Supplementary Table S2. Calculation of probability values (CHITEST) and false discovery rate (FDR) for miRNAs whose expression is altered in at least 45% of the tumors, excluding the miRNAs deregulated miRNAs in more than 90 % of the patients.

	Observed_range (TCGA data)					**Expected_range**						
miRNA	**Classical (50)**	**Mesenchymal (56)**	**Neural (27)**	**Proneural (55)**	**Total**	**Classical (50)**	**Mesenchymal (56)**	**Neural (27)**	**Proneural (55)**	**Total**	**CHITEST (p value)**	**FDR**
hsa-mir-379	47	47	25	48	167	44	50	24	49	167	0.94838614	0.9483861
hsa-mir-9*	27	21	13	27	88	23	26	13	26	88	0.64572222	0.6652896
hsa-mir-769-5p	43	53	21	40	157	42	47	23	46	157	0.62803307	0.6672851
hsa-mir-320	24	24	10	31	89	24	27	13	26	89	0.61629703	0.6759387
hsa-mir-370	24	29	16	21	90	24	27	13	26	90	0.57459155	0.6512038
hsa-mir-299-5p	25	31	15	21	92	24	27	13	27	92	0.56723605	0.6650354
hsa-mir-15b	46	42	17	44	149	40	44	21	44	149	0.55988779	0.6798637
hsa-mir-451	23	22	13	32	90	24	27	13	26	90	0.54775189	0.6897616
hsa-mir-376a	20	30	16	23	89	24	27	13	26	89	0.53335448	0.6974636
hsa-mir-23a	49	54	23	39	165	44	49	24	48	165	0.41103372	0.5590059
hsa-mir-149	36	49	17	34	136	36	41	20	40	136	0.39942805	0.5658564
hsa-mir-29c	47	42	16	47	152	40	45	22	44	152	0.39048826	0.5772435
hsa-mir-210	38	50	18	34	140	37	42	20	41	140	0.38104901	0.5888939
hsa-mir-25	45	40	15	45	145	39	43	21	42	145	0.37706612	0.610488
hsa-mir-93	40	34	19	49	142	38	42	20	42	142	0.36267714	0.6165511
hsa-mir-106b	43	37	16	48	144	38	43	21	42	144	0.3525261	0.6308362
hsa-mir-29b	45	35	20	51	151	40	45	22	44	151	0.26334662	0.4974325
hsa-mir-377	26	42	24	36	128	34	38	18	37	128	0.25447242	0.5089448
hsa-mir-487b	27	27	11	40	105	28	31	15	31	105	0.21017079	0.4466129
hsa-mir-15a	42	31	13	35	121	32	36	17	35	121	0.18634326	0.4223781
hsa-mir-142-3p	26	44	15	26	111	30	33	16	32	111	0.14578767	0.3540558
hsa-mir-383	34	26	8	31	99	26	29	14	29	99	0.13804116	0.3610307
hsa-mir-195	37	22	13	32	104	28	31	15	30	104	0.10735952	0.3041853
hsa-mir-92b	45	31	23	32	131	35	39	19	38	131	0.08631044	0.2667777
hsa-mir-148a	29	40	13	19	101	27	30	15	30	101	0.06128502	0.2083691
hsa-mir-10b	33	26	19	49	127	34	38	18	37	127	0.056904	0.2149707
hsa-mir-34a	38	46	14	21	119	32	35	17	35	119	0.0150595	0.0640029
hsa-mir-106a	34	18	11	41	104	28	31	15	30	104	0.0088728	0.0430965
hsa-mir-155	43	53	16	24	136	36	41	20	40	136	0.00723736	0.0410117
hsa-let-7i	39	18	12	22	91	24	27	13	27	91	0.00464277	0.0315708
hsa-mir-20a	34	18	9	46	107	28	32	15	31	107	0.00083188	0.0070709
hsa-mir-130b	33	15	9	44	101	27	30	15	30	101	0.00041455	0.0046982
hsa-mir-222	13	21	18	50	102	27	30	15	30	102	1.8352E-05	0.000312
hsa-mir-221	11	15	17	47	90	24	27	13	26	90	1.5926E-06	5.415E-05

The table shows the number of patients with alterations in the respective miRNA in each GBM subtype (observed range). The expected number of patients with alterations in the corresponding miRNA (expected range) was calculated using the formula: TS*TA/TP, where TS is the total number of patients in the specific subtype (indicated between brackets), TA is the sum of the number of patients with alterations in the four subtypes and TP is the total number of patients (188). Probability values were calculated using the Excel CHITEST function (Microsoft Excel 2003, Microsoft, USA). This algorithm uses the chi-square test ($\chi2$) to calculate the probability of the differences between two supplied data sets (observed and expected frequencies) to be simply due to sampling error or to be real. The FDR is a statistical method used in multiple hypothesis testing to correct for multiple comparisons. The FDR of a set of predictions is the expected percent of false predictions in the set of predictions. Changes were considered significant ($p<0.05$) if the FDR was smaller than 0.05.