Supplementary Figure Legends

Supplementary Figure 1. **HILIC HPLC chromatograms used in library generation for SWATH analysis.** 30 µg of tryptic peptides from normal endometrium and endometrial cancer tissues were fractionated by HILIC-HPLC into 15 fractions prior to LC-MS/MS. Dotted lines indicated collected fractions.

Supplementary Figure 2. **List of candidate proteins that are overexpressed during premenopausal vs postmenopausal in endometrial cancer compared to controls.** IHC data and information on these highlighted proteins (EWSR1, TUBA1A, TIGAR, CENPV, COL1A2, S100A16, and NEBL) in endometrial cancer as described in the Human Protein Atlas (HPA).

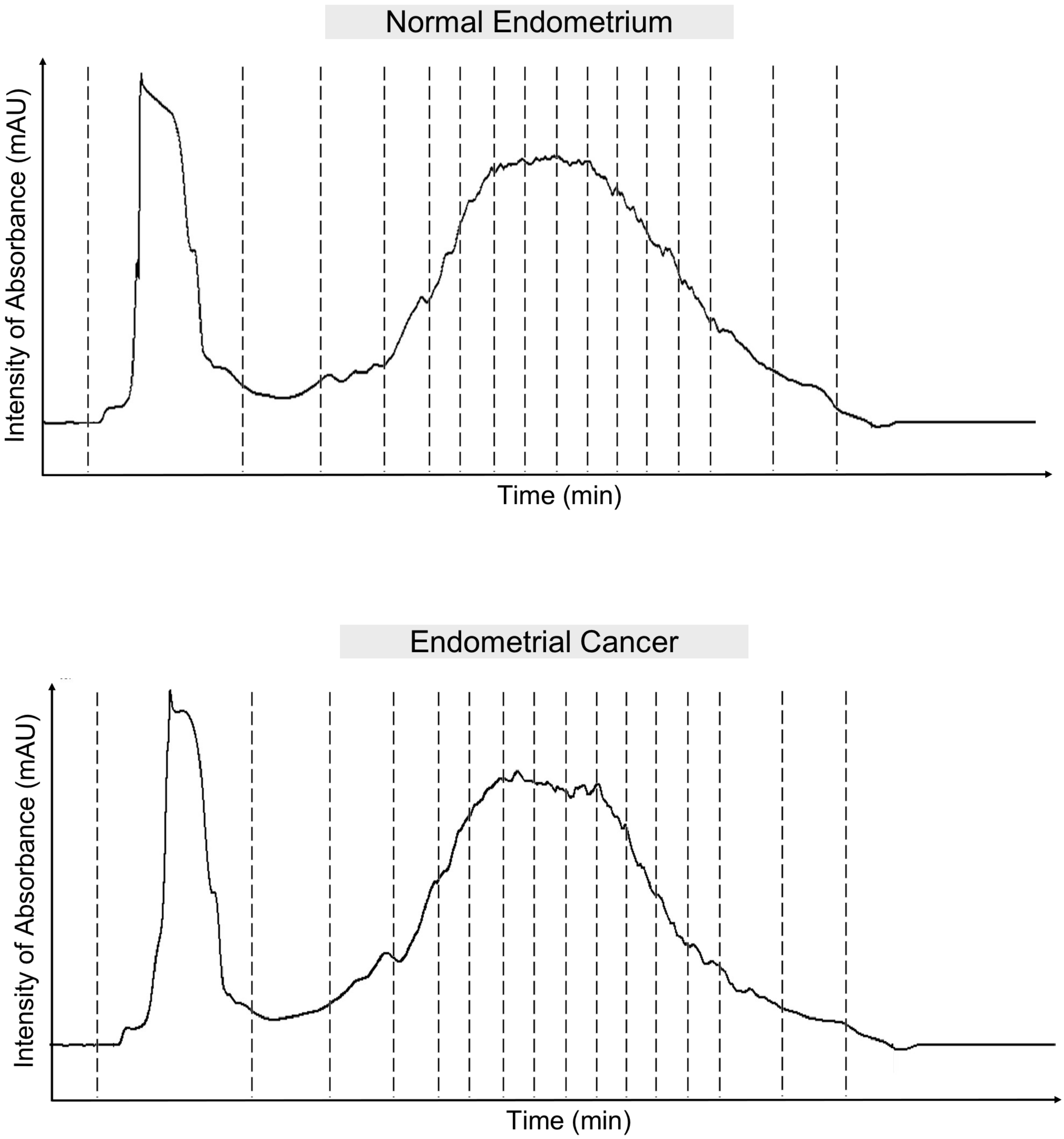
Supplementary Figure 3. **List of candidate proteins that are overexpressed in macroscopic tumors compared to microscopic tumors.** IHC data and information on these highlighted proteins (ECHS1, PHGDH, YWHAE, HADH, SRP68, and CAPRIN1) in endometrial cancer as described in the Human Protein Atlas (HPA).

Supplementary Figure 4. **Ingenuity pathway analysis of endometrial cancer patients (Patient 1 to Patient 6).** The top 10 significantly altered canonical pathways in endometrial cancer tissue associated with individual patients are shown along the x-axis of the bar chart. The ratio (orange dots connected by a line) indicates the number of proteins from the dataset that map to the pathway listed divided by the total number of proteins that map to the canonical pathway within the IPA database. The yellow line represents the threshold of p-value < 0.05 as calculated by Fischer’s test.

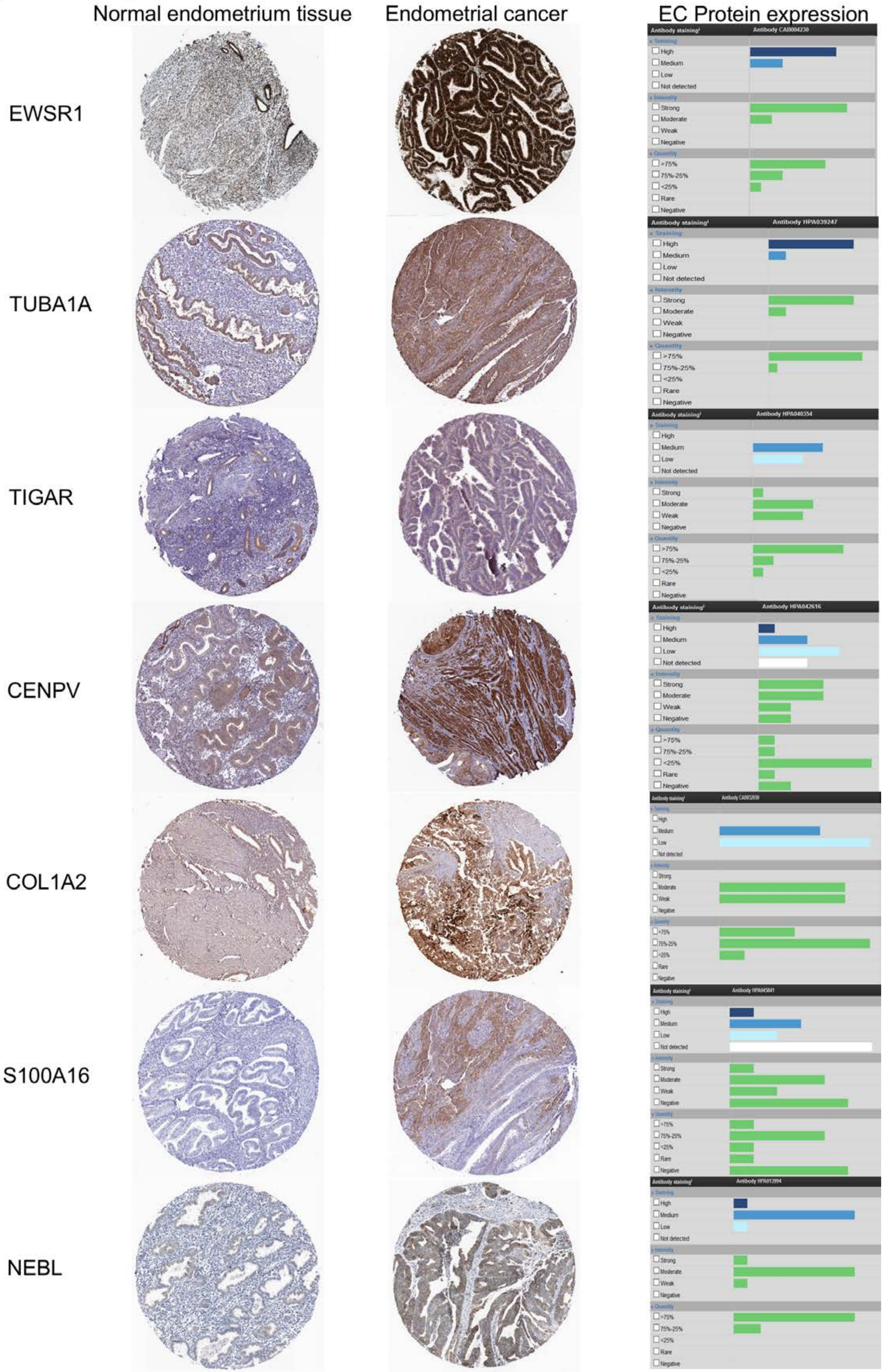
Supplementary Figure 5. **Ingenuity pathway analysis of endometrial cancer patients (Patient 7 to Patient 14).** The top 10 significantly altered canonical pathways in endometrial cancer tissue associated with individual patients are shown along the x-axis of the bar chart. The ratio (orange dots connected by a line) indicates the number of proteins from the dataset that map to the pathway listed divided by the total number of proteins that map to the canonical pathway within the IPA database. The yellow line represents the threshold of p value < 0.05 as calculated by Fischer’s test.

Supplementary Figure 6. **Ingenuity pathway analysis in endometrial cancer patients (Patient 15 to Patient 20).** The top 10 significantly altered canonical pathways in endometrial cancer tissue associated with individual patients are shown along the x-axis of the bar chart. The ratio (orange dots connected by a line) indicates the number of proteins from the dataset that map to the pathway listed divided by the total number of proteins that map to the canonical pathway within the IPA database. The yellow line represents the threshold of p-value < 0.05 as calculated by Fischer's test.

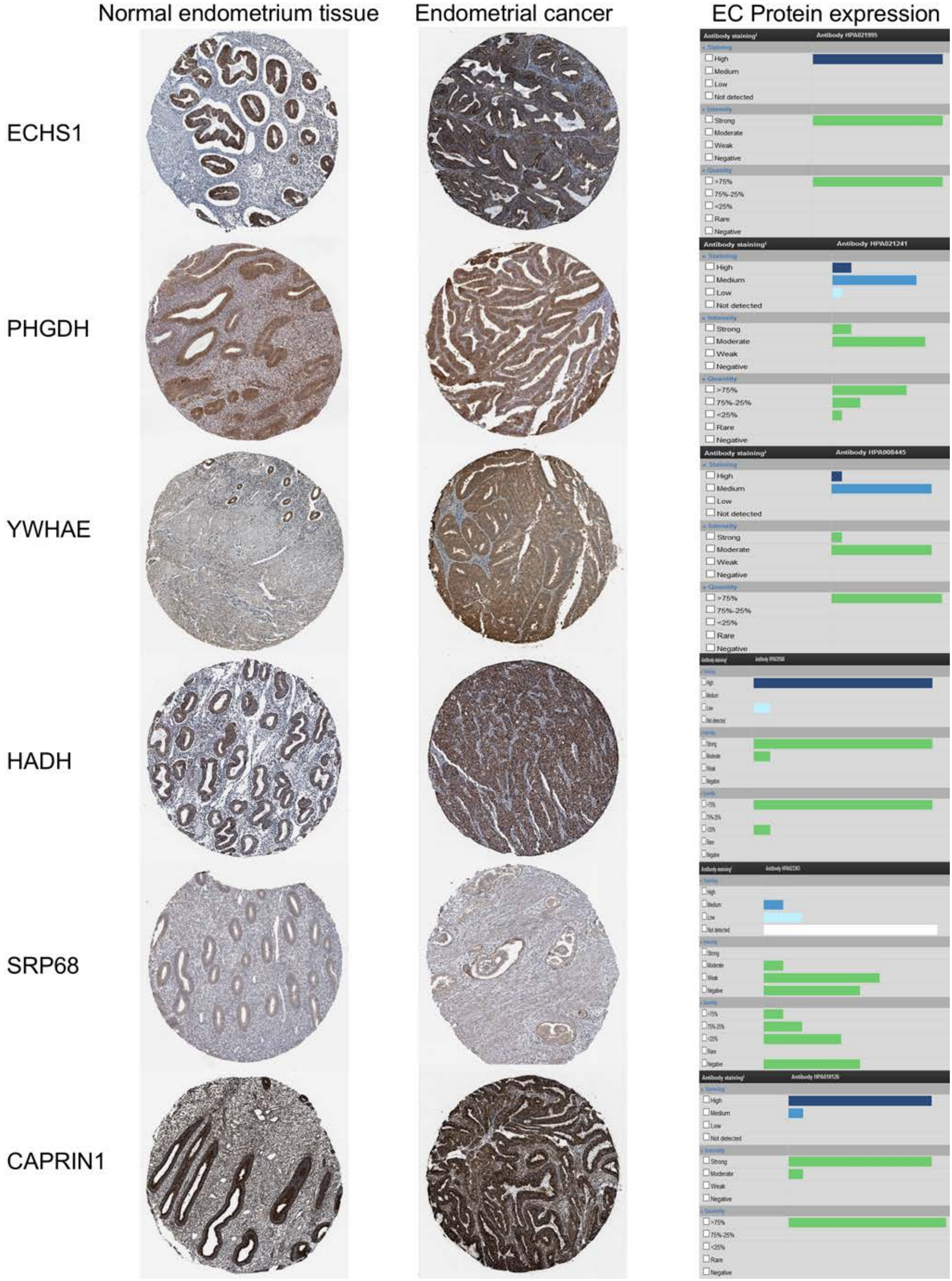
Supplementary Figure 1



Supplementary Figure 2

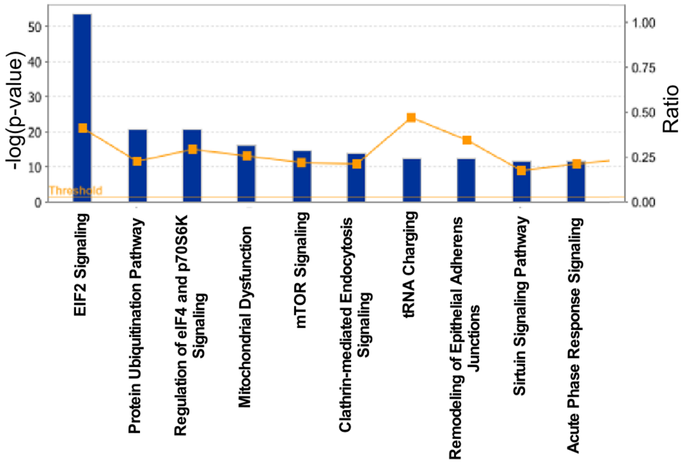


Supplementary Figure 3

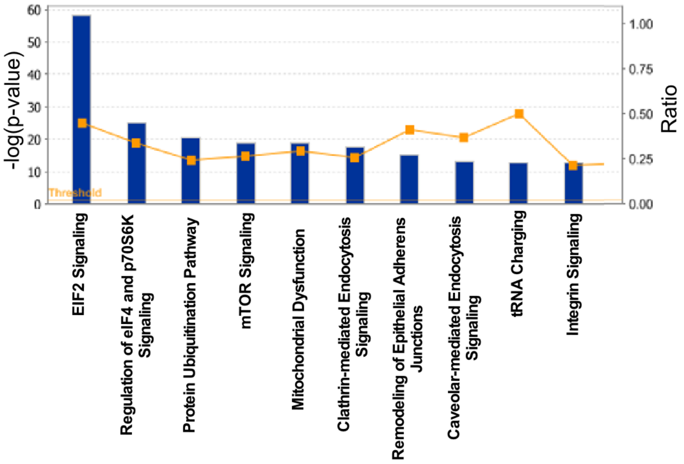


Supplementary Figure 4

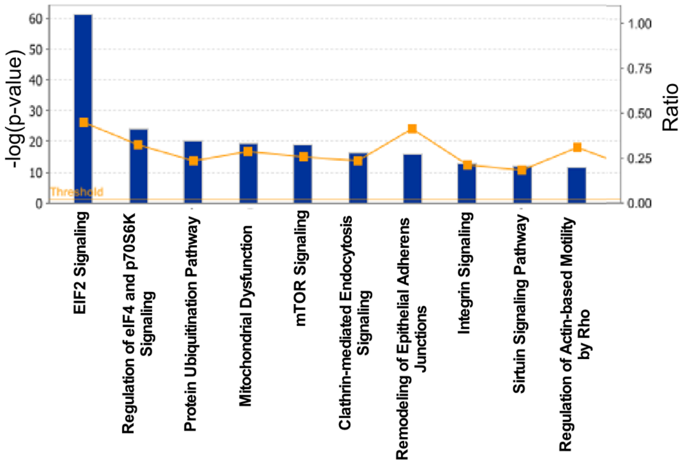
(A) Patient 1 - Top 10 canonical pathways



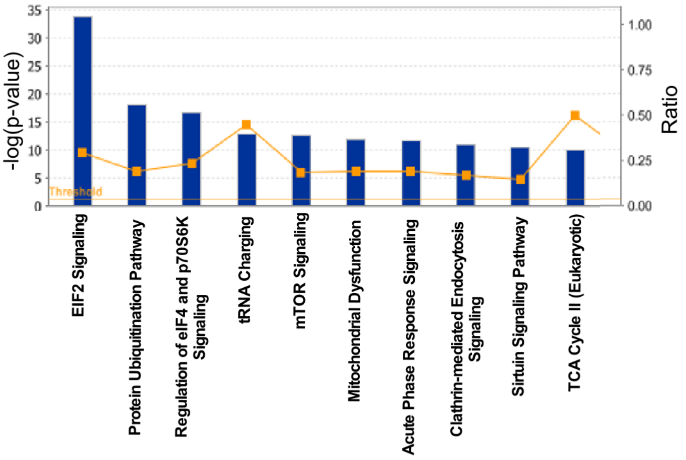
(B) Patient 2 - Top 10 canonical pathways



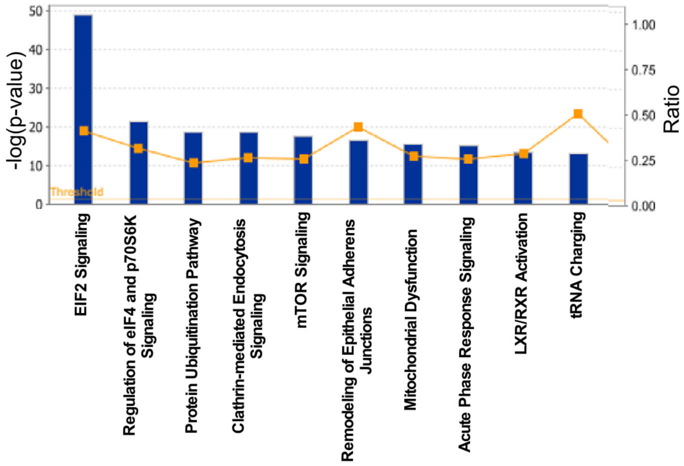
(C) Patient 3 - Top 10 canonical pathways



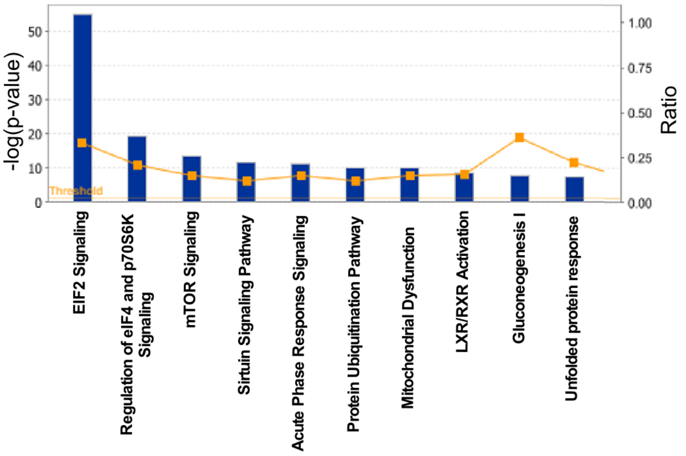
(D) Patient 4 - Top 10 canonical pathways



(E) Patient 5 - Top 10 canonical pathways

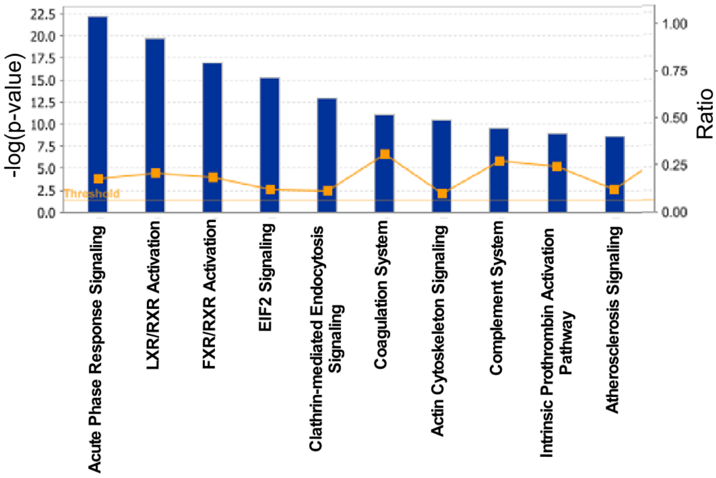


(E) Patient 6 - Top 10 canonical pathways

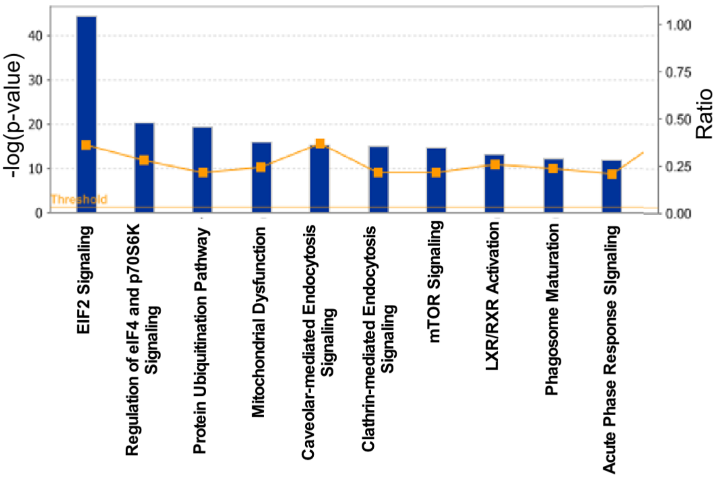


Supplementary Figure 5

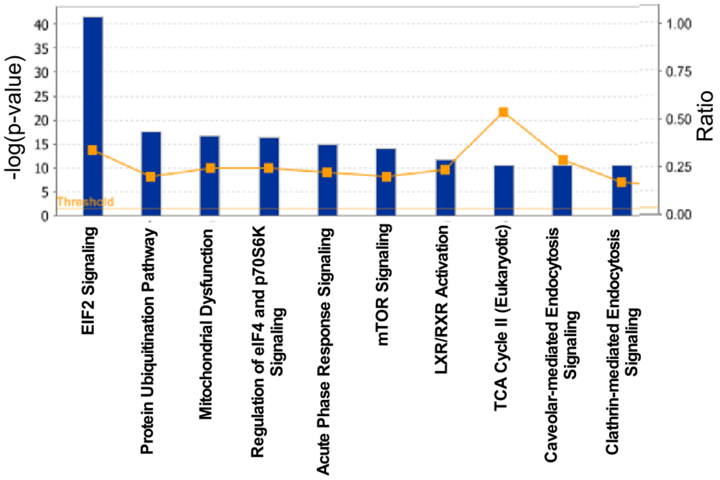
(A) Patient 7 - Top 10 canonical pathways



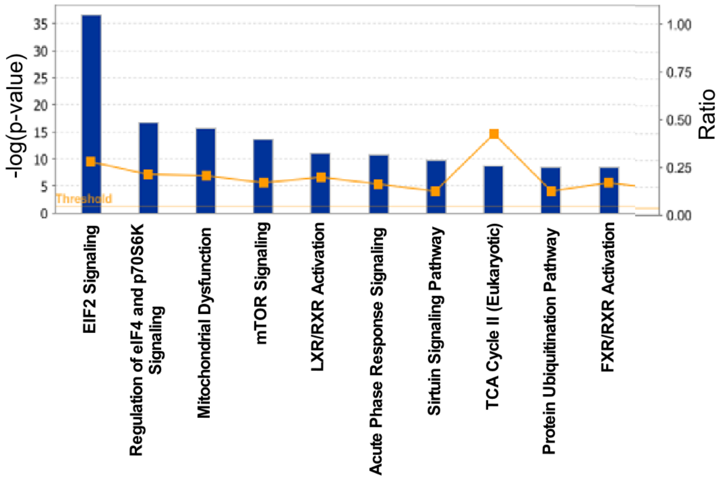
(B) Patient 8 - Top 10 canonical pathways



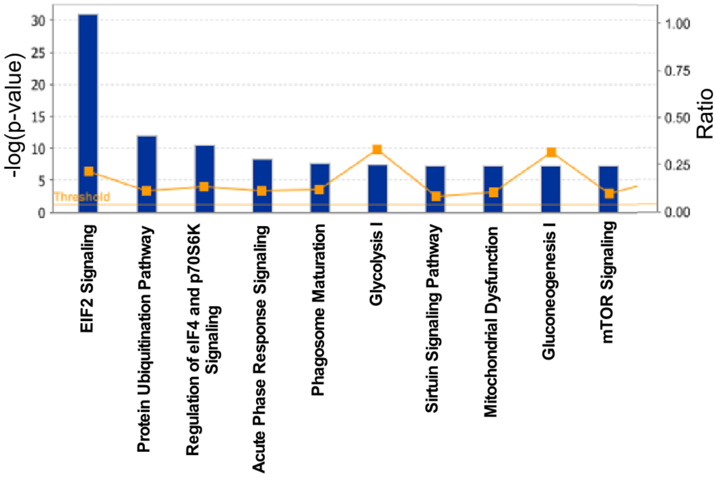
(C) Patient 9 - Top 10 canonical pathways



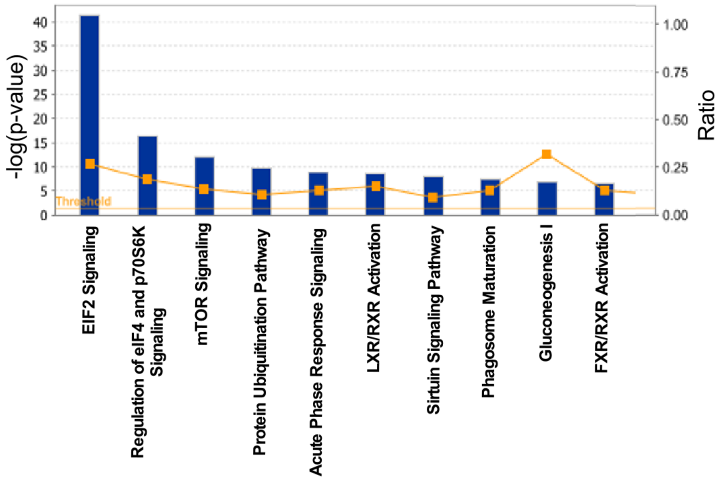
(D) Patient 10 - Top 10 canonical pathways



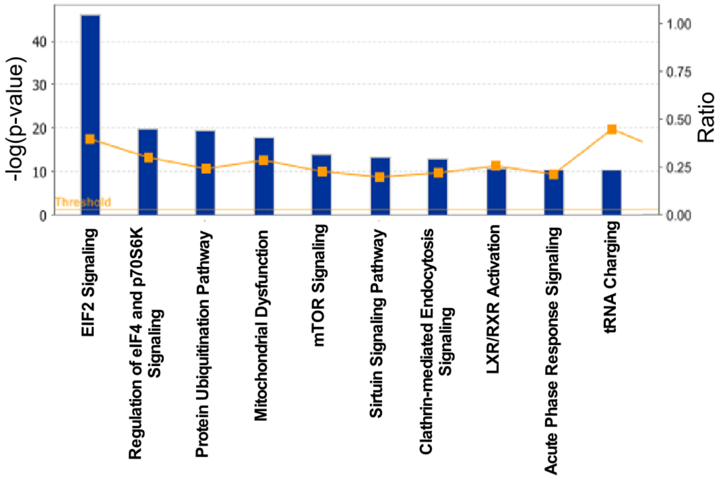
(E) Patient 11 - Top 10 canonical pathways



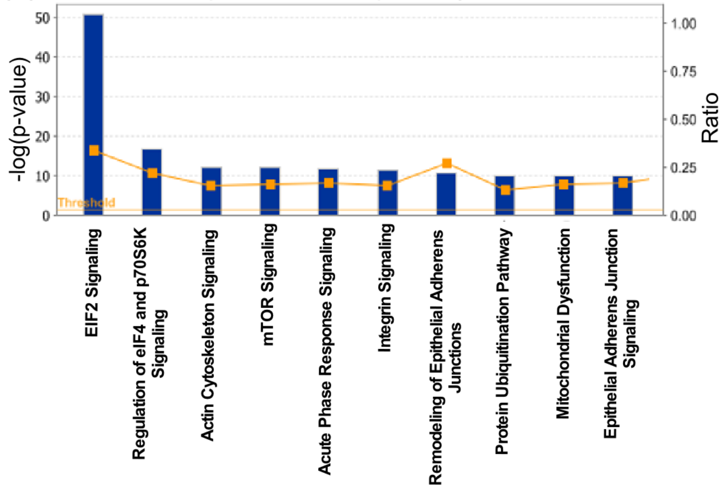
(F) Patient 12 - Top 10 canonical pathways



(G) Patient 13 - Top 10 canonical pathways

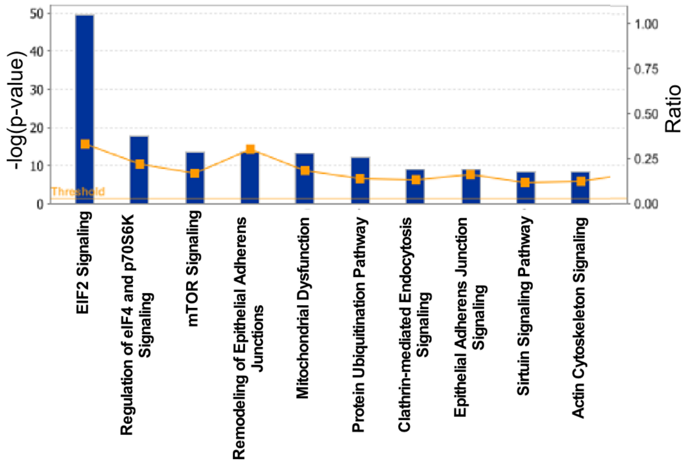


(H) Patient 14 - Top 10 canonical pathways

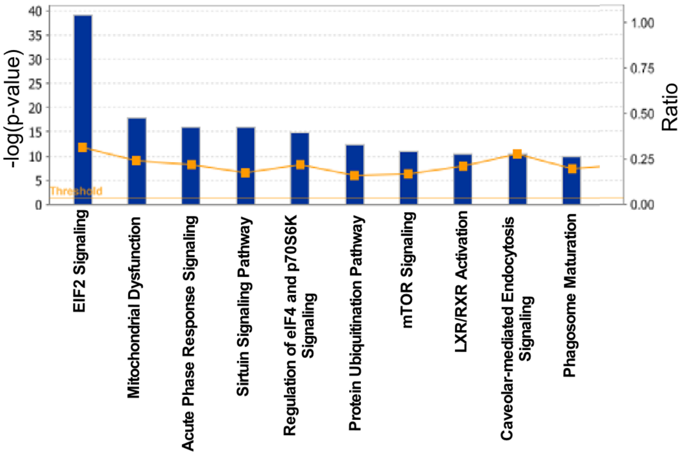


Supplementary Figure 6.

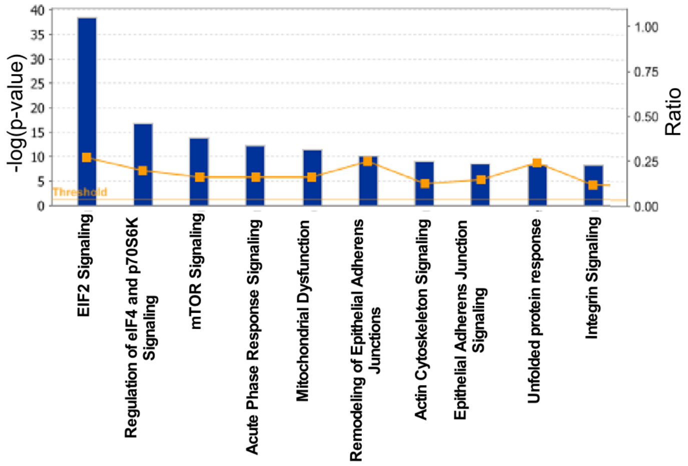
(A) **Patient 15** - Top 10 canonical pathways



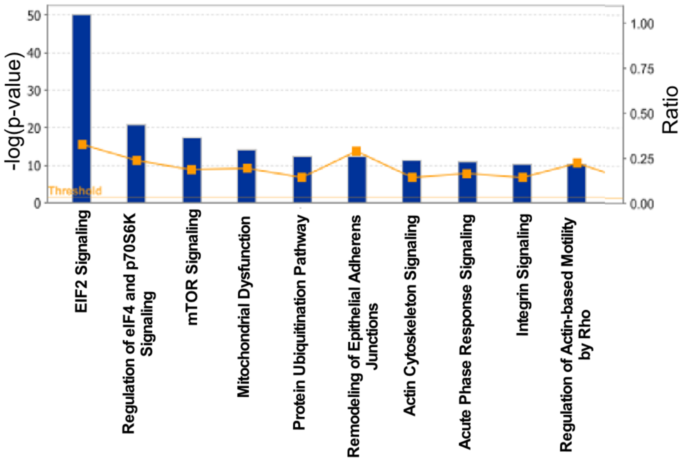
(B) **Patient 16** - Top 10 canonical pathways



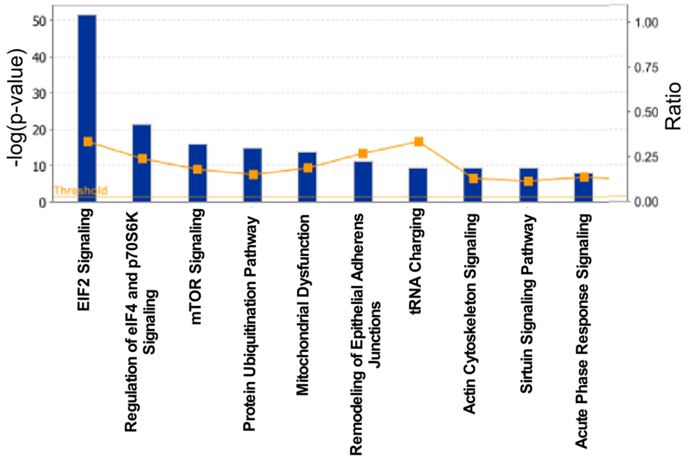
(C) **Patient 17** - Top 10 canonical pathways



(D) **Patient 18** - Top 10 canonical pathways



(E) **Patient 19** - Top 10 canonical pathways



(F) **Patient 20** - Top 10 canonical pathways