



**Figure S4: Identification of variant KPC-2 (in *K. pneumoniae*) from spiked urine samples.** Overview on array data obtained after DNA extraction from spiked urine samples (10 dilution steps + no template control (NTC)) followed by hybridization. Listed are the average absolute perfect match (PM) signal intensities for every SNP position of sense and anti-sense probes. In addition the corresponding  $MM_{\max}/PM$  ratios are presented for every SNP position. Once the threshold is reached ( $MM_{\max}/PM > 0.7$ ) the probes are not used for discrimination anymore (marked in dark grey). The same applies for the average absolute PM signal. Once the signal intensity is below the LOD, the probe set is not used for discrimination anymore, also shown in dark grey. Furthermore, the standard deviation (SD) is monitored and a probe set is flagged once the SD is larger than 30% of the PM signal, shown in light grey. The probe sets which fulfil all criteria are then used for discrimination and the identified variant is shown at the bottom of the table. This is shown for extractions carried out with Qiagen and Norgen in duplicates. In all cases variant KPC-2 was correctly identified to a concentration of 120 cells / ml urine (Qiagen) and 120 and 40 cells / ml urine (Norgen). A summary of the final results is shown in Figure 4.