Contaminants from outside the Arctic are transported to the Arctic regions. As an example, industrial emissions since the 19th century industrial revolution have resulted in increased concentrations of contaminants in ice cores from the Greenland ice sheet.

One of the reasons, that this is important is because the ongoing climate change is resulting in increased melting of the frozen environments in which some of these contaminants are stored.

In this paper we were interested in assessing whether the microbial communities from around the Greenland ice sheet have the genetic potential to resist and degrade contaminants.

We sampled microbe-mineral aggregates called cryoconite from 5 regions around the Greenland ice sheet as shown here in Figure 1.

Cryoconite melts into the ice due to its lower albedo and forms cryoconite holes. We extracted DNA from these cryoconite samples and obtained metagenomes, the total pool of genetic information from these samples.

From this metagenomic data we assessed the presence of genes known to confer resistance to or degradation of a selected list of contaminants known to the Arctic. These include PCB, PAH and the heavy metals lead and mercury.

The main result is shown here in Figure 4. Panel A shows the number of times genes for degradation of PCB were found in the samples from the 5 regions. Note that the counts are normalized to the counts of a set of bacterial housekeeping genes. What you can see in panel A is that the Tasiilaq samples from East Greenland had the highest counts of genes for PCB degradation. This is an interesting result since the human population of Tasiilaq has previously been shown to have the highest concentration of PCB in their fat tissue compared to other regions of Greenland.

Panel B shows the results for PAH degradation genes. PAHs, polycyclic aromatic hydrocarbons form by incomplete combustion. The highest numbers of genes for PAH degradation were found in samples from the Kangerlussuaq and Thule regions. These two regions are also the locations of the two largest airports of Greenland.

Panel E shows the non-normalized counts of genes for resistance to various heavy metals found in the 34 samples. We included this panel to show what the
actual counts were. The highest count is found in one of the Tasiilaq samples. In this sample genes for degradation of heavy metals were found more than 18000 times. With metagenomic data it can be difficult to say whether these counts are high or significant.

Therefore, as a negative control, we searched for the same genes in publicly available metagenomic datasets from healthy human guts, which we assumed not to be contaminated. For all of the genes that we found in the Greenland ice sheet the count in the human gut samples were zero with no exception.

We also clustered genomic fragments based on co-abundance across samples resulting in putative microbial genomes.

For seven out of 24 putative genomes, the closest neighbor found in the microbial RAST database was an organism isolated from a heavily contaminated habitat.

Based on these results we argue that we should not consider the Greenland ice sheet a pristine environment. This is because the presence of contaminants is suggested by the resistance and degradation potential of the resident microbial communities. Finally, we argue that we should pay more attention to the potential release of contaminants from the Greenland ice sheet.