Supplemental Table S1b. The miRNA alignments in the table are based on miRNAs predicted to regulate the 3’UTR of EZH2 using miRBase (http://microrna.sanger.ac.uk/targets/v5/). The 3’UTR miRNA binding sites of EZH2 are presented and extracted from the Ensemble database (ENST00000320356). Of the miRNAs deregulated in GBM, only miR-101, miR-98, miR-137 and miR-139 were predicted to target the 3’-UTR of EZH2. miR-101 showed the highest binding predictions and was predicted to bind the EZH2 3’-UTR twice.

<table>
<tr><th>miRNA ID</th><th>Score</th><th>Start</th><th>End</th><th>Alignment miRNA
3’UTR</th><th>Species</th><th>No. hits within 3’-UTR</th><th>Confirmed deregulated in GBM</th></tr>
<tr><td>hsa-miR-101</td><td>18,8608</td><td>101</td><td>121</td><td>AGUCAAUAGUGUCAUGACAU
| | || || |||||||||
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<tr><td>hsa-miR-127-5p</td><td>18,761</td><td>28</td><td>49</td><td>uagUCUCGGGAGACUCGAAGUC
   | |||: || ||||||||
gaaACAGCTGCCTTAGCTTCAG</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-101</td><td>18,6322</td><td>45</td><td>66</td><td>AAGUCAAUAGUG-UCAUGACAU
||||| | | | ||||||||:
TTCAGGAACCTCGAGTACTGTG</td><td>8</td><td>2</td><td>Down</td></tr>
<tr><td>hsa-miR-23a*</td><td>18,5336</td><td>35</td><td>56</td><td>uuuaGGGUAGGGGUCCUUGGGG
    |::| |::||||||||:|
ctgcCTTAGCTTCAGGAACCTC</td><td>2</td><td>1</td><td></td></tr>
<tr><td>hsa-let-7f</td><td>18,4199</td><td>1</td><td>14</td><td>uugauauguUAGAUGAUGGAGu
         ||||:|||||||
--------cATCTGCTACCTCc</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-765</td><td>18,2893</td><td>1</td><td>18</td><td>guaGUGGAAGGAAGAGGAGGu
   ||:|| |: |||||||
---CATCTGCTACCTCCTCCc</td><td>2</td><td>1</td><td></td></tr>
<tr><td>hsa-let-7a</td><td>18,0788</td><td>1</td><td>14</td><td>uugauauguUGGAUGAUGGAGu
         |:||:|||||||
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<tr><td>hsa-let-7b</td><td>18,0788</td><td>1</td><td>14</td><td>uuggugugu UGGAUGAUGGAGu
         |:||:|||||||
--------cATCTGCTACCTCc</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-let-7c</td><td>18,0788</td><td>1</td><td>14</td><td>uugguauguUGGAUGAUGGAGu
         |:||:|||||||
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<tr><td>hsa-let-7d</td><td>18,0788</td><td>1</td><td>14</td><td>uugauacguUGGAUGAUGGAGa
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<tr><td>hsa-miR-217</td><td>17,8748</td><td>193</td><td>220</td><td>aGGUUAGUCAAGGAC-----UACGUCAU
 |||:| | ||::|| ||||||||
aCCAGTGAATTTTTGCAATAATGCAGTA</td><td>5</td><td>2</td><td></td></tr>
<tr><td>hsa-miR-139-5p</td><td>17,8514</td><td>47</td><td>68</td><td>GACCUCUGUGCACGUGACAUCU
| ||| | || |:|||||:|:
CAGGAACCTCGAGTACTGTGGG</td><td>7</td><td>1</td><td>Down</td></tr>
<tr><td>hsa-miR-19b-2*</td><td>17,8514</td><td>94</td><td>116</td><td>ACUUUACG-UUUGGACGUUUUGa
|||||| | :||::||||||::
TGAAATTCTGAATTTGCAAAGTa</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-630</td><td>17,8514</td><td>231</td><td>253</td><td>uGGAAGGGAC-CAUGUCUUAUGA
 :| |::|| || ||||||||
tTCAACTTTGAATAAAGAATACT</td><td>6</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-20a*</td><td>17,624</td><td>198</td><td>219</td><td>gaaauucacgagUAUUACGUCA
            ||||||||||
tgaattttgcaATAATGCAGT</td><td>3</td><td>1</td><td></td></tr>
<tr><td>hsa-let-7e</td><td>17,5103</td><td>1</td><td>14</td><td>uugauauguUGGAGGAUGGAGu
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<tr><td>hsa-let-7g</td><td>17,5103</td><td>1</td><td>14</td><td>uugacauguUUGAUGAUGGAGu
         | ||:|||||||
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<tr><td>hsa-let-7i</td><td>17,5103</td><td>1</td><td>14</td><td>uugucguguUUGAUGAUGGAGu
         | ||:|||||||
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<tr><td>hsa-miR-595</td><td>17,4891</td><td>211</td><td>231</td><td>ucUGUGUGGUGCCGUGUGAAG
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taATGCAGTATGGTACATTTT</td><td>6</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-26a</td><td>17,2829</td><td>236</td><td>257</td><td>ucggauaggacCUAAUGAACUU
           || ||||||||
ctttgaataaaGAATACTTGAA</td><td>7</td><td>1</td><td></td></tr>
</table>

<table>
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<tr><td>hsa-miR-98</td><td>17,1692</td><td>1</td><td>14</td><td>uuguuauguUGAAUGAUGGAGu
         |: |:|||||||
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<tr><td>hsa-miR-944</td><td>17,0555</td><td>109</td><td>131</td><td>gaguaggcuACA-UGUUAUUAAA
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gcaaagtacTGTAAGAATAATTT</td><td>7</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-26b</td><td>17,0319</td><td>237</td><td>257</td><td>uggauaggacUUAAUGAACUU
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tttgaataaaGAATACTTGAA</td><td>7</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-539</td><td>16,9418</td><td>213</td><td>234</td><td>UGUGUGGUUCCUAUUAAAGAGg
|::|| :| || ||||:||
ATGCAGTATGGTACATTTTTCa</td><td>4</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-646</td><td>16,8821</td><td>22</td><td>40</td><td>cGGAGUCUCCGUCGACGaa
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tCCTCTGAAACAGCTGCct</td><td>3</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-498</td><td>16,8566</td><td>76</td><td>98</td><td>CUUUUUGCGGGGGACCGAACUUU
|||||| | : |:||||||
GAAAAAGAACATGCAGTTTGAAA</td><td>5</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-33a</td><td>16,8033</td><td>198</td><td>218</td><td>ACGUUACGUUGAUGUUACGUg
|| | | : :| |:||||||
TGAATTTTTGCAATAATGCAg</td><td>6</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-330-3p</td><td>16,7435</td><td>168</td><td>192</td><td>AGAGACGUC--CGGCACACGAAACG
|||| ||| || |||:||||:
TCTCACCAGCTGCAAAGTGTTTTGT</td><td>4</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-27a</td><td>16,6889</td><td>47</td><td>68</td><td>cgCCUUGAAUC-GGUGACACUU
  ||||| | | :||||||::
caGGAACCTCGAGTACTGTGGG</td><td>6</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-138</td><td>16,6303</td><td>154</td><td>178</td><td>gccGGACUAA--GUGUUGUGGUCGA
   ::| ||| | : ||||||||
actTTTTATTGCCTTCTCACCAGCT</td><td>8</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-99a*</td><td>16,6007</td><td>125</td><td>146</td><td>gucUGGGUAUCUUCGCUCGAAc
   |:::|||| | :|||:||
ataATTTATAGTAATGAGTTTa</td><td>2</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-20a</td><td>16,5172</td><td>53</td><td>75</td><td>gauggaCGUGAUAUUCGUGAAAU
      |:|||:|::||| ||||
cctcgaGTACTGTGGGCAATTTA</td><td>5</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-219-1-3p</td><td>16,487</td><td>137</td><td>158</td><td>gccCUGCAGGUCUGAGUUGAGA
   || |: | | ||||||:|
aatGAGTTTAAAAATCAACTTT</td><td>2</td><td>2</td><td></td></tr>
<tr><td>hsa-miR-23b*</td><td>16,487</td><td>37</td><td>56</td><td>uuuAGUCGUACGGUCCUUGGGu
   |:||| | ||||||||:
gccTTAGCTT--CAGGAACCTc</td><td>2</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-106b</td><td>16,4603</td><td>55</td><td>75</td><td>uagaCGUGACAGUCGUGAAAU
    |:||||| :||| ||||
tcgaGTACTGTGGGCAATTTA</td><td>5</td><td>1</td><td></td></tr>
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 |:|| |: | :||||||:
cAGGAACCTCGAGTACTGTGG</td><td>6</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-871</td><td>16,4041</td><td>85</td><td>107</td><td>GUACUGACCGUGAUUAGACUUAu
|||| :: | |||||||
CATGCAGTTTGAAATTCTGAATt</td><td>5</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-382</td><td>16,3733</td><td>56</td><td>75</td><td>GCUUAGGUGGUGCUUGUUGAAg
|||:| ||:::|::|||:||
CGAGT--ACTGTGGGCAATTTa</td><td>1</td><td>2</td><td></td></tr>
<tr><td>hsa-miR-27b</td><td>16,346</td><td>47</td><td>68</td><td>cgUCUUGAAUC-GGUGACACUU
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caGGAACCTCGAGTACTGTGGG</td><td>6</td><td>1</td><td></td></tr>
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| | | : :|| :||||||
GAATTTTTGCAATAATGCAg</td><td>6</td><td>1</td><td></td></tr>
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      ||||||| ||||||
ccccccTCCTCTG-AAACAGct</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-99b*</td><td>16,2596</td><td>125</td><td>146</td><td>gccUGGGUGUCUGUGCUCGAAc
   |:::|:|| |:|||:||
ataATTTATAGTAATGAGTTTa</td><td>2</td><td>1</td><td></td></tr>
<tr><td>hsa-miR-567</td><td>16,1778</td><td>68</td><td>90</td><td>caagacaggaccUUCUUGUAUGa
            ||||||||:|
gcaatttagaaaAAGAACATGCa</td><td>1</td><td>1</td><td></td></tr>
<tr><td>hsa-let-7g</td><td>16,1459</td><td>22</td><td>42</td><td>uuGACAUGUUUGAUGAUGGAGU
  || |: |||| :||:|||:|
tcCTCTG-AAACAGCTGCCTTA</td><td>6</td><td>2</td><td></td></tr>
</table>

hsa-miR-199a-3p	16,1459	99	120	auuggUUACACGUCUGAUGACA ||| |||| | |||||| ttctgAATTTGCAAAGTACTGT	5	1	
hsa-miR-26a-1*	16,1459	106	129	gcACG-UUCAUUG-GUUCUUAUcc ||| ||||| : :||||||| ttTGCAAAGTACTGTAAGAATAat	1	1	
hsa-miR-26a-2*	16,1459	107	129	cuuugUUCAUUA-GUUCUUAUcc ||||| | :||||||| ttgcaAAGTACTGTAAGAATAat	1	2	
hsa-miR-548a-3p	16,0322	76	96*	CGUUUUCAUUAACGGUCAAAac | ||||| | || |||||| GAAAAAGAACATG-CAGTTTga	5	1	
hsa-miR-590-5p	16,0322	124	145	gacgUGAAAAUACUUAUUCGAG |:|| || |||:||:|: aataATTTATAGTAATGAGTTT	5	1	
hsa-let-7i	15,9185	21	42	uugucgugUUUGAUGAUGGAGU |||| :||:|||:| ctcctctgAAACAGCTGCCTTA	6	1	
hsa-miR-26a-2*	15,9185	232	253	cuUUGUUCAUUAGUUCUUAUcc ||| ||| ||||||| tcAACTTTGAATAAAGAATAct	1	2	
hsa-miR-137	15,8384	119	141	gAUGCGCAUAAGAAUUCGUUAUU || | || |:| ||:|||:| gTAAGAATAATTTATAGTAATGA	6	2	Down
hsa-miR-217	15,8384	71	93	agguuagucaaggacUACGUCAu ||||||| atttagaaaaagaacATGCAGTt	5	2	
hsa-miR-34c-5p	15,8384	147	167	cgUUAGUCGAUUGAUGUGACGGA ||||| || :| :|:||||| aaAATCAACT–TTTTATTGCCT	5	1	
hsa-miR-10a*	15,8047	184	205	auaAGGGGAUCUAUGCUUAAAc |::: || ::|||||| gtgTTTTGTACCAGTGAATTTt	1	3	
hsa-miR-200a*	15,8047	105	126	aGGUCGUGACAGGCCAUUCUac :: ||| || | |||||| aTTTGCAAAGTACTGTAAGAat	1	1	
hsa-miR-625*	15,8047	116	137	acuccccCUUUCAAGAUAUCAg ||| |:|||||| actgtaaGAATAATTTATAGTa	1	1	
hsa-miR-200b	15,691	202	223	AGUAGUAAUGGUCCGUCAUAau |: |:: |: | ||||||| TTTTTGCAATAATGCAGTATgg	4	1	
hsa-miR-219-1-3p	15,691	221	239	GCCCUGCAGGUCUGAGUUGAGA :|| || |:: :||||||:| TGGTACATTT---TTCAACTTT	3	2	
hsa-miR-382	15,691	111	132	gcUUAGGUGGUGCUUGUUGAAg |:| | :| |||:||:|| aaAGTACTGTAAGAATAATTTa	1	2	
hsa-miR-501-5p	15,5773	230	251	AGAGUGGGUCCCUGUUUCCUAa |:||| |: | |:|||| || TTTCAACTTTGAATAAAGAATa	2	1	
hsa-miR-801	15,5373	50	73	cagcuaaggCGUGCGUCUCGUUAG |:|| |:|||||: gaacctcgaGTACTGTGGGCAATT	4	1	
hsa-miR-137	15,499	191	213	gAUGCGCAUAAGAAUUCGUUAUU ||| ||: :|| ||||||| gTACCAGTGAATTTTTGCAATAA	5	2	Down
hsa-miR-10b*	15,4636	87	110	uaaggGGAUCUUA--GCUUAGACa ::|: ||| :||||:|| tgcagTTTGAAATTCTGAATTTGc	2	1	
hsa-miR-10a*	15,3499	88	109	auaaggggaucuAUGCUUAAAC | :||||||| gcagtttgaaatTCTGAATTTG	2	3	
hsa-miR-518d-3p	15,3173	170	191	cGAGGUU-UCCCUUCGCGAAAC | |||: | |||:|:|||| tCACCAGCTGCAAAGTGTTTTG	6	1	
hsa-miR-10a*	15,1225	125	146	auaaGGGGAUCUAUGCUUAAAc ::: ||| |:||:||| ataaTTTATAGTAATGAGTTTa	1	3	
hsa-miR-126	15,1225	206	228	GCGUAAUAAUG-AGUGCCAUGcu :||| || |:| :|:||||| TGCAATAATGCAGTATGGTACat	6	1	
hsa-miR-518a-3p	14,8951	169	191	aGGUCGUU-UCCCUUCGCGAAAg :|| ||: | |||:|:||| cTCACCAGCTGCAAAGTGTTTTg	6	1	

<table>
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|||:|:||||
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CAC-CAGCTGCAAAGTGTTTT</td><td>6</td><td>1</td><td></td></tr>
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| |||:||||:
ctcgagtacTGTGGGCAATTt</td><td>2</td><td>1</td><td>Down</td></tr>
</table>