Office of Chief Medical Examiner – New York City
PowerPlex® Fusion System Amplification Kit on the Applied Biosystems 3130*xl* Genetic Analyzer using GeneMarker HID v. 2.8.2 Analysis Software
Validation Report

August 29, 2016

Contents

1. Introduction

The PowerPlex® Fusion system is a 24 locus system that includes all CODIS and ESS loci. The loci included are: Amelogenin, D3S1358, D1S1656, D2S441, D10S1248, D13S317, Penta E, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, D22S1045, DYS391, and FGA.

Before an established method or procedure may be employed in a forensic laboratory, an internal validation must be completed to show that the method performs as expected. This validation summary outlines a set of experiments that shows conformance with the FBI Quality Assurance Standards for DNA Casework Laboratories (https://www.fbi.gov/about-us/lab/biometric-analysis/codis/qas_testlabs) and the validation guidelines outlined by the Scientific Working Group on DNA Analysis Methods (SWGDAM) (http://swgdam.org/SWGDAM_Validation_Guidelines_APPROVED_Dec_2012.pdf). These experiments were designed to demonstrate the sensitivity and reliability of the PowerPlex® Fusion system. The studies completed were: sensitivity and stochastic studies, mixtures studies, precision, reproducibility, repeatability, known, non-probative evidence samples and mock evidence samples and contamination assessment.

2. FBI Quality Assurance Standard and SWGDAM Recommended Studies

Standard 8.3.1: Internal validation studies conducted after the date of this revision shall include as applicable: known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies, mixture studies, and contamination assessment. Internal validation studies shall be documented and summarized. The technical leader shall approve the internal validation studies.

3. Materials and Methods

3.A.1 DNA Amplification

DNA amplification was performed on an Applied Biosystems GeneAmp® PCR 9700 following the cycling parameters described in the PowerPlex® Fusion System technical manual using 29 cycles (TMD039). The protocol is 96°C for 1 minute, 29 cycles of 94°C for 10 seconds, 59°C for 1 minute, 72°C for 30 seconds, followed by 60°C for 10 minutes and a 4°C soak. A 12.5µl reaction was 2.5µl of 5X PowerPlex® Fusion master mix, 2.5µl of 5X PowerPlex® Fusion primer mix, and 7.5µl of DNA/water was added for all of the reactions. Negative controls contained 7.5µl water and the reaction mix. Please refer to Appendix A for the lot numbers of the reagents that were used during the validation. Applied Biosystems GeneAmp® PCR 9700 806F TC1 (serial number 805S6101009), Applied Biosystems GeneAmp® PCR 9700 806F-TC2 (serial number 805S7022692) and Applied Biosystems GeneAmp® PCR 9700 806F-TC3 (serial number 805S7022760) were used for the validation study .

3.A.2 Data Analysis

Spectral resolution was established using the PowerPlex® Fusion 5C matrix standard (TMD049). One microliter of amplified or allelic ladder was combined with 9.5µl of Hi-Di formamide and 0.5µl of the WEN Internal Lane Standard 500. The samples were heat denatured for 3 minutes at 95°C followed by an immediate chill for 3 minutes at 4°C. The samples were run on two 3130*xl* (Athena serial number 1594-010 and Newton 18231-006) genetic analyzers. Injection condition tested was 3kV for 5 second injection using a 2000 second run time. The data was analyzed using GeneMarkerHID v 2.8.2. Upon completion of the sensitivity study, the analytical threshold was calculated. As per the OCME-NYC, a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter in addition to the disabling of the pull-up correction was used for the rest of the validation.

3.A.3 Sensitivity Study

A sensitivity study was performed using the two extracted DNA samples, DNA1 and DNA 2. The final DNA templates tested were 4ng, 2ng, 1ng, 500pg, 250pg, 125pg, 100pg, 75pg, 50pg, 30pg, 25pg, 15pg, 7.5pg and 3.25pg. These samples were used to establish the analytical threshold and stochastic threshold as described in section 3.A.4. This study was also used to determine at which concentration allelic drop out first appears.

3.A.4 Analytical Threshold, and Stochastic Threshold

The analytical threshold is the point above which a peak can reliably be distinguished from baseline noise. The peak is either allelic or attributable to some known artifact such as pull-up or stutter. If a peak is not above the analytical threshold, it cannot be reliably considered to be a part of any developed DNA profile. If a true allelic peak is below the analytical threshold, that peak is considered to have “dropped out” of the profile. Any peak that is present above an analytical threshold that isn’t diagnosable artifact or due to a true allele from a known contributor would be considered to have ‘dropped-in’ to the profile.

The analytical threshold was calculated by Promega using two different methods of determination. Process #1 used the SWGDAM Interpretation Guidelines for Autosomal STR Typing recommendation. This method uses two times the intensity of the difference between the highest peak and lowest peak within the noise data. For this study, the sensitivity series, DNA 1 and DNA 2 from data generated on both Athena and Newton were reviewed. Process #2 targeted the limit of detection, a point at which the signal in the form of data peaks can be reliably distinguished from noise (LOD) and the limit of quantitation, a point in which signal can be reliably quantified (LOQ). 1ng and 500pg samples from sensitivity series, DNA 1 and DNA 2 that were injected on both Athena and Newton, were analyzed looking for the highest background noise in RFUs per dye lane. The average of the highest noise peak plus three times the standard deviation resulted in the LOD per dye lane. The average of the highest noise peaks plus ten times the standard deviation resulted in the LOQ per dye lane.

A stochastic threshold is the RFU level above which a single peak representing an allele at a locus can be determined to be a homozygote. If a single peak is observed below the stochastic threshold, then it must be assumed that a paired peak has potentially “dropped out” of the DNA profile. The stochastic threshold was calculated using the sensitivity series. The profiles were examined to determine the heterozygous loci in which one of the sister alleles had dropped below the analytical threshold. The average peak height of the surviving sister alleles was determined along with the standard deviation. Three times the standard deviation was added to the average to determine the stochastic threshold.

3.A.5 Known and Non-Probative Evidence Samples/ Mock Casework Samples

Amplification of known samples and non-probative evidence samples allows the laboratory to provide evidence of concordance using the new amplification system. For this study, ten known samples and twenty-four mock casework samples were amplified. Mock samples were generated from various touched items. In addition, all known and mock samples were amplified by two separate operators.

3.A.6 Precision

Sizing precision is critical for accurate genotyping. The migration of each allele in the ladder was evaluated. Thirteen ladders were run on each CE instrument (Athena and Newton). The average base pair size, standard deviation, minimum size, maximum size and range of base pair size was calculated for each allele present in the allelic ladder.

3.A.7 Reproducibility

The 2800M DNA sample supplied in the PowerPlex® Fusion amplification kit (0.25ng/µL) and the NIST SRM 2391c samples were used for the reproducibility study. The 2800M was amplified on all plates during the validation project; NIST SRM 2391c samples were amplified alongside known, mock casework and mixture samples. A combined total of 30 positive controls were injected throughout the validation on the CE instrument with the extracted DNA samples. In addition, 2800M and NIST SRM 2391c samples were amplified by two operators to show the reproducibility of the kit on different thermal cyclers and different operators.

3.A.8 Mixture Study

Mixture samples are commonly encountered in forensic casework samples. This study demonstrates the ability to detect major and minor profiles in samples, as well as the ability of the amplification kit to show mixtures at different ratios of contributors. For this study, two mixture series were generated using the following ratios: two person (20:1, 15:1 10:1, 4:1, 2:1, 1:1, 1:2, 1:4, 1:10, 1:15, and 1:20), three person (5:1:1, 5:5:1, 1:1:1 1:2:1, 3:2:1, and 5:2:1), four person (1:1:1:1, 1:3:3:1, and 1:3:5:1). Mixtures were amplified at four different target amounts: C1= 750pg, C2=500pg, C3=250pg, and C4=100pg. Two person mixtures were evaluated for % profile obtained of the minor contributor using only unshared alleles. Three and four person mixtures were evaluated for the total number of alleles obtained. The three and four person mixtures will be evaluated during the OCME-NYC validation of STRmix® software program.

3.A.9 Contamination Assessment

Negative controls were run to assess contamination. A combined total of 35 negative controls were injected throughout the validation on both CE instruments. Each negative control was analyzed using the 50 RFU analytical threshold with a 3% minimum heterozygote filter and 3% global max filter.

3.A.10 Thermocycler Performance Check

Performance checks were conducted on ten thermocyclers. Seven replicates of 2800M were amplified using 750pg of input DNA. Alongside the seven replicates of 2800M, a negative control was run on each thermocycler. The results were evaluated using peak height and peak height ratios. Applied Biosystems GeneAmp® PCR 9700 705A TC11 (serial number 805S6101085, Applied Biosystems GeneAmp® PCR 9700 705A-TC12 (serial number 805S6101963), Applied Biosystems GeneAmp® PCR 9700 705A-TC13 (serial number 805S6101955), Applied Biosystems GeneAmp® PCR 9700 714C-TC6 (serial number 805S3110458), Applied Biosystems GeneAmp® PCR 9700 714C-TC8 (serial number 805S6101028), Applied Biosystems GeneAmp® PCR 9700 714C-TC9 (serial number 805S6101954), Applied Biosystems GeneAmp® PCR 9700 714C-TC11 (serial number 805S6101023), Applied Biosystems GeneAmp® PCR 9700 806C-TC6 (serial number 805S3120439), Applied Biosystems GeneAmp® PCR 9700 806F-TC1 (serial number 805S6101009), Applied Biosystems GeneAmp® PCR 9700 806F-TC2 (serial number 805S7022692), Applied Biosystems GeneAmp® PCR 9700 806F-TC3 (serial number 805S7022760), and Applied Biosystems GeneAmp® PCR 9700 610J-TC1 (serial number 805S3120445) were used for the performance check study

4. **Results**

4.A.1 Analytical Threshold, and Stochastic Threshold

Following SWGDAM guidelines, process #1 used by Promega reviewed data generated from 2ng, 1ng, 500pg, 250pg, 125pg, 100pg, 75pg, 50pg, 30pg, 25pg, 15pg, 7.5pg, 3.25pg and 0pg on both Newton and Athena (Table 1). Process #2 used by Promega determined the LOD and LOQ of both the 1ng and 500pg samples that were injected on both Newton and Athena. (Table 2). In addition the analytical threshold was calculated by the OCME. As per the OCME, "Analysis of all the negative samples that were run for the Mock Evidence/R&R and Mixture studies was performed at 1 RFU, deleting any peaks that were obviously not noise, and exported the heights of the noise peaks that were called. 167 total data points were determined on Newton and 34 data points were determined on Athena. The average heights of all the noise peaks called was calculated and added to three times the standard deviation to arrive at the analytical threshold. Newton's average analytical threshold was 38.06 RFU, and Athena's was 27.24 RFU. The average for both instruments was 32.65 RFU. Considering the data above and in preparation for the STRmix validation project, 500pg samples were analyzed at varying analytical thresholds ranging from 1rfu to 80rfus. When considering the results of analysis at 40 RFU and 50 RFU, significantly fewer artifacts were present with the 50 RFU analytical threshold." The analytical threshold calculation described above by the OCME-NYC are shown in Table 3. As per the OCME-NYC, a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter was used for the rest of the validation. The analysis methods used to analyze the remainder of the validation data can be found in Appendix C. A stochastic threshold of 300 RFU can be used on both Athena and Newton (Table 4). The stochastic threshold tables can be found in Appendix C.

Due to the large number of artifacts that were observed using a 50 RFU analytical threshold, the OCME performed a global filter evaluation. As per the OCME, "A large number of artifacts were observed across all runs and between instruments. Troubleshooting steps of lowering input amount to 500pg and diluting the instrument matrix to make it less saturated were not successful in removing these artifacts. A global filter was evaluated to determine if artifacts could be reduced without excessive loss of data. Analysis of a portion of the samples run on both Athena and Newton was performed. A Global Max filter was applied during the run wizard, as well as a Min Heterozygote Imbalance (%) filter within the panel settings across all the locations. These samples were analyzed with a 10% filter, 8% filter, 5% filter and 4% filter set in both locations. After evaluation of a 4% filter it was noticed that almost half of the lost alleles could be recovered by going down to a 3% filter, while still greatly reducing the number of artifacts. For all samples, evidence and exemplars, it was decided a filter of 3% would be applied for the Global Max filter during the run wizard and across all locations within the panel for the Min Heterozygote Imbalance (%) filter."

Table 1: Analytical threshold calculated by Promega using Process #1 using sensitivity series and a calculation of 2* (maximum noise peak height – minimum noise peak height)

	Athena DNA1				Athena DNA 2				Newton DNA 1				Newton DNA 2			
	MIN	MAX	Difference	2X's	MIN	MAX	Difference	2X's	MIN	MAX	Difference	2X's	MIN	MAX	Difference	2X's
2ng	1	60	59	118	1	54	53	106	1	60	59	118	1	83	82	164
1ng	1	31	30	60	1	33	32	64	1	31	30	60	1	46	45	90
500pg	1	21	20	40	1	20	19	38	1	21	20	40	1	28	27	54
250pg	1	15	14	28	1	14	13	26	1	15	14	28	1	23	22	44
150pg	1	11	10	20	1	11	10	20	1	11	10	20	1	16	15	30
125pg	1	10	9	18	1	11	10	20	1	10	9	18	1	16	15	30
100pg	1	10	9	18	1	11	10	20	1	10	9	18	1	20	19	38
75pg	1	10	9	18	1	11	10	20	1	10	9	18	1	15	14	28
50pg	1	9	8	16	1	10	9	18	1	9	8	16	1	15	14	28
30pg	1	8	7	14	1	9	8	16	1	8	7	14	1	13	12	24
25pg	1	8	7	14	1	9	8	16	1	8	7	14	1	13	12	24
15pg	1	8	7	14	1	8	7	14	1	8	7	14	1	16	15	30
7.5pg	1	8	7	14	1	8	7	14	1	8	7	14	1	12	11	22
3.25pg	1	8	7	14	1	8	7	14	1	8	7	14	1	14	13	26
0pg	1	8	7	14	1	8	7	14	1	8	7	14	1	12	11	22

Table 2: Analytical threshold calculated by Promega using Process #2 using sensitivity samples near the optimal target.

Athena DNA1

DNA Template	Background rfu *(per dye channel)*	Average Background *(per template)*
1ng	33	37
	29	
	36	
	48	
500pg	12	26
	28	
	31	
	31	

Athena DNA2

DNA Template	Background rfu *(per dye channel)*	Average Background *(per template)*
1ng	32	29
	26	
	36	
	22	
500pg	12	24
	23	
	31	
	31	

Newton DNA1

DNA Template	Background rfu *(per dye channel)*	Average Background *(per template)*
1ng	55	56
	56	
	58	
	53	
500pg	21	31
	32	
	39	
	33	

Newton DNA2

DNA Template	Background rfu *(per dye channel)*	Average Background *(per template)*
1ng	57	54
	40	
	68	
	49	
500pg	39	36
	39	
	42	
	22	

1ng and 500pg	Average	STDEV	Limit of Detection (LOD) *AVG + 3XSTDEV*	Limit of Quantitation (LOQ) *AVG + 10XSTDEV*
FL	33	16	81	195
JOE	34	10	64	134
TMR	43	12	79	165
CXR	36	11	71	151
OVERALLL =	36	13	76	170

500pg only	Average	STDEV	Limit of Detection (LOD) *AVG + 3XSTDEV*	Limit of Quantitation (LOQ) *AVG + 10XSTDEV*
FL	21	13	59	148
JOE	31	7	51	98
TMR	36	6	53	92
CXR	29	5	44	78
OVERALLL =	29	9	56	120

Table 3: Analytical threshold calculated by OCME-NYC for casework at 29 cycles

Amplification Negative Noise Peaks at 1 RFU		
	Newton	**Athena**
Total Data Points	178	34
Average	15.64	13.82
Standard Deviation	9.61	11.09
Avg + 3x Std Dev	44.47	47.10
Average between Newton and Athena	45.79	

Table 4: Stochastic threshold for casework at 29 cycles for 3kV 5 sec.

		Average Height of Surviving Sister Allele	Standard Deviation	Maximum Peak Height of a Surviving Sister Allele	STOCHASTIC THRESHOLD
Athena	**DNA 1**	87	37	252	199
	DNA 2	94	44	251	227
Newton	**DNA 1**	103	53	320	262
	DNA 2	106	61	381	288

4.A.2 Sensitivity

The sensitivity data was analyzed using a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter. The samples that were used in the calculation were the 1ng, 500pg, 250pg, 125pg, 100pg, 75pg, 50pg, 30pg, 25pg, 15pg, 7.5pg, 3.25pg and 0pg for DNA1 and DNA2.

Full profiles in at least one replicate were obtained down to 50pg for DNA 1 on both Athena and Newton with 29 cycles; 75pg for DNA 2 (Table 5). Drop out in at least one replicate was first observed at 125pg for DNA 1 on both Athena and Newton; 100pg for DNA 2 on Athena and 50pg on Newton. As per the OCME a target optimal amount of 750pg would be appropriate for extracted DNA. The peak heights decreased with a decrease in template amount (Table 6-10). The decrease in template amount also decreased the peak height ratios for each of the DNA samples (Table 11-15). There were two instances of drop-in on Newton. Both were seen using a 50pg target amount; DNA 1 replicate A at 54 RFU and DNA 2 replicate C at 53 RFU (Figure 1).

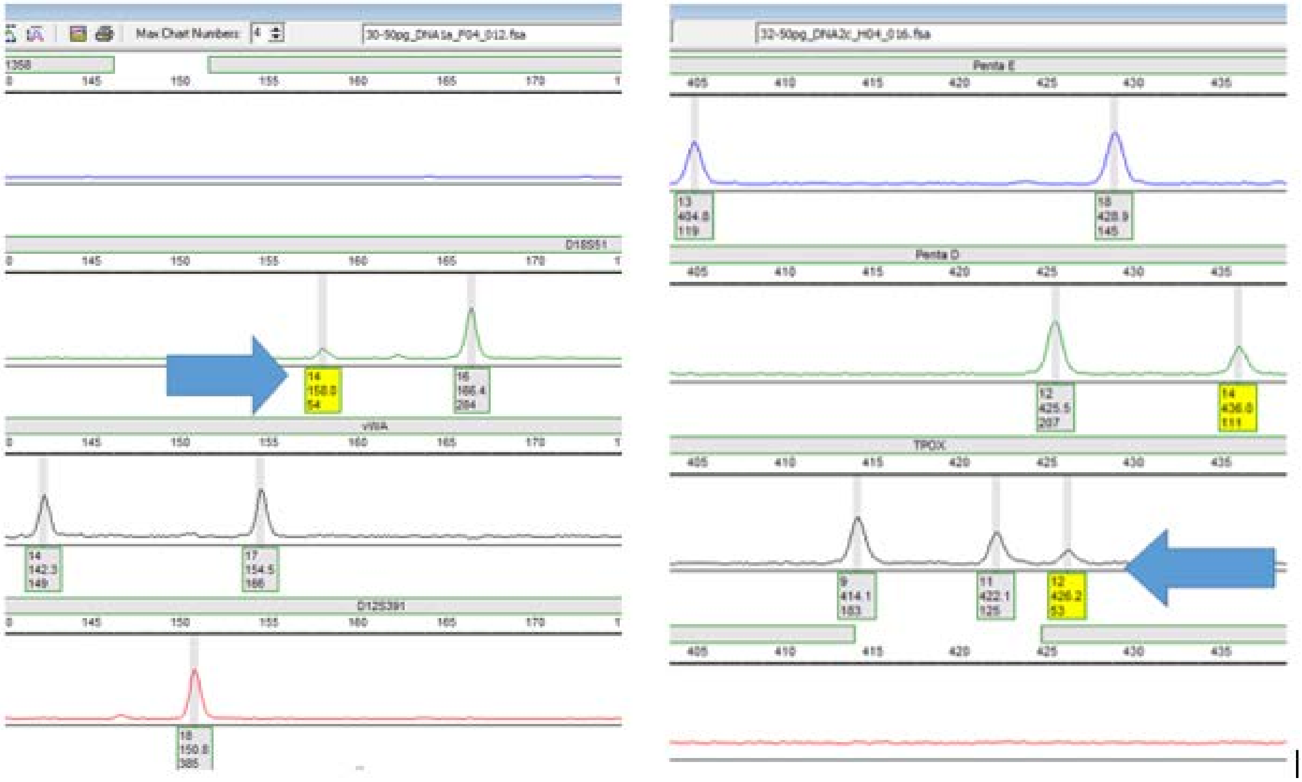
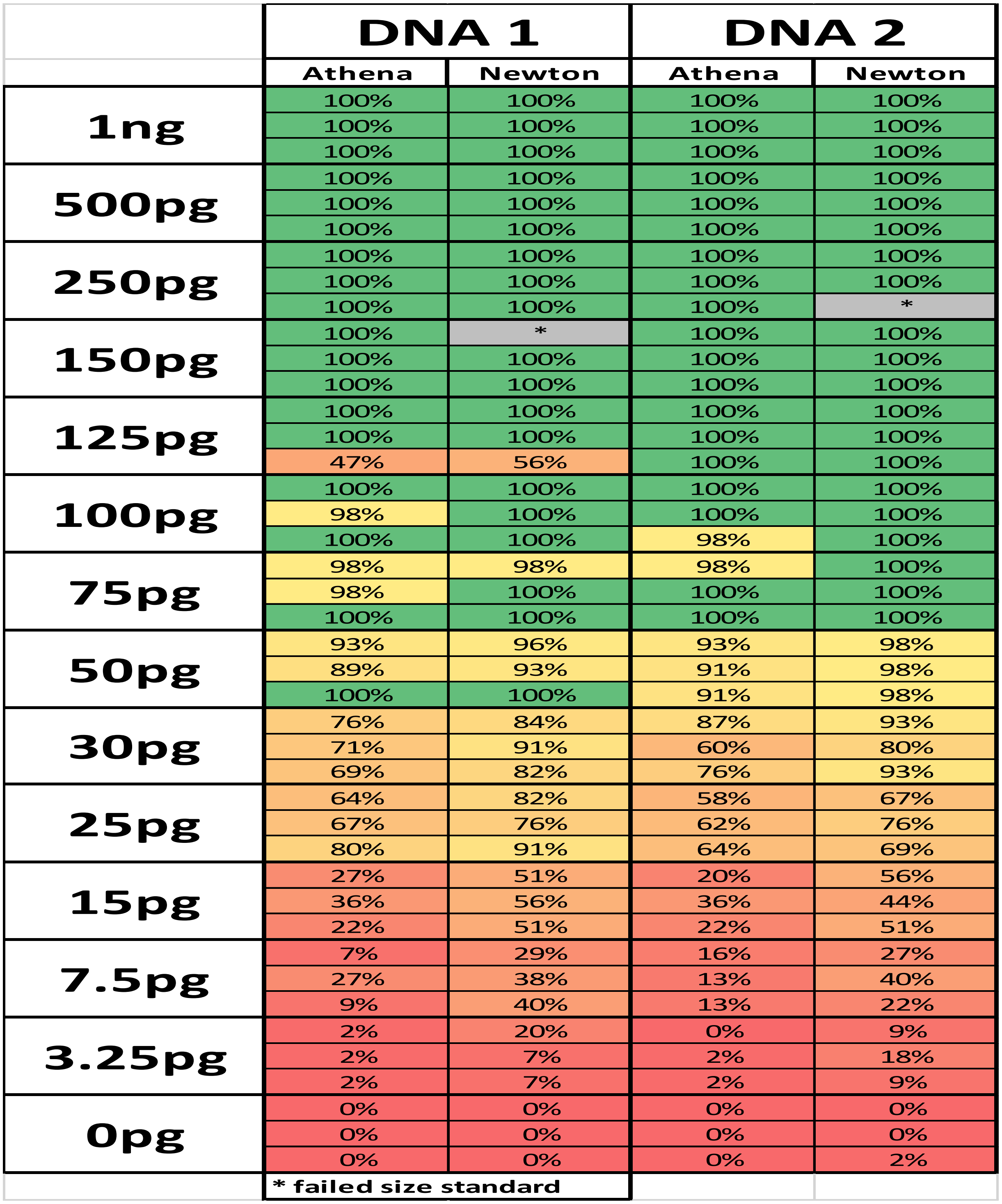


Figure 1: Instances of drop-in observed on Newton. Left side is DNA 1 replicate A with drop-in at D18S51 with an allelic assignment of 14 at 54 RFU. Right side is DNA 2 replicate C with an allelic assignment of 12 at 53 RFU.

Table 5: Percent profile obtained for each sensitivity series using a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter at a 3kV 5 sec injection parameter. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the percent profile observed.



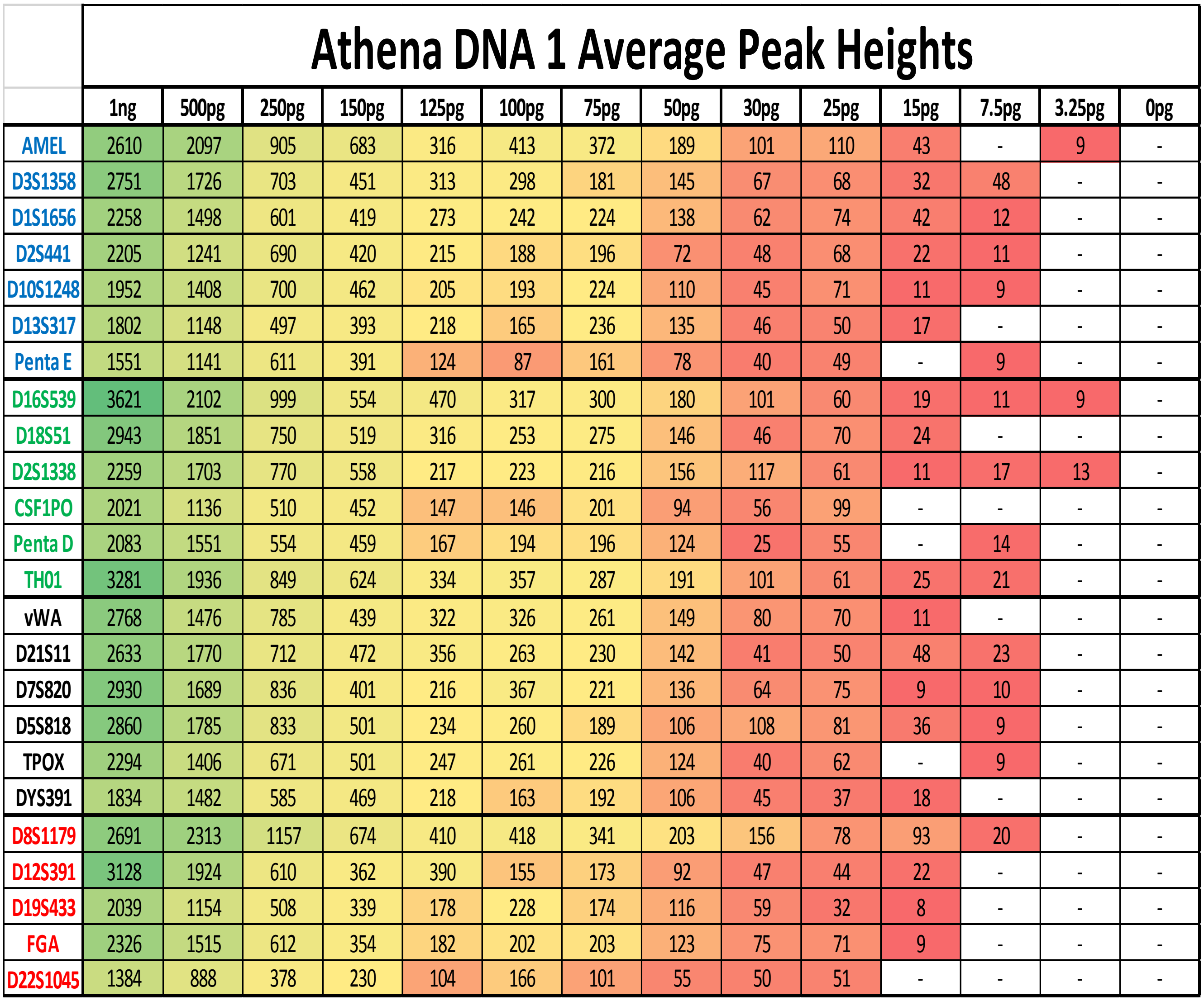
	DNA 1		DNA 2	
	Athena	Newton	Athena	Newton
1ng	100%	100%	100%	100%
	100%	100%	100%	100%
	100%	100%	100%	100%
500pg	100%	100%	100%	100%
	100%	100%	100%	100%
	100%	100%	100%	100%
250pg	100%	100%	100%	100%
	100%	100%	100%	100%
	100%	100%	100%	*
150pg	100%	*	100%	100%
	100%	100%	100%	100%
	100%	100%	100%	100%
125pg	100%	100%	100%	100%
	100%	100%	100%	100%
	47%	56%	100%	100%
100pg	100%	100%	100%	100%
	98%	100%	100%	100%
	100%	100%	98%	100%
75pg	98%	98%	98%	100%
	98%	100%	100%	100%
	100%	100%	100%	100%
50pg	93%	96%	93%	98%
	89%	93%	91%	98%
	100%	100%	91%	98%
30pg	76%	84%	87%	93%
	71%	91%	60%	80%
	69%	82%	76%	93%
25pg	64%	82%	58%	67%
	67%	76%	62%	76%
	80%	91%	64%	69%
15pg	27%	51%	20%	56%
	36%	56%	36%	44%
	22%	51%	22%	51%
7.5pg	7%	29%	16%	27%
	27%	38%	13%	40%
	9%	40%	13%	22%
3.25pg	2%	20%	0%	9%
	2%	7%	2%	18%
	2%	7%	2%	9%
0pg	0%	0%	0%	0%
	0%	0%	0%	0%
	0%	0%	0%	2%

* failed size standard

Table 6: Average peak heights from both Athena and Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the range of peak heights. The white cells represent loci that had complete dropout in all replicates.

	Average Peak Heights													
	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	3049	2502	1038	787	469	433	428	229	133	117	83	25	18	-
D3S1358	3329	2110	825	533	429	353	294	205	96	98	39	56	19	-
D1S1656	2949	1835	805	506	428	284	279	150	72	98	42	21	-	-
D2S441	2846	1618	735	539	293	270	232	99	94	67	34	17	-	-
D10S1248	2488	1768	861	542	327	246	284	172	79	77	44	21	9	-
D13S317	2461	1595	723	530	333	234	267	170	89	72	32	24	9	-
Penta E	2062	1516	760	516	250	144	235	119	57	62	19	11	-	-
D16S539	3998	2415	1051	568	511	339	338	207	147	88	44	28	12	-
D18S51	3475	2135	996	548	454	286	312	168	93	92	40	11	8	-
D2S1338	2670	1952	835	607	406	276	284	208	141	64	24	21	15	-
CSF1PO	2460	1477	626	468	253	193	223	110	81	89	31	14	10	-
Penta D	2418	1787	802	464	305	226	260	143	68	72	41	22	-	-
TH01	3796	2094	988	659	440	369	332	206	130	71	70	45	10	-
vWA	3254	1835	865	526	387	360	286	181	92	74	23	20	11	-
D21S11	3096	1869	858	489	443	305	290	185	88	64	44	30	9	-
D7S820	3596	2012	971	520	392	365	293	176	91	94	18	22	18	9
D5S818	3595	1998	917	573	369	284	252	140	121	70	45	28	9	-
TPOX	2859	1662	822	559	363	298	263	143	72	88	38	25	12	-
DYS391	2264	1733	684	426	285	200	238	127	56	41	37	39	21	-
D8S1179	3160	2525	1215	722	496	479	383	233	170	109	86	25	19	-
D12S391	3632	2037	773	362	424	179	195	117	72	50	28	19	-	-
D19S433	2461	1419	613	394	254	237	215	103	105	39	17	16	8	-
FGA	2972	1864	740	423	325	285	261	169	91	77	31	13	13	-
D22S1045	1907	1212	520	307	204	199	168	78	65	65	31	13	9	-

Table 7: Average peak heights for DNA 1 from Athena at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the range of peak heights. The white cells represent loci that had complete dropout in all replicates.



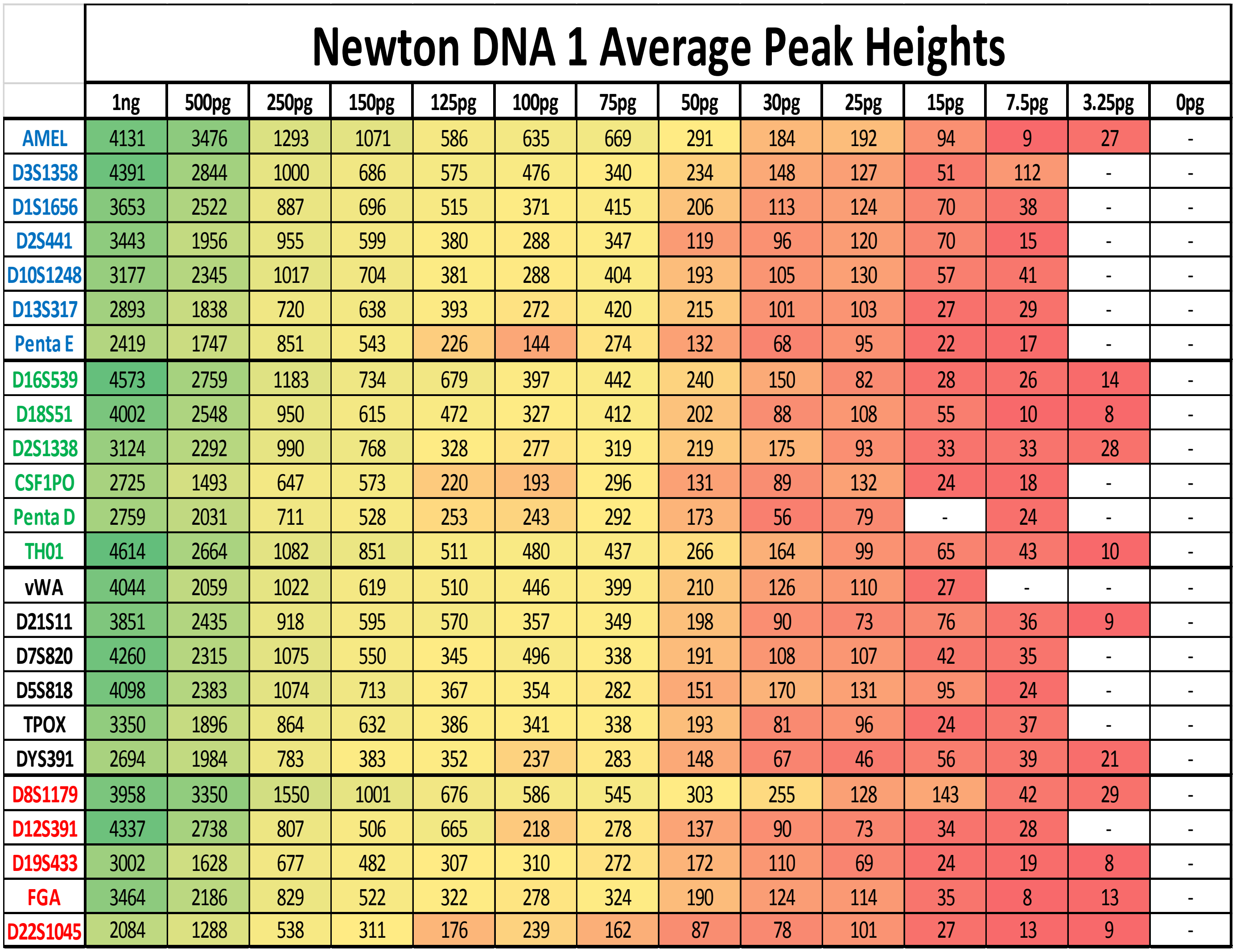
Athena DNA 1 Average Peak Heights

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	2610	2097	905	683	316	413	372	189	101	110	43	-	9	-
D3S1358	2751	1726	703	451	313	298	181	145	67	68	32	48	-	-
D1S1656	2258	1498	601	419	273	242	224	138	62	74	42	12	-	-
D2S441	2205	1241	690	420	215	188	196	72	48	68	22	11	-	-
D10S1248	1952	1408	700	462	205	193	224	110	45	71	11	9	-	-
D13S317	1802	1148	497	393	218	165	236	135	46	50	17	-	-	-
Penta E	1551	1141	611	391	124	87	161	78	40	49	-	9	-	-
D16S539	3621	2102	999	554	470	317	300	180	101	60	19	11	9	-
D18S51	2943	1851	750	519	316	253	275	146	46	70	24	-	-	-
D2S1338	2259	1703	770	558	217	223	216	156	117	61	11	17	13	-
CSF1PO	2021	1136	510	452	147	146	201	94	56	99	-	-	-	-
Penta D	2083	1551	554	459	167	194	196	124	25	55	-	14	-	-
TH01	3281	1936	849	624	334	357	287	191	101	61	25	21	-	-
vWA	2768	1476	785	439	322	326	261	149	80	70	11	-	-	-
D21S11	2633	1770	712	472	356	263	230	142	41	50	48	23	-	-
D7S820	2930	1689	836	401	216	367	221	136	64	75	9	10	-	-
D5S818	2860	1785	833	501	234	260	189	106	108	81	36	9	-	-
TPOX	2294	1406	671	501	247	261	226	124	40	62	-	9	-	-
DYS391	1834	1482	585	469	218	163	192	106	45	37	18	-	-	-
D8S1179	2691	2313	1157	674	410	418	341	203	156	78	93	20	-	-
D12S391	3128	1924	610	362	390	155	173	92	47	44	22	-	-	-
D19S433	2039	1154	508	339	178	228	174	116	59	32	8	-	-	-
FGA	2326	1515	612	354	182	202	203	123	75	71	9	-	-	-
D22S1045	1384	888	378	230	104	166	101	55	50	51	-	-	-	-

Table 8: Average peak heights for DNA 2 from Athena at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the range of peak heights. The white cells represent loci that had complete dropout in all replicates.

	Athena DNA 2 Average Peak Heights													
	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	2095	1635	726	511	365	269	240	161	88	61	75	18	-	-
D3S1358	2326	1417	607	356	305	252	231	161	58	69	16	-	-	-
D1S1656	2200	1204	643	324	341	200	168	92	32	72	9	-	-	-
D2S441	2205	1233	549	420	220	236	134	71	83	23	-	13	-	-
D10S1248	1822	1231	643	363	268	186	182	141	60	37	22	10	-	-
D13S317	1977	1272	618	401	274	189	151	118	77	48	-	12	-	-
Penta E	1691	1204	573	427	252	128	188	91	44	41	-	-	-	-
D16S539	3351	2016	860	408	372	284	251	164	137	90	51	26	9	-
D18S51	2935	1707	948	429	428	246	225	129	93	81	32	9	-	-
D2S1338	2207	1585	708	446	453	251	244	175	110	37	22	-	9	-
CSF1PO	2200	1384	555	354	274	179	162	82	64	55	22	-	-	-
Penta D	2108	1490	778	364	341	203	227	104	78	68	32	20	-	-
TH01	2937	1548	823	463	368	269	242	138	92	52	69	49	-	-
vWA	2493	1543	663	411	287	281	192	147	59	49	9	15	-	-
D21S11	2373	1348	736	360	341	247	233	158	80	54	13	22	-	-
D7S820	2949	1660	804	455	409	253	244	149	74	75	10	-	-	-
D5S818	3098	1590	747	432	362	220	219	118	67	30	20	22	-	-
TPOX	2429	1404	751	447	339	241	201	97	60	83	31	17	-	-
DYS391														
D8S1179	2325	1730	821	466	349	372	244	159	101	89	36	13	-	-
D12S391	2737	1362	637	221	246	138	125	87	41	29	-	-	-	-
D19S433	1861	1152	505	289	204	162	161	39	96	18	-	-	-	-
FGA	2418	1487	596	317	313	264	199	135	54	44	29	-	-	-
D22S1045	1687	1064	437	267	209	154	160	56	38	44	-	-	-	-

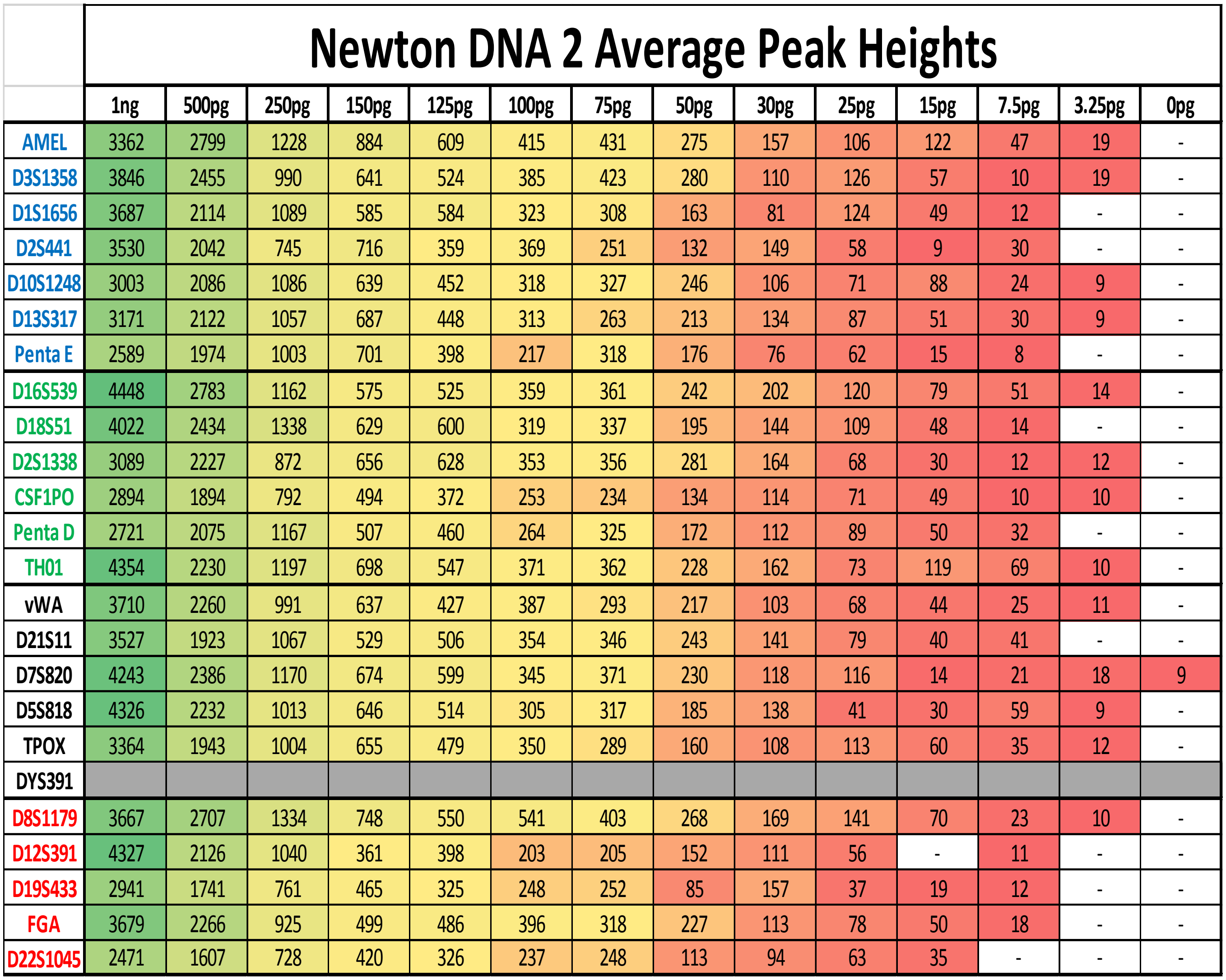
Table 9: Average peak heights for DNA 1 from Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the range of peak heights. The white cells represent loci that had complete dropout in all replicates.



Newton DNA 1 Average Peak Heights

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	4131	3476	1293	1071	586	635	669	291	184	192	94	9	27	-
D3S1358	4391	2844	1000	686	575	476	340	234	148	127	51	112	-	-
D1S1656	3653	2522	887	696	515	371	415	206	113	124	70	38	-	-
D2S441	3443	1956	955	599	380	288	347	119	96	120	70	15	-	-
D10S1248	3177	2345	1017	704	381	288	404	193	105	130	57	41	-	-
D13S317	2893	1838	720	638	393	272	420	215	101	103	27	29	-	-
Penta E	2419	1747	851	543	226	144	274	132	68	95	22	17	-	-
D16S539	4573	2759	1183	734	679	397	442	240	150	82	28	26	14	-
D18S51	4002	2548	950	615	472	327	412	202	88	108	55	10	8	-
D2S1338	3124	2292	990	768	328	277	319	219	175	93	33	33	28	-
CSF1PO	2725	1493	647	573	220	193	296	131	89	132	24	18	-	-
Penta D	2759	2031	711	528	253	243	292	173	56	79	-	24	-	-
TH01	4614	2664	1082	851	511	480	437	266	164	99	65	43	10	-
vWA	4044	2059	1022	619	510	446	399	210	126	110	27	-	-	-
D21S11	3851	2435	918	595	570	357	349	198	90	73	76	36	9	-
D7S820	4260	2315	1075	550	345	496	338	191	108	107	42	35	-	-
D5S818	4098	2383	1074	713	367	354	282	151	170	131	95	24	-	-
TPOX	3350	1896	864	632	386	341	338	193	81	96	24	37	-	-
DYS391	2694	1984	783	383	352	237	283	148	67	46	56	39	21	-
D8S1179	3958	3350	1550	1001	676	586	545	303	255	128	143	42	29	-
D12S391	4337	2738	807	506	665	218	278	137	90	73	34	28	-	-
D19S433	3002	1628	677	482	307	310	272	172	110	69	24	19	8	-
FGA	3464	2186	829	522	322	278	324	190	124	114	35	8	13	-
D22S1045	2084	1288	538	311	176	239	162	87	78	101	27	13	9	-

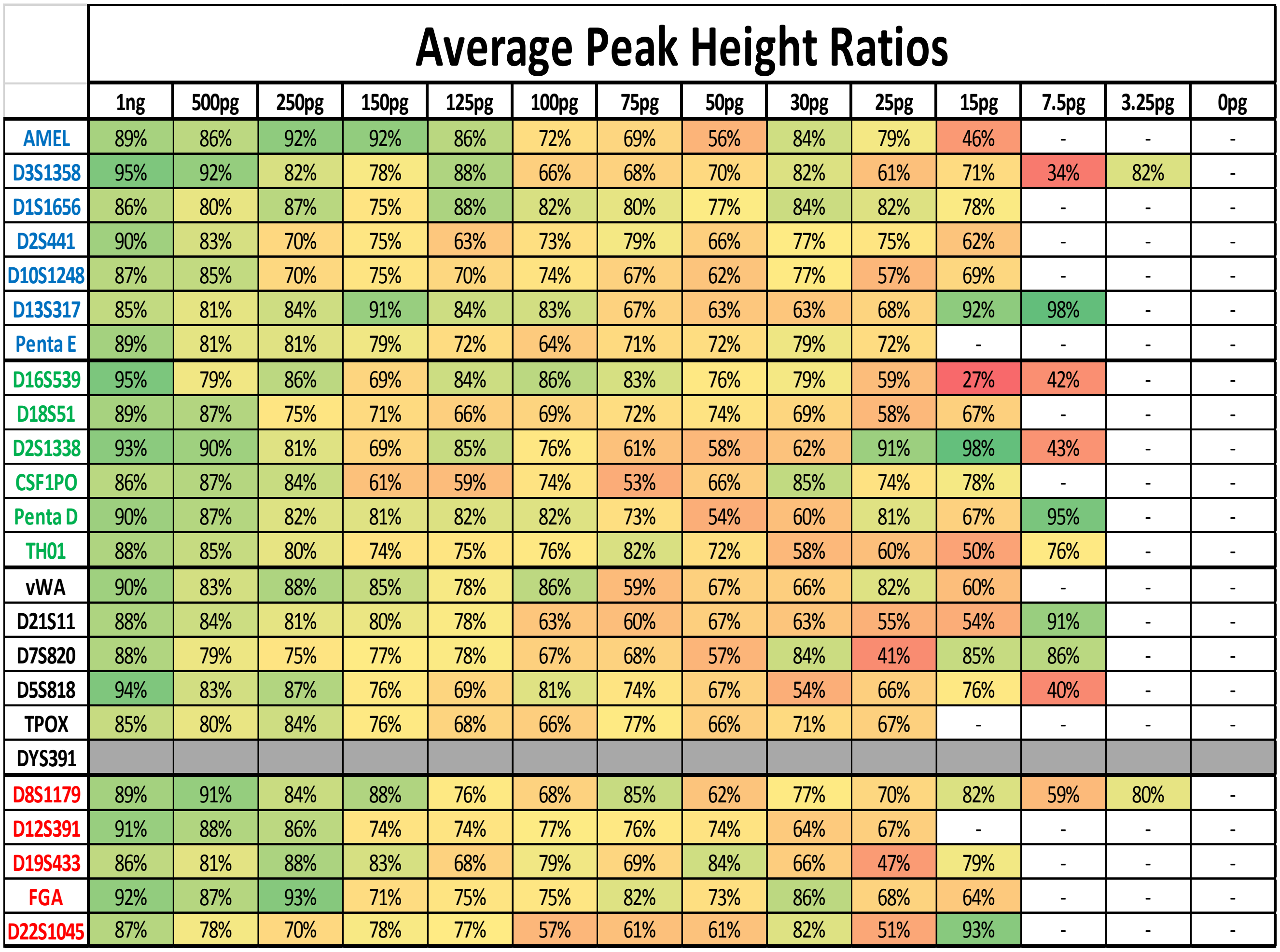
Table 10: Average peak heights for DNA 2 from Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height (red), the average (yellow) and the highest peak height (dark green). The heat map allows for a quick visualization of the range of peak heights. The white cells represent loci that had complete dropout in all replicates.



Newton DNA 2 Average Peak Heights

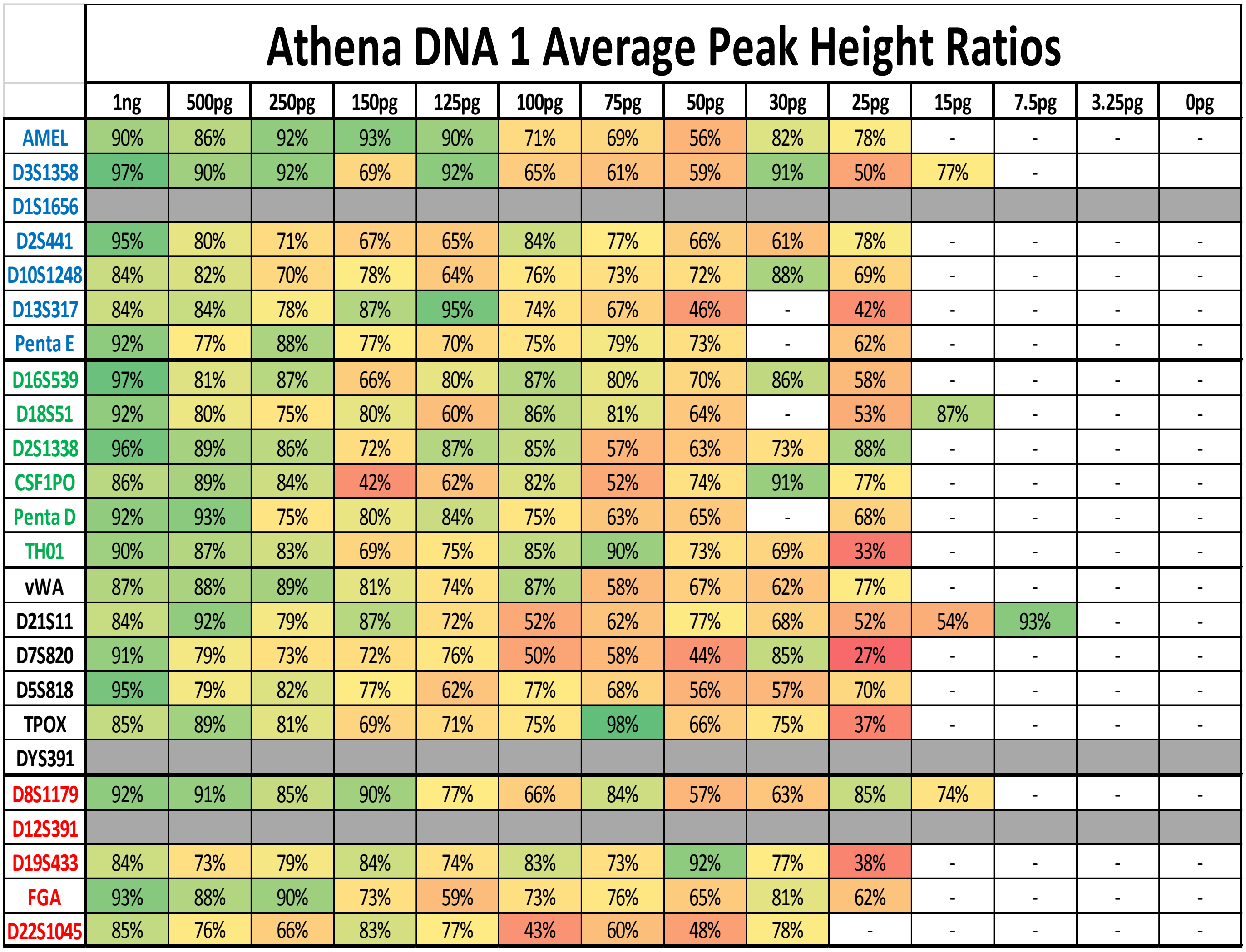
	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	3362	2799	1228	884	609	415	431	275	157	106	122	47	19	-
D3S1358	3846	2455	990	641	524	385	423	280	110	126	57	10	19	-
D1S1656	3687	2114	1089	585	584	323	308	163	81	124	49	12	-	-
D2S441	3530	2042	745	716	359	369	251	132	149	58	9	30	-	-
D10S1248	3003	2086	1086	639	452	318	327	246	106	71	88	24	9	-
D13S317	3171	2122	1057	687	448	313	263	213	134	87	51	30	9	-
Penta E	2589	1974	1003	701	398	217	318	176	76	62	15	8	-	-
D16S539	4448	2783	1162	575	525	359	361	242	202	120	79	51	14	-
D18S51	4022	2434	1338	629	600	319	337	195	144	109	48	14	-	-
D2S1338	3089	2227	872	656	628	353	356	281	164	68	30	12	12	-
CSF1PO	2894	1894	792	494	372	253	234	134	114	71	49	10	10	-
Penta D	2721	2075	1167	507	460	264	325	172	112	89	50	32	-	-
TH01	4354	2230	1197	698	547	371	362	228	162	73	119	69	10	-
vWA	3710	2260	991	637	427	387	293	217	103	68	44	25	11	-
D21S11	3527	1923	1067	529	506	354	346	243	141	79	40	41	-	-
D7S820	4243	2386	1170	674	599	345	371	230	118	116	14	21	18	9
D5S818	4326	2232	1013	646	514	305	317	185	138	41	30	59	9	-
TPOX	3364	1943	1004	655	479	350	289	160	108	113	60	35	12	-
DYS391														
D8S1179	3667	2707	1334	748	550	541	403	268	169	141	70	23	10	-
D12S391	4327	2126	1040	361	398	203	205	152	111	56	-	11	-	-
D19S433	2941	1741	761	465	325	248	252	85	157	37	19	12	-	-
FGA	3679	2266	925	499	486	396	318	227	113	78	50	18	-	-
D22S1045	2471	1607	728	420	326	237	248	113	94	63	35	-	-	-

Table 11: Average peak height ratios for both Athena and Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height ratio (red), the average (yellow) and the highest peak height ratio (dark green). The heat map allows for a quick visualization of the range of peak heights ratios. The gray cells represent the Y-STR locus with no heterozygous calculation. The white cells represent loci in with complete dropout in all replicates.



	Average Peak Height Ratios													
	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	89%	86%	92%	92%	86%	72%	69%	56%	84%	79%	46%	-	-	-
D3S1358	95%	92%	82%	78%	88%	66%	68%	70%	82%	61%	71%	34%	82%	-
D1S1656	86%	80%	87%	75%	88%	82%	80%	77%	84%	82%	78%	-	-	-
D2S441	90%	83%	70%	75%	63%	73%	79%	66%	77%	75%	62%	-	-	-
D10S1248	87%	85%	70%	75%	70%	74%	67%	62%	77%	57%	69%	-	-	-
D13S317	85%	81%	84%	91%	84%	83%	67%	63%	63%	68%	92%	98%	-	-
Penta E	89%	81%	81%	79%	72%	64%	71%	72%	79%	72%	-	-	-	-
D16S539	95%	79%	86%	69%	84%	86%	83%	76%	79%	59%	27%	42%	-	-
D18S51	89%	87%	75%	71%	66%	69%	72%	74%	69%	58%	67%	-	-	-
D2S1338	93%	90%	81%	69%	85%	76%	61%	58%	62%	91%	98%	43%	-	-
CSF1PO	86%	87%	84%	61%	59%	74%	53%	66%	85%	74%	78%	-	-	-
Penta D	90%	87%	82%	81%	82%	82%	73%	54%	60%	81%	67%	95%	-	-
TH01	88%	85%	80%	74%	75%	76%	82%	72%	58%	60%	50%	76%	-	-
vWA	90%	83%	88%	85%	78%	86%	59%	67%	66%	82%	60%	-	-	-
D21S11	88%	84%	81%	80%	78%	63%	60%	67%	63%	55%	54%	91%	-	-
D7S820	88%	79%	75%	77%	78%	67%	68%	57%	84%	41%	85%	86%	-	-
D5S818	94%	83%	87%	76%	69%	81%	74%	67%	54%	66%	76%	40%	-	-
TPOX	85%	80%	84%	76%	68%	66%	77%	66%	71%	67%	-	-	-	-
DYS391														
D8S1179	89%	91%	84%	88%	76%	68%	85%	62%	77%	70%	82%	59%	80%	-
D12S391	91%	88%	86%	74%	74%	77%	76%	74%	64%	67%	-	-	-	-
D19S433	86%	81%	88%	83%	68%	79%	69%	84%	66%	47%	79%	-	-	-
FGA	92%	87%	93%	71%	75%	75%	82%	73%	86%	68%	64%	-	-	-
D22S1045	87%	78%	70%	78%	77%	57%	61%	61%	82%	51%	93%	-	-	-

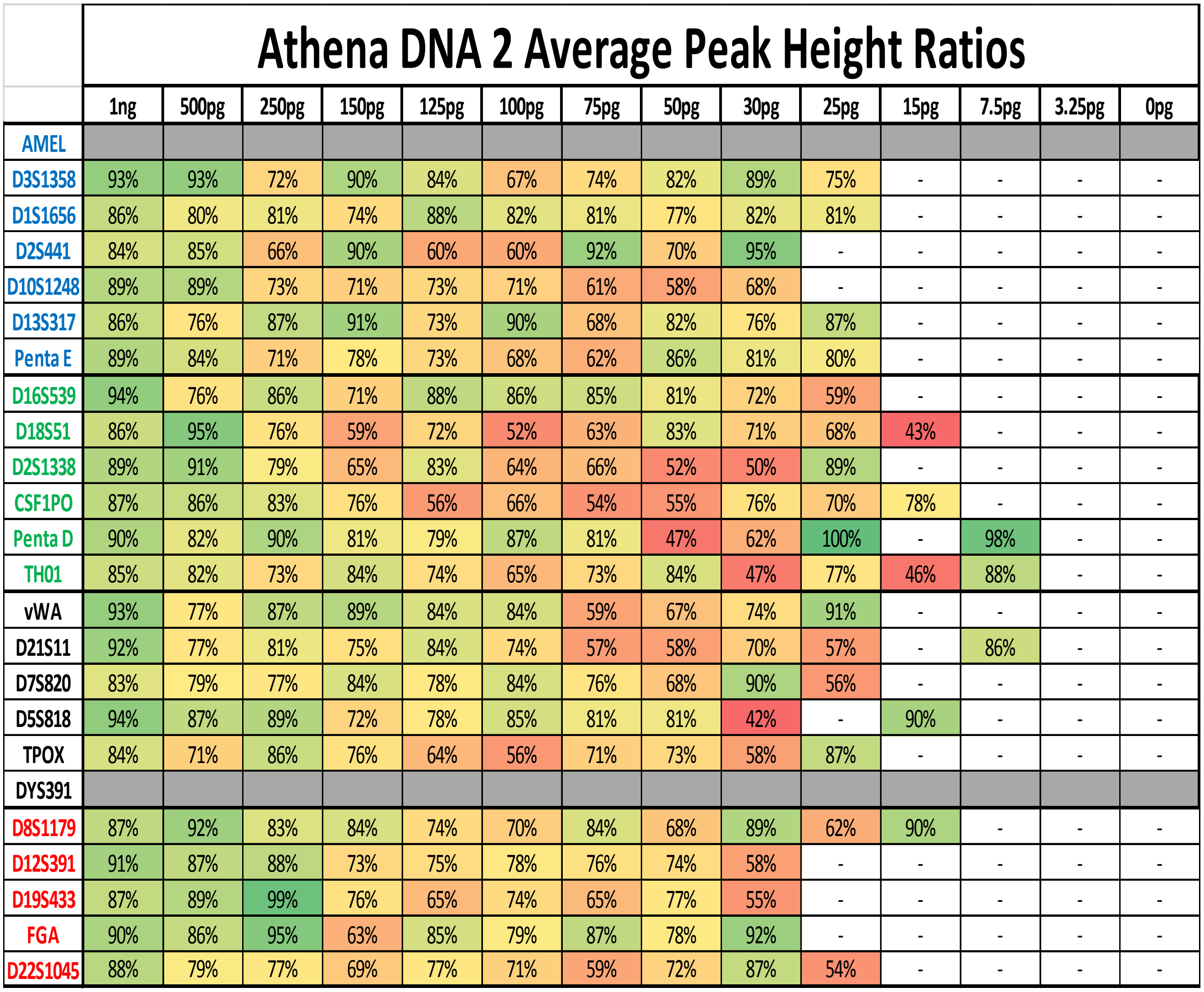
Table 12: Average peak height ratios for DNA 1 from Athena at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height ratio (red), the average (yellow) and the highest peak height ratio (dark green). The heat map allows for a quick visualization of the range of peak heights ratios. The gray cells represent the Y-STR locus with no heterozygous calculation. The white cells represent loci in with complete dropout in all replicates.



Athena DNA 1 Average Peak Height Ratios

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	90%	86%	92%	93%	90%	71%	69%	56%	82%	78%	-	-	-	-
D3S1358	97%	90%	92%	69%	92%	65%	61%	59%	91%	50%	77%	-		
D1S1656														
D2S441	95%	80%	71%	67%	65%	84%	77%	66%	61%	78%	-	-	-	-
D10S1248	84%	82%	70%	78%	64%	76%	73%	72%	88%	69%	-	-	-	-
D13S317	84%	84%	78%	87%	95%	74%	67%	46%	-	42%	-	-	-	-
Penta E	92%	77%	88%	77%	70%	75%	79%	73%	-	62%	-	-	-	-
D16S539	97%	81%	87%	66%	80%	87%	80%	70%	86%	58%	-	-	-	-
D18S51	92%	80%	75%	80%	60%	86%	81%	64%	-	53%	87%	-	-	-
D2S1338	96%	89%	86%	72%	87%	85%	57%	63%	73%	88%	-	-	-	-
CSF1PO	86%	89%	84%	42%	62%	82%	52%	74%	91%	77%	-	-	-	-
Penta D	92%	93%	75%	80%	84%	75%	63%	65%	-	68%	-	-	-	-
TH01	90%	87%	83%	69%	75%	85%	90%	73%	69%	33%	-	-	-	-
vWA	87%	88%	89%	81%	74%	87%	58%	67%	62%	77%	-	-	-	-
D21S11	84%	92%	79%	87%	72%	52%	62%	77%	68%	52%	54%	93%	-	-
D7S820	91%	79%	73%	72%	76%	50%	58%	44%	85%	27%	-	-	-	-
D5S818	95%	79%	82%	77%	62%	77%	68%	56%	57%	70%	-	-	-	-
TPOX	85%	89%	81%	69%	71%	75%	98%	66%	75%	37%	-	-	-	-
DYS391														
D8S1179	92%	91%	85%	90%	77%	66%	84%	57%	63%	85%	74%	-	-	-
D12S391														
D19S433	84%	73%	79%	84%	74%	83%	73%	92%	77%	38%	-	-	-	-
FGA	93%	88%	90%	73%	59%	73%	76%	65%	81%	62%	-	-	-	-
D22S1045	85%	76%	66%	83%	77%	43%	60%	48%	78%	-	-	-	-	-

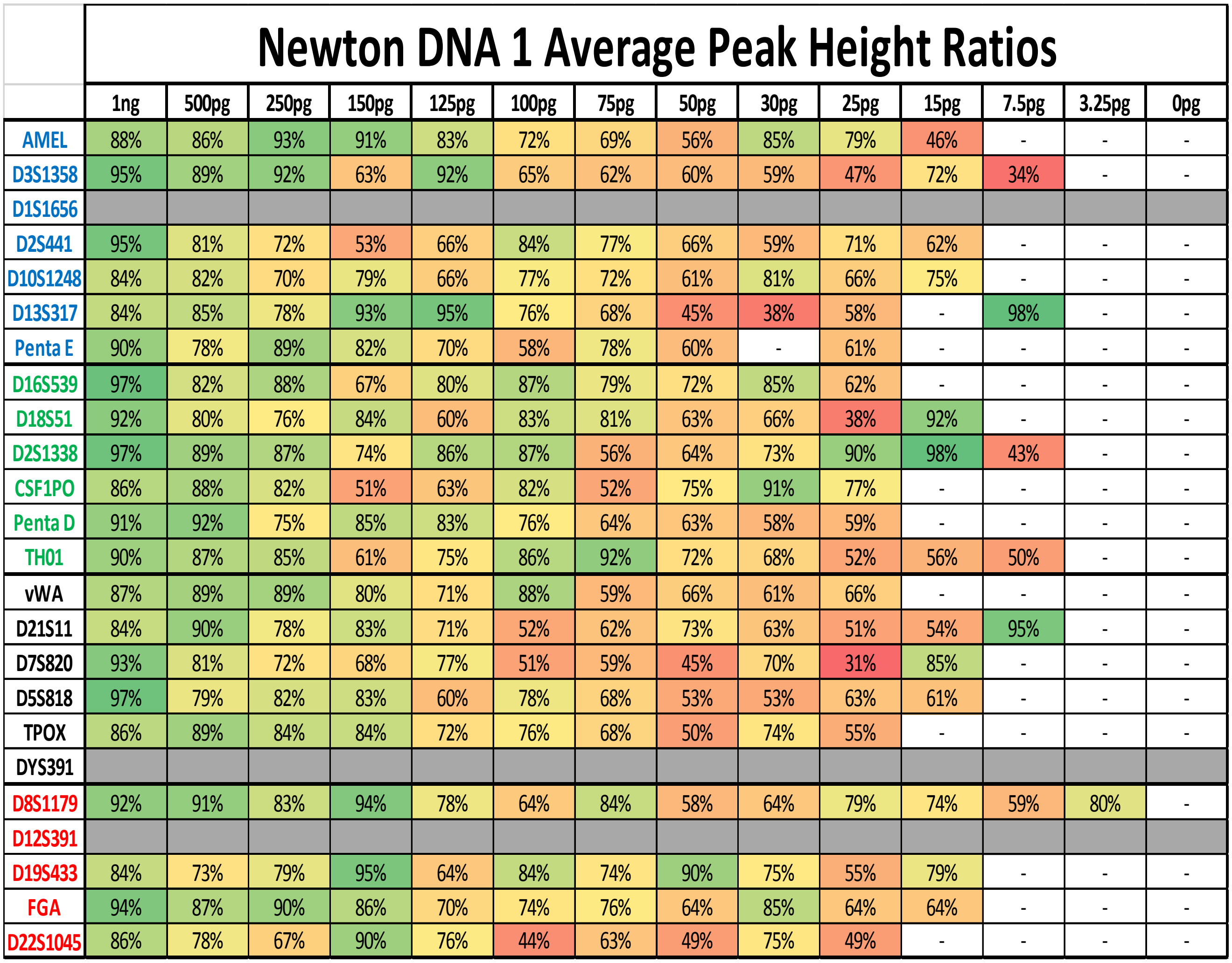
Table 13: Average peak height ratios for DNA 2 from Athena at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height ratio (red), the average (yellow) and the highest peak height ratio (dark green). The heat map allows for a quick visualization of the range of peak heights ratios. The gray cells represent the Y-STR locus with no heterozygous calculation. The white cells represent loci in with complete dropout in all replicates.



Athena DNA 2 Average Peak Height Ratios

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL														
D3S1358	93%	93%	72%	90%	84%	67%	74%	82%	89%	75%	-	-	-	-
D1S1656	86%	80%	81%	74%	88%	82%	81%	77%	82%	81%	-	-	-	-
D2S441	84%	85%	66%	90%	60%	60%	92%	70%	95%	-	-	-	-	-
D10S1248	89%	89%	73%	71%	73%	71%	61%	58%	68%	-	-	-	-	-
D13S317	86%	76%	87%	91%	73%	90%	68%	82%	76%	87%	-	-	-	-
Penta E	89%	84%	71%	78%	73%	68%	62%	86%	81%	80%	-	-	-	-
D16S539	94%	76%	86%	71%	88%	86%	85%	81%	72%	59%	-	-	-	-
D18S51	86%	95%	76%	59%	72%	52%	63%	83%	71%	68%	43%	-	-	-
D2S1338	89%	91%	79%	65%	83%	64%	66%	52%	50%	89%	-	-	-	-
CSF1PO	87%	86%	83%	76%	56%	66%	54%	55%	76%	70%	78%	-	-	-
Penta D	90%	82%	90%	81%	79%	87%	81%	47%	62%	100%	-	98%	-	-
TH01	85%	82%	73%	84%	74%	65%	73%	84%	47%	77%	46%	88%	-	-
vWA	93%	77%	87%	89%	84%	84%	59%	67%	74%	91%	-	-	-	-
D21S11	92%	77%	81%	75%	84%	74%	57%	58%	70%	57%	-	86%	-	-
D7S820	83%	79%	77%	84%	78%	84%	76%	68%	90%	56%	-	-	-	-
D5S818	94%	87%	89%	72%	78%	85%	81%	81%	42%	-	90%	-	-	-
TPOX	84%	71%	86%	76%	64%	56%	71%	73%	58%	87%	-	-	-	-
DYS391														
D8S1179	87%	92%	83%	84%	74%	70%	84%	68%	89%	62%	90%	-	-	-
D12S391	91%	87%	88%	73%	75%	78%	76%	74%	58%	-	-	-	-	-
D19S433	87%	89%	99%	76%	65%	74%	65%	77%	55%	-	-	-	-	-
FGA	90%	86%	95%	63%	85%	79%	87%	78%	92%	-	-	-	-	-
D22S1045	88%	79%	77%	69%	77%	71%	59%	72%	87%	54%	-	-	-	-

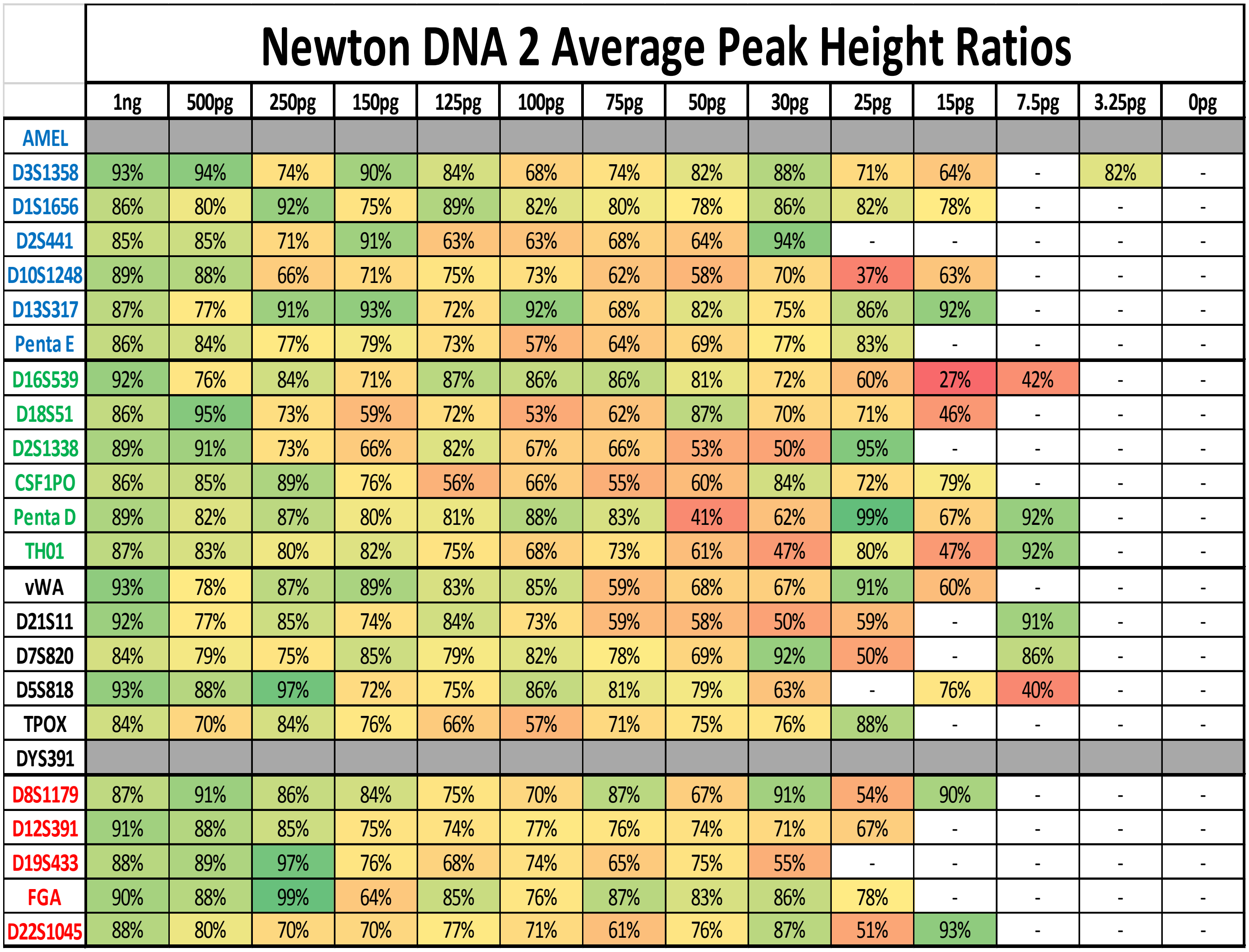
Table 14: Average peak height ratios for DNA 1 from Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height ratio (red), the average (yellow) and the highest peak height ratio (dark green). The heat map allows for a quick visualization of the range of peak heights ratios. The gray cells represent the Y-STR locus with no heterozygous calculation. The white cells represent loci in with complete dropout in all replicates.



Newton DNA 1 Average Peak Height Ratios

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL	88%	86%	93%	91%	83%	72%	69%	56%	85%	79%	46%	-	-	-
D3S1358	95%	89%	92%	63%	92%	65%	62%	60%	59%	47%	72%	34%	-	-
D1S1656														
D2S441	95%	81%	72%	53%	66%	84%	77%	66%	59%	71%	62%	-	-	-
D10S1248	84%	82%	70%	79%	66%	77%	72%	61%	81%	66%	75%	-	-	-
D13S317	84%	85%	78%	93%	95%	76%	68%	45%	38%	58%	-	98%	-	-
Penta E	90%	78%	89%	82%	70%	58%	78%	60%	-	61%	-	-	-	-
D16S539	97%	82%	88%	67%	80%	87%	79%	72%	85%	62%	-	-	-	-
D18S51	92%	80%	76%	84%	60%	83%	81%	63%	66%	38%	92%	-	-	-
D2S1338	97%	89%	87%	74%	86%	87%	56%	64%	73%	90%	98%	43%	-	-
CSF1PO	86%	88%	82%	51%	63%	82%	52%	75%	91%	77%	-	-	-	-
Penta D	91%	92%	75%	85%	83%	76%	64%	63%	58%	59%	-	-	-	-
TH01	90%	87%	85%	61%	75%	86%	92%	72%	68%	52%	56%	50%	-	-
vWA	87%	89%	89%	80%	71%	88%	59%	66%	61%	66%	-	-	-	-
D21S11	84%	90%	78%	83%	71%	52%	62%	73%	63%	51%	54%	95%	-	-
D7S820	93%	81%	72%	68%	77%	51%	59%	45%	70%	31%	85%	-	-	-
D5S818	97%	79%	82%	83%	60%	78%	68%	53%	53%	63%	61%	-	-	-
TPOX	86%	89%	84%	84%	72%	76%	68%	50%	74%	55%	-	-	-	-
DYS391														
D8S1179	92%	91%	83%	94%	78%	64%	84%	58%	64%	79%	74%	59%	80%	-
D12S391														
D19S433	84%	73%	79%	95%	64%	84%	74%	90%	75%	55%	79%	-	-	-
FGA	94%	87%	90%	86%	70%	74%	76%	64%	85%	64%	64%	-	-	-
D22S1045	86%	78%	67%	90%	76%	44%	63%	49%	75%	49%	-	-	-	-

Table 15: Average peak height ratios for DNA 2 from Newton at 3kV 5s for the sensitivity series from 1ng down to 0pg using 29 cycles. The three color heat map was used to represent the lowest peak height ratio (red), the average (yellow) and the highest peak height ratio (dark green). The heat map allows for a quick visualization of the range of peak heights ratios. The gray cells represent the Y-STR locus with no heterozygous calculation. The white cells represent loci in with complete dropout in all replicates.



Newton DNA 2 Average Peak Height Ratios

	1ng	500pg	250pg	150pg	125pg	100pg	75pg	50pg	30pg	25pg	15pg	7.5pg	3.25pg	0pg
AMEL														
D3S1358	93%	94%	74%	90%	84%	68%	74%	82%	88%	71%	64%	-	82%	-
D1S1656	86%	80%	92%	75%	89%	82%	80%	78%	86%	82%	78%	-	-	-
D2S441	85%	85%	71%	91%	63%	63%	68%	64%	94%	-	-	-	-	-
D10S1248	89%	88%	66%	71%	75%	73%	62%	58%	70%	37%	63%	-	-	-
D13S317	87%	77%	91%	93%	72%	92%	68%	82%	75%	86%	92%	-	-	-
Penta E	86%	84%	77%	79%	73%	57%	64%	69%	77%	83%	-	-	-	-
D16S539	92%	76%	84%	71%	87%	86%	86%	81%	72%	60%	27%	42%	-	-
D18S51	86%	95%	73%	59%	72%	53%	62%	87%	70%	71%	46%	-	-	-
D2S1338	89%	91%	73%	66%	82%	67%	66%	53%	50%	95%	-	-	-	-
CSF1PO	86%	85%	89%	76%	56%	66%	55%	60%	84%	72%	79%	-	-	-
Penta D	89%	82%	87%	80%	81%	88%	83%	41%	62%	99%	67%	92%	-	-
TH01	87%	83%	80%	82%	75%	68%	73%	61%	47%	80%	47%	92%	-	-
vWA	93%	78%	87%	89%	83%	85%	59%	68%	67%	91%	60%	-	-	-
D21S11	92%	77%	85%	74%	84%	73%	59%	58%	50%	59%	-	91%	-	-
D7S820	84%	79%	75%	85%	79%	82%	78%	69%	92%	50%	-	86%	-	-
D5S818	93%	88%	97%	72%	75%	86%	81%	79%	63%	-	76%	40%	-	-
TPOX	84%	70%	84%	76%	66%	57%	71%	75%	76%	88%	-	-	-	-
DYS391														
D8S1179	87%	91%	86%	84%	75%	70%	87%	67%	91%	54%	90%	-	-	-
D12S391	91%	88%	85%	75%	74%	77%	76%	74%	71%	67%	-	-	-	-
D19S433	88%	89%	97%	76%	68%	74%	65%	75%	55%	-	-	-	-	-
FGA	90%	88%	99%	64%	85%	76%	87%	83%	86%	78%	-	-	-	-
D22S1045	88%	80%	70%	70%	77%	71%	61%	76%	87%	51%	93%	-	-	-

4.A.3 Known Non Probative and Mock Casework Samples

All known non-probative samples were amplified using a 750pg target amount; mock casework samples were amplified targeting 750pg or max input volume. Known, non-probative and mock casework samples were amplified by two separate operators and injected for 3kV 5sec. Samples were analyzed using a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter. All ten known samples and mock casework samples were reviewed for concordance. The known, non-probative and mock casework samples had consistent genotypes with those provided. All known non-probative samples generated full profiles. Some mock casework displayed inconsistent results when compared to the provided results. These inconsistencies are most likely due to the nature of touched samples and the variations in overall target amount leading to drop out. In addition, multiple alleles not assigned to the original donor where called using PowerPlex® Fusion System (Tables 16-21).

Table 16: Mock casework key for profiles generated during the PowerPlex® Fusion internal validation.

	Touched Item	SA pg/ul
Mock 1	bottle	63.2
Mock 2	bottle	2155.4
Mock 3	bottle	276.3
Mock 4	bottle	463.7
Mock 5	bottle	173.0
Mock 6	bottle	53.3
Mock 7	bottle	474.9
Mock 8	bottle	1344.9
Mock 9	bottle	1803.5
Mock 10	Rubber Piece	24.9
Mock 11	Altoid Tin	5.8
Mock 12	Scissors	2.9
Mock 13	Fork Handle	516.8
Mock 14	Glasses Piece	62.1
Mock 15	Altoid Tin	3.6
Mock 16	Hair Drier	7.6
Mock 17	Timer	16.5
Mock 18	Ice Cream Scoop	190.6
Mock 19	Spoon Handle	6.7
Mock 20	Brown Sunglasses	25.2
Mock 21	Stress Toy	53.6
Mock 22	Ear Buds	9.8
Mock 23	Aviator Sunglasses	7.0
Mock 24	Cup	10.9

Table 17: Known profile success for operator 1. The bolded profiles were provided by the OCME-NYC and the non-bolded samples below are the observed profile during the validation.

	Known Samples Newton Operator 1																							
	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Known 1	**X Y**	**16 17**	**15 16**	**10 14**	**16**	**8 9**	**12 18**	**9 11**	**13 15**	**17 25**	**11 12**	**11 12**	**7 9**	**16 18**	**29 31.2**	**8 10**	**11**	**11**	**10**	**11 14**	**19 21**	**13**	**22 23**	**16 17**
Known_1	X Y	16 17	15 16	10 14	16	8 9	12 18	9 11	13 15	17 25	11 12	11 12	7 9	16 18	29 31.2	8 10	11	11	10	11 14	19 21	13	22 23	16 17
Known 2	**X Y**	**14 16**	**16.3 17.3**	**11 14**	**13 16**	**9**	**14 19**	**12 13**	**14 17**	**16 19**	**10**	**9 10**	**6 8**	**15 18**	**29 32.2**	**9 10**	**10 11**	**8 9**	**9**	**13**	**17 22**	**13 14**	**18 22**	**15**
Known_2	X Y	14 16	16.3 17.3	11 14	13 16	9	14 19	12 13	14 17	16 19	10	9 10	6 8	15 18	29 32.2	9 10	10 11	8 9	9	13	17 22	13 14	18 22	15
Known 3	**X Y**	**15 16**	**14 16**	**10 12**	**15 16**	**11**	**5 7**	**10 11**	**16 21**	**18 19**	**12**	**10 11**	**6 9**	**14 16**	**27 31**	**8 11**	**12 13**	**8 11**	**10**	**12 13**	**18 20**	**12**	**23 24**	**17**
Known_3	X Y	15 16	14 16	10 12	15 16	11	5 7	10 11	16 21	18 19	12	10 11	6 9	14 16	27 31	8 11	12 13	8 11	10	12 13	18 20	12	23 24	17
Known 4	**X Y**	**16**	**12**	**10 14**	**14 17**	**11 13**	**12 13**	**12**	**14 18**	**20 22**	**10 11**	**9 11**	**8 9.3**	**14 17**	**29 31.2**	**8 12**	**11 12**	**9 11**	**10**	**12 13**	**18 21**	**12 14**	**23**	**11 15**
Known_4	X Y	16	12	10 14	14 17	11 13	12 13	12	14 18	20 22	10 11	9 11	8 9.3	14 17	29 31.2	8 12	11 12	9 11	10	12 13	18 21	12 14	23	11 15
Known 5	**X Y**	**16**	**12 16**	**12 14**	**14 17**	**10 14**	**5 12**	**11**	**13 18**	**19 25**	**11 12**	**11 12**	**6 7**	**16 18**	**27 29**	**10**	**12 13**	**8**	**10**	**12 14**	**20 22**	**13 14.2**	**21 22**	**15 17**
Known_5	X Y	16	12 16	12 14	14 17	10 14	5 12	11	13 18	19 25	11 12	11 12	6 7	16 18	27 29	10	12 13	8	10	12 14	20 22	13 14.2	21 22	15 17
Known 6	**X Y**	**15 16**	**16 18.3**	**12 14**	**13 14**	**8 10**	**16 20**	**10 12**	**14**	**19 22**	**10 11**	**9 13**	**7 9.3**	**14 17**	**29**	**8**	**11**	**8 11**	**9**	**10 15**	**19 21**	**12.2 14.2**	**18 21**	**16 17**
Known_6	X Y	15 16	16 18.3	12 14	13 14	8 10	16 20	10 12	14	19 22	10 11	9 13	7 9.3	14 17	29	8	11	8 11	9	10 15	19 21	12.2 14.2	18 21	16 17
Known 7	**X**	**16 17**	**13 15**	**11 14**	**15**	**12 13**	**5 8**	**9 11**	**16 18**	**16 24**	**10**	**8 13**	**7 8**	**15 19**	**29 32.2**	**9 11**	**12 13**	**9**	**	**14 15**	**15 17**	**14 14.2**	**22**	**15 16**
Known_7	X	16 17	13 15	11 14	15	12 13	5 8	9 11	16 18	16 24	10	8 13	7 8	15 19	29 32.2	9 11	12 13	9	-	14 15	15 17	14 14.2	22	15 16
Known 8	**X**	**15 16**	**15 17.3**	**11**	**14**	**10 11**	**12 22**	**10 12**	**12 14**	**20**	**12**	**8 12**	**7 8**	**16 19**	**31 32.2**	**11 12**	**7 9**	**8 11**	**	**16**	**18 20**	**13 15.2**	**19 23**	**16**
Known_8	X	15 16	15 17.3	11	14	10 11	12 22	10 12	12 14	20	12	8 12	7 8	16 19	31 32.2	11 12	7 9	8 11	-	16	18 20	13 15.2	19 23	16
Known 9	**X**	**15 16**	**15 16**	**11**	**13 14**	**8 12**	**5 12**	**11 12**	**14 19**	**17 23**	**10 12**	**8 12**	**7 9**	**14**	**30 31**	**9.1 10**	**10 12**	**8 10**	**	**10 14**	**22**	**13 14**	**24 26**	**15**
Known_9	X	15 16	15 16	11	13 14	8 12	5 12	11 12	14 19	17 23	10 12	8 12	7 9	14	30 31	9.1 10	10 12	8 10	-	10 14	22	13 14	24 26	15
Known 10	**X**	**17**	**11 15**	**10 14**	**13**	**12 13**	**7 12**	**9 10**	**15 18**	**19 23**	**10 12**	**9 10**	**6 7**	**14 18**	**29 30**	**10 11**	**11 12**	**8**	**	**13**	**17 18**	**12.2 15.2**	**20 26**	**15 16**
Known_10	X	17	11 15	10 14	13	12 13	7 12	9 10	15 18	19 23	10 12	9 10	6 7	14 18	29 30	10 11	11 12	8	-	13	17 18	12.2 15.2	20 26	15 16

** and – represent loci where no alleles were present.

Table 18: Known profile success for operator 2. The top bolded profiles were provided by the OCME-NYC and the non-bolded samples below are the observed profile during the validation.

Known Samples Newton Operator 2

	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Known 1	**X Y**	**16 17**	**15 16**	**10 14**	**16**	**8 9**	**12 18**	**9 11**	**13 15**	**17 25**	**11 12**	**11 12**	**7 9**	**16 18**	**29 31.2**	**8 10**	**11**	**11**	**10**	**11 14**	**19 21**	**13**	**22 23**	**16 17**
Known_1	X Y	16 17	15 16	10 14	16	8 9	12 18	9 11	13 15	17 25	11 12	11 12	7 9	16 18	29 31.2	8 10	11	11	10	11 14	19 21	13	22 23	16 17
Known 2	**X Y**	**14 16**	**16.3 17.3**	**11 14**	**13 16**	**9**	**14 19**	**12 13**	**14 17**	**16 19**	**10**	**9 10**	**6 8**	**15 18**	**29 32.2**	**9 10**	**10 11**	**8 9**	**9**	**13**	**17 22**	**13 14**	**18 22**	**15**
Known_2	X Y	14 16	16.3 17.3	11 14	13 16	9	14 19	12 13	14 17	16 19	10	9 10	6 8	15 18	29 32.2	9 10	10 11	8 9	9	13	17 22	13 14	18 22	15
Known 3	**X Y**	**15 16**	**14 16**	**10 12**	**15 16**	**11**	**5 7**	**10 11**	**16 21**	**18 19**	**12**	**10 11**	**6 9**	**14 16**	**27 31**	**8 11**	**12 13**	**8 11**	**10**	**12 13**	**18 20**	**12**	**23 24**	**17**
Known_3	X Y	15 16	14 16	10 12	15 16	11	5 7	10 11	16 21	18 19	12	10 11	6 9	14 16	27 31	8 11	12 13	8 11	10	12 13	18 20	12	23 24	17
Known 4	**X Y**	**16**	**12**	**10 14**	**14 17**	**11 13**	**12 13**	**12**	**14 18**	**20 22**	**10 11**	**9 11**	**8 9.3**	**14 17**	**29 31.2**	**8 12**	**11 12**	**9 11**	**10**	**12 13**	**18 21**	**12 14**	**23**	**11 15**
Known_4	X Y	16	12	10 14	14 17	11 13	12 13	12	14 18	20 22	10 11	9 11	8 9.3	14 17	29 31.2	8 12	11 12	9 11	10	12 13	18 21	12 14	23	11 15
Known 5	**X Y**	**16**	**12 16**	**12 14**	**14 17**	**10 14**	**5 12**	**11**	**13 18**	**19 25**	**11 12**	**11 12**	**6 7**	**16 18**	**27 29**	**10**	**12 13**	**8**	**10**	**12 14**	**20 22**	**13 14.2**	**21 22**	**15 17**
Known_5	X Y	16	12 16	12 14	14 17	10 14	5 12	11	13 18	19 25	11 12	11 12	6 7	16 18	27 29	10	12 13	8	10	12 14	20 22	13 14.2	21 22	15 17
Known 6	**X Y**	**15 16**	**16 18.3**	**12 14**	**13 14**	**8 10**	**16 20**	**10 12**	**14**	**19 22**	**10 11**	**9 13**	**7 9.3**	**14 17**	**29**	**8**	**11**	**8 11**	**9**	**10 15**	**19 21**	**12.2 14.2**	**18 21**	**16 17**
Known_6	X Y	15 16	16 18.3	12 14	13 14	8 10	16 20	10 12	14	19 22	10 11	9 13	7 9.3	14 17	29	8	11	8 11	9	10 15	19 21	12.2 14.2	18 21	16 17
Known 7	**X**	**16 17**	**13 15**	**11 14**	**15**	**12 13**	**5 8**	**9 11**	**16 18**	**16 24**	**10**	**8 13**	**7 8**	**15 19**	**29 32.2**	**9 11**	**12 13**	**9**	**	**14 15**	**15 17**	**14 14.2**	**22**	**15 16**
Known_7	X	16 17	13 15	11 14	15	12 13	5 8	9 11	16 18	16 24	10	8 13	7 8	15 19	29 32.2	9 11	12 13	9	-	14 15	15 17	14 14.2	22	15 16
Known 8	**X**	**15 16**	**15 17.3**	**11**	**14**	**10 11**	**12 22**	**10 12**	**12 14**	**20**	**12**	**8 12**	**7 8**	**16 19**	**31 32.2**	**11 12**	**7 9**	**8 11**	**	**16**	**18 20**	**13 15.2**	**19 23**	**16**
Known_8	X	15 16	15 17.3	11	14	10 11	12 22	10 12	12 14	20	12	8 12	7 8	16 19	31 32.2	11 12	7 9	8 11	-	16	18 20	13 15.2	19 23	16
Known 9	**X**	**15 16**	**15 16**	**11**	**13 14**	**8 12**	**5 12**	**11 12**	**14 19**	**17 23**	**10 12**	**8 12**	**7 9**	**14**	**30 31**	**9.1 10**	**10 12**	**8 10**	**	**10 14**	**22**	**13 14**	**24 26**	**15**
Known_9	X	15 16	15 16	11	13 14	8 12	5 12	11 12	14 19	17 23	10 12	8 12	7 9	14	30 31	9.1 10	10 12	8 10	-	10 14	22	13 14	24 26	15
Known 10	**X**	**17**	**11 15**	**10 14**	**13**	**12 13**	**7 12**	**9 10**	**15 18**	**19 23**	**10 12**	**9 10**	**6 7**	**14 18**	**29 30**	**10 11**	**11 12**	**8**	**	**13**	**17 18**	**12.2 15.2**	**20 26**	**15 16**
Known_10	X	17	11 15	10 14	13	12 13	7 12	9 10	15 18	19 23	10 12	9 10	6 7	14 18	29 30	10 11	11 12	8	-	13	17 18	12.2 15.2	20 26	15 16

** and – represent loci where no alleles were present.

Table 19: Mock casework profile success for operator 1. The bolded profiles were provided by the OCME-NYC and the non-bolded samples below are the observed profile during the validation. Yellow cells indicated drop out. Red allele labels indicate additional labeled alleles not assigned to the original donor.

	Mock Samples Newton Operator 1																							
	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mock 1	**X**	**14 16**	**14**	**14 15**	**11 15**	**8 13**	**5 13**	**10 11**	**18 19**	**19 24**	**10**	**10**	**6 9**	**16**	**29 31**	**9 11**	**12 13**	**8 11**	******	**10 15**	**15 OB**	**13.2 14**	**22 23**	**10 16**
Mock_1	X	14 16	14	14 15	11 15	8 13	5 13	10 11	18 19	19 24	10	10	6 9	16	29 31	9 11	12 13	8 11	-	10 15	15 OB	13.2 14	22 23	10 16
Mock 2	**X Y**	**15 16**	**17**	**11 15**	**14 15**	**11 13**	**5 13**	**12**	**11 13**	**17 21**	**10 11**	**7 13**	**7**	**14 17**	**25.2 30**	**8 10**	**12**	**8**	**10**	**13 15**	**20 24**	**14 15**	**20 23**	**16**
Mock_2	X Y	15 16	17	11 15	14 15	11 13	5 13	12	11 13	17 21	10 11	7 13	7	14 17	25.2 30	8 10	12	8	10	13 15	20 24	14 15	20 23	16
Mock 3	**X**	**15 16**	**13 15**	**10 11**	**13 14**	**12 13**	**10 19**	**11 13**	**13 17**	**17**	**11 12**	**11 14**	**8 9**	**16 18**	**29 30**	**8 9**	**11 12**	**9 11**	******	**14 16**	**16 20**	**16**	**25**	**15**
Mock_3	X	15 16	13 15	10 11	13 14	12 13	10 19	11 13	13 17	17	11 12	11 14	8 9	16 18	29 30	8 9	11 12	9 11	-	14 16	16 20	16	25	15
Mock 4	**X**	**15 17**	**17.3 18.3**	**10 15**	**12 13**	**11 12**	**10 19**	**12 13**	**17 18**	**20 25**	**10**	**9**	**6 9.3**	**15 18**	**30**	**10 13**	**10 13**	**8 11**	******	**14 15**	**18 22**	**13.2 15**	**21 23**	**16 17**
Mock_4	X	15 17	17.3 18.3	10 15	12 13	11 12	10 19	12 13	17 18	20 25	10	9	6 9.3	15 18	30	10 13	10 13	8 11	-	14 15	18 22	13.2 15	21 23	16 17
Mock 5	**X**	**15 16**	**14 18.3**	**11.3 14**	**14**	**8 11**	**11 20**	**12**	**16 17**	**16 18**	**12**	**9 13**	**9 9.3**	**17 19**	**30 31.2**	**8 11**	**11 12**	**8 9**	******	**12 13**	**19 20**	**12 13**	**20 25**	**15 16**
Mock_5	X	15 16	14 18.3	11.3 14	14	8 11	11 20	12	16 17	16 18	12	9 13	9 9.3	17 19	30 31.2	8 11	11 12	8 9	-	12 13	19 20	12 13	20 25	15 16
Mock 6	**X**	**17**	**11 15**	**10 14**	**13**	**12 13**	**7 12**	**9 10**	**15 18**	**19 23**	**10 12**	**9 10**	**6 7**	**14 18**	**29 30**	**10 11**	**11 12**	**8**	******	**13**	**17 18**	**12.2 15.2**	**20 26**	**15 16**
Mock_6	X	17	11 15	10 14	13	12 13	7 12	9 10	15 18	19 23	10 12	9 10	6 7	14 18	29 30	10 11	11 12	8	-	13	17 18	12.2 15.2	20 26	15 16
Mock 7	**X**	**17 18**	**12 14.3**	**11 14**	**14**	**11 13**	**7 15**	**12**	**14 16**	**20 25**	**10 11**	**10 12**	**6 7**	**18**	**30**	**9 12**	**11 12**	**8**	******	**12 14**	**17.3 25**	**12 14.2**	**21 23**	**11 15**
Mock_7	X	17 18	12 14.3	11 14	14	11 13	7 15	12	14 16	20 25	10 11	10 12	6 7	18	30	9 12	11 12	8	-	12 14	17.3 25	12 14.2	21 23	11 15
Mock 8	**X**	**17 18**	**12 13**	**11**	**14**	**11**	**13 14**	**11 13**	**14 17**	**17 20**	**10 11**	**9 10**	**6 9.3**	**17 19**	**29 32.2**	**8 10**	**11 13**	**8**	******	**15**	**15 21**	**14 15**	**21 23**	**14 15**
Mock_8	X	17 18	12 13	11	14	11	13 14	11 13	14 17	17 20	10 11	9 10	6 9.3	17 19	29 32.2	8 10	11 13	8	-	15	15 21	14 15	21 23	14 15
Mock 9	**X**	**15 18**	**14 15**	**11 11.3**	**15 19**	**11 12**	**7 11**	**11 12**	**16 17**	**17 20**	**11 12**	**13**	**6 9.3**	**14 16**	**30.2 32**	**9**	**9 13**	**8**	******	**14**	**20 21**	**13.2 16**	**25**	**11 15**
Mock_9	X	15 18	14 15	11 11.3	15 19	11 12	7 11	11 12	16 17	17 20	11 12	13	6 9.3	14 16	30.2 32	9	9 13	8	-	14	20 21	13.2 16	25	11 15
Mock 10	**X**	**14**	**16.3 17.3**	**11 11.3**	**14 17**	**12 13**	**15**	**9 11**	**12 15**	**16 26**	**10 11**	**9 15**	**6 10**	**17 19**	**30**	**10**	**11 12**	**8**	******	**10 12**	**17.3 21**	**14**	**20 21**	**15 16**
Mock_10	X	14	16.3 17.3	11 11.3	14 17	12 13	15	9 11	12 15	16 26	10 11	9 15	6 10	17 19	30	10	11 12	8	-	10 12	17.3 21	14	20 21	15 16
Mock 11	**X**	**15 16**	**14**	**10 14**	**13 14**	**11 12**	**11 12**	**11 13**	**14 17**	**18 22**	**11 12**	**9 10**	**6 9.3**	**16 18**	**32.2 33.2**	**8 12**	**11 13**	**8 9**	******	**11 13**	**21 22**	**12 14**	**18 22**	**15 16**
Mock_11	X	15 16	16 17	10 14	13	12		11 13	14 20				6 9.3	16	31		12 13		-	8 13		12		
Mock 12	**X Y**	**16 17**	**14 16.3**	**11 14**	**13 17**	**11 12**	**7 14**	**9 10**	**14 18**	**20**	**9 12**	**11 13**	**9.3**	**16**	**28 29**	**9 11**	**12 13**	**8 11**	**10**	**14**	**17 21**	**14**	**20.2 21**	**11 15**
Mock_12	Y									20			7 9.3		28			8	-	14		14		
Mock 13	**X**	**15 17**	**17 17.3**	**10 11**	**14**	**8 10**	**18 20**	**8 11**	**14 16**	**17 19**	**10 11**	**9 12**	**6 7**	**17 18**	**29**	**10 11**	**11 12**	**8**	******	**14 15**	**17 18**	**13 14**	**19 22**	**11 15**
Mock_13	X	15 17	17 17.3	10 11	14	8 10	18 20	8 11	14 16	17 19	10 11	9 12	6 7	17 18	29	10 11	11 12	8	-	14 15	17 18	13 14	19 22	11 15
Mock 14	**X**	**14 16**	**14**	**10 11**	**13**	**11 12**	**5 8**	**11 12**	**17 18**	**22**	**8 10**	**9 11**	**7 8**	**16 18**	**28 30**	**8 9**	**10 12**	**9 10**	******	**12 15**	**19**	**12 15**	**20 22**	**12 17**
Mock_14	X	14 16	14	10 11	13	11 12	5 8	11 12	17 18	22	8 10	9 11	7 8	16 18	28 30	8 9	10 12	9 10	-	12 15	19	12 15	20 22	12 17
Mock 15	**X**	**15 16**	**15 17.3**	**11**	**14**	**10 11**	**12 22**	**10 12**	**12 14**	**20**	**12**	**8 12**	**7 8**	**16 19**	**31 32.2**	**11 12**	**7 9**	**8 11**	******	**16**	**18 20**	**13 15.2**	**19 23**	**16**
Mock_15	X Y	15 19		11				12 13	14 18	19 20	12		6 7 8 9	15	31	11	7		-	13				
Mock 16	**X**	**14 16**	**14**	**11 14**	**14**	**9 13**	**5 7**	**12 13**	**12 16**	**16 18**	**12**	**11 14**	**7 9**	**17**	**31.2 32.2**	**8 10**	**10 13**	**8**	******	**9 14**	**21 23**	**13 15.2**	**20 23**	**12 16**
Mock_16	X	14 16	14	11 14	14	9 13	7	11 12 13	16 18	16 17 18	12	14	7 9	17		8 10	10 13	8	-	9 14		15.2	20 23	
Mock 17	**X**	**14 18**	**15.3 16**	**11.3 14**	**14 16**	**11 12**	**7 13**	**12 13**	**14 15**	**17 18**	**11 13**	**9 13**	**9 9.3**	**17**	**28 30**	**11**	**11**	**9 11**	******	**12**	**22 23**	**12 15**	**22 23**	**15 16**
Mock_17	X	14 17 18	14 15 15.3 16	11.3 14	14 16	11 12	7 13	12 13	14 15	17 18 24	11 13	9 13	9 9.3	17	28 30	11	11	9 11	-	12	22 23	12 15	22 23	15 16
Mock 18	**X**	**15 17**	**17.3 18.3**	**10 15**	**12 13**	**11 12**	**10 19**	**12 13**	**17 18**	**20 25**	**10**	**9**	**6 9.3**	**15 18**	**30**	**10 13**	**10 13**	**8 11**	******	**14 15**	**18 22**	**13.2 15**	**21 23**	**16 17**
Mock_18	X	15 17	17.3 18.3	10 15	12 13	11 12	10 19	12 13	17 18	20 25	10	9	6 9.3	15 18	30	10 13	10 13	8 11	-	14 15	18 22	13.2 15	21 23	11 16 17
Mock 19	**X**	**16**	**11 17.3**	**14**	**13 16**	**8 13**	**10 13**	**8 11**	**14 15**	**19 23**	**11**	**11 13**	**6 9.3**	**14 16**	**30 31**	**10 12**	**11 13**	**8 11**	******	**12 15**	**19.3 21**	**13 16**	**20 22**	**15 17**
Mock_19	X Y	16	11 17.3	14	13 15 16	8 13	10	8 11	14 15	19 23		11 13	6 9.3	16 17	30 31	10	11	8	-	12 15	19.3	13 16	20 22	15
Mock 20	**X**	**16**	**14 17**	**10**	**13 15**	**9 10**	**12 15**	**11**	**14**	**19 22**	**10 11**	**12**	**6**	**16 17**	**30 31.2**	**11**	**11 13**	**8**	******	**12 13**	**17 19**	**13 15.2**	**24 25**	**16**
Mock_20	X Y	16	14 17	10 11	13 14 15	9 10 13	5 12 15	11 12	11 14 16	17 19 20 21 22	10 11	7 12	6 7	16 17	30 31.2	8 9 11	11 12 13	8	-	12 13 14 15	17 17.3 19	13 14 15 15.2	20 23 24 25	16
Mock 21	**X**	**14 16**	**14**	**14 15**	**11 15**	**8 13**	**5 13**	**10 11**	**18 19**	**19 24**	**10**	**10**	**6 9**	**16**	**29 31**	**9 11**	**12 13**	**8 11**	******	**10 15**	**15 OB**	**13.2 14**	**22 23**	**10 16**
Mock_21	X	14 16	14	14 15	11 15	8 13	5 13	10 11 12 13	12 14 18 19	19 24	10 11	10	6 8 9	16	29 31	9 11	12 13	8 11	-	10 13 15	15 OB	13.2 14	22 23	10 16
Mock 22	**X Y**	**14 16**	**15.3 16.3**	**10**	**13 15**	**12 13**	**10 12**	**11 12**	**13 17**	**19**	**10 11**	**11 13**	**7 9.3**	**14 16**	**29 30**	**10 11**	**11 13**	**9 11**	**10**	**11 14**	**15 21**	**14 15**	**24**	**11 15**
Mock_22	X Y	14 15 16	15.3 16.3	10	15 16	12 13	10 12	10 11 12	12 13 17	19	11	11 13	7 9.3	14 16	29 30	10 11	11	9 11	-	11 13 14	15 21	14 15	24	15
Mock 23	**X**	**15 16**	**16.3 17.3**	**11**	**13**	**11 14**	**12 15**	**9 11**	**17 19**	**20 24**	**7 10**	**11 13**	**7 9.3**	**15**	**28 29**	**10 11**	**12**	**9 11**	******	**11 13**	**17**	**12 13**	**19 24**	**15**
Mock_23	X	15 16	16.3 17.3	11	13	11		9 11 12	17 19	20	7 10	11 13	7 9.3	15	29	10 11	12	9 11	-	11 13	17	12 13		15
Mock 24	**X**	**16**	**14**	**10 14**	**13 15**	**11 12**	**7 19**	**10 13**	**15 16**	**16 19**	**11 12**	**12 15**	**7 8**	**15 19**	**28 30**	**10**	**13**	**8 9**	******	**14 15**	**19 21**	**14 15.2**	**18.2 25**	**15 16**
Mock_24	X	16	14	10 14	13 15	11 12	7 19	10 13	15 16	16 19	11 12	12 15	7 8	15 19	28 30	10	13	8	-	14 15	19 21	14 15.2	18.2 25	15 16

** and – represent loci where no alleles were present.

Table 20: Mock casework profile success for operator 2. The bolded profiles were provided by the OCME-NYC and the non-bolded samples below are the observed profile during the validation. Yellow cells indicated drop out. Red allele labels indicate additional labeled alleles not assigned to the original donor.

	Mock Samples Newton Operator 2																							
	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mock 1	**X**	**14 16**	**14**	**14 15**	**11 15**	**8 13**	**5 13**	**10 11**	**18 19**	**19 24**	**10**	**10**	**6 9**	**16**	**29 31**	**9 11**	**12 13**	**8 11**	**	**10 15**	**15 OB**	**13.2 14**	**22 23**	**10 16**
Mock_1	X	14 16	14	14 15	11 15	8 13	5 13	10 11	18 19	19 24	10	10	6 9	16	29 31	9 11	12 13	8 11	-	10 15	15 OB	13.2 14	22 23	10 16
Mock 2	**X Y**	**15 16**	**17**	**11 15**	**14 15**	**11 13**	**5 13**	**12**	**11 13**	**17 21**	**10 11**	**7 13**	**7**	**14 17**	**25.2 30**	**8 10**	**12**	**8**	**10**	**13 15**	**20 24**	**14 15**	**20 23**	**16**
Mock_2	X Y	15 16	17	11 15	14 15	11 13	5 13	12	11 13	17 21	10 11	7 13	7	14 17	25.2 30	8 10	12	8	10	13 15	20 24	14 15	20 23	16
Mock 3	**X**	**15 16**	**13 15**	**10 11**	**13 14**	**12 13**	**10 19**	**11 13**	**13 17**	**17**	**11 12**	**11 14**	**8 9**	**16 18**	**29 30**	**8 9**	**11 12**	**9 11**	**	**14 16**	**16 20**	**16**	**25**	**15**
Mock_3	X	15 16	13 15	10 11	13 14	12 13	10 19	11 13	13 17	17	11 12	11 14	8 9	16 18	29 30	8 9	11 12	9 11	-	14 16	16 20	16	25	15
Mock 4	**X**	**15 17**	**17.3 18.3**	**10 15**	**12 13**	**11 12**	**10 19**	**12 13**	**17 18**	**20 25**	**10**	**9**	**6 9.3**	**15 18**	**30**	**10 13**	**10 13**	**8 11**	**	**14 15**	**18 22**	**13.2 15**	**21 23**	**16 17**
Mock_4	X	15 17	17.3 18.3	10 15	12 13	11 12	10 19	12 13	17 18	20 25	10	9	6 9.3	15 18	30	10 13	10 13	8 11	-	14 15	18 22	13.2 15	21 23	16 17
Mock 5	**X**	**15 16**	**14 18.3**	**11.3 14**	**14**	**8 11**	**11 20**	**12**	**16 17**	**16 18**	**12**	**9 13**	**9 9.3**	**17 19**	**30 31.2**	**8 11**	**11 12**	**8 9**	**	**12 13**	**19 20**	**12 13**	**20 25**	**15 16**
Mock_5	X	15 16	14 18.3	11.3 14	14	8 11	11 20	12	16 17	16 18	12	9 13	9 9.3	17 19	30 31.2	8 11	11 12	8 9	-	12 13	19 20	12 13	20 25	15 16
Mock 6	**X**	**17**	**11 15**	**10 14**	**13**	**12 13**	**7 12**	**9 10**	**15 18**	**19 23**	**10 12**	**9 10**	**6 7**	**14 18**	**29 30**	**10 11**	**11 12**	**8**	**	**13**	**17 18**	**12.2 15.2**	**20 26**	**15 16**
Mock_6	X	17	11 15	10 14	13	12 13	7 12	9 10	15 18	19 23	10 12	9 10	6 7	14 18	29 30	10 11	11 12	8	-	13	17 18	12.2 15.2	20 26	15 16
Mock 7	**X**	**17 18**	**12 14.3**	**11 14**	**14**	**11 13**	**7 15**	**12**	**14 16**	**20 25**	**10 11**	**10 12**	**6 7**	**18**	**30**	**9 12**	**11 12**	**8**	**	**12 14**	**17.3 25**	**12 14.2**	**21 23**	**11 15**
Mock_7	X	17 18	12 14.3	11 14	14	11 13	7 15	12	14 16	20 25	10 11	10 12	6 7	18	30	9 12	11 12	8	-	12 14	17.3 25	12 14.2	21 23	11 15
Mock 8	**X**	**17 18**	**12 13**	**11**	**14**	**11**	**13 14**	**11 13**	**14 17**	**17 20**	**10 11**	**9 10**	**6 9.3**	**17 19**	**29 32.2**	**8 10**	**11 13**	**8**	**	**15**	**15 21**	**14 15**	**21 23**	**14 15**
Mock_8	X	17 18	12 13	11	14	11	13 14	11 13	14 17	17 20	10 11	9 10	6 9.3	17 19	29 32.2	8 10	11 13	8	-	15	15 21	14 15	21 23	14 15
Mock 9	**X**	**15 18**	**14 15**	**11 11.3**	**15 19**	**11 12**	**7 11**	**11 12**	**16 17**	**17 20**	**11 12**	**13**	**6 9.3**	**14 16**	**30.2 32**	**9**	**9 13**	**8**	**	**14**	**20 21**	**13.2 16**	**25**	**11 15**
Mock_9	X	15 18	14 15	11 11.3	15 19	11 12	7 11	11 12	16 17	17 20	11 12	13	6 9.3	14 16	30.2 32	9	9 13	8	-	14	20 21	13.2 16	25	11 15
Mock 10	**X**	**14**	**16.3 17.3**	**11 11.3**	**14 17**	**12 13**	**15**	**9 11**	**12 15**	**16 26**	**10 11**	**9 15**	**6 10**	**17 19**	**30**	**10**	**11 12**	**8**	**	**10 12**	**17.3 21**	**14**	**20 21**	**15 16**
Mock_10	X	14	16.3 17.3	11 11.3	14 17	12 13	15	9 11	12 15	16 26	10 11	9 15	6 10	17 19	30	10	11 12	8	-	10 12	17.3 21	14	20 21	15 16
Mock 11	**X**	**15 16**	**14**	**10 14**	**13 14**	**11 12**	**11 12**	**11 13**	**14 17**	**18 22**	**11 12**	**9 10**	**6 9.3**	**16 18**	**32.2 33.2**	**8 12**	**11 13**	**8 9**	**	**11 13**	**21 22**	**12 14**	**18 22**	**15 16**
Mock_11	X	15 16	14	10				11 13	17 **20**			9 **12**	**7** 9.3	18	32.2	8 **10** 12		8 9	-	**8** 11 13	21			16
Mock 12	**X Y**	**16 17**	**14 16.3**	**11 14**	**13 17**	**11 12**	**7 14**	**9 10**	**14 18**	**20**	**9 12**	**11 13**	**9.3**	**16**	**28 29**	**9 11**	**12 13**	**8 11**	**10**	**14**	**17 21**	**14**	**20.2 21**	**11 15**
Mock_12	X	17						**11**					**6** 9.3	16			12		-	14				
Mock 13	**X**	**15 17**	**17 17.3**	**10 11**	**14**	**8 10**	**18 20**	**8 11**	**14 16**	**17 19**	**10 11**	**9 12**	**6 7**	**17 18**	**29**	**10 11**	**11 12**	**8**	**	**14 15**	**17 18**	**13 14**	**19 22**	**11 15**
Mock_13	X	15 17	17 17.3	10 11	14	8 10	18 20	8 11	14 16	17 19	10 11	9 12	6 7	17 18	29	10 11	11 12	8	-	14 15	17 18	13 14	19 22	11 15
Mock 14	**X**	**14 16**	**14**	**10 11**	**13**	**11 12**	**5 8**	**11 12**	**17 18**	**22**	**8 10**	**9 11**	**7 8**	**16 18**	**28 30**	**8 9**	**10 12**	**9 10**	**	**12 15**	**19**	**12 15**	**20 22**	**12 17**
Mock_14	X	14 16	14	10 11	13	11 12	5 8	11 12	17 18	22	8 10	9 11	7 8	16 18	28 30	8 9	10 12	9 10	-	12 15	19	12 15	20 22	12 17
Mock 15	**X**	**15 16**	**15 17.3**	**11**	**14**	**10 11**	**12 22**	**10 12**	**12 14**	**20**	**12**	**8 12**	**7 8**	**16 19**	**31 32.2**	**11 12**	**7 9**	**8 11**	**	**16**	**18 20**	**13 15.2**	**19 23**	**16**
Mock_15	X Y	15 16				10 11		10 12	12 **18**	20				**15**		**10** 11	7		-	**13**		13	23	
Mock 16	**X**	**14 16**	**14**	**11 14**	**14**	**9 13**	**5 7**	**12 13**	**12 16**	**16 18**	**12**	**11 14**	**7 9**	**17**	**31.2 32.2**	**8 10**	**10 13**	**8**	**	**9 14**	**21 23**	**13 15.2**	**20 23**	**12 16**
Mock_16	X	14 16	14	**13** 14	14		7	**11** 12 13	12 **14 15** 16	16 18 **19**	12	11 14	7 9	17 **19**	31.2 32.2	8	10 13	8	-	9 14		13 15.2	20 23	16
Mock 17	**X**	**14 18**	**15.3 16**	**11.3 14**	**14 16**	**11 12**	**7 13**	**12 13**	**14 15**	**17 18**	**11 13**	**9 13**	**9 9.3**	**17**	**28 30**	**11**	**11**	**9 11**	**	**12**	**22 23**	**12 15**	**22 23**	**15 16**
Mock_17	X	14 18	15 16 **17.3**	11.3 14	14 16	11 12	7 13	12 13	14 15	17 18	11 13	9 13	9 9.3	17	28 30	11	11	9 11	-	12	22 23	12 15	22 23	15 16
Mock 18	**X**	**15 17**	**17.3 18.3**	**10 15**	**12 13**	**11 12**	**10 19**	**12 13**	**17 18**	**20 25**	**10**	**9**	**6 9.3**	**15 18**	**30**	**10 13**	**10 13**	**8 11**	**	**14 15**	**18 22**	**13.2 15**	**21 23**	**16 17**
Mock_18	X	15 17	17.3 18.3	10 15	12 13	11 12	10 19	12 13	17 18	20 25	10	9	6 9.3	15 18	30	10 13	10 13	8 11	-	14 15	18 22	13.2 15	21 23	16 17
Mock 19	**X**	**16**	**11 17.3**	**14**	**13 16**	**8 13**	**10 13**	**8 11**	**14 15**	**19 23**	**11**	**11 13**	**6 9.3**	**14 16**	**30 31**	**10 12**	**11 13**	**8 11**	**	**12 15**	**19.3 21**	**13 16**	**20 22**	**15 17**
Mock_19	X Y	16	11 17.3	14	13		10 13	8 11 **12**	14 15	19 23	11	13	6 9.3	14 16	31	10 12	13	8 11	-	12 15	19.3	13 16	22	15
Mock 20	**X**	**16**	**14 17**	**10**	**13 15**	**9 10**	**12 15**	**11**	**14**	**19 22**	**10 11**	**12**	**6**	**16 17**	**30 31.2**	**11**	**11 13**	**8**	**	**12 13**	**17 19**	**13 15.2**	**24 25**	**16**
Mock_20	X **Y**	16 **17**	14 **14.3** 17	10 **11**	13 **14** 15	9 10 **13**	**5** 12 **13** 15	11 **12**	**11 13** 14	**22 25**	10 11	12	6 **7**	**14** 16 17	30 31.2	**8 9** 11	11 **12** 13	8	-	12 13 **15**	17 19 **24**	**12** 13 **14** 15.2	**23** 24 25	**11** 16
Mock 21	**X**	**14 16**	**14**	**14 15**	**11 15**	**8 13**	**5 13**	**10 11**	**18 19**	**19 24**	**10**	**10**	**6 9**	**16**	**29 31**	**9 11**	**12 13**	**8 11**	**	**10 15**	**15 OB**	**13.2 14**	**22 23**	**10 16**
Mock_21	X	14 **15** 16	**12 13** 14	14 15	11 15	8 13	5 13	10 11	**15 16** 18 19	19 24	10	10	6 **7 8** 9	16	29 31	9 11	**11** 12 13	8 11	-	10 **14** 15	15 OB	13.2 14	22 23	10 16
Mock 22	**X Y**	**14 16**	**15.3 16.3**	**10**	**13 15**	**12 13**	**10 12**	**11 12**	**13 17**	**19**	**10 11**	**11 13**	**7 9.3**	**14 16**	**29 30**	**10 11**	**11 13**	**9 11**	**10**	**11 14**	**15 21**	**14 15**	**24**	**11 15**
Mock_22	X Y	14 **15** 16	15.3 16.3	10	13	12	10 12	11 12	**12** 13 **16** 17	19	11	11	7 9.3	14 16	29 30	10 11	11 13	9	-	11 **13** 14	15 21	14 15	24	15
Mock 23	**X**	**15 16**	**16.3 17.3**	**11**	**13**	**11 14**	**12 15**	**9 11**	**17 19**	**20 24**	**7 10**	**11 13**	**7 9.3**	**15**	**28 29**	**10 11**	**12**	**9 11**	**	**11 13**	**17**	**12 13**	**19 24**	**15**
Mock_23	X	15 16	16.3 **17** 17.3	11	13	11 14	12 15	9 11 **12**	17 19	20 24		11 13	7 9.3	15	29	10	12		-	11 13	17	12 13	19 24	15
Mock 24	**X**	**16**	**14**	**10 14**	**13 15**	**11 12**	**7 19**	**10 13**	**15 16**	**16 19**	**11 12**	**12 15**	**7 8**	**15 19**	**28 30**	**10**	**13**	**8 9**	**	**14 15**	**19 21**	**14 15.2**	**18.2 25**	**15 16**
Mock_24	X	**15** 16	14	10 14	13 15	**9** 11 12	7 19	10 **11 12** 13	15 16	16 19	11 12	12 15	7 8	15 19	28 30	10	13	8 9	-	14 15	19 21	14 15.2	18.2 25	16

** and – represent loci where no alleles were present.

4.A.4 Precision

The precision assessment was done using 13 allelic ladders that were run in conjunction with the sensitivity samples at 3kV 5s on Athena, and 13 allelic ladders at 3kV 5s on Newton. The size of the alleles (in bp) was evaluated. The highest standard deviation observed on Athena was 0.1 (Figure 2). The highest standard deviation observed on Newton was 0.1 (Figure 3). Three times the standard deviation is less 0.5bp.

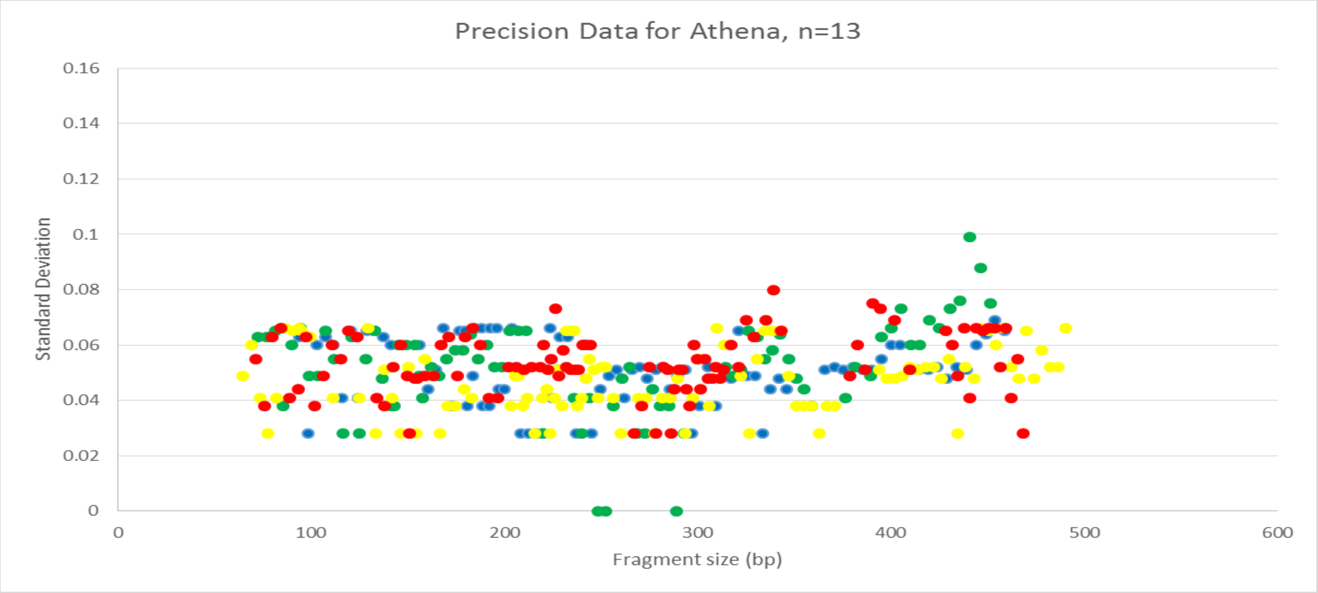


Figure 2: Precision of the PowerPlex® Fusion system on a 3130*xl* Genetic Analyzer. Thirteen ladders were run on the Applied Biosystems® 3130*xl* using a 3kV, 5 second injection on Athena. For each allele, the average fragment size (in bases) was plotted against the standard deviation of the mean size observed. Generally, a standard deviation of 0.16 (3* st.dev < 0.5) is an acceptable precision for the system.

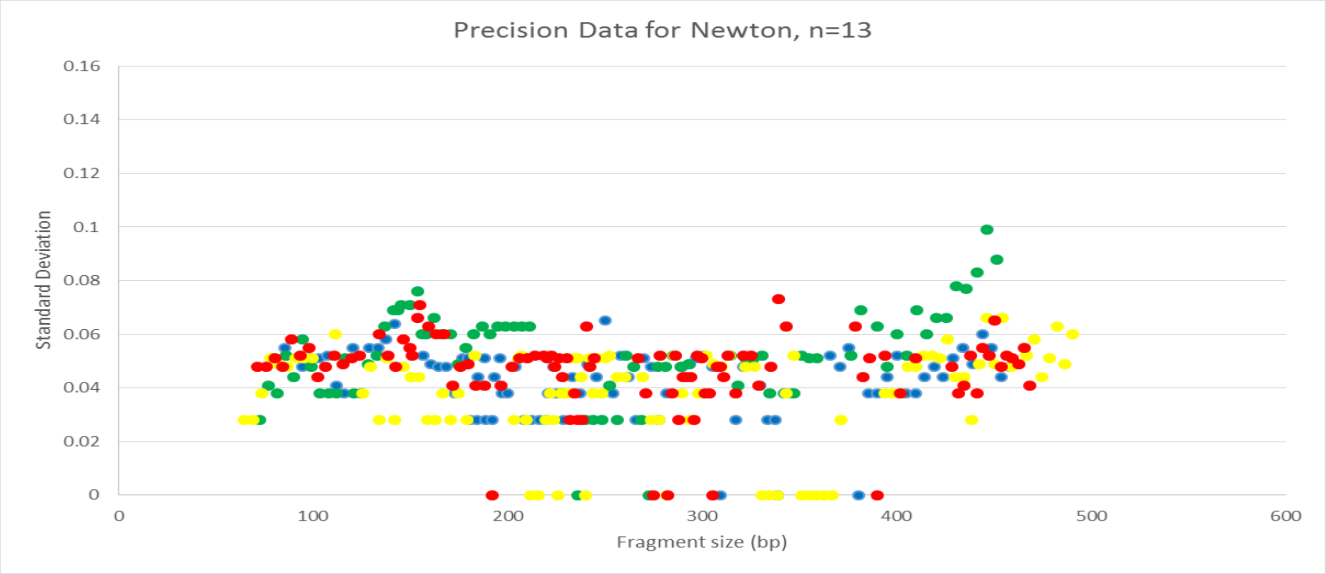


Figure 3: Precision of the PowerPlex® Fusion system on a 3130*xl* Genetic Analyzer. Thirteen ladders were run on the Applied Biosystems® 3130*xl* using a 3kV, 5 second injection on Newton. For each allele, the average fragment size (in bases) was plotted against the standard deviation of the mean size observed. Generally, a standard deviation of 0.16 (3* st.dev < 0.5) is an acceptable precision for the system.

4.A.5 Reproducibility and Repeatability

Positive controls were amplified on each amplification plate. Every positive control (2800M) resulted in the same profile which is concordant with the profile provided in TMD045 Appendix 9.A in the Technical Manual (Table 22). Replicates of 2800M were also amplified by two different operators and injected on both Athena and Newton. All profiles yielded the correct genotype. (Table 23) NIST SRM 2391c samples were also amplified by two different operators. One replicate of NIST C amplified by operator 1 initially resulted in an OB at DYS391; the sample was re-injected. The subsequent re-injection results in the correct allelic assignment of 11 at DYS391.All results were concordant with the NIST 2391c certificate with the exception of NIST D at D12S391 allele 19. Allele 19 not called due to resolution between the 18.3 and 19 allele. (Table 24) (Figure 4). The resolution of 18.3 and 19 at D12S391 is concordant with the results obtained during the PowerPlex® Fusion developmental validation.

Table 22: Genotype results of all positive controls amplified during the validation.

		OCME Repeatability of 2800M																							
		AMEL	**D3S1358**	**D1S1656**	**D2S441**	**D10S1248**	**D13S317**	**Penta E**	**D16S539**	**D18S51**	**D2S1338**	**CSF1PO**	**Penta D**	**TH01**	**vWA**	**D21S11**	**D7S820**	**D5S818**	**TPOX**	**DYS391**	**D8S1179**	**D12S391**	**D19S433**	**FGA**	**D22S1045**
	2800M	**XY**	**17 18**	**12 13**	**10 14**	**13 15**	**9 11**	**7 14**	**9 13**	**16 18**	**22 25**	**12**	**12 13**	**6 9.3**	**16 19**	**29 31.2**	**8 11**	**12**	**11**	**10**	**14 15**	**18 23**	**13 14**	**20 23**	**16**
Athena	02-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	24-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	24-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	24-Amplification_Positive	failed size standard																							
	26-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	27-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	28-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	52-Amp_Pos_a	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	52-Amp_Pos_a	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	53-Amp_Pos_b	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	53-Amp_Pos_b	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	54-Amp_Pos_c	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	54-Amp_Pos_c	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
Newton	02-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	24-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	26-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	27-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	28-Amplification_Positive	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	52-Amp_Pos_a	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	52-Amp_Pos_a	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	53-Amp_Pos_b	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	53-Amp_Pos_b	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	54-Amp_Pos_c	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	54-Amp_Pos_c	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16

Table 23: Results of 2800M amplified by two different operators and injected on both Newton and Athena.

			OCME Reproducibility of 2800M																							
			AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
		2800M	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
Newton	Operator 1	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
	Operator 2	09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
Athena		09-Amp_Pos_1	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		10-Amp_Pos_2	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		11-Amp_Pos_3	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16
		12-Amp_Pos_4	XY	17 18	12 13	10 14	13 15	9 11	7 14	9 13	16 18	22 25	12	12 13	6 9.3	16 19	29 31.2	8 11	12	11	10	14 15	18 23	13 14	20 23	16

Table 24: Results of NIST SRM 2391c sample concordance.

OCME Reproducibility of 2391c NIST

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
	NIST A	**X**	**15 16**	**17.3**	**10**	**15 16**	**8**	**5 10**	**10 11**	**12 15**	**18 23**	**10**	**9 13**	**8 9.3**	**18 19**	**28 32.2**	**11**	**11 12**	**8**	**-**	**13 14**	**18.3 22**	**13 14**	**21 23**	**15**
Operator 1	NISTA1	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
	NISTA1	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
	NISTA2	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
	NISTA2	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
Operator 2	NISTA1	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
	NISTA2	X	15 16	17.3	10	15 16	8	5 10	10 11	12 15	18 23	10	9 13	8 9.3	18 19	28 32.2	11	11 12	8	-	13 14	18.3 22	13 14	21 23	15
	NIST B	**XY**	**15 19**	**11 14**	**10 14**	**13**	**9 12**	**7 15**	**10 13**	**13 16**	**17**	**10 11**	**8 12**	**6 9.3**	**17 18**	**32 32.2**	**10**	**12 13**	**8 11**	**10**	**10 13**	**19 24**	**16 16.2**	**20 23**	**15 17**
Operator 1	NISTB1	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
	NISTB1	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
	NISTB2	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
	NISTB2	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
Operator 2	NISTB1	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
	NISTB2	XY	15 19	11 14	10 14	13	9 12	7 15	10 13	13 16	17	10 11	8 12	6 9.3	17 18	32 32.2	10	12 13	8 11	10	10 13	19 24	16 16.2	20 23	15 17
	NIST C	**XY**	**16 18**	**11 15**	**10**	**12 16**	**11**	**12 13**	**10**	**16 19**	**19**	**10 12**	**10 11**	**6 8**	**16 18**	**29 30**	**10 12**	**10 11**	**11**	**11**	**10 17**	**19 23**	**13.2 15.2**	**24 26**	**16**
Operator 1	NISTC1	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
	NISTC1	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
	NISTC2	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
	NISTC2**	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	**OB**	10 17	19 23	13.2 15.2	24 26	16
	NISTC2	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
Operator 2	NISTC1	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
	NISTC2	XY	16 18	11 15	10	12 16	11	12 13	10	16 19	19	10 12	10 11	6 8	16 18	29 30	10 12	10 11	11	11	10 17	19 23	13.2 15.2	24 26	16
	NIST D	**XY**	**15 16 18**	**11 15 17.3**	**10**	**12 15 16**	**8 11**	**5 10 12 13**	**10 11**	**12 15 16 19**	**18 19 23**	**10 12**	**9 10 11 13**	**6 8 9.3**	**16 18 19**	**28 29 30 32.2**	**10 11 12**	**10 11 12**	**8 11**	**11**	**10 13 14 17**	**18.3 19 22 23**	**13 13.2 14 15.2**	**21 23 24 26**	**15 16**
Operator 1	NISTD1	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16
	NISTD1	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16
	NISTD2	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16
	NISTD2	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16
Operator 2	NISTD1	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16
	NISTD2	XY	15 16 18	11 15 17.3	10	12 15 16	8 11	5 10 12 13	10 11	12 15 16 19	18 19 23	10 12	9 10 11 13	6 8 9.3	16 18 19	28 29 30 32.2	10 11 12	10 11 12	8 11	11	10 13 14 17	18.3 22 23	13 13.2 14 15.2	21 23 24 26	15 16

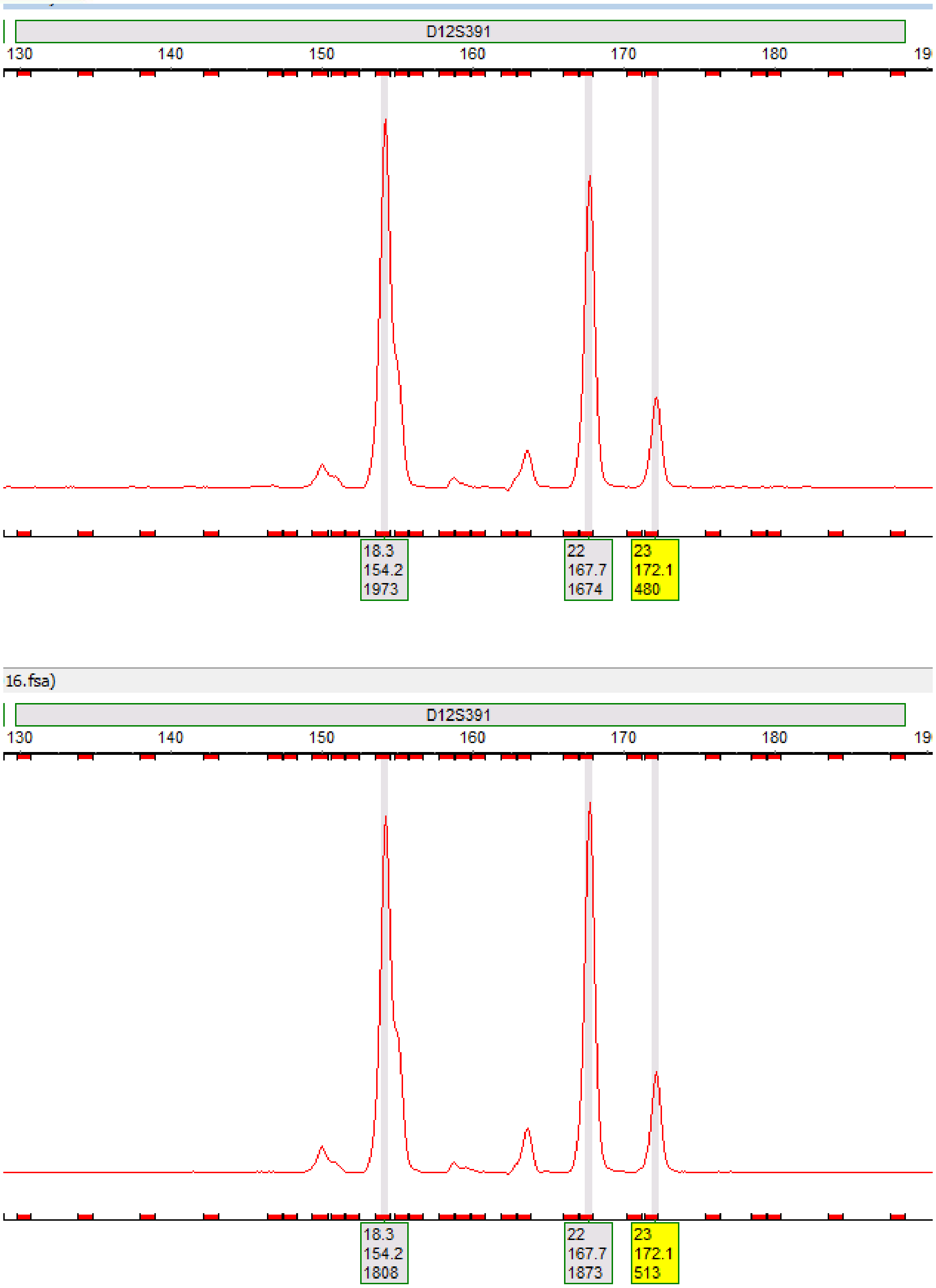


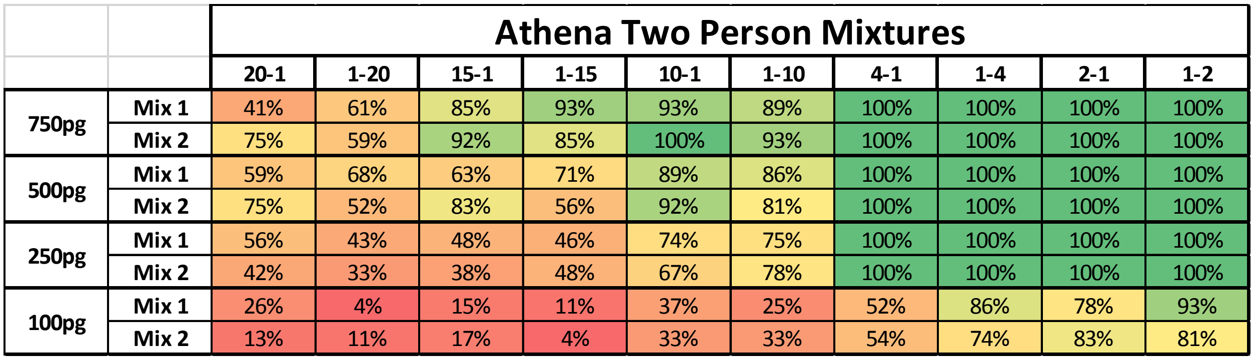
Figure 4: NIST SRM 2391c sample D Applied Biosystems® 3130*xl* injected on Athena using 3kv 5 sec injection parameter.

4.A.6 Mixture Study

Eighty-eight two person mixtures were amplified during this validation study. Two person mixtures were generated using samples 6M and 22F (mixture 1) and 15M and 5F (mixture 2). Profiles were compared and a composite profile was generated containing only unshared alleles in the minor contributor. The mixtures were then compared to determine what percentage of the unique minor alleles was detected in each mixture ratio. For two person mixtures injected on Athena, 100% of the unique alleles from the minor donor was obtained at 2-1 and 4-1 mixtures using a 750pg, 500pg, and 250pg for both mixture series. Mixture series #2 obtained a full profile at a 750pg 10-1 ratio (Tables 25). Two person mixtures injected on Newton obtained 100% of the minor alleles for 2-1 mixtures down to 100pg and 4-1 mixtures down to 250pg for both mixture series. Mixture series #2 obtained a full profile at a 750pg 10-1 ratio (Table 26).
Forty-eight three person mixtures were amplified during this study. Three person mixtures were generated using samples 12F, 13M, and 6M, (mixture 1), and 17M, 27F, and 9M (mixture 2). Twelve four person mixtures were generated using 17M, 27F, 9M, and 28F. Three and four person mixtures were evaluated for the total number of alleles obtained. Three person mixtures obtained full profiles for mixture #1 on Athena and Newton at a 5-1-1, 5-5-1, 1-1-1, 1-2-1,3-2-1, and 5-2-1 at 750pg; 1-1-1, 1-2-1, 3-2-1, and 5-2-1 at 500pg; 5-1-1, 1-2-1, 3-2-1, and 5-2-1 at 250pg. Full profiles were obtained for mixture #2 on Athena and Newton at a 1-1-1, 1-2-1, 3-2-1, and 5-2-1 at 750pg; 1-1-1, 1-2-1, and 3-2-1 at 500pg. Four person mixtures obtained full profiles on both Athena and Newton using a 750pg target at 1-1-1-1 and 1-3-3-1. (Table 27 and 28). See Appendix E for individual mixture results.

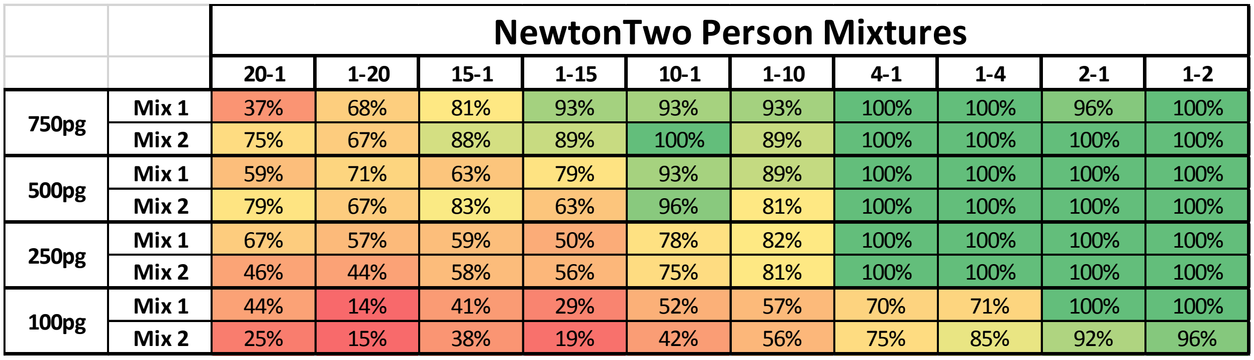
There were numerous instances of pull-up noticed throughout both mixture series on both instruments. Mixtures amplified using 750pg target amount at times had a significant amount of pull up seen in the sample. As expected, when lowering the target amount of DNA amplified the instances of pull up decreased as well (Table 29 and 30).

Table 25: Percentage of minor profile obtained for two person mixtures injected at 3kV 5 sec on Athena



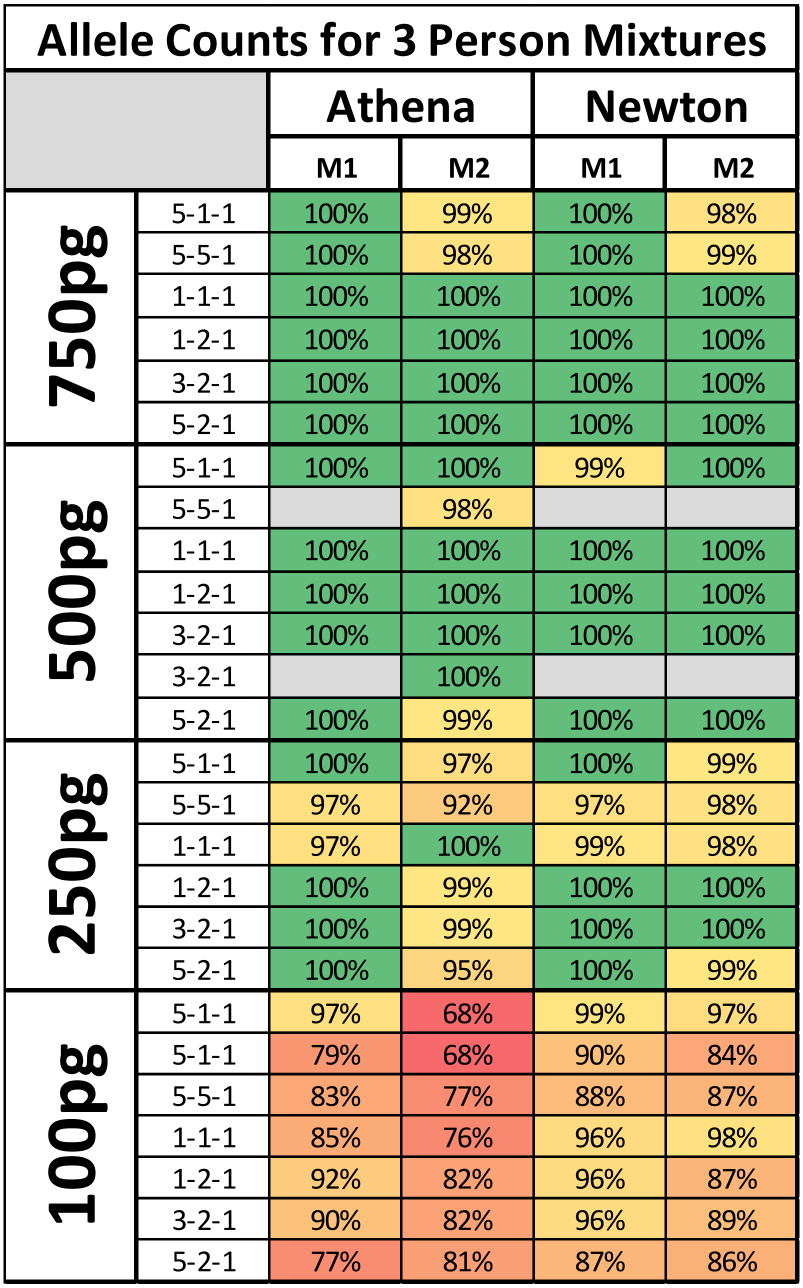
		Athena Two Person Mixtures									
		20-1	**1-20**	**15-1**	**1-15**	**10-1**	**1-10**	**4-1**	**1-4**	**2-1**	**1-2**
750pg	**Mix 1**	41%	61%	85%	93%	93%	89%	100%	100%	100%	100%
	Mix 2	75%	59%	92%	85%	100%	93%	100%	100%	100%	100%
500pg	**Mix 1**	59%	68%	63%	71%	89%	86%	100%	100%	100%	100%
	Mix 2	75%	52%	83%	56%	92%	81%	100%	100%	100%	100%
250pg	**Mix 1**	56%	43%	48%	46%	74%	75%	100%	100%	100%	100%
	Mix 2	42%	33%	38%	48%	67%	78%	100%	100%	100%	100%
100pg	**Mix 1**	26%	4%	15%	11%	37%	25%	52%	86%	78%	93%
	Mix 2	13%	11%	17%	4%	33%	33%	54%	74%	83%	81%

Table 26: Percentage of minor profile obtained for two person mixtures injected at 3kV 5 sec on Newton



		NewtonTwo Person Mixtures									
		20-1	**1-20**	**15-1**	**1-15**	**10-1**	**1-10**	**4-1**	**1-4**	**2-1**	**1-2**
750pg	**Mix 1**	37%	68%	81%	93%	93%	93%	100%	100%	96%	100%
	Mix 2	75%	67%	88%	89%	100%	89%	100%	100%	100%	100%
500pg	**Mix 1**	59%	71%	63%	79%	93%	89%	100%	100%	100%	100%
	Mix 2	79%	67%	83%	63%	96%	81%	100%	100%	100%	100%
250pg	**Mix 1**	67%	57%	59%	50%	78%	82%	100%	100%	100%	100%
	Mix 2	46%	44%	58%	56%	75%	81%	100%	100%	100%	100%
100pg	**Mix 1**	44%	14%	41%	29%	52%	57%	70%	71%	100%	100%
	Mix 2	25%	15%	38%	19%	42%	56%	75%	85%	92%	96%

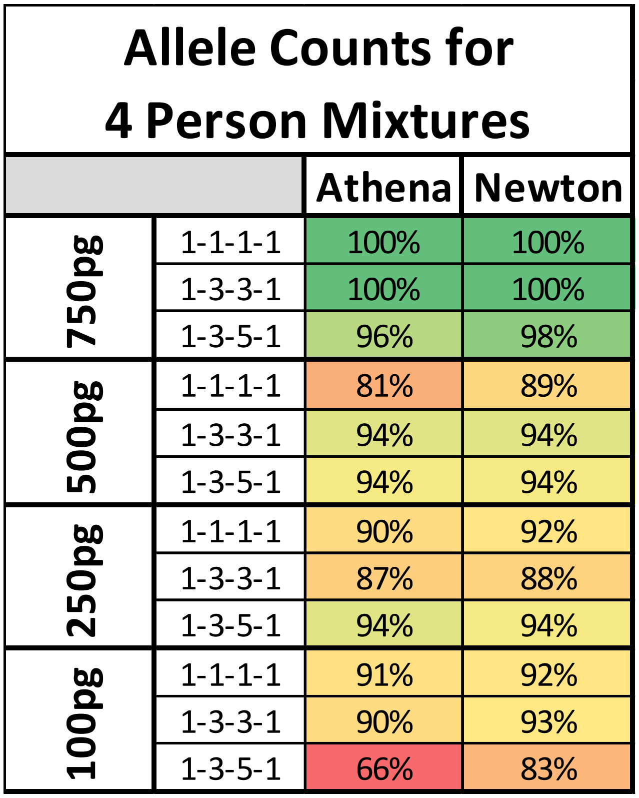
Table 27: Percentage of total alleles obtained for three person mixtures injected at 3kV 5 sec



Allele Counts for 3 Person Mixtures

		Athena		Newton	
		M1	M2	M1	M2
750pg	5-1-1	100%	99%	100%	98%
	5-5-1	100%	98%	100%	99%
	1-1-1	100%	100%	100%	100%
	1-2-1	100%	100%	100%	100%
	3-2-1	100%	100%	100%	100%
	5-2-1	100%	100%	100%	100%
500pg	5-1-1	100%	100%	99%	100%
	5-5-1		98%		
	1-1-1	100%	100%	100%	100%
	1-2-1	100%	100%	100%	100%
	3-2-1	100%	100%	100%	100%
	3-2-1		100%		
	5-2-1	100%	99%	100%	100%
250pg	5-1-1	100%	97%	100%	99%
	5-5-1	97%	92%	97%	98%
	1-1-1	97%	100%	99%	98%
	1-2-1	100%	99%	100%	100%
	3-2-1	100%	99%	100%	100%
	5-2-1	100%	95%	100%	99%
100pg	5-1-1	97%	68%	99%	97%
	5-1-1	79%	68%	90%	84%
	5-5-1	83%	77%	88%	87%
	1-1-1	85%	76%	96%	98%
	1-2-1	92%	82%	96%	87%
	3-2-1	90%	82%	96%	89%
	5-2-1	77%	81%	87%	86%

Table 28: Percentage of total alleles obtained for four person mixtures injected at 3kV 5 sec



Allele Counts for
4 Person Mixtures

		Athena	Newton
750pg	1-1-1-1	100%	100%
	1-3-3-1	100%	100%
	1-3-5-1	96%	98%
500pg	1-1-1-1	81%	89%
	1-3-3-1	94%	94%
	1-3-5-1	94%	94%
250pg	1-1-1-1	90%	92%
	1-3-3-1	87%	88%
	1-3-5-1	94%	94%
100pg	1-1-1-1	91%	92%
	1-3-3-1	90%	93%
	1-3-5-1	66%	83%

Table 29: Instances of pull up documented when analyzing Mixture 1 using GeneMarkerHID v.2.8.2 using a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter.

Mixture 1			
		Athena	**Newton**
750pg	**20-1**	5	6
	15-1	3	7
	10-1	4	3
	4-1	2	4
	2-1	3	2
	1-1	2	5
	1-2	4	1
	1-4	13	7
	1-10	0	4
	1-15	2	1
	1-20	4	2
500pg	**20-1**	2	1
	15-1	0	1
	10-1	2	2
	4-1	0	1
	2-1	1	8
	1-1	1	9
	1-2	0	4
	1-4	0	4
	1-10	5	2
	1-15	0	5
	1-20	7	2
250pg	**20-1**	0	2
	15-1	2	1
	10-1	1	2
	4-1	0	0
	2-1	0	0
	1-1	0	2
	1-2	3	0
	1-4	1	3
	1-10	1	2
	1-15	0	2
	1-20	0	0
100pg	**20-1**	0	0
	15-1	0	0
	10-1	0	0
	4-1	0	0
	2-1	0	0
	1-1	0	0
	1-2	0	0
	1-4	0	0
	1-10	0	0
	1-15	0	0
	1-20	0	0

Table 30: Instances of pull up documented when analyzing Mixture 2 using GeneMarkerHID v.2.8.2 using a 50 RFU threshold with a 3% minimum heterozygote filter and 3% global max filter.

Mixture 2			
		Athena	Newton
750pg	20-1	2	4
	15-1	4	4
	10-1	1	1
	4-1	1	3
	2-1	5	2
	1-1	4	5
	1-2	3	0
	1-4	7	9
	1-10	3	6
	1-15	2	2
	1-20	4	1
500pg	20-1	1	1
	15-1	0	1
	10-1	0	1
	4-1	0	1
	2-1	3	0
	1-1	1	2
	1-1	1	1
	1-2	0	3
	1-4	0	6
	1-10	4	1
	1-15	1	3
	1-20	6	1
250pg	20-1	0	1
	15-1	0	0
	10-1	0	0
	4-1	0	1
	2-1	0	0
	1-1	0	0
	1-2	2	0
	1-4	0	4
	1-10	0	2
	1-15	0	0
	1-20	0	0
100pg	20-1	0	0
	15-1	0	0
	10-1	0	0
	4-1	0	0
	2-1	0	0
	1-1	0	0
	1-2	0	0
	1-4	0	0
	1-10	0	0
	1-15	0	0
	1-20	0	0

4.A.7 Contamination Assessment

Thirty-five negative controls were examined throughout the validation study. One negative control injected on Newton generated an allele call of 10 at D7S820. This result was not reproducible (Table 31).

Table 31: Results of contamination assessment

		OCME Contamination Assessment																							
		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Athena	03-Amplification_Negative																								
	13-Amp_Neg_1																								
	14-Amp_Neg_2																								
	15-Amp_Neg_3																								
	17-Amp_Neg_4																								
	29-Amplification_Negative																								
	30-Amplification_Negative																								
	31-Amplification_Negative																								
	49-0pg_a																								
	49-0pg_a																								
	50-0pg_b																								
	50-0pg_b																								
	51-0pg_c																								
	51-0pg_c																								
	72-Amplification_Negative																								
Newton	03-Amplification_Negative																								
	13-Amp_Neg_1																								
	13-Amp_Neg_1																								
	14-Amp_Neg_2																								
	14-Amp_Neg_2																								
	15-Amp_Neg_3																								
	15-Amp_Neg_3																								
	17-Amp_Neg_4																								
	17-Amp_Neg_4																								
	17-Amp_Neg_4**	failed size standard																							
	29-Amplification_Negative																								
	30-Amplification_Negative																								
	31-Amplification_Negative																								
	72-Amplification_Negative																								
	49-0pg_a																								
	49-0pg_a																								
	50-0pg_b																								
	50-0pg_b																								
	51-0pg_c															10									
	51-0pg_c																								
	**Sample was reinjected and the run is shown in the row above																								

4.A.8 Thermocycler Performance Check

Ten thermocyclers were performance checked using 2800M. All positive controls yielded the correct genotype; all negative controls were negative. Three positive controls run on 806F-TC3, 610J-TC1, and 705A-TC12, had failed size standards. Thermocyclers were also compared by peak heights and peak height ratios (Table 32 and 33)

Table 32: Average peak heights generated during the performance check of 10 internal OCME-NYC thermocyclers

	Performance Check Peak Heights									
	610J-TC1	**705A-TC11**	**705A-TC12**	**705A-TC13**	**714C-TC6**	**714C-TC8**	**714C-TC9**	**714C-TC11**	**806C-TC6**	**806F-TC3**
AMEL	1786	1840	2009	1961	1797	1828	1980	1997	1965	2149
D3S1358	2259	2026	2177	2080	1929	2373	2260	2087	2128	2587
D1S1656	2297	2149	2196	2009	2061	2353	2322	2238	2162	2651
D2S441	1727	1657	1861	1770	1718	1857	1786	1848	1817	1851
D10S1248	1669	1665	1769	1469	1589	1798	1712	1684	1732	1967
D13S317	1660	1591	1774	1576	1495	1709	1652	1685	1747	1770
Penta E	1416	1369	1543	1537	1513	1407	1461	1600	1545	1632
D16S539	3329	3425	3103	3092	3476	3692	3121	3419	3852	3316
D18S51	2537	2718	2540	2383	2441	2835	2557	2562	2686	2717
D2S1338	2405	2447	2494	2411	2398	2434	2419	2438	2514	2364
CSF1PO	2090	2005	2338	2017	1943	2124	2043	2058	2058	2147
Penta D	1461	1570	1936	1654	1583	1304	1607	1652	1677	1803
TH01	3464	3291	3392	3373	3544	3554	3286	3466	3851	3386
vWA	2343	2824	2311	2267	2140	2861	2174	2218	2682	2339
D21S11	2463	2236	2192	1876	1995	2301	2330	2011	2230	2610
D7S820	2300	2422	2473	2218	2174	2277	2245	2246	2515	2471
D5S818	2552	2331	2595	2444	2299	2390	2538	2384	2530	2518
TPOX	2279	2168	2357	2072	2047	2130	2137	2006	2283	2275
DYS391	2275	2182	2275	2171	2077	2086	2047	2105	2216	2219
D8S1179	1652	1688	1963	1987	1782	1749	2070	1961	1968	2592
D12S391	2364	2180	2272	2267	2176	2605	2332	2205	2482	2795
D19S433	1601	1548	1646	1559	1667	1562	1573	1644	1726	1710
FGA	1848	1870	2130	1959	1826	1865	1882	1971	2048	2025
D22S1045	1233	1461	1522	1447	1283	1335	1324	1388	1438	1446

Table 33: Average peak height ratios generated during the performance check of 10 internal OCME-NYC thermocyclers. The gray cells represent loci with no heterozygous calculations.

	Performance Check Peak Height Ratios									
	610J-TC1	**705A-TC11**	**705A-TC12**	**705A-TC13**	**714C-TC6**	**714C-TC8**	**714C-TC9**	**714C-TC11**	**806C-TC6**	**806F-TC3**
AMEL	85%	93%	94%	91%	91%	92%	90%	84%	91%	96%
D3S1358	80%	90%	92%	92%	93%	90%	89%	90%	86%	91%
D1S1656	90%	95%	90%	90%	89%	88%	91%	90%	88%	94%
D2S441	91%	89%	90%	91%	88%	90%	87%	88%	89%	90%
D10S1248	92%	93%	91%	89%	88%	90%	92%	94%	90%	85%
D13S317	92%	86%	93%	90%	86%	94%	86%	85%	89%	89%
Penta E	88%	88%	91%	91%	85%	88%	89%	92%	87%	88%
D16S539	90%	90%	94%	88%	90%	93%	90%	92%	90%	91%
D18S51	87%	94%	89%	86%	93%	90%	91%	88%	89%	94%
D2S1338	91%	87%	91%	89%	90%	91%	87%	88%	93%	87%
CSF1PO										
Penta D	86%	88%	88%	87%	87%	83%	89%	87%	86%	96%
TH01	89%	92%	91%	89%	92%	89%	94%	94%	89%	88%
vWA	90%	89%	88%	94%	92%	92%	89%	90%	92%	91%
D21S11	93%	84%	90%	92%	88%	88%	93%	87%	90%	90%
D7S820	87%	94%	89%	94%	87%	93%	88%	89%	87%	85%
D5S818										
TPOX										
DYS391										
D8S1179	84%	88%	90%	83%	94%	87%	84%	92%	93%	87%
D12S391	83%	79%	91%	87%	85%	89%	83%	84%	87%	85%
D19S433	93%	87%	88%	87%	88%	91%	85%	90%	86%	80%
FGA	91%	89%	78%	85%	93%	92%	90%	92%	87%	85%
D22S1045										

5. Conclusion

The PowerPlex® Fusion system was evaluated on the Applied Biosystems® GeneAmp® PCR 9700 thermal cycler. Samples were amplified using the extracted DNA protocol at half reaction with 29 cycles. The amplified product was run using a 3kV 5 second injection with a 2000 second run time on two Applied Biosystems® 3130*xl*. As per the OCME-NYC, an analytical threshold of 50 RFU with a 3% minimum heterozygote filter and 3% global max filter was used for the validation with 29 cycles. A stochastic threshold of 300 RFU was established. The results showed that the system was capable of producing reliable and reproducible results. The precision of the system is within the recommended range. The studies performed in this validation meet the criteria for an internal validation and have shown that the PowerPlex® Fusion is suitable for use in a forensic laboratory.

6. References

Quality Assurance Standards for Forensic DNA Testing Laboratories (effective July 1, 2009)

SWGDAM Validation Guidelines – Approved December 2012 (SWGDAM.org)

Butler, J.M. (2010) Fundamentals of Forensic DNA Typing, San Diego; Elsevier Academic Press, Chapter 13 “Quality Assurance”, p. 300

Butler, J.M. (2012) Advanced Topics in Forensic DNA Typing: Methodology, San Diego: Elsevier Academic Press, Chapter 7 “Quality Assurance and Validation”, p. 183

PowerPlex® Fusion System Technical Manual TMD039, Revision Date 6/16 from Promega Corporation

PowerPlex® 5C Matrix Standard Technical Manual TMD049, Revision Date 10/15 from Promega Corporation

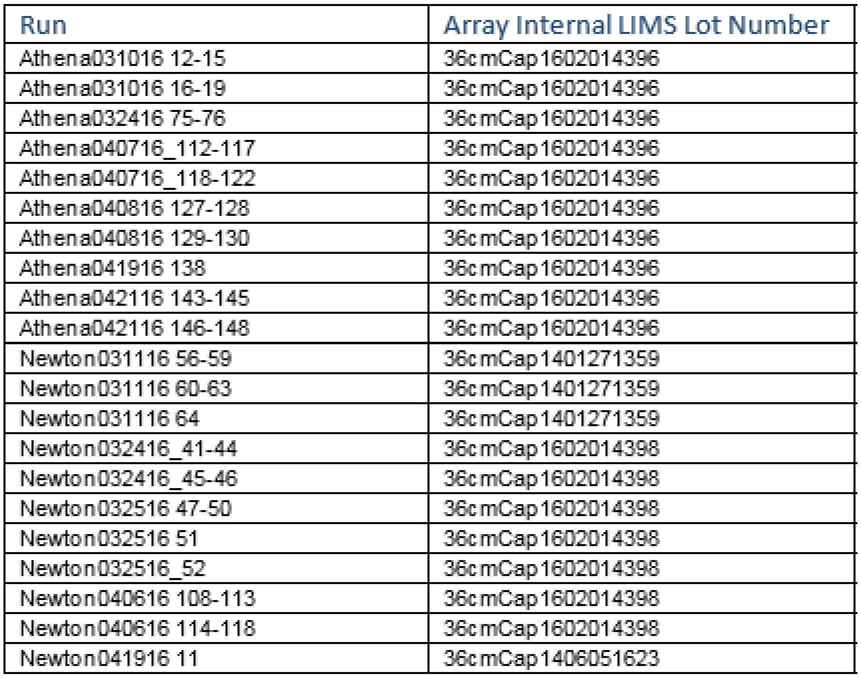
Internal Validation Guide of Autosomal STR Systems for Forensic Laboratories, Promega Reference Manual (2013)

Erica L.R Butts, M.C. Kline, D.L. Duewer, C. R. Hill, H.M. Butler, P. M Vallone. NIST validation studies on the 3500 Genetic Analyzer. Forensic Science International: Genetics Supplement Series 3. 2011 e184-185.

7. Appendix A – Lot Numbers

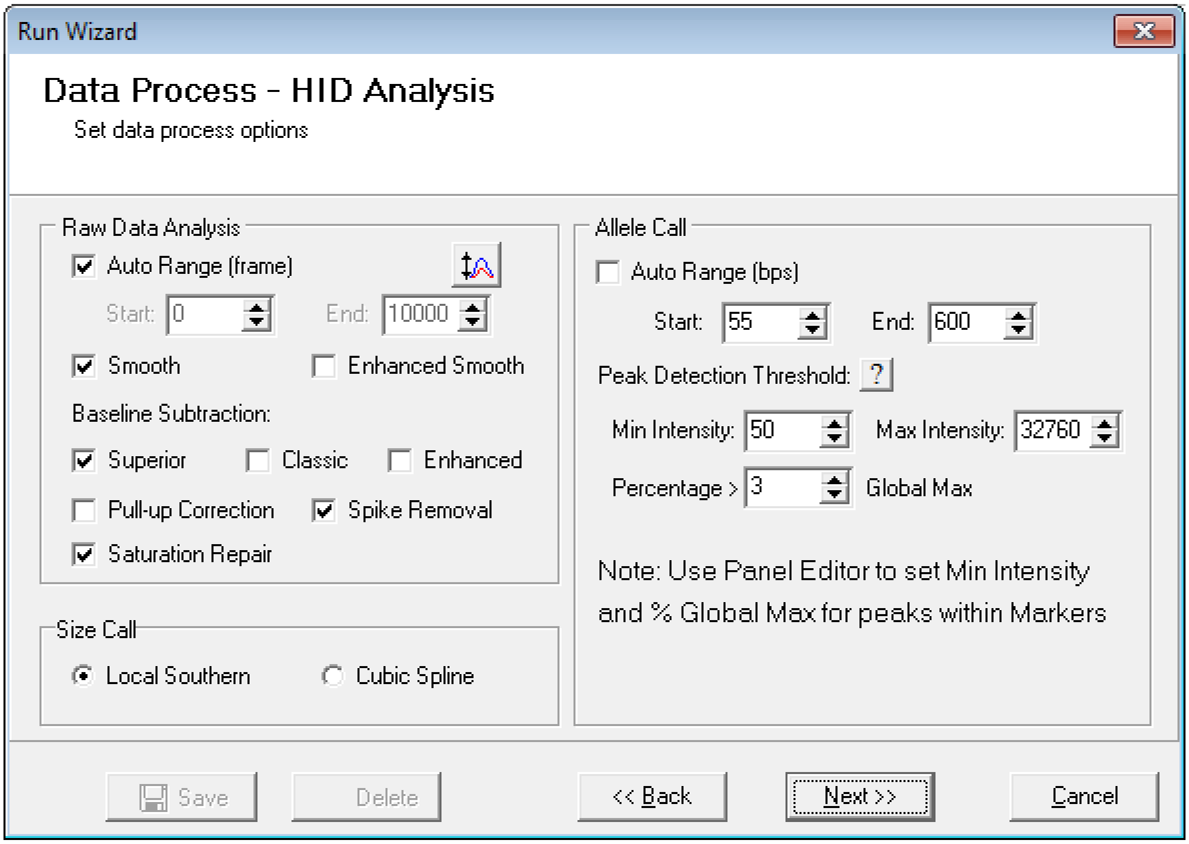
Pre-Amplification Product	**Manufacturer**	**Catalog Number**	**Lot Number**	**Expiration Date**
PowerPlex® 5C Matrix Standard	Promega	DG4850	183166	07/23/2017
PowerPlex® Fusion kit	Promega	DC2408	154236	10/20/2017
PowerPlex® Fusion 5X Master Mix	Promega	DP207A	140564	11/06/2017
PowerPlex® Fusion 5X Primer Pair Mix	Promega	DK236B	148691	01/04/2018
2800M Control DNA	Promega	DD710A	118893	10/06/2019
Water, Amplification Grade	Promega	DW099A	135976	10/27/2019
Post Amplification Product	**Manufacturer**	**Catalog Number**	**Lot Number**	**Expiration Date**
PowerPlex® Fusion Allelic Ladder Mix	Promega	DG381B	120080	10/20/2017
WEN ILS 500	Promega	DG500A	183317	10/20/2018
Array (16 capillary)	Applied Biosystems	4404687	See table below	
Polymer (POP 4) 960 samples	Applied Biosystems	4393710	10224026	05/07/2016

Array lot numbers used during the validation study



Run	Array Internal LIMS Lot Number
Athena031016 12-15	36cmCap1602014396
Athena031016 16-19	36cmCap1602014396
Athena032416 75-76	36cmCap1602014396
Athena040716_112-117	36cmCap1602014396
Athena040716_118-122	36cmCap1602014396
Athena040816 127-128	36cmCap1602014396
Athena040816 129-130	36cmCap1602014396
Athena041916 138	36cmCap1602014396
Athena042116 143-145	36cmCap1602014396
Athena042116 146-148	36cmCap1602014396
Newton031116 56-59	36cmCap1401271359
Newton031116 60-63	36cmCap1401271359
Newton031116 64	36cmCap1401271359
Newton032416_41-44	36cmCap1602014398
Newton032416_45-46	36cmCap1602014398
Newton032516 47-50	36cmCap1602014398
Newton032516 51	36cmCap1602014398
Newton032516_52	36cmCap1602014398
Newton040616 108-113	36cmCap1602014398
Newton040616 114-118	36cmCap1602014398
Newton041916 11	36cmCap1406051623

8. Appendix B – Analysis Methods



Run Wizard

Data Process - HID Analysis

Set data process options

Raw Data Analysis

☑ Auto Range (frame)

Start: 0 End: 10000

☑ Smooth ☐ Enhanced Smooth

Baseline Subtraction:

☑ Superior ☐ Classic ☐ Enhanced

☐ Pull-up Correction ☑ Spike Removal

☑ Saturation Repair

Size Call

● Local Southern ○ Cubic Spline

Allele Call

☐ Auto Range (bps)

Start: 55 End: 600

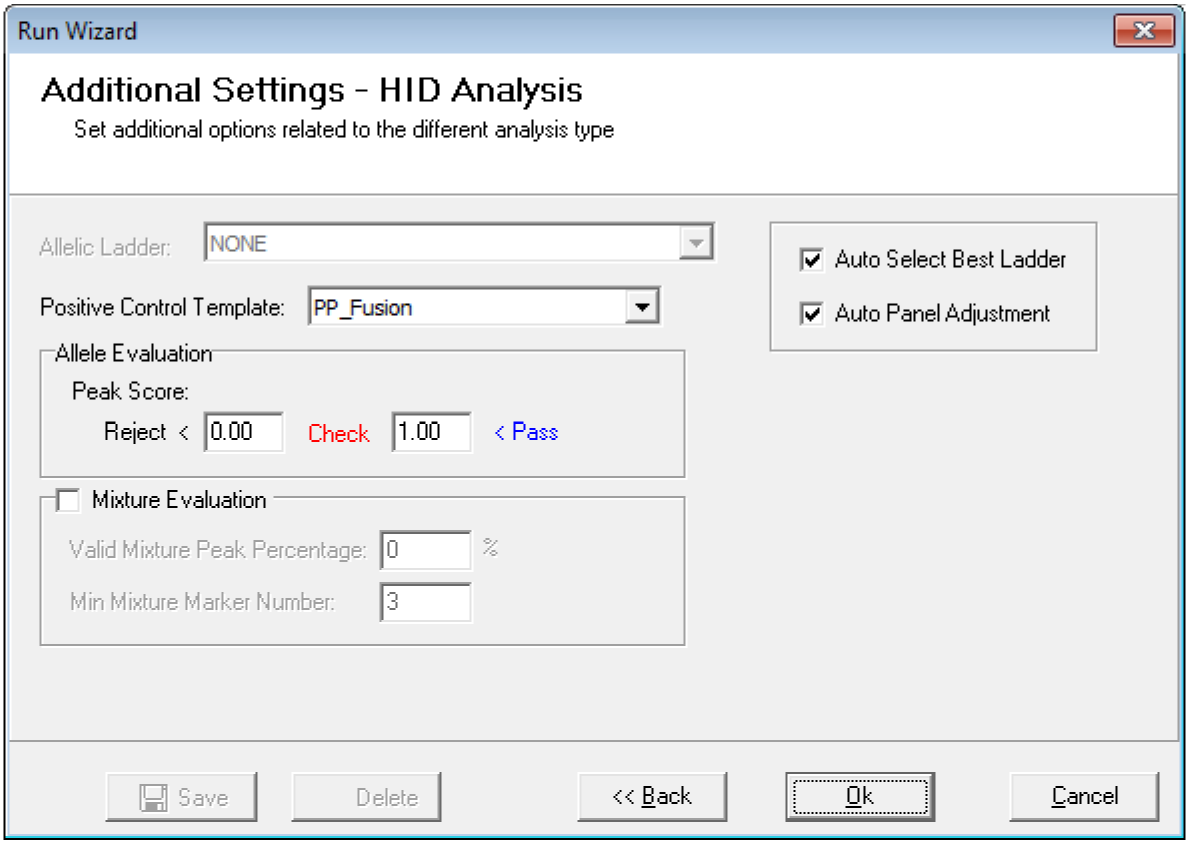
Peak Detection Threshold: ?

Min Intensity: 50 Max Intensity: 32760

Percentage > 3 Global Max

Note: Use Panel Editor to set Min Intensity and % Global Max for peaks within Markers

Run Wizard, Additional Settings



Additional Settings - HID Analysis

Set additional options related to the different analysis type

Allelic Ladder: NONE

Positive Control Template: PP_Fusion

Allele Evaluation

Peak Score:

Reject < 0.00 Check 1.00 < Pass

☐ Mixture Evaluation

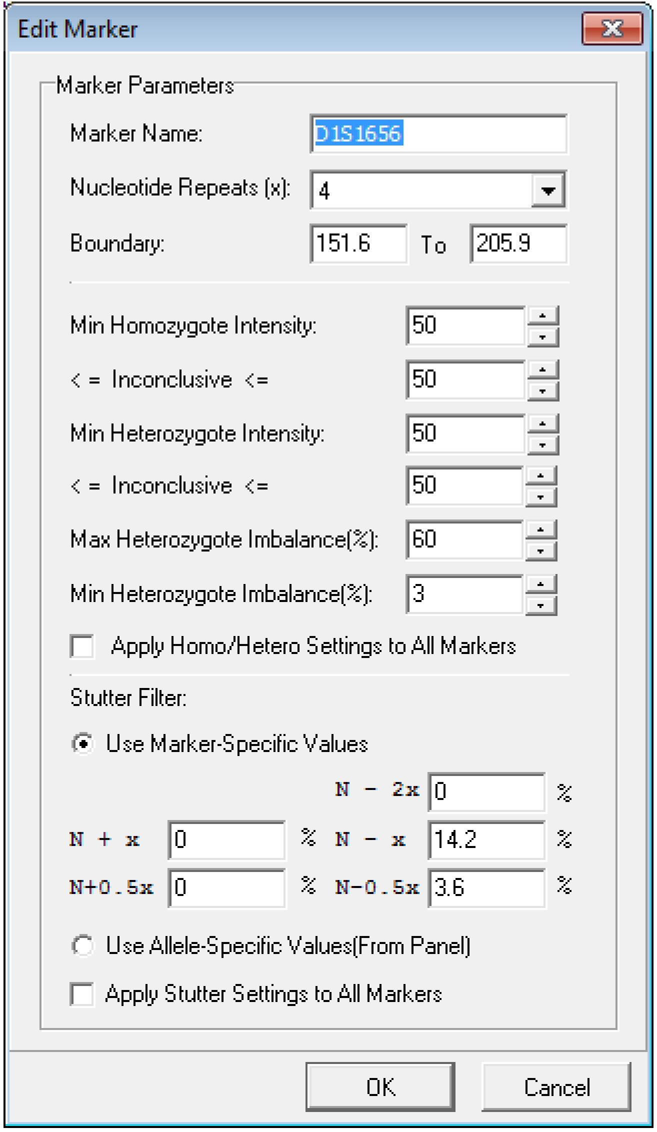
Valid Mixture Peak Percentage: 0 %

Min Mixture Marker Number: 3

☑ Auto Select Best Ladder

☑ Auto Panel Adjustment

Panel Editor, Edit Marker



Edit Marker

Marker Parameters

Marker Name: D1S1656

Nucleotide Repeats (x): 4

Boundary: 151.6 To 205.9

Min Homozygote Intensity: 50

< = Inconclusive <= 50

Min Heterozygote Intensity: 50

< = Inconclusive <= 50

Max Heterozygote Imbalance(%): 60

Min Heterozygote Imbalance(%): 3

☐ Apply Homo/Hetero Settings to All Markers

Stutter Filter:

● Use Marker-Specific Values

N - 2x 0 %

N + x 0 % N - x 14.2 %

N+0.5x 0 % N-0.5x 3.6 %

○ Use Allele-Specific Values(From Panel)

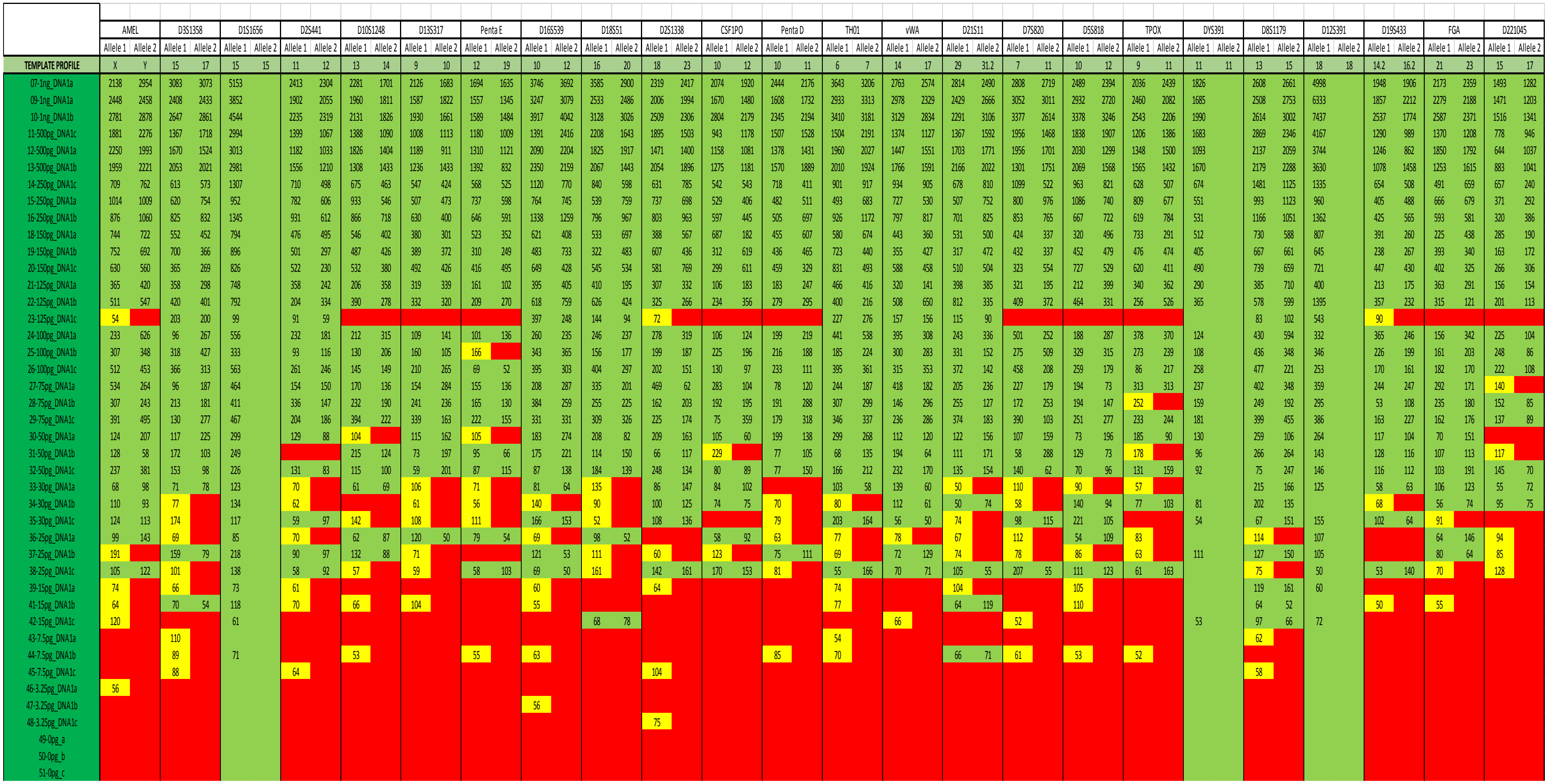
☐ Apply Stutter Settings to All Markers

Promega Stutter Percentages used in GeneMarker v.2.8.2

Promega Stutter Percentages			
AMEL	0%	N-x	Minus
D3S1358	11.9%	N-x	Minus
D1S1656	14.2%	N-x	Minus
	3.6%	N-0.5x	Minus
D2S441	9.2%	N-x	Minus
D10S1248	12.4%	N-x	Minus
D13S317	9.8%	N-x	Minus
Penta E	7.6%	N-x	Minus
D16S539	10.2%	N-x	Minus
D18S51	14.6%	N-x	Minus
D2S1338	13.9%	N-x	Minus
CSF1PO	9.5%	N-x	Minus
Penta D	6.8%	N-x	Minus
TH01	4.6%	N-x	Minus
vWA	11.2%	N-x	Minus
D21S11	11.6%	N-x	Minus
D7S820	11.0%	N-x	Minus
D5S818	9.5%	N-x	Minus
TPOX	5.5%	N-x	Minus
DYS391	8.7%	N-x	Minus
D8S1179	10.9%	N-x	Minus
D12S391	15.8%	N-x	Minus
D19S433	11.0%	N-x	Minus
FGA	12.1%	N-x	Minus
D22S1045	16.4%	N-x	Minus
	8.6%	N+x	Plus

9. Appendix C – Stochastic Threshold Tables

Stochastic threshold for 29 cycles for DNA 1 Athena



	AMEL		D3S1358		D1S1656		D2S441		D10S1248		D13S317		Penta E		D16S539		D18S51		D2S1338		CSF1PO		Penta D		TH01		vWA		D21S11		D7S820		D5S818		TPOX		DYS391		D8S1179		D12S391		D19S433		FGA		D221045	
	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
TEMPLATE PROFILE	X	Y	15	17	15	15	11	12	13	14	9	10	12	19	10	12	16	20	18	23	10	12	10	11	6	7	14	17	29	31.2	7	11	10	12	9	11	11	11	13	15	18	18	14.2	16.2	21	23	15	17
07-1ng_DNA1a	2138	2954	3083	3073	5153		2413	2304	2281	1701	2126	1683	1694	1635	3746	3692	3585	2900	2319	2417	2074	1920	2444	2176	3643	3206	2763	2574	2814	2490	2808	2719	2489	2394	2036	2439	1826		2608	2661	4998		1948	1906	2173	2359	1493	1282
09-1ng_DNA1a	2448	2458	2408	2433	3852		1902	2055	1960	1811	1587	1822	1557	1345	3247	3079	2533	2486	2006	1994	1670	1480	1608	1732	2933	3313	2978	2329	2429	2666	3052	3011	2932	2720	2460	2082	1685		2508	2753	6333		1857	2212	2279	2188	1471	1203
10-1ng_DNA1b	2781	2878	2647	2861	4544		2235	2319	2131	1826	1930	1661	1589	1484	3917	4042	3128	3026	2509	2306	2804	2179	2345	2194	3410	3181	3129	2834	2291	3106	3377	2614	3378	3246	2543	2206	1990		2614	3002	7437		2537	1774	2587	2371	1516	1341
11-500pg_DNA1c	1881	2276	1367	1718	2994		1399	1067	1388	1090	1008	1113	1180	1009	1391	2416	2208	1643	1895	1503	943	1178	1507	1528	1504	2191	1374	1127	1367	1592	1956	1468	1838	1907	1206	1386	1683		2869	2346	4167		1290	989	1370	1208	778	946
12-500pg_DNA1a	2250	1993	1670	1524	3013		1182	1033	1826	1404	1189	911	1310	1121	2090	2204	1825	1917	1471	1400	1158	1081	1378	1431	1960	2027	1447	1551	1703	1771	1956	1701	2030	1299	1348	1500	1093		2137	2059	3744		1246	862	1850	1792	644	1037
13-500pg_DNA1b	1959	2221	2053	2021	2981		1556	1210	1308	1433	1236	1433	1392	832	2350	2159	2067	1443	2054	1896	1275	1181	1570	1889	2010	1924	1766	1591	2166	2022	1301	1751	2069	1568	1565	1432	1670		2179	2288	3630		1078	1458	1253	1615	883	1041
14-250pg_DNA1c	709	762	613	573	1307		710	498	675	463	547	424	568	525	1120	770	840	598	631	785	542	543	718	411	901	917	934	905	678	810	1099	522	963	821	628	507	674		1481	1125	1335		654	508	491	659	657	240
15-250pg_DNA1a	1014	1009	620	754	952		782	606	933	546	507	473	737	598	764	745	539	759	737	698	529	406	482	511	493	683	727	530	507	752	800	976	1086	740	809	677	551		993	1123	960		405	488	666	679	371	292
16-250pg_DNA1b	876	1060	825	832	1345		931	612	866	718	630	400	646	591	1338	1259	796	967	803	963	597	445	505	697	926	1172	797	817	701	825	853	765	667	722	619	784	531		1166	1051	1362		425	565	593	581	320	386
18-150pg_DNA1a	744	722	552	452	794		476	495	546	402	380	301	523	352	621	408	533	697	388	567	687	182	455	607	580	674	443	360	531	500	424	337	320	496	733	291	512		730	588	807		391	260	225	438	285	190
19-150pg_DNA1b	752	692	700	366	896		501	297	487	426	389	372	310	249	483	733	322	483	607	436	312	619	436	465	723	440	355	427	317	472	432	337	452	479	476	474	405		667	661	645		238	267	393	340	163	172
20-150pg_DNA1c	630	560	365	269	826		522	230	532	380	492	426	416	495	649	428	545	534	581	769	299	611	459	329	831	493	588	458	510	504	323	554	727	529	620	411	490		739	659	721		447	430	402	325	266	306
21-125pg_DNA1a	365	420	358	298	748		358	242	206	358	319	339	161	102	395	405	410	195	307	332	106	183	183	247	466	416	320	141	398	385	321	195	212	399	340	362	290		385	710	400		213	175	363	291	156	154
22-125pg_DNA1b	511	547	420	401	792		204	334	390	278	332	320	209	270	618	759	626	424	325	266	234	356	279	295	400	216	508	650	812	335	409	372	464	331	256	526	365		578	599	1395		357	232	315	121	201	113
23-125pg_DNA1c	54		203	200	99		91	59							397	248	144	94	72						227	276	157	156	115	90									83	102	543		90					
24-100pg_DNA1a	233	626	96	267	556		232	181	212	315	109	141	101	136	260	235	246	237	278	319	106	124	199	219	441	538	395	308	243	336	501	252	188	287	378	370	124		430	594	332		365	246	156	342	225	104
25-100pg_DNA1b	307	348	318	427	333		93	116	130	206	160	105	166		343	365	156	177	199	187	225	196	216	188	185	224	300	283	331	152	275	509	329	315	273	239	108		436	348	346		226	199	161	203	248	86
26-100pg_DNA1c	512	453	366	313	563		261	246	145	149	210	265	69	52	395	303	404	297	202	151	130	97	233	111	395	361	315	353	372	142	458	208	259	179	86	217	258		477	221	253		170	161	182	170	222	108
27-75pg_DNA1a	534	264	96	187	464		154	150	170	136	154	284	155	136	208	287	335	201	469	62	283	104	78	120	244	187	418	182	205	236	227	179	194	73	313	313	237		402	348	359		244	247	292	171	140	
28-75pg_DNA1b	307	243	213	181	411		336	147	232	190	241	236	165	130	384	259	255	225	162	203	192	195	191	288	307	299	146	296	255	127	172	253	194	147	252		159		249	192	295		53	108	235	180	152	85
29-75pg_DNA1c	391	495	130	277	467		204	186	394	222	339	163	222	155	331	331	309	326	225	174	75	359	179	318	346	337	236	286	374	183	390	103	251	277	233	244	181		399	455	386		163	227	162	176	137	89
30-50pg_DNA1a	124	207	117	225	299		129	88	104		115	162	105		183	274	208	82	209	163	105	60	199	138	299	268	112	120	122	156	107	159	73	196	185	90	130		259	106	264		117	104	70	151		
31-50pg_DNA1b	128	58	172	103	249				215	124	73	197	95	66	175	221	114	150	66	117	229		77	105	68	135	194	64	111	171	58	288	129	73	178		96		266	264	143		128	116	107	113	117	
32-50pg_DNA1c	237	381	153	98	226		131	83	115	100	59	201	87	115	87	138	184	139	248	134	80	89	77	150	166	212	232	170	135	154	140	62	70	96	131	159	92		75	247	146		116	112	103	191	145	70
33-30pg_DNA1a	68	98	71	78	123		70		61	69	106		71		81	64	135		86	147	84	102			103	58	139	60	50		110		90		57				215	166	125		58	63	106	123	55	72
34-30pg_DNA1b	110	93	77		134		62				61		56		140		90		100	125	74	75	70		80		112	61	50	74	58		140	94	77	103	81		202	135			68		56	74	95	75
35-30pg_DNA1c	124	113	174		117		59	97	142		108		111		166	153	52		108	136			79		203	164	56	50	74		98	115	221	105			54		67	151	155		102	64	91			
36-25pg_DNA1a	99	143	69		85		70		62	87	120	50	79	54	69		98	52			58	92	63		77		78		67		112		54	109	83				114		107				64	146	94	
37-25pg_DNA1b	191		159	79	218		90	97	132	88	71				121	53	111		60		123		75	111	69		72	129	74		78		86		63		111		127	150	105				80	64	85	
38-25pg_DNA1c	105	122	101		138		58	92	57		59		58	103	69	50	161		142	161	170	153	81		55	166	70	71	105	55	207	55	111	123	61	163			75		50		53	140	70		128	
39-15pg_DNA1a	74		66		73		61								60				64						74				104				105						119	161	60							
41-15pg_DNA1b	64		70	54	118		70		66		104				55										77				64	119			110						64	52			50		55			
42-15pg_DNA1c	120				61												68	78									66				52						53		97	66	72							
43-7.5pg_DNA1a			110																						54														62									
44-7.5pg_DNA1b			89		71				53				55		63								85		70				66	71	61		53		52													
45-7.5pg_DNA1c			88				64												104																				58									
46-3.25pg_DNA1a	56																																															
47-3.25pg_DNA1b															56																																	
48-3.25pg_DNA1c																			75																													
49-0pg_a																																																
50-0pg_b																																																
51-0pg_c																																																

Stochastic threshold for 29 cycles for DNA 2 Athena

	AMEL		D3S1358		D1S1656		D2S441		D10S1248		D13S317		Penta E		D16S539		D18S51		D2S1338		CSF1PO		Penta D		TH01		vWA		D21S11		D7S820		D5S818		TPOX		DYS391		D8S1179		D12S391		D19S433		FGA		D221045	
	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
TEMPLATE PROFILE	X	X	16	17	16	17.3	11	14	14	15	8	11	13	18	10	11	15	17	17	24	13	14	12	14	7	9	15	19	30	32.2	10	12	9	13	9	11	11	11	11	13	15	21	15.2	16.2	21	22	15	16
07-1ng_DNA2a	4096		2319	2337	2297	2592	2198	2775	1932	1636	2375	2546	1997	1599	3370	3476	3289	2889	2422	2691	2593	2241	2206	2414	2671	2289	2402	2456	2057	2366	3225	2278	2576	3008	2077	2525			2185	1709	2413	2419	2082	1730	2155	2422	1674	1469
09-1ng_DNA2a	3663		2103	1884	2032	1705	2000	1923	1580	1456	1381	1753	1509	1451	2801	2450	2326	2644	2018	1671	2022	1766	2008	1773	2779	3415	2642	2221	2267	2247	3023	2903	3176	3047	2925	2175			1924	2181	2910	2237	1659	1950	2473	2036	1665	1699
10-1ng_DNA2b	4812		2783	2531	2121	2451	1888	2447	2045	2280	2038	1767	1873	1716	4076	3931	3562	2899	2166	2274	2430	2150	2246	2003	3414	3051	2585	2652	2782	2521	3453	2814	3391	3388	2378	2491			3049	2901	3272	3172	1797	1950	2720	2700	2023	1593
11-500pg_DNA2c	2911		1361	1286	976	1158	1074	924	1438	1170	1246	995	938	884	1521	2198	1652	1554	1562	1376	1528	1317	1315	1237	1211	1557	1549	1116	1256	1446	1439	1671	1457	1668	1190	1660			1910	1816	1361	1251	1009	1094	1373	1388	965	1067
12-500pg_DNA2a	3560		1365	1538	1088	1451	1574	1419	1241	1300	1685	1249	1437	1209	2827	1711	2109	2148	1864	1826	1513	1216	1654	1356	1763	1623	1910	1709	1266	1692	2097	1664	1621	2059	1765	1368			1503	1814	1402	1520	1594	1229	1789	1869	1364	865
13-500pg_DNA2b	3336		1454	1495	1150	1400	1351	1055	1179	1057	1401	1055	1575	1178	1931	1906	1433	1344	1533	1347	1418	1309	1991	1389	1369	1766	1751	1224	1439	989	1278	1813	1333	1400	1485	954			1681	1654	1484	1151	977	1009	1522	983	1153	967
14-250pg_DNA2c	1567		609	524	745	709	367	437	738	315	656	557	447	563	897	719	1139	635	665	461	480	428	1018	796	926	989	601	678	679	798	809	1120	643	614	596	695			802	1012	717	604	464	468	530	532	456	395
15-250pg_DNA2a	1334		741	457	562	493	644	362	670	772	609	628	814	558	909	817	918	1035	688	523	601	670	750	720	574	856	654	777	665	773	723	567	739	812	794	641			750	840	725	631	481	490	634	638	641	345
16-250pg_DNA2b	1452		535	773	842	506	939	547	640	723	704	555	646	412	851	968	894	1065	918	994	671	477	676	709	592	1003	596	670	631	871	721	884	928	748	927	851			838	685	547	596	568	561	579	662	373	410
18-150pg_DNA2a	1125		363	289	199	368	382	429	223	336	298	363	361	452	577	423	581	287	550	242	260	294	456	417	379	450	401	448	365	328	523	525	254	414	317	433			440	432	229	196	267	199	188	294	281	174
19-150pg_DNA2b	879		390	388	356	322	423	489	393	539	342	337	446	455	377	204	447	319	604	669	464	320	290	361	534	399	540	493	329	153	404	300	393	654	528	357			370	466	255	159	212	375	434	196	282	372
20-150pg_DNA2c	1060		335	371	391	306	390	407	290	398	552	515	306	541	401	468	333	604	379	231	464	322	272	386	493	525	269	315	519	467	552	427	427	448	488	560			623	465	282	203	335	345	442	348	292	203
21-125pg_DNA2a	631		329	339	318	352	322	264	371	420	367	273	207	334	332	264	713	446	517	443	317	189	338	446	339	320	210	205	288	315	409	402	349	246	438	281			268	171	360	252	239	145	297	300	202	196
22-125pg_DNA2b	720		191	218	281	341	147	250	184	103	188	241	295	181	359	431	486	310	569	446	371	261	299	277	394	397	349	226	436	264	454	327	492	430	529	314			446	578	225	151	152	252	420	338	138	187
23-125pg_DNA2c	836		455	300	393	359	96	242	303	228	229	347	242	254	423	422	320	291	406	339	364	140	404	280	174	583	387	345	373	370	336	523	371	281	279	194			281	347	226	261	251	185	299	222	329	201
24-100pg_DNA2a	480		235	348	169	119	209	364	88	204	155	166	121	178	260	219	360	256	240	299	242	182	289	262	434	412	321	244	275	311	318	282	166	224	275	342			451	260	111	160	225	141	331	169	255	111
25-100pg_DNA2b	465		293	344	278	281	218	227	286	228	242	263	123	183	264	317	274	109	217	338	216	133	174	144	248	119	257	285	216	311	234	177	265	303	334	196			241	293	149	123	125	141	323	282	124	123
26-100pg_DNA2c	668		95	194	155	199	86	311	149	163	164	141	162		303	339	327	148	280	130	184	115	163	184	134	264	310	269	223	145	238	271	187	172	236	65			411	577	157	128	200	142	237	241	128	181
27-75pg_DNA2a	404		199	162	188	178	229		206	132	104	160	67	230	294	251	174	115	235	329	94	186	248	397	296	262	107	318	165	380	275	125	218	120	233	194			264	279	170	81	142	249	188	224	214	239
28-75pg_DNA2b	385		262	301	149	245	118	137	225	159	78	126	217	157	179	245	269	83	89	118	88	152	198	186	211	223	178	204	142	296	237	282	146	164	166	185			267	234	108	98	57	104	198	176	123	74
29-75pg_DNA2c	648		159	304	115	130	162	159	120	249	250	189	250	208	264	271	339	369	461	230	158	291	154	177	123	335	220	125	183	233	271	272	328	336	121	304			248	172	138	154	225	188	216	192	241	69
30-50pg_DNA2a	281		157	117	57	87	60	74	133	71	120	131	134	124	129	163	146	171	142	201	139	64	175		227		240	181	227	213	108	198	68		101	66			195	146	115	90	79	102	192	107	60	76
31-50pg_DNA2b	336		142	152	95	84	96		78	129	135	165	125		182	227	139	122	150	275	55		170	72	188	213	169	100	179	90	134	94	86	60	102	120			169	58	80	64	51		67	77	58	89
32-50pg_DNA2c	347		225	174	227		125	73	165	268	64	90	73	92	154	130	85	112	65	219	91	142	136	69	112	89	77	116	55	185	199	160	257	235	112	78			187	197	68	105			190	175	53	
33-30pg_DNA2a	244		99	97	78	64	61	66	75	61	60	71	80	65	127	286	69	118	111	74	90	80	126		74	128	105	55	62		166		98	231	50				122		60		76	121	81	76	90	78
34-30pg_DNA2b	142				52		72		61	112	70	81	121		92	85	147		218	71			124		96		85		188		75	84	72		97				251				68	99	80	88	60	
35-30pg_DNA2c	144		67	84			148	151	52		114	66			101	129	121	100	123	64	129	82	133	82	69	186	54	52	94	134	56	62			135	78			109	122	69	119	157	52				
36-25pg_DNA2a	153		56		119	113	136		107		85	98	124		89	60	55						132				80		91		131		108		73	98			80	128	65		50		137		52	96
37-25pg_DNA2b	93		78	51	56				117				69	55	55	87	121	51	63	71	70	69	103	103	87	73	83		85		75	135			97	98			140						59		57	
38-25pg_DNA2c	121		123	105	86	58					104				171	77	125	134	87		56	137	68		88	61	61	67	53	93	110		74		134				114	69	106		55		70		57	
39-15pg_DNA2a	128														140		134	57	60				71		73										109										53			
41-15pg_DNA2b	131								64						94				72		57	73	120		94		54		78		57		63	57	77				102						63			
42-15pg_DNA2c	189		96		52				66						72										78	168													59	53					55			
43-7.5pg_DNA2a	109						77				70														60	59			60	70																		
44-7.5pg_DNA2b															102		52						60	59			87												77									
45-7.5pg_DNA2c									58						51										76	99							132		103													
46-3.25pg_DNA2a																																																
47-3.25pg_DNA2b															52																																	
48-3.25pg_DNA2c																			53																													
49-0pg_a																																																
50-0pg_b																																																
51-0pg_c																																																

Stochastic threshold for 29 cycles for DNA 1 Newton

	AMEL		D3S1358		D1S1656		D2S441		D10S1248		D13S317		Penta E		D16S539		D18S51		D2S1338		CSF1PO		Penta D		TH01		vWA		D21S11		D7S820		D5S818		TPOX		DYS391		D8S1179		D12S391		D19S433		FGA		D221045	
	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
TEMPLATE PROFILE	X	Y	15	17	15	15	11	12	13	14	9	10	12	19	10	12	16	20	18	23	10	12	10	11	6	7	14	17	29	31.2	7	11	10	12	9	11	11	11	13	15	18	18	14.2	16.2	21	23	15	17
07-1ng_DNA1a	3357	4718	4921	4821	8203		3596	3487	3584	2637	3227	2564	2443	2346	4848	4873	5041	4131	3278	3329	2800	2549	3259	2888	5153	4540	4102	3815	4222	3636	4056	4070	3593	3487	2942	3498	2677		4052	4132	7705		2949	2874	3373	3656	2302	2005
09-1ng_DNA1a	3757	3746	3733	3871	6194		2880	3134	3085	2854	2460	2792	2302	1980	3992	3827	3329	3226	2646	2653	2150	1917	2097	2256	4511	5101	4793	3759	3911	4295	4846	4720	4557	4299	3809	3251	2675		3803	4262	9095		2772	3360	3419	3311	2211	1803
10-1ng_DNA1b	4468	4739	4308	4694	7523		3732	3827	3723	3178	3407	2907	2880	2560	4845	5051	4175	4108	3575	3264	3882	3049	3160	2891	4349	4029	4143	3652	3012	4031	4301	3566	4362	4290	3527	3074	2730		3506	3993	9221		3505	2553	3634	3390	2197	1983
11-500pg_DNA1c	2777	3392	2043	2606	4680		1967	1500	2090	1622	1485	1632	1646	1422	1655	2825	2726	2000	2338	1867	1149	1414	1809	1854	1860	2711	1739	1420	1691	2000	2403	1872	2246	2371	1504	1733	2088		3744	3046	5215		1634	1234	1757	1536	1048	1239
12-500pg_DNA1a	4195	3628	3058	2758	5630		2139	1838	3375	2561	2140	1637	2214	1927	2973	3099	2754	2890	2162	2077	1666	1519	1971	2061	2921	2955	2182	2296	2492	2625	2841	2598	2929	1885	1939	2134	1590		3382	3255	5935		1932	1321	2934	2792	1001	1630
13-500pg_DNA1b	3234	3632	3317	3284	4823		2389	1905	2120	2304	1919	2216	2049	1226	3127	2877	2887	2032	2757	2549	1682	1529	2035	2458	2876	2661	2488	2231	3027	2776	1774	2401	2748	2121	2137	1931	2275		3262	3413	5279		1549	2098	1787	2312	1314	1497
14-250pg_DNA1c	1169	1226	1008	935	2187		1128	809	1147	794	910	715	944	874	1409	987	1143	832	898	1106	766	744	1018	588	1185	1197	1284	1246	919	1102	1486	715	1328	1124	860	705	956		2108	1594	1851		911	729	721	946	991	372
15-250pg_DNA1a	1379	1370	837	1017	1319		1001	804	1281	750	681	640	947	774	851	835	653	904	882	845	627	475	568	600	602	813	869	632	598	905	948	1200	1299	902	949	844	679		1197	1408	1183		509	603	831	871	486	385
16-250pg_DNA1b	1194	1419	1104	1099	1816		1205	783	1167	961	843	528	810	757	1548	1465	980	1186	1010	1200	739	533	627	863	1211	1485	1031	1069	902	1079	1105	998	854	935	815	1011	713		1580	1413	1809		556	754	813	791	452	543
19-150pg_DNA1b	1222	1139	1128	594	1470		773	478	759	660	597	590	484	377	642	952	444	650	811	571	405	778	562	577	1035	642	510	610	436	651	614	489	620	667	637	640	551		1012	1044	1013		358	395	586	530	239	258
20-150pg_DNA1c	1017	907	591	430	1312		796	347	817	581	728	637	604	708	809	534	683	684	733	957	368	740	562	409	1084	643	768	589	649	645	399	698	906	658	744	507	599		1022	926	1011		591	585	535	437	348	400
21-125pg_DNA1a	669	768	665	543	1356		611	427	376	640	548	587	286	178	567	589	604	287	457	496	159	267	271	373	712	638	503	222	618	590	496	305	323	628	516	545	453		632	1142	653		328	268	584	477	257	246
22-125pg_DNA1b	923	1007	784	772	1555		376	609	733	534	619	604	390	500	902	1101	935	641	502	405	357	537	422	450	622	341	789	1054	1314	541	659	611	741	510	410	843	602		963	1014	2365		606	397	540	221	353	201
23-125pg_DNA1c	62	89	350	337	181		155	104							560	353	220	143	107						332	419	240	252	203	153									140	165	969		75	170	58	50		
24-100pg_DNA1a	306	815	126	355	696		281	223	249	360	125	156	108	143	286	261	278	254	286	320	99	122	181	199	521	650	468	363	264	359	498	258	172	274	350	340	109		524	757	394		412	280	175	361	219	100
25-100pg_DNA1b	492	549	507	683	547		143	181	210	326	250	170	265	73	437	467	209	253	266	249	296	260	288	254	312	381	482	467	546	253	440	842	496	508	433	385	171		695	543	545		354	311	247	317	391	138
26-100pg_DNA1c	869	776	640	545	984		469	433	285	297	411	517	161	114	532	400	553	416	305	237	215	164	361	174	515	498	421	474	521	196	626	311	385	288	157	381	432		684	312	369		255	249	290	277	385	198
27-75pg_DNA1a	895	438	163	316	778		245	238	295	230	258	478	250	220	281	381	462	285	650	89	385	144	110	167	327	265	593	252	287	322	313	258	267	103	425	441	330		573	500	527		354	365	429	250	201	
28-75pg_DNA1b	621	495	443	375	853		652	280	459	368	462	462	306	237	622	395	408	354	249	321	301	308	299	450	504	485	246	480	408	203	275	414	303	226	65	387	247		449	338	519		93	177	402	312	248	146
29-75pg_DNA1c	688	877	243	500	861		353	316	677	394	576	283	373	257	488	482	464	496	339	265	112	524	268	456	516	527	372	448	590	281	599	166	377	418	338	373	271		664	743	623		267	375	264	289	228	151
30-50pg_DNA1a	212	339	209	364	500		207	144	187	75	192	283	58	178	248	360	284	115	289	236	146	88	280	188	406	380	149	166	161	215	148	210	90	270	270	137	181		363	161	385		171	148	106	228		
31-50pg_DNA1b	219	93	291	172	411		58		363	210	119	323	155	111	243	305	160	223	99	175	320		112	159	91	187	283	95	157	253	84	416	195	110	54	275	133		409	415	223		198	175	171	182	189	
32-50pg_DNA1c	344	538	224	141	323		186	116	173	147	84	291	124	164	116	170	244	185	334	180	110	122	102	196	224	310	327	240	183	221	197	90	99	141	188	236	131		112	359	216		176	166	154	301	223	110
33-30pg_DNA1a	116	158	126	128	196		116		98	117	75	172	111		118	93	190		115	204	115	136	55		164	99	202	91	79	56	168		126		60	83			336	267	204		89	93	173	191	85	115
34-30pg_DNA1b	210	179	146	78	260		115	64	86	67	111		102		221		75	138	158	196	116	113	62	107	136		192	99	85	126	54	97	238	147	122	162	117		335	221	64		111	75	98	122	154	116
35-30pg_DNA1c	224	218	327	84	223		108	175	259		59	187	194		246	223	69	54	168	206	51		113		333	252	92	79	64	128	150	180	349	157	59		85		116	257	269		178	111	157			
36-25pg_DNA1a	201	291	153		185		83	142	137	184	248	105	155	108	120		166	89	68		97	145	104	53	119	82	56	141	119		194		91	193	146				216		203		79	55	122	273	177	84
37-25pg_DNA1b	275		233	112	320		120	130	187	119	96		61		137	62	128		74		139		83	125	85		92	155	94		93		58	104	74	52	137		166	194	135				101	84	111	56
38-25pg_DNA1c	182	203	181	83	240		96	151	57	96	98	73	86	162	96	75	217	50	196	217	219	189	107		79	227	107	107	150	77	272	85	155	182	85	218			81	113	98		82	199	103		179	
39-15pg_DNA1a	123	73	104		121		95		73						92		63	62	91		60				107				156		59	50	68	173	60		57		193	260	102						78	
41-15pg_DNA1b	113		116	84	193		114	73	106	80	161		62		73										149	84	63		104	194	52		184						98	79			63	80	59	92	83	
42-15pg_DNA1c	62	192			103		52	86	80				72				94	111	53	54	81				52		98				89		79	66	85		110		138	91	103				58			
43-7.5pg_DNA1a	54		205	76	80				78		65														84						50				74		51		105		50						75	
44-7.5pg_DNA1b			190	59	147				107				99		99		57				55		143		116	58			105	111	101		77		87						67							
45-7.5pg_DNA1c			140				92		58		55	56			55				138	60	52										56		64		60		65		94	55	50				50			
46-3.25pg_DNA1a	104																50		59						59														53	66			50		79		55	
47-3.25pg_DNA1b	59														85																								57									
48-3.25pg_DNA1c																			110										52								62											
49-0pg_a																																																
50-0pg_b																																																
51-0pg_c																																																

Stochastic threshold for 29 cycles for DNA 2 Newton

	AMEL		D3S1358		D1S1656		D2S441		D10S1248		D13S317		Penta E		D16S539		D18S51		D2S1338		CSF1PO		Penta D		TH01		vWA		D21S11		D7S820		D5S818		TPOX		DYS391		D8S1179		D12S391		D19S433		FGA		D221045	
	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
TEMPLATE PROFILE	X	X	16	17	16	17.3	11	14	14	15	8	11	13	18	10	11	15	17	17	24	13	14	12	14	7	9	15	19	30	32.2	10	12	9	13	9	11	11	11	11	13	15	21	15.2	16.2	21	22	15	16
07-1ng_DNA2a	6784		3961	3918	3963	4394	3578	4504	3243	2729	3851	4169	3172	2493	4814	5130	4819	4308	3668	3989	3696	3142	3144	3487	4119	3606	3804	3879	3256	3741	5014	3508	4052	4578	3209	3869			3762	2962	4186	4262	3571	2954	3709	4101	2874	2495
09-1ng_DNA2a	5914		3500	3099	3355	2827	3094	2996	2386	2198	1959	2447	1924	1826	3757	3305	3063	3509	2624	2084	2303	1987	2195	1939	4566	5613	4262	3590	3682	3600	4517	4348	4387	4209	3859	2815			3331	3795	4803	3768	2641	3123	3626	2995	2091	2168
10-1ng_DNA2b	7475		4511	4087	3484	4097	3109	3901	3575	3887	3508	3092	3322	2797	4995	4687	4642	3790	3038	3130	3367	2871	2943	2616	4294	3926	3317	3406	3629	3256	4371	3699	4517	4213	3163	3267			4221	3931	4569	4373	2618	2741	3874	3770	2876	2322
11-500pg_DNA2c	4595		2224	2084	1619	1919	1667	1445	2293	1864	1962	1574	1451	1351	1970	2844	2257	2091	2056	1854	2006	1720	1702	1613	1635	2075	2133	1560	1710	1970	1954	2272	1965	2206	1557	2201			2796	2617	1954	1820	1433	1539	1939	1961	1369	1506
12-500pg_DNA2a	6133		2415	2694	1900	2576	2614	2351	2135	2219	2827	2092	2354	1977	3894	2344	2973	2996	2574	2492	2050	1606	2225	1840	2494	2328	2739	2462	1751	2340	2919	2397	2208	2833	2408	1813			2347	2864	2208	2352	2366	1835	2744	2792	1963	1267
13-500pg_DNA2b	6066		2624	2691	2101	2569	2350	1827	2140	1863	2437	1842	2703	2008	2856	2790	2231	2056	2366	2018	2072	1911	2986	2083	2118	2728	2747	1919	2230	1539	1961	2812	2056	2126	2246	1430			2823	2792	2496	1927	1603	1668	2506	1654	1906	1629
14-250pg_DNA2c	2685		1037	911	1326	1247	637	747	1391	598	1202	1042	876	1014	1223	968	1607	915	1024	726	743	652	1477	1154	1285	1371	864	976	994	1178	1159	1625	960	913	920	1058			1241	1547	1100	928	767	762	869	863	747	646
15-250pg_DNA2a	2228		1263	750	938	845	1024	573	1112	1243	970	1014	1267	855	1297	1159	1329	1502	989	749	842	930	1039	996	849	1284	979	1145	963	1133	1059	836	1086	1093	1131	906			1214	1332	1153	979	734	779	994	974	983	534
18-150pg_DNA1a	1865		625	498	358	640	629	701	385	573	499	588	575	710	787	568	809	418	764	350	353	389	606	553	550	670	588	660	534	468	748	771	369	595	465	622			659	666	369	315	408	308	283	441	419	266
19-150pg_DNA2b	1558		729	723	667	597	754	871	708	981	611	615	762	773	553	306	682	500	920	1012	672	461	430	542	860	651	895	811	540	240	639	485	633	1042	836	554			641	812	442	283	358	642	742	349	479	622
20-150pg_DNA2c	1882		610	663	695	552	656	682	503	682	933	878	508	879	568	668	468	896	557	333	648	440	370	539	686	768	407	459	736	655	772	626	594	640	682	771			982	726	432	325	525	549	650	530	432	302
21-125pg_DNA2a	1029		538	558	519	589	492	419	624	684	584	425	316	517	449	358	971	600	697	591	421	248	451	588	481	459	301	280	396	447	572	570	477	323	594	390			391	263	554	395	349	232	451	449	301	282
22-125pg_DNA2b	1214		342	387	507	590	263	420	326	185	316	406	474	288	495	601	663	424	758	595	489	340	379	359	580	581	506	332	623	396	640	468	696	570	718	441			682	891	354	241	234	387	611	489	201	265
23-125pg_DNA2c	1411		794	522	676	620	160	397	505	389	378	578	391	403	621	623	491	450	611	513	530	205	579	406	267	911	600	545	588	588	526	820	577	443	431	300			483	589	382	459	420	329	519	394	562	345
24-100pg_DNA2a	696		347	511	258	183	311	529	148	326	210	232	171	239	329	269	467	336	337	404	293	223	349	328	557	552	417	334	377	427	410	335	216	260	344	417			666	374	163	230	331	212	478	241	331	157
25-100pg_DNA2b	707		444	528	437	426	319	324	403	324	335	356	148	209	335	389	329	137	265	401	230	140	171	145	396	199	379	435	306	464	309	251	340	378	424	242			382	459	226	178	175	207	449	374	135	139
26-100pg_DNA2c	1085		166	313	277	355	170	561	342	365	385	357	122	413	394	438	445	201	472	236	393	240	272	320	182	341	404	350	334	214	347	418	343	290	508	166			568	798	233	188	326	236	404	431	268	389
27-75pg_DNA2a	694		347	273	323	300	77	380	344	224	171	271	118	352	396	345	252	164	339	463	134	257	340	531	420	367	162	460	241	536	397	201	303	161	328	261			411	404	263	127	213	375	287	333	317	355
28-75pg_DNA2b	765		519	580	297	497	233	270	446	325	156	242	399	297	281	387	428	133	141	186	140	237	313	296	342	368	287	331	235	471	383	446	240	261	262	282			466	436	198	179	92	179	343	302	201	131
29-75pg_DNA2c	1128		286	531	198	230	268	275	206	419	418	317	401	338	380	379	498	546	681	324	220	417	225	247	193	482	332	186	267	328	404	394	464	472	172	427			411	287	217	246	348	303	342	301	377	105
30-50pg_DNA2a	449		270	200	98	154	102	123	239	118	214	231	243	220	169	216	204	224	213	300	217	98	61	249	302	61	313	235	313	297	154	273	93		152	107			307	213	180	142	108	160	291	175	93	121
31-50pg_DNA2b	641		273	294	186	171	176	89	153	247	263	318	243	87	295	368	230	218	260	473	60	88	283	123	301	361	284	172	310	157	229	167	149	109	181	210			311	106	155	124	98		131	138	113	168
32-50pg_DNA2c	559		361	281	371		193	111	274	446	104	147	119	145	219	185	125	167	106	333	134	205	207	111	193	151	119	177	87	292	312	244	408	350	183	125			329	341	119	190	79	65	323	306	83	100
33-30pg_DNA2a	429		186	176	138	120	106	117	131	111	102	122	142	110	191	423	115	185	172	109	127	120	183		127	213	163	89	58	97	262		154	353	83	89			223		110	58	119	205	148	123	154	133
34-30pg_DNA2b	252				90		124		104	187	117	137	202		125	116	207		302	100	61	58	168		64	147	71	128	269	50	117	129	103	69	134				381		73	74	106	151	123	136	78	94
35-30pg_DNA2c	262		134	164	64	75	269	278	104		210	117			156	199	201	157	195	107	197	123	198	122	114	309	87	79	154	218	97	104	83	64	215	125			194	214	133	216	265	96	68	81	55	51
36-25pg_DNA2a	268		62	103	207	192	222		171		139	161	195		122	80	85		52	52			179				105		124		183		141		98	122			126	199	105	70	68		198		70	137
37-25pg_DNA2b	165		127	89	88		59		187	70	52		98	81	77	116	158	70	87	97	90	90	135	134	118	107	124		130		100	188			140	135			204	55			66		90	70	85	
38-25pg_DNA2c	201		205	172	148	106	65				168				221	103	170	173	118		75	173	83		124	86	85	93	82	139	154	73	102		181				155	109	161		88		110		87	
39-15pg_DNA2a	224		68	72	77	70			73	61	78				56	204	199	91	90		62		101	68	103	61	71		65						167				89				51		96		68	
41-15pg_DNA2b	212								98	64					117				88		70	89	132		169	56	85	51	124		81		103	78	117				167				62		100			
42-15pg_DNA2c	298		51	151	90	58	55		163	67	110	119	91		94						71				104	220	55		52						77				87	78					105		69	74
43-7.5pg_DNA2a	192						122		50		118										60				84	86			87	96			57								63				55			
44-7.5pg_DNA2b	89				73						60		50		68	161	83		71				92	100			147				57	66	66		75				137				73		54			
45-7.5pg_DNA2c			58				56		92						74										113	132			64				66	166	137													
46-3.25pg_DNA2a																											63				53		54						57									
47-3.25pg_DNA2b	58		50	61					51		51				85																57				73													
48-3.25pg_DNA2c	53																		72		58				59																							
49-0pg_a																																																
50-0pg_b																																																
51-0pg_c																																	54															

10. Appendix D – Mixture Results

Mixture Results generated for 2 person Mixture Series 1 on Athena

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 1	**6 M**	**X Y**	**15 17**	**15**	**10 12**	**13 15**	**8 9**	**11 17**	**9 11**	**15 16**	**19 23**	**12**	**9**	**9**	**14 19**	**30**	**9.1 11**	**11 12**	**10**	**10**	**14**	**19 20**	**12 13**	**23 25**	**11 16**
	22 F	**X**	**15 17**	**15 16**	**11**	**14**	**8 11**	**11 19**	**11**	**13 19**	**17**	**11**	**11 15**	**6 9**	**17 18**	**27 31.2**	**8 10**	**9 11**	**8**	******	**14 16**	**21**	**13.2 15**	**21 24**	**11 15**
750pg	**20-1**	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	15 16 19	17 19 23	11 12	9	6 9	14 19	30	9.1 11	11 12	8 10	10	14	19 20 21	12 13	21 23 25 26	11 16
	15-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30	9.1 10 11	9 11 12	8 10	10	14	19 20 21	12 13 13.2 15	21 23 24 25	11 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16 19	17 19 23	11 12	9 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	11 12	14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-15	X Y	15 17	15 16	10 11 12	13 14	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-20	X	15 17	15 16	11	14	8 9 11	11 19	11	13 15 16 19	17 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 10 11	9 11 12	8 10		14 16	19 21	12 13 13.2 15	21 24 25	11 15 16
500pg	**20-1**	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16	17 19 23	11 12	9 11	9	14 18 19	27 30	8 9.1 11	9 11 12	10	10	14	19 20 21	12 13 15	21 23 24 25	11 16
	15-1	X Y	15 17	15	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9	6 9	14 17 18 19	30	8 9.1 11	9 11 12	8 10	10	14 16	19 20 21	12 13	21 23 25	11 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16	17 19 23	11 12	9 15	6 9	14 17 18 19	27 30 31.2	9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	10 11 12	14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10		14 16	19 21	13 13.2 15	21 23 24 25	11 15 16
	1-15	X	15 17	15 16	11 12	14	8 11	11 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	21	13 13.2 15	21 23 24 25	11 15 16
	1-20	X	15 17	15 16	10 11 12	14	8 9 11	11 17 19	9 11	13 15 16 19	17	11 12	9 11 15	6 9	14 17 18	27 30 31.2	8 9.1 10 11	9 11 12	8	10	14 15 16	19 21	12 13 13.2 15	21 23 24 25	11 15
250pg	**20-1**	X Y	15 17	15	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16	17 19 23	11 12	9 15	9	14 17 18 19	30	8 9.1 11	9 11 12	10	10	14	19 20 21	12 13	21 23 24 25	11 15 16
	15-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9	11 17	9 11	15 16 19	19 23	11 12	9	9	14 17 18 19	30	8 9.1 10 11	11 12	8 10	10	14	19 20 21	12 13	21 23 25	11 15 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9	11 17	9 11	13 15 16 19	17 19 23	11 12	9	6 8 9	14 18 19	27 30	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 15	21 23 24 25	11 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2 35	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	11 12	13 14 15	8 9 11	11 19	11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10	9 11 12	8 10	10	14 16	19 20 21	13.2 15	21 23 24 25	11 15
	1-15	X	15 17	15 16	10 11	14 15	8 11	11 19	9 11	13 19	17	11 12	9 11 15	6 9	14 17 18	27 31.2	8 9.1 10 11	9 11	8 10	10	14 15 16	21	12 13 13.2 15	21 24 25	11 15
	1-20	X	15 17	15 16	11	14 15	8 11	11 19	11	13 15 16 19	17 19 23	11	9 11 15	6 9	14 17 18	27 31.2	8 10 11	9 11 12	8 10		14 16	19 21	12 13.2 15	21 24	11 15
100pg	**20-1**	X Y	15 17	15	10 12	13 15	8 9	11 17	9 11	15 16	17 19 23	11 12	9 11	9	14 18 19	30	9.1 11	11 12	8 10	10	14 16	19 20	12 13	23 24 25	11 16
	15-1	X Y	15 17	15	10 12	13 15	8 9	11 17	9 11	13 15 16	19 23	11 12	9	6 9	14 19	30	8 9.1 11	11 12	10	10	14	19 20	12 13	23 25	11 16
	10-1	X Y	15 17	15	10 11 12	13 14 15	8 9	11 17	9 11	15 16	19 23	11 12	9 11 15	6 9	14 19	27 30 31.2	9.1 11	11 12	8 10	10	14	19 20 21	12 13	23 24 25	11 15 16
	4-1	X Y	15 17	15	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16 19	19 23	11 12	9	6 9	14 18 19	27 30	9.1 10 11	9 11 12	8 10	10	14	19 20 21	12 13	23 24 25	11 16
	2-1	X Y	15 17	15	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	9.1 11	9 11 12	8 10	10	14 16	19 20 21	12 13	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11	13 14 15	8 9 11	11	9 11	13 15 16 19	17 19	11 12	9 11	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	13.2 15	21 23 24 25	11 15
	1-2	X Y	15 17	15 16	10 11	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10		14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X	15 17	15 16	11 12	13 14	8 9 11	11 17 19	11	13 16 19	17	11 12	9 11 15	6 9	14 17 18	27 30 31.2	8 10 11	9 11 12	8 10	10	14 16	21	13.2 15	21 24	11 15
	1-10	X	15 17	15 16	10 11	14	8 11	11 19	11	13 15 19	17	11	9 11 15	6 9	14 17 18	27 30 31.2	8 10	9 11	8		14 16	20 21	13.2 15	21 24	11 15
	1-15	X	15 17	15 16	11	13 14	8 11	11 19	11	13 19	17	11 12	11	6 9	17 18	27 31.2	8 10 11	9 11	8		14 16	21	13.2 15	21 24	11 15
	1-20	X	15 17	15 16	11 12	14	8 11	11 19	11	13 19	17	11	11 15	6 9	17 18	27 31.2	8 10	9 11	8		14 16	21	13.2 15	21 24	11 15

Promega

Mixture Results generated for 2 person Mixture Series 2 on Athena

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 2	**15 M**	**X Y**	**17 18**	**12 14**	**11**	**13 14**	**9 12**	**5 12**	**11 13**	**15 20**	**17 25**	**12**	**11 14**	**8 9.3**	**17**	**29 30**	**9 10**	**10 12**	**11**	**10**	**12 13**	**19 21**	**14 14.2**	**18 24**	**15**
	5 F	**X**	**14 16**	**14**	**11 14**	**14**	**9 13**	**5 7**	**12 13**	**12 16**	**16 18**	**12**	**11 14**	**7 9**	**17**	**31.2 32.2**	**8 10**	**10 13**	**8**	******	**9 14**	**21 23**	**13 15.2**	**20 23**	**12 16**
750pg	**20-1**	X Y	14 16 17 18	12 14	11	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 24	12 15
	15-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20 21	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	9 10	10 12 13	8 11	10	12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	10-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 11 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13 14	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 11 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-15	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 10	10 12 13	8 11		9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-20	X	14 16 17 18	12 14	11 14	14	9 13	5 7 12	11 12 13 14	12 16 20	16 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 10	10 12 13	8		9 12 14	19 21 23	13 14 15.2	20 23	12 15 16
500pg	**20-1**	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	9 10	10 12	8 11	10	9 12 13	19 21	13 14 14.2 15.2	18 24	12 15 16
	15-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 20 21	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2	18 20 23 24	15 16
	10-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	15 16
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13 14	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 18 25	12	11 14	7 8 9 9.3	17	29 31.2 32.2	8 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-15	X	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 16 20	16 18 25	12	11 14	7 8 9 9.3	17	30 31.2 32.2	8 10	10 13	8		9 13 14	19 21 23	13 15.2	18 20 23	12 15 16
	1-20	X	14 16 17	14	11 14	14	9 12 13	5 7 12	11 12 13 14	12 15 16	16 18 25	12	11 14	7 8 9 9.3	17	29 31.2 32.2	8 10	10 11 12 13	8 11		9 12 13 14	18.3 21 23	13 14 15.2	20 23	12 16
250pg	**20-1**	X Y	16 17 18	12 14	11	13 14	9 12 13	5 12	11 12 13	15 20	17 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12	11	10	9 12 13 14	19 21	13 14 14.2	18 24	15
	15-1	X Y	14 16 17 18	12 14	11	13 14	9 12	5 12	11 12 13	12 15 16 20	17 25	12	11 14	8 9 9.3	17	29 30 31.2	9 10	10 12	11	10	9 12 13	19 21	14 14.2	18 23 24	15
	10-1	X Y	14 17 18	12 14	11 14	13 14	9 12	5 12	11 12 13	12 15 20	16 17 25	12	11 14	8 9 9.3	17	29 30	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	14 14.2 15.2	18 20 23 24	12 15
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 11 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11		9 12 13 14	19 21 23	13 14.2 15.2	18 20 23	12 15 16
	1-15	X	14 16 17 18	14	11 14	14	9 12 13	5 7	11 12 13	12 16	16 17 18	12	11 14	7 9 9.3	17	29 31.2 32.2	8 10	10 12 13	8		9 12 14	19 21 23	13 14 15.2	20 23 24	12 15 16
	1-20	X Y	14 16	14	11 14	14	9 12 13	5 7	11 12 13	12 16	16 18	12	11 14	7 8 9	17	29 30 31.2 32.2	8 10	10 12 13	8		9 12 14	19 21 23	13 14.2 15.2	20 23	12 16
100pg	**20-1**	X Y	17 18	12 14	11	13 14	9 12	5 12	11 13	15 20	17 25	12	11 14	8 9.3	17	29 30 32.2	9 10	10 12	8 11	10	12 13	19 21	14 14.2	18 24	15
	15-1	X Y	17 18	12 14	11	13 14	9 12	5 12	11 13	15 20	17 25	12	11 14	7 8 9 9.3	17	29 30	9 10	10 12	11	10	12 13 14	19 21	14 14.2	18 24	15
	10-1	X Y	14 17 18	12 14	11	13 14	9 12	5 12	11 12 13	15 16 20	16 17 18 25	12	11 14	8 9.3	17	29 30	9 10	10 12	8 11	10	12 13 14	19 21	14 14.2	18 23 24	15
	4-1	X Y	16 17 18	14	11	13 14	9 12	5 12	11 12 13	12 15 16 20	16 17 25	12	11 14	7 8 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	12 13 14	19 21 23	14 14.2	18 23 24	15
	2-1	X Y	14 17 18	12 14	11 14	13 14	9 12	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14 14.2 15.2	20 23	12 15 16
	1-4	X	14 16 18	14	11 14	13 14	9 12 13	5 7	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14.2 15.2	18 20 23	12 15 16
	1-10	X	14 16 17	14	11 14	14	9 12 13	5 7	11 12 13	12 16	16 18 25	12	11 14	7 8 9	17	30 31.2 32.2	8 10	10 12 13	8	10	9 14	21 23	13 15.2	20 23 24	12 16
	1-15	X	14 16	14	11 14	14	9 13	5 7	12 13	12 16	16 18	12	11 14	7 9	17	31.2 32.2	8 10	10 12 13	8		9 14	21 23	13 15.2	20 23	12 16
	1-20	X	14 16	14	11 14	14	9 13	5 7	12 13	12 16	16 18	12	11 14	7 9	17	30 31.2 32.2	8 10	10 13	8		9 14	21 23	13 14.2 15.2	20 23	12 15 16

Mixture Results generated for 2 person Mixture Series 1 on Newton

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 1	**6 M**	**X Y**	**15 17**	**15**	**10 12**	**13 15**	**8 9**	**11 17**	**9 11**	**15 16**	**19 23**	**12**	**9**	**9**	**14 19**	**30**	**9.1 11**	**11 12**	**10**	**10**	**14**	**19 20**	**12 13**	**23 25**	**11 16**
	22 F	**X**	**15 17**	**15 16**	**11**	**14**	**8 11**	**11 19**	**11**	**13 19**	**17**	**11**	**11 15**	**6 9**	**17 18**	**27 31.2**	**8 10**	**9 11**	**8**	**	**14 16**	**21**	**13.2 15**	**21 24**	**11 15**
750pg	**20-1**	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	15 16 19	17 19 23	11 12	9	9	14 19	30	9.1 11	11 12	8 10	10	14	19 20 21	12 13	23 25	11 15 16
	15-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11	6 9	14 17 18 19	27 30	9.1 10 11	9 11 12	8 10	10	14	19 20 21	12 13 13.2 15	21 23 24 25	11 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16 19	17 19 23	11 12	9 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 14 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-15	X Y	15 17	15 16	10 11 12	13 14	8 9 11	11 17 19	9 11	13 15 16 19 20	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-20	X	15 17	15 16	11	14	8 9 11	11 17 19	11	13 15 16 19	17 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	6 8 10 11	9 11 12	8 10	10	14 16	19 21	12 13 13.2 15	21 24 25	11 15 16
500pg	**20-1**	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16	17 19 23	11 12	9 11	9	14 18 19	27 30	8 9.1 11	9 11 12	10	10	14	19 20 21	12 13 13.2 15	21 23 24 25	11 16
	15-1	X Y	15 17	15	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9	6 9	14 17 18 19	30	8 9.1 11	9 11 12	8 10	10	14 16	19 20 21	12 13 15	21 23 25	11 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 25	11 15 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	10 11 12	14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 21	12 13 13.2 15	21 23 24 25	11 15
	1-15	X	15 17	15 16	11 12	14	8 9 11	11 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	21	12 13 13.2 15	21 23 24 25	11 15 16
	1-20	X	15 17	15 16	10 11 12	14	8 9 11	11 17 19	9 11	13 15 16 19	17	11 12	9 11 15	6 9	14 17 18	27 30 31.2	8 9.1 10 11	9 11 12	8	10	14 15 16	19 21	12 13 13.2 15	21 23 24 25	11 15
250pg	**20-1**	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16	17 19 23	11 12	9 15	9	14 17 18 19	30	8 9.1 10 11	9 11 12	10	10	14	19 20 21	12 13	21 23 24 25	11 15 16
	15-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	15 16 19	17 19 23	11 12	9	9	14 17 18 19	30	8 9.1 10 11	11 12	8 10	10	14	19 20 21	12 13 13.2	21 23 25	11 15 16
	10-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17	9 11	13 15 16 19	17 19 23	11 12	9	6 9	14 18 19	27 30	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 8 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-10	X Y	15 17	15 16	11 12	13 14 15	8 9 11	11 19	11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13.2 15	21 23 24 25	11 15
	1-15	X	15 17	15 16	10 11	14 15	8 11	11 19	9 11	13 19	17	11 12	9 11 15	6 9	14 17 18	27 31.2	8 9.1 10 11	9 11	8 10	10	14 15 16	19 21	12 13 13.2 15	21 24 25	11 15
	1-20	X	15 17	15 16	11	14 15	8 9 11	11 19	11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18	27 31.2	8 10 11	9 11 12	8 10		14 16	19 21	12 13 13.2 15	21 23 24	11 15
100pg	**20-1**	X Y	15 17	15	10 11 12	13 14 15	8 9	11 17	9 11	15 16	17 19 23	11 12	9 11	9	14 18 19	30	8 9.1 10 11	11 12	8 10	10	14 16	19 20	12 13	23 24 25	11 15 16
	15-1	X Y	15 17	15	10 11 12	13 14 15	8 9	11 17	9 11	13 15 16	19 23	11 12	9 11	6 9	14 19	30 31.2	8 9.1 11	11 12	10	10	14	19 20 21	12 13 15	23 24 25	11 16
	10-1	X Y	15 17	15	10 11 12	13 14 15	8 9	11 17	9 11	15 16	17 19 23	11 12	9 11 15	6 9	14 19	27 30 31.2	9.1 11	11 12	8 10	10	14	19 20 21	12 13 15	23 24 25	11 15 16
	4-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	19 23	11 12	9	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14	19 20 21	12 13	21 23 24 25	11 16
	2-1	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-1	X Y	15 16 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-2	X Y	15 17	15 16	10 11 12	13 14 15	8 9 11	11 17 19	9 11	13 14 15 16 19	17 19 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 9.1 10 11	9 11 12	8 10	10	14 15 16	19 20 21	12 13 13.2 15	21 23 24 25	11 15 16
	1-4	X	15 17	15 16	10 11 12	13 14	8 9 11	11 19	9 11	13 15 16 19	17 23	11 12	9 11 15	6 9	14 17 18 19	27 30 31.2	8 10	9 11 12	8 10	10	14 16	20 21	13.2 15	21 23 24 25	11 15 16
	1-10	X	15 17	15 16	10 11	14 15	8 11	11 17 19	9 11	13 15 16 19	17 23	11 12	9 11 15	6 9	14 17 18	27 30 31.2	8 10 11	9 11 12	8 10		14 16	20 21	12 13.2 15	21 24	11 15
	1-15	X Y	15 17	15 16	11 12	13 14	8 11	11 17 19	11	13 15 19	17	11 12	11 15	6 9	17 18	27 31.2	8 10 11	9 11	8		14 16	21	13.2 15	21 23 24 25	11 15
	1-20	X	15 17	15 16	11 12	14	8 11	11 19	11	13 19	17	11	11 15	6 9	17 18	27 31.2	8 10 11	9 11	8 10		14 16	21	13.2 15	21 23 24	11 15

Mixture Results generated for 2 person Mixture Series 2 on Newton

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 2	**15 M**	**X Y**	**17 18**	**12 14**	**11**	**13 14**	**9 12**	**5 12**	**11 13**	**15 20**	**17 25**	**12**	**11 14**	**8 9.3**	**17**	**29 30**	**9 10**	**10 12**	**11**	**10**	**12 13**	**19 21**	**14 14.2**	**18 24**	**15**
	5 F	**X**	**14 16**	**14**	**11 14**	**14**	**9 13**	**5 7**	**12 13**	**12 16**	**16 18**	**12**	**11 14**	**7 9**	**17**	**31.2 32.2**	**8 10**	**10 13**	**8**	**	**9 14**	**21 23**	**13 15.2**	**20 23**	**12 16**
750pg	**20-1**	X Y	14 16 17 18	12 14	11	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 24	12 15
	15-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	15 16 20 21	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	9 10	10 12 13	8 11	10	12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	10-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	30 31.2 32.2	8 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-15	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-20	X	14 16 17 18	12 14	11 14	14	9 13	5 7 12	11 12 13	12 16 20	16 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 10	10 12 13	8	10	9 12 13 14	19 21 23	13 14 15.2	20 23	12 15 16
500pg	**20-1**	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 20	17 18 25	12	11 14	8 9 9.3	17	29 30 31.2 32.2	9 10	10 12 13	8 11	10	9 12 13	19 21 23	13 14 14.2 15.2	18 24	12 15 16
	15-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 20 21	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2	18 20 23 24	15 16
	10-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20 21	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 30.2 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 18 25	12	11 14	7 8 9 9.3	17	29 31.2 32.2	8 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-15	X	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 16 20	16 18 25	12	11 14	7 8 9 9.3	17	30 31.2 32.2	8 10	10 13	8	10	9 13 14	19 21 23	13 15.2	18 20 23 24	12 15 16
	1-20	X	14 16 17 18	12 14	11 14	14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 18 25	12	11 14	7 8 9 9.3	17	29 31.2 32.2	8 10	10 12 13	8 11		9 12 13 14	19 21 23	13 14 15.2	20 23	12 16
250pg	**20-1**	X Y	16 17 18	12 14	11	13 14	9 12 13	5 12	11 12 13	15 16 20	17 25	12	11 14	7 8 9 9.3	17	29 30 31.2	9 10	10 12	11	10	9 12 13 14	19 21	13 14 14.2 15.2	18 20 24	15
	15-1	X Y	14 16 17 18	12 14	11	13 14	9 12	5 7 12	11 12 13	12 15 16 20	17 25	12	11 14	8 9 9.3	17	29 30 31.2	9 10	10 12	8 11	10	9 12 13 14	19 21	13 14 14.2	18 23 24	15 16
	10-1	X Y	14 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 20	16 17 25	12	11 14	8 9 9.3	17	29 30	9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	14 14.2 15.2	18 20 23 24	12 15
	4-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-4	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	12 14	11 14	14	9 12 13	5 7	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11		9 12 13 14	19 21 23	13 14.2 15.2	18 20 23	12 15 16
	1-15	X	14 16 17 18	12 14	11 14	14	9 12 13	5 7	11 12 13	12 16 20	16 17 18	12	11 14	7 9 9.3	17	29 31.2 32.2	8 10	10 12 13	8		9 12 14	19 21 23	13 14 15.2	20 23 24	12 15 16
	1-20	X Y	14 16 17	14	11 14	14	9 12 13	5 7	11 12 13	12 16	16 18	12	11 14	7 8 9	17	29 30 31.2 32.2	8 10	10 12 13	8		9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23	12 16
100pg	**20-1**	X Y	14 17 18	12 14	11	13 14	9 12	5 12	11 13	15 20	17 25	12	11 14	8 9.3	17	29 30 32.2	9 10	10 12	8 11	10	12 13 14	19 21	13 14 14.2	18 24	15
	15-1	X Y	14 16 17 18	12 14	11	13 14	9 12	5 12	11 13	15 16 19 20	17 25	12	11 14	7 8 9 9.3	17	29 30 32.2	9 10	10 12 13	11	10	12 13 14	19 21	13 14 14.2	18 24	15 16
	10-1	X Y	14 16 17 18	12 14	11	13 14	9 12 13	5 12	11 12 13	15 16 20	16 17 18 25	12	11 14	8 9.3	17	29 30	9 10	10 12	8 11	10	12 13 14	19 21	14 14.2	18 23 24	15 16
	4-1	X Y	16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	14 14.2	18 23 24	15
	2-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15
	1-1	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-2	X Y	14 16 17 18	12 14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 8 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	19 21 23	13 14 14.2 15.2	18 20 23	12 15 16
	1-4	X	14 16 18	14	11 14	13 14	9 12 13	5 7 12	11 12 13	12 15 16 20	16 17 18 25	12	11 14	7 9 9.3	17	29 30 31.2 32.2	8 9 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14 14.2 15.2	18 20 23 24	12 15 16
	1-10	X Y	14 16 17 18	14	11 14	14	9 12 13	5 7	11 12 13	12 16	16 18 25	12	11 14	7 8 9 9.3	17	30 31.2 32.2	8 10	10 12 13	8 11	10	9 12 13 14	21 23	13 14.2 15.2	20 23 24	12 16
	1-15	X	14 16	12 14	11 14	14	9 12 13	5 7	12 13	12 16	16 18	12	11 14	7 9	17	31.2 32.2	8 10	10 12 13	8		9 12 14	21 23	13 15.2	20 23 24	12 15 16
	1-20	X	14 16	14	11 14	14	9 13	5 7	11 12 13	12 16	16 18	12	11 14	7 8 9	17	30 31.2 32.2	8 10	10 13	8		9 14	21 23	13 14.2 15.2	20 23	12 15 16

Mixture Results generated for 3 person Mixture Series 1 on Athena. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 1	**12F**	X	16	14 17	10	13 15	9 10	12 15	11	14	19 22	10 11	12	6	16 17	30 31.2	11	11 13	8	**	12 13	17 19	13 15.2	24 25	16
	13M	X Y	15 16	14 16	10	13 14	8	14 17	9 13	13 14	23 24	10	10 11	6 7	14 20	29	11 12	13	8	10	11 14	20	15.2 16	22	11 17
	6M	X Y	15 17	15	10 12	13 15	8 9	11 17	9 11	15 16	19 23	12	9	9	14 19	30	9.1 11	11 12	10	10	14	19 20	12 13	23 25	11 16
750pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 18 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 12 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 18 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
500pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13 16	14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	21 22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13 16	13 14 15 16 18.2	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25 50.2	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 12 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13 16	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
250pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2	22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10	13 14 15	8 9 10	12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 12 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 12 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16 17
100pg	5-1-1	X Y	15 16	14 15 16 17	10	13 14 15	8 9 10	12 15 17	9 11 13	14 16	19 22 23 24	10 11	9 11 12	6 9	14 16 17 20	29 30 31.2	11	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	23 24 25	16
	5-5-1	X Y	15 16 17	14 15 16 17	10	13 14 15	8 9	15 17	9 11 13	13 14	19 22 23 24	10 11 12	10 11 12	6 7 9	14 16 17 20	29 30 31.2	9.1 11 12	11 12 13	8	10	11 12 13 14	17 19 20	13 15.2 16	22 24 25	16 17
	1-1-1	X Y	15 16 17	14 15 17	10 12	13 14 15	8 9	12 15 17	9 11 13	13 14 15 16	19 22 23 24	10 12	9 12	6 7 9	14 16 17 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 14	17 19 20	13 15.2 16	22 23 24 25	11 16
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	15.2 16	22 23 24 25	11 16
	3-2-1	X Y	15 16 17	14 15 16 17	10	13 15	8 9 10	14 17	9 11 13	13 14 15	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 16 17	10	13 14 15	8 9 10	12 15	9 11	13 14 16	19 22 23	10 11	9 11 12	6 7 9	14 16 17	29 30 31.2	11	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2	22 24 25	11 16

Mixture Results generated for 3 person Mixture Series 2 on Athena. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 2	17M	X Y	14 16	11 17	10 14	14	8 12	12	11 12	13 14	19 23	10 13	9 13	6 8	14 17	30 31	11	13	8	10	12 14	18	12 16	20 22	16
	27F	X	12 15	12 15	11 13	14	11 14	7 14	11	18 20	20	12	9 10	9 9.3	16 19	28 29	10	8 12	6 10	**	14	15 18	14.2	21 28	15 16
	9M	X Y	15 16	17	11 14	13 14	8	12 18	11	14 15	19 25	11 12	10 12	9	15 18	30	10 11	10 11	11	10	10 13	17 21	13.2 15.2	23 25	11 15
750pg	5-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	**7** 9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-5-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-1-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31 **32**	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
500pg	5-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 **15.2** 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-5-1	X Y	12 14 15 16	11 12 15 **16** 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31 **32**	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 16	20 21 22 23 28	11 15 16
	1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21.2**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
250pg	5-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 14.2 15.2 16	20 21 22 23 25 28	15 16
	5-5-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	14	8 11 12 14	7 12 14	11 12	13 14 15 18 20	19 20 23	10 11 12 13	9 10 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10	10	10 12 13 14	15 17 18 21	12 13.2 14.2 16	20 21 22 23 25 28	15 16
	1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23	10 11 12 13	9 10 12 13	6 8 9 9.3	14 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	12 13 14	15 17 18 21	12 14.2 15.2 16	20 21 22 23 28	11 15 16
100pg	5-1-1	X Y	14 15 16	11 15 17	10 13 14	13 14	8 12	12	11 12	13 14 15 20	19 23	10 11 12 13	9 10 13	6 8 9 9.3	14 16 17	30 31	10 11	10 12 13	6 8 11	10	10 12 13 14	15 18 21	12 16	20 23	15 16
	5-1-1	X Y	14 15 16	11 15 17	10 13 14	13 14	8 12	12	11 12	13 14 15 20	19 23	10 11 12 13	9 10 13	6 8 9 9.3	14 16 17	30 31	10 11	10 12 13	6 8 11	10	10 12 13 14	15 18 21	12 16	20 23	15 16
	5-5-1	X Y	12 14 15 16	11 15 17	10 11 13 14	14	8 11 12 14	12 14	11 12	13 14 18 20	19 20 23	10 12 13	9 10 12 13	6 8 9 9.3	14 16 17 19	28 30 31	10 11	8 12 13	6 8 10	10	10 12 13 14	15 18	12 14.2 16	20 21 22	15 16
	1-1-1	X Y	12 14 15 16	11 12 17	11	13 14	8 11	7 12 14 18	11 12	13 14 15 18 20	19 23 25	10 11 12	9 10	8 9 9.3	15 16 18 19	28 29 30 31	10 11	10 11 12 13	8 10 11	10	10 12 13 14	17 18 21	12 14.2 15.2	23 25 28	11 16
	1-2-1	X Y	12 14 15 16	12 15 17	11 13 14	13 14	8 11 12 14	7 12 14 18	11	13 14 15 18 20	19 20	10 12	9 10 13	6 8 9	15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18	12 13.2 14.2 15.2	21 25 28	15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 14	13 14	8 12 14	7 12	11 12	13 14 15 18 20	19 20 23 25	12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 12 13	6 8 10 11	10	12 13 14	15 17 18	12 13.2 14.2	20 22 25 28	15 16
	5-2-1	X Y	12 14 15 16	11 12 17	10 11 13 14	13 14	8 11 12	7 12 14	11 12	13 14 15 20	19 20 23	10 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17	28 29 30 31	10 11	8 10 12 13	6 8 10 11	10	10 12 13 14	15 18	12 14.2 16	20 21 22 28	16

Mixture Results generated for 3 person Mixture Series 1 on Newton. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 1	12F	X	16	14 17	10	13 15	9 10	12 15	11	14	19 22	10 11	12	6	16 17	30 31.2	11	11 13	8	**	12 13	17 19	13 15.2	24 25	16
	13M	X Y	15 16	14 16	10	13 14	8	14 17	9 13	13 14	23 24	10	10 11	6 7	14 20	29	11 12	13	8	10	11 14	20	15.2 16	22	11 17
	6M	X Y	15 17	15	10 12	13 15	8 9	11 17	9 11	15 16	19 23	12	9	9	14 19	30	9.1 11	11 12	10	10	14	19 20	12 13	23 25	11 16
750pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 **12** 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 **16** 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 **13** 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	**27.1** 29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
500pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 **18** 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 **12** 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	**27.1** 29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 **12** 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	**10** 14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
250pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2	22 23 24 25	11 16 17
	5-5-1	X Y	15 16 17	14 15 16 17	10	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 **12** 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 **12** 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16 17
100pg	5-1-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	12 15 17	9 11 13	14 15 16	19 22 23 24	10 11	9 10 11 12	6 7 9	14 16 17 20	29 30 31.2	11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16
	5-5-1	X Y	15 16 17	14 15 16 17	10	13 14 15	8 9	12 15 17	9 11 13	13 14	19 22 23 24	10 11 12	10 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16 17
	1-1-1	X Y	15 16 17	14 15 17	10 12	13 14 15	8 9 10	11 12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 11 12	6 7 9	14 16 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16 17
	1-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	12 14 15 17	9 11 13	13 14 15 16	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 17 19 20	29 30 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2 16	22 23 24 25	11 16
	3-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	12 14 17	9 11 13	13 14 15	19 22 23 24	10 11 12	9 10 11 12	6 7 9	14 16 17 19 20	29 30 **30.2** 31.2	9.1 11 12	11 12 13	8 10	10	11 12 13 14	17 19 20	12 13 15.2	22 23 24 25	11 16 17
	5-2-1	X Y	15 16 17	14 15 16 17	10 12	13 14 15	8 9 10	12 15 17	9 11	13 14 15 16	19 22 23	10 11 12	9 11 12	6 7 9	14 16 17	29 30 31.2	11	11 12 13	8 10	10	11 12 13 14	17 19 20	13 15.2 16	22 23 24 25	11 16 17

Mixture Results generated for 3 person Mixture Series 2 on Newton. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
Mixture 2	17M	X Y	14 16	11 17	10 14	14	8 12	12	11 12	13 14	19 23	10 13	9 13	6 8	14 17	30 31	11	13	8	10	12 14	18	12 16	20 22	16
	27F	X	12 15	12 15	11 13	14	11 14	7 14	11	18 20	20	12	9 10	9 9.3	16 19	28 29	10	8 12	6 10	**	14	15 18	14.2	21 28	15 16
	9M	X Y	15 16	17	11 14	13 14	8	12 18	11	14 15	19 25	11 12	10 12	9	15 18	30	10 11	10 11	11	10	10 13	17 21	13.2 15.2	23 25	11 15
750pg	5-1-1	X Y	**11** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13 **14**	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-5-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	**6** 10 11	8 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-1-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	**10** 14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	**9** 12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31 **32**	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
500pg	5-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-5-1	X Y	12 14 15 16	11 12 15 **16** 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20 **21**	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	**10** 14 15 16 17 18 19	28 29 30 31 **32**	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14 **15**	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 **6.1** 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 **13** 14	7 12 **13** 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
250pg	5-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	15 16
	5-5-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 **6.1** 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10	10	10 12 13 14	15 17 18 21	12 13.2 14.2 16	20 21 22 23 25 28	11 15 16
	1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 **17** 18 **19** 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	5-2-1	X Y	12 14 15 16	11 12 **13** 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 **19** 20	19 20 23	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	12 13 14	15 17 18 21	12 14.2 15.2 16	20 21 22 23 25 28	11 15 16
100pg	5-1-1	X Y	14 15 16	11 12 15 **16** 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 20	19 20 23	10 11 12 13	9 10 13	6 8 9 9.3	14 16 17	28 30 31	10 11	10 12 13	6 8 10 11	10	10 12 13 14	15 18 21	12 13.2 14.2 16	20 21 22 23	15 16
	5-5-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	14	8 11 12 14	7 12 14	11 12	13 14 18 19 20	19 20 23	10 12 13	9 10 12 13	6 8 9 9.3	14 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10	10	10 12 13 14	15 18 21	12 14.2 16	20 21 22 25	15 16
	1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 18 20	19 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	21 22 23 25 28	11 15 16
	1-2-1	X Y	12 14 15 16	12 15 17	11 13 14	13 14	8 11 12 14	7 12 14 18	11	13 14 15 18 20	19 20 25	10 12	9 10 12 13	6 8 9	15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 10 11	10	10 12 13 14	15 17 18	12 13.2 14.2 15.2	20 21 22 25 28	15 16
	3-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12 14	7 12 18	11 12	13 14 15 18 20	19 20 23 25	12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 12 13	6 8 10 11	**9** 10	10 12 13 14	15 17 18	12 13.2 14.2 16	20 22 25 28	15 16
	5-2-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12	7 12 14 18	11 12	13 14 15 20	19 20 23 25	10 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17	28 29 30 31	10 11	8 10 12 13	6 8 10 11	10	10 12 13 14	15 18	12 14.2 16	20 21 22 28	15 16

Mixture Results generated for 4 person on Athena. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
	17M	X Y	14 16	11 17	10 14	14	8 12	12	11 12	13 14	19 23	10 13	9 13	6 8	14 17	30 31	11	13	8	10	12 14	18	12 16	20 22	16
	27F	X	12 15	12 15	11 13	14	11 14	7 14	11	18 20	20	12	9 10	9 9.3	16 19	28 29	10	8 12	6 10	**	14	15 18	14.2	21 28	15 16
	9M	X Y	15 16	17	11 14	13 14	8	12 18	11	14 15	19 25	11 12	10 12	9	15 18	30	10 11	10 11	11	10	10 13	17 21	13.2 15.2	23 25	11 15
	28F	X	16 17	16 17.3	11 14	14 15	8 11	13 18	10 11	15 17	17 24	13 14	12 14	7 9	15 19	30 32.2	10 12	9 13	9 11	**	11 13	15 21	15.2 16.2	21 22	15 16
750pg	1-1-1-1	X Y	12 14 15 16 17	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 13 14 18	10 11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16 17	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 13 14 18	10 11 12	13 14 15 17 18 20 21.2	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 14 18	10 11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
500pg	1-1-1-1	X Y	12 14 15 16	11 12 15 17	10 11 13 14	13 14	8 11 12	7 12 14 18	10 11 12	13 14 15 18 20	19 20 23 25	11 12 13	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	9 10 11 12 13	6 8 9 11	10	10 12 13 14	15 17 18 21	12 13.2 15.2 16	20 21 23 25	11 15 16
	1-3-3-1	X Y	9 12 14 15 16	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	19 20 23 25	10 11 12 13 14	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
250pg	1-1-1-1	X Y	12 14 15 16	11 12 15 16 17	10 11 13 14	13 14 15	8 11 12 14	7 12 14 18	11 12	13 14 15 17 18 20 21.2	19 20 23 24 25	10 11 12 13 14	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11	8 10 11 12 13	6 8 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16	11 12 15 16 17	10 11 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 17 18 20	17 19 20 23 25	10 11 12 13	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	12 13 14 15 17 18 20 21.2	17 19 20 23 24 25	10 11 12 13	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
100pg	1-1-1-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	19 20 23 24 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 9 10 11 12 13	6 8 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14 15	8 11 14	7 12 14 18	11 12	13 14 15 17 18 20 21.2	19 20 23 25	10 11 12 13	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16	11 12 17	10 11 14	13 14	8 11	12 18	11 12	13 14 15 18 20	19 20 25	10 11 12 13	9 10 12	8 9	14 15 16 18	28 29 30 31	10 11	8 10 11 12 13	8 9 10 11	10	10 13 14	17 18 21	12 13.2 14.2 15.2	21 23 25	15 16

Mixture Results generated for 4 person on Newton. Red numbers indicate artifacts potentially due to pull up or elevated stutter.

		AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	DYS391	D8S1179	D12S391	D19S433	FGA	D22S1045
	17M	X Y	14 16	11 17	10 14	14	8 12	12	11 12	13 14	19 23	10 13	9 13	6 8	14 17	30 31	11	13	8	10	12 14	18	12 16	20 22	16
	27F	X	12 15	12 15	11 13	14	11 14	7 14	11	18 20	20	12	9 10	9 9.3	16 19	28 29	10	8 12	6 10	**	14	15 18	14.2	21 28	15 16
	9M	X Y	15 16	17	11 14	13 14	8	12 18	11	14 15	19 25	11 12	10 12	9	15 18	30	10 11	10 11	11	10	10 13	17 21	13.2 15.2	23 25	11 15
	28F	X	16 17	16 17.3	11 14	14 15	8 11	13 18	10 11	15 17	17 24	13 14	12 14	7 9	15 19	30 32.2	10 12	9 13	9 11	**	11 13	15 21	15.2 16.2	21 22	15 16
750pg	1-1-1-1	X Y	12 14 15 16 17	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 13 14 18	10 11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13 14	6 **6.1** 7 8 9 9.3	**10** 14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16 17	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 13 14 18	10 11 12	13 14 15 17 18 **19** 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16 17	11 12 15 16 17 17.3	10 11 13 14	13 14 15	8 11 12 14	7 12 14 18	10 11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
500pg	1-1-1-1	X Y	12 14 15 16	11 12 15 17 17.3	10 11 13 14	13 14	8 11 12	7 12 13 14 18	10 11 12	13 14 15 17 18 20	17 19 20 23 25	10 11 12 13	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	9 10 11 12 13	6 8 9 10 11	10	10 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	**9** 12 14 15 16	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	**12** 17 19 20 23 24 25	10 11 12 13	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14 **14.1**	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	19 20 23 25	10 11 12 13 14	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
250pg	1-1-1-1	X Y	**11** 12 14 15 16	11 12 15 16 17	10 11 13 14	13 14 15	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13 14	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31 32.2	10 11	8 10 11 12 13	6 8 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 14	13 14	8 11 12 14	7 12 14 18	11 12	13 14 15 17 18 20	17 19 20 23 25	10 11 12 13	9 10 12 13	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11	8 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16	20 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	**12** 13 14 15 17 18 20	17 19 20 23 24 25	10 11 12 13	9 10 12 13 14	6 7 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14 **14.1**	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
100pg	1-1-1-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14	8 11 12 14	7 12 13 14 18	11 12	13 14 15 17 18 20	19 20 23 24 25	10 11 12 13 14	9 10 12 13	6 8 9 9.3	**10** 14 15 16 17 18 19	28 29 30 31	10 11	8 9 10 11 12 13	6 8 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-3-1	X Y	12 14 15 16 17	11 12 15 16 17	10 11 13 14	13 14 15	8 11 14	7 12 13 14 18	11 12	13 14 15 17 18 20	19 20 23 25	10 11 12 13 14	9 10 12 13	6 8 9 9.3	14 15 16 17 18 19	28 29 30 31	10 11 12	8 9 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2 16 16.2	20 21 22 23 25 28	11 15 16
	1-3-5-1	X Y	12 14 15 16	11 12 15 17 17.3	10 11 13 14	13 14	8 11	7 12 14 18	11 12	13 14 15 18 20	17 19 20 23 25	10 11 12 13	9 10 12 13	8 9	14 15 16 17 18	28 29 30 31 32.2	10 11 12	8 10 11 12 13	6 8 9 10 11	10	10 11 12 13 14	15 17 18 21	12 13.2 14.2 15.2	21 22 23 24 25	11 15 16

Addendum to the Powerplex Fusion Validation, Genemarker HID v2.8.2 Analysis Software Validation, and STRmix Validation

Global filter and DNA input amount evaluation

A large number of artifacts were observed using a 50 RFU analytical threshold. Therefore, a Global Filter evaluation was conducted. Lowering the input amount to 500pg and diluting the instrument matrix to make it less saturated were not successful in removing these artifacts. A global filter was evaluated to determine if artifacts could be reduced without excessive loss of data. Analysis of a portion of the samples run on both Athena and Newton was performed. A Global Max filter was applied during the run wizard, as well as a Min Heterozygote Imbalance (%) filter within the panel settings across all the locations. These samples were analyzed with a 10% filter, 8% filter, 5% filter, 4% filter, and 3% filter set in both locations. After evaluation it was noticed that almost half of the lost alleles could be recovered by going down to a 3% filter, while still greatly reducing the number of artifacts. Therefore, for all evidence and exemplar samples, it was decided that a filter of 3% would be applied for the Global Max filter during the run wizard and across all locations within the panel for the Min Heterozygote Imbalance (%) filter.

However, after beginning work on the STRmix® validation it was determined that the Global Max filter and Min Heterozygote Imbalance filter could not be used during analysis since the filters were removing potential low-level stutter peaks which STRmix® needed to properly analyze the sample. Therefore, to be able to remove both filters, a lower input amount of 525pg was decided upon to achieve fewer artifacts. This is justified because samples amplified with a 525pg input amount achieved the same accuracy and comparable peak height ratios as samples amplified with a 750pg input amount.

The final decision for Powerplex Fusion @ 29 cycles stands as follows:

Global Max Filter: 0%
Min Heterozygote Imbalance Filter: 0%
Optimum DNA Input Amount: 525pg

Based on sensitivity studies and mixture studies, the minimum DNA Input Amount has been set at 37.5pg.