

Supplementary material

Supplementary Table S1. Summary of raw reads generated for each library from IsoSeq, RNAseq and CAGEseq sequencing

	Isoseq			RNA seq	CAGEseq
	ZMW*	Full-length reads	Mapped reads	Raw reads	Raw reads
Fetal Liver	557,868	205,952	205,904	78,492,675	15,141,599
Fetal Lung	519,277	394,189	394,170	90,713,379	2,944,730
Liver	459,570	342,585	342,517	77,648,618	19,113,216
Lung	NA**	NA**	NA**	69,662,155	37,473,013
Blood	574,977	410,796	408,585	68,392,292	4,986,447
Thyroid	570,816	403,006	402,991	67,905,471	18,954,871
Spleen	486,355	376,649	376,635	74,322,017	6,164,132
Kidney	521,514	370,574	370,550	76,661,390	20,244,459
Muscle	315,986	211,985	211,953	80,903,660	7,414,926
Ovary	490,676	364,170	364,116	NA**	12,315,069
Uterus	530,312	394,387	394,307	NA**	12,211,715

* ZMW means Zero mode waveguide

** NA means sequencing data is not available

Supplementary Table S2. Summary of read length for each tissue generated from ISOseq sequencing

Library	Average read length	Maximum length
Blood	1647	6696
Foetal Lung	1847	6997
Foetal Liver	1563	6178
Kidney	2056	10305
Liver	1438	6284
Muscle	1375	5508
Ovary	1381	4557
Spleen	1949	8202
Thyroid	2141	7474
Uterus	1619	10096

INTRON SPANNING READS FROM RNA-SEQ DATA

RNAseq intron spanning reads were used to support the presence of novel isoform. RNAseq alignments were visualised in IGV and intron spanning read counts were extracted directly from the alignments.

Supplementary Table S3. Intron spanning read for IGF1 from RNAseq data.

	INTRON 1	INTRON 2	INTRON 3
Spleen	87	90	82
Thyroid	70	74	77

Supplementary Table S4. Intron spanning read for RPS20 from RNAseq data.

	INTRON 1	INTRON 2	INTRON 3
Kidney	1062	4304	4295
Blood	3190	13110	12963
Foetal liver	2737	11499	11892
Foetal lung	1961	7668	7864
Liver	844	3128	3386
Muscle	1231	5070	5054
Spleen	4954	19253	19210
Thyroid	6169	23903	24789

Supplementary Table S5. Intron spanning read for RTKN2 from RNAseq data.

	1	2	3	4	5	6	7	8	9	10	11
Foetal lung	1	20	12	26	19	10	5	14	22	21	11
Thyroid	6	10	5	12	7	1	5	4	4	5	4
Spleen	-	-	2	2	2	4	1	2	3	2	1

Supplementary Table S6. Intron spanning read for SERPINA7 from RNAseq data.

	INTRON 1	INTRON 2	INTRON 3	INTRON 4
Foetal liver	1505	1297	1526	321
Foetal lung	533	395	446	87

Supplementary Figure S1: Histogram shows the size distribution of all ISO-seq libraries.

