| M6           | MEgreen      | 571                 | 0.727294    | 4.71E-15 | 1.65E-14 | 12.98429145                                 |

In the results section p 662, the text should read, “Although there was no overlap of pathway enrichment of repressed genes in the single-gene analysis, we did find overlap on the network levels between the M6 (previously labeled M8) and S6 module.”

The revised Figure 5B shows the same overlapping enriched pathways across modules using the new muscle modules, including the important finding of T cell activation and signaling in both networks. Here, I show the similarities across the top three modules from both tissues:

In the results section p 662, there are 614 hub genes (previously 615) in the muscle network.

In the results section, p 664, sixteen (previously nineteen) cell types were significantly enriched in muscle, and CD8+ T cells and gamma-delta T cells are no longer enriched in cases. Figure 6A has been updated below to reflect the 16 cell types. The most enriched cells, macrophages and dendritic cells, are the same.
In Supplementary Table 4, B2M and NMI are included in the top 30 hub genes in the muscle network, and IFIT5 and HERC6 are now numbers 31 and 33 top hub genes, respectively.

In the results section on page 663, in muscle, 109 (previously 133) genes were classified as ISGs, of which 3 (previously 14) were exclusively stimulated by type I IFN, whereas, 106 were stimulated by both type I and type II IFN.

We sincerely apologize for these errors. We are happy to see that removing this study with duplicates does not change the main interpretations and conclusions of our manuscript. We hope that you find this work informative and useful to your own research programs.

Sincerely,
Jessica Neely & Marina Sirota