Figure 1 A comparison of parameters estimated by the MATLAB and R implementations of ISOpure for the Bhattacharjee dataset. Each plot shows the entries of a parameter estimated using ISOpureR plotted against the corresponding entries estimated using the MATLAB code. The parameter is an average over 50 models run with different initial conditions. The line $y = x$ is indicated in black, and the linear regression line, or robust regression line for $\theta$, is dashed orange. (A) Parameters from the Cancer Profile Estimation step of ISOpure are: (i) $\nu$, the hyper-parameter for the Dirichlet distribution over $\theta$, (ii) $\theta$, the proportion of a patient sample from a known healthy-tissue profile, (iii) $m$, the average mRNA abundance cancer profile, (iv) $\alpha$, the fraction of cancer cells for every patient sample, (v) $\omega$ a hyper-parameter for the Dirichlet distribution over $m$. (B) Parameters from the Patient Profile Estimation step of ISOpure are (i) $\nu$, the hyper-parameter for the Dirichlet distribution over $\theta$, (ii) $\theta$, the proportion of a patient sample from a known healthy-tissue profile, (iii) $c_n$, the purified mRNA abundance cancer profile for each patient.
Figure 2. A comparison of parameters estimated by the MATLAB and R implementations of ISOpure for the Wallace dataset. Each plot shows the entries of a parameter estimated using ISOpureR plotted against the corresponding entries estimated using the MATLAB code. The parameter is an average over 50 models run with different initial conditions. The line $y = x$ is indicated in black, and the linear regression line, or robust regression line for $\theta$, is dashed orange. A description of the parameters from the Cancer Profile Estimation step (A) and the Patient Profile Estimation step (B) of ISOpure is given in Figure 1.
Figure 3. A comparison of parameters estimated by the MATLAB and R implementations of ISOpure for the Wang dataset. Each plot shows the entries of a parameter estimated using ISOpureR plotted against the corresponding entries estimated using the MATLAB code. The parameter is an average over 25 MATLAB models run with different initial conditions and 13 R models; models converging to a local minimum were omitted. The line $y = x$ is indicated in black, and the linear regression line, or robust regression line for $\theta$, is dashed orange. A description of the parameters from the Cancer Profile Estimation step (A) and the Patient Profile Estimation step (B) of ISOpure is given in Figure 1.