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| --- |
| **Table S6.** Subnetworks statistics. |
| **Network** | **Subnetwork** | **Seed genes** | ***P*-valuea** | ***P*adja** | **ESa** | **NESa** | **GO BP termb** | **KEGG Termb** |
| skin (top 15) | cluster\_4\_size\_32 | *UBE2Z* | 0.032322 | 0.080806 | -0.4161 | -1.53117 | RNA interferenceRNA export from nucleusglutamine metabolic process | Spliceosome |
| breast (top 30) | cluster\_3\_size\_94 | *LINC00639**ANAPC13**CEP63* | 0.018819 | 0.037638 | -0.3183 | -1.47748 | regulation of mRNA polyadenylation |  |
| fibroblast (top 30) | cluster\_2\_size\_35 | *MUC16* | 0.013054 | 0.039163 | -0.58043 | -1.71602 | cornification |  |
| aGene-set enrichment analysis with using height information from DL Taylor *et al*. bOver-representation analysis. |