**Supplementary Table 2.** Significantly enriched pathways detected in pathway enrichment analysis and targets prediction (Diana mirPath v.3 web-based computational tool) of the 66* upregulated miRNAs in metastatic tumors compared to those in normal surrounding liver.

| KEGG pathway                                | p-value          |
|---------------------------------------------|------------------|
| 1. Fatty acid biosynthesis (hsa00061)       | <1e-325          |
| 2. Prion diseases (hsa05020)                | <1e-325          |
| 3. ECM-receptor interaction (hsa04512)      | <1e-325          |
| 4. Adherens junction (hsa04520)             | 1.893252e-11     |
| 5. Viral carcinogenesis (hsa05203)          | 2.014489e-11     |
| 6. Proteoglycans in cancer (hsa05205)       | 2.625722e-11     |
| 7. Hippo signaling pathway (hsa04390)       | 8.28115e-10      |
| 8. Cell cycle (hsa04110)                    | 8.251494e-07     |
| 9. Lysine degradation (hsa00310)            | 2.515057e-06     |
| 10. Protein processing in endoplasmic reticulum | 1.718417e-05   |
| 11. Hepatitis B (hsa05161)                  | 3.304304e-05     |
| 12. p53 signaling pathway (hsa04115)        | 6.020478e-05     |
| 13. Fatty acid metabolism (hsa01212)        | 0.0001324588     |
| 14. Pathways in cancer (hsa05200)           | 0.0003046663     |
| 15. Chronic myeloid leukemia (hsa05220)     | 0.001297946      |
| 16. TGF-beta signaling pathway (hsa04350)   | 0.007290645      |
| 17. Glioma (hsa05214)                       | 0.008409624      |
| 18. Thyroid hormone signaling pathway (hsa04919) | 0.02322047  |

*Of the 73 miRNAs shown in Table 1, four miRNAs (miR-378d, miR-378a-5p, miR-146b-3p and miR-203a) were downregulated in tumors. Out of the rest 69 miRNAs, three miRNAs (miR-127-3p, miR-543 and miR-127-5p) were excluded because they were not recognized by Diana mirPath v.3 web-based computational tool.