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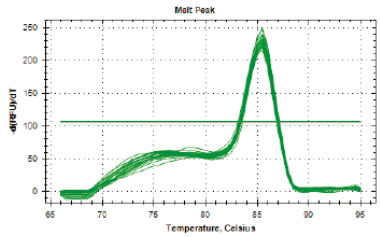

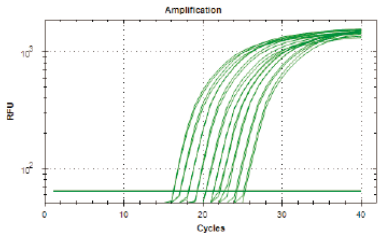

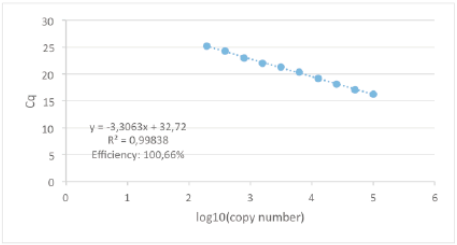

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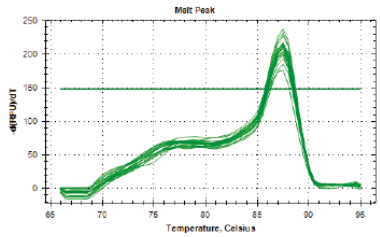

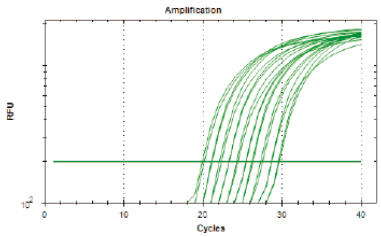

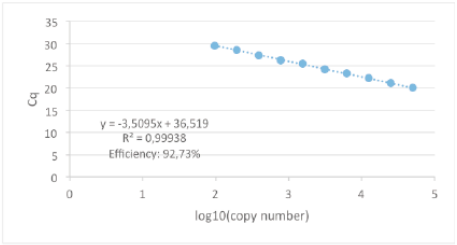

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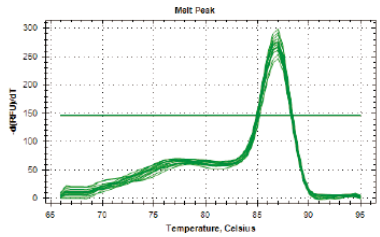

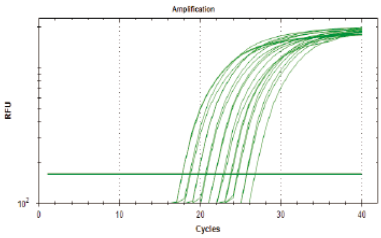

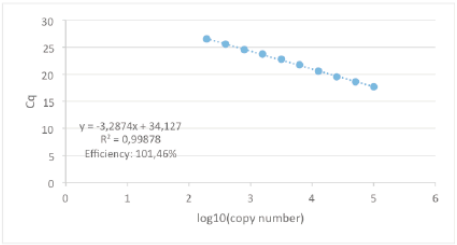

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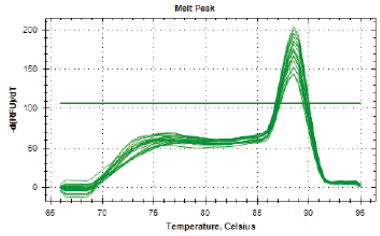

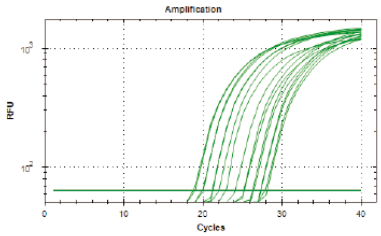

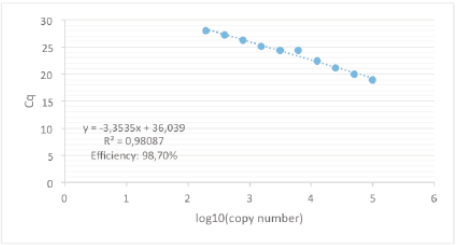

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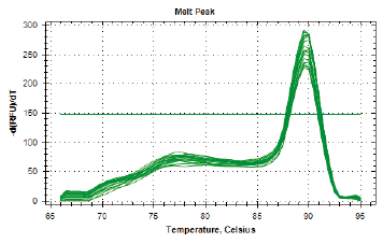

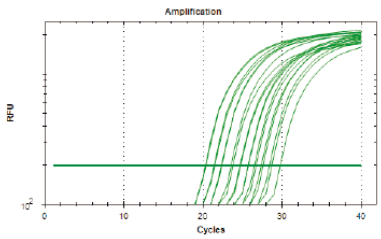

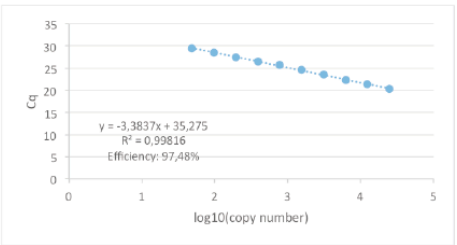

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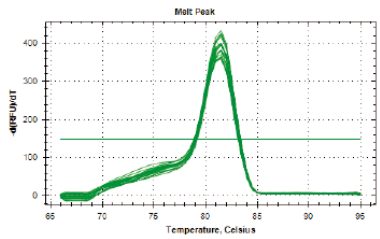

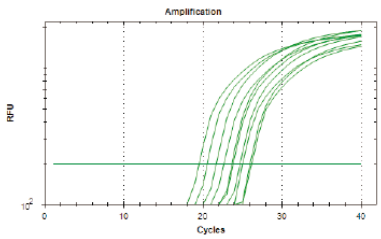

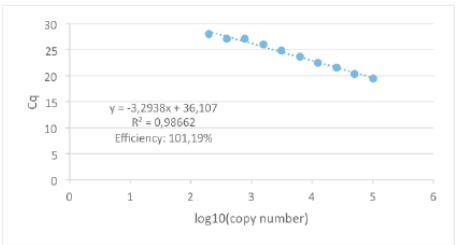

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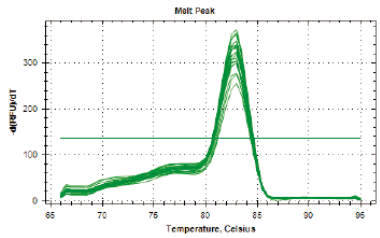

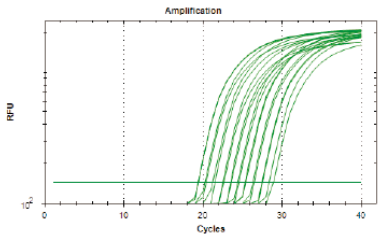

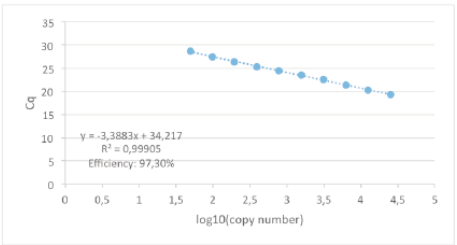

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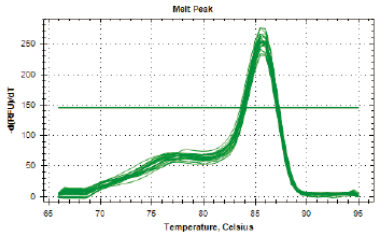

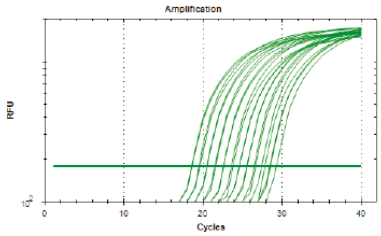

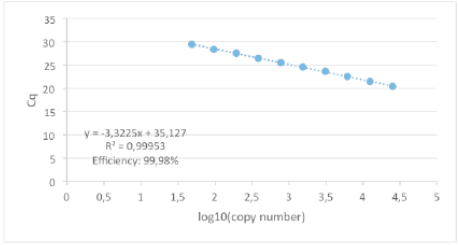

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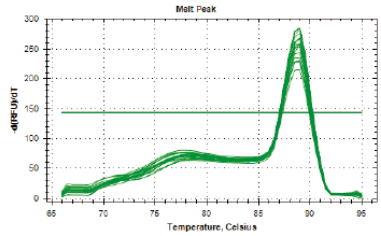

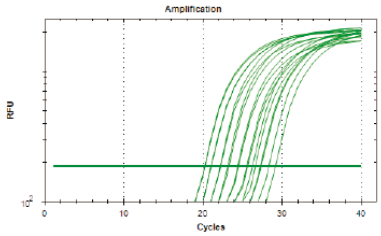

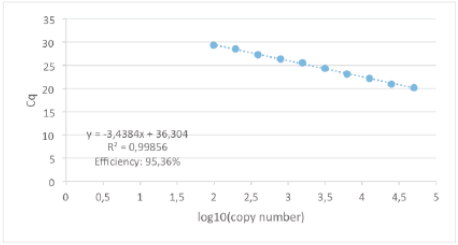

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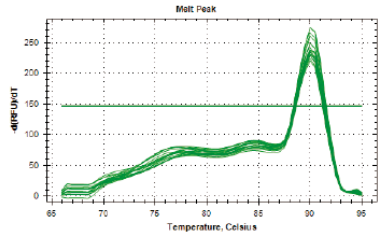

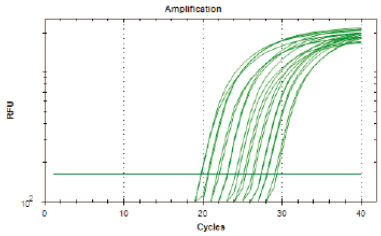

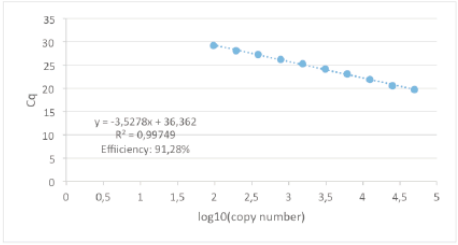

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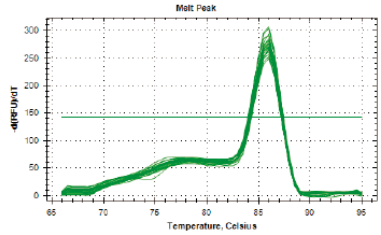

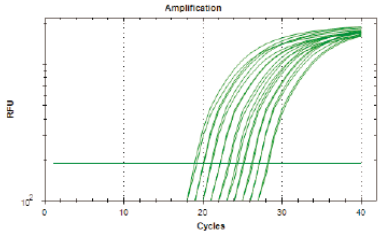

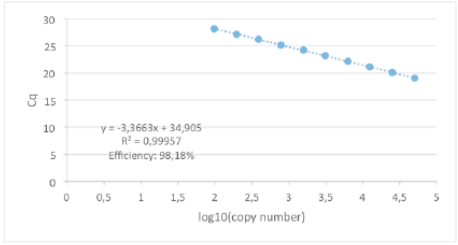

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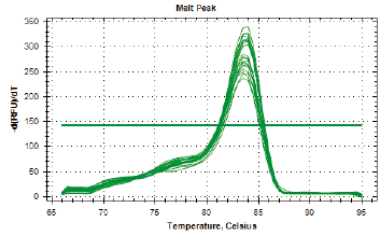

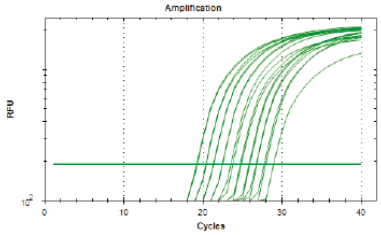

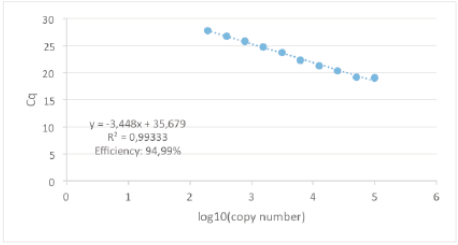

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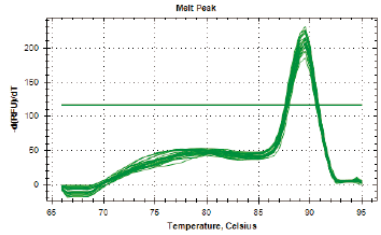

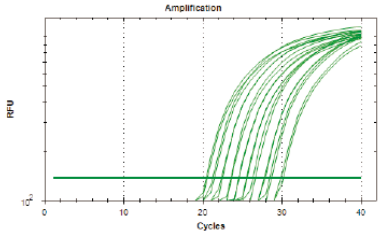

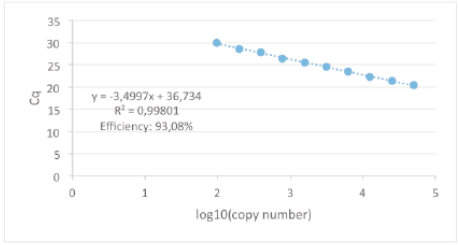

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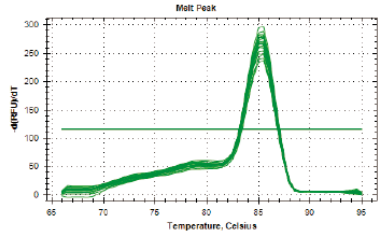

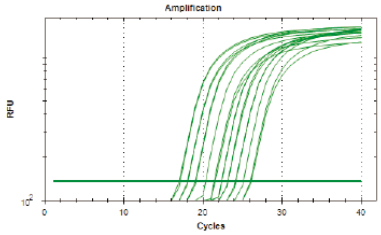

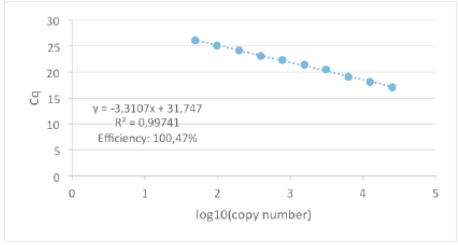

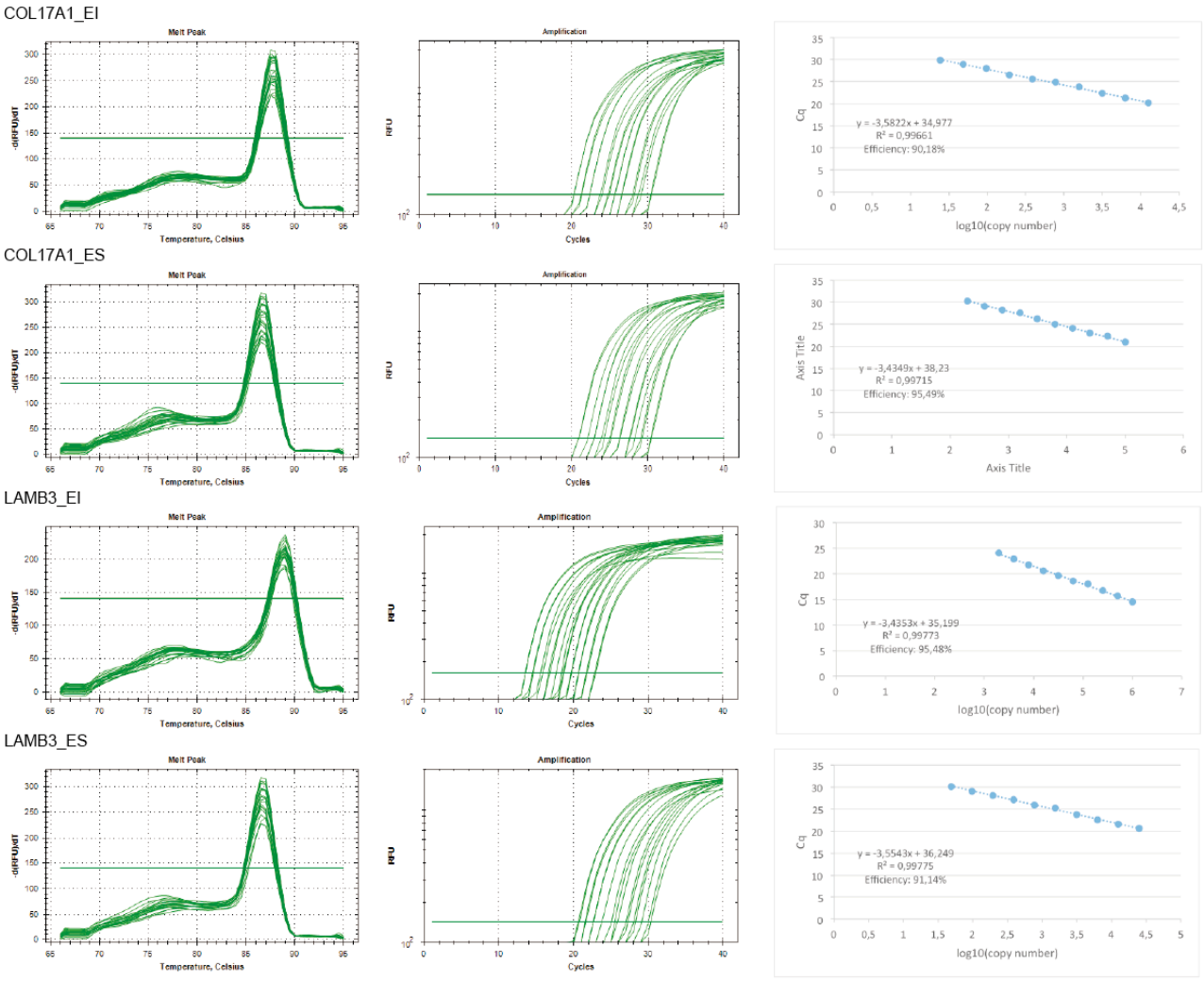

Supplemental Figure S6. Amplification efficiency determination via standard curve analysis. The amplification efficiency of the qRT-PCR for each primer set used in Figure 1C was determined by analyzing serially diluted cDNAs. For each set of primers melt peak curves, amplification traces and corresponding calibration curves were shown and slope and amplification efficiency were calculated. A single peak in the melt peak curves indicates that the qRT-PCR reactions are specific and a single product is amplified. Slope of calibration curves comprised between -3.1 and -3.6, R^2 values that demonstrated a good linear relationship between Cq values and the cDNA concentration and amplification efficiency comprised between 90% and 110% for each set of primers are shown in the standard curves and are indicative of a suitable condition for qRT-PCR.