|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Number of Human miRNAs****analyzed** | **Samples setting** | **Method** | **Up-regulated****miRNAs** | **Down-regulated miRNAs** | **References** |
| 180  | 3 fresh GBMs, versus 8 NBs  | Microarray | **-21,** -138, -347, -291-5', -135 | -*198, -188*, -202  | [[24](#_ENREF_23)] |
| 245 | 9 fresh GBMs versus 9 ANBs10 GBM cell lines versus 4NBs  | Microarray  | **-10b,** -130a, -**221**, -125b-1, -125b-2, -9-2, **-21, -25**, -123-**221**, -**23a**, 23b, -222-prec, **-21*,*** *-24-1,- 24-2, -191,- 220* | **-128a**, **-181c**, **-181a**, **-181b** -125b-1, -197, **-181b**, **-181a**, -125b-2, **-181c**,  | [[15](#_ENREF_24)] |
| 756  | 26 fresh GBMs versus 13 AAs  | Microarray  | **-16, -21**, -22, -24, **-**34a**,** -126, -142-5p, -143, -146b-5p, **-155**, -193a-3p, -199a/b-3p, -335, 376c, -381, -**451**, -509-3-5p, -513a-5p, -552, -886-3p/5p | **-128**, -219-2-3p | [[43](#_ENREF_39)] |
| 248  | Unspecified # fresh mouse GBMs versus ANBs  | Microarray | -383, -519d, **-21,** -516-3p, -26a, **-10b,** -**486**, -**451**  | -124a, **-137**, -**323,** **-139,** -**218**, **-128-2**, -483**, -128-1**, -299,- 511-1, -190 | [[31](#_ENREF_36)] |
| 435  | 5 GBM cell lines, 1 AA cell line, and 1 commercial RNA  | Microarray  | -*23b*, -**23a**, -222, -**221**, -106, **-15b**, -**21**  | -451, **-124,** -495, -223, -**329**, -126, -219, -1, -**330**, -342, -**323,** -127, **-128,** **-132**, -95 , **-137** | [[20](#_ENREF_43)] |
| 8  | 10 fresh GBMs, 10 AAs, 8 LGAs, versus 4 NBs  | qRT-PCR | **-21,** -**221**  | **-181b**  | [[25](#_ENREF_25)] |
| 192  | 4 fresh GBMs, 4 AAs vs 4 NBs  | qRT-PCR | **-10b, -21,** **-155**, -**210**  | -**7**, -**31**, **-107**, **-124,** -124b, -129, **-137**, **-138**, **-139,** -187, -203, -**218**, -101, **-128a**, **-132**, -133a, -133b, -149, -153, -154\*, -185, -29b, -**323,** -328, -**330**  | [[47](#_ENREF_30)] |
| 723 | CD133+ (stem) vs CD133- (non-stem) cells from 3 GBM tissues  | Microarray  | -**451**, -**486**, -425, **-16**, -107, -185  | None found  | [[16](#_ENREF_40)] |
| 365  | 8 fresh GBMs vs 4 AAs  | qRT-PCR | **-15b**, **-21,** -135b, -196a, **-196b**, -363  | -105, -128b, -184, -302b, -302d, -367, -383, -504, -517c, -601  | [[32](#_ENREF_37)] |
| 127  | 3 fresh GBMs versus ANB  | Microarray  | **-10b, -21,** -183, -**92b**, **-106b**  | -302c , -**379**, -**329**, -134, -369-3p | [[44](#_ENREF_21)] |
| 157  | 4 fresh secondary GBMs versus LGGs  | qRT-PCR | -9, -15a, **-16**, -17, -19a, **-20a**, **-21, -25**, -28, -130b, -140, -**210**  | -184, -328  | [[40](#_ENREF_38)] |
| 1145 | 82 fresh GBMs versus 5 NBs  | Microarray  | -518b, -566  | -181d, -524-5p, -1227  | [[55](#_ENREF_35)] † |
| whole-genome small RNA sequencing | 3 GBM stem cell lines vs 3 normal neural stem cell lines  | Microarray AND NGS  | **-10a**, **-10b,** -140-5p, -204, -424, **-**34a**,** -193a-5p, -455-5p  | **-124,** -874  | [[17](#_ENREF_41)] |
| 875  | 3 fresh GBMs vs 3 NBs  | NGS  | Most 10 up-regulated: **-10b,** -96, -10b\*, -182, -135a\*, -21\*, **-21,** -542-3p, **-148a**, -**92b**  | Most 10 down-regulated: -433, -7-1\*, -129\*, -628-5p, -935, -**218**, -**31**, -876-3p, -1258, **-132**  | [[33](#_ENREF_27)] |
| 8 | 22 FFPE-dissected GBMs vs 6 NBs | qRT-PCR | **-21,** -125b | **-128a**, -**222**, -**221**, **-181b**, **-181c**, **-181a** | [[65](#_ENREF_32)] |
| 282 | 12 fresh GBMs, 12 fresh O versus 4 fresh NBs | Microarray AND qRT-PCR | **-21,** **-155**, let-7f, let-7a, **-16**, **-15b**, **-**9, -**210** | **-132**, **-128, -7,** -330-3p, -139-5p, **-124** | [[37](#_ENREF_28)] |
| 8 | 38 FFPE GBMs vs 6 NBs and 4 commercial RNAs | qRT-PCR | -196a, **-196b**, -**21** | **-128a**, -**221**, -195, -**222**, **-181c** | [[66](#_ENREF_29)] |
| 866 | 7 GBM cell lines: migrating cells vs non migrating cells  | Microarray  | *-99a\*, -767-3p, -202\*, -556-3p, -655, -451, -495, -579, -223, -381, -329, -769-3p, -524-3p, -93\*, -220a, -491-5p, -200c\*, -133b, -19b-1\*, -520h, -92b, -657, -891a, -326, -541\**  | -16, -30c, -15b, let-7f, let-7a, -23b, -103, **-107**, -24, -93, -15a, -151-5p, -23a, -30b, let-7e, -30a, -29a, -455-3p, let-7b , -25, let-7c, -106b, -92a, let-7d, -125b, -125a-5p, -**222**, let-7g, -17, -20a, -29c, let-7i, -26a, -574-3p, **-181b**, -30e, -320, -99a, -424, **-181a**,-10b**,** -17\*, -140-5p, -197, -151-3p, -30e\* | [[18](#_ENREF_42)] |
| 305  | 222 GBMs vs 10 NBs (data from TGCA)  | Microarray  | -**20a**, **-106a**, -**17-5p**, **-148a**, -146b, -200b, -193a | -**221**, -**222**, -**31**  | [[49](#_ENREF_33)] |
| whole-genome small RNA sequencing (according to miRBASE v 16.0) | 6 fresh GBMs versus 3 NBs  | NGS  | -10b\*, **-10b,** -891a, **-93,** **-196b**, -21\*, -320d, -217, -4448, **-25**, -660, **-21,** -320c, -296-3p, -**92b**, **-10a**, -92a, let-7i\*, -148a\* | **-124,** -95, **-132**, -139-5p, **-7,** -543, let-7d, -323-3p, **-128,** -598, -103a, -103b, -139-3p, -487b, -873, -323b-3p, -1381\*, -301b, **-107**, -411-3p, -124\*, -342-3p, -379\*, -212, let-7g, -153, -181d, -22, -889, -885-5p, -**379**, **-138**, let-7e, -**218**, -**221**, -136, -24, -4787-3p, -126, -548i, -382, -1270, -495, -2392, -1273d, -767-5p, -770-5p, -504, -490-3p | [[48](#_ENREF_31)] |
| >1000  | 35 FFPE GBMs: short-term vs long-term survivors  | Microarray  | miR-3163  | -539, -1305, -1260, let-7a  | [[63](#_ENREF_44)] |
| 534  | 240 GBMs vs 10 NBs (data from TGCA)  | Microarray  | -15a, **-15b**, **-16**, **-17-5p**, -**25,** -92, -**93**, **-106a**, **-106b**, -320, -502, -532, -590, -660 | -487a, -**323,** -**329**, -**218** | [[28](#_ENREF_26)]  |
| NS | 261 GBMs vs 10 NBs (data from TGCA) | Microarray | **-21, -10b,** -**210**, -27a, **-25**, **-15b**, -**23a**, -**92b**, **-106b**, -92, **-155**, **-93,** -339, -494, -565, -130b, **-**34a**, -16**, **-20a**, -320, **-106a**, -19b, -100, **-17-5p**, -424 | -124a, **-139,** -134, **-7,** -**218**, -338, -129, 2-19, -128b, **-128a**, -136, -410, **-138**, -29b, -29c, -491, **-132**, -**379**, -377, -149, -769-5p, -**330**, -**323** | [[50](#_ENREF_34)] |
| 474 | 3 fresh GBMs vs 2 NBs | Microarray | **-10b**, -182, **-10a**, -183, **21**, **-148a**, -503, -505, -**451**, -144, -542-5p, -542-3p, -26a, -142-3p, -199b, **-15b**, -550, -**25**, 9\*, -**92b**, -142-5p, -27a, -**23a**, -**486**, -362, -532, -**93**, **-106b**, -223 | None found | [[34](#_ENREF_18)] |

**Supplementary Table 1: MiRNAs profiling studies in glioblastoma**

GBM: Glioblastoma, AA: Anaplastic Astrocytoma, NB: Normal Brain, ANB: Adjacent Normal Brain, LGA: Low Grade Astrocytoma, LGG: Low Grade Glioma, O: Oligodendroglioma, DA: Diffuse Astrocytoma, NS: Not Specified, NGS: Next Generation Sequencing, qRT-PCR: quantitative Realt-Time PCR, ISH: in situ hybridization, TGCA: The Cancer Genome Atlas Datasets, FFPE: Formalin-Fixed Paraffin-Embedded. In bold: miRNAs reported up- or down-regulated in at least 3 studies. Only miRNAs showed a fold change greater than or equal to two-fold: were considered. MiRNAs showed a fold change smaller than two-fold are reported in italic font and they were not considered for GBM profiling analysis. † The authors considered a cut-off fold change >1.5.