Technology Overview

Besides Tp53, there are few genes identified as frequently mutated in esophageal adenocarcinomas (EAC). Assessing somatic chromosome alterations from SNP arrays, Brian Reid’s lab developed a risk prediction model using 29 risk prediction features representing 86 chromosomal regions for EAC with high accuracy (AUC score of 0.94), which outperforms Tp53. These researchers interrogated the cancer risk and progression of a 248 Barrett’s esophagus patient cohort spanning 25 years. The longitudinal study included 1,272 biopsies and 79 patients that progressed to early-stage EAC. This procedure for developing the prediction model can be adapted to other technology platforms, beyond SNP arrays, to assess genomic instability, disease progression, and prediction in other diseases.

Applications

- Detect and predict risk for EAC
- Provide guidance on treatment and/or prevention strategies based on risk and detection of EAC

Advantages

- Higher accuracy than Tp53
- Improve early diagnosis of EAC

Market Overview

In the US, Barrett’s esophagus affects about 1.3-5.6% of the general population. This condition is the strongest risk factor for esophageal cancer (EAC) with a 10 to 30 fold increased risk. EAC is one of the fast growing cancers in the world. It affects approximately 17,000 people each year in the US and in 2012, there were over 450,000 new cases worldwide. EAC has a poor prognosis and when caught early the 5-year survival rate jumps to 40% from 10%. In the US, $1.6 billion was spent on esophageal cancer-related expenditures in 2016 with $0.7 billion occurring in the last year of life. Additionally, the global cancer and tumor profiling market is expected to reach $61.8 billion by 2021 at a CAGR of 19% from 2016-2021.