in this study. Small study numbers may explain our failure to replicate the findings of Wachman et al, in whose study SNPs in both *OPRM1* and *COMT* predicted NAS.[9]

The strengths of this small pilot study are that mothers and babies were cared for in one facility, with a practiced and consistent approach to management of NAS. Persons caring for the babies were unaware of the infant's genotype. Even within a small number of patients, genomic variation in *CYP2B6* between treated and untreated babies was significant.

Future studies should consider maternal genotype and its relationship to infant genotype and/or the prediction of NAS as well as associated maternal polydrug use.

Conclusion

Genomic variation in *CYP2B6* in the newborn is associated with severity of NAS; this has not previously been reported. Better understanding of the role of pharmacogenetics in the etiology of NAS may result in improved care for mother and baby.

Note
This study was undertaken as part of a PhD cosponsored by Bournemouth University and Randox. Royal Bournemouth Hospital donated the space for sample analysis.

Authors' Contributions
Helen Mactier was involved in study concept and sample collection and wrote the manuscript. Poppy McLaughlin analyzed samples and data, contributed to manuscript revisions, and approved the final version. Cheryl Gillis recruited patients and collected samples, contributed to manuscript revisions, and approved the final version. Michael David Osselton conceived the study, oversaw analysis of samples, contributed to manuscript revisions, and approved the final version.

Conflict of Interest
None.

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