得到一些测序数据集

39个流通池产生的数据

测序分析和碱基检测评估：

将reads比对到20号染色体，用以下三个方法评估，得到碱基检测器之间比较和同聚物解析

Oxford Nanopore Technologies: the Metrichor cloud-based service; Nanonet, an open-source recurrent neural network (RNN); and Scrappie, a transducer neural network

然后组装测序数据集，和illumina的比较

Comparisons against independent Illumina data from GM12878 yielded a slightly higher accuracy estimate of 95.74%.Despite the low consensus accuracy, contiguity was good。

分析不包括初级组装的数据，这些典型代表的重复序列，像长串连重复序列，短散在重复序列，卫星DNA等

The majority of sequences represented particular repeat classes e.g. LINEs, SINEs etc., as described in SI Figure 8. These were observed in similar proportion in the primary assembly, with the exception of satellite DNAs known to be enriched in human centromeric regions.

测定单核苷酸多态性和结构变异的敏感性

用SVTyper，一个贝叶斯的结构变异器检测，首先用illumina的数据得到变异结果，然后用改进版本的SVTyper来检测纳米孔测序的数据

nanopore data recovered approximately 93% of high-confidence SVs with a false-positive rate of approximately 6% (Methods). Illumina and nanopore genotypes agreed at 82% of heterozygous and 91% of homozygous alternate sites.

鉴定全基因组纳米孔中的结构变异，并与先前的PacBio进行比较。 给出插入，删除，重复和串联扩展/收缩的SV与GRCh38的直方图。分为小（50-500bp）和大（500-10000bp）类别的结构变异。 PacBio下的结果显示的插入和缺失率峰值在300bp。 相比之下，纳米孔显示出强大的缺失偏差，其中大多数变异是<500bp的缺失。预期Scrappie读数的组装将进一步减少观察到的缺失偏差。

5’胞嘧啶甲基化检测signalAlign

一种受控的甲基化样本