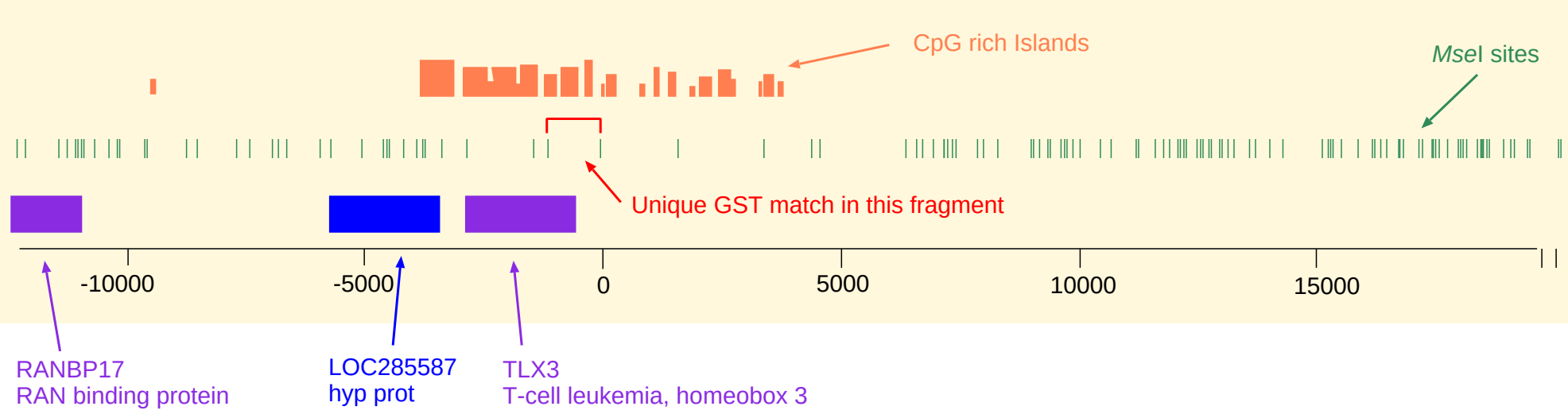
Finding heavily methylated regions in Human DNA

Methylation-regulation irregularities may play a role in cancer development. By running *Mse*I fragments from cancerous cell DNA through a methylation column and then collecting GSTs from the fragment ends, its is possible to locate the fragments to unique positions in chromosome sequences.

There are roughly 40 million *Mse*I sites in the Human Genome. A test protocol conducted on pancreatic cancer cell DNA has yielded over a hundred GSTS, the bulk matching unique sites in the Human Genome. This diagram shows the neighborhood of one such match in chromsome 5. The fragment matched contains a very CpG rich island, believe to play an important role in regulation in cancer cells.