Supplementary Figure S1

A

Hypomethylated genes

Hypermethylated genes

B

ROC curve

<table>
<thead>
<tr>
<th>cut off value</th>
<th>0.2</th>
<th>0.4</th>
<th>0.6</th>
<th>0.8</th>
<th>1</th>
<th>1.2</th>
<th>1.4</th>
<th>1.6</th>
<th>1.8</th>
<th>2</th>
<th>2.2</th>
<th>2.4</th>
</tr>
</thead>
<tbody>
<tr>
<td>sensitivity(%)</td>
<td>96.2</td>
<td>92.3</td>
<td>92.3</td>
<td>88.5</td>
<td>88.5</td>
<td>76.9</td>
<td>57.7</td>
<td>46.2</td>
<td>38.5</td>
<td>15.4</td>
<td>11.5</td>
<td>3.85</td>
</tr>
<tr>
<td>specificity(%)</td>
<td>12.5</td>
<td>33.3</td>
<td>45.8</td>
<td>54.2</td>
<td>62.5</td>
<td>70.8</td>
<td>83.3</td>
<td>83.3</td>
<td>87.5</td>
<td>91.7</td>
<td>91.7</td>
<td>95.8</td>
</tr>
<tr>
<td>false-positive rate</td>
<td>0.875</td>
<td>0.667</td>
<td>0.542</td>
<td>0.458</td>
<td>0.375</td>
<td>0.292</td>
<td>0.167</td>
<td>0.167</td>
<td>0.125</td>
<td>0.083</td>
<td>0.083</td>
<td>0.042</td>
</tr>
</tbody>
</table>
Supplementary Figure S2

- **ANGPT2**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **FAR1**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **L1TD1**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **RADIL**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **SFRP1**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **MZB1**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **DERL3**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **CCK**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **PBX4**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **OCIAD2**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM

- **KCNK6**
  - Relative expression level (no treatment)
  - 5-aza-dCyt, concentrations: 1 μM, 5 μM, 10 μM
Supplementary Figure S3

Primary HCC

<table>
<thead>
<tr>
<th>L81</th>
<th>L82</th>
<th>L83</th>
<th>L84</th>
<th>L85</th>
<th>L86</th>
<th>L87</th>
<th>L88</th>
<th>L89</th>
<th>L92</th>
<th>L97</th>
<th>L98</th>
<th>L99</th>
<th>L100</th>
<th>L101</th>
<th>L102</th>
<th>L104</th>
</tr>
</thead>
<tbody>
<tr>
<td>NT</td>
<td>NT</td>
<td>NT</td>
<td>NT</td>
<td>NT</td>
<td>NT</td>
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<td>NT</td>
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<td>NT</td>
</tr>
</tbody>
</table>

BstU1

Region 3

Methylation

Silencing

FAR1

Relative mRNA expression (paired N)

Tumor-specific hypermethylation (T >20%, N <20%)

>50% decreased expression in tumor tissue

8/17 (47.1%) Silencing/Methylation

6/17 (35.3%)

5/8 (62.5%)
**Supplementary Figure S4**

<table>
<thead>
<tr>
<th>Region</th>
<th>Methylation (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Total</td>
</tr>
<tr>
<td>HLE</td>
<td>98.3</td>
</tr>
<tr>
<td>HLE + 5-aza-dCyd</td>
<td>57.4</td>
</tr>
</tbody>
</table>

The figure shows the methylation percentages across different regions of the MZB1 gene. The methylation levels are indicated by filled bars, with higher percentages shown in darker shades. The table provides the total methylation percentage and the specific percentage for Region 8.