

A foundation for reliable spatial proteomics experiments
data analysis
Supplementary tables

Trans-localisations

	from	to
AT5G45160	ER membrane	TGN
AT5G61840	Golgi	PM
AT1G27390	Mitochondrion	Plastid
AT2G47840	Plastid	ER
AT2G14720	TGN	Golgi
AT4G26690	PM	Vacuola
AT2G21410	vacuole	Mitochondrion

Table 1: The seven marker proteins that have been trans-localised and their destination organelles. The destination profiles have been computed by averaging the fractions of the destination organelle markers.

	svm	svm.scores
AT5G45160.1	ER membrane	0.97
AT5G45160.3	TGN	0.78
AT5G61840.1	Golgi	0.87
AT5G61840.3	PM	0.94
AT1G27390.1	Mitochondrion	0.87
AT1G27390.3	Plastid	0.94
AT2G47840.1	Plastid	0.54
AT2G47840.3	ER membrane	0.97
AT2G14720.1	TGN	0.82
AT2G14720.3	Golgi	0.92
AT4G26690.1	PM	0.93
AT4G26690.3	vacuole	0.89
AT2G21410.1	vacuole	0.72
AT2G21410.3	Mitochondrion	0.93

Table 2: Classification details of the 7 in silico trans-localised proteins. The rows ending with .1 show results for the first replicate and the second replicate, corresponding to the changes in localisation, are suffixed by a .3. The `svm` column defines the classification result and the `svm.scores` gives the classification posterior probability.

	svm	svm.scores
AT4G11010.1	Plastid	1.00
AT4G11010.3	Plastid	1.00
AT5G22640.1	Plastid	0.60
AT5G22640.3	Plastid	0.89
AT5G27850.1	Ribosome	0.58
AT5G27850.3	Ribosome	0.76
AT1G76270.1	Golgi	0.35
AT1G76270.3	Golgi	0.94
AT2G18690.1	vacuole	0.39
AT2G18690.3	ER lumen	0.43
AT2G30930.1	PM	0.37
AT2G30930.3	vacuole	0.89
AT3G62700.1	ER lumen	0.27
AT3G62700.3	vacuole	0.85
AT4G31430.1	PM	0.53
AT4G31430.3	Golgi	0.92
AT5G50370.1	Plastid	0.87
AT5G50370.3	Mitochondrion	0.86

Table 3: Details of the non-trans-localised proteins that had greater distance score than the smallest trans-localised protein. The `svm` column defines the classification result and the `svm.scores` gives the classification posterior probability. The protein identifiers ending with .1 are those of the first replicate and the .3 correspond to the second replicate after in silico trans-localisation.

Concerted trans-localisations

	svm	svm.scores
AT2G45060.1	Mitochondrion	0.95
AT2G45060.3	Plastid	0.91
AT3G02090.1	Mitochondrion	0.86
AT3G02090.3	Plastid	0.87
AT3G16480.1	Mitochondrion	0.63
AT3G16480.3	Plastid	0.91
AT3G51010.1	Mitochondrion	0.93
AT3G51010.3	Plastid	0.89
AT3G58840.1	Mitochondrion	0.93
AT3G58840.3	Plastid	0.80
AT3G59280.1	Mitochondrion	0.91
AT3G59280.3	Plastid	0.89
AT3G59820.1	Mitochondrion	0.93
AT3G59820.3	Plastid	0.91
AT4G05020.1	Mitochondrion	0.93
AT4G05020.3	Plastid	0.92
AT4G26410.1	Mitochondrion	0.93
AT4G26410.3	Plastid	0.79
AT4G27585.1	Mitochondrion	0.94
AT4G27585.3	Plastid	0.89
AT4G28220.1	Mitochondrion	0.91
AT4G28220.3	Plastid	0.90
AT4G28390.1	Mitochondrion	0.79
AT4G28390.3	Plastid	0.93
AT4G29130.1	Mitochondrion	0.89
AT4G29130.3	Plastid	0.94
AT4G29480.1	Mitochondrion	0.85
AT4G29480.3	Plastid	0.83
AT4G30010.1	Mitochondrion	0.93
AT4G30010.3	Plastid	0.90

Table 4: Classification results for the concerted trans-localisations from the mitochondrion (first replicate ending with .1) and second, in silico perturbed replicate (.3 suffix), showing the expected plastid localisation.