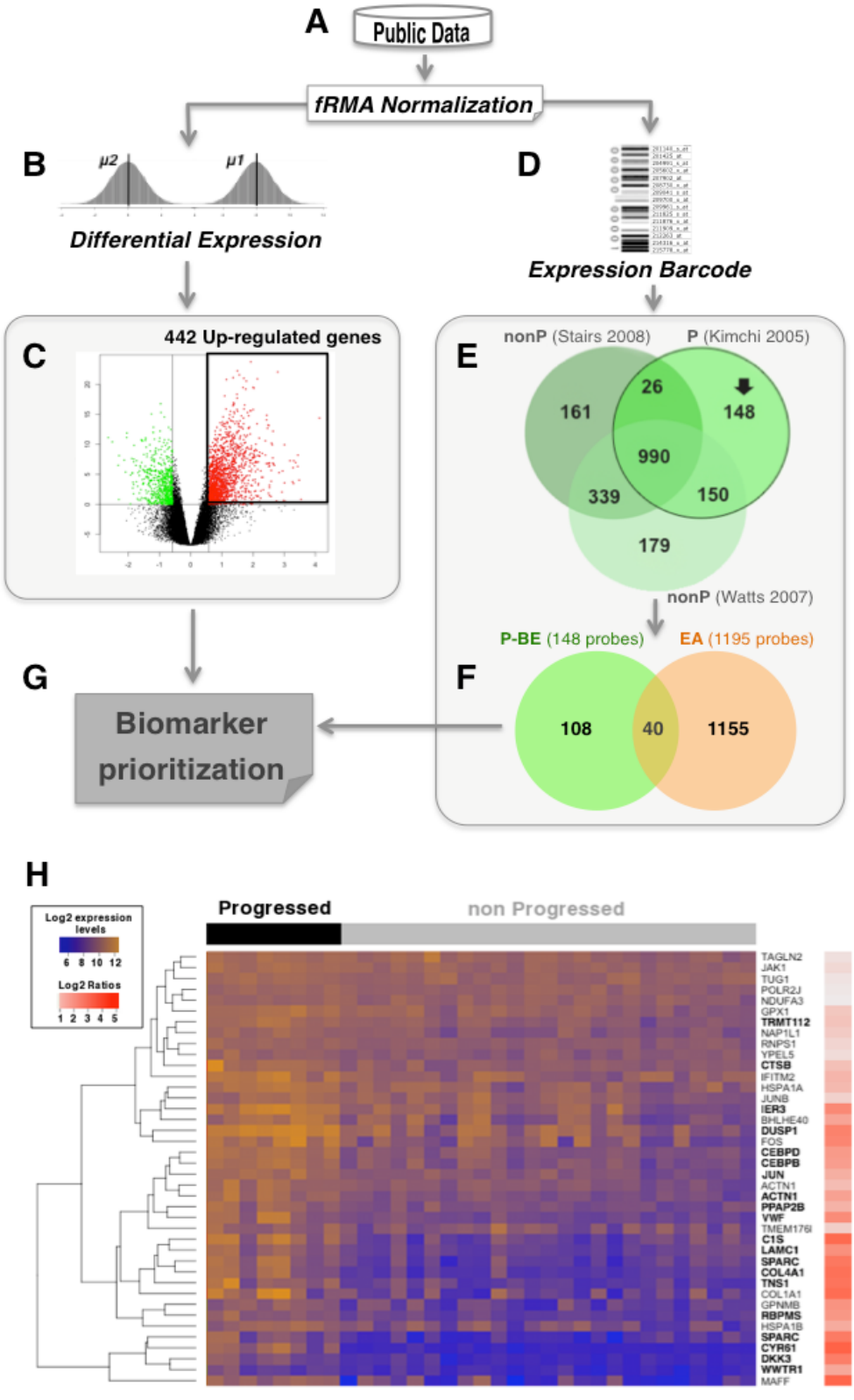

S1 Fig. An original bioinformatics prioritization framework allowed the identification of at risk BE biomarkers. **A.** Publicly available microarray datasets on BE and/or EA were

normalized with the fRMA algorithm. BE samples associated with progression to EA were retrieved from Kimchi *et al.* [1] and assigned to the P-BE group and EA-free BE samples were retrieved from Watts *et al.* [2] and Stairs *et al.* [3] and assigned to nonP-BE group. **B.** Comparison of P-BE versus nonP-BE samples with a differential expression approach which, **C.** resulted in the identification of 442 unique up-regulated genes in P-BE. **D.** Calculation of expression barcodes was performed per individual sample. **E.** P-BE-exclusive probe sets (148) were defined via intersection of P-BE and nonP-BE barcodes. **F.** Forty malignancy-associated progression probe sets were achieved by crossing 148 P-BE barcoded probe sets with EA-associated barcodes. **G.** Integration of barcode and differential expression results to further trim promising candidates for downstream validation. **H.** Combined barcode and differential expression prioritized 20 probe sets associated with BE malignant progression to be validated in downstream experimental settings. In total, 19 unique up-regulated genes (in bold) differentiate P-BE from nonP-BE.

References

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