

Supplementary Table 1: *Reliability of Quantifications for Detected Spots, Pinnacle Method*: Summary of coefficient of variation (%CV) for each protein load group for all spots automatically detected (i.e. no hand editing) by Pinnacle.

Study	Protein Load	Number of Spots	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	937	391 (0.42)	22.9	9.9	16.4	21.5	28.1	38.3
	7.5µg	937	779 (0.83)	14.6	5.0	9.3	12.6	17.1	28.9
	10µg	937	629 (0.67)	18.9	7.5	13.3	17.2	21.7	32.3
	15µg	937	811 (0.87)	15.0	5.9	9.8	12.5	16.6	27.9
	30µg	937	301 (0.32)	24.0	13.4	18.8	22.5	26.4	36.6
	40µg	937	566 (0.60)	19.3	8.7	13.7	18.0	23.1	33.8
	50µg	937	745 (0.79)	16.9	8.3	12.5	15.6	19.0	30.9
SH	5µg	1322	952 (0.72)	16.6	3.5	8.5	13.6	20.9	37.5
	10µg	1322	52 (0.04)	48.4	22.3	38.6	48.8	58.3	71.4
	25µg	1322	590 (0.45)	24.6	7.2	14.8	21.7	30.0	52.0
	50µg	1322	956 (0.72)	16.2	3.2	7.8	12.8	21.0	41.5
	100µg	1322	191 (0.14)	35.8	12.6	25.3	35.6	44.9	61.0
	150µg	1322	597 (0.45)	23.2	7.0	15.7	21.0	28.2	46.3
D1	Fent	719	464 (0.65)	19.0	5.6	11.4	16.8	23.7	39.8
	Control	719	230 (0.32)	32.3	10.7	17.9	26.6	37.9	73.8
D2	Fent	1136	673 (0.59)	21.6	5.7	11.4	17.2	25.4	55.2
	Control	1136	398 (0.35)	34.5	10.5	17.0	25.0	37.8	91.3

Supplementary Table 2: *Reliability of Quantifications for Detected Spots, SameSpots*: Summary of coefficient of variation (%CV) for each protein load group for all spots automatically detected (i.e. no hand editing) by SameSpots.

Study	Protein Load	Number of Spots	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	688	99 (0.14)	37.7	14.8	23.7	32.7	43.7	74.2
	7.5µg	688	373 (0.54)	24.6	8.7	13.6	18.7	28.7	54.7
	10µg	688	284 (0.41)	27.0	10.3	16.3	21.8	31.8	58.0
	15µg	688	421 (0.61)	21.7	8.4	12.4	17.1	25.2	50.0
	30µg	688	119 (0.17)	29.6	15.3	21.5	26.0	32.9	51.9
	40µg	688	287 (0.42)	25.1	11.5	16.9	21.6	28.2	45.8
	50µg	688	214 (0.31)	26.1	14.7	19.2	22.6	27.4	42.6
SH	5µg	1037	542 (0.52)	22.5	4.8	11.3	19.1	29.3	50.5
	10µg	1037	71 (0.07)	46.8	17.6	35.6	47.1	58.1	74.3
	25µg	1037	400 (0.39)	27.3	6.2	15.3	24.2	35.0	61.0
	50µg	1037	620 (0.60)	20.8	3.6	9.4	16.3	27.2	53.2
	100µg	1037	230 (0.22)	34.7	8.9	21.8	32.4	45.6	67.0
	150µg	1037	379 (0.37)	27.1	8.0	16.9	24.7	34.1	54.7
D1	Fent	1094	270 (0.25)	32.5	11.8	20.1	27.1	38.7	72.6
	Control	1094	12 (0.01)	55.1	26.9	37.9	47.8	63.5	111.7
D2	Fent	1410	432 (0.30)	32.8	10.7	18.4	26.3	39.5	79.8
	Control	1410	297 (0.21)	40.0	12.6	21.5	31.3	47.7	97.0

Supplementary Table 3: *Reliability of Quantifications for Detected Spots, SameSpots – PG adjusted*: Summary of coefficient of variation (%CV) for each protein load group for all spots automatically detected (i.e. no hand editing) by SameSpots, with PG for spot detection.

Study	Protein Load	Number of Spots	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	1033	434 (0.42)	24.9	9.0	16.1	21.8	28.3	42.4
	7.5µg	1025	720 (0.70)	20.1	5.8	10.4	14.8	21.9	37.9
	10µg	1032	631 (0.61)	23.6	7.8	13.4	18.0	23.6	67.6
	15µg	1032	693 (0.67)	20.9	7.2	11.6	16.1	22.7	49.1
	30µg	1032	453 (0.44)	25.7	11.4	17.1	21.1	26.5	50.7
	40µg	1032	621 (0.60)	22.0	9.3	14.4	18.4	23.5	43.5
	50µg	1032	648 (0.63)	21.6	9.8	15.0	18.4	22.2	37.8
SH	5µg	1305	691 (0.53)	21.5	4.7	11.4	19.1	29.1	45.6
	10µg	1305	84 (0.06)	47.6	18.3	36.7	48.2	59.3	76.3
	25µg	1305	456 (0.35)	27.7	7.1	16.3	25.0	35.7	57.4
	50µg	1305	773 (0.59)	20.5	3.6	10.1	17.1	27.3	49.7
	100µg	1305	233 (0.18)	37.7	10.4	24.3	35.8	49.6	70.5
	150µg	1305	435 (0.33)	27.4	8.4	17.7	25.3	34.1	53.9
D1	Fent	1319	303 (0.23)	33.2	11.8	20.8	28.1	42.1	70.6
	Control	1319	16 (0.01)	54.2	26.9	38.5	48.1	61.7	99.3
D2	Fent	1928	484 (0.25)	32.8	11.1	20.0	28.6	40.9	66.1
	Control	1928	334 (0.17)	39.8	12.8	23.2	33.8	49.9	83.8

Supplementary Table 4: *Reliability of Quantifications for Detected Spots, SameSpots – hand edited version*: Summary of coefficient of variation (%CV) for each protein load group for all spots detected by SameSpots, after hand editing spots and spot boundaries in SameSpots.

Study	Protein Load	Number of Spots	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	899	408 (0.45)	22.8	8.9	15.9	21.0	27.5	39.7
	7.5µg	898	673 (0.75)	17.3	5.9	10.2	14.3	20.0	31.2
	10µg	899	609 (0.68)	19.7	7.5	12.5	16.6	21.9	36.9
	15µg	899	665 (0.74)	18.1	7.2	11.6	15.3	20.3	35.1
	30µg	899	416 (0.46)	22.9	11.1	16.6	20.5	25.3	36.5
	40µg	899	577 (0.64)	19.9	8.9	14.0	17.8	22.2	34.6
	50µg	899	548 (0.61)	20.3	10.1	15.2	18.7	22.4	31.2
SH	5µg	1244	675 (0.54)	10.9	4.6	11.3	18.6	27.5	45.8
	10µg	1244	63 (0.05)	48.7	19.8	37.1	48.6	59.6	76.7
	25µg	1244	460 (0.37)	26.6	6.2	15.9	23.9	34.1	56.2
	50µg	1244	815 (0.66)	18.6	3.6	8.9	15.3	24.2	45.9
	100µg	1244	281 (0.23)	34.4	9.5	21.5	32.7	45.3	65.7
	150µg	1244	439 (0.35)	27.0	8.2	17.1	24.4	33.6	54.2
D1	Fent	1153	282 (0.24)	30.0	11.5	20.1	26.8	36.5	57.6
	Control	1153	12 (0.01)	51.0	27.3	37.9	46.7	58.8	91.9
D2	Fent	1390	492 (0.35)	27.2	10.1	17.5	24.0	33.2	54.9
	Control	1390	349 (0.25)	32.6	12.1	20.0	28.6	40.2	67.5

Supplementary Table 5: *Reliability of Quantifications for Detected Spots, SameSpots PG –hand edited version:* Summary of coefficient of variation (%CV) for each protein load group for all spots detected by SameSpots, after hand editing spots and spot boundaries using PG interface.

Study	Protein Load	Number of Spots	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	1081	463 (0.43)	23.3	8.9	15.9	21.6	28.2	40.6
	7.5µg	1077	784 (0.73)	17.9	5.9	10.4	14.9	20.7	34.7
	10µg	1081	707 (0.65)	20.6	7.6	12.8	17.1	22.3	40.7
	15µg	1081	759 (0.70)	19.1	7.1	11.9	16.1	21.5	37.5
	30µg	1081	473 (0.44)	23.9	11.2	17.0	21.1	26.1	41.3
	40µg	1081	641 (0.59)	20.8	8.9	14.5	18.6	23.5	36.4
	50µg	1081	639 (0.59)	20.7	10.1	15.1	18.7	22.8	32.6
SH	5µg	1383	734 (0.53)	21.6	4.7	11.6	19.1	28.4	47.9
	10µg	1383	77 (0.06)	48.9	18.7	37.4	49.2	60.1	78.0
	25µg	1383	494 (0.36)	27.2	6.6	15.9	24.6	34.7	56.4
	50µg	1383	872 (0.63)	19.3	3.8	9.5	16.2	25.3	46.7
	100µg	1383	279 (0.20)	35.6	10.4	22.8	33.9	46.1	68.4
	150µg	1383	466 (0.34)	27.6	8.5	17.2	24.7	34.0	55.7
D1	Fent	1255	304 (0.24)	29.9	11.8	20.1	27.0	36.7	57.5
	Control	1255	14 (0.01)	50.7	26.7	37.7	47.0	58.0	90.0
D2	Fent	1458	506 (0.35)	27.5	10.1	17.5	24.4	33.5	54.9
	Control	1458	346 (0.24)	32.6	12.4	20.6	29.3	40.2	65.8

Supplementary Table 6: *Reliability of Quantifications for Detected Spots, Progenesis PG240 Method*: Summary of coefficient of variation (%CV) for each protein load group for all spots automatically detected (i.e. no hand editing) by Progenesis PG240 on aligned gel images.

Study	Protein Load	Number of Spots*	Number of spots with %CV<20	%CV					
				Mean	Q05	Q25	Median	Q75	Q95
NC	0.5µg	566	69 (0.12)	82.7	15.4	26.4	44.8	131.9	200.0
	7.5µg	654	296 (0.45)	53.6	7.9	13.4	21.9	70.4	200.0
	10µg	706	227 (0.32)	53.9	10.8	18.1	25.9	70.1	200.0
	15µg	737	376 (0.51)	41.4	7.8	13.2	19.6	37.1	200.0
	30µg	945	147 (0.16)	42.9	14.7	23.1	31.8	67.2	200.0
	40µg	970	315 (0.32)	39.7	10.2	17.8	25.7	44.1	118.1
	50µg	994	198 (0.20)	38.1	15.3	21.3	27.3	39.9	91.4
SH	5µg	391	63 (0.16)	79.7	11.5	26.9	68.9	111.7	173.2
	10µg	562	8 (0.01)	94.7	29.5	60.4	88.6	120.0	173.2
	25µg	688	120 (0.17)	67.3	10.5	25.1	46.7	94.9	173.2
	50µg	902	225 (0.25)	54.8	7.6	20.0	39.9	86.8	173.2
	100µg	1089	88 (0.08)	72.2	15.2	38.3	61.3	97.6	173.2
	150µg	969	161 (0.17)	50.4	11.3	24.1	37.5	63.7	143.5

*The number of spots in this table corresponds to the number of spots that do not have all zeros for Progenesis for the specified protein load.