# Supplementary Materials: Identification of More Feasible MicroRNA–mRNA Interactions within Multiple Cancers Using Principal Component Analysis Based Unsupervised Feature Extraction

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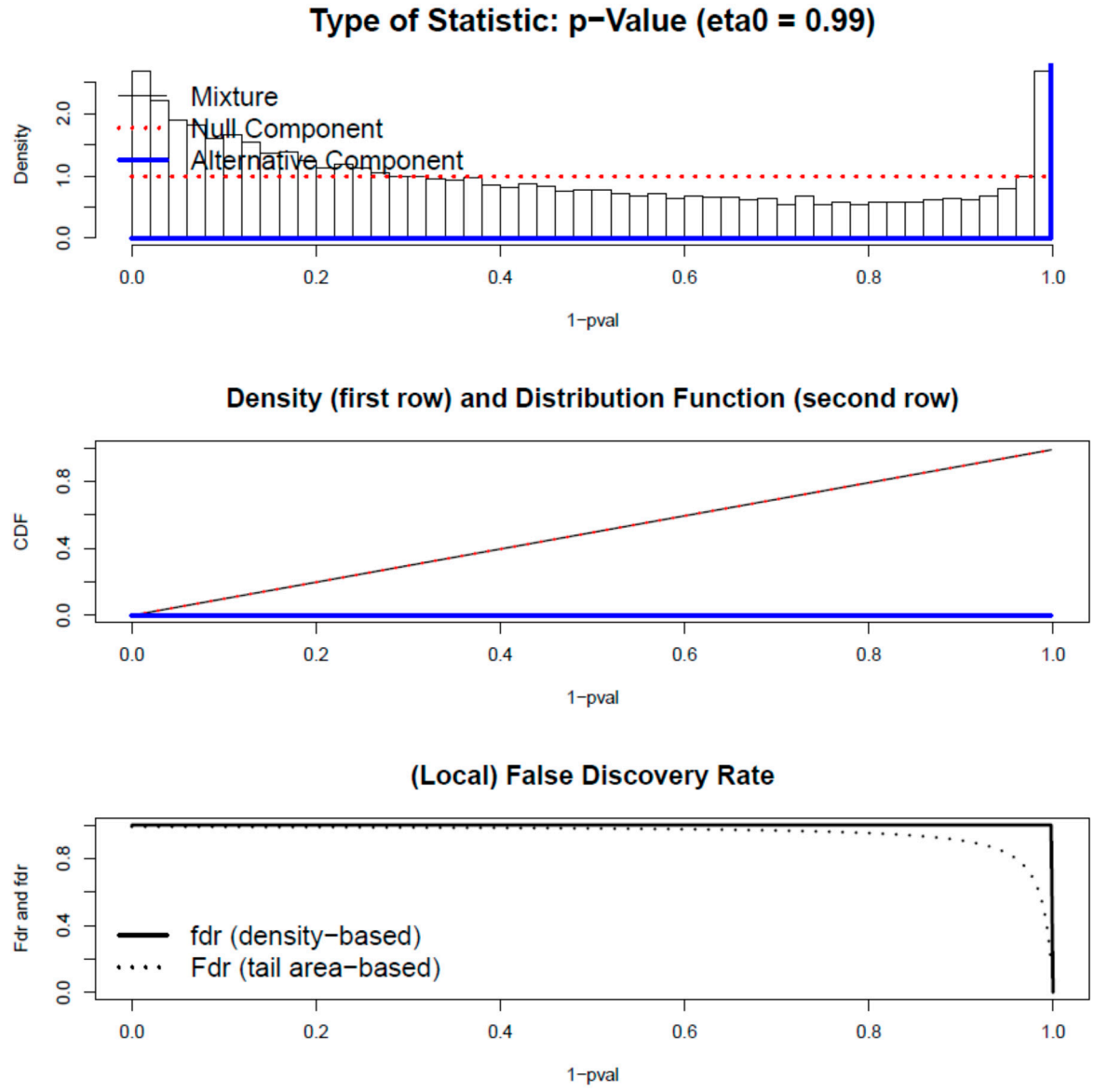


**Figure S1.** fdrtool's output: mRNA in HCC. **Top**: histogram of 1-*P*; **Middle**: Density and cumulative density of 1-*P*; **Bottom**: (Local) False Discovery Rate.

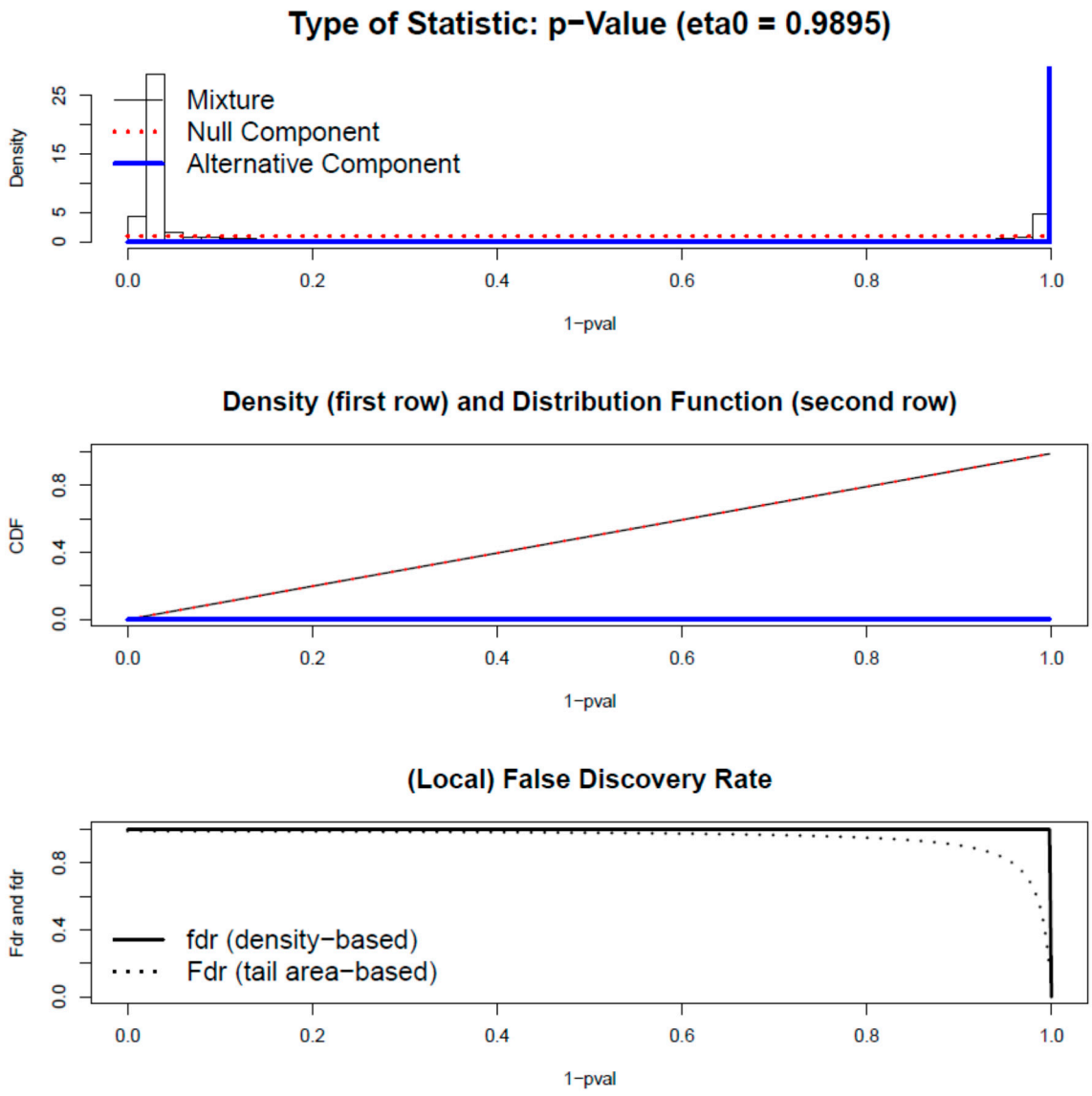


**Figure S2.** fdrtool's output: miRNA in HCC.

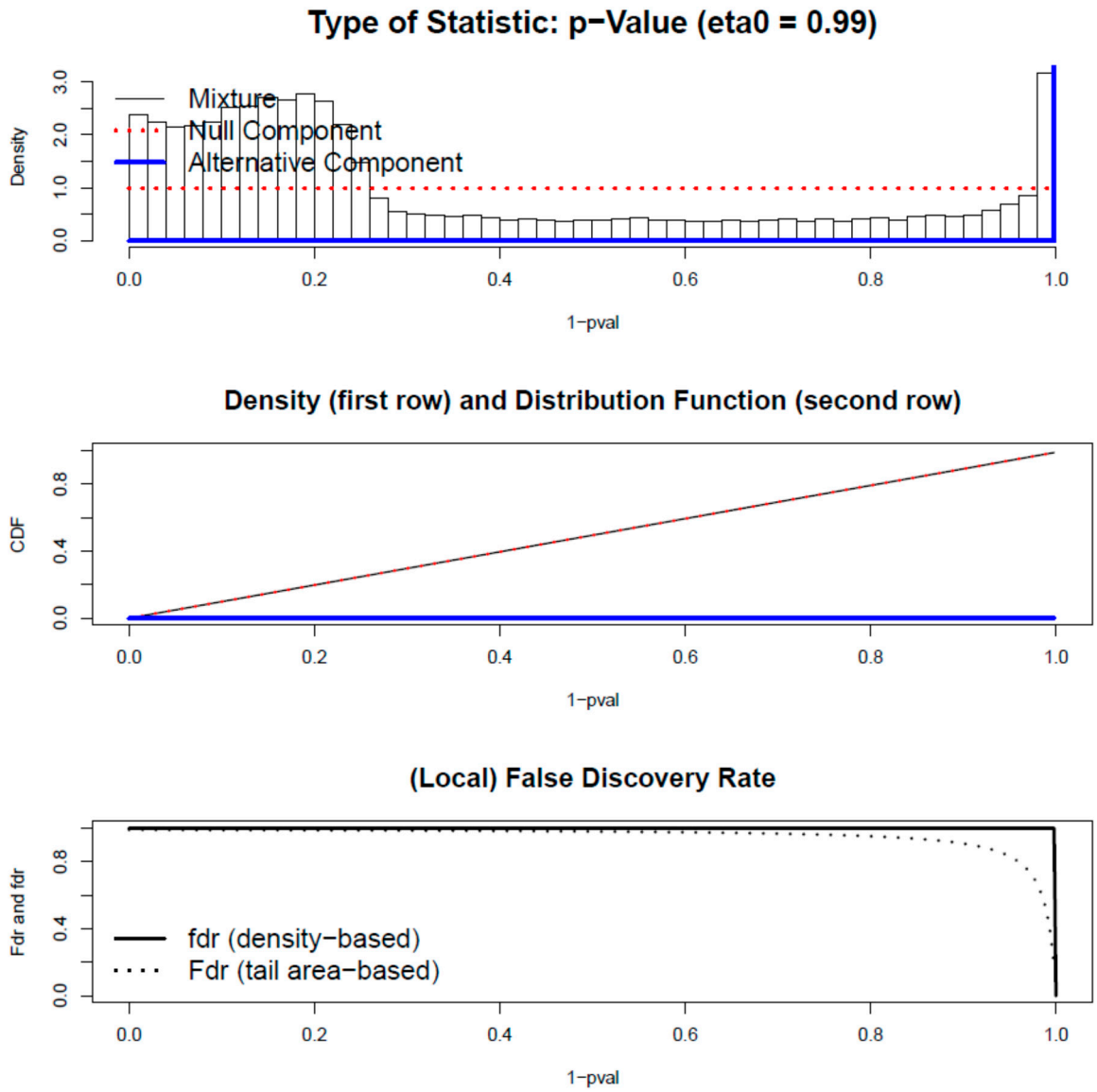


**Figure S3.** fdrtool's output: mRNA in NSCLC.

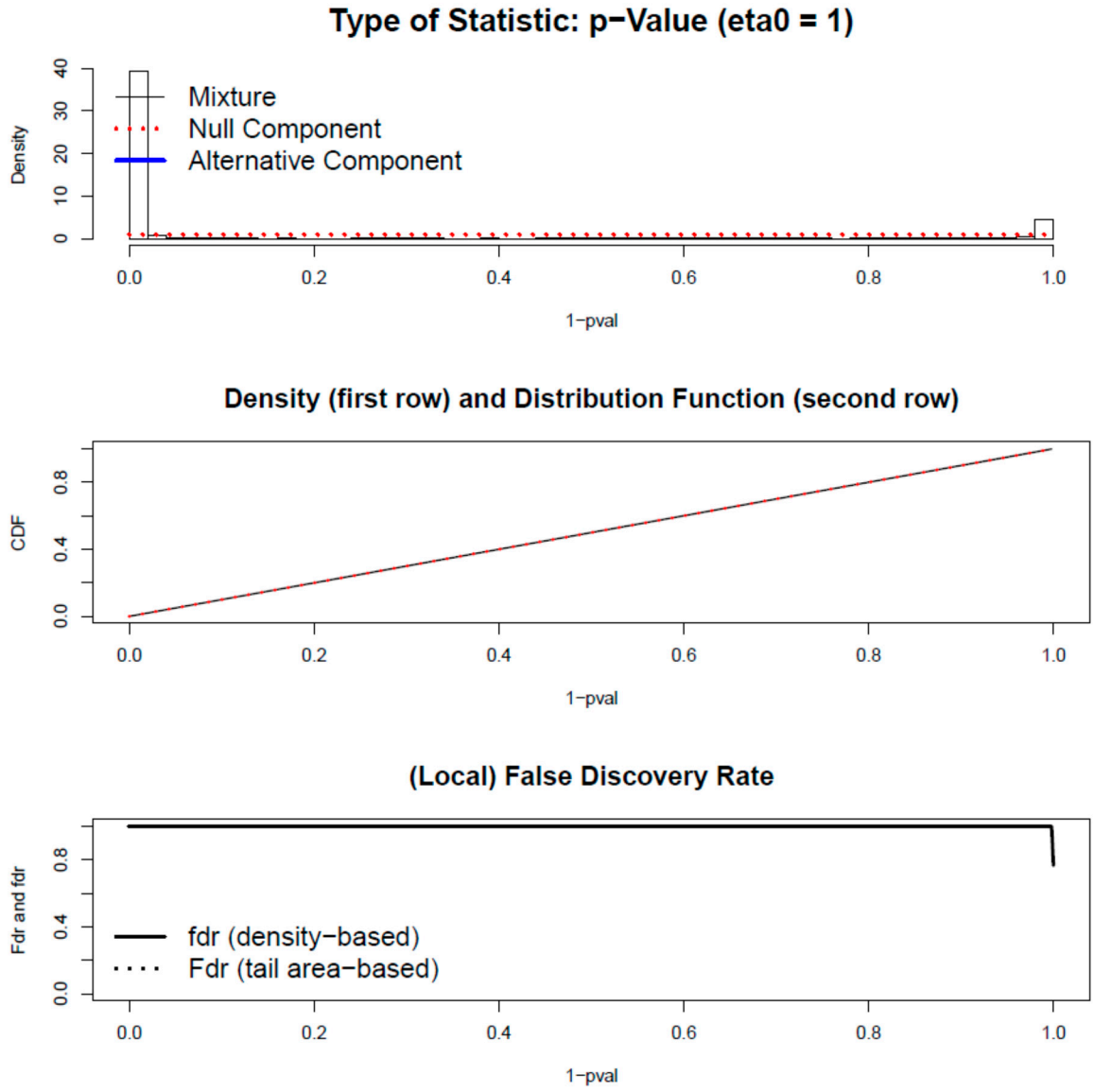


**Figure S4.** fdrtool's output: miRNA in NSCLC.

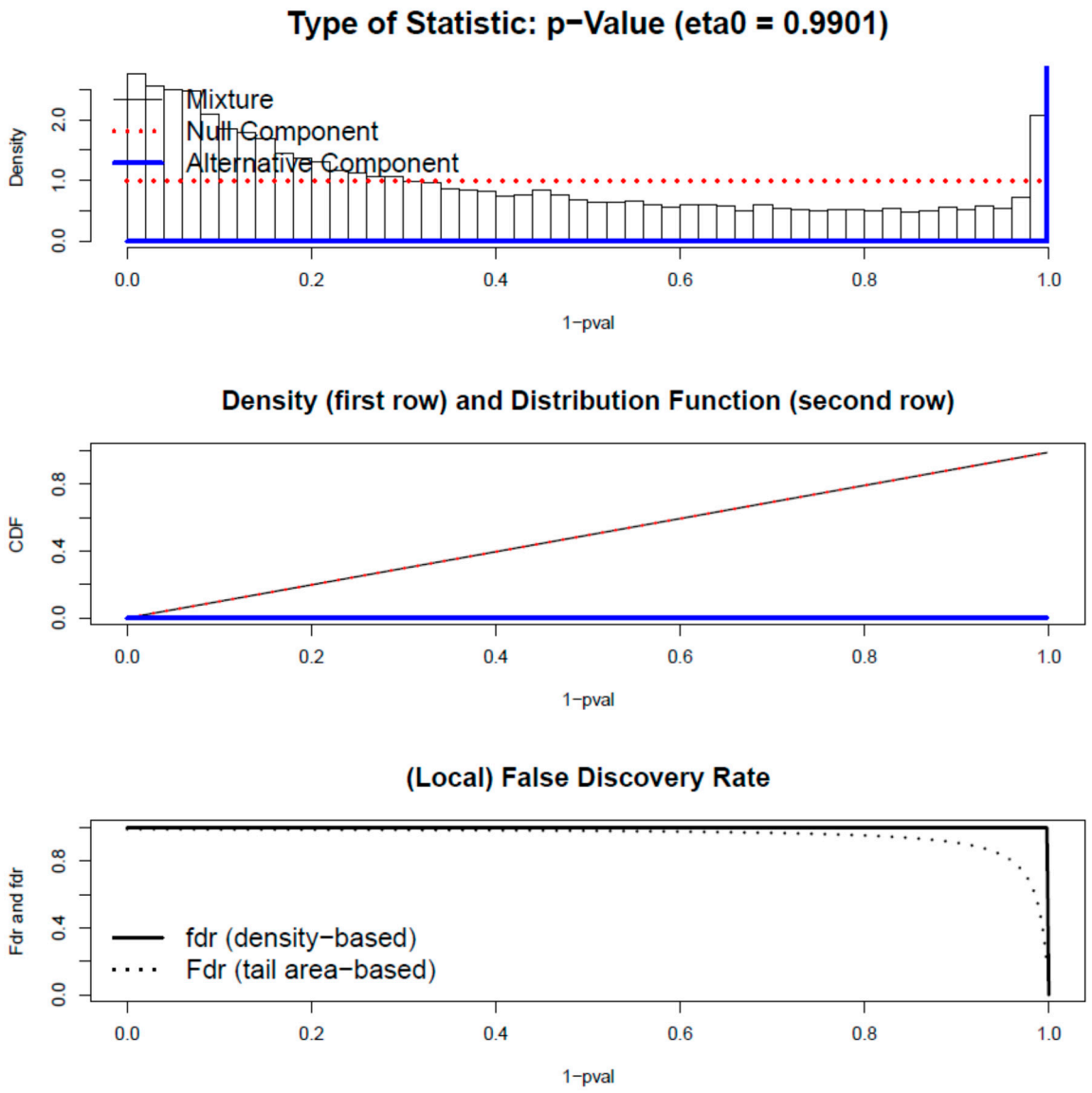


**Figure S5.** fdrtool's output: mRNA in ESCC.

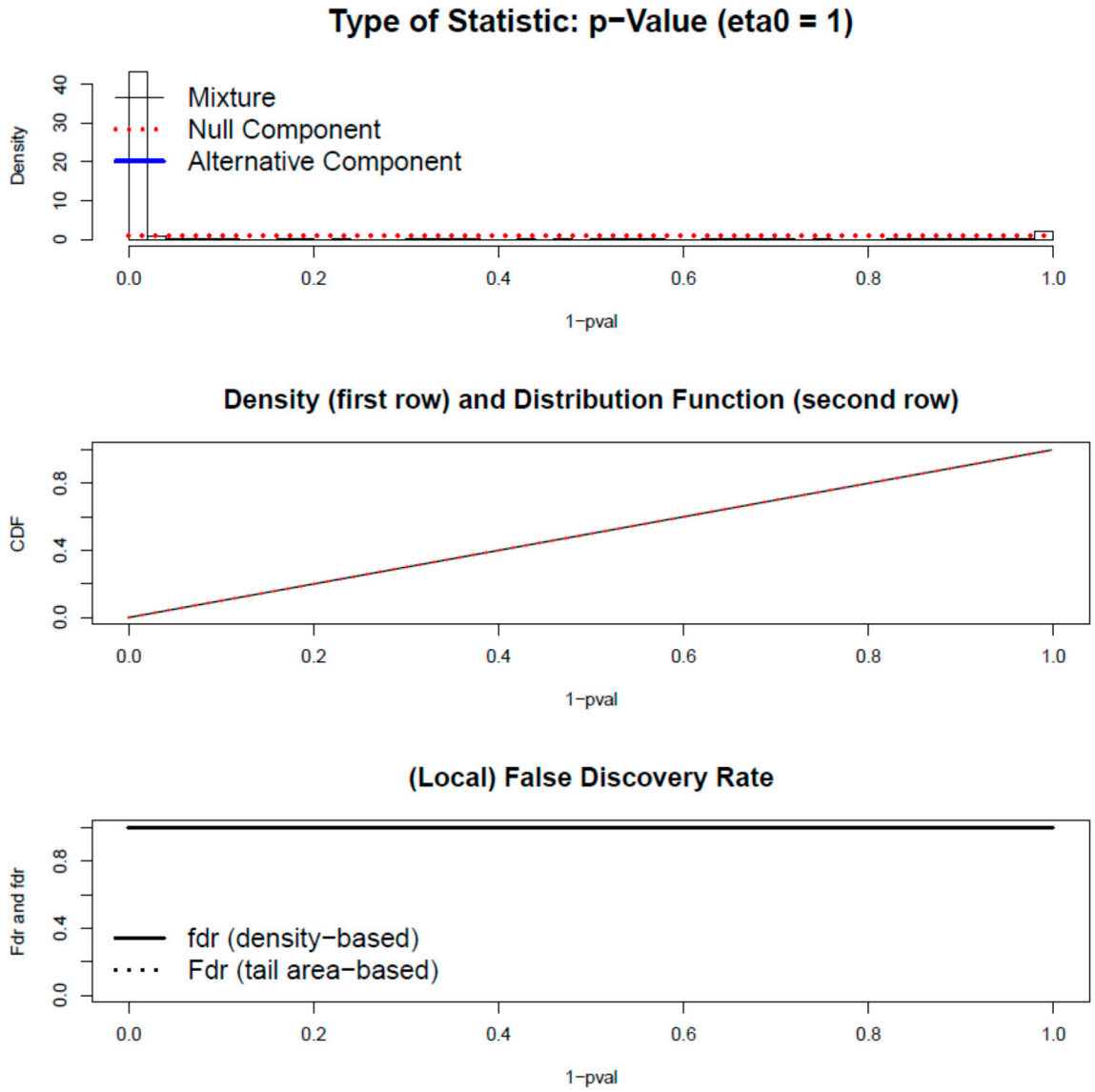


**Figure S6.** fdrtool's output: miRNA in ESCC.

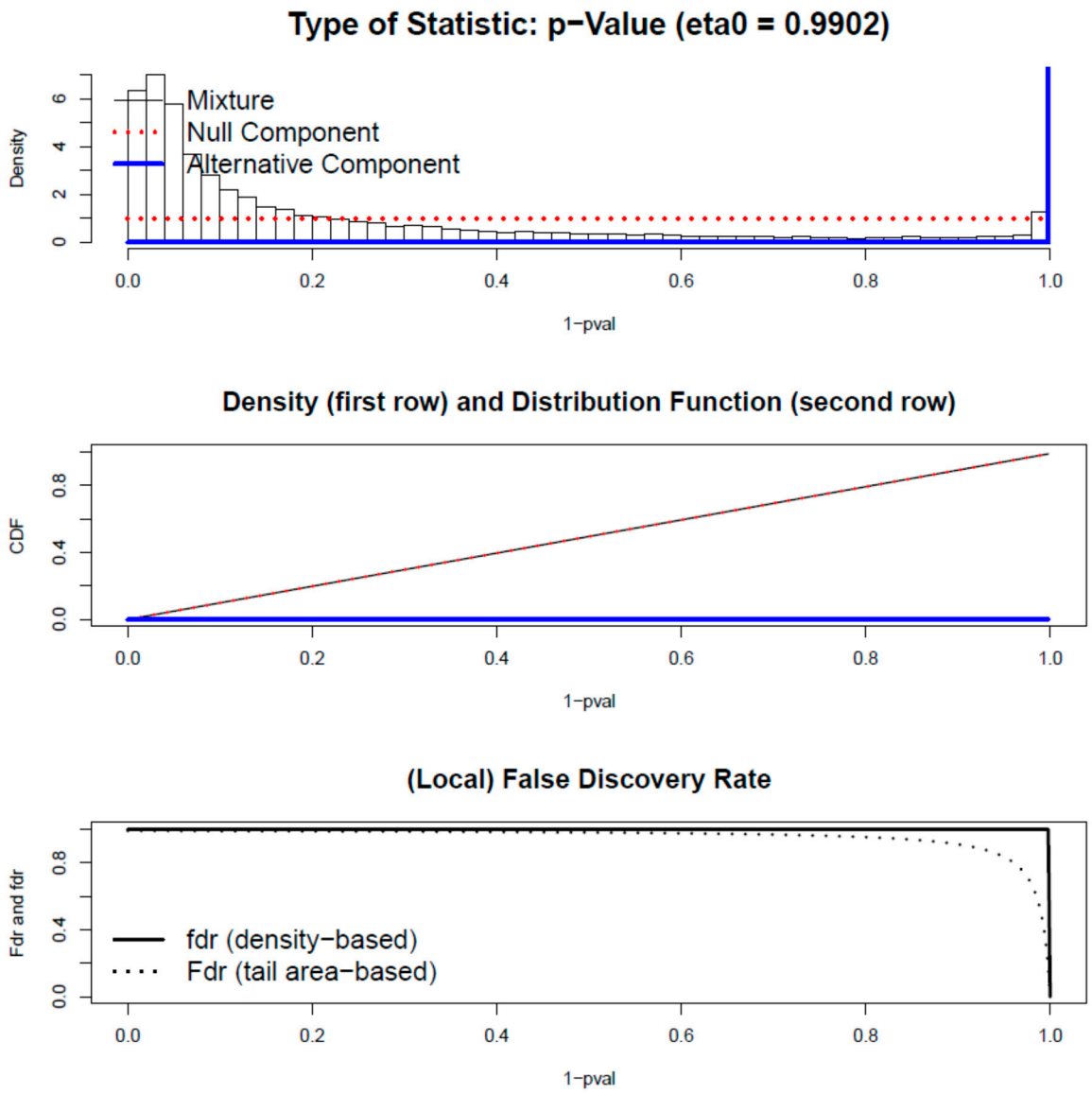


**Figure S7.** fdrtool's output: mRNA in prostate cancer.

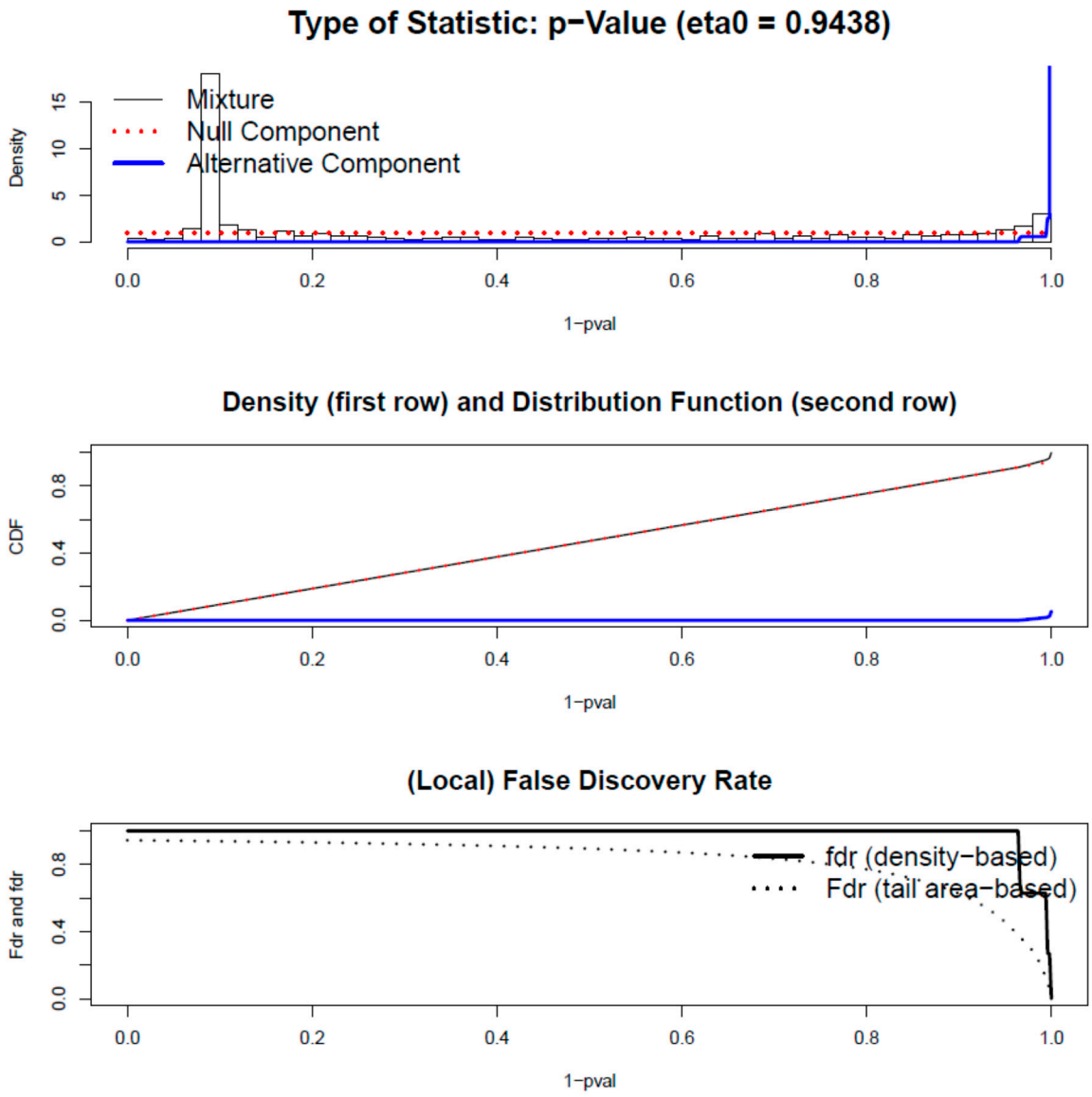


**Figure S8.** fdrtool's output: miRNA in prostate cancer.

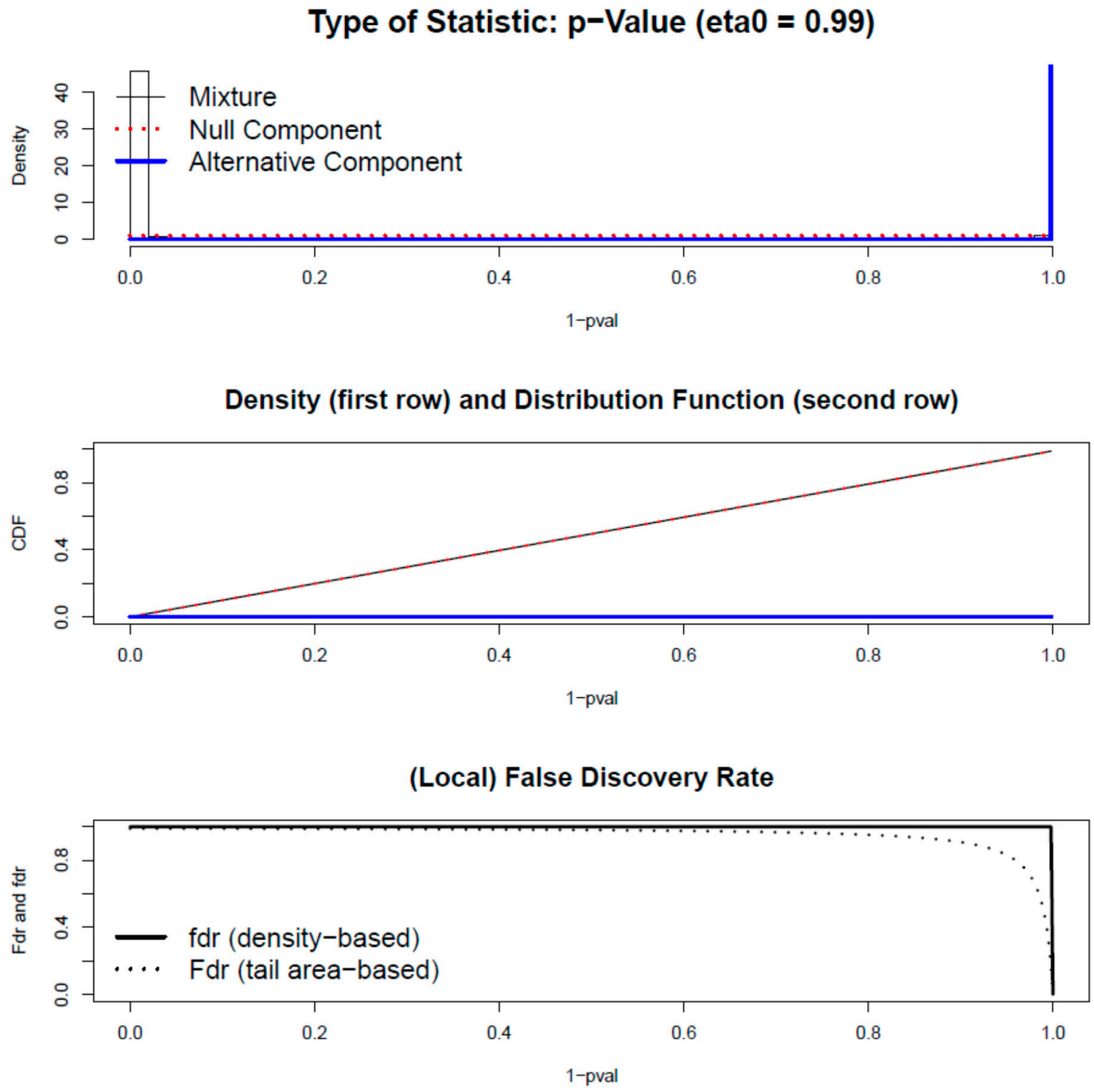


**Figure S9.** fdrtool's output: mRNA in colon/colorectal cancer.

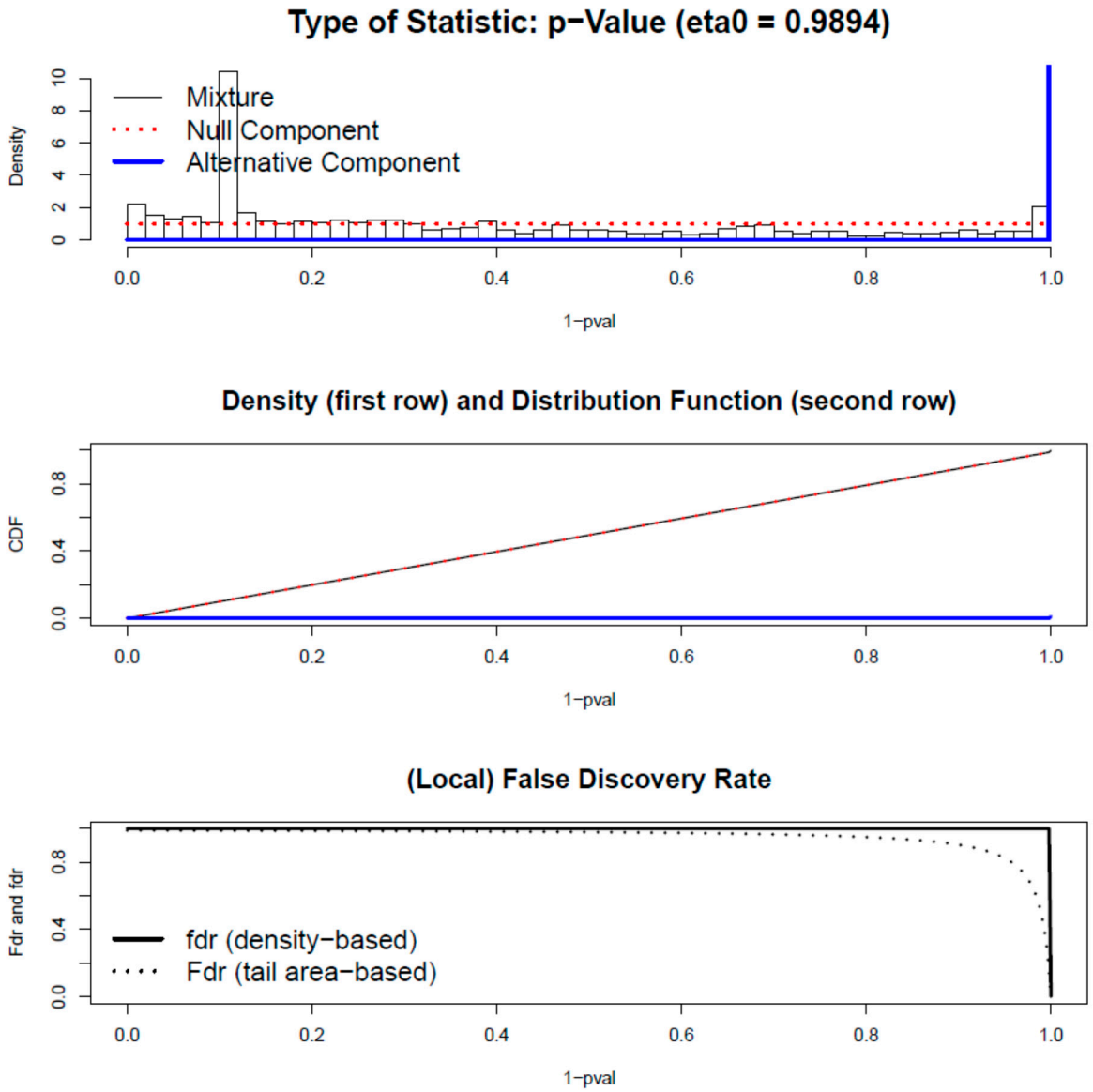


**Figure S10.** fdrtool's output: miRNA in colon/colorectal cancer.

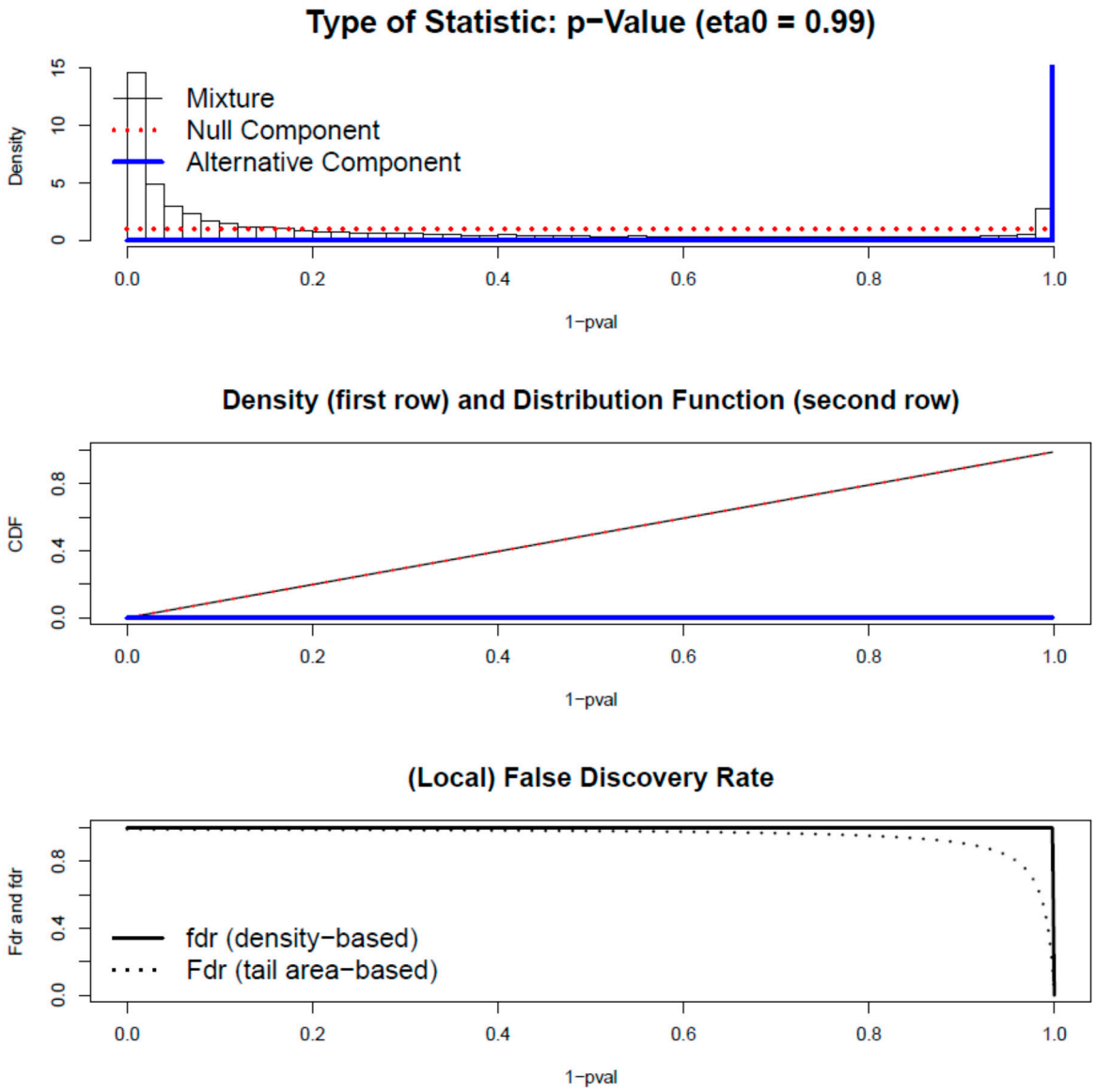


**Figure S11.** fdrtool's output: mRNA in breast cancer.

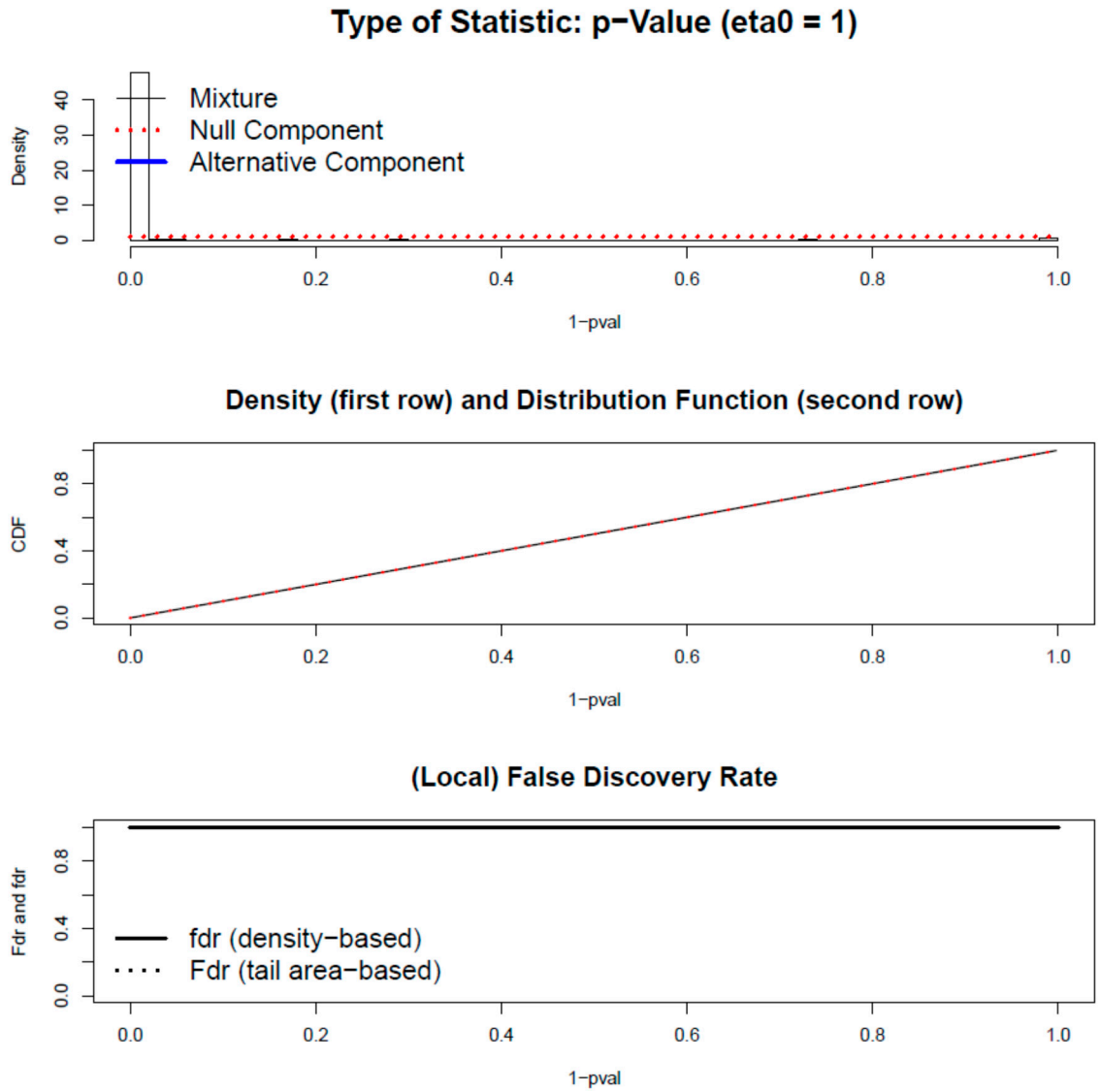


**Figure S12.** fdrtool's output: miRNA in breast cancer.

**Table S1.** miRNA–mRNA interaction pairs identified in the HCC samples. $T > N$: upregulated in tumors, $T < N$: upregulated in normal tissues. The starbase column lists the number of cancer cell lines associated with significant reciprocal correlations among the identified pairs. If several miRNAs share the same seed sequence, their numbers are stated separately and connected by a + symbol.

| **miRNAs** ($T > N$) | **Gene** ($T < N$) | **Function in HCC** | **Starbase** |
|---|---|---|---|
| miR-93 | | activates the c-Met/PI3K/Akt pathway [1] | |
| | ESR1 | tumor suppressor [2], promoter methylation [3] | 0 |
| | CXCL2 | therapeutic target [4], promotes cell proliferation and metastasis [5] | 0 |
| miR-25 | | various roles [6], promotes cell growth [7] | |
| miR-92a | | deregulation [8], contributes to tumor growth [9], preserves sur- vival [10] | |
| | CD69 | CD4(+) CD69(+) CD25(−) T cells were identified in HCC tis- sues [11] | 6 + 10 |
| miR-15b | | induces endoplasmic reticulum stress and apoptosis [12] | |
| | CD69 | see miR-25/92a | 0 |
| | GHR | related to proliferation [13], targets a long non-coding RNA that in-creases EGFR expression [14], distinct therapy treatments between positive/negative tumors [13] | 0 |
| | GLS2 | tumor suppressor [15], epigenetic silencing [16] | 4 |
| miR-148a | | repression of HCC cell malignancy [17] | 4 |
| | ESR1 | see miR-93 | |
| miR-125b | | attenuates epithelial-mesenchymal transitions [18] | |
| | TAT | Loss of one TAT allele [19] | 0 |
| let-7a | | promising tools against systemic HCC [8] | |
| | STAB2 | upregulation [20], downregulation suppresses tumor [20] | 0 |
| | GHR | see miR-15b | 0 |

**Table S2.** miRNA–mRNA interaction pairs identified in HCC samples (continued).

| **miRNAs** ($T < N$) | **Gene** ($T > N$) | **Function in HCC** | **Starbase** |
|---|---|---|---|
| miR-20a | | Reduced expression promotes HCC [21] | |
| | SLC40A1 | haplotype [22] | 9 |
| | HSPA8 | upregulation [23] | 4 |
| | GPR88 | — | 0 |
| | PDE3B | involved in development and metabolism of HCV [24] | 2 |
| miR-214 | | recurrence of HCC [25] | |
| | PEG10 | upregulation [26], associated with poor survival and tumor recurrence [27], promote carcinogenesis [28] | 0 |
| miR-195 | | suppresses angiogenesis and metastasis of HCC [29] | |
| | GPR88 | see miR-20a | 0 |
| | GABRE | upregulation [30] | 0 |
| miR-200b | | suppression of HCC [31] | |
| | CCNA2 | AAV2 integration in CCNA2 [32], associated with low survival sub-class [33] | 4 |
| miR-29c | | suppression of HCC [34] | |
| | B3GNT5 | — | 8 |
| miR-30d | | promotes tumor invasion and metastasis [35] | |
| | B3GNT5 | see miR-29c | 8 |

**Table S3.** miRNA–mRNA interaction pairs identified in the NSCLC samples. *T* > *N*: upregulated in tumors, *T* < *N*: upregulated in normal tissues. For a description of the numbers in the starbase column, see Table S1.

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-30a | | inhibits tumor proliferation [36] | |
| miR-30d | | inhibits tumor proliferation [37] | |
| | BNC1 | hypermethylation [38] | 0 + 0 |
| | PIGX | candidate driver genes [39] | 5 + 4 |
| | GCLC | drug resistance [40] | 3 + 2 |
| | THBS2 | correlated with decreased vascularity [41] | 0 + 0 |
| | HMGB3 | overexpression as biomarker [42] | 0 + 0 |
| | PFN2 | epigenetic regulation of other genes [43] | 5 + 4 |
| | FOXD1 | association with poor prognosis [44] | 4 + 7 |
| | CYP24A1 | independent prognostic marker of survival [45] | 5 + 5 |
| | PITX1 | decreased expression [46] | 7 + 7 |
| | BMP7 | reported biological impact [47] | 0 + 0 |
| | MXRA5 | frequent mutation [48] | 0 + 0 |
| | SLC7A11 | contributes to pathogenesis [49] | 6 + 6 |
| | FAP | clinical implications [50] | 8 + 11 |
| | BCL11A | overexpression predicts survival and relapse [51] | 3 + 5 |
| | ADAM12 | diagnostic marker of proliferation, migration and invasion [52] | 0 + 0 |
| | ITGA6 | downregulation in cancer stem cells [53] | 5 + 4 |
| | MARK1 | inhibitor, new target agent [54] | 0 + 0 |
| | NEFL | candidate biomarker of recurrence and survival [55] | 5 + 8 |
| | GRHL1 | decreased expression in cell lines [56] | 0 + 0 |
| | SLC41A2 | — | 3 + 6 |
| | GDA | — | 1 + 4 |
| | CDCA7 | possible subtype-specific expression [57] | 9 + 6 |
| | FRMD6 | — | 6 + 11 |
| | CTHRC1 | associated with tumor aggressiveness and poor prognosis [58] | 10 + 8 |
| | FBXO32 | — | 0 + 0 |
| | C3orf58 | — | 4 + 1 |
| | PPP1R14C | — | 2 + 4 |
| | E2F7 | upregulated in NSCLC treatment [59] | 10 + 5 |
| | SIX1 | target of tumor suppressor miRNA [60] | 9 + 5 |
| | FAM83F | FAM83B, which belongs to the same protein family as FAM83F, is a novel biomarker [61] | 0 + 0 |

**Table S4.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-221 | | Growth inhibitor [62] | |
| | ATP11B | — | 0 |
| | TFAP2A | — | 3 |
| | FAT2 | subtype-specific biomarker [63] | 0 |
| | IGF2BP2 | — | 0 |
| miR-130a | | targets some genes [64] | |
| | SLC2A1 | reported polymorphisms [65] | 2 |
| | CALB1 | suggested roles [66] | 0 |
| | TP63 | isoform expression [67] | 2 |
| | BCL11A | see miR-30a/30d | 1 |
| | SULF1 | dysregulation [68] | 0 |
| | ADAM12 | see miR-30a/30d | 3 |
| | CEP55 | overexpression and modulation of tumor migration and invasion [69] | 3 |
| | GDA | see miR-30a/30d | 6 |
| | FRMD6 | see miR-30a/30d | 4 |
| | E2F7 | see miR-30a/30d | 2 |
| miR-100 | | tumor suppressor [70] | |
| | FGFR3 | mutation [71] | 6 |
| | GRHL1 | miR-30a/30d | 7 |
| miR-223 | | potent tumor suppressor [72] | |
| | PFN2 | miR-30a/30d | 0 |
| | ECT2 | overexpression [73] | 3 |
| miR-143 | | inhibits NSCLC cell growth and metastasis [74] | |
| | COL1A1 | overexpression [75] | 0 |
| | COL5A1 | — | 0 |
| | PLAU | subtype-specific expression [76] | 0 |
| | KLF5 | inhibits apoptosis [77] | 8 |
| | SLC7A11 | chemoresistance [78] | 4 |
| | ITGA6 | miR-30a/30d | 2 |
| | GOLM1 | overexpression [79] | 5 |
| | COL5A2 | overexpression [80] | 0 |
| | FAM83F | see miR-30a/30d | 0 |

**Table S5.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-145 | | inhibits NSCLE proliferation [81] | |
| | ABCC1 | drug resistance [82] | 3 |
| | HMGB3 | miR-30a/30d | 6 |
| | TFRC | frequent amplification [83] | 7 |
| | KLF5 | miR-143 | 4 |
| | SULF1 | see miR-130a | 0 |
| | PSAT1 | sustains proliferation [84] | 6 |
| miR-125b | | downregulation promotes NSCLC invasion and migration [85] | |
| | HMGB3 | miR-30a/30d | 7 |
| | MMP11 | correlated with higher-grade NSCLC [86] | 0 |
| | CYP24A1 | miR-30a/30d | 0 |
| | RAPGEFL1 | — | 0 |
| | GRHL1 | miR-30a/30d | 5 |
| | VANGL2 | — | 0 |
| | FAM83F | see miR-30a/30d | |
| miR-195 | | tumor suppressor [87] | |
| | ANLN | plays a critical role in NSCLC [88] | 7 |
| | AK4 | promotes metastasis [88] | 0 |
| | KCNN4 | associated with poor prognosis [89] | 1 |
| | CXCL10 | blood biomarker [90] | 1 |
| | KIF23 | overexpression [91] | 8 |
| | PTHLH | increased in the serum and urine of NSCLE patients [92] | 3 |
| | HMGA2 | overexpression [93] | 8 |
| | LRRC15 | — | 0 |
| | RAPGEFL1 | see miR-125b | 0 |
| | FZD10 | overexpression [94] | 1 |
| | PLUNC | biomarker [95] | 0 |
| | RGMA | — | 0 |
| | SLC41A2 | see miR-30a/30d | 2 |
| | KCTD1 | — | 5 |
| | FAM110C | — | 3 |
| | E2F7 | see miR-30a/30d | 8 |
| | PRR11 | cell cycle progression [96] | 0 |
| | ODZ2 | biomarker [97] | 0 |

**Table S6.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-26a | | drug resistance [98] | |
| | COL1A2 | potential therapeutic target [99] | 0 |
| | PLOD2 | prognostic variables [100] | 8 |
| | ADM | regulates NSCLC [101] | 7 |
| | LOXL2 | downregulation [102] | 10 |
| | COL5A1 | see miR-143 | 8 |
| | COL11A1 | overexpression [103] | 0 |
| | TFAP2A | see miR-221 | 5 |
| | COL10A1 | overexpression [104] | 0 |
| | WNT5A | promotes angiogenesis [105] | 2 |
| | CILP | — | 0 |
| | HMGA2 | see miR-195 | 6 |
| | JAG1 | prognostic biomarkers [106] | 4 |
| | TP63 | see miR-130a | 0 |
| | SLC7A11 | see miR-143 | 6 |
| | BCL11A | see miR-30a/30d | 2 |
| | SULF1 | see miR-130a | 0 |
| | ADAM12 | see miR-30a/30d | 0 |
| | ITGA6 | see miR-143 | 5 |
| | MARK1 | see miR-30a/30d | 3 |
| | HAS3 | abundant expression [107] | 0 |
| | VANGL2 | see miR-125b | 1 |
| | E2F7 | miR-30a/30d | 8 |
| | LPAR3 | — | 4 |
| | GRHL3 | — | 0 |

**Table S7.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-29a | | aberrant methylation [108] | |
| | COL1A1 | see miR-143 | 4 |
| | COL3A1 | upregulation [109] | 4 |
| | SLC16A1 | — | 7 |
| | COL1A2 | see miR-26a | 0 |
| | LOXL2 | see miR-26a | 6 |
| | COL5A1 | see miR-26a | 4 |
| | COL11A1 | see miR-26a | 0 |
| | DSG3 | biomarker [110] | 0 |
| | PTHLH | see miR-195 | 5 |
| | UPK1B | a part of classifier [111] | 0 |
| | BCL11A | see miR-30a/30d | 4 |
| | ADAM12 | see miR-30a/30d | 6 |
| | COL4A6 | frequently mutated=[48] | 0 |
| | ITGA6 | see miR-30a/30d | 6 |
| | RAPGEFL1 | see miR-125b | 0 |
| | COL5A2 | see miR-143 | 6 |
| | HAS3 | see miR-26a | 3 |
| | KCTD1 | see miR-195 | 6 |
| | E2F7 | see miR-30a/30d | 9 |

**Table S8.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-106a | | promotes growth and metastasis of NSCLC [112] | |
| miR-17 | | cancer development [113] | |
| | IGSF10 | differently expressed [114] | 0 + 0 |
| | SLC4A4 | — | 0 + 0 |
| | LMO3 | cell growth and metastasis [115] | 0 + 0 |
| | NR4A2 | tumor suppressor [116] | 5 + 6 |
| | HLF | — | 0 + 0 |
| | FOXF1 | drives NSCLC progression [117] | 8 + 9 |
| | SMAD6 | contributes to patient survival [118] | 4 + 8 |
| | CD69 | detected expression [119] | 6 + 9 |
| | DLC1 | tumor suppressor [120] | 9 + 9 |
| | TMEM100 | downregulation [114] | 9 + 8 |
| | TBX3 | overexpression [121] | 5 + 6 |
| | COL4A3 | correlated with poor prognosis [122] | 0 + 0 |
| | NTN4 | — | 6 + 10 |
| | SCD5 | abundance [123] | 4 + 5 |
| | TMTC1 | — | 6 + 9 |
| | PTPN21 | mutations [124] | 9 + 8 |
| | NEDD4L | prognostic marker [125] | 3 + 4 |
| | ANKRD29 | — | 9 + 11 |
| | GLDN | — | 0 + 0 |
| | ATP11A | — | 6 + 3 |
| | GPR133 | mutation [126] | 7 + 10 |
| | NCKAP5 | downregulation [114] | 4 + 6 |

**Table S9.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-141 | | biomarker [127] | |
| miR-200a | | targets multiple NSCLC prognostic markers [128] | |
| | PLCB4 | downregulation [129] | 0 + 0 |
| | LMO3 | see miR-106a/17 | 5 + 5 |
| | HLF | see miR-106a/17 | 0 + 0 |
| | GPM6B | — | 0 + 0 |
| | PDZD2 | — | 0 + 0 |
| | PTCH1 | suppressed by miR-212 [130] | 4 + 0 |
| | GATA6 | tumor inhibitor [131] | 6 + 5 |
| | FOXA2 | downregulated [132] | 0 + 0 |
| | DLC1 | see miR-106a/17 | 11 + 9 |
| | ATP8A1 | downregulated [133] | 5 + 5 |
| | CLIC5 | downregulated [134] | 0 + 0 |
| | SLC1A1 | polymorphisms [65] | 4 + 3 |
| | PCDH9 | possible association with NSCLC development, metastasis and prognosis [135] | 11 + 8 |
| | SOX17 | promoter of methylation in plasma-circulating tumors DNA [136] | 0 + 0 |
| | SCD5 | see miR-106a/17 | 5 + 4 |
| | SEMA6A | downregulation [137] | 0 + 0 |
| | HSPC159 | — | 0 + 0 |
| | TMTC1 | see miR-106a/17 | 0 + 0 |
| | SYNPO2 | upregulated under HDACi treatment [138] | 0 + 0 |
| | SCN7A | associated with good survival [139] | 0 + 0 |
| | ADRB1 | ADRB1-specific or non-selective drug improves survival [140] | 4 + 2 |
| | NCKAP5 | see miR-106a/17 | 3 + 2 |
| | PAQR5 | — | 2 + 3 |

**Table S10.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-200b | | targets multiple NSCLC prognostic markers [128] | |
| miR-200c | | inhibits invasion and metastasis [141] | |
| | DUSP1 | promotes angiogenesis, invasion and metastasis [142] | 7 + 10 |
| | FHL1 | downregulation [143] | 10 + 9 |
| | SLC4A4 | see miR-106a/17 | 0 + 0 |
| | REEP1 | upregulated under both 5-dAzaC treatment and BRG1 re-expression [144] | 4 + 5 |
| | HLF | see miR-106a/17 | 0 + 0 |
| | DACH1 | tumor suppressor [145] | 0 + 1 |
| | FOXF1 | see miR-106a/17 | 9 + 8 |
| | GPM6A | differential expression [146] | 7 + 8 |
| | CHRDL1 | aberrant gene expression [147] | 0 + 0 |
| | PTCH1 | see miR-141/200a | 2 + 3 |
| | DLC1 | see miR-106a/17 | 8 + 9 |
| | KLF4 | metastasis regulation [148] | 4 + 2 |
| | COL4A3 | see miR-106a/17 | 6 + 6 |
| | PTPN21 | see miR-106a/17 | 7 + 8 |
| | SEMA6D | — | 5 + 3 |
| | NEDD4L | see miR-106a/17 | 1 + 1 |
| | AFF3 | — | 0 + 0 |
| | GCOM1 | downregulation [149] | 3 + 5 |
| | MAMDC2 | aberrant methylation [150] | 7 + 10 |
| | PAQR5 | see miR-141/200a | 0 + 0 |

**Table S11.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-205 | | drives malignant phenotype [151] | |
| | LPCAT1 | upregulation [152] | 4 |
| | SLC4A4 | see miR-106a/17 | 0 |
| | FOXF1 | see miR-106a/17 | 7 |
| | TBX3 | see miR-106a/17 | 0 |
| | SCD5 | see miR-106a/17 | 0 |
| | AFF3 | see miR-200b/200c | 0 |
| | GCOM1 | see miR-200b/200c | 0 |
| | LRRK2 | — | 0 |
| miR-21 | | restrains cell proliferation and migration [153] | |
| | THBD | can be used as a part of survival prediction [154] | 0 |
| | PDZD2 | see miR-141/200a | 8 |
| | CD69 | see miR-106a/17 | 0 |
| | PTCH1 | see miR-141/200a | 0 |
| | OLR1 | can be used as a part of prognosis prediction [155] | 2 |
| | LIFR | — | 11 |
| | ARHGEF26 | — | 0 |
| | SOX7 | downregulation [156] | 7 |
| | KCNT2 | — | 0 |

**Table S12.** miRNA–mRNA interaction pairs identified in NSCLC samples (continued).

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in NSCLC** | **Starbase** |
|---|---|---|---|
| miR-19b | | circulating biomarker [157] | |
| | TGM2 | cisplatin resistance marker [158] | 9 |
| | EDNRB | Aberrant promoter methylation [159] | 8 |
| | REEP1 | see miR-200b/200c | 3 |
| | HLF | see miR-106a/17 | 0 |
| | DLC1 | see miR-106a/17 | 8 |
| | LIMCH1 | inclusion in tumorgenesis [160] | 9 |
| | PARM1 | — | 8 |
| | CAB39L | — | 0 |
| | FRAS1 | knockdown reduces A549 cell migration and invasion [161] | 3 |
| | HSPC159 | see miR-141/200a | 0 |
| | PTPN21 | see miR-106a/17 | 9 |
| | VSIG10 | — | 2 |
| | SEMA6D | see miR-200b/200c | 4 |
| | ARHGEF26 | see miR-21 | 0 |
| | SYNPO2 | see miR-141/200a | 0 |
| | ADRB1 | see miR-141/200a | 9 |
| | LRRK2 | see miR-205 | 0 |
| | ATP11A | see miR-106a/17 | 2 |
| | SCN4B | — | 0 |
| | NCKAP5 | see miR-106a/17 | 6 |
| | KCNT2 | see miR-21 | 0 |

**Table S13.** miRNA–mRNA interaction pairs identified in ESCC samples. *T* > *N*: upregulated in tumors, *T* < *N*: upregulated in normal tissues. For a description of the numbers in the starbase column, see Table S1.

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in ESCC** | **Starbase** |
|---|---|---|---|
| miR-203 | | G1 arrest [162],downregulation [163] | |
| | BIRC5 | overexpression [164] | 1 |
| | TP63 | tumor suppressor [165] | 0 |
| (*T* > *N* | (*T* < *N*) | | |
| miR-223 | | clinically significant [166]; overexpression regulates the ubiquitin ligase FBXW7 [167] | |
| | HLF | lineage - specifically essential for tumor growth [168] | 0 |
| | SORBS1 | significantly shortened tandem 3′ UTRs [169] | 6 |

**Table S14.** miRNA–mRNA interaction pairs identified in prostate cancer samples. $T > N$: upregulated in tumors, $T < N$: upregulated in normal tissues. For a description of the numbers in the starbase column, see Table S1.

| **miRNAs** ($T > N$) | **Gene** ($T < N$) | **Function in Prostate Cancer** | **Starbase** |
|---|---|---|---|
| miR-136 | | biomarker [170] | |
| | EIF4B | related to anticancer activity [171] | 6 |
| | HOXC10 | aberrant expression [172] | 0 |
| miR-145 | | suppress the androgen receptor [173] | |
| | TFRC | biomarker [174] | 7 |
| | EIF4B | see miR-136 | 0 |
| | KIAA0355 | — | 0 |
| | USP31 | — | 2 |
| | ZDHHC8 | — | 0 |
| miR-22 | | overexpression in DU145 [175] | |
| | KIAA0355 | see miR-145 | 7 |
| | PTEN | genomic rearrangement [176] | 2 |
| | ZNF827 | — | 0 |
| miR-494 | | suppress proliferation, invasion, and migration [177] | |
| | C14orf43 | — | 2 |
| | YEATS2 | — | 1 |
| | PTEN | see miR-22 | 1 |
| | USP31 | see miR-145 | 1 |
| | USP27X | — | 0 |

**Table S15.** miRNA–mRNA interaction pairs identified in prostate cancer samples (continued).

| **miRNAs** ($T < N$) | **Gene** ($T > N$) | **Function in Prostate Cancer** | **Starbase** |
|---|---|---|---|
| let-7a/7f | | inclusion in tumorgenesis [178] | |
| | NXT2 | — | 0 + 1 |
| | ANKRD12 | — | 1 + 2 |
| | FOXP1 | tumor suppressor [179] | 3 + 1 |
| | RTCD1 | — | 7 + 5 |
| | PLEKHG6 | — | 0 + 0 |
| miR-200a | | tumor suppressor [180] | |
| | FOXP1 | see let-7a/7f | 6 |
| miR-200b | | tumor suppressor [180] | |
| | FOXP1 | see let-7a/7f | 0 |
| | CADM1 | inactivated by methylation promoter [181] | 2 |
| | PFN2 | — | 0 |
| miR-20b | | reported importance [182] | |
| | ANKRD12 | see let-7a/7f | 3 |
| | RGNEF | — | 3 |
| | PFN2 | see miR-200b | 1 |

**Table S16.** miRNA–mRNA interaction pairs identified in colorectal/colon cancer samples. *T* > *N*: upregulated in tumors, *T* < *N*: upregulated in normal tissues. For a description of the numbers in the starbase column, see Table S1.

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in Colorectal/Colon Cancer** | **Starbase** |
|---|---|---|---|
| miR-182 | | deregulation promotes proliferation [183] | |
| | FN1 | upregulation [184] | 0 |
| miR-183 | | overexpression [185] | |
| | EEF2 | knockdown inhibits growth [186] | 4 |
| miR-96 | | overexpression [187] | |
| | FN1 | see miR-182 | 9 |
| (*T* > *N*) | (*T* < *N*) | | |
| miR-133a | | tumor suppressor [188] | |
| | PTPRO | sensitization [189] | 0 |
| miR-137 | | tumor suppressor [190] | |
| | SLC25A5 | — | 3 |
| miR-149 | | tumor suppressor [191] | |
| | IGJ | downregulation [192] | 0 |
| miR-30a | | targets the insulin receptor [193] | |
| | MYH11 | down-regulated expression correlates with poor prognosis [194] | 0 |
| | CEACAM1 | regulates metastasis [195] | 0 |

**Table S17.** miRNA–mRNA interaction pairs identified in breast cancer samples. *T* > *N*: upregulated in tumors, *T* < *N*: upregulated in normal tissues. For a description of the numbers in the starbase column, see Table S1.

| **miRNAs** (*T* > *N*) | **Gene** (*T* < *N*) | **Function in Breast Cancer** | **Starbase** |
|---|---|---|---|
| let-7i | | regulates self-renewal and tumorigenicity [196] | |
| | AMT | subtype-specific downregulation [197] | 4 |
| | GHR | up-expression [198] | 0 |
| | HOXA9 | modulates tumor phenotype [199] | 0 |
| miR-148a | | inhibits migration of breast cancer cells [200] | |
| | CNN1 | possible therapeutic target [201] | 0 |
| | FOSB | overexpression [202] | 0 |
| | TNXB | adhesion modulation [203] | 0 |
| miR-19b | | regulates tissue factor expression [204] | |
| | NCALD | frequent amplification [205] | 0 |
| | HOXA9 | see let-7i | 1 |
| | IRX4 | — | 0 |
| | CXCL12 | promotes metastasis [206] | 0 |
| | MATN2 | downregulation [207] | 9 |
| miR-21 | | overexpression [208] | |
| | MSX1 | — | 6 |
| | MATN2 | see miR-19b | 9 |
| miR-23a | | overexpression [209] | |
| | SFRP1 | associated with neoadjuvant chemotherapy [210] | 0 |
| | FOSB | see miR-148a | 0 |
| | CXCL12 | see miR-19b | 5 |
| miR-24 | | enhances tumor invasion and metastasis [211] | |
| | NCALD | see miR-19b | 0 |

**Table S18.** miRNA–mRNA interaction pairs identified in breast cancer samples (continued).

| **miRNAs** (*T* < *N*) | **Gene** (*T* > *N*) | **Function in Breast Cancer** | **Starbase** |
|---|---|---|---|
| let-7b | | regulates self-renewal and tumorigenicity [196] | |
| | ICOS | associated with poor prognosis [212] | 0 |
| | SYT1 | possible biomarker [213] | 0 |
| | ERO1L | associated with overall good survival [214] | 4 |
| | CTSC | metastasis [215] | 3 |
| | S100A8 | aggression [216] | 0 |
| | RDH10 | — | 4 |
| miR-125b | | targets ARID3B [217] | |
| | DUSP6 | silencing inhibits proliferation [218] | 5 |
| | CCR2 | coordinates survival and motility [219] | 0 |
| | BIN2 | also known as breast cancer-associated protein 1 [220] | 0 |
| | WARS | good prognostic marker [221] | 5 |
| | PDE7A | — | 4 |
| | GALNT7 | — | 5 |
| | GLS | promotes proliferation [222] | 0 |
| miR-143 | | tumor suppressor [223] | |
| | WHSC1 | positive regulator of ER$\alpha$ signaling [224] | 0 |
| | ITGA6 | overexpression [225] | 2 |
| miR-145 | | tumor suppressor [223] | |
| | DUSP6 | see miR-125b | 1 |
| | RPS6KB1 | alteration [226] | 3 |
| | ITPR2 | fused with ETV6 [227] | 0 |
| miR-22 | | biomarker [228] | |
| | FOSL1 | overexpression inhibition decreases cell growth [229] | 2 |

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