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Cover image: Pictured is a harbor seal (*Phoca vitulina*). Joseph I. Hoffman et al. used high-throughput sequencing to accurately estimate the genome-wide heterozygosity of individual seals stranded on the Dutch Waddensee coast. Without using a pedigree, this approach revealed strong evidence of reduced resistance to lungworm infection due to inbreeding in this natural population. See the article by Hoffman et al. on pages 3775–3780. Image courtesy of Oliver Krüger (Bielefeld University, Bielefeld, Germany).

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CORRECTIONS