

Table S1. Information on the Donors Whose Tissues Were Used in the Present Study

Donor ID	Age (y)	Gender	Tissue	Past Medical History
9478	87	M	temporal lobe, gray matter	Multiple infarcts/CVA
9499	81	M	temporal lobe, gray matter	Multiple lacunar infarcts
9517	83	M	temporal lobe, gray matter	Lacunar infarcts
10337	86	M	temporal lobe, gray matter	Multiple lacunar infarcts
30	76	M	Retina and RPE	Stroke, Alzheimer's disease, peripheral vascular disease, abdominal aortic aneurysm, hypertension, chronic obstructive pulmonary disease, peptic ulcer disease, depression.
32	68	M	Retina and RPE	Ischemic bowel infarction, coronary bypass, chronic kidney disease, hypertension, osteoarthritis, tobacco use, occasional EtOH use.
38	79	M	Retina and RPE	Sepsis, diabetes for 10 years, chronic lymphocytic leukemia, hypertension, osteoarthritis, deep vein thrombosis, stroke
39	82	M	Retina and RPE	Lung cancer, end stage renal disease, history of chemo- and radiation treatment.

Table S2. Peptides and MRM Transitions.

MRM transitions (<i>m/z</i>)				
Protein/Peptides	Q1 (charge)	Q3 (type, charge)		
CYP7B1				
AFSISQLQK	511.29 (+2)	803.46 (y^7 ,+1)	716.43 (y^6 ,+1)	603.35 (y^5 ,+1)
¹⁵ N-AFSISQLQK	517.27 (+2)	813.43 (y^7 ,+1)	725.40 (y^6 ,+1)	611.32 (y^5 ,+1)
QVFEPQLLK	551.32 (+2)	874.50 (y^7 ,+1)	727.44 (y^6 ,+1)	598.39 (y^5 ,+1)
¹⁵ N-QVFEPQLLK	557.30 (+2)	883.48 (y^7 ,+1)	735.41 (y^6 ,+1)	605.37 (y^5 ,+1)
CYP11A1				
NFLPLLDVSR	622.85 (+2)	983.59 (y^9 ,+1)	870.50 (y^8 ,+1)	547.28 (y^5 ,+1)
¹⁵ N-NFLPLLDVSR	630.33 (+2)	995.55 (y^9 ,+1)	881.47 (y^8 ,+1)	555.26 (y^5 ,+1)
YLVNDLVLR	552.82 (+2)	828.49 (y^7 ,+1)	729.43 (y^6 ,+1)	615.38 (y^5 ,+1)
¹⁵ N-YLVNDLVLR	559.31 (+2)	839.46 (y^7 ,+1)	739.40 (y^6 ,+1)	623.36 (y^5 ,+1)
CYP27A1				
LYPVVPTNSR	573.32 (+2)	869.48 (y^8 ,+1)	673.36 (y^6 ,+1)	574.29 (y^5 ,+1)
¹⁵ N-LYPVVPTNSR	580.30 (+2)	881.45 (y^8 ,+1)	683.33 (y^6 ,+1)	583.27 (y^5 ,+1)
IQHPFGSVPGYGVR	554.29 (+3)	795.41 (y^7 ,+1)	698.36 (y^6 ,+1)	551.29 (y^5 ,+1)
¹⁵ N-IQHPFGSVPGYGVR	561.27 (+3)	805.39 (y^7 ,+1)	707.34 (y^6 ,+1)	559.27 (y^5 ,+1)
CYP46A1				
LLEEETLIDFVR	693.88 (+2)	1160.58 (y^{10} ,+1)	1031.54 (y^9 ,+1)	773.45 (y^7 ,+1)
¹⁵ N-LLEEETLIDFVR	701.35 (+2)	1173.54 (y^{10} ,+1)	1043.50 (y^9 ,+1)	783.42 (y^7 ,+1)
VLQDVFLDWAK	667.36 (+2)	1121.56 (y^9 ,+1)	993.50 (y^8 ,+1)	779.41 (y^6 ,+1)
¹⁵ N-VLQDVFLDWAK	674.37 (+2)	1133.53 (y^9 ,+1)	1003.47 (y^8 ,+1)	787.38 (y^6 ,+1)
VIDLAFSR	460.76 (+2)	708.37 (y^6 ,+1)	593.34 (y^5 ,+1)	480.26 (y^4 ,+1)
¹⁵ N-VIDLAFSR	466.25 (+2)	717.34 (y^6 ,+1)	601.32 (y^5 ,+1)	487.24 (y^4 ,+1)
CPR				
GVATNWLR	458.75 (+2)	760.41 (y^6 ,+1)	689.37 (y^5 ,+1)	588.33 (y^4 ,+1)
¹⁵ N-GVATNWLR	465.23 (+2)	771.38 (y^6 ,+1)	699.34 (y^5 ,+1)	597.30 (y^4 ,+1)
NPFLAAVTTNR	602.33 (+2)	992.55 (y^9 ,+1)	845.48 (y^8 ,+1)	732.40 (y^7 ,+1)
¹⁵ N-NPFLAAVTTNR	610.30 (+2)	1005.51 (y^9 ,+1)	857.45 (y^8 ,+1)	743.37 (y^7 ,+1)
FdR				
LTELLLR	429.28 (+2)	744.46 (y^6 ,+1)	643.41 (y^5 ,+1)	514.37 (y^4 ,+1)
¹⁵ N-LTELLLR	434.26 (+2)	753.44 (y^6 ,+1)	651.39 (y^5 ,+1)	521.35 (y^4 ,+1)
TATEKPGVEEAAR	433.56 (+3)	768.40 (y^8 ,+1)	517.27 (y^5 ,+1)	563.80 (y^{11} ,+2)
¹⁵ N-TATEKPGVEEAAR	439.21 (+3)	779.37 (y^8 ,+1)	525.25 (y^5 ,+1)	571.27 (y^{11} ,+2)
Fdx				
ITVHFINR	333.86 (+3)	443.75 (y^7 ,+2)	393.23 (y^6 ,+2)	343.69 (y^5 ,+2)
¹⁵ N-ITVHFINR	338.52 (+3)	450.23 (y^7 ,+2)	399.21 (y^6 ,+2)	349.17 (y^5 ,+2)

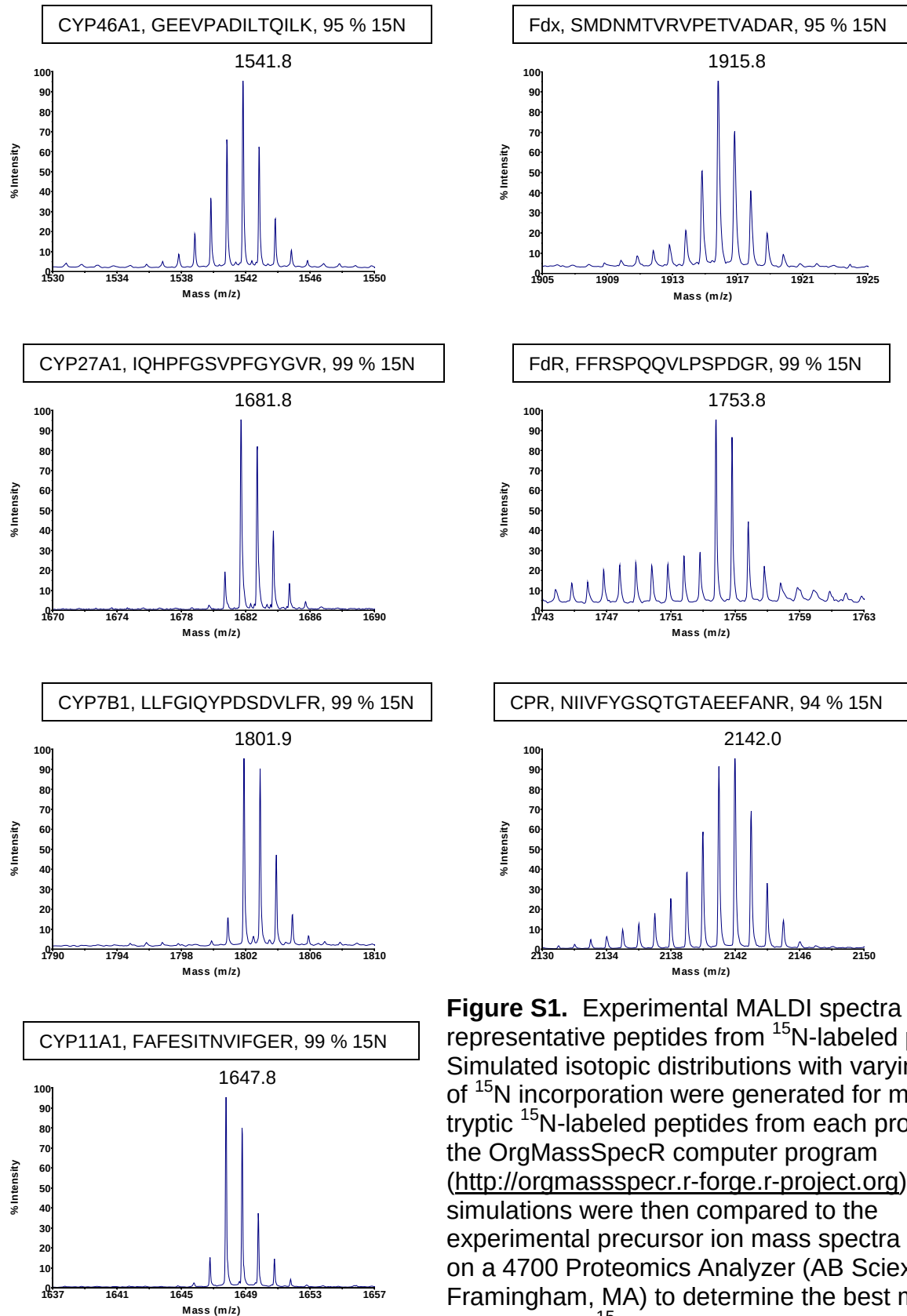
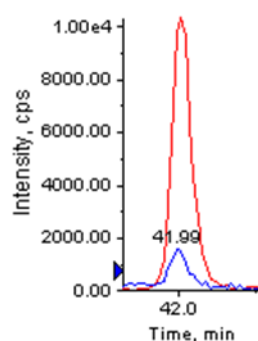
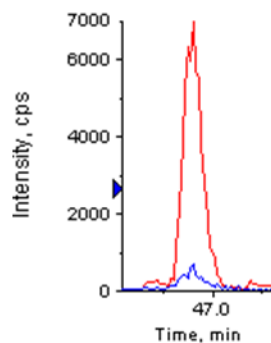


Figure S1. Experimental MALDI spectra for representative peptides from ^{15}N -labeled proteins. Simulated isotopic distributions with varying percent of ^{15}N incorporation were generated for multiple tryptic ^{15}N -labeled peptides from each protein, using the OrgMassSpecR computer program (<http://orgmassspecr.r-forge.r-project.org>). These simulations were then compared to the experimental precursor ion mass spectra acquired on a 4700 Proteomics Analyzer (AB Sciex, Framingham, MA) to determine the best match and therefore the ^{15}N incorporation.

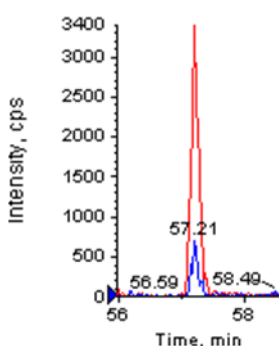
CYP27A1-LYPVVPTNSR



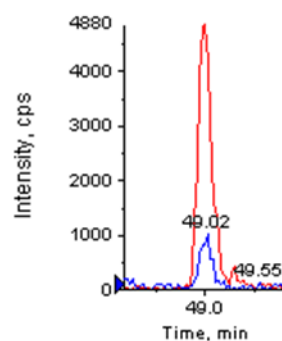
CYP27A1-IQHPFGSVPFYGVR



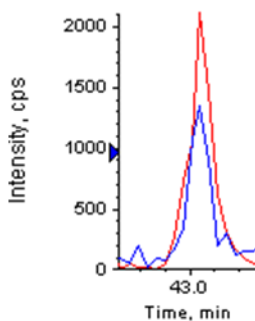
CYP46A1-VLQDVFLDWAK



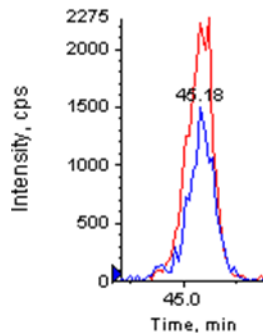
CYP46A1-LLEEETLIDFVR



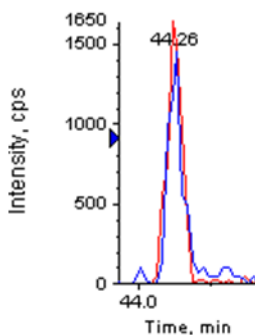
CPR-GVATNWLR



CPR-NPFLAAVTTNR



FdR-LTELLLR



FdR-TATEKPGVEEAAR

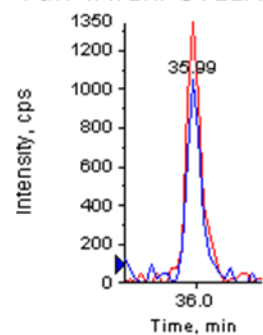
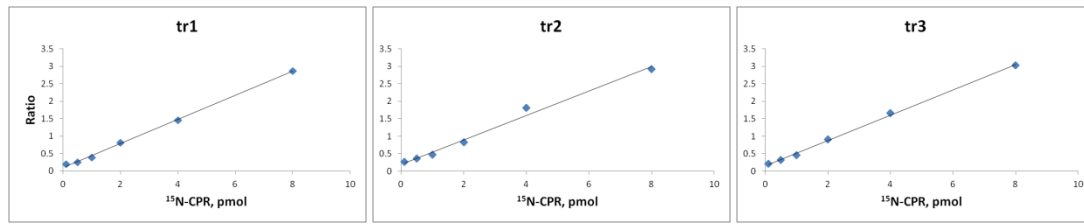
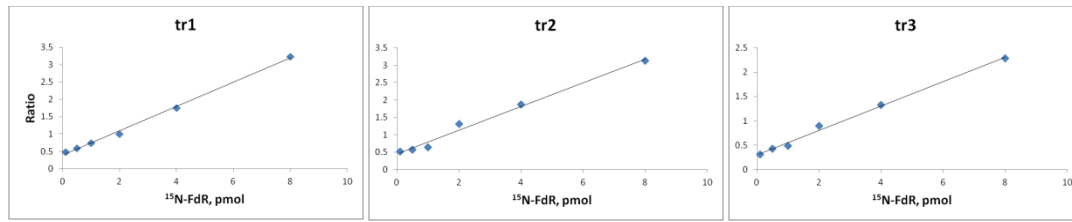


Figure S2. Extracted ion chromatograms of selected transitions from two different peptides per protein show comparable heavy/light ratios and therefore comparable quantification. Heavy (^{15}N -labeled) and light (non-labeled) peaks are shown in red and blue, respectively.

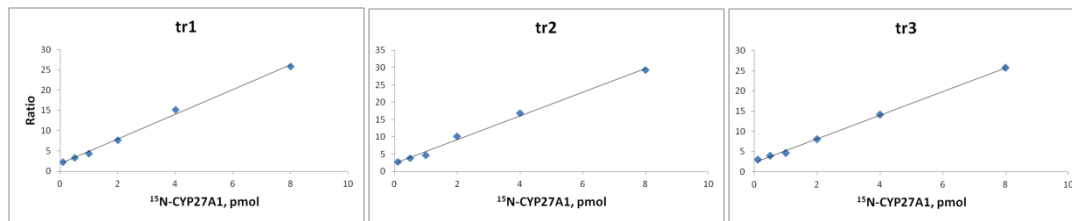
CPR, NPFLAAVTTNR



FdR, TATEKPGVEEAAR



CYP27A1, LYPVVPTNSR



CYP46A1, VLQDVFLDWAK

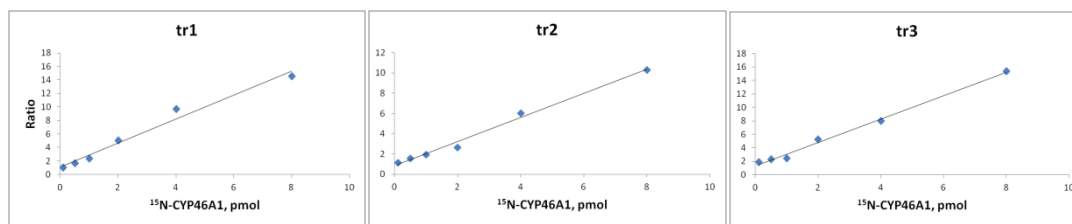


Figure S3. Calibration curves for quantification of CPR, FdR, CYP27A1, and CYP46A1 in the temporal lobe. The area ratio of a corresponding heavy (^{15}N -labeled) peptide to light (non-labeled) peptide was plotted versus amount of ^{15}N -labeled standard. Individual transitions (tr1, tr2, and tr3) are shown. The Q1 and Q3 values for these transitions are summarized in the Table S2.