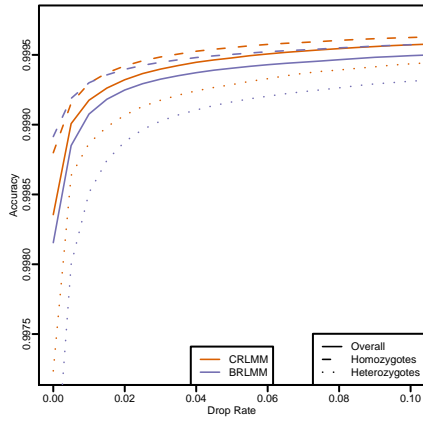
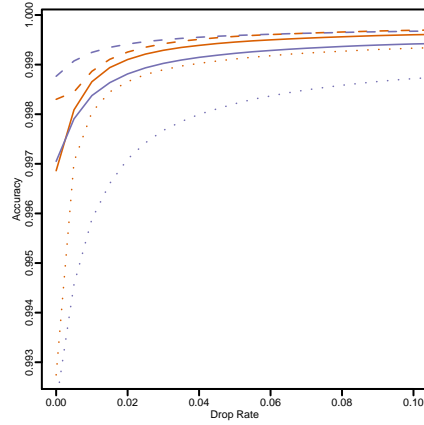


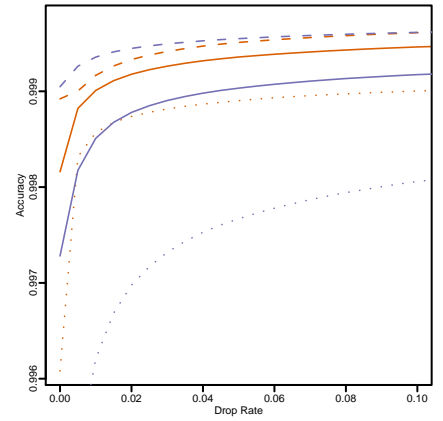
Supplemental Figure 1A



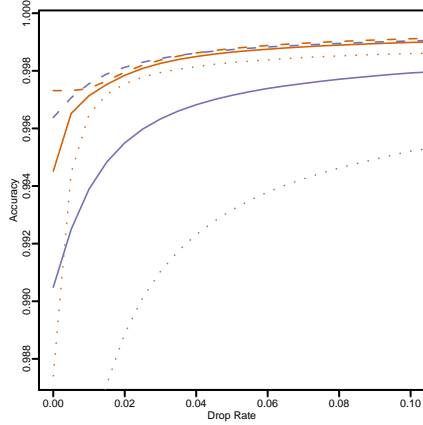
Supplemental Figure 1B



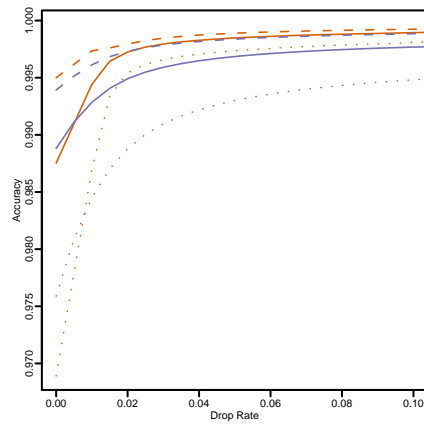
Supplemental Figure 1C



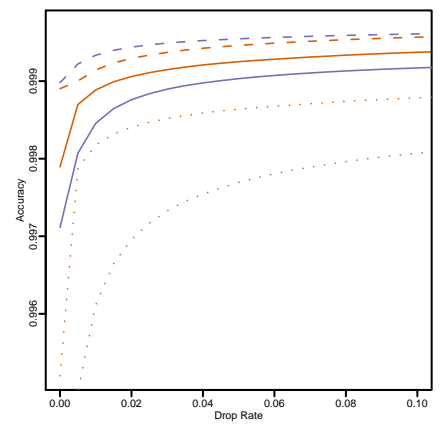
Supplemental Figure 1D



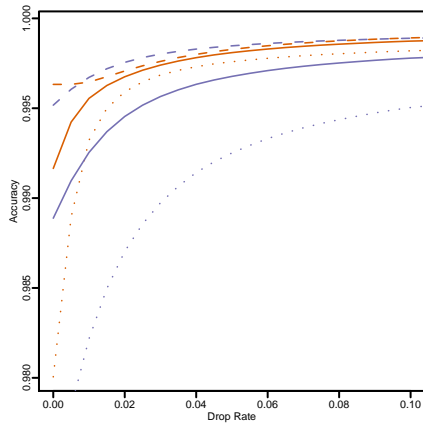
Supplemental Figure 1E



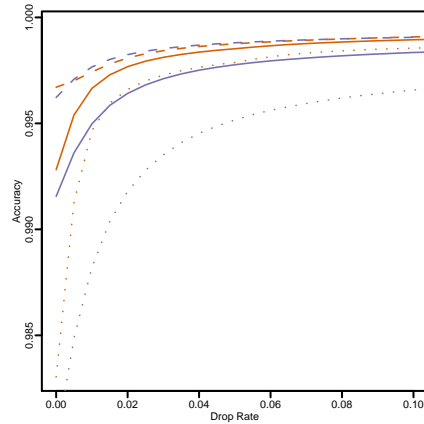
Supplemental Figure 1F



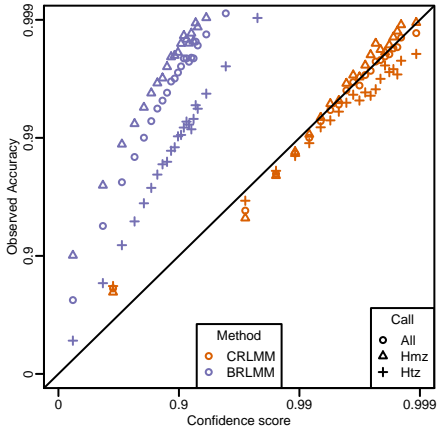
Supplemental Figure 1G



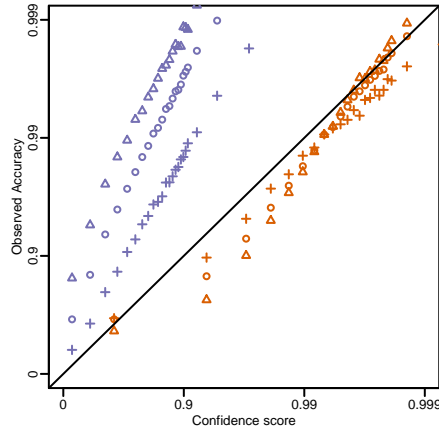
Supplemental Figure 1H



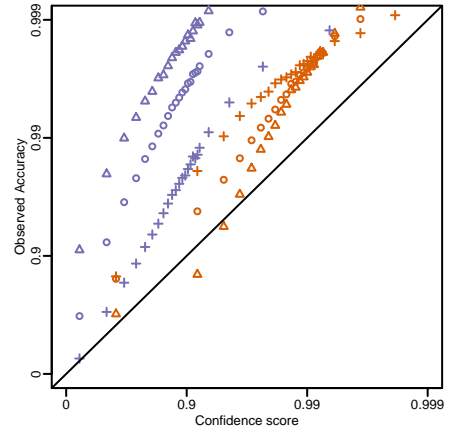
Supplemental Figure 2A



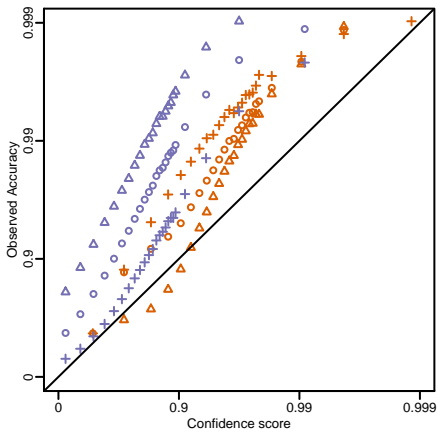
Supplemental Figure 2B



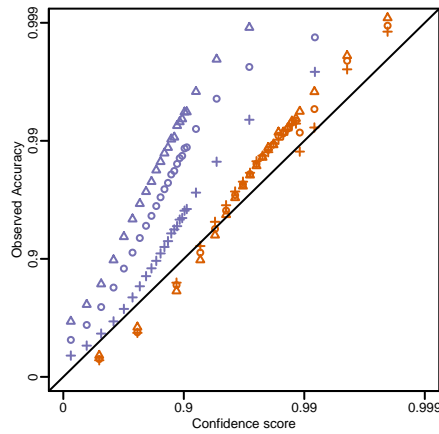
Supplemental Figure 2C



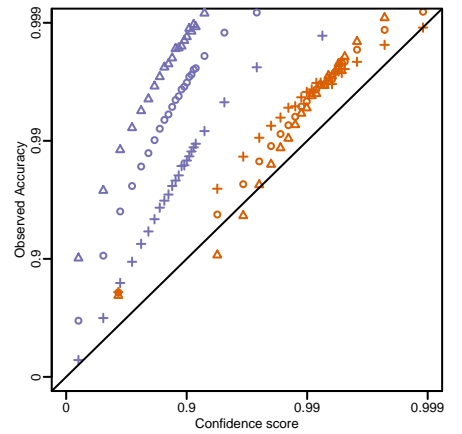
Supplemental Figure 2D



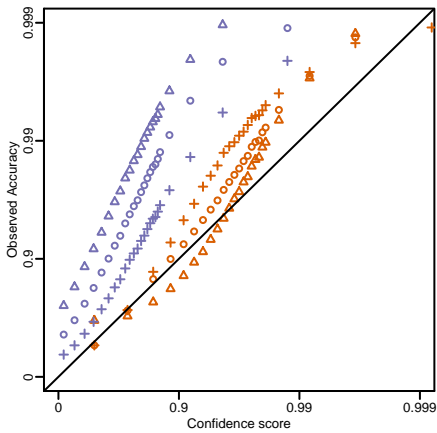
Supplemental Figure 2E



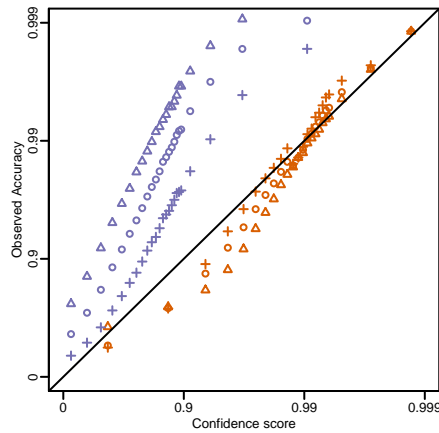
Supplemental Figure 2F



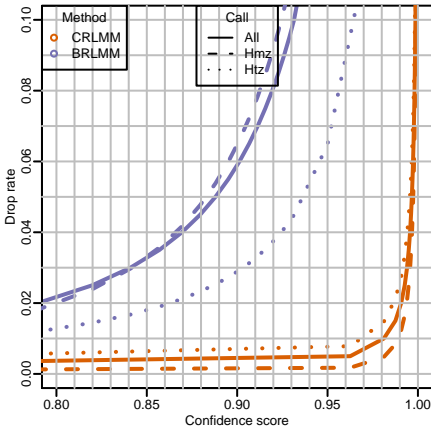
Supplemental Figure 2G



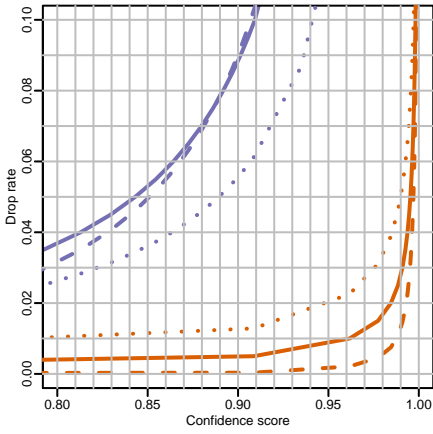
Supplemental Figure 2H



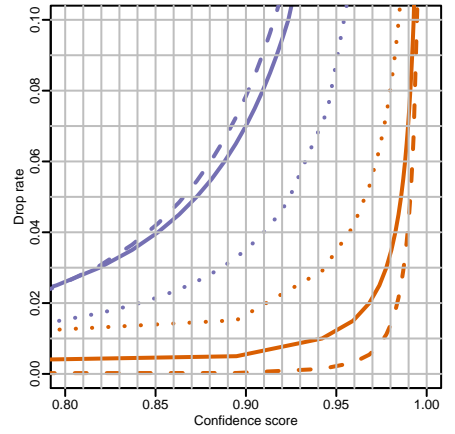
Supplemental Figure 3A



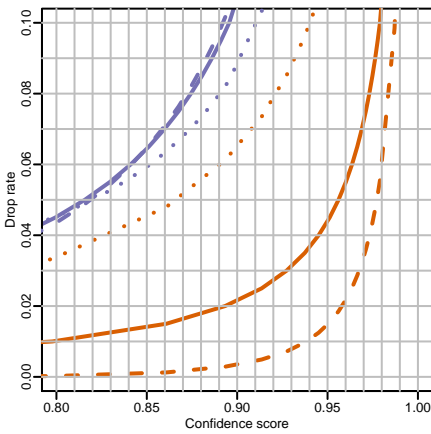
Supplemental Figure 3B



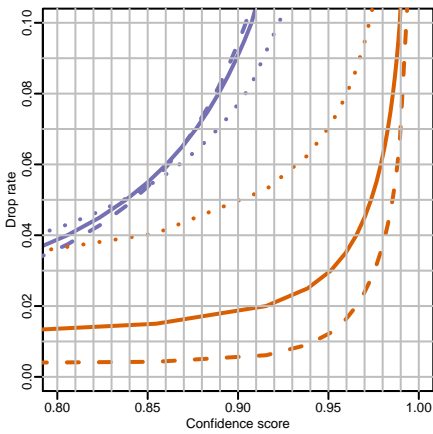
Supplemental Figure 3C



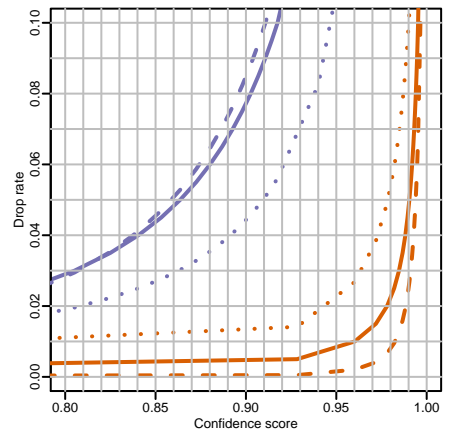
Supplemental Figure 3D



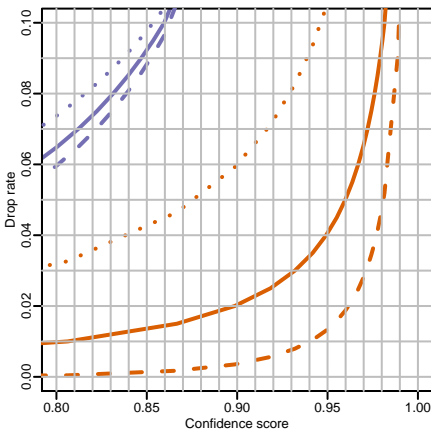
Supplemental Figure 3E



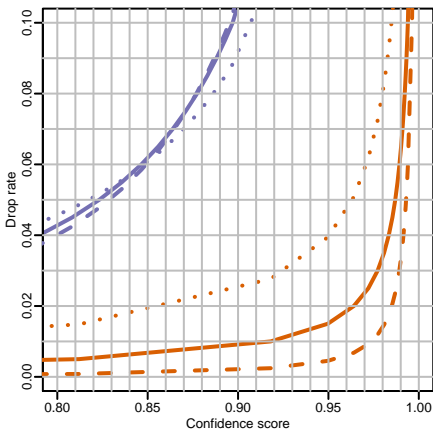
Supplemental Figure 3F



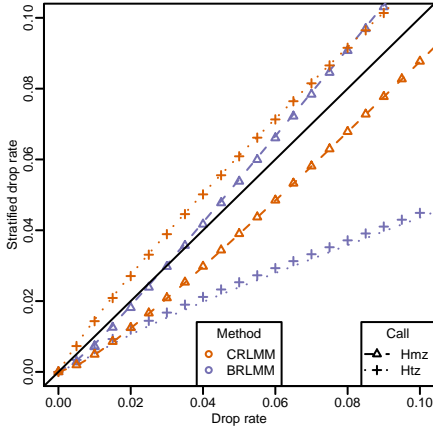
Supplemental Figure 3G



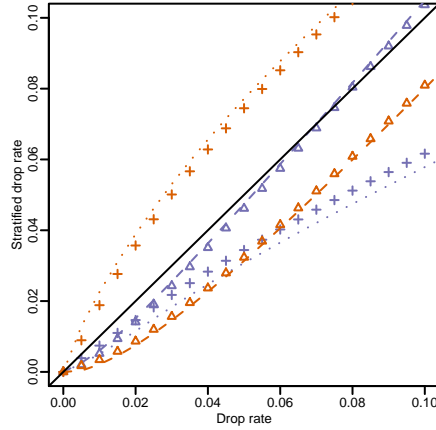
Supplemental Figure 3H



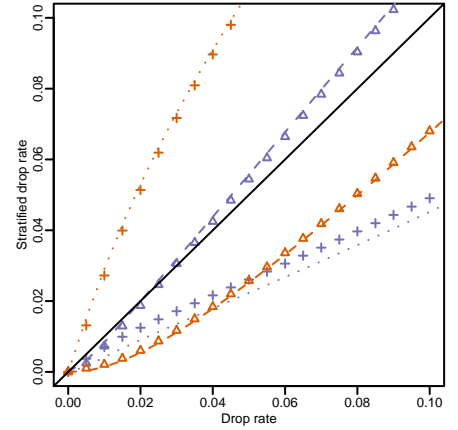
Supplemental Figure 4A



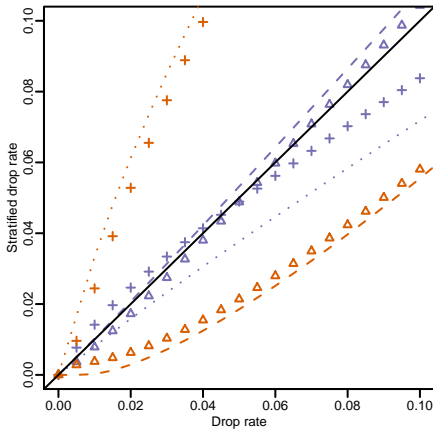
Supplemental Figure 4B



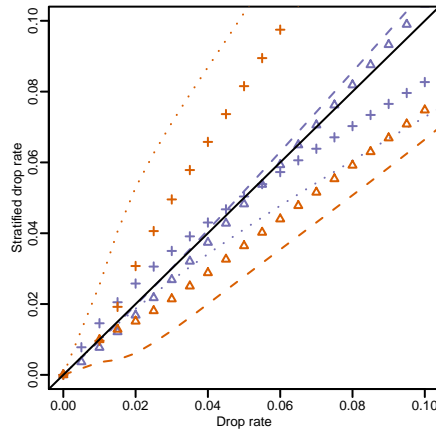
Supplemental Figure 4C



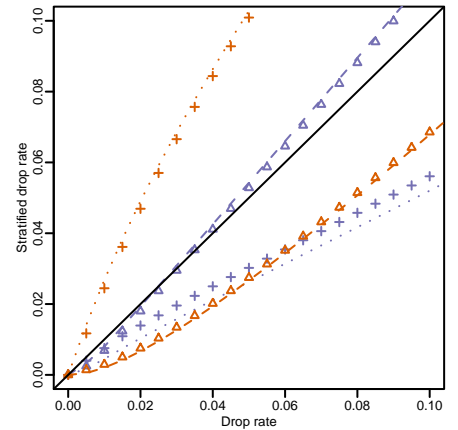
Supplemental Figure 4D



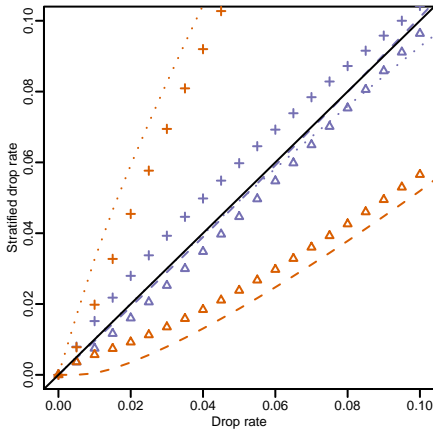
Supplemental Figure 4E



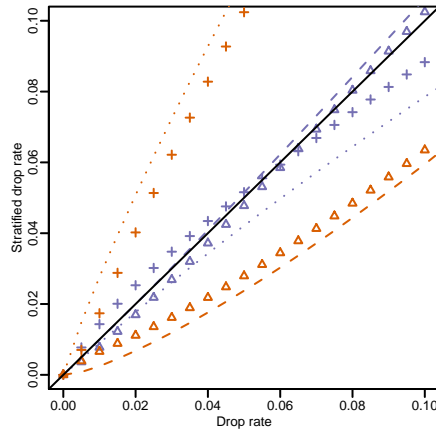
Supplemental Figure 4F



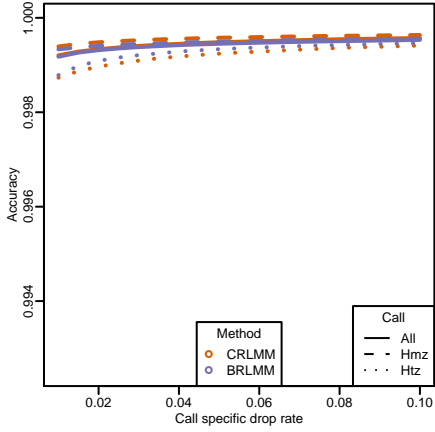
Supplemental Figure 4G



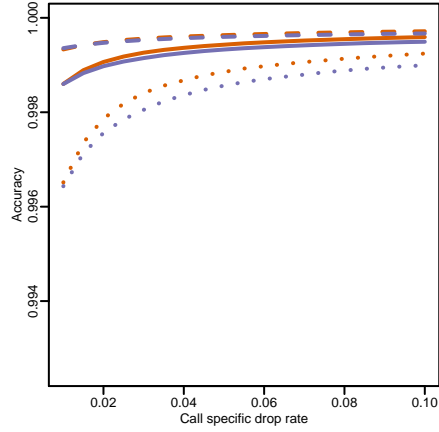
Supplemental Figure 4H



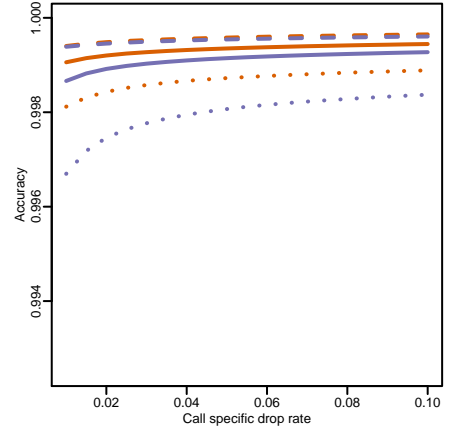
Supplemental Figure 5A



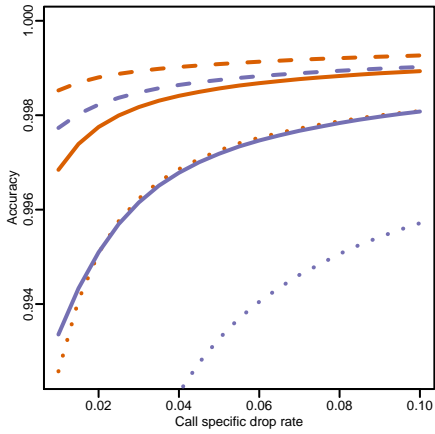
Supplemental Figure 5B



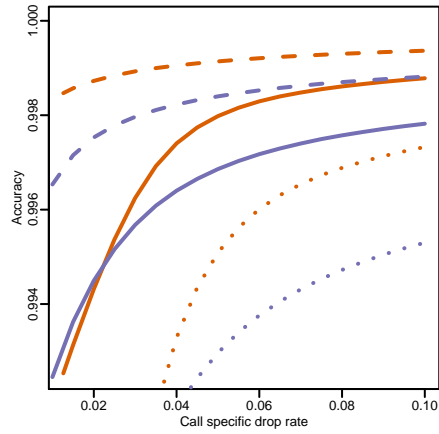
Supplemental Figure 5C



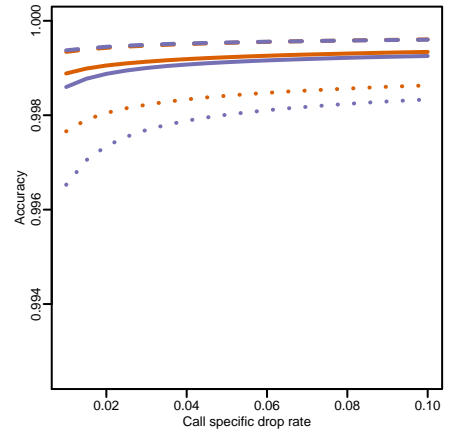
Supplemental Figure 5D



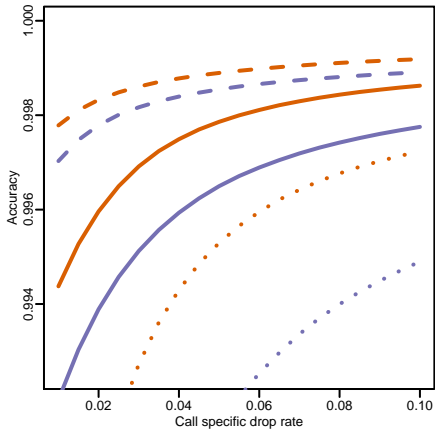
Supplemental Figure 5E



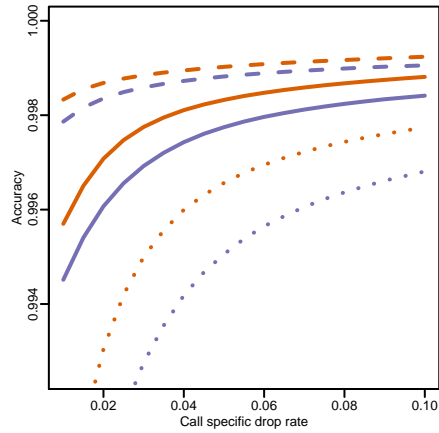
Supplemental Figure 5F



Supplemental Figure 5G



Supplemental Figure 5H



## SUPPLEMENTAL FIGURE LEGENDS

**Supplemental Figure 1:** Accuracy versus dropped rate plots (ADPs) comparing CRLMM and BRLMM for each HapMap dataset are shown in separate plots. The curves are further stratified between heterozygotes and homozygotes as determined by the HapMap gold standard. A) 269 Affymetrix high-quality XBA arrays. B) 269 Affymetrix high-quality HIND arrays. C) 270 Affymetrix high-quality STY arrays. D) 152 Broad Institute first-pass STY arrays. E) 95 Affymetrix first-pass STY arrays. F) 270 Affymetrix high-quality NSP arrays. G) 152 Broad Institute first-pass NSP arrays. H) 95 Affymetrix first-pass NSP arrays.

**Supplemental Figure 2:** Confidence measure versus accuracy plots (CAPs) comparing CRLMM and BRLMM for each HapMap dataset are shown in separate plots. The curves are further stratified between heterozygotes and homozygotes as determined by the HapMap gold standard. A) 269 Affymetrix high-quality XBA arrays. B) 269 Affymetrix high-quality HIND arrays. C) 270 Affymetrix high-quality STY arrays. D) 152 Broad Institute first-pass STY arrays. E) 95 Affymetrix first-pass STY arrays. F) 270 Affymetrix high-quality NSP arrays. G) 152 Broad Institute first-pass NSP arrays. H) 95 Affymetrix first-pass NSP arrays.

**Supplemental Figure 3:** The drop rate versus confidence measure are shown for CRLMM and BRLMM. The curves are further stratified between heterozygotes and homozygotes as determined by the HapMap gold standard. A) 269 Affymetrix high-quality XBA arrays. B) 269 Affymetrix high-quality HIND arrays. C) 270 Affymetrix high-quality STY arrays. D) 152 Broad Institute first-pass STY arrays. E) 95 Affymetrix first-pass STY arrays. F) 270 Affymetrix high-quality NSP arrays. G) 152 Broad Institute first-pass NSP arrays. H) 95 Affymetrix first-pass NSP arrays.

**Supplemental Figure 4:** Validity of drop rates using called data. Drop rates stratified by homozygote and heterozygote calls are plotted against the non-stratified drop rates. The stratification is performed with HapMap gold standard calls (lines) and algorithm

derived calls (triangles and crosses). That the curves derived from HapMap and algorithm results are by and large equivalent demonstrates call rates for homozygotes and heterozygotes from algorithms are valid. Thus in the end, by also using the confidence metric of CRLMM, one can achieve a data set in which all calls are both above a pre-specified accuracy threshold and have equivalent drop rates between homozygotes and heterozygotes. A) 269 Affymetrix high-quality XBA arrays. B) 269 Affymetrix high-quality HIND arrays. C) 270 Affymetrix high-quality STY arrays. D) 152 Broad Institute first-pass STY arrays. E) 95 Affymetrix first-pass STY arrays. F) 270 Affymetrix high-quality NSP arrays. G) 152 Broad Institute first-pass NSP arrays. H) 95 Affymetrix first-pass NSP arrays.

**Supplemental Figure 5:** ADPs are plotted as in Supplemental Figure 1 except that the drop rate is forced to be the same for both heterozygous and homozygous calls. A) 269 Affymetrix high-quality XBA arrays. B) 269 Affymetrix high-quality HIND arrays. C) 270 Affymetrix high-quality STY arrays. D) 152 Broad Institute first-pass STY arrays. E) 95 Affymetrix first-pass STY arrays. F) 270 Affymetrix high-quality NSP arrays. G) 152 Broad Institute first-pass NSP arrays. H) 95 Affymetrix first-pass NSP arrays.