Table S5 Comparison of gene-level abundance results from alignment of 30 million simulated DO reads to NCBIM37 and individualized DO transcriptomes

			Number of genes with estimates x% from Ground Truth			
Aligned to	**Mismatches Allowed**	**Genes above threshold**	**< 5%**	**< 10%**	**> 10%**	**> 50%**
30M DO Reads						
NCBIM37	3	13,260	7,371	10,995 (83%)	2,265 (17%)	355
DO IRG	3	13,209	9,829	11,696 (89%)	1,501 (11%)	262
NCBIM37	0	13,222	2,301	4,800 (36%)	8,422 (64%)	728
DO IRG	0	13,196	9,136	11,169 (85%)	2,012 (15%)	249

Gene estimates in the simulated DO sample are improved by read alignment to the individualized transcriptome (≤3 mismatches), yielding 33% more gene estimates (N= +2,458) within 5% of the ground truth value and 34% fewer estimates (N= -764) that deviate more than 10% from the ground truth. Gene-level abundance results for perfect matching reads (i.e. 0 mismatches) are also shown.