





The heatmap displays the percentage of high-frequency alleles (0.1 and 0.2) across various populations, categorized by 'not_truncated' and 'truncated' groups. The y-axis lists populations: W_Scotland, Kat, cod3M, Celtic, Faroe, GB, Northsea, Coas, GM, W_Baltic, cod3NO, NE_Arctic, NGulf, cod3Ps, Iceland, and cod2J3KL. The x-axis lists the same populations. The legend indicates that 0.1 is represented by a light green color and 0.2 by a light orange color. The 'not_truncated' group shows high percentages of high-frequency alleles across most populations, while the 'truncated' group shows low percentages.

The heatmap displays the Total AUC for various datasets and methods, categorized into 'not_truncated' and 'truncated' groups. The color scale ranges from 500 (light blue) to 2000 (dark blue). The datasets listed on the y-axis are: W_Scotland, Kat, cod3M, Celtic, Faroe, GB, Northsea, Coas, GM, W_Baltic, cod3NO, NE_Arctic, NGulf, cod3p's, Iceland, and cod2J3KL. The methods listed on the x-axis are: W_Scotland, Kat, cod3M, Celtic, Faroe, GB, Northsea, Coas, GM, W_Baltic, cod3NO, NE_Arctic, NGulf, cod3p's, Iceland, and cod2J3KL. The 'not_truncated' group shows higher AUC values (darker blue) for most datasets compared to the 'truncated' group, which shows lower AUC values (lighter blue).

Cod Populations (increasing maximum age) split by truncated and not truncated distributions