Supplementary Figures: Indirect comparisons between one methylated gene and 31 other genes.

**Figure S1.** The diagnostic accuracy of 1/CDH1 compared with the other 31 methylated genes. OR >1 means that 1/CDH1 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S2. The diagnostic accuracy of 2/SOX17 compared with the other 31 methylated genes. OR >1 means that 2/SOX17 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
**Figure S3.** The diagnostic accuracy of 3/CDO1 compared with the other 31 methylated genes. OR >1 means that 3/CDO1 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S4. The diagnostic accuracy of 4/ZFP42 compared with the other 31 methylated genes. OR >1 means that 4/ZFP42 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
### Figure S5. The diagnostic accuracy of S/TAC1 compared with the other 28 methylated genes. OR >1 means that S/TAC1 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S6. The diagnostic accuracy of 6/H-cadherin compared with the other 31 methylated genes. OR >1 means that 6/H-cadherin had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S7. The diagnostic accuracy of 7/FHIT compared with the other 31 methylated genes. OR >1 means that 7/FHIT had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S8. The diagnostic accuracy of 8/PCDH20 compared with the other 31 methylated genes. OR >1 means that 8/PCDH20 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S9. The diagnostic accuracy of 9/Dab2 compared with the other 31 methylated genes. OR >1 means that 9/Dab2 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S10. The diagnostic accuracy of 10/Dcr2 compared with the other 31 methylated genes. OR >1 means that 10/Dcr2 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S11. The diagnostic accuracy of 11/SULF2 compared with the other 31 methylated genes. OR >1 means that 11/SULF2 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S12. The diagnostic accuracy of 12/Kifla compared with the other 31 methylated genes. OR >1 means that 12/Kifla had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S13. The diagnostic accuracy of 13/Dal-1 compared with the other 31 methylated genes. OR >1 means that 13/Dal-1 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S14. The diagnostic accuracy of 14/Jph3 compared with the other 31 methylated genes. OR >1 means that 14/Jph3 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S15. The diagnostic accuracy of 15/RASSF2 compared with the other 31 methylated genes. OR >1 means that 15/RASSF2 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S16. The diagnostic accuracy of 16/TCF21 compared with the other 31 methylated genes. OR >1 means that 16/TCF21 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S17. The diagnostic accuracy of 17/CXCL compared with the other 31 methylated genes. OR >1 means that 17/CXCL had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S18. The diagnostic accuracy of 18/MAGE compared with the other 31 methylated genes. OR >1 means that 18/MAGE had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S19. The diagnostic accuracy of 19/HOXA compared with the other 31 methylated genes. OR >1 means that 19/HOXA had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S20. The diagnostic accuracy of 20/RARβ compared with the other 31 methylated genes. OR >1 means that 20/RARβ had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S21. The diagnostic accuracy of 21/FAM19A4 compared with the other 31 methylated genes. OR >1 means that 21/FAM19A4 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S22. The diagnostic accuracy of 22/PHACTR3 compared with the other 31 methylated genes. OR >1 means that 22/PHACTR3 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S23. The diagnostic accuracy of 23/DAPK compared with the other 31 methylated genes. OR >1 means that 23/DAPK had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S24. The diagnostic accuracy of 24/3OST2 compared with the other 28 methylated genes. OR >1 means that 24/3OST2 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S25. The diagnostic accuracy of 25/PRDM14 compared with the other 31 methylated genes. OR >1 means that 25/PRDM14 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S26. The diagnostic accuracy of 26/GATA compared with the other 31 methylated genes. OR >1 means that 31/GATA had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S27. The diagnostic accuracy of 27/MGMT compared with the other 31 methylated genes. OR >1 means that 27/MGMT had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S28. The diagnostic accuracy of 28/PAX5 compared with the other 31 methylated genes. OR >1 means that 28/PAX5 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S29. The diagnostic accuracy of 29/CYGB compared with the other 31 methylated genes. OR >1 means that 29/CYGB had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S30. The diagnostic accuracy of 30/\textit{APC} compared with the other 31 methylated genes. OR >1 means that 30/\textit{APC} had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S31. The diagnostic accuracy of 31/p16 compared with the other 31 methylated genes. OR >1 means that 31/p16 had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
Figure S32. The diagnostic accuracy of 32/RASSF1A compared with the other 31 methylated genes. OR >1 means that 32/RASSF1A had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.
| Value   | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 | 0.80 | 0.81 | 0.82 | 0.83 | 0.84 | 0.85 | 0.86 | 0.87 | 0.88 | 0.89 | 0.90 | 0.91 | 0.92 | 0.93 | 0.94 | 0.95 | 0.96 | 0.97 | 0.98 | 0.99 | 1.00 | 1.01 | 1.02 | 1.03 | 1.04 | 1.05 | 1.06 | 1.07 | 1.08 | 1.09 | 1.10 | 1.11 | 1.12 | 1.13 | 1.14 | 1.15 |
|---------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 0.64    | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.65    | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.66    | 0.26 | 0.27 | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.67    | 0.24 | 0.25 | 0.26 | 0.27 | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.68    | 0.22 | 0.23 | 0.24 | 0.25 | 0.26 | 0.27 | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.69    | 0.21 | 0.22 | 0.23 | 0.24 | 0.25 | 0.26 | 0.27 | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |
| 0.70    | 0.20 | 0.21 | 0.22 | 0.23 | 0.24 | 0.25 | 0.26 | 0.27 | 0.28 | 0.29 | 0.30 | 0.31 | 0.32 | 0.33 | 0.34 | 0.35 | 0.36 | 0.37 | 0.38 | 0.39 | 0.40 | 0.41 | 0.42 | 0.43 | 0.44 | 0.45 | 0.46 | 0.47 | 0.48 | 0.49 | 0.50 | 0.51 | 0.52 | 0.53 | 0.54 | 0.55 | 0.56 | 0.57 | 0.58 | 0.59 | 0.60 | 0.61 | 0.62 | 0.63 | 0.64 | 0.65 | 0.66 | 0.67 | 0.68 | 0.69 | 0.70 | 0.71 | 0.72 | 0.73 | 0.74 | 0.75 | 0.76 | 0.77 | 0.78 | 0.79 |

In column the methylated gene compared with the other 31 methylated genes; in row the other 31 methylated genes compared with the methylated gene. OR > 1 means that the methylated gene had a higher diagnostic accuracy, and 95% CI excluding 1 was considered significant.