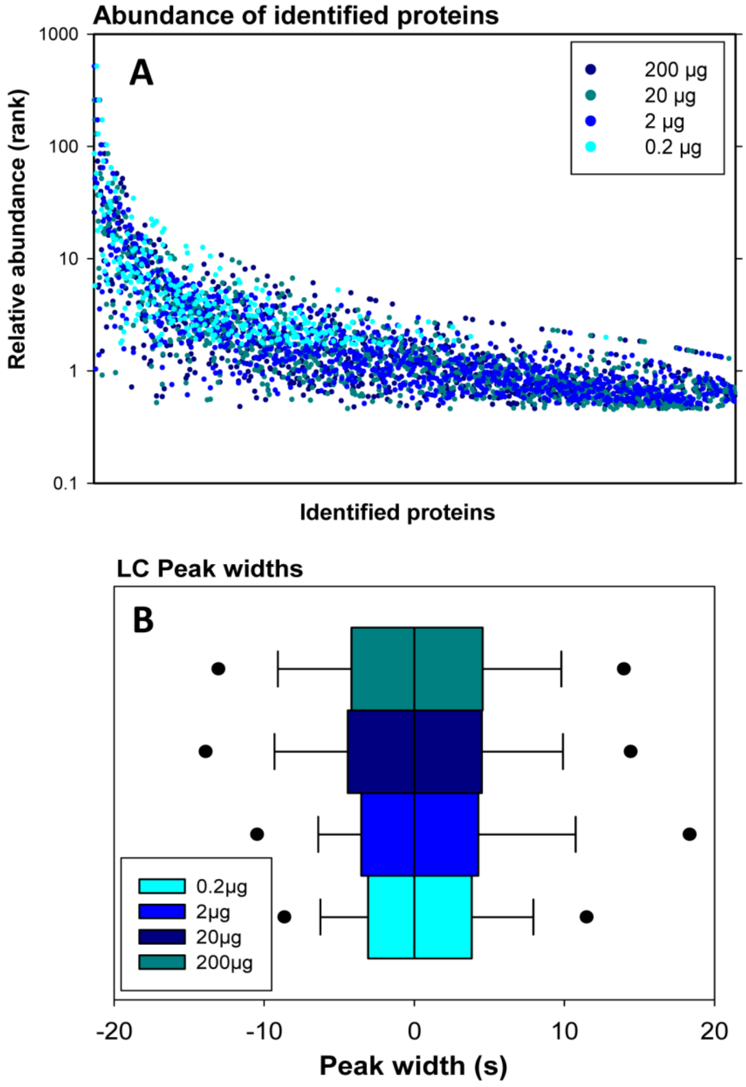
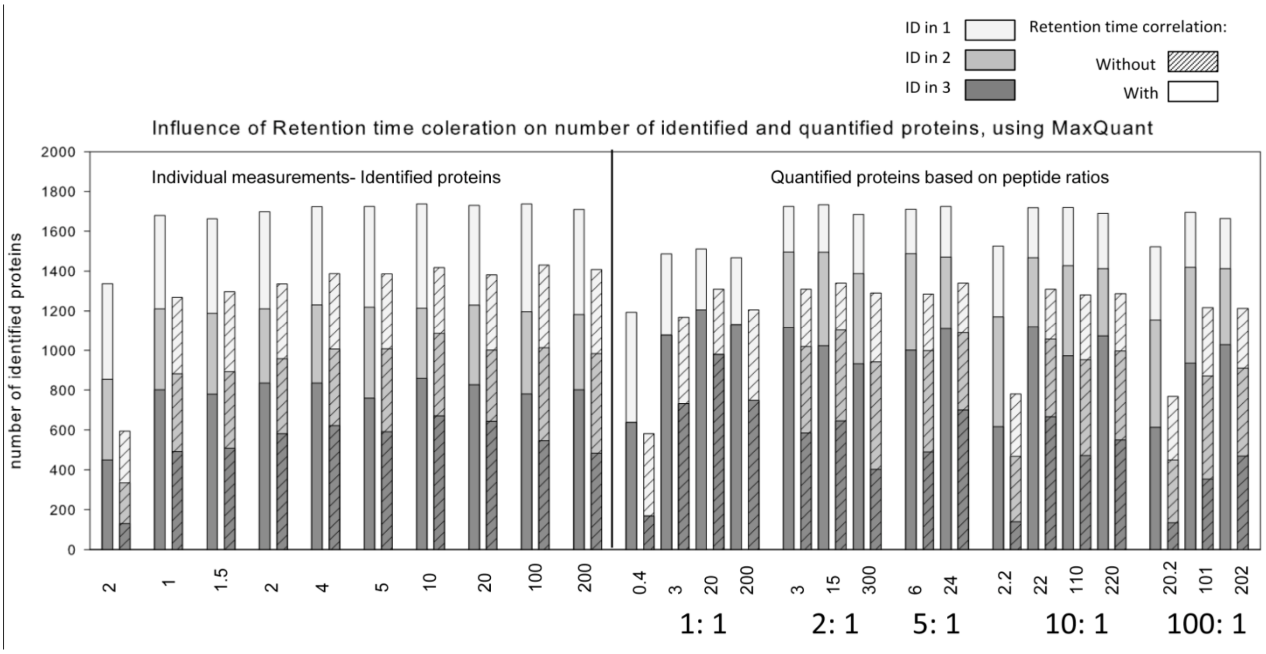
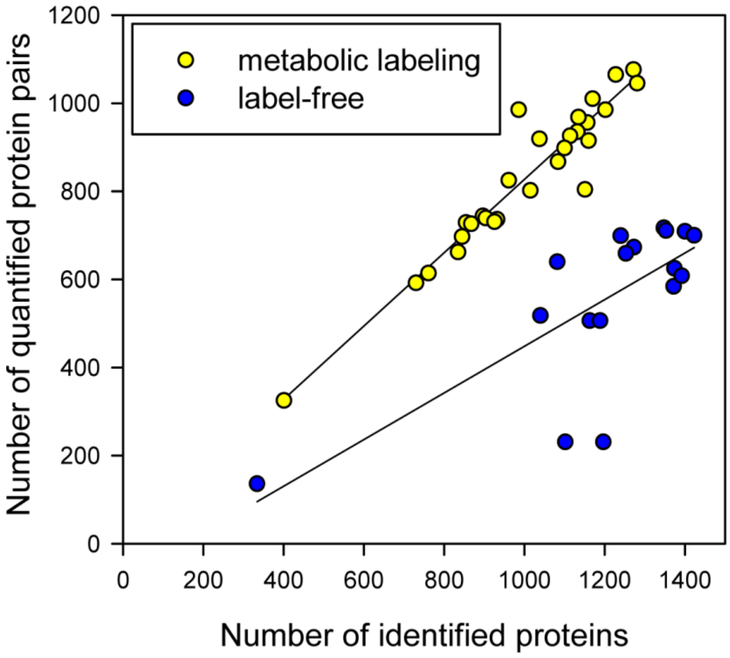
Supplementary Figure 1: Protein identifications and chromatographic properties under different protein loadings. (**A**) Relationship between protein abundance in the sample and its identification by MS/MS in different total protein sample amounts. (**B**) Box plot of peak widths during liquid chromatography as aligned on the median for different protein amounts loaded.



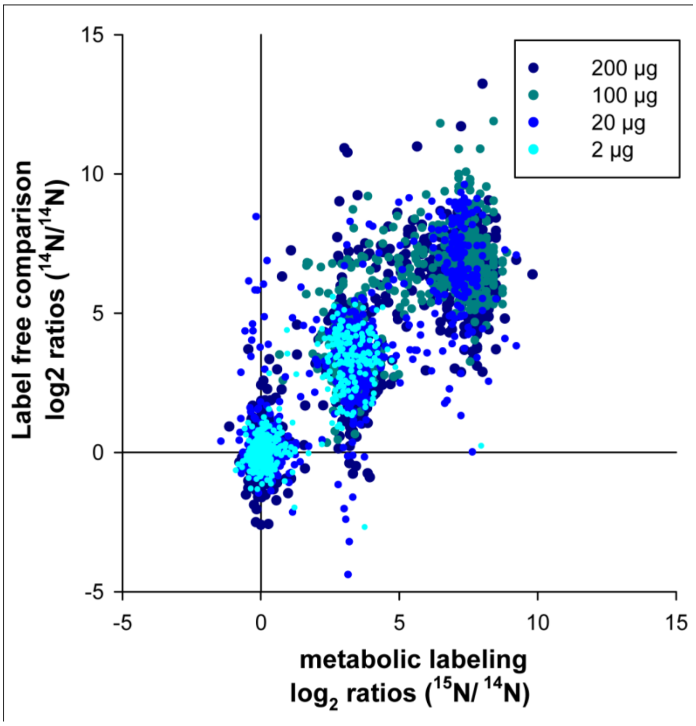
Supplementary Figure 2: Number of identified proteins increases if non-fragmented peaks are included based on retention time correlation of accurate masses.



Supplementary Figure 3: Relationship between quantified proteins and identified proteins for metabolic labeling and label-free approach.



Supplementary Figure 4: Direct comparison of abundance $\log_2$-ratios for peptides identified by both methods and at different total protein amounts.



Supplementary Tables

Supplementary Table 1: Nomenclature and composition of raw data files submitted to the Tranche database. **A**: Metabolic labeling approach; **B**: Label free approach.

A: Metabolic labeling dataset

	Isotope (µg)	**composition**	***.raw file name**	
ratio	**15N**	**14N**	**sample**	**Technical Replicas**
0.01	0.2	20	Rq	4,5,6
0.01	1	100	Rw	4,5,6
0.01	2	200	Rxx	4,5,6
0.1	0.2	2	Rk	4,5,6
0.1	2	20	Rt	4,5,6
0.1	10	100	Re	4,5,6
0.1	20	200	Rf	4,5,6
0.2	1	5	Rm	4,5,6
0.2	4	20	Ru	4,5,6
0.5	1	2	Rc	4,5,6
0.5	5	10	Ro	4,5,6
0.5	100	200	Rzz	4,5,6
1	0.2	0.2	Ri	4,5,6
1	1.5	1.5	Rl	4,5,6
1	10	10	Ra	4,5,6
1	100	100	Ry	4,5,6
2	2	1	Rd	4,5,6
2	10	5	Rp	4,5,6
2	200	100	Rz	4,5,6
5	5	1	Rn	4,5,6
5	20	4	Rv	4,5,6
10	2	0.2	Rj	4,5,6
10	20	2	Rs	4,5,6
10	100	10	Rg	4,5,6
10	200	20	Rh	4,5,6
100	20	0.2	Rr	4,5,6
100	100	1	Rx	4,5,6
100	200	2	Ryy	4,5,6

B: Label-free dataset

	*.raw file name	
14N (µg)	**sample**	**Technical Replicas**
0.2	14g	4,5,6
1	14a	4,5,6
1.5	14h	4,5,6
2	14b	4,5,6
4	14i	4,5,6
5	14j	4,5,6
10	14c	4,5,6
20	14d	4,5,6
100	14e	4,5,6
200	14f	4,5,6

Supplementary Table 2: Summary of the technical comparison between metabolic labeling and label free proteomic approach for Arabidopsis thaliana cell cultures. The values represented are based on three technical replicates for each mixing ratio and show the number of uniquely identified and quantified peptides and proteins. Ratios of peptides from multiple replicates have been averaged and these values have been used for the calculation of the median, average ratio per sample and the standard deviation from this average ratio.

sample	Expected ratio	Log2 (expect ratio)	Protein amount (µg)	**Identified Proteins**	**Quant. Proteins**	**Quant. Peptides**	**median**	**average**	**stdev**
Rq	0.01	-6.64	20.2	1157	956	2917	-5.23	-4.95	1.52
Rw	0.01	-6.64	101	1272	1076	3372	-5.28	-5.03	1.59
Rxx	0.01	-6.64	202	1132	935	2925	-5.45	-5.15	1.58
Rk	0.1	-3.32	2.2	1038	919	3249	-3.47	-3.33	0.88
Rt	0.1	-3.32	22	1170	1010	3559	-3.38	-3.27	0.77
Re	0.1	-3.32	110	1228	1065	3570	-3.32	-3.21	0.74
Rf	0.1	-3.32	220	1114	926	3046	-3.50	-3.39	0.75
Rm	0.2	-2.32	6	961	825	3339	-2.25	-2.21	0.56
Ru	0.2	-2.32	24	1135	968	3913	-2.40	-2.37	0.62
Rc	0.5	-1.00	3	855	729	3049	-0.86	-0.83	0.66
Ro	0.5	-1.00	15	868	726	3102	-0.92	-0.94	0.46
Rzz	0.5	-1.00	300	897	744	2427	-1.06	-1.08	0.45
Ri	1	0.00	0.4	401	325	1067	-0.26	-0.38	1.13
Rl	1	0.00	3	730	592	2591	0.19	0.34	0.80
Ra	1	0.00	20	835	662	2685	0.10	0.08	0.52
Ry	1	0.00	200	845	697	2571	0.02	-0.01	0.43
Rd	2	1.00	3	761	614	2559	1.16	1.11	0.59
Rp	2	1.00	15	932	736	2773	1.19	1.13	0.63
Rz	2	1.00	300	904	739	2780	1.11	1.05	0.62
Rn	5	2.32	6	926	731	2553	2.28	2.08	0.95
Rv	5	2.32	24	1084	867	2892	2.51	2.34	0.91
Rj	10	3.32	2.2	1015	802	2577	3.90	3.44	1.66
Rs	10	3.32	22	986	985	3468	3.51	3.20	1.28
Rg	10	3.32	110	1151	804	2385	3.39	3.07	1.23
Rh	10	3.32	220	1100	898	2652	3.43	3.07	1.34
Rr	100	6.64	20.2	1202	985	3269	4.21	3.62	2.87
Rx	100	6.64	101	1160	915	2829	4.36	3.65	2.82
Ryy	100	6.64	202	1281	1045	2954	4.17	3.71	2.92
14g :14g	1	0.00	0.4	334	136	234	-0.02	-0.13	1.01
14h : 14h	1	0.00	3	1040	518	1334	0.00	0.05	0.96
14c : 14c	1	0.00	20	1082	640	1993	0.00	-0.08	1.03
14e : 14e	1	0.00	200	1189	506	1384	0.00	-0.07	1.18
14b :14a	2	1.00	3	1240	699	2219	0.92	1.02	0.80
14c : 14j	2	1.00	15	1273	673	2495	0.35	0.43	0.81
14f :14e	2	1.00	300	1400	709	2194	1.22	1.28	0.82
14j : 14a	5	2.32	6	1253	659	2145	2.20	2.26	1.01
14d : 14i	5	2.32	24	1348	717	2505	2.06	2.05	0.79

14b :14g	10	3.32	2.2	1102	231	552	2.31	2.25	1.31
14d : 14b	10	3.32	22	1353	711	2413	2.95	2.98	1.02
14e : 14c	10	3.32	110	1374	625	2111	3.56	3.44	1.07
14f : 14d	10	3.32	220	1423	700	2269	3.64	3.65	0.98
14d : 14g	100	6.64	20.2	1197	231	549	5.24	5.08	1.67
14e :14a	100	6.64	101	1372	584	1828	6.26	6.35	1.37
14f : 14b	100	6.64	202	1392	608	1877	6.59	6.77	1.03
14g			0.20	334					
14h			1.50	1040					
14a			1.00	1036					
14b			2.00	1093					
14i			4.00	1100					
14j			5.00	1092					
14c			10.00	1082					
14d			20.00	1186					
14e			100.00	1189					
14f			200.00	1163					

Supplementary Table 3: Influence of retention time correlation (RTC) in the number of quantified proteins based on peptide ratios. The percent of increase for quantified proteins from MaxQuant has been applied to estimate the expected influence of RTC on the label free data quantified by MSQuant.

		MaxQuant			**MsQuant**		
Protein ammount (µg)	**Ratio**	**Qquantified without RTC**	**Quantified with RTC**	**%increase with RTC**	**Label-free quantified without RTC**	**Estimated quantified prot. using increase in Percent for RTC from MaxQuant**	**Metabolic Labeling quantified without RTC**
0.4	1: 1	582	1193	105	136	279	325
3		1168	1486	27	518	659	592
20		1310	1511	15	640	738	662
200		1205	1468	22	506	616	697
3	2:1	1309	1725	32	699	921	614
15		1339	1733	29	673	871	736
300		1290	1685	31	709	926	739
6	5:1	1285	1711	33	659	877	731
24		1339	1724	29	717	923	867
2.2	10:1	781	1526	95	231	451	802
22		1309	1719	31	711	934	985
110		1280	1720	34	625	840	804
220		1287	1691	31	700	920	898
20.2	100:1	768	1522	98	231	458	985
101		1217	1695	39	584	813	915
202		1213	1664	37	608	834	1045