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3 ***Supplementary Figure 1: Barrett's Methylation candidates***

4 These data were from Alvi et al 2013. (A) Boxplots representing the methylation level of the
5 differentially methylated genes in Barrett's compared to normal tissue. (B) Heatmap
6 representing the non-supervised hierarchical clustering of patients according to the
7 methylation level of genes of interest.
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13 ***Supplementary Figure 2: Methylation level of B3GAT2, CDX2 and Vimentin***

14 Boxplots representing the methylation level of the B3GAT2, CDX2 and Vimentin (VIM)
15 genes in Barrett's compared to normal tissue from Alvi et al 2013 dataset.
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20 ***Supplementary Figure 3: Methylation levels of our identified markers according to the***
21 ***length of the Barrett's segment using the Cytosponge™.***
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23 Dotplot presenting sensitivity variation by circumferential (C) and maximal (M) Barrett's
24 length.
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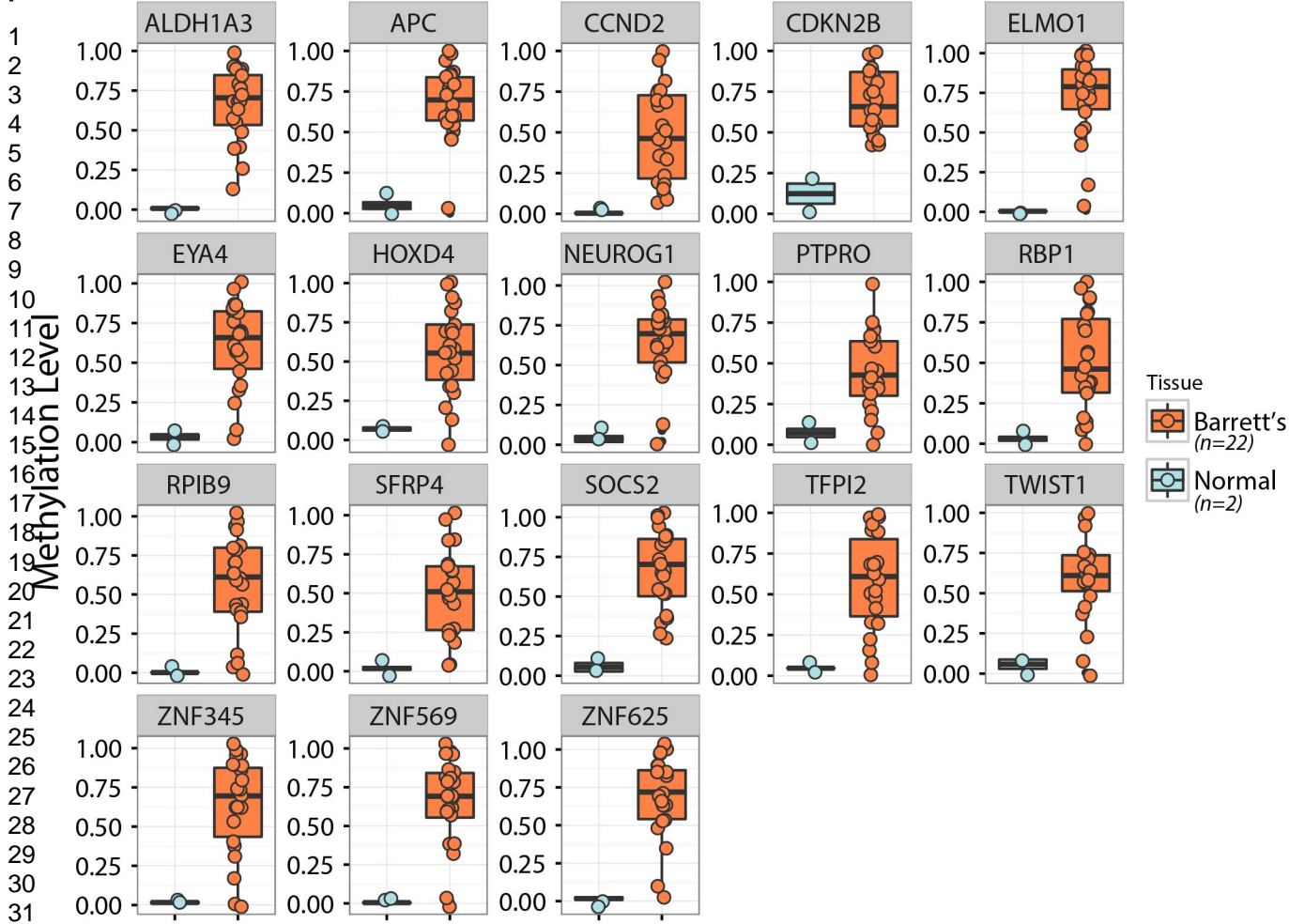
28 ***Supplementary Figure 4: Methylation status in dysplasia and adenocarcinoma.***

29 Boxplot of normalised beta values showing hypermethylation of each gene candidate in
30 Barrett's and Oesophageal adenocarcinoma biopsies compared to normal tissue – data
31 extracted from Alvi's dataset (Alvi et al., 2013)
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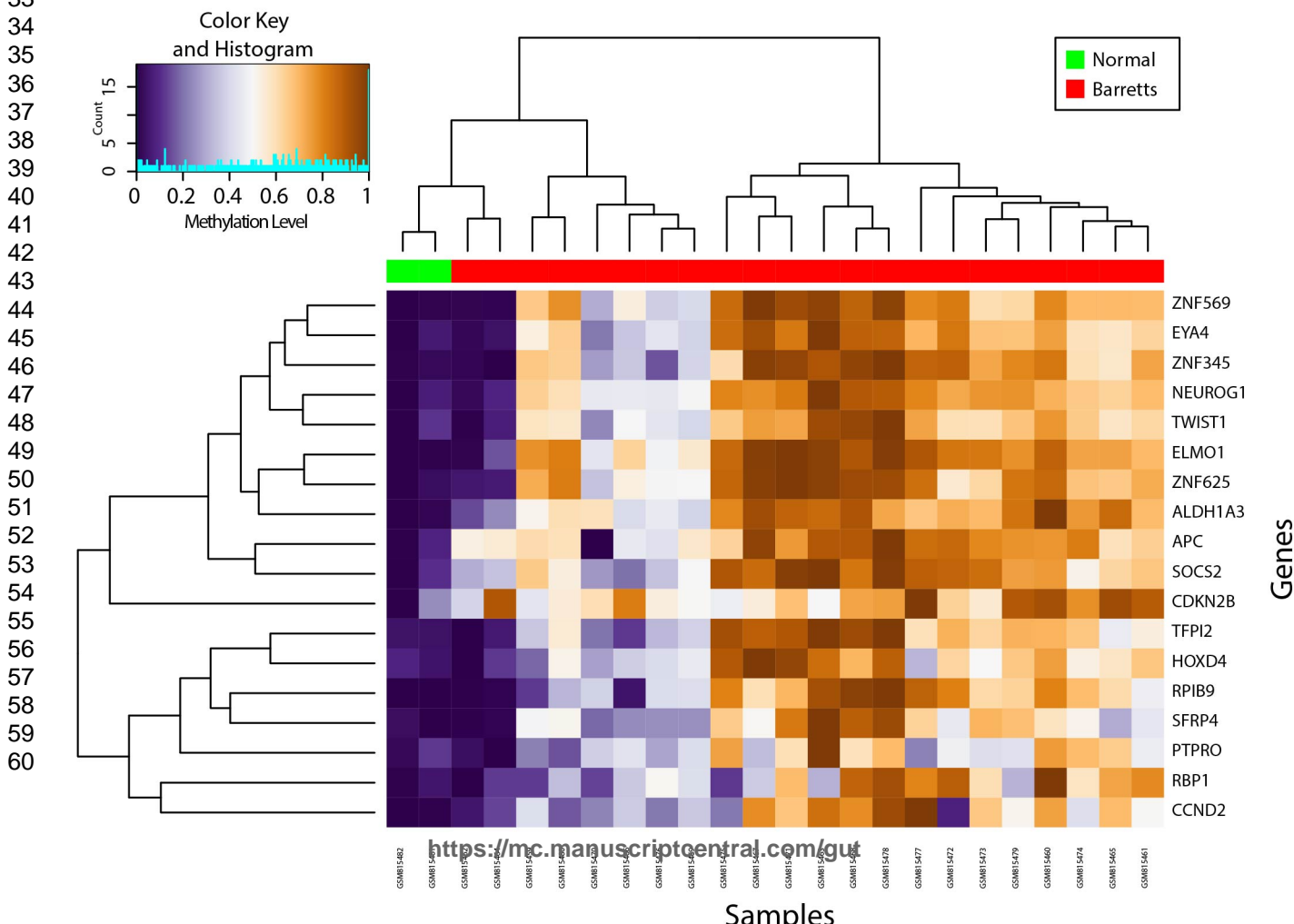
35 **References**

36 Alvi MA, Liu X, O'Donovan M, et al. DNA methylation as an adjunct to histopathology to
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38 detect prevalent, inconspicuous dysplasia and early-stage neoplasia in Barrett's
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40 esophagus. *Clin Cancer Res* 2013;19(4):878-88. doi: 10.1158/1078-0432.CCR-12-2880
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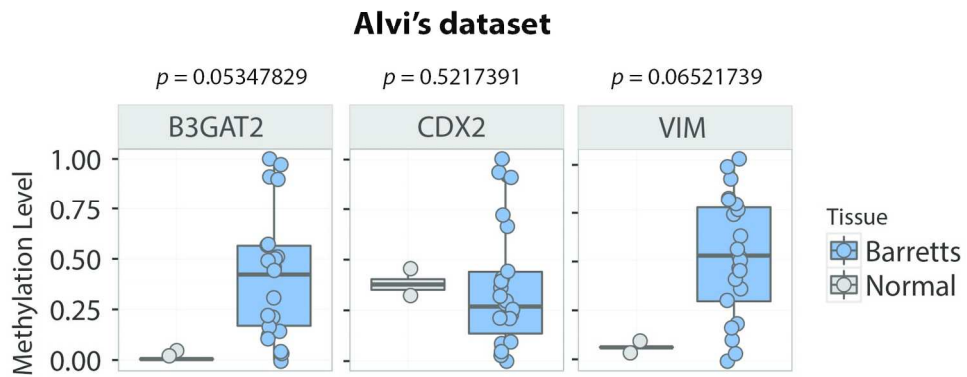
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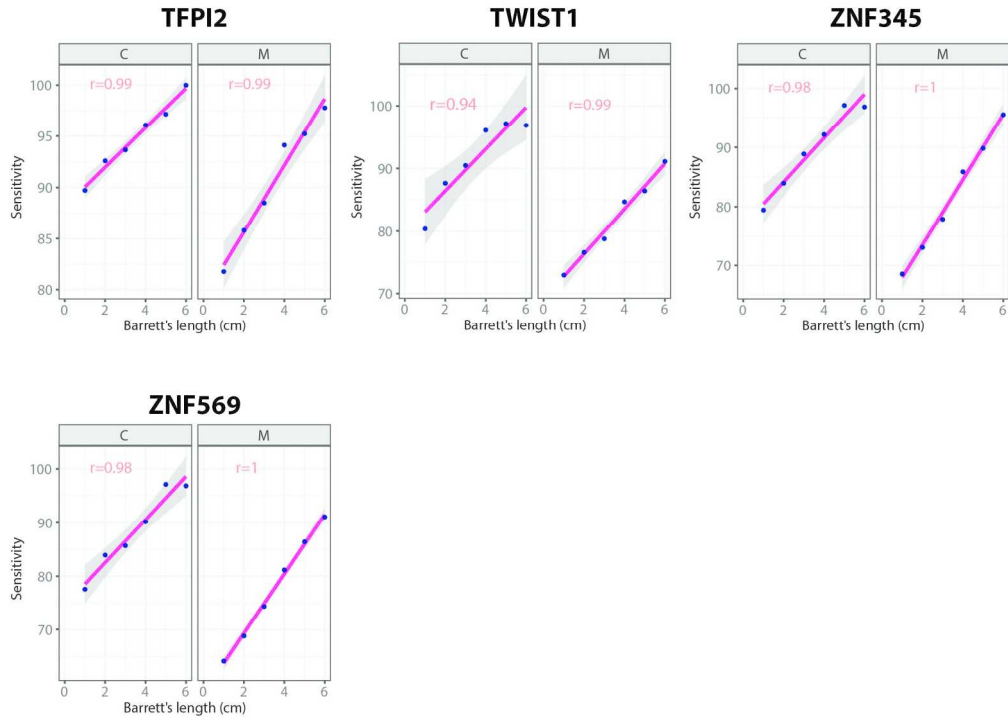
Supplementary Figure 2



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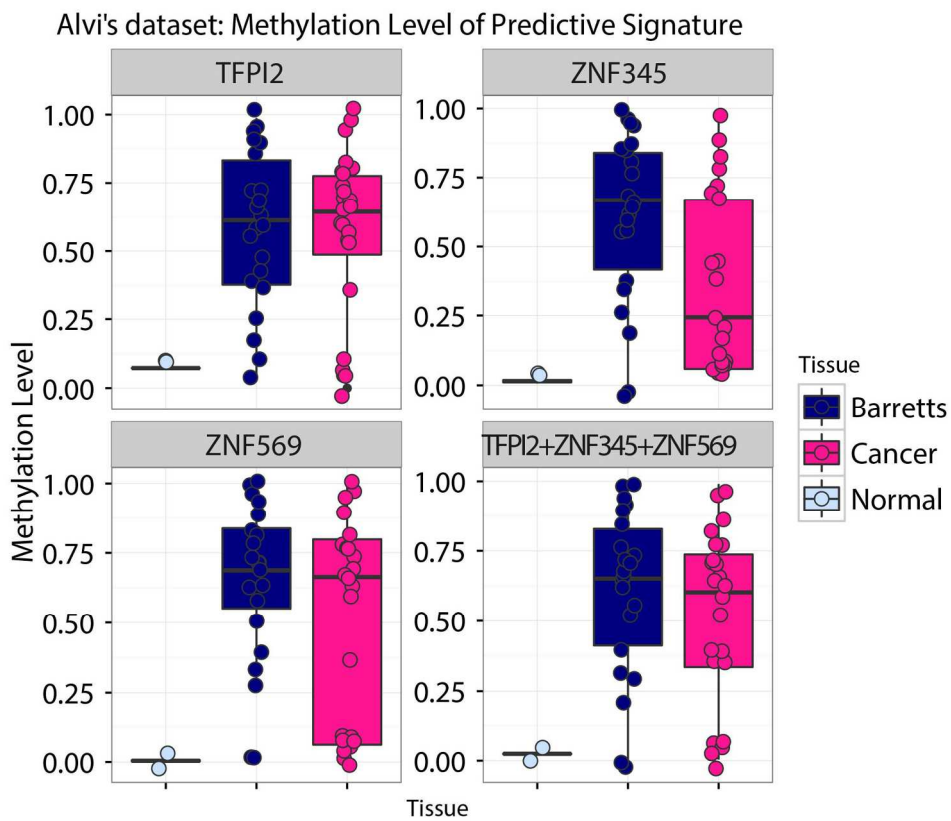
Supplementary Figure 3



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Review Only

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