Bankoff et al. Table 2

	Human reference coding region size (bp)	BEAT with aye-aye sequence reads[1]			Untrimmed aye-aye *de novo* assembly[2]				Trimmed aye-aye *de novo* assembly[2]			
Gene		bp recovered	% coverage	% identity to reference	bp recovered	% coverage	% identity to reference	% identity to BEAT	bp recovered	% coverage	% identity to reference	% identity to BEAT
CDH23	8976	8952	99.73	92.76	7863	87.60	92.81	98.99	7139	79.53	93.14	99.52
KCNQ4	1713	1713	100	94.74	1013	59.14	90.97	95.63	815	47.58	91.78	96.93
OTOF	5634	5605	99.49	92.73	4190	74.37	91.63	98.56	3854	68.41	92.53	99.77
PCDH15	4194	4189	99.88	94.84	4009	95.59	94.51	98.98	3581	85.38	94.86	99.75
PJVK	840	840	100	96.07	840	100	96.07	100	840	100	-	-
SLC26A5	2016	2016	100	94.81	1968	97.62	94.70	98.93	1687	83.68	95.14	99.70
TMC1	2116	1969	93.05	94.29	1886	89.13	92.21	96.04	905	42.77	94.59	99.11

Table 2. Comparison of *de novo* genome assembly and BEAT methods for reconstruction of aye-aye gene coding regions using the same shotgun sequence read data for both methods.

[1] Analysis based on BEAT reconstructions from the same shotgun sequencing read data used in Perry, Reeves et al. (2012), a subset of the sequence read data used in the full analysis of this paper.

[2] Analysis based on BLAST reconstructions of scaffolds from aye-aye *de novo* assembly published in Perry, Reeves et al. (2012). Sequences assembled from the aye-aye *de novo* assembly were scanned for regions with more than one non-identical mapping scaffold; these scaffolds were allowed to contribute to the consensus in the "Untrimmed" group, and removed from the "Trimmed" group.