Supplemental Materials

Molecular Biology of the Cell

Meyer et al.

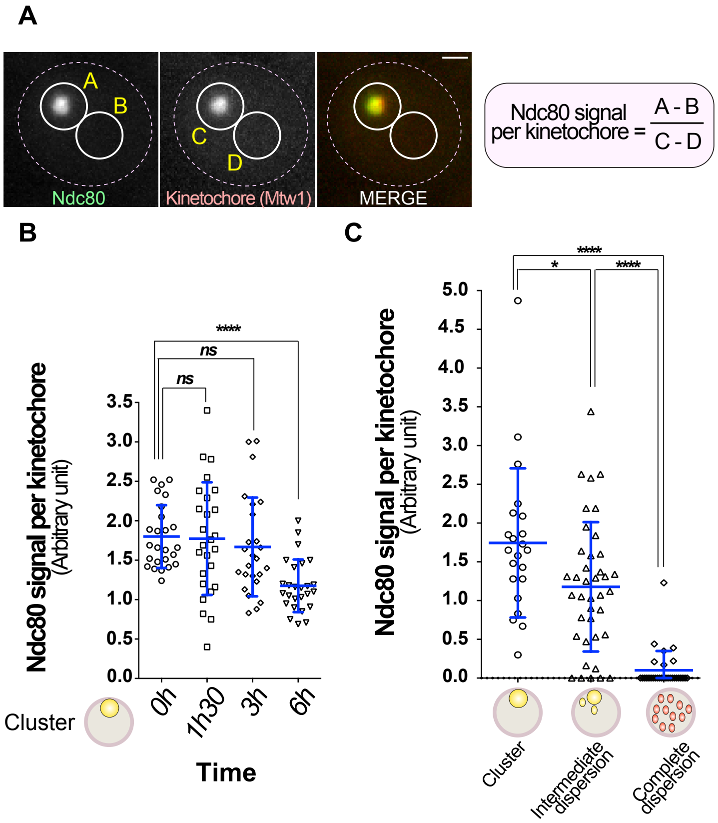
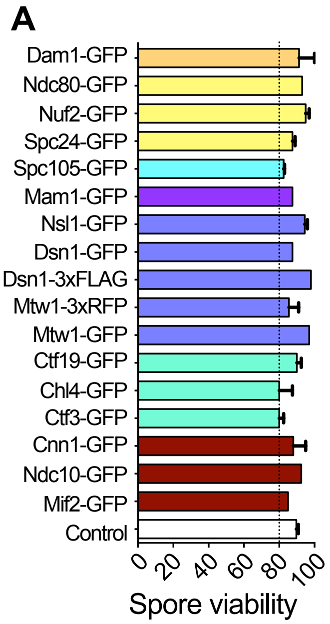
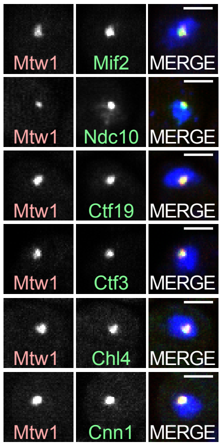


Figure S1. Quantification of Ndc80 association with kinetochores during meiosis I. Wild-type diploid cells expressing Ndc80-GFP and Mtw1-3xmCherry were switched to sporulation medium (T = 0 h). The strains used were *ndt80* mutants that arrest in pachytene. Cells with clustered centromeres (1 focus), intermediate dispersion (<4 Mtw1 foci), or complete dispersion (>4 Mtw1 foci) were used for quantification of Ndc80 signal ($n \geq 22$). (A) To quantify the relative amount of Ndc80 (using Ndc80-GFP) per kinetochore (using Mtw1-RFP), images were collected as seven slice Z series (0.5 µm intervals). A summed projection of these images was then used for analysis of GFP and RFP fluorescence intensity. An area (A) containing the kinetochores (Mtw1-mCherry) signal was first selected and the signal in this area in the Ndc80 (GFP) channel was determined. This value was corrected for background signal by selecting a nearby, same-sized area (B) and determining the GFP signal in this area, which was then subtracted from value (A). The total Mtw1 signal (mCherry) in the selected area was determined (C) and the background value subtracted (D). The corrected GFP value (A minus B) was then divided by the corrected mCherry value (C minus D) to obtain a normalized Ndc80/Mtw1 value for that cell. These values were then plotted. Scale bar, 1µm. (B) Ndc80 signals at clustered centromeres at times after meiotic induction. For panel (B), the area of analysis was 0.5µm in diameter. (C) Ndc80 signals at clustered, intermediate dispersed and completely dispersed kinetochores 3 hours after meiotic induction. For panel (C) the area of analysis was expanded to 1.1µm diameter in all cells tested to allow inclusion of dispersed kinetochores. Graphs show values of individual cells, average and one standard deviation. Student's t-tests were used to evaluate the significance of observed differences. *$p<0.05$, ****$p<0.0001$.

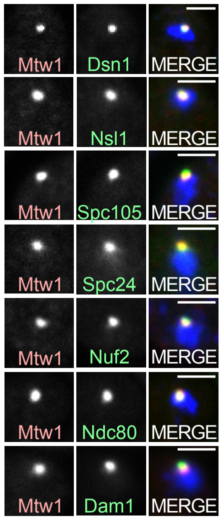


B Constitutive Centromere Associated Network



Complex	*S.cerevisae*	Human	
	Cse4	CENP-A	
	Mif2	CENP-C	
Cnn1/Wip1 Complex	**Cnn1**	CENP-T	
	Wip1	CENP-W	
	Mhf1	CENP-S	
	Mhf2	CENP-X	
CBF3 Complex	**Ndc10**		
	Cep3		
	Ctf13		
	Skp1		
CTF19 complex	**Ctf19**	CENP-P	**Sub complex COMA**
	Mcm21	CENP-O	
	Okp1	CENP-Q	
	Ame1	CENP-U	
	Ctf3	CENP-I	
	Mcm16	CENP-H	
	Mcmc22	CENP-K	
	Chl4	CENP-N	
	Iml3/Mcm19	CENP-L	
	Nkp1		
	Nkp2		

C KMN network and Dam1 complex



Complex	*S.cerevisae*	Human
Mtw1/MIS12/ MIND Complex (M)	**Mtw1**	MIS12
	Dsn1	DSN1
	Nsl1	NSL1
	Nnf1	NNF1
Spc105/KNL1 Complex (K)	**Spc105**	KNL1
	Kre28	ZWINT1
NDC80 Complex (N)	**Ndc80**	NDC80 (HEC1)
	Nuf2	NUF2
	Spc24	SPC24
	Spc25	SPC25
DAM1 Complex	**Dam1**	
	Ask1	
	Hsk3	
	Dad1	
	Dad2	
	Dad3	
	Dad4	
	Duo1	
	Spc19	
	Spc34	

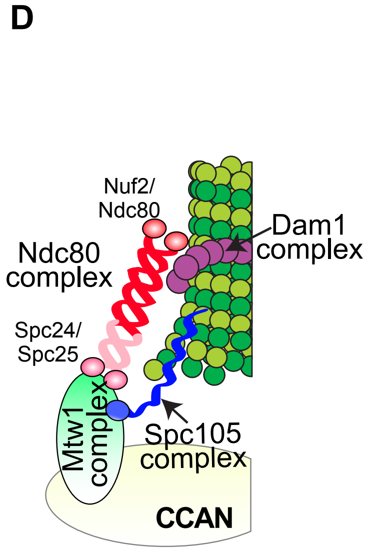


Figure S2. Kinetochore structure when cells enter meiosis. (A) Tetrad dissection was used to quantify the effect of tagging each kinetochore component on spore viability. (B-C) Wild-type diploid cells expressing Mtw1-3xmCherry and GFP-tagged kinetochore proteins were switched to sporulation medium and fluorescence microscopy was used to monitor the presence of the individual components on the kinetochore cluster that is characteristic of cells at meiotic entry. Tables (B) and (C) list components of the kinetochore and the names of the mammalian homologs. All components tested (red in the tables) were detectable in the kinetochore cluster suggesting kinetochores are intact at meiotic entry. A representative image of a cell with each GFP-tagged component at the time of meiotic induction is shown. Scale bars = 2µm. (D) Cartoon showing kinetochore sub-complexes.

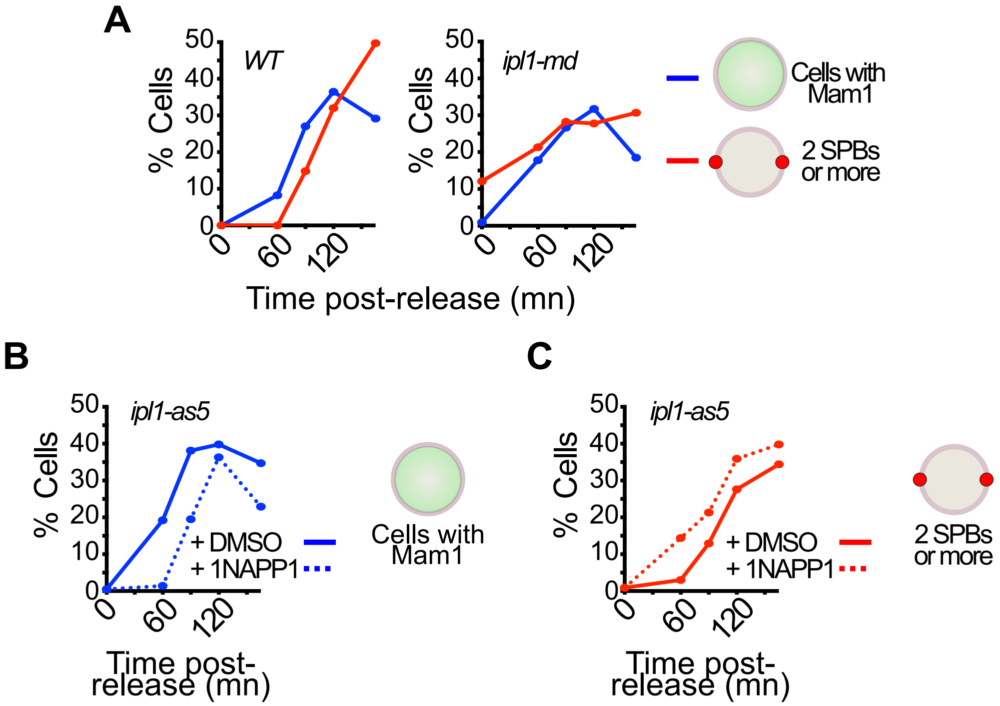
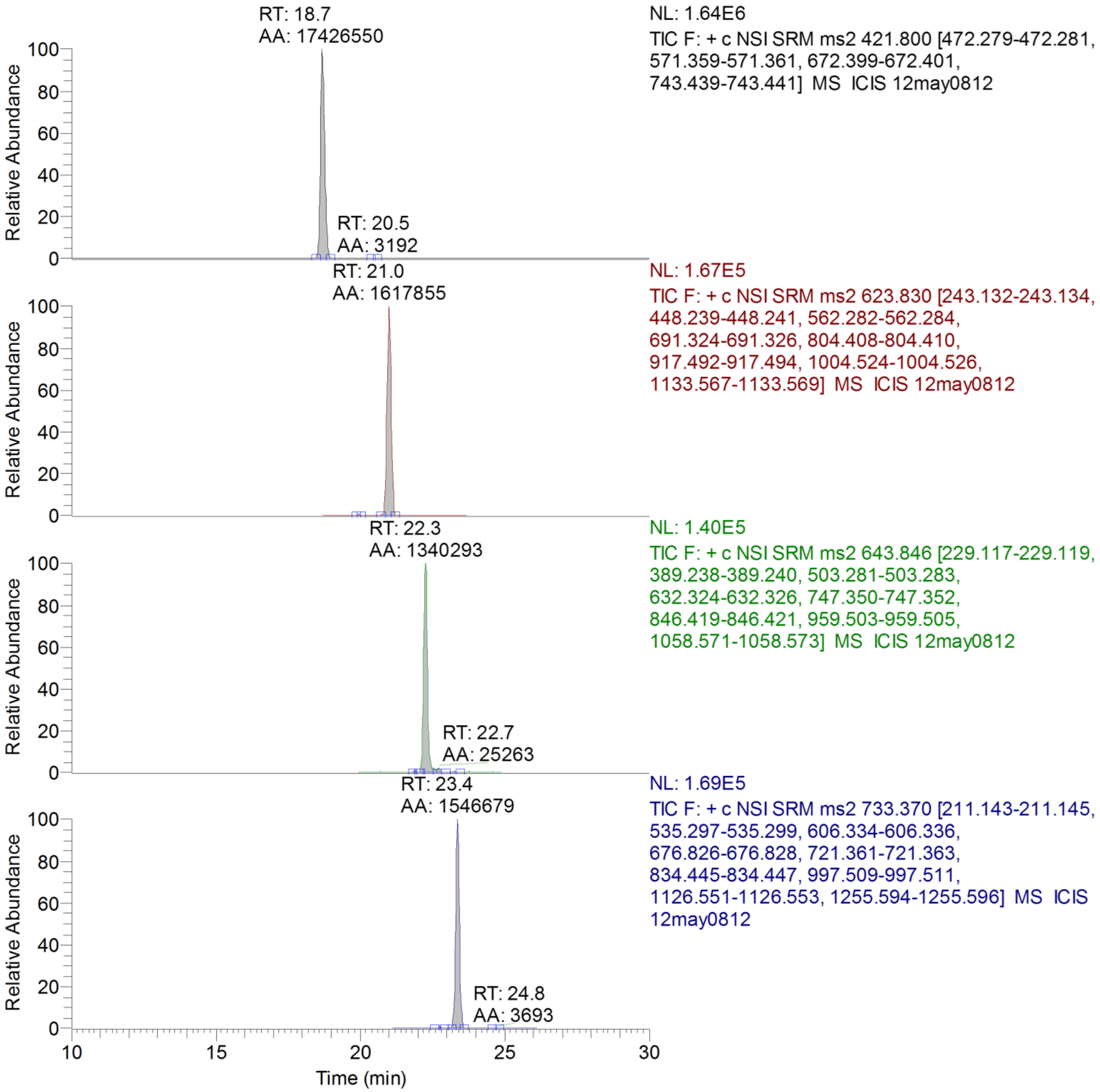


Figure S3. Effect of Ipl1 inactivation on spindle formation and Mam1 expression. (A-C) Wild-type and *ipl1* mutant (*ipl1-md* and *ipl1-as5/ipl1-md*) cells carrying a monopolin marker (*MAM1-GFP*), a kinetochore marker (*MTW1-GFP*), and also a SPB marker (*SPC42-DsRed*) in the *ipl1* mutants were sporulated and released from a pachytene arrest (*P_{GAL1}-NDT80 GAL4-ER*) at 6 hours after meiotic induction by the addition of 5 μM β-estradiol. (A) For wild-type and *ipl1-md* mutants, cells with Mam1 or with two SPBs or more were scored (n≥ 100 for all time points). (B-C) Ipl1-as5 was inhibited (dashed lines) or not (straight lines) by adding 50μM 1NA-PP1 or DMSO upon the release from pachytene arrest. Cells with Mam1 (B) or with two SPBs or more (C) were counted. (n≥ 100 for all time points). In all experiments, *ipl1* mutants formed spindles earlier due to the role of Ipl1 in preventing precocious spindle assembly (Kim et al., 2013). Mam1 was expressed with similar kinetics in wild-type cells and *ipl1* mutants, suggesting that the failures in Mam1 loading in Ipl1 mutants is not due to a dramatic reduction or delay in expression.

MTW1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15
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25
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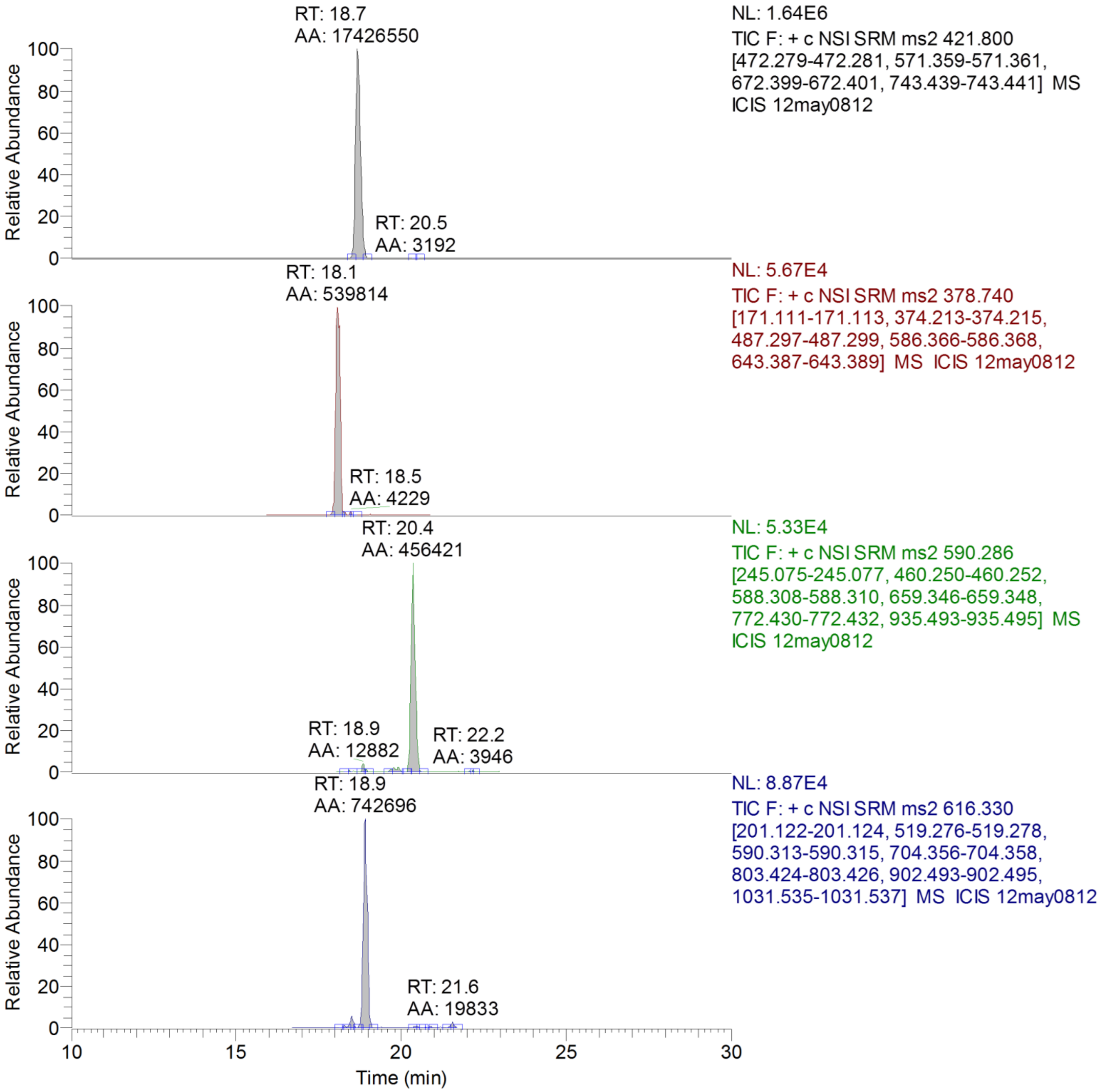
Time (min)

NSL1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RT: 22.2
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Time (min)

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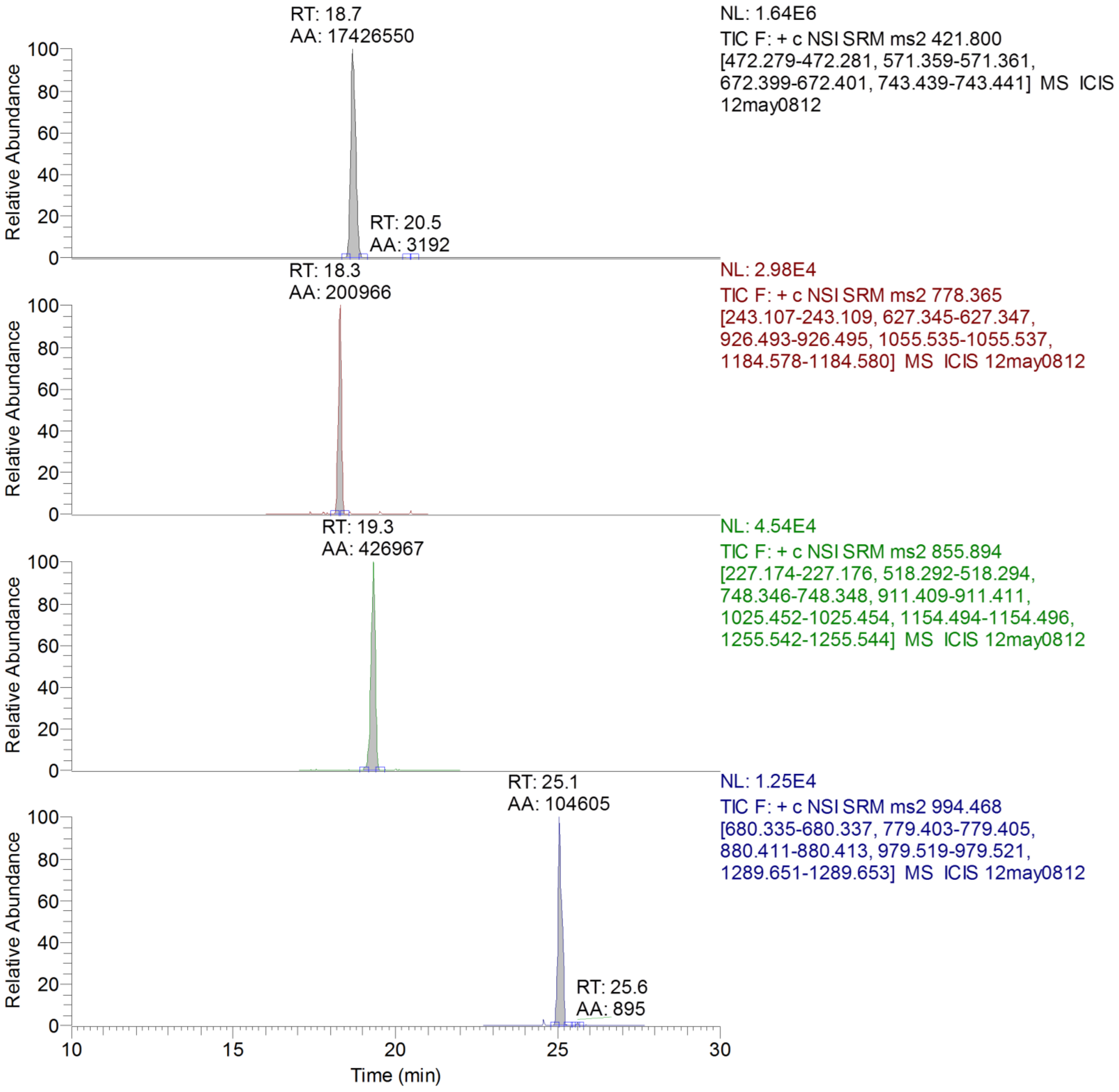
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Time (min)
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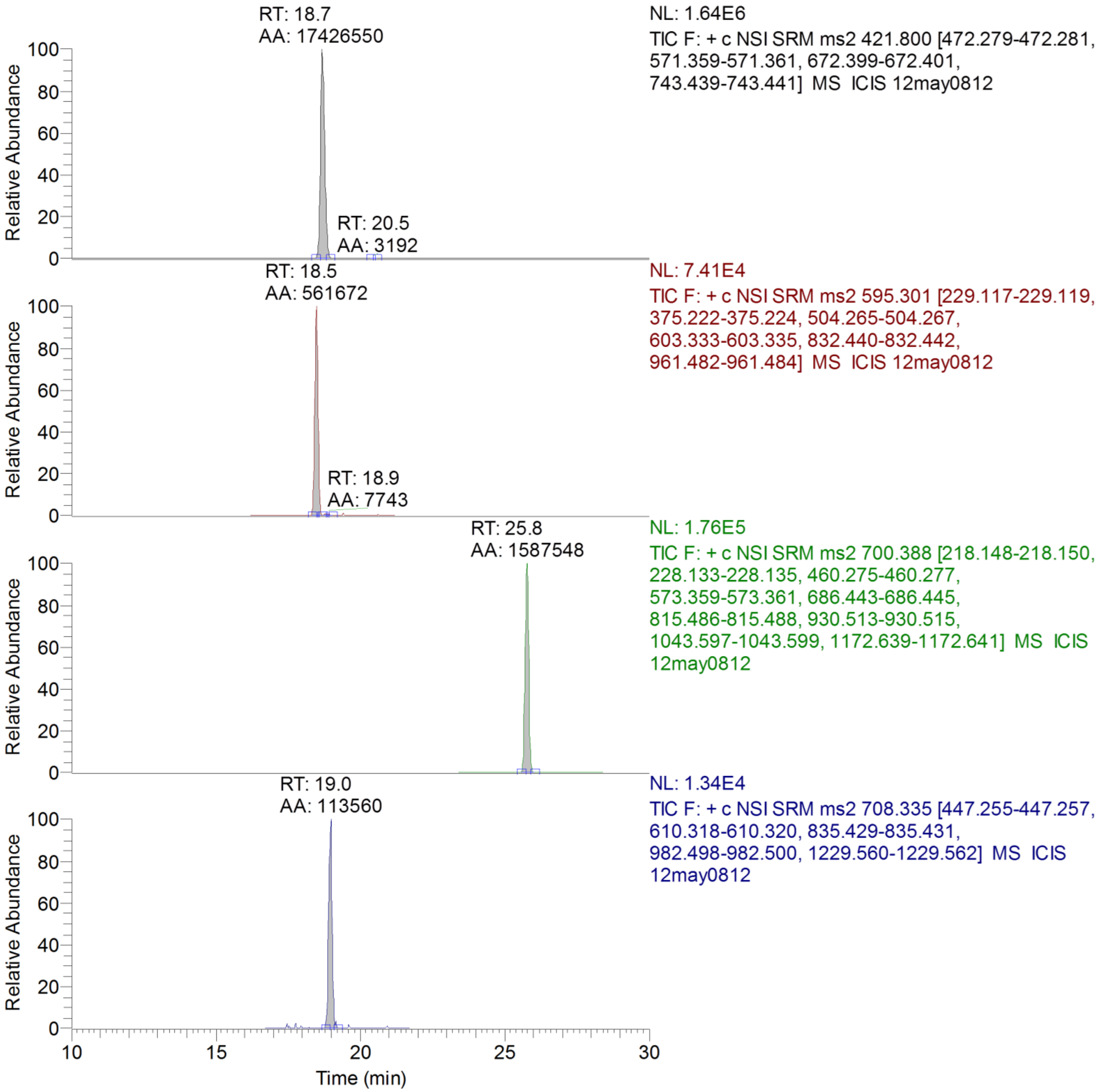
NNF1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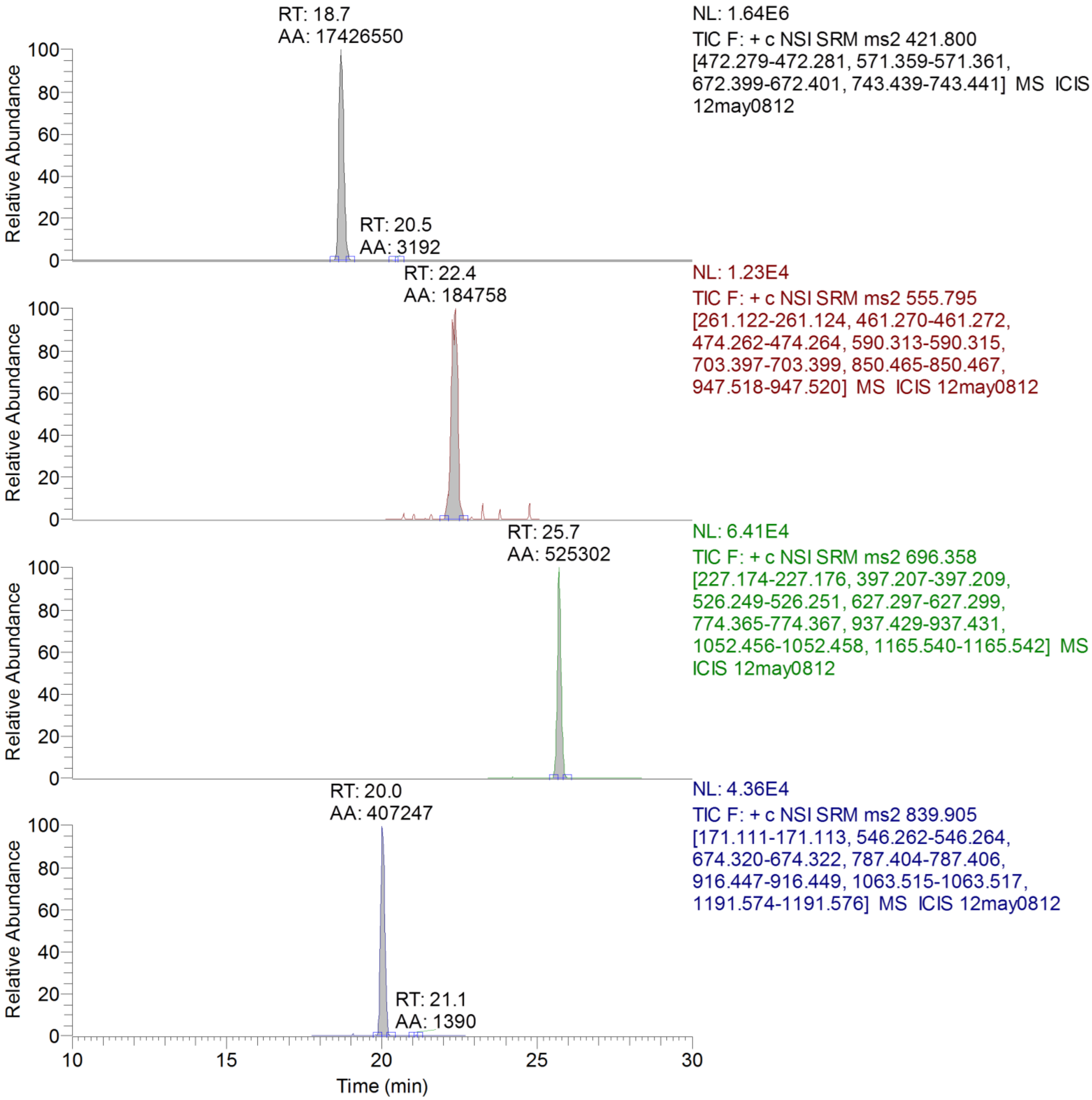
Time (min)

NDC80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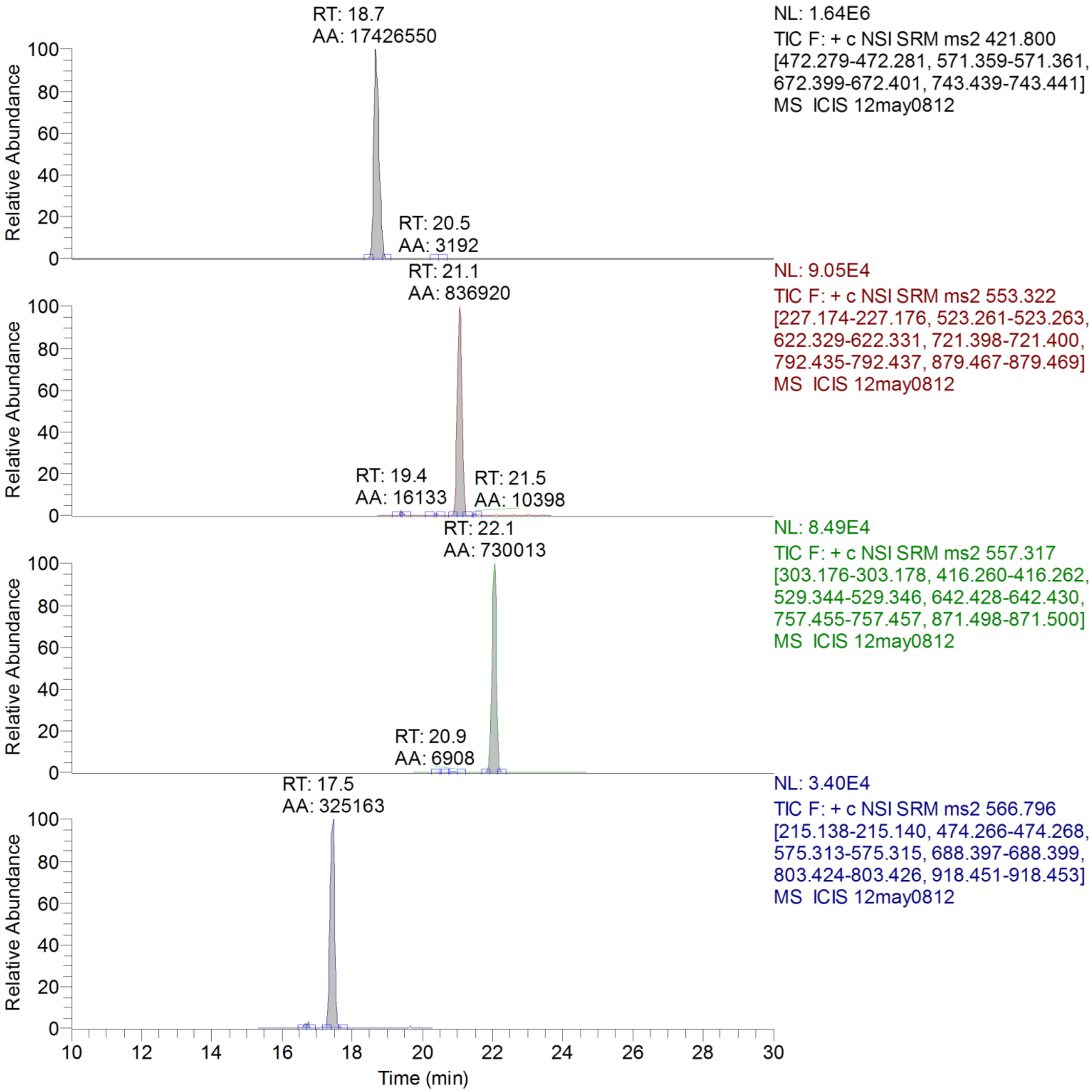
Time (min)

NUF2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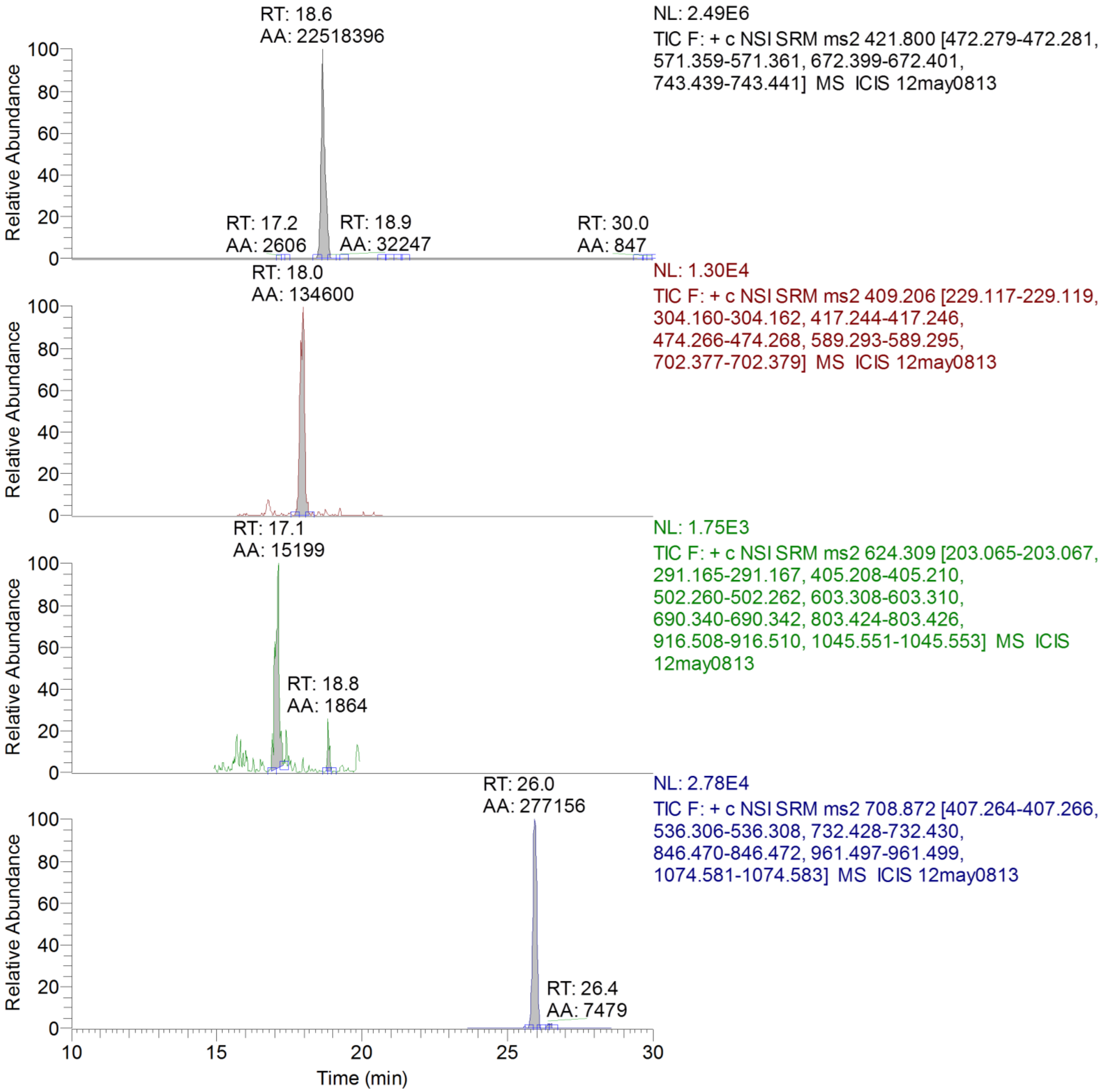
SPC24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RT: 18.9
AA: 32247
RT: 30.0
AA: 847
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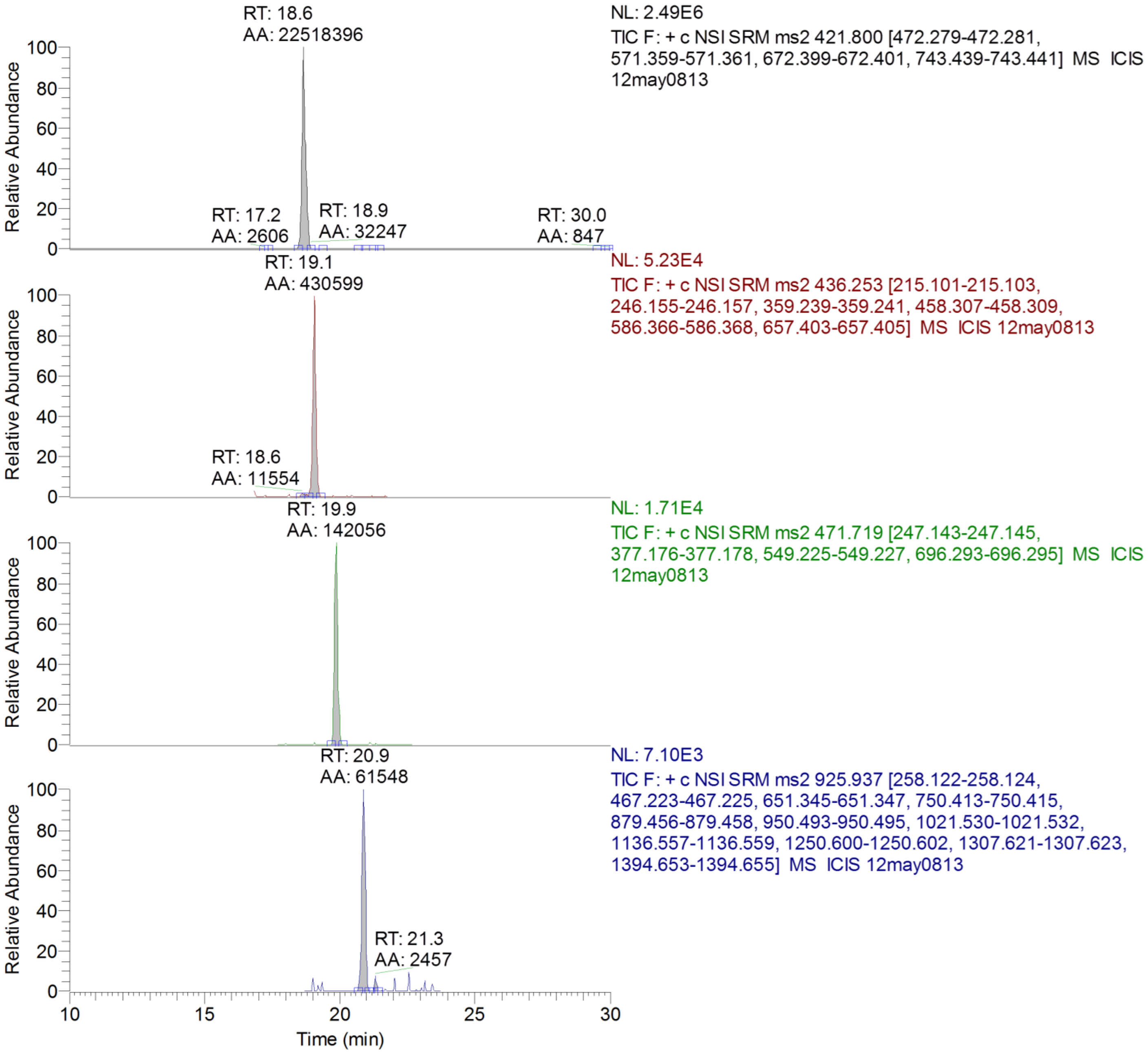
SPC25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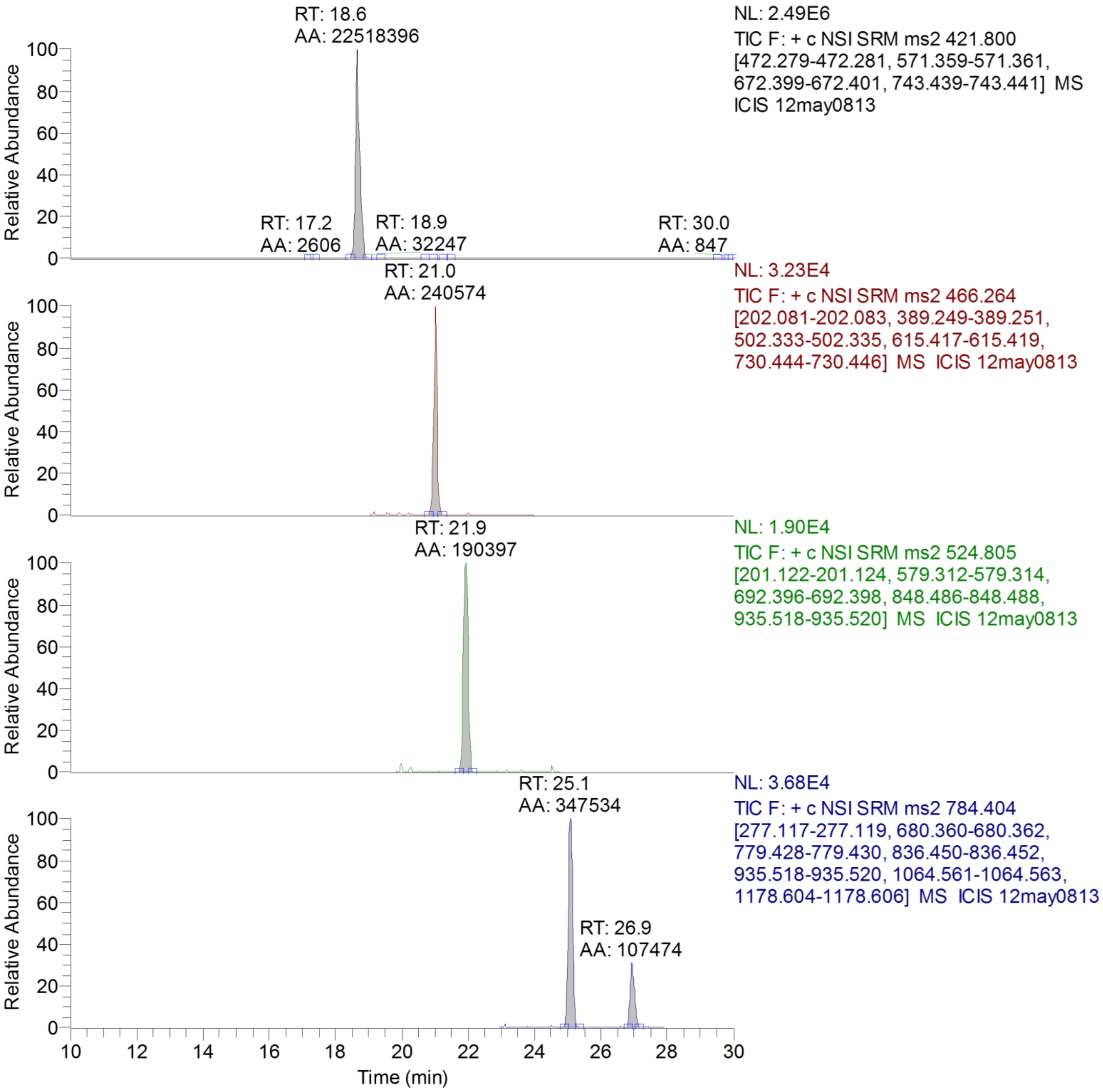
Time (min)

SPC105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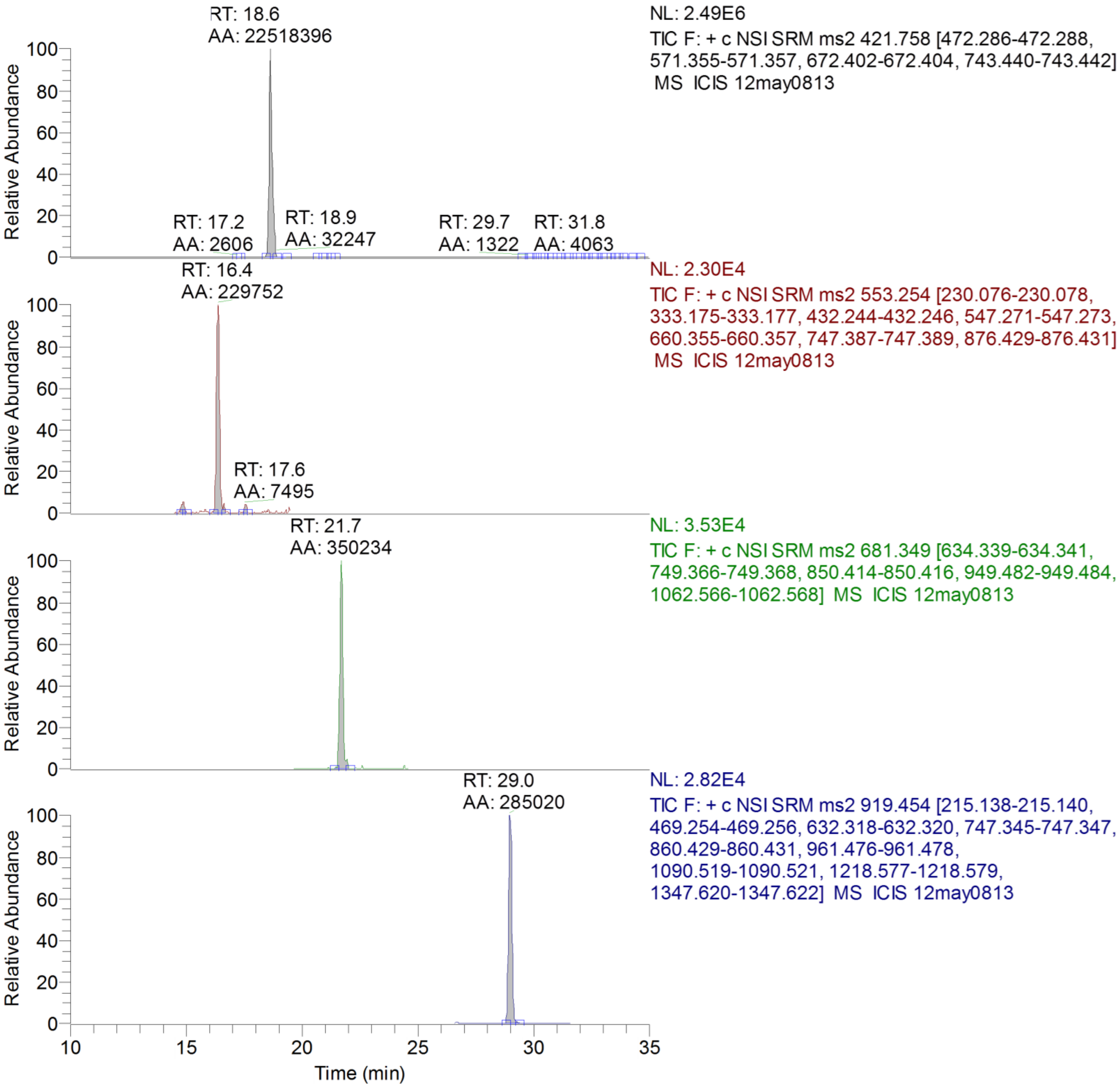
KRE28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AA: 285020
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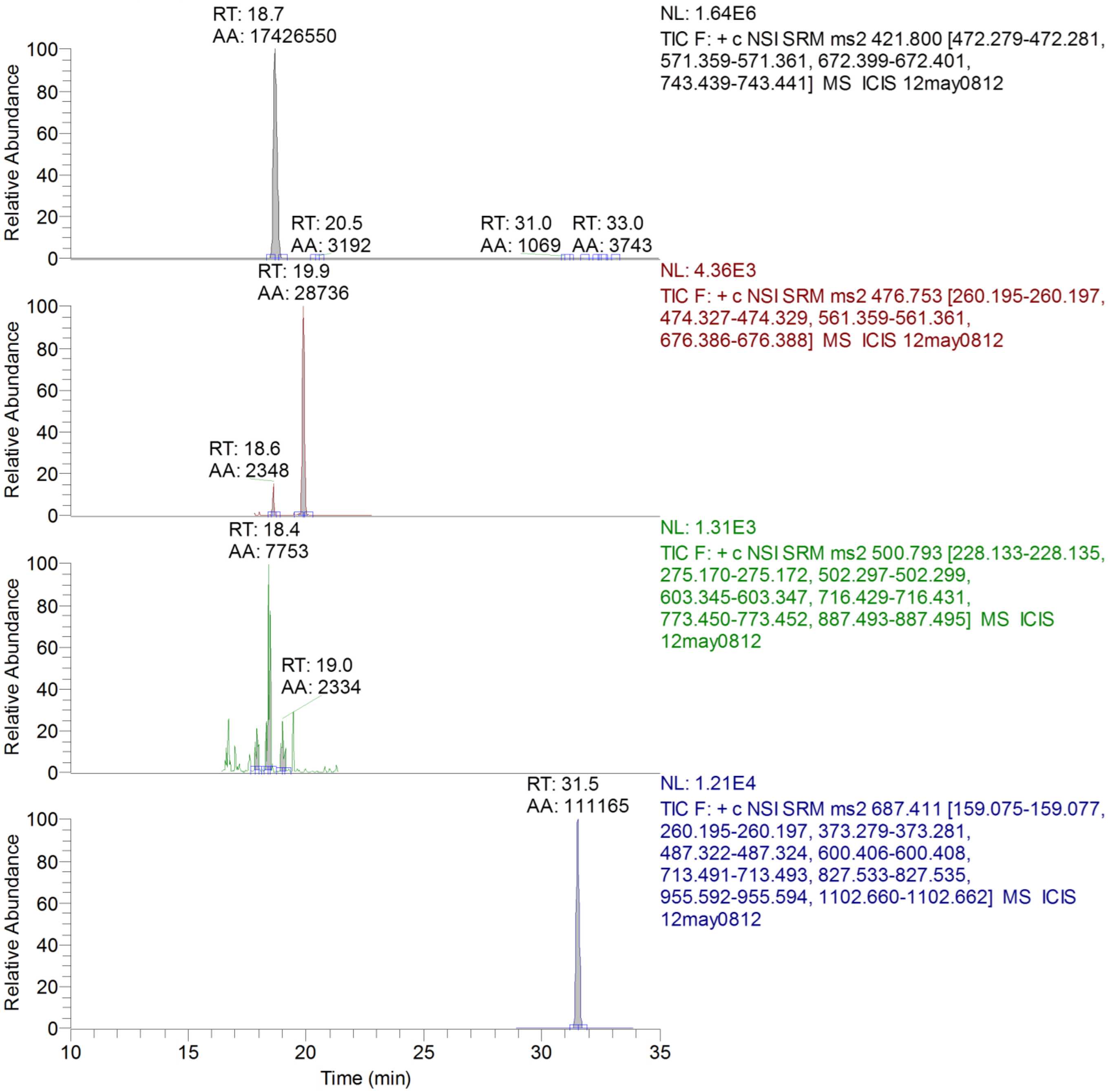
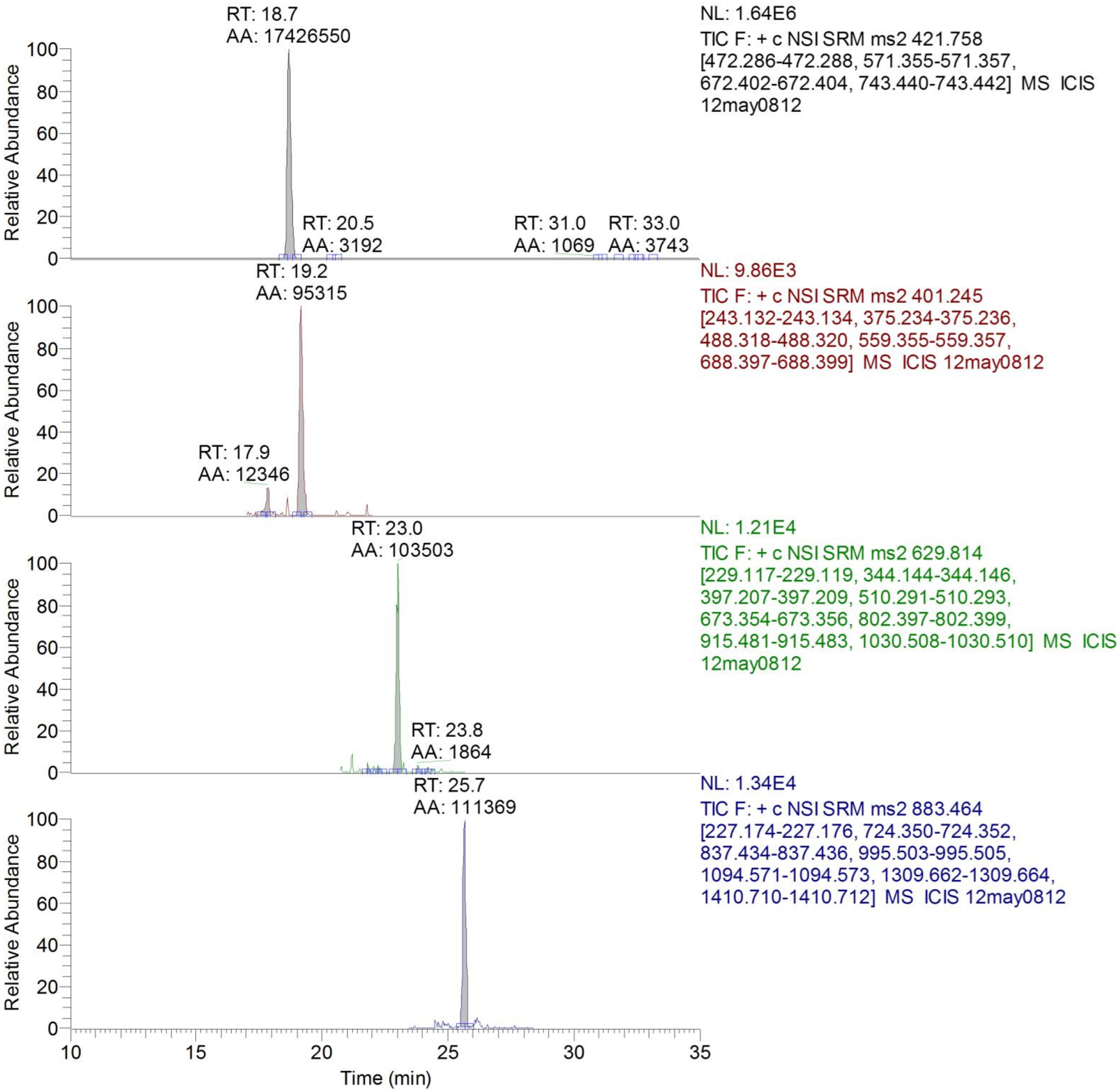
TIC F: + c NSI SRM ms2 919.454 [215.138-215.140, 469.254-469.256, 632.318-632.320, 747.345-747.347, 860.429-860.431, 961.476-961.478, 1090.519-1090.521, 1218.577-1218.579, 1347.620-1347.622] MS ICIS 12may0813
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
35
Time (min)

CTF19

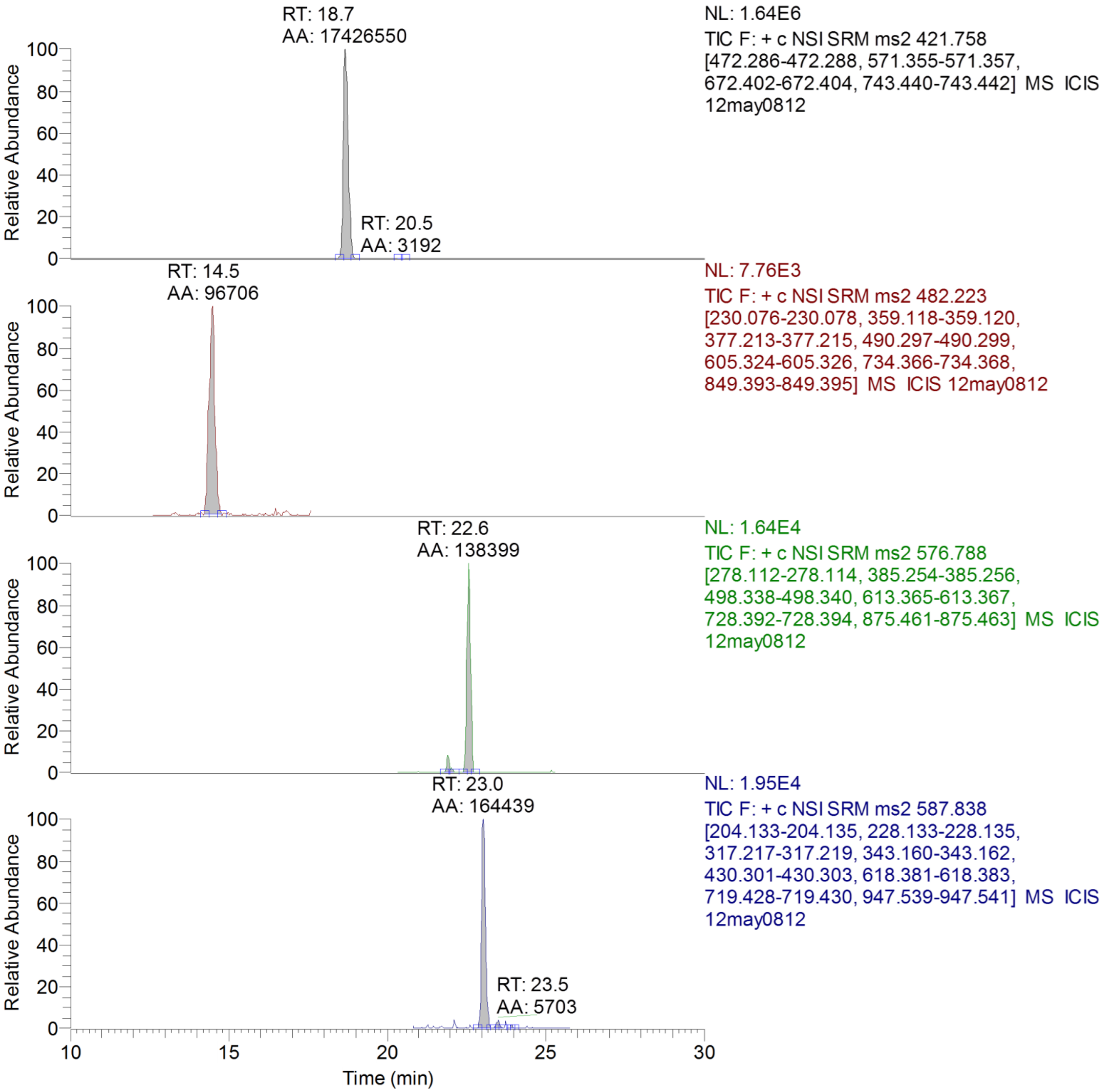

RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
RT: 31.0
AA: 1069
RT: 33.0
AA: 3743
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.800 [472.279-472.281, 571.359-571.361, 672.399-672.401, 743.439-743.441] MS ICIS 12may0812
RT: 19.9
AA: 28736
RT: 18.6
AA: 2348
NL: 4.36E3
TIC F: + c NSI SRM ms2 476.753 [260.195-260.197, 474.327-474.329, 561.359-561.361, 676.386-676.388] MS ICIS 12may0812
RT: 18.4
AA: 7753
RT: 19.0
AA: 2334
NL: 1.31E3
TIC F: + c NSI SRM ms2 500.793 [228.133-228.135, 275.170-275.172, 502.297-502.299, 603.345-603.347, 716.429-716.431, 773.450-773.452, 887.493-887.495] MS ICIS 12may0812
RT: 31.5
AA: 111165
NL: 1.21E4
TIC F: + c NSI SRM ms2 687.411 [159.075-159.077, 260.195-260.197, 373.279-373.281, 487.322-487.324, 600.406-600.408, 713.491-713.493, 827.533-827.535, 955.592-955.594, 1102.660-1102.662] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
35
Time (min)

OKP1

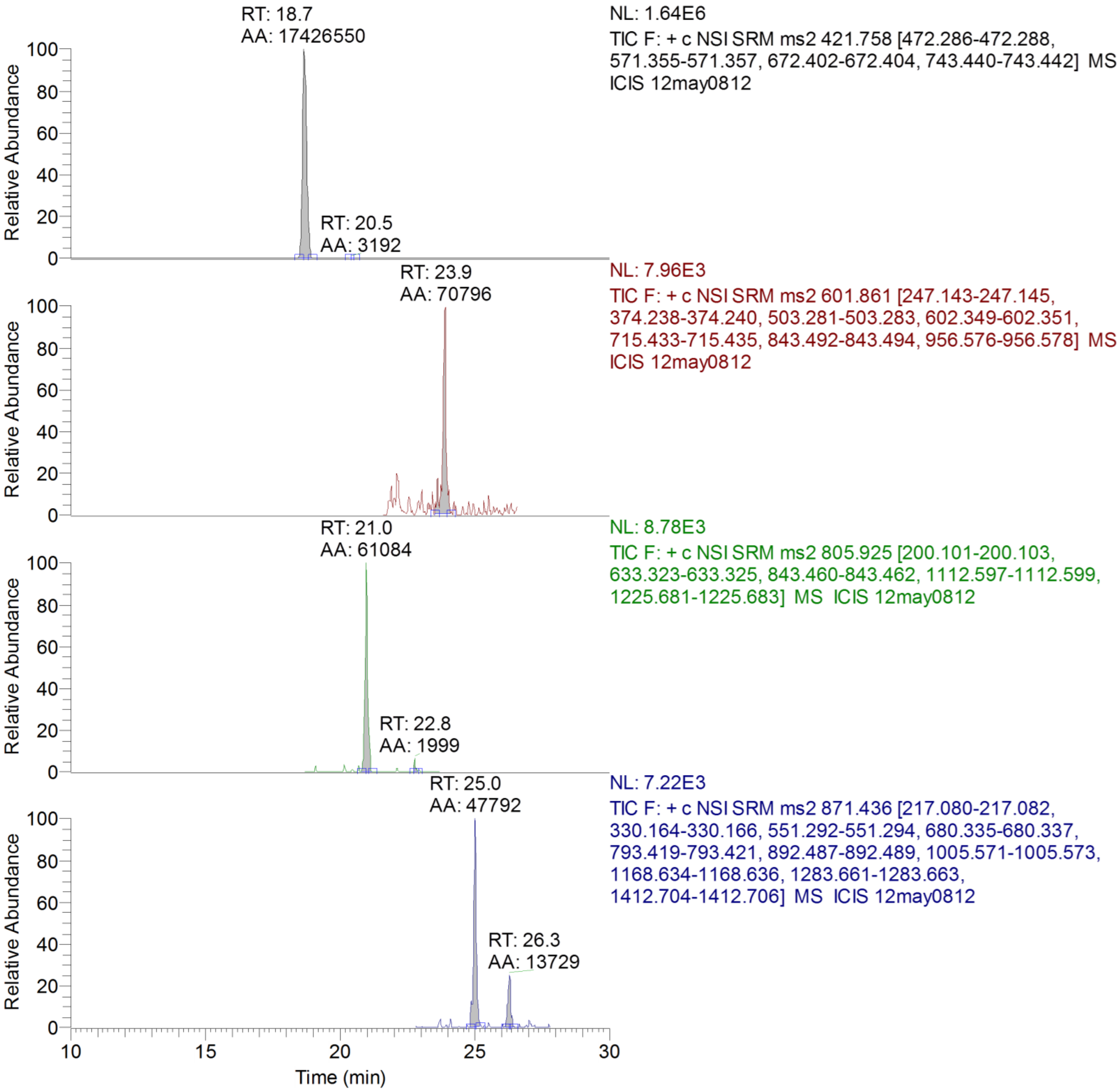


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
RT: 31.0
AA: 1069
RT: 33.0
AA: 3743
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.758 [472.286-472.288, 571.355-571.357, 672.402-672.404, 743.440-743.442] MS ICIS 12may0812
RT: 19.2
AA: 95315
RT: 17.9
AA: 12346
NL: 9.86E3
TIC F: + c NSI SRM ms2 401.245 [243.132-243.134, 375.234-375.236, 488.318-488.320, 559.355-559.357, 688.397-688.399] MS ICIS 12may0812
RT: 23.0
AA: 103503
RT: 23.8
AA: 1864
NL: 1.21E4
TIC F: + c NSI SRM ms2 629.814 [229.117-229.119, 344.144-344.146, 397.207-397.209, 510.291-510.293, 673.354-673.356, 802.397-802.399, 915.481-915.483, 1030.508-1030.510] MS ICIS 12may0812
RT: 25.7
AA: 111369
NL: 1.34E4
TIC F: + c NSI SRM ms2 883.464 [227.174-227.176, 724.350-724.352, 837.434-837.436, 995.503-995.505, 1094.571-1094.573, 1309.662-1309.664, 1410.710-1410.712] MS ICIS 12may0812
Relative Abundance
100
80
60
40
20
0
10
15
20
25
30
35
Time (min)

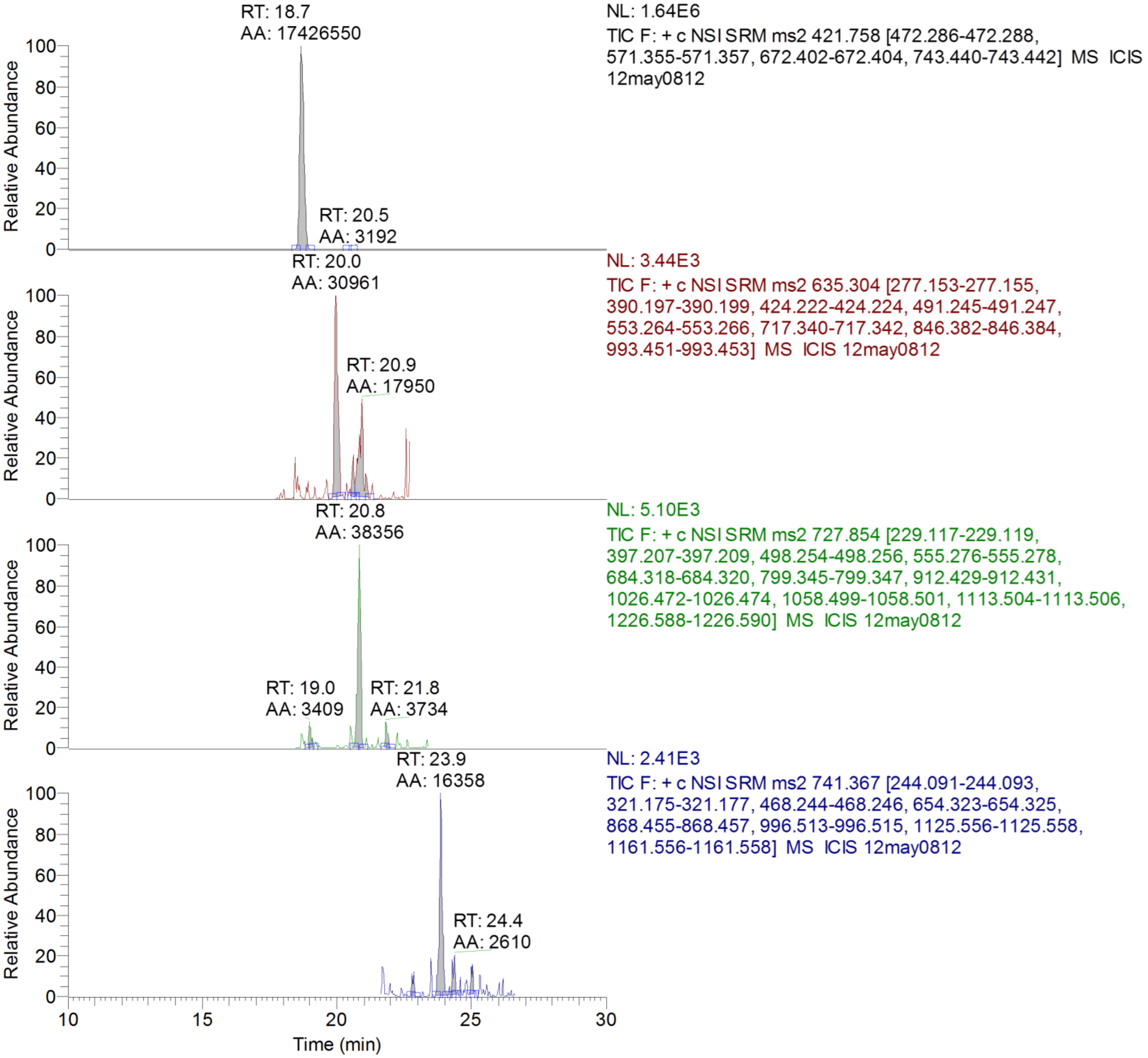
AME1


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.758 [472.286-472.288, 571.355-571.357, 672.402-672.404, 743.440-743.442] MS ICIS 12may0812
RT: 14.5
AA: 96706
NL: 7.76E3
TIC F: + c NSI SRM ms2 482.223 [230.076-230.078, 359.118-359.120, 377.213-377.215, 490.297-490.299, 605.324-605.326, 734.366-734.368, 849.393-849.395] MS ICIS 12may0812
RT: 22.6
AA: 138399
NL: 1.64E4
TIC F: + c NSI SRM ms2 576.788 [278.112-278.114, 385.254-385.256, 498.338-498.340, 613.365-613.367, 728.392-728.394, 875.461-875.463] MS ICIS 12may0812
RT: 23.0
AA: 164439
RT: 23.5
AA: 5703
NL: 1.95E4
TIC F: + c NSI SRM ms2 587.838 [204.133-204.135, 228.133-228.135, 317.217-317.219, 343.160-343.162, 430.301-430.303, 618.381-618.383, 719.428-719.430, 947.539-947.541] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
Time (min)

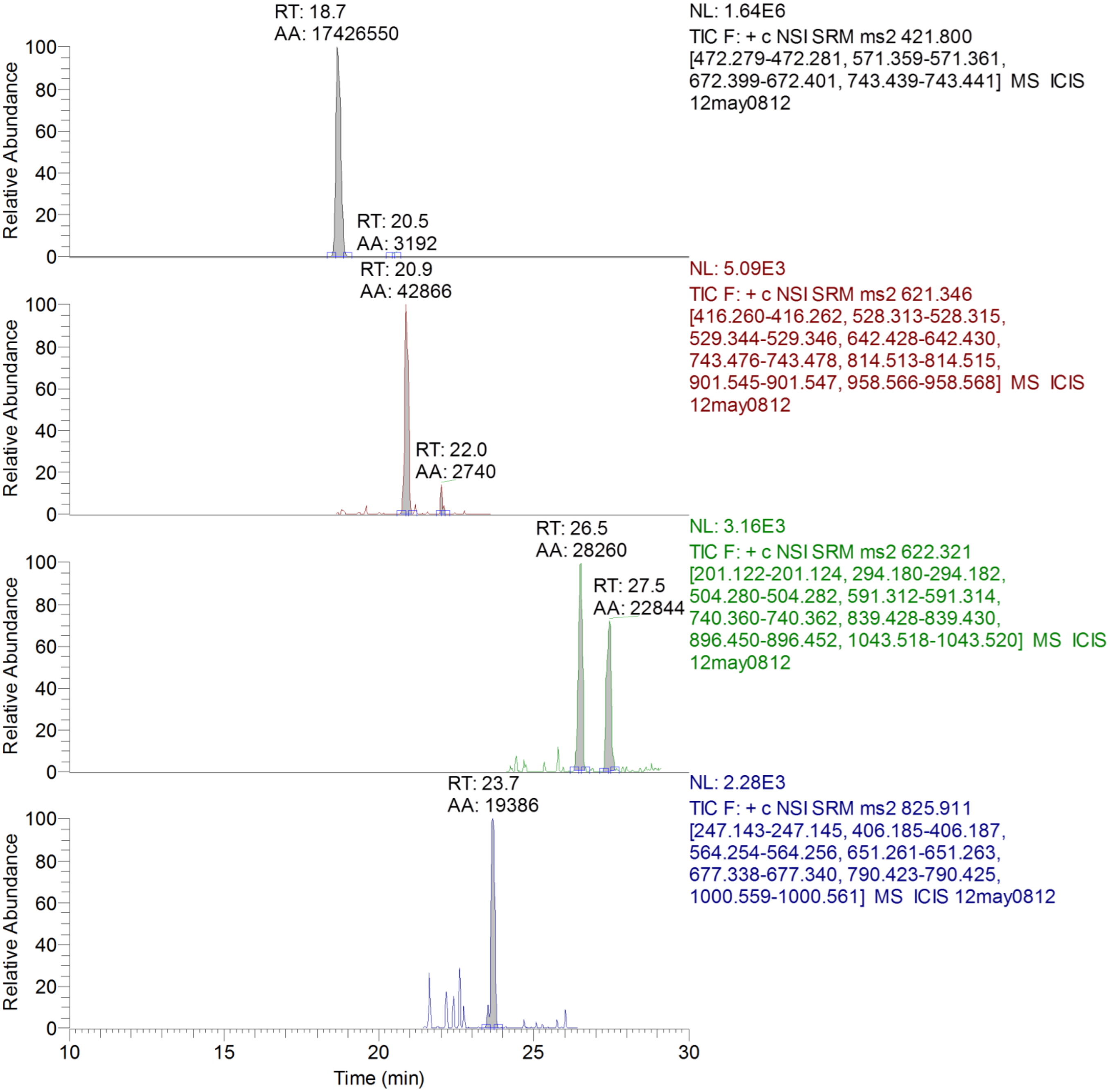
MCM21


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.758 [472.286-472.288, 571.355-571.357, 672.402-672.404, 743.440-743.442] MS ICIS 12may0812
RT: 23.9
AA: 70796
NL: 7.96E3
TIC F: + c NSI SRM ms2 601.861 [247.143-247.145, 374.238-374.240, 503.281-503.283, 602.349-602.351, 715.433-715.435, 843.492-843.494, 956.576-956.578] MS ICIS 12may0812
RT: 21.0
AA: 61084
RT: 22.8
AA: 1999
NL: 8.78E3
TIC F: + c NSI SRM ms2 805.925 [200.101-200.103, 633.323-633.325, 843.460-843.462, 1112.597-1112.599, 1225.681-1225.683] MS ICIS 12may0812
RT: 25.0
AA: 47792
RT: 26.3
AA: 13729
NL: 7.22E3
TIC F: + c NSI SRM ms2 871.436 [217.080-217.082, 330.164-330.166, 551.292-551.294, 680.335-680.337, 793.419-793.421, 892.487-892.489, 1005.571-1005.573, 1168.634-1168.636, 1283.661-1283.663, 1412.704-1412.706] MS ICIS 12may0812
Relative Abundance
100
80
60
40
20
0
10
15
20
25
30
Time (min)

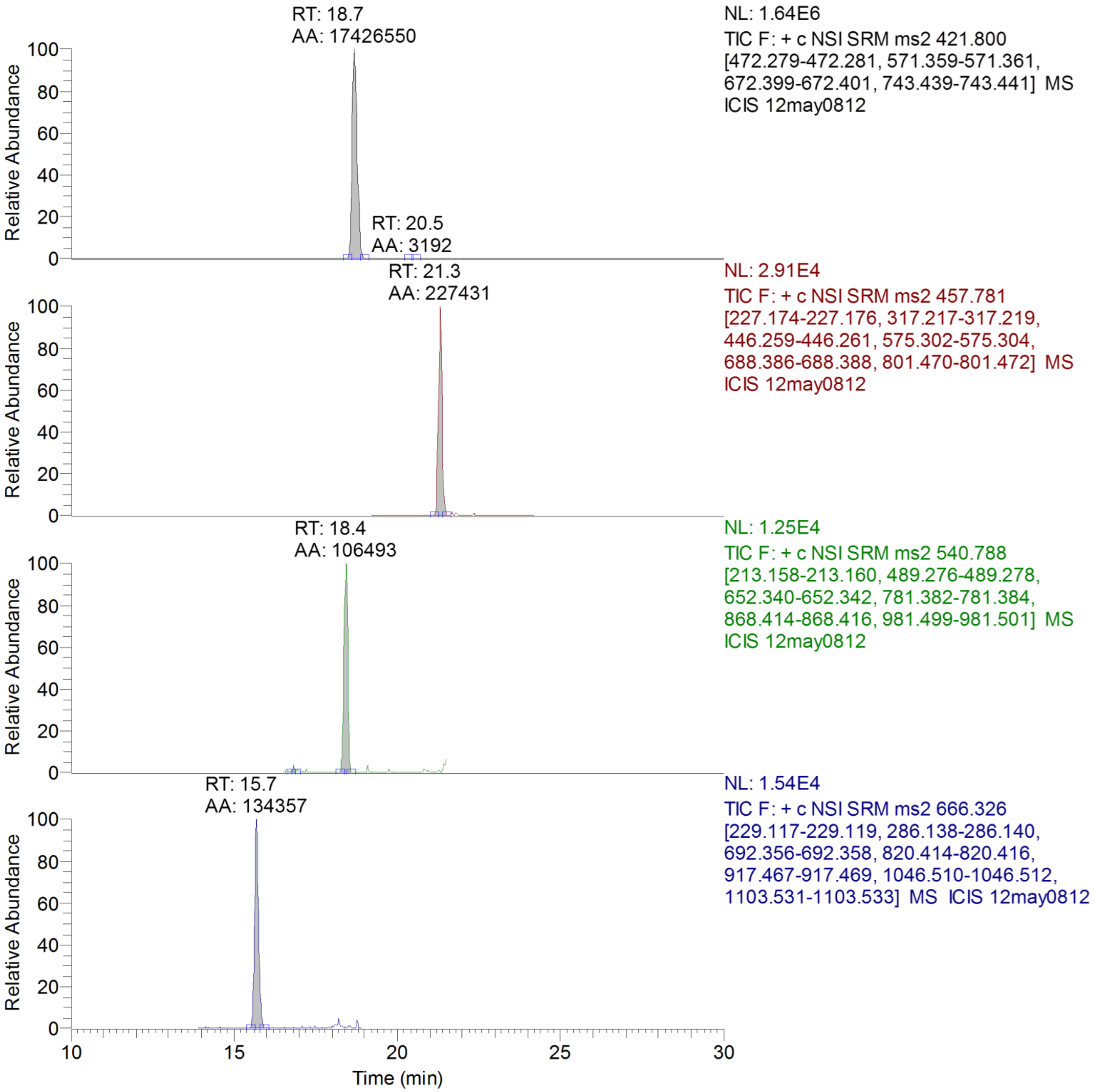
MCM19


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.758 [472.286-472.288, 571.355-571.357, 672.402-672.404, 743.440-743.442] MS ICIS 12may0812
RT: 20.0
AA: 30961
RT: 20.9
AA: 17950
NL: 3.44E3
TIC F: + c NSI SRM ms2 635.304 [277.153-277.155, 390.197-390.199, 424.222-424.224, 491.245-491.247, 553.264-553.266, 717.340-717.342, 846.382-846.384, 993.451-993.453] MS ICIS 12may0812
RT: 20.8
AA: 38356
RT: 19.0
AA: 3409
RT: 21.8
AA: 3734
NL: 5.10E3
TIC F: + c NSI SRM ms2 727.854 [229.117-229.119, 397.207-397.209, 498.254-498.256, 555.276-555.278, 684.318-684.320, 799.345-799.347, 912.429-912.431, 1026.472-1026.474, 1058.499-1058.501, 1113.504-1113.506, 1226.588-1226.590] MS ICIS 12may0812
RT: 23.9
AA: 16358
RT: 24.4
AA: 2610
NL: 2.41E3
TIC F: + c NSI SRM ms2 741.367 [244.091-244.093, 321.175-321.177, 468.244-468.246, 654.323-654.325, 868.455-868.457, 996.513-996.515, 1125.556-1125.558, 1161.556-1161.558] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
Time (min)

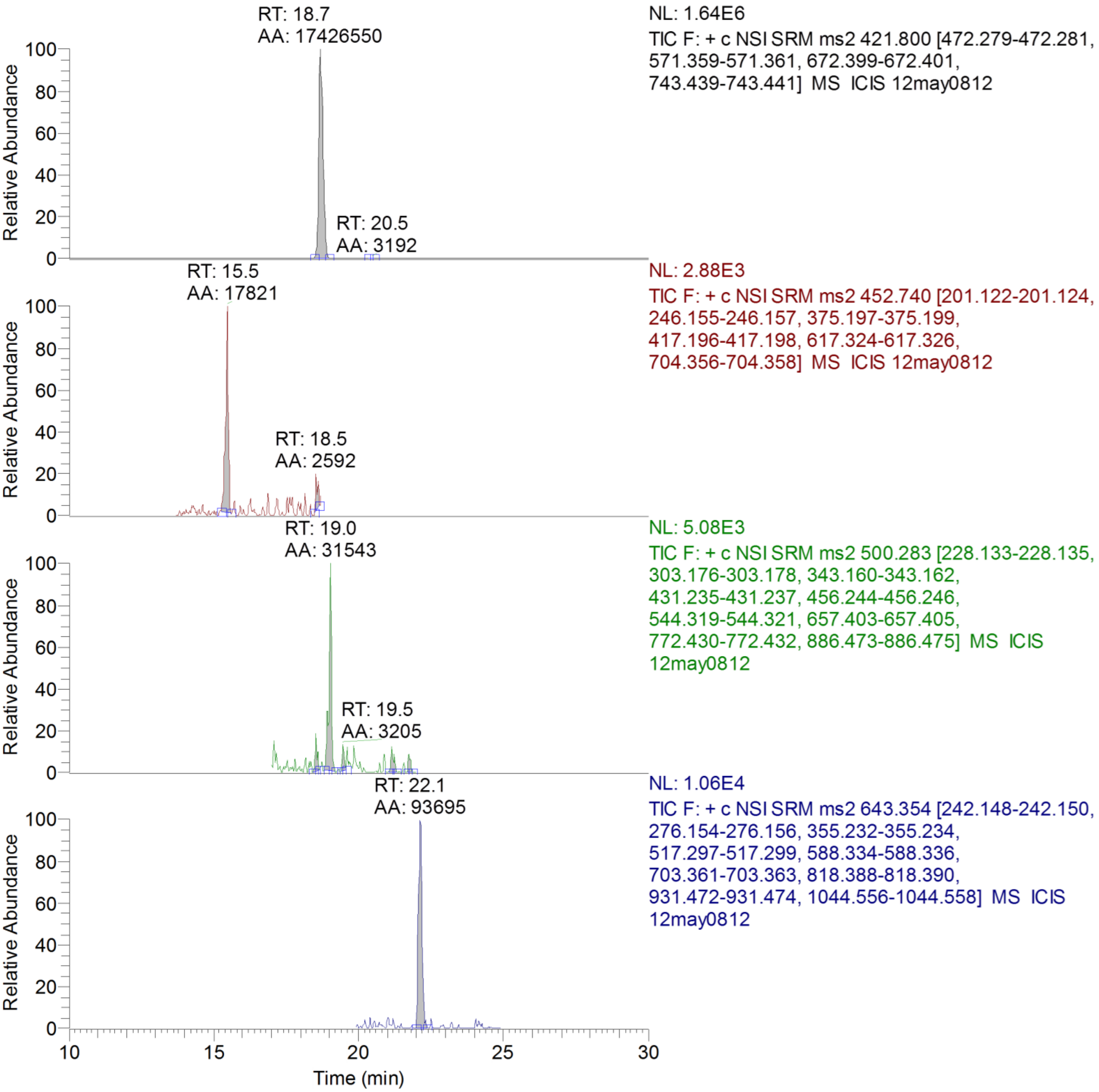
CTF3


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.800 [472.279-472.281, 571.359-571.361, 672.399-672.401, 743.439-743.441] MS ICIS 12may0812
RT: 20.9
AA: 42866
RT: 22.0
AA: 2740
NL: 5.09E3
TIC F: + c NSI SRM ms2 621.346 [416.260-416.262, 528.313-528.315, 529.344-529.346, 642.428-642.430, 743.476-743.478, 814.513-814.515, 901.545-901.547, 958.566-958.568] MS ICIS 12may0812
RT: 26.5
AA: 28260
RT: 27.5
AA: 22844
NL: 3.16E3
TIC F: + c NSI SRM ms2 622.321 [201.122-201.124, 294.180-294.182, 504.280-504.282, 591.312-591.314, 740.360-740.362, 839.428-839.430, 896.450-896.452, 1043.518-1043.520] MS ICIS 12may0812
RT: 23.7
AA: 19386
NL: 2.28E3
TIC F: + c NSI SRM ms2 825.911 [247.143-247.145, 406.185-406.187, 564.254-564.256, 651.261-651.263, 677.338-677.340, 790.423-790.425, 1000.559-1000.561] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
Time (min)

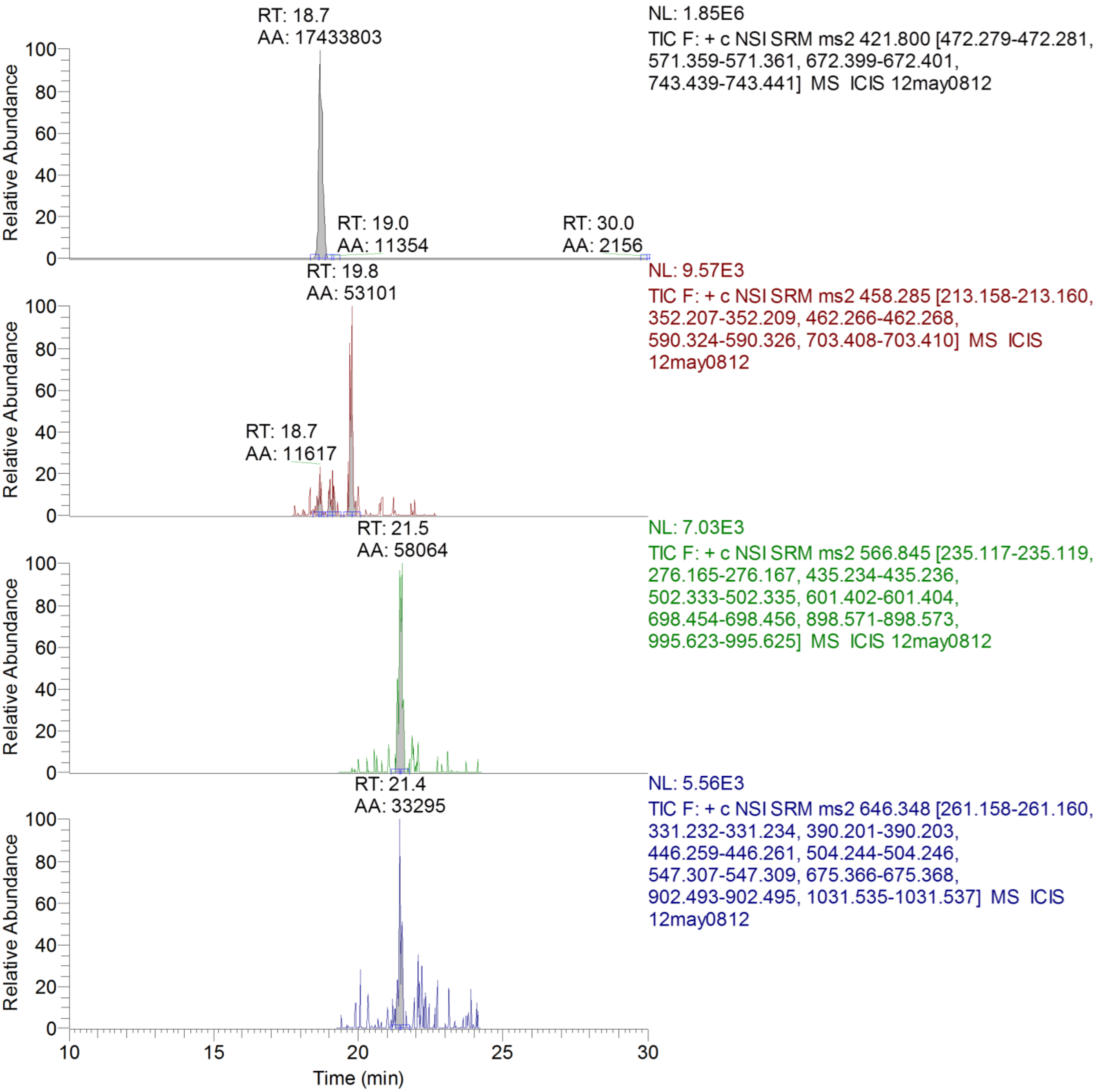
NKP1


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.800 [472.279-472.281, 571.359-571.361, 672.399-672.401, 743.439-743.441] MS ICIS 12may0812
RT: 21.3
AA: 227431
NL: 2.91E4
TIC F: + c NSI SRM ms2 457.781 [227.174-227.176, 317.217-317.219, 446.259-446.261, 575.302-575.304, 688.386-688.388, 801.470-801.472] MS ICIS 12may0812
RT: 18.4
AA: 106493
NL: 1.25E4
TIC F: + c NSI SRM ms2 540.788 [213.158-213.160, 489.276-489.278, 652.340-652.342, 781.382-781.384, 868.414-868.416, 981.499-981.501] MS ICIS 12may0812
RT: 15.7
AA: 134357
NL: 1.54E4
TIC F: + c NSI SRM ms2 666.326 [229.117-229.119, 286.138-286.140, 692.356-692.358, 820.414-820.416, 917.467-917.469, 1046.510-1046.512, 1103.531-1103.533] MS ICIS 12may0812
Relative Abundance
100
80
60
40
20
0
10
15
20
25
30
Time (min)

NKP2


RT: 18.7
AA: 17426550
RT: 20.5
AA: 3192
NL: 1.64E6
TIC F: + c NSI SRM ms2 421.800 [472.279-472.281, 571.359-571.361, 672.399-672.401, 743.439-743.441] MS ICIS 12may0812
RT: 15.5
AA: 17821
RT: 18.5
AA: 2592
NL: 2.88E3
TIC F: + c NSI SRM ms2 452.740 [201.122-201.124, 246.155-246.157, 375.197-375.199, 417.196-417.198, 617.324-617.326, 704.356-704.358] MS ICIS 12may0812
RT: 19.0
AA: 31543
RT: 19.5
AA: 3205
NL: 5.08E3
TIC F: + c NSI SRM ms2 500.283 [228.133-228.135, 303.176-303.178, 343.160-343.162, 431.235-431.237, 456.244-456.246, 544.319-544.321, 657.403-657.405, 772.430-772.432, 886.473-886.475] MS ICIS 12may0812
RT: 22.1
AA: 93695
NL: 1.06E4
TIC F: + c NSI SRM ms2 643.354 [242.148-242.150, 276.154-276.156, 355.232-355.234, 517.297-517.299, 588.334-588.336, 703.361-703.363, 818.388-818.390, 931.472-931.474, 1044.556-1044.558] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
10
15
20
25
30
Time (min)

CHL4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AA: 17433803
RT: 19.0
AA: 11354
RT: 30.0
AA: 2156
NL: 1.85E6
TIC F: + c NSI SRM ms2 421.800 [472.279-472.281, 571.359-571.361, 672.399-672.401, 743.439-743.441] MS ICIS 12may0812
RT: 19.8
AA: 53101
RT: 18.7
AA: 11617
NL: 9.57E3
TIC F: + c NSI SRM ms2 458.285 [213.158-213.160, 352.207-352.209, 462.266-462.268, 590.324-590.326, 703.408-703.410] MS ICIS 12may0812
RT: 21.5
AA: 58064
NL: 7.03E3
TIC F: + c NSI SRM ms2 566.845 [235.117-235.119, 276.165-276.167, 435.234-435.236, 502.333-502.335, 601.402-601.404, 698.454-698.456, 898.571-898.573, 995.623-995.625] MS ICIS 12may0812
RT: 21.4
AA: 33295
NL: 5.56E3
TIC F: + c NSI SRM ms2 646.348 [261.158-261.160, 331.232-331.234, 390.201-390.203, 446.259-446.261, 504.244-504.246, 547.307-547.309, 675.366-675.368, 902.493-902.495, 1031.535-1031.537] MS ICIS 12may0812
Relative Abundance
0
20
40
60
80
100
Time (min)
10
15
20
25
30

Figure S4. Representative chromatograms for each yeast kinetochore peptide detected in these analyses. For each protein, four chromatograms are shown. The top chromatogram is the trypsin peptide VATVSLPR that is used as a common marker in all analyses. The subsequent three chromatograms show the selective detection of the three peptides used to measure each kinetochore protein. The response for each protein is the sum of the integrated peak area, denoted AA in the chromatograms, for the three peptides that are monitored.

Abbreviations in these chromatograms
RT: – the retention time for the chromatographic peak
AA: – the automatically integrated peak area
NL: – normalized, the value used for data normalization in that chromatogram
TIC: – total ion current, the ion intensity for all fragment ions is used
F: + c NSI SRM ms2 – details of the data filtering to use positive ions in the centroid mode from nanospray ionization in a selected reaction monitoring tandem mass spectrometry experiment
MS ICIS: – a mass spectrometry experiment with the peak area measured using the Interactive Chemical Information System peak detection and integration algorithm

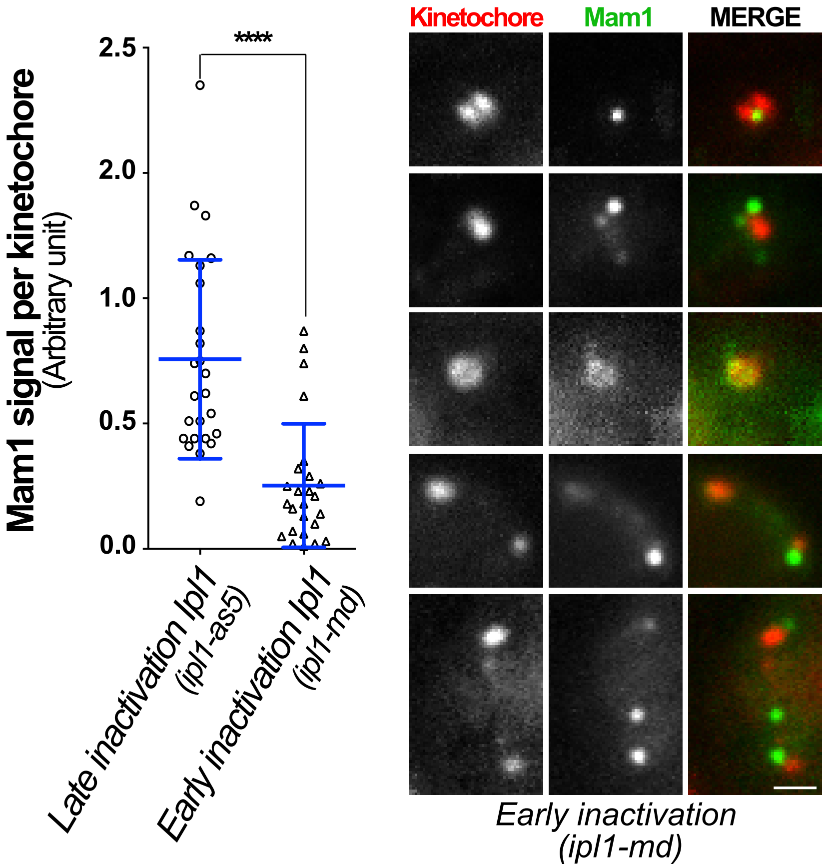

Figure S5. Quantifying the Mam1 signal at kinetochores in *ipl1* mutants. *ipl1-md*, and *ipl1-as5*/*ipl1-md (ipl1-as5)* diploid cells expressing Mam1-GFP and Mtw1-3xmCherry were switched to sporulation medium and released from a pachytene arrest (P_{GAL1}*-NDT80 GAL4-ER*) at 4.5 hours by the addition of 5 µM β-estradiol. Ipl1-as5 was inhibited by the addition of 50 µM 1NA-PP1 at the time of the release. As in Supplemental Figure S1, we the defined area around the kinetochores and measured the total signal I this area in the Mam1 channel (GFP) (A). We corrected for background by subtracting the signal in the GFP channel in an equivalently-sized close area (B). This value was divided divided by the corrected signal in the kinetochore channel (mCherry) for the same area (C minus D). Using this formula, we scored, for each cell (n≥ 25), the relative amount of Mam1 per kinetochore between the early inactivation of Ipl1 (using *ipl1-md* mutant) and late inactivation (using *ipl1-as5* with 1NA-PP1 inhibitor) at 150mn after the release. Graph shows values of individual cells, average, and one standard deviation. The student's t-test was used to evaluate the significance of observed differences. ****p<0.0001. The panel on the right shows representative images of Mam1-GFP patterns observed in *ipl1-md* cells. Note that these mutant cells frequently feature one or more bright foci of Mam1 signal that is not co-localized with kinetochores. Scale bar, 1µm.

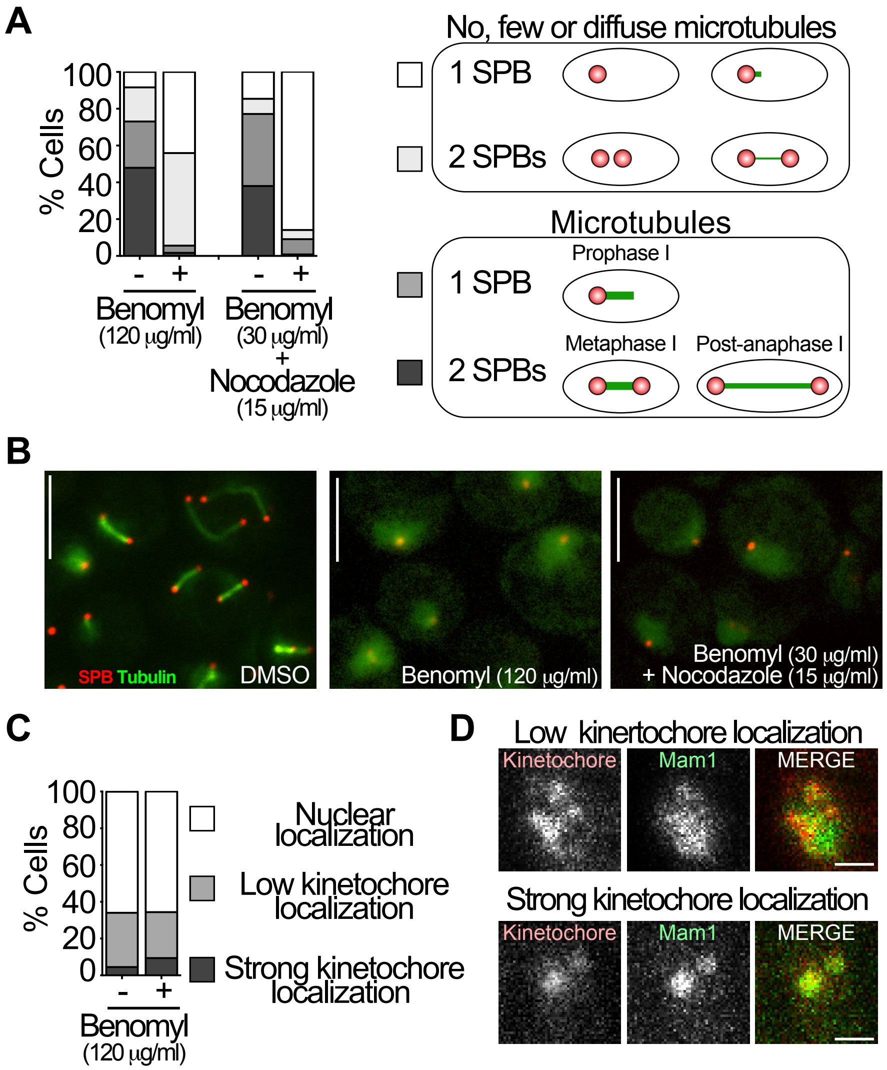

Figure S6. Effect of benomyl and nocodazole on microtubule dynamics and monopolin loading. (A-B) Wild-type diploid cells carrying SPB (Spc42-DsRed) and spindle (Tub1-GFP) markers were sporulated and released from a pachytene arrest (*P_{GAL1}-NDT80 GAL4-ER*) at 6 hours by the addition of 5 µM β-estradiol. Cells were scored according to Tubulin-GFP distribution as shown in (B) with either no or diffuse staining of Tub1-GFP with one (white) or two SPBs (light grey), or with strong staining of Tub1-GFP with one (medium grey) or two SPBs (dark grey). Benomyl (30 µg/ml) and nocodazole (15 µg/ml) were added to the cells at the time of release. Scale bars = 5 µm. (C) *ipl1-md* diploid cells carrying Mam1-GFP and Mtw1-3xmCherry were sporulated and released from a pachytene arrest (*P_{GAL1}-NDT80 GAL4-ER*) at 6 hours by the addition of 5 µM β-estradiol. The protocol is summarized in Figure 6A. T=0 represents the time when cells were released from the arrest. Benomyl (120µg/ml) was added to the cells at the time of release. Cells were categorized according to Mam1-GFP distribution as shown in Figure 6E. (D) Representative cells for Figure 7B with low and strong kinetochore localization of Mam1-GFP in diploid cells are shown. Scale bars = 1 µm.

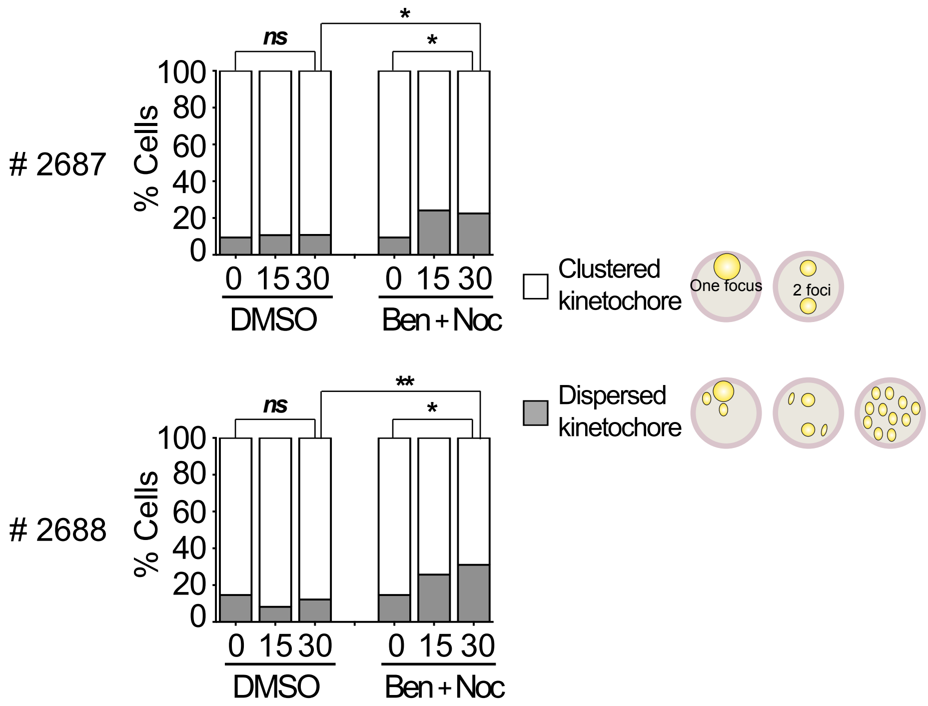

Figure S7. Effect of benomyl and nocodazole on kinetochore release in *ipl1*cells. *ipl1-md* diploid cells expressing Ndc80-GFP and Mtw1-3xmCherry were switched to sporulation medium. The strains used were *ndt80* mutants that arrest in pachytene. DMSO or benomyl (30 µg/ml) and nocodazole (15 µg/ml) were added to the cells 6 hours after induction of meiosis (T=0). Using the Mtw1-3xmCherry signal, cells were scored as having clustered kinetochores (< 3 kinetochore foci, white box) or dispersed kinetochores (≥ 3 kinetochore foci, dark grey box). Two zygotes (DRM2687 and DRM2688) were used. (n≥ 50 per time-point). Fisher's exact tests were used to evaluate the significance of observed differences. *p<0.05, **p<0.01.

Table S1: Diploid strain list

Diploid	**Parents strain**	**Figure**
DRM1845	X454 * Y421	Fig1A
DRM1846	X455 * Y422	Fig1A
DRM1811	X1679 * Y1599	Fig1B-E, Fig3E “Ndc80”, FigS1
DRM1812	X1680 * Y1600	Fig1B-E, Fig3E “Ndc80”
DRM2431	X1460 * Y1425	Fig1F
DRM1839	X1475 * Y1439	Fig2B “Mif2-GFP”, FigS2B “Mif2”
DRM1840	X1476 * Y1440	Fig2B “Mif2-GFP”, FigS2B “Mif2”
DRM1841	X1477 * Y1441	Fig2B “Ndc10-GFP”, FigS2B “Ndc10”
DRM1842	X1478 * Y1442	Fig2B “Ndc10-GFP”, FigS2B “Ndc10”
DRM1843	X2001 * Y1789	Fig2B “Cnn1-GFP”, FigS2B “Cnn1”
DRM1844	X2002 * Y1790	Fig2B “Cnn1-GFP”, FigS2B “Cnn1”
DHC164 (3x)	X1447 * Y1420	Fig2D-E, Fig3A-B, D
DRM1833	X1469 * Y1433	Fig2D “Ctf19-GFP”, FigS2B “Ctf19”
DRM1834	X1470 * Y1434	Fig2D “Ctf19-GFP”, FigS2B “Ctf19”
DRM1837	X1473 * Y1437	Fig2E “Ctf3-GFP”, FigS2B “Ctf3”
DRM1838	X1474 * Y1438	Fig2E “Ctf3-GFP”, FigS2B “Ctf3”
DRM1829	X1365 * Y1339	Fig3A “Dsn1-GFP”, Fig3F “Dsn1”, FigS2B “Dsn1”
DRM1830	X1366 * Y1340	Fig3A “Dsn1-GFP”, Fig3F “Dsn1”, FigS2B “Dsn1”
DRM2291, 2323	X1957 * Y1763	Fig3A “Nsl1-GFP”, Fig3F “Nsl1”, FigS2B “Nsl1”
DRM2292, 2324	X1958 * Y1764	Fig3A “Nsl1-GFP”, Fig3F “Nsl1”, FigS2B “Nsl1”
DRM1825	X1363 * Y1337	Fig3B “Spc105-GFP”, Fig3F “Spc105”, FigS2B “Spc105”
DRM1826	X1364 * Y1338	Fig3B “Spc105-GFP”, Fig3F “Spc105”, FigS2B “Spc105”
DRM1831	X1367 * Y1341	Fig3C “Spc24-GFP”
DRM1832	X1368 * Y1342	Fig3C “Spc24-GFP”
DRM2295, 2327	X1959 * Y1765	Fig3C “Nuf2-GFP”, Fig3F “Nuf2”, FigS2B “Nuf2”
DRM2296, 2328	X1960 * Y1766	Fig3C “Nuf2-GFP”, Fig3F “Nuf2”, FigS2B “Nuf2”
DRM1821	X1335 * Y1275	Fig3C “Ndc80-GFP”, FigS2B “Ndc80”
DRM1822	X1336 * Y1276	Fig3C “Ndc80-GFP”, FigS2B “Ndc80”
DRM2395	X873 * Y1763	Fig3D “Nsl1”
DRM2396	X874 * Y1764	Fig3D “Nsl1”
DRM2397	X873 * Y1599	Fig3D “Ndc80”
DRM2398	X874 * Y1600	Fig3D “Ndc80”
DRM2399	X873 * Y1765	Fig3D “Nuf2”
DRM2400	X874 * Y1766	Fig3D “Nuf2”
DRM2401	X873 * Y1757	Fig3D “Spc24”
DRM2402	X874 * Y1758	Fig3D “Spc24”
DRM2403	X873 * Y1783	Fig3D “Spc25”
DRM2404	X874 * Y1784	Fig3D “Spc25”
DRM1823	X1355 * Y1335	Fig3E “Dam1-GFP”, Fig3F “Dam1”, FigS2B “Dam1”
DRM1824	X1356 * Y1336	Fig3E “Dam1-GFP”, Fig3F “Dam1”, FigS2B “Dam1”
DRM2297, 2329	X1955 * Y1757	Fig3F “Spc24”, FigS2B “Spc24”
DRM2298, 2330	X1956 * Y1758	Fig3F “Spc24”, FigS2B “Spc24”
DRM1849	X2080 * Y1859	Fig4A “*cdc28-as1*”
DRM1850	X2081 * Y1859	Fig4A “*cdc28-as1*”

Diploid	**Parents strain**	**Figure**
DCH1801	X1531 * Y1492	Fig4B “*ndt80 cdc28-as1*”
DCH1802	X1706 * Y1494	Fig4B “*ndt80 cdc28-as1*”
DRM1005	X871 * Y909	Fig4C “*WT*”
DRM1006	X872 * Y910	Fig4C “*WT*”
DRM2447	X2151 * Y1921	Fig4C “*cdc6-md*”
DRM2448	X2152 * Y1922	Fig4C “*cdc6-md*”
DRM2319	X1217 * Y1192	Fig4D “*WT*”
DRM2320	X1218 * Y1192	Fig4D “*WT*”
DRM2321	X2019 * Y1799	Fig4D “*cdc6-md*”
DRM2322	X2020 * Y1800	Fig4D “*cdc6-md*”
DRM1817	X1519 * Y1471	Fig5A “*WT*”
DRM1818	X1520 * Y1472	Fig5A “*WT*”
DRM1783	X1589 * Y1511	Fig5A “*ipl1-md*”
DRM1784	X1590 * Y1514	Fig5A “*ipl1-md*”
DRM2432	X2120 * Y1426	Fig5B “*ipl1-md*”
DCH1793	X1611 * Y1529	Fig5C “*WT*”
DCH1794	X1612 * Y1530	Fig5C “*WT*”
DCH1795	X1609 * Y1527	Fig5C “*ipl1-md*”
DCH1796	X1610 * Y1528	Fig5C “*ipl1-md*”
DCH1789	X1603 * Y1521	Fig5D “*WT*”
DCH1790	X1604 * Y1522	Fig5D “*WT*”
DCH1791	X1601 * Y1519	Fig5D “*ipl1-md*”
DCH1792	X1602 * Y1520	Fig5D “*ipl1-md*”
DHC197 (3x), DHC266 (2x), DHC268 (2x), DRM1903	X1446 * Y1419	Fig5E “*WT*” Fig5E “*WT*” Fig5E “*WT*” FigS2A “Dsn1-3xFLAG”
DHC200 (3x), DHC267 (2x)	X1571 * Y1500	Fig5E “*ipl1-md*” Fig5E “*ipl1-md*”
DRM2433	X1675 * Y1583	Fig6B-C “*WT*”
DRM2435	X1691 * Y1586	Fig6D-E “*ipl1-md*”
DRM2437	X1691 * Y1582	Fig6D-E “*ipl1-as5/ipl1-md*”
DRM2438	X1692 * Y1582	Fig6D-E “*ipl1-as5/ipl1-md*”
DRM2557, DRM2611	X1673 * Y1585	Fig7A-B, FigS5 “*ipl1-md*”, FigS6C “*ipl1-md*”
DRM2558, DRM2612	X1674 * Y1586	Fig7A-B, FigS5 “*ipl1-md*”, FigS6C “*ipl1-md*”
DRM2589	X2289 * Y2133	Fig7B “*ndc80-md*”
DRM2590	X2290 * Y2134	Fig7B “*ndc80-md*”
DRM2591	X2287 * Y2131	Fig7B, FigS6D “*ipl1-md ndc80-md*”
DRM2592	X2298 * Y2132	Fig7B, FigS6D “*ipl1-md ndc80-md*”
DRM2687	X1677 * Y2119	Fig7C “*ndt80 ipl1-md*”, FigS7
DRM2688	X1678 * Y2120	Fig7C “*ndt80 ipl1-md*”, FigS7
DRM2303	X2047 * Y1477	FigS2A “Dam1-GFP”
DRM2304	X2048 * Y1478	FigS2A “Dam1-GFP”
DRM2228	X1294 * Y1192	FigS2A “Ndc80-GFP”

Diploid	**Parents strain**	**Figure**
DRM2287	X1999 * Y1787	FigS2A "Nuf2-GFP"
DRM2288	X2000 * Y1788	FigS2A "Nuf2-GFP"
DRM2243	X2005 * Y1481	FigS2A "Spc24-GFP"
DRM2244	X2006 * Y1482	FigS2A "Spc24-GFP"
DRM2245	X2007 * Y1479	FigS2A "Spc105-GFP"
DRM2246	X2008 * Y1480	FigS2A "Spc105-GFP"
DRM2459	X2046 * Y1475	FigS2A "Mam1-GFP"
DRM2285	X1997 * Y1785	FigS2A "Nsl1-GFP"
DRM2286	X1998 * Y1786	FigS2A "Nsl1-GFP"
DRM2247	X2009 * Y1473	FigS2A "Dsn1-GFP"
DRM2237	X1287 * Y1279	FigS2A "Mtw1-RFP"
DRM2238	X1288 * Y1280	FigS2A "Mtw1-RFP"
DRM2263	X454 * Y399	FigS2A "Mtw1-GFP"
DRM2264	X455 * Y400	FigS2A "Mtw1-GFP"
DRM2317	X2049 * Y1815	FigS2A "Ctf19-GFP"
DRM2318	X2050 * Y1816	FigS2A "Ctf19-GFP"
DRM2305	X2051 * Y1817	FigS2A "Chl4-GFP"
DRM2306	X2052 * Y1818	FigS2A "Chl4-GFP"
DRM2307	X2053 * Y1819	FigS2A "Ctf3-GFP"
DRM2308	X2054 * Y1820	FigS2A "Ctf3-GFP"
DRM2225	X1907 * Y1731	FigS2A "Cnn1-GFP"
DRM2226	X1908 * Y1732	FigS2A "Cnn1-GFP"
DRM2331	X2055 * Y1823	FigS2A "Ndc10-GFP"
DRM2332	X2056 * Y1824	FigS2A "Ndc10-GFP"
DRM2333	Y1821 * Y1822	FigS2A "Mif2-GFP"
DRM00	X55 * Y8	FigS2A "Control"
DRM2343	X55 * Y169	FigS2A "Control"
DRM2344	X206 * Y170	FigS2A "Control"
DRM1835	X1471 * Y1435	FigS2B "Chl4"
DRM1836	X1472 * Y1436	FigS2B "Chl4"
DRM2729	X1673 * Y1581	FigS5 "*ipl1-as5*"
DRM2730	X1674 * Y1582	FigS5 "*ipl1-as5*"
DRM2561	X1581 * Y1507	FigS6A-B
DRM2562	X1582 * Y1508	FigS6A-B

Table S2: Haploid strain list

X454	MATa, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3
Y421	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3, SPC42-[MDE1145: URA3 SPC42-DSRed]
X455	MAT∝, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3
Y422	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3, SPC42-[MDE1145: URA3 SPC42-DSRed]
X1679	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
Y1599	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NDC80-EGFP-TRP1
X1680	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
Y1600	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NDC80-EGFP-TRP1
X1460	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, NDC80-EGFP-KanMx4, MTW1-13xMYC-TRP1, ndt80::LEU2
Y1425	MAT∝, leu2, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1, SPC42-[MDE1145: URA3 SPC42-DSRed], MTW1-13xMYC-HIS3MX, ndt80::LEU2
X1475	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, MIF2-yeGFP-TRP1
Y1439	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, MIF2-yeGFP-TRP1
X1476	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, MIF2-yeGFP-TRP1
Y1440	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, MIF2-yeGFP-TRP1
X1477	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, NDC10-yeGFP-TRP1
Y1441	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, NDC10-yeGFP-TRP1

X1478	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, NDC10-yeGFP-TRP1
Y1442	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, NDC10-yeGFP-TRP1
X2001	MATa, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CNN1-yeGFP-TRP1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1
Y1789	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, CNN1-yeGFP-TRP1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1
X2002	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CNN1-yeGFP-TRP1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1
Y1790	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, CNN1-yeGFP-TRP1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1
X1447	MATa, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, ndt80::LEU2, Dsn1-3XFLAG-KanMX
Y1420	MAT∝, ura3-1, trp1-Δ63, leu2-?, tyr1-2, lys2-2, met13-c, cyh2-1, ndt80::LEU2, his3-Δ1, Dsn1-3xFLAG-KanMX
X1469	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CTF19-yeGFP-TRP1
Y1433	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CTF19-yeGFP-TRP1
X1470	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CTF19-yeGFP-TRP1
Y1434	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CTF19-yeGFP-TRP1
X1473	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CTF3-yeGFP-TRP1
Y1437	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CTF3-yeGFP-TRP1
X1474	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CTF3-yeGFP-TRP1
Y1438	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CTF3-yeGFP-TRP1

X1365	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, DSN1-yeGFP-TRP1
Y1339	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, DSN1-yeGFP-TRP1
X1366	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, DSN1-yeGFP-TRP1
Y1340	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, DSN1-yeGFP-TRP1
X1957	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NSL1-yeGFP-TRP1
Y1763	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, NSL1-yeGFP-TRP1, natNT2-PGAL1-NDT80
X1958	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NSL1-yeGFP-TRP1
Y1764	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, NSL1-yeGFP-TRP1, natNT2-PGAL1-NDT80
X1363	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, SPC105-yeGFP-TRP1
Y1337	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, SPC105-yeGFP-TRP1
X1364	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, SPC105-yeGFP-TRP1
Y1338	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, SPC105-yeGFP-TRP1
X1367	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, SPC24-yeGFP-TRP1
Y1341	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, SPC24-yeGFP-TRP1
X1368	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, SPC24-yeGFP-TRP1
Y1342	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, SPC24-yeGFP-TRP1

X1959	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NUF2-yeGFP-TRP1
Y1765	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, NUF2-yeGFP-TRP1, natNT2-PGAL1-NDT80
X1960	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NUF2-yeGFP-TRP1
Y1766	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, NUF2-yeGFP-TRP1, natNT2-PGAL1-NDT80
X1335	MATa, met13-d, trp1-Δ63, tyr1-1, ura3-13, his3-Δ1, can1-R, leu2, lys2-1, KanMX-PGAL1-NDT80, NDC80-EGFP-TRP1, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1
Y1275	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1
X1336	MAT∝, met13-d, trp1-Δ63, tyr1-1, ura3-13, his3-Δ1, can1-R, leu2, lys2-1, KanMX-PGAL1-NDT80, NDC80-EGFP-TRP1, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1
Y1276	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1
X1355	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, DAM1-yeGFP-TRP1
Y1335	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, DAM1-yeGFP-TRP1
X1356	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, DAM1-yeGFP-TRP1
Y1336	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, URA3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, DAM1-yeGFP-TRP1
X1955	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], SPC24-yeGFP-TRP1, natNT2-PGAL1-NDT80
Y1757	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, natNT2-PGAL1-NDT80, SPC24-yeGFP-TRP1
X1956	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-ura3::hphNT1], SPC24-yeGFP-TRP1, natNT2-PGAL1-NDT80
Y1758	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, natNT2-PGAL1-NDT80, SPC24-yeGFP-TRP1

X2080	MAT∝, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3, cdc28-as1
X2081	MAT∝, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3, cdc28-as1
Y1859	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3, SPC42-[MDE1145: URA3 SPC42-DSRed], cdc28-as1
X1531	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), NDC80-EGFP-TRP1, natNT2-PGAL1-NDT80, cdc28-as1
Y1492	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1, cdc28-as1, SPC42-[MDE1145: URA3 SPC42-DSRed]
X1706	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC42-[MDE1145: URA3::HIS SPC42-DSRed], cdc28-as1, NDC80-EGFP-TRP1, natNT2-PGAL1-NDT80
Y1494	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1, cdc28-as1
X1519	MATa, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC42-[MDE1145: URA3::HIS SPC42-DSRed], NDC80-EGFP-TRP1, natNT2-PGAL1-NDT80
Y1471	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
X1520	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC42-[MDE1145: URA3::HIS SPC42-DSRed], NDC80-EGFP-TRP1, natNT2-PGAL1-NDT80
Y1472	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
X1589	MATa, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, NDC80-EGFP-TRP1, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
Y1511	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, NDC80-EGFP-TRP1
X1590	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, NDC80-EGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
Y1514	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, NDC80-EGFP-TRP1, SPC42-[MDE1145: URA3 SPC42-DSRed]
X1611	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], SPC24-yeGFP-TRP1
Y1529	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, SPC24-yeGFP-TRP1

X1612	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], SPC24-yeGFP-TRP1
Y1530	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, SPC24-yeGFP-TRP1
X1609	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], SPC24-yeGFP-TRP1, PCLB2-3HA-IPL1 KanMX6
Y1527	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, SPC24-yeGFP-TRP1
X1610	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], SPC24-yeGFP-TRP1, PCLB2-3HA-IPL1 KanMX6
Y1528	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, SPC24-yeGFP-TRP1
X1603	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], DAM1-yeGFP-TRP1
Y1521	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, DAM1-yeGFP-TRP1
X1604	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], DAM1-yeGFP-TRP1
Y1522	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, DAM1-yeGFP-TRP1
X1601	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], DAM1-yeGFP-TRP1
Y1519	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, DAM1-yeGFP-TRP1
X1602	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], DAM1-yeGFP-TRP1
Y1520	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, DAM1-yeGFP-TRP1
X2120	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, NDC80-EGFP-KanMx4, MTW1-13xMYC-TRP1, ndt80::LEU2, PCLB2-3HA-IPL1 KanMX6
Y1426	MATa, leu2, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1, PCLB2-3HA-IPL1 KanMX6, SPC42-[MDE1145: URA3 SPC42-DSRed], MTW1-13xMYC-HIS3MX, ndt80::LEU2

X1446	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, Dsn1-3FLAG-kanMX
Y1419	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, Dsn1-3xFLAG-KanMX
X1571	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, Dsn1-3FLAG-kanMX, PCLB2-3HA-IPL1 KanMX6
Y1500	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, Dsn1-3xFLAG-KanMX, PCLB2-3HA-IPL1 KanMX6
X1675	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80
Y1583	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, MAM1-yeGFP-TRP1
X1691	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
Y1586	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1
X1692	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, SPC42-[MDE1145: URA3::HIS SPC42-DSRed], natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
Y1582	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, ipl1ΔKAN:ipl1-as5-MYC:HIS3:LEU2, MAM1-yeGFP-TRP1
X2047	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), DAM1-yeGFP-TRP1
Y1477	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, DAM1-yeGFP-TRP1
X2048	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), DAM1-yeGFP-TRP1
Y1478	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, DAM1-yeGFP-TRP1
X1294	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, NDC80-EGFP-TRP1
Y1192	MATa, leu2, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1
X1999	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3-13, NUF2-yeGFP-TRP1
Y1787	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NUF2-yeGFP-TRP1
X2000	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3-13, NUF2-yeGFP-TRP1
Y1788	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NUF2-yeGFP-TRP1

X2005	MATa, can1-R, leu2, lys2-1, met13-d, trp1-Δ63, tyr1-1, ura3-13, his3-Δ1, SPC24-yeGFP-TRP1
Y1481	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, SPC24-yeGFP-TRP1
X2006	MAT∝, can1-R, leu2, lys2-1, met13-d, trp1-Δ63, tyr1-1, ura3-13, his3-Δ1, SPC24-yeGFP-TRP1
Y1482	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, SPC24-yeGFP-TRP1
X2007	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC105-yeGFP-TRP1
Y1479	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, SPC105-yeGFP-TRP1
X2008	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC105-yeGFP-TRP1
Y1480	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, SPC105-yeGFP-TRP1
X2046	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, MAM1-yeGFP-TRP1
Y1475	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, MAM1-yeGFP-TRP1
X1997	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3-13, NSL1-yeGFP-TRP1
Y1785	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NSL1-yeGFP-TRP1
X1998	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, ura3-13, NSL1-yeGFP-TRP1
Y1786	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NSL1-yeGFP-TRP1
X2009	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), DSN1-yeGFP-TRP1
Y1473	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, DSN1-yeGFP-TRP1
X1287	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1
Y1279	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1
X1288	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1
Y1280	MATa, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1
Y399	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3
Y400	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3
X2049	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CTF19-yeGFP-TRP1
Y1815	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CTF19-

	yeGFP-TRP1

X2050	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CTF19-yeGFP-TRP1
Y1816	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CTF19-yeGFP-TRP1
X2051	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CHL4-yeGFP-TRP1
Y1817	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CHL4-yeGFP-TRP1
X2052	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CHL4-yeGFP-TRP1
Y1818	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CHL4-yeGFP-TRP1
X2053	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CTF3-yeGFP-TRP1
Y1819	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CTF3-yeGFP-TRP1
X2054	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CTF3-yeGFP-TRP1
Y1820	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, CTF3-yeGFP-TRP1
X1907	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CNN1-yeGFP-TRP1
Y1731	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, CNN1-yeGFP-TRP1
X1908	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), CNN1-yeGFP-TRP1
Y1732	MATa,leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, ura3-1, CNN1-yeGFP-TRP1
X2055	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), NDC10-yeGFP-TRP1
Y1823	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC10-yeGFP-TRP1
X2056	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), NDC10-yeGFP-TRP1
Y1824	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC10-yeGFP-TRP1
Y1821	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MIF2-yeGFP-TRP1
Y1822	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MIF2-yeGFP-TRP1
X55	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R
Y8	MAT∝, ura3-1, trp1-63, his3-1, HIS7, leu2, met13-c, tyr1-2, ade2, cyh2-1 (R)
Y169	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1
X206	MAT∝, ura3-13, trp1-Δ63, leu2, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1
Y170	MATa, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1

X1471	MATa, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CHL4-yeGFP-TRP1
Y1435	MAT∝, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CHL4-yeGFP-TRP1
X1472	MAT∝, ura3-13, trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), KanMX-PGAL1-NDT80, SPC42-[OPL29: URA3 SPC42-CFP], MTW1-3xmCherry-hphNT1, CHL4-yeGFP-TRP1
Y1436	MATa, leu2, lys2-2, met13-c, tyr1-2, trp1-Δ63, cyh2-1, his3-Δ1, KanMX-PGAL1-NDT80, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::HIS], MTW1-3xmCherry-hphNT1, CHL4-yeGFP-TRP1
X873	MATa, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, ndt80::LEU2
Y1783	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, natNT2-PGAL1-NDT80, SPC25-yeGFP-TRP1
X874	MAT∝, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, ndt80::LEU2
Y1784	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-3xmCherry-hphNT1, natNT2-PGAL1-NDT80, SPC25-yeGFP-TRP1
X871	MATa, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3, ndt80::LEU2
Y909	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3, SPC42-[MDE1145: URA3 SPC42-DSRed], ndt80::LEU2, his7-1
X872	MAT∝, ura3-13, trp1-Δ63, leu2-?, tyr1-1, lys2-1, met13-d, can1-R, his3-Δ1, MTW1-GFP-URA3, ndt80::LEU2
Y910	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, MTW1-GFP-URA3, SPC42-[MDE1145: URA3 SPC42-DSRed], ndt80::LEU2
X2151	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, PSCC1-CDC6 KanMX6, MTW1-GFP-URA3, ndt80::LEU2
Y1921	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, PSCC1-CDC6 KANMX6, SPC42-[MDE1145: URA3 SPC42-DSRed], MTW1-GFP-URA3, ndt80::LEU2
X2152	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, PSCC1-CDC6 KanMX6, MTW1-GFP-URA3, ndt80::LEU2
Y1922	MATa, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, PSCC1-CDC6 KANMX6, SPC42-[MDE1145: URA3 SPC42-DSRed], MTW1-GFP-URA3, ndt80::LEU2
X1217	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, NDC80-EGFP-KanMx4, SPC42-[MDE1145: URA3 SPC42-DSRed]
X1218	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, NDC80-EGFP-KanMx4, SPC42-[MDE1145: URA3 SPC42-DSRed]
Y1192	MATa, leu2, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, NDC80-EGFP-TRP1

X2019	MATa, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, PSCC1-CDC6 KanMX6, NDC80-EGFP-KanMx4, SPC42-[MDE1145: URA3 SPC42-DSRed]
Y1799	MAT∝, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, PSCC1-CDC6 KANMX6, NDC80-EGFP-TRP1
X2020	MAT∝, ura3-13, trp1-Δ63, his3-Δ1, leu2-?, met13-d, tyr1-1, lys2-1, can1-R, PSCC1-CDC6 KanMX6, NDC80-EGFP-KanMx4, SPC42-[MDE1145: URA3 SPC42-DSRed]
Y1800	MATa, leu2-?, lys2-2, met13-c, tyr1-2, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, PSCC1-CDC6 KANMX6, NDC80-EGFP-TRP1
X1673	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
Y1585	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1
X1674	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6
X2289	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-NDC80 KanMX6
Y2133	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1, PCLB2-3HA-NDC80 KanMX6
X2290	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-NDC80 KanMX6
Y2134	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1, PCLB2-3HA-NDC80 KanMX6
X2287	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, PCLB2-3HA-NDC80 KanMX6
Y2131	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1, PCLB2-3HA-NDC80 KanMX6
X2298	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], MAM1-yeGFP-TRP1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, PCLB2-3HA-NDC80 KanMX6
Y2132	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, PCLB2-3HA-IPL1 KanMX6, MAM1-yeGFP-TRP1, MTW1-3xmCherry-hphNT1, PCLB2-3HA-NDC80 KanMX6

X1677	MATa, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], PCLB2-3HA-IPL1 KanMX6, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
Y2119	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NDC80-EGFP-TRP1, PCLB2-3HA-IPL1 KanMX6
X1678	MAT∝, trp1-Δ63, his3-Δ1, leu2, met13-d, tyr1-1, lys2-1, can1-R, MTW1-3xmCherry-hphNT1, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], PCLB2-3HA-IPL1 KanMX6, natNT2-PGAL1-NDT80, NDC80-EGFP-TRP1
Y2120	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, NDC80-EGFP-TRP1, PCLB2-3HA-IPL1 KanMX6
X1581	MATa, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC42-[MDE1145: URA3::HIS SPC42-DSRed], natNT2-PGAL1-NDT80
Y1507	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3::pAFS125[PHIS3-GFP-TUB1, URA3], trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80
X1582	MAT∝, ura3::pKB80 [PGPD1-GAL4(848)-ER-URA3::hphNT1], trp1-63, his3-1, leu2, met13-d, tyr1-1, lys2-1, can1 (R), SPC42-[MDE1145: URA3::HIS SPC42-DSRed], natNT2-PGAL1-NDT80
Y1508	MATa, leu2, lys2-2, tyr1-2, met13-c, ura3::pAFS125[PHIS3-GFP-TUB1, URA3], trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80
Y1581	MAT∝, leu2, lys2-2, tyr1-2, met13-c, ura3-1, trp1-Δ63, cyh2-1, his3-Δ1, natNT2-PGAL1-NDT80, MTW1-3xmCherry-hphNT1, ipl1ΔKAN:ipl1-as5-MYC:HIS3:LEU2, MAM1-yeGFP-TRP1

Table S3. Descriptors used for the selected reaction monitoring experiment. Each protein was quantified by the detecion of three peptides formed in a tryptic digest. The m/z resolution was set to 0.7Da for both the parent ion m/z and production ion m/z. The collision energy was set based on the parent ion m/z. Scheduling was used to defined a time window in which the peptide eluted, as seen in the start time and end time.

Parent ion, m/z	Fragment ion, m/z	Collision energy, eV	Start time	End time	Charge	Peptide sequence	Gene name
623.83	243.13	25	18.7	23.7	+	LESLLENSVDK	*MTW1*
623.83	448.24	25	18.7	23.7	+	LESLLENSVDK	
623.83	562.28	25	18.7	23.7	+	LESLLENSVDK	
623.83	691.33	25	18.7	23.7	+	LESLLENSVDK	
623.83	804.41	25	18.7	23.7	+	LESLLENSVDK	
623.83	917.49	25	18.7	23.7	+	LESLLENSVDK	
623.83	1004.53	25	18.7	23.7	+	LESLLENSVDK	
623.83	1133.57	25	18.7	23.7	+	LESLLENSVDK	
643.85	229.12	25	19.9	24.9	+	DLVIVDENELK	
643.85	389.24	25	19.9	24.9	+	DLVIVDENELK	
643.85	503.28	25	19.9	24.9	+	DLVIVDENELK	
643.85	632.33	25	19.9	24.9	+	DLVIVDENELK	
643.85	747.35	25	19.9	24.9	+	DLVIVDENELK	
643.85	846.42	25	19.9	24.9	+	DLVIVDENELK	
643.85	959.50	25	19.9	24.9	+	DLVIVDENELK	
643.85	1058.57	25	19.9	24.9	+	DLVIVDENELK	
733.37	211.14	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	535.30	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	606.34	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	676.83	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	721.36	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	834.45	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	997.51	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	1126.55	28	21.1	26.1	+	IPEEYLDANVFR	
733.37	1255.60	28	21.1	26.1	+	IPEEYLDANVFR	
378.74	171.11	16	15.9	20.9	+	IGVLQAR	*NSL1*
378.74	374.21	16	15.9	20.9	+	IGVLQAR	
378.74	487.30	16	15.9	20.9	+	IGVLQAR	
378.74	586.37	16	15.9	20.9	+	IGVLQAR	
378.74	643.39	16	15.9	20.9	+	IGVLQAR	
590.29	245.08	23	18.0	23.0	+	DEYLAQLDGR	
590.29	460.25	23	18.0	23.0	+	DEYLAQLDGR	
590.29	588.31	23	18.0	23.0	+	DEYLAQLDGR	
590.29	659.35	23	18.0	23.0	+	DEYLAQLDGR	
590.29	772.43	23	18.0	23.0	+	DEYLAQLDGR	
590.29	935.49	23	18.0	23.0	+	DEYLAQLDGR	
616.33	201.12	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	519.28	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	590.31	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	704.36	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	803.43	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	902.49	24	16.7	21.7	+	SLEVVNADTVGK	
616.33	1031.54	24	16.7	21.7	+	SLEVVNADTVGK	
778.37	243.11	30	16.0	21.0	+	NQEEEGELEHLTK	*DSN1*
778.37	627.35	30	16.0	21.0	+	NQEEEGELEHLTK	
778.37	926.49	30	16.0	21.0	+	NQEEEGELEHLTK	
778.37	1055.54	30	16.0	21.0	+	NQEEEGELEHLTK	
778.37	1184.58	30	16.0	21.0	+	NQEEEGELEHLTK	
855.89	227.18	32	17.0	22.0	+	ILDNTENYDDTELR	
855.89	518.29	32	17.0	22.0	+	ILDNTENYDDTELR	
855.89	748.35	32	17.0	22.0	+	ILDNTENYDDTELR	

855.89	911.41	32	17.0	22.0	+	ILDNTENYDDTELR	
855.89	1025.45	32	17.0	22.0	+	ILDNTENYDDTELR	
855.89	1154.50	32	17.0	22.0	+	ILDNTENYDDTELR	
855.89	1255.54	32	17.0	22.0	+	ILDNTENYDDTELR	
994.47	680.34	35	22.7	27.7	+	DIPEEDFYTVVGNASFGK	
994.47	779.40	35	22.7	27.7	+	DIPEEDFYTVVGNASFGK	
994.47	880.41	35	22.7	27.7	+	DIPEEDFYTVVGNASFGK	
994.47	979.52	35	22.7	27.7	+	DIPEEDFYTVVGNASFGK	
994.47	1289.65	35	22.7	27.7	+	DIPEEDFYTVVGNASFGK	
595.30	229.12	24	16.2	21.2	+	DLETQVEVEK	*NNF1*
595.30	375.22	24	16.2	21.2	+	DLETQVEVEK	
595.30	504.27	24	16.2	21.2	+	DLETQVEVEK	
595.30	603.33	24	16.2	21.2	+	DLETQVEVEK	
595.30	832.44	24	16.2	21.2	+	DLETQVEVEK	
595.30	961.48	24	16.2	21.2	+	DLETQVEVEK	
700.39	218.15	28	23.4	28.4	+	LNELDELILEAK	
700.39	228.13	28	23.4	28.4	+	LNELDELILEAK	
700.39	460.28	28	23.4	28.4	+	LNELDELILEAK	
700.39	573.36	28	23.4	28.4	+	LNELDELILEAK	
700.39	686.44	28	23.4	28.4	+	LNELDELILEAK	
700.39	815.49	28	23.4	28.4	+	LNELDELILEAK	
700.39	930.51	28	23.4	28.4	+	LNELDELILEAK	
700.39	1043.60	28	23.4	28.4	+	LNELDELILEAK	
700.39	1172.64	28	23.4	28.4	+	LNELDELILEAK	
708.34	187.11	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
708.34	447.26	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
708.34	610.32	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
708.34	835.43	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
708.34	982.50	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
708.34	1229.56	28	16.7	21.7	+	VSSC[160]FPQYVNSK	
555.80	261.12	22	20.1	25.1	+	YPFLESINK	*NDC80*
555.80	461.27	22	20.1	25.1	+	YPFLESINK	
555.80	474.26	22	20.1	25.1	+	YPFLESINK	
555.80	590.31	22	20.1	25.1	+	YPFLESINK	
555.80	703.40	22	20.1	25.1	+	YPFLESINK	
555.80	850.47	22	20.1	25.1	+	YPFLESINK	
555.80	947.52	22	20.1	25.1	+	YPFLESINK	
696.36	227.18	27	23.4	28.4	+	LLIDYFTESYK	
696.36	397.21	27	23.4	28.4	+	LLIDYFTESYK	
696.36	526.25	27	23.4	28.4	+	LLIDYFTESYK	
696.36	627.30	27	23.4	28.4	+	LLIDYFTESYK	
696.36	774.37	27	23.4	28.4	+	LLIDYFTESYK	
696.36	937.43	27	23.4	28.4	+	LLIDYFTESYK	
696.36	1052.46	27	23.4	28.4	+	LLIDYFTESYK	
696.36	1165.54	27	23.4	28.4	+	LLIDYFTESYK	
839.91	171.11	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	546.26	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	674.32	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	787.41	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	916.45	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	1063.52	32	17.7	22.7	+	GISTEQFELQNQER	
839.91	1191.58	32	17.7	22.7	+	GISTEQFELQNQER	
553.32	227.18	22	18.7	23.7	+	LLSAVVNYAR	*NUF2*
553.32	523.26	22	18.7	23.7	+	LLSAVVNYAR	
553.32	622.33	22	18.7	23.7	+	LLSAVVNYAR	
553.32	721.40	22	18.7	23.7	+	LLSAVVNYAR	
553.32	792.44	22	18.7	23.7	+	LLSAVVNYAR	
553.32	879.47	22	18.7	23.7	+	LLSAVVNYAR	

557.32	303.18	22	19.7	24.7	+	ELNDLLIQR	
557.32	416.26	22	19.7	24.7	+	ELNDLLIQR	
557.32	529.35	22	19.7	24.7	+	ELNDLLIQR	
557.32	642.43	22	19.7	24.7	+	ELNDLLIQR	
557.32	757.46	22	19.7	24.7	+	ELNDLLIQR	
557.32	871.50	22	19.7	24.7	+	ELNDLLIQR	
566.80	215.14	23	15.3	20.3	+	TLDDLTAQQK	
566.80	474.27	23	15.3	20.3	+	TLDDLTAQQK	
566.80	575.31	23	15.3	20.3	+	TLDDLTAQQK	
566.80	688.40	23	15.3	20.3	+	TLDDLTAQQK	
566.80	803.43	23	15.3	20.3	+	TLDDLTAQQK	
566.80	918.45	23	15.3	20.3	+	TLDDLTAQQK	
409.21	229.12	17	15.7	20.7	+	DLDGLER	*SPC24*
409.21	304.16	17	15.7	20.7	+	DLDGLER	
409.21	417.25	17	15.7	20.7	+	DLDGLER	
409.21	474.27	17	15.7	20.7	+	DLDGLER	
409.21	589.29	17	15.7	20.7	+	DLDGLER	
409.21	702.38	17	15.7	20.7	+	DLDGLER	
624.31	203.07	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	291.17	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	405.21	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	502.26	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	603.31	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	690.34	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	803.43	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	916.51	25	14.9	19.9	+	DSEIISTPNGSK	
624.31	1045.55	25	14.9	19.9	+	DSEIISTPNGSK	
708.87	407.27	27	23.6	28.6	+	DNLLDNPVEFLK	
708.87	536.31	27	23.6	28.6	+	DNLLDNPVEFLK	
708.87	732.43	27	23.6	28.6	+	DNLLDNPVEFLK	
708.87	846.47	27	23.6	28.6	+	DNLLDNPVEFLK	
708.87	961.50	27	23.6	28.6	+	DNLLDNPVEFLK	
708.87	1074.58	27	23.6	28.6	+	DNLLDNPVEFLK	
436.25	215.10	18	16.8	21.8	+	DVAQVLAR	*SPC25*
436.25	246.16	18	16.8	21.8	+	DVAQVLAR	
436.25	359.24	18	16.8	21.8	+	DVAQVLAR	
436.25	458.31	18	16.8	21.8	+	DVAQVLAR	
436.25	586.37	18	16.8	21.8	+	DVAQVLAR	
436.25	657.40	18	16.8	21.8	+	DVAQVLAR	
471.72	247.14	19	17.7	22.7	+	FVFGDDSR	
471.72	377.18	19	17.7	22.7	+	FVFGDDSR	
471.72	549.23	19	17.7	22.7	+	FVFGDDSR	
471.72	696.29	19	17.7	22.7	+	FVFGDDSR	
925.94	258.12	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	467.22	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	651.35	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	750.41	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	879.46	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	950.49	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	1021.53	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	1136.56	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	1250.60	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	1307.62	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
925.94	1394.65	35	18.7	23.7	+	WAAQSGNDAAEVALYER	
466.26	202.08	19	19.0	24.0	+	SNDILTLR	*SPC105*
466.26	389.25	19	19.0	24.0	+	SNDILTLR	
466.26	502.33	19	19.0	24.0	+	SNDILTLR	
466.26	615.42	19	19.0	24.0	+	SNDILTLR	

466.26	730.45	19	19.0	24.0	+	SNDILTLR	
524.81	201.12	21	19.8	24.8	+	ISGVLPSFTK	
524.81	579.31	21	19.8	24.8	+	ISGVLPSFTK	
524.81	692.40	21	19.8	24.8	+	ISGVLPSFTK	
524.81	848.49	21	19.8	24.8	+	ISGVLPSFTK	
524.81	935.52	21	19.8	24.8	+	ISGVLPSFTK	
784.40	277.12	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	680.36	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	779.43	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	836.45	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	935.52	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	1064.56	30	22.9	27.9	+	EFINEVGVGFLDTK	
784.40	1178.61	30	22.9	27.9	+	EFINEVGVGFLDTK	
553.25	230.08	22	14.5	19.5	+	NDESLDVEGK	*KRE28*
553.25	333.18	22	14.5	19.5	+	NDESLDVEGK	
553.25	432.25	22	14.5	19.5	+	NDESLDVEGK	
553.25	547.27	22	14.5	19.5	+	NDESLDVEGK	
553.25	660.36	22	14.5	19.5	+	NDESLDVEGK	
553.25	747.39	22	14.5	19.5	+	NDESLDVEGK	
553.25	876.43	22	14.5	19.5	+	NDESLDVEGK	
681.35	634.34	26	19.6	24.6	+	AGGNIVTDIEASSK	
681.35	749.37	26	19.6	24.6	+	AGGNIVTDIEASSK	
681.35	850.42	26	19.6	24.6	+	AGGNIVTDIEASSK	
681.35	949.48	26	19.6	24.6	+	AGGNIVTDIEASSK	
681.35	1062.57	26	19.6	24.6	+	AGGNIVTDIEASSK	
919.45	215.14	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	469.26	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	632.32	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	747.35	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	860.43	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	961.48	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	1090.52	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	1218.58	35	26.6	31.6	+	LTYLEQETLDYFFR	
919.45	1347.62	35	26.6	31.6	+	LTYLEQETLDYFFR	
476.75	260.20	20	17.8	22.8	+	FEDSTLLK	*CTF19*
476.75	474.33	20	17.8	22.8	+	FEDSTLLK	
476.75	561.36	20	17.8	22.8	+	FEDSTLLK	
476.75	676.39	20	17.8	22.8	+	FEDSTLLK	
500.79	228.13	20	16.4	21.4	+	INGLTNLQK	
500.79	275.17	20	16.4	21.4	+	INGLTNLQK	
500.79	502.30	20	16.4	21.4	+	INGLTNLQK	
500.79	603.35	20	16.4	21.4	+	INGLTNLQK	
500.79	716.43	20	16.4	21.4	+	INGLTNLQK	
500.79	773.45	20	16.4	21.4	+	INGLTNLQK	
500.79	887.49	20	16.4	21.4	+	INGLTNLQK	
687.41	159.08	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	260.20	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	373.28	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	487.32	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	600.41	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	713.49	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	827.53	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	955.59	27	28.9	33.9	+	TGIFQNLINLLK	
687.41	1102.66	27	28.9	33.9	+	TGIFQNLINLLK	
401.25	243.13	17	17.0	22.0	+	LEAILSR	*OKP1*
401.25	375.24	17	17.0	22.0	+	LEAILSR	
401.25	488.32	17	17.0	22.0	+	LEAILSR	
401.25	559.36	17	17.0	22.0	+	LEAILSR	

401.25	688.40	17	17.0	22.0	+	LEAILSR	
629.81	229.12	25	20.7	25.7	+	DLDIEYIYSK	
629.81	344.15	25	20.7	25.7	+	DLDIEYIYSK	
629.81	397.21	25	20.7	25.7	+	DLDIEYIYSK	
629.81	510.29	25	20.7	25.7	+	DLDIEYIYSK	
629.81	673.36	25	20.7	25.7	+	DLDIEYIYSK	
629.81	802.40	25	20.7	25.7	+	DLDIEYIYSK	
629.81	915.48	25	20.7	25.7	+	DLDIEYIYSK	
629.81	1030.51	25	20.7	25.7	+	DLDIEYIYSK	
883.46	227.18	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	724.35	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	837.44	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	995.50	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	1094.57	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	1309.66	33	23.4	28.4	+	LLETNTVSALDSVFEK	
883.46	1410.71	33	23.4	28.4	+	LLETNTVSALDSVFEK	
482.22	230.08	20	12.6	17.6	+	NDEDLTTR	*AME1*
482.22	359.12	20	12.6	17.6	+	NDEDLTTR	
482.22	377.21	20	12.6	17.6	+	NDEDLTTR	
482.22	490.30	20	12.6	17.6	+	NDEDLTTR	
482.22	605.33	20	12.6	17.6	+	NDEDLTTR	
482.22	734.37	20	12.6	17.6	+	NDEDLTTR	
482.22	849.39	20	12.6	17.6	+	NDEDLTTR	
576.79	278.11	23	20.3	25.3	+	YNFDDIPIR	
576.79	385.26	23	20.3	25.3	+	YNFDDIPIR	
576.79	498.34	23	20.3	25.3	+	YNFDDIPIR	
576.79	613.37	23	20.3	25.3	+	YNFDDIPIR	
576.79	728.39	23	20.3	25.3	+	YNFDDIPIR	
576.79	875.46	23	20.3	25.3	+	YNFDDIPIR	
587.84	204.13	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	228.13	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	317.22	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	343.16	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	430.30	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	618.38	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	719.43	24	20.8	25.8	+	LNDLTSTLLGK	
587.84	947.54	24	20.8	25.8	+	LNDLTSTLLGK	
601.86	247.14	24	21.6	26.6	+	VFLQLVEVQK	*MCM21*
601.86	374.24	24	21.6	26.6	+	VFLQLVEVQK	
601.86	503.28	24	21.6	26.6	+	VFLQLVEVQK	
601.86	602.35	24	21.6	26.6	+	VFLQLVEVQK	
601.86	715.43	24	21.6	26.6	+	VFLQLVEVQK	
601.86	843.49	24	21.6	26.6	+	VFLQLVEVQK	
601.86	956.58	24	21.6	26.6	+	VFLQLVEVQK	
805.93	200.10	31	18.7	23.7	+	AQADIPATPIPYEPK	
805.93	633.32	31	18.7	23.7	+	AQADIPATPIPYEPK	
805.93	843.46	31	18.7	23.7	+	AQADIPATPIPYEPK	
805.93	1112.60	31	18.7	23.7	+	AQADIPATPIPYEPK	
805.93	1225.68	31	18.7	23.7	+	AQADIPATPIPYEPK	
871.44	217.08	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	330.17	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	551.29	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	680.34	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	793.42	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	892.49	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	1005.57	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	1168.64	33	22.8	27.8	+	SELEDYIVLENVYR	
871.44	1283.66	33	22.8	27.8	+	SELEDYIVLENVYR	

871.44	1412.71	33	22.8	27.8	+	SELEDYIVLENVYR	
635.30	277.15	25	17.7	22.7	+	LYFEPETQDK	*MCM19*
635.30	390.20	25	17.7	22.7	+	LYFEPETQDK	
635.30	424.22	25	17.7	22.7	+	LYFEPETQDK	
635.30	491.25	25	17.7	22.7	+	LYFEPETQDK	
635.30	553.27	25	17.7	22.7	+	LYFEPETQDK	
635.30	717.34	25	17.7	22.7	+	LYFEPETQDK	
635.30	846.38	25	17.7	22.7	+	LYFEPETQDK	
635.30	993.45	25	17.7	22.7	+	LYFEPETQDK	
727.85	229.12	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	397.21	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	498.26	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	555.28	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	684.32	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	799.35	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	912.43	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	1026.47	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	1058.50	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	1113.51	28	18.4	23.4	+	LDISNLDEGTYSK	
727.85	1226.59	28	18.4	23.4	+	LDISNLDEGTYSK	
741.37	244.09	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	321.18	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	468.25	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	654.32	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	868.46	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	996.51	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	1125.56	29	21.6	26.6	+	ENIEQITWFSSK	
741.37	1161.56	29	21.6	26.6	+	ENIEQITWFSSK	
621.35	416.26	24	18.6	23.6	+	DAPGSATLILQR	CTF3
621.35	528.31	24	18.6	23.6	+	DAPGSATLILQR	
621.35	529.35	24	18.6	23.6	+	DAPGSATLILQR	
621.35	642.43	24	18.6	23.6	+	DAPGSATLILQR	
621.35	743.48	24	18.6	23.6	+	DAPGSATLILQR	
621.35	814.51	24	18.6	23.6	+	DAPGSATLILQR	
621.35	901.55	24	18.6	23.6	+	DAPGSATLILQR	
621.35	958.57	24	18.6	23.6	+	DAPGSATLILQR	
622.32	201.12	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	294.18	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	504.28	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	591.31	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	740.36	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	839.43	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	896.45	24	24.1	29.1	+	SLFGVSPDFFK	
622.32	1043.52	24	24.1	29.1	+	SLFGVSPDFFK	
825.91	247.14	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	406.19	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	564.26	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	651.26	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	677.34	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	790.42	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
825.91	1000.56	31	21.4	26.4	+	VFSSDDPLLLSAAC[160]R	
457.78	227.18	19	19.2	24.2	+	LLLEEAVK	*NKP1*
457.78	317.22	19	19.2	24.2	+	LLLEEAVK	
457.78	446.26	19	19.2	24.2	+	LLLEEAVK	
457.78	575.30	19	19.2	24.2	+	LLLEEAVK	
457.78	688.39	19	19.2	24.2	+	LLLEEAVK	
457.78	801.47	19	19.2	24.2	+	LLLEEAVK	
540.79	213.16	22	16.5	21.5	+	VLSEYSNLR	

540.79	489.28	22	16.5	21.5	+	VLSEYSNLR	
540.79	652.34	22	16.5	21.5	+	VLSEYSNLR	
540.79	781.38	22	16.5	21.5	+	VLSEYSNLR	
540.79	868.42	22	16.5	21.5	+	VLSEYSNLR	
540.79	981.50	22	16.5	21.5	+	VLSEYSNLR	
666.33	229.12	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	286.14	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	692.36	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	820.42	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	917.47	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	1046.51	26	13.9	18.9	+	VEGEPQSTSIER	
666.33	1103.53	26	13.9	18.9	+	VEGEPQSTSIER	
452.74	201.12	19	13.7	18.7	+	VTSELEAR	*NKP2*
452.74	246.16	19	13.7	18.7	+	VTSELEAR	
452.74	375.20	19	13.7	18.7	+	VTSELEAR	
452.74	417.20	19	13.7	18.7	+	VTSELEAR	
452.74	617.33	19	13.7	18.7	+	VTSELEAR	
452.74	704.36	19	13.7	18.7	+	VTSELEAR	
500.28	228.13	20	17.0	22.0	+	INDLLQQR	
500.28	303.18	20	17.0	22.0	+	INDLLQQR	
500.28	343.16	20	17.0	22.0	+	INDLLQQR	
500.28	431.24	20	17.0	22.0	+	INDLLQQR	
500.28	456.25	20	17.0	22.0	+	INDLLQQR	
500.28	544.32	20	17.0	22.0	+	INDLLQQR	
500.28	657.40	20	17.0	22.0	+	INDLLQQR	
500.28	772.43	20	17.0	22.0	+	INDLLQQR	
500.28	886.47	20	17.0	22.0	+	INDLLQQR	
643.35	242.15	25	19.9	24.9	+	LQILDDAIQEK	
643.35	276.16	25	19.9	24.9	+	LQILDDAIQEK	
643.35	355.23	25	19.9	24.9	+	LQILDDAIQEK	
643.35	517.30	25	19.9	24.9	+	LQILDDAIQEK	
643.35	588.34	25	19.9	24.9	+	LQILDDAIQEK	
643.35	703.36	25	19.9	24.9	+	LQILDDAIQEK	
643.35	818.39	25	19.9	24.9	+	LQILDDAIQEK	
643.35	931.47	25	19.9	24.9	+	LQILDDAIQEK	
643.35	1044.56	25	19.9	24.9	+	LQILDDAIQEK	
458.29	213.16	19	17.7	22.7	+	LVLQSISR	*CHL4*
458.29	352.21	19	17.7	22.7	+	LVLQSISR	
458.29	462.27	19	17.7	22.7	+	LVLQSISR	
458.29	590.33	19	17.7	22.7	+	LVLQSISR	
458.29	703.41	19	17.7	22.7	+	LVLQSISR	
566.85	235.12	23	19.3	24.3	+	HPSLPVLITR	
566.85	276.17	23	19.3	24.3	+	HPSLPVLITR	
566.85	435.24	23	19.3	24.3	+	HPSLPVLITR	
566.85	502.33	23	19.3	24.3	+	HPSLPVLITR	
566.85	601.40	23	19.3	24.3	+	HPSLPVLITR	
566.85	698.46	23	19.3	24.3	+	HPSLPVLITR	
566.85	898.57	23	19.3	24.3	+	HPSLPVLITR	
566.85	995.62	23	19.3	24.3	+	HPSLPVLITR	
646.35	261.16	25	19.2	24.2	+	FIENLQTDLAK	
646.35	331.23	25	19.2	24.2	+	FIENLQTDLAK	
646.35	390.20	25	19.2	24.2	+	FIENLQTDLAK	
646.35	446.26	25	19.2	24.2	+	FIENLQTDLAK	
646.35	504.25	25	19.2	24.2	+	FIENLQTDLAK	
646.35	547.31	25	19.2	24.2	+	FIENLQTDLAK	
646.35	675.37	25	19.2	24.2	+	FIENLQTDLAK	
646.35	902.49	25	19.2	24.2	+	FIENLQTDLAK	
646.35	1031.54	25	19.2	24.2	+	FIENLQTDLAK	

421.76	472.29	17	5	35	+	VATVSLPR	porcine trypsin
421.76	571.36	15	5	35	+	VATVSLPR	
421.76	672.40	15	5	35	+	VATVSLPR	
421.76	743.44	17	5	35	+	VATVSLPR	
523.29	661.36	25	5	35	+	LSSPATLNSR	
523.29	758.42	19	5	35	+	LSSPATLNSR	
523.29	845.45	17	5	35	+	LSSPATLNSR	
523.29	932.48	21	5	35	+	LSSPATLNSR	
395.24	361.24	18	15.4	20.4	+	LVTDLTK	bovine serum albumin
395.24	476.27	16	15.4	20.4	+	LVTDLTK	
395.24	577.32	12	15.4	20.4	+	LVTDLTK	
395.24	676.39	14	15.4	20.4	+	LVTDLTK	
464.25	359.24	19	17.7	22.7	+	YLYEIAR	
464.25	488.28	15	17.7	22.7	+	YLYEIAR	
464.25	651.35	15	17.7	22.7	+	YLYEIAR	
464.25	764.43	17	17.7	22.7	+	YLYEIAR	
582.32	595.31	19	19.9	24.9	+	LVNELTEFAK	
582.32	708.39	19	19.9	24.9	+	LVNELTEFAK	
582.32	837.44	19	19.9	24.9	+	LVNELTEFAK	
582.32	951.48	19	19.9	24.9	+	LVNELTEFAK	