**Thank you for your interest to present your work at xMAP® Connect 2017!**

* Prepare a presentation title, the title included on the submission should be suitable for published material.
* Abstract text is limited to 3000 characters (approx 500 words).
* We ask to use 4 core elements: 1) background and aim, 2) methods, 3) results, 4) conclusions. We kindly ask you to use the format below.
* Please ensure the submission has been approved by all authors.
* By submitting an abstract, you agree to be present the 8th and 9th of November at the congress, should your abstract be selected.
* Please indicate if you would like to be a speaker or present a poster.

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| **Title:**  **25-Plex Malaria MagPlex-TAG™ assay to detect human host and parasite genetic markers** |
| 1) Background and aim:  In malaria field studies, assessment of host and parasite genetic markers is often necessary to understand parasite epidemiology. However, current assays are time consuming and require a high volume of template. Here, we developed a MagPlex-TAG™ microsphere based multiplex assay that analyses multiple single nucleotide polymorphisms (SNPs) in one reaction.  Our assay contains eight epidemiologically important human markers such as glucose-6-phosphate dehydrogenase (G6PD) deficiency SNPs and common haemoglobin mutations as well as seventeen parasite markers of drug resistance.  2) Methods:  The MagPlex-TAG™ microsphere assay developed here requires only 5 µl of template DNA for the multiplex reactions. The twenty-five markers are combined in an allele specific primer extension (ASPE) and after hybridisation, read on a MAGPIX®.  3) Results:  In a pilot study on 120 field samples collected in Burkina Faso and in The Gambia, the MagPlex-TAG™ microsphere assay gave similar results for all samples compared to established genotyping assays. The assay is sensitive and fast, and results for 96 samples are available in 6-7 hours.  4) Conclusion:  We believe this multiplex assay will become an important tool for malaria epidemiology studies as it allows the identification of individuals likely to develop haemolysis during antimalarial treatment (G6PD deficient individuals) and of individuals that are protected against or at risk of severe malaria disease (e.g. individuals with haemoglobin S mutation are protected). It will also allow rigorous monitoring of the drug resistance status in patient samples, which is important to adequately inform government and policy makers. |