Table S4. Enrichment of important biological pathways among miRNAs differentially expressed between OBIS and OBIR patients by regulated genes.

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| --- | --- | --- |
| **Reactome annotation** | **p-Value** | **miRNAs** |
| Gene Expression | 7.55e-16 | |  |  | | --- | --- | | hsa-miR-125a-5p | ↓ | | hsa-miR-197-3p | ↑ | | hsa-miR-23b-3p | ↑ | | hsa-miR-204-5p | ↓ | | hsa-miR-320a | ↓ | | hsa-miR-99b-5p | ↓ | | hsa-miR-125b-5p | ↓ | |
| Translation | 3.09e-7 |
| Generic Transcription Pathway | 4.61e-7 |
| Eukaryotic Translation Initiation | 4.61e-7 |
| Cap-dependent Translation Initiation | 4.61e-7 |
| Cellular responses to stress | 5.36e-7 |
| 3' -UTR-mediated translational regulation | 0.00000656 |
| Eukaryotic Translation Elongation | 0.0000289 |
| Eukaryotic Translation Termination | 0.0000395 |
| Activation of Matrix Metalloproteinases | 0.00252 |