Supplementary Table 1. List of raw reads and per sample assembly statistics.

BioSample	Data	ID	Tissue	Number of raw reads	Effective library size	Normalized expression	Gene Ontology term assignment				
							Transcript number	Unigene number	Normalized expression		Representative terms (average unigene expression)
SAMN15147518	SRR11936462	G	**gonad**	51,105,632	1,908,614	523,444	23130	14203	365,838	70%	biological_process / reproductive process (93)
SAMN15147519	SRR11936461	jel	**intestine**	50,670,370	1,070,765	933,160	30013	16363	657,294	70%	molecular_function / chitin binding (3215)
SAMN15147520	SRR11936460	Mozg	**brain**	56,467,492	1,309,984	762,752	31971	17811	510,813	67%	molecular_function / structural constituent of myelin sheath (798)
SAMN15147521	SRR11936459	Ngl	**head kidney**	40,697,110	1,327,568	752,763	30570	16623	530,929	71%	biological_process / antigen processing and presentation (538)
SAMN15147522	SRR11936458	oko	**eye**	49,715,066	1,060,061	942,593	31501	17534	692,401	73%	molecular_function / structural constituent of eye lens (1985)
SAMN15147523	SRR11936457	se	**heart**	65,349,164	797,850	1,252,196	28974	15950	973,445	78%	biological_process / circulatory system process (1365)
SAMN15147524	SRR11936456	skd	**skin, lower body part**	46,383,752	523,601	1,907,930	25730	15029	1,538,874	81%	biological_process / response to cold (3775)
SAMN15147525	SRR11936455	skg	**skin, upper body part**	51,767,234	1,161,900	859,983	30859	16825	614,989	72%	biological_process / response to cold (5069)
SAMN15147526	SRR11936454	sled	**spleen**	53,686,144	1,298,240	769,680	28407	15928	559,540	73%	molecular_function / oxygen carrier activity (6452)
SAMN15147527	SRR11936453	W	**liver**	44,331,924	417,704	2,392,067	23737	13870	1,952,990	82%	molecular_function / lipid transporter activity (5285)

Filtering of the assembly by expression level was performed according to the Trinity manual available at:
https://github.com/trinityrnaseq/trinityrnaseq/wiki/Trinity-Transcript-Quantification
The following scripts, distributed with Trinity were used to estimate transcript abundance:
First,
$TRINITY_HOME/util/align_and_estimate_abundance.pl
was used to count reads mapping to each contig, separately for each sample.
Then,
$TRINITY_HOME/util/abundance_estimates_to_matrix.pl
was run to construct a matrix of normalized expression values. These normalized expression values are formally in “transcripts per million of reads” (TPM). The matrix was then utilized to perform filtering by expression by tritoconstrictor script.
After all filtering steps the final assembly was again subject to the same abundance estimation and normalisation procedure, and the table presents the results of this analysis.
For each tissue/sample large proportion of the expression belongs to transcripts with assigned GO terms, providing tissue-specific expression profile.
Expression values for individual transcripts are listed in Supplementary Table 3.