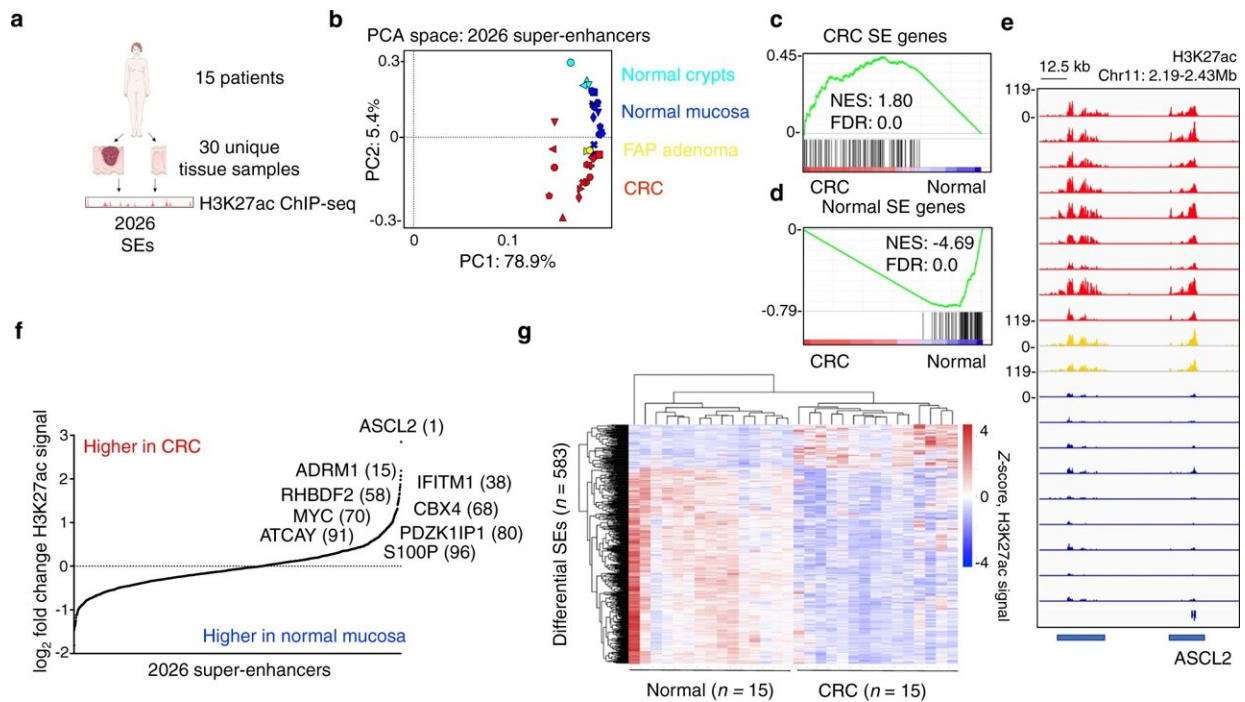


# Study identifies new gene that drives colon cancer

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Recurrently dysregulated super-enhancers in CRC patients. **a** Study overview. Figure adapted from SMART Servier Medical Art, reproduced with permission, licensed under a Creative Commons Attribution 3.0 unported license. **b** PCA of H3K27ac signal at 2026 SEs in CRC ( $n = 15$  independent tissue samples), normal mucosa ( $n = 15$ ), crypts ( $n = 4$ ), and FAP adenomas ( $n = 2$ ). **c, d** GSEA between SE proximal genes and differentially expressed genes between CRC and normal. **e** H3K27ac ChIP-seq track near *ASCL2*. Two proximal SEs are underlined. The y-axes of all ChIP-seq tracks are scaled the same. **f** 2026 SEs by  $\log_2$  fold change in H3K27ac signal with 12 candidate SE target genes based on overlap of ranking and recurrence annotated. **g** Heatmap of H3K27ac signal at 583 differentially expressed SEs ( $P$

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