Figure S3: PR curve for transcripts. If any transfrag that overlaps any part of a transcript (as opposed to only the exons) is scored positive, the van Bakel et al. dataset [1] shows much higher precision, indicating that many of their negative calls (transfrags detected outside of exons) from Figure 1 result from transfrags in introns. A similar analysis for the Clark et al. data is shown for comparison.