

**FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS**

<b>Manual Appendix for PowerPlex Fusion Stutter Information</b>		
Status: Published		Document ID: 57011
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**Appendix for PowerPlex® Fusion Stutter**

Table 1. Locations without STRmix™ stutter modeling organized (a) by location and (b) by stutter type for STRmix™ and GeneMarker®. \*There are no DBS filters in GeneMarker®. (X)-marked locations are NOT modeled by STRmix™. Note: All locations model back stutter and are not included in the tables.

(a) Stutter modeling by location

	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E
FS						
HBS						X
DBS*	X			X	X	X
	D16S539	D18S51	D2S1338	CSF1PO	Penta D	
FS				X	X	
HBS	X			X	X	
DBS*	X			X	X	
	TH01	vWA	D21S11	D7S820	D5S818	TPOX
FS	X					X
HBS		X	X		X	X
DBS*	X	X		X	X	X
	D8S1179	D12S391	D19S433	FGA	D22S1045	
FS						
HBS	X	X	X	X	X	
DBS*			X		X	

(b) Stutter modeling by stutter type

	FS	HBS	DBS*		FS	HBS	DBS*
D3S1358			X	TH01	X		X
D1S1656				vWA		X	X
D2S441				D21S11		X	
D10S1248			X	D7S820			X
D13S317			X	D5S818		X	X
Penta E		X	X	TPOX	X	X	X
D16S539		X	X	D8S1179		X	
D18S51				D12S391		X	
D2S1338				D19S433		X	X
CSF1PO	X	X	X	FGA		X	
Penta D	X	X	X	D22S1045		X	X

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Table 2. Methods for stutter modeling used by STRmix™ and GeneMarker® by location. For locations that use longest uninterrupted sequence (LUS) or Average, if value is not available, the allele regression line is then used. \*There are no DBS filters in GeneMarker®.

Locus	Back Stutter	Forward Stutter	Half Back Stutter	Double Back Stutter*
D3S1358	Average	Average	Average	
D1S1656	LUS	Average	Allele Regression	Average
D2S441	Average	Average	Average	Average
D10S1248	Allele Regression	Average	Average	
D13S317	Allele Regression	Average	Average	
Penta E	Average	Average		
D16S539	Allele Regression	Average		
D18S51	Allele Regression	Average	Average	Average
D2S1338	Average	Average	Allele Regression	Allele Regression
CSF1PO	Allele Regression			
Penta D	Average			
TH01	LUS		Average	
vWA	Average	Average		
D21S11	Average	Average		Average
D7S820	Allele Regression	Average	Average	
D5S818	Allele Regression	Average		
TPOX	Average			
DYS391				
D8S1179	Average	Average		Average
D12S391	Allele Regression	Average		Allele Regression
D19S433	Average	Average		
FGA	Average	Average		Average
D22S1045	Allele Regression	Average		

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Table 3. Allele-specific stutter filters used in GeneMarker® analysis at NYC OCME. Values highlighted in blue show allele-specific averages. LUS assignments and values based on LUS calculations are highlighted in orange (D1S1656 and TH01).

D3S1358				D1S1656				D2S441				D10S1248				D13S317				Penta E				
Allele	BS	FS	HBS	Allele	LUS	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS
8	3.15%	1.50%	2.34%	8	8	7.29%	6.12%	2.42%	8	8.01%	8.25%	2.25%	8	3.18%	3.68%	1.89%	5	1.47%	3.03%	3.34%	4	1.81%	7.13%	
9	3.94%	1.64%	2.37%	9	9	8.26%	6.09%	2.48%	9	7.95%	8.32%	2.43%	9	4.08%	3.84%	1.89%	6	2.20%	3.26%	3.40%	5	2.11%	1.00%	
10	4.74%	1.78%	2.41%	10	9.5	8.75%	6.06%	2.53%	9.1	3.58%	8.33%	2.44%	10	4.97%	4.00%	1.90%	7	2.94%	3.49%	3.45%	6	2.40%	7.17%	
11	5.54%	1.92%	2.44%	11	11	10.20%	12.44%	2.59%	10	5.99%	7.36%	0.77%	11	5.87%	4.17%	1.90%	7.1	3.02%	3.52%	3.46%	7	1.29%	7.18%	
12	6.33%	2.06%	2.47%	12	11.5	10.69%	3.91%	2.65%	10.1	7.89%	8.40%	2.62%	12	6.76%	7.02%	1.91%	8	3.68%	2.52%	3.15%	8	2.05%	7.20%	
13	7.13%	2.20%	2.50%	13	12	11.17%	8.86%	2.70%	11	8.02%	4.52%	1.21%	13	7.66%	2.69%	1.92%	8.1	3.76%	3.75%	3.51%	9	3.30%	7.22%	
14	7.57%	1.13%	2.54%	13.3	11	10.20%	5.96%	2.72%	11.3	1.97%	15.86%	2.83%	14	8.55%	5.87%	1.92%	9	4.42%	0.42%	2.96%	10	2.09%	1.76%	
14.3	8.17%	2.39%	2.55%	14	13.5	12.63%	5.24%	2.76%	12	11.11%	1.88%	2.95%	15	9.44%	4.00%	1.26%	10	5.16%	2.94%	3.04%	11	4.55%	7.25%	
15	8.48%	1.03%	1.82%	14.3	9	8.26%	5.93%	2.78%	12.3	7.78%	8.57%	3.00%	16	10.34%	6.25%	1.93%	11	5.90%	3.75%	3.51%	11.4	4.02%	7.26%	
15.1	8.80%	2.50%	2.57%	15	14	13.11%	2.75%	2.82%	13	4.17%	10.86%	3.12%	17	11.23%	0.91%	1.93%	12	6.64%	3.45%	3.86%	12	3.96%	5.47%	
15.2	8.88%	2.51%	2.57%	15.3	10.5	9.72%	7.00%	2.84%	13.1	7.73%	8.62%	3.14%	18	12.13%	5.30%	1.94%	12.3	6.86%	4.72%	3.75%	13	4.62%	7.28%	
15.3	8.96%	2.53%	2.58%	16	15.33	14.40%	3.57%	2.88%	13.3	7.72%	8.64%	3.18%	19	13.02%	5.46%	1.94%	13	7.37%	3.48%	3.81%	14	4.37%	0.96%	
16	10.06%	2.14%	4.48%	16.2		13.66%	5.88%	2.89%	14	7.00%	10.40%	6.49%					13.3	7.60%	4.95%	3.80%	14.2	4.85%	7.31%	
16.2	9.68%	2.66%	2.61%	16.3	11	10.20%	1.72%	2.89%	14.3	7.67%	8.71%	3.35%					14	8.11%	10.75%	4.22%	15	5.09%	1.02%	
17	10.31%	2.86%	3.36%	17	16	15.05%	2.00%	2.93%	15	4.92%	2.67%	3.47%					15	8.85%	2.00%	3.90%	15.2	5.15%	7.32%	
17.1	10.40%	2.78%	2.64%	17.1		14.09%	5.85%	2.94%	16	7.58%	8.84%	3.65%					16	9.59%	5.57%	3.95%	16	4.71%	7.34%	
17.2	10.48%	2.80%	2.64%	17.3	12	11.17%	6.63%	2.95%	17	7.53%	8.91%	3.82%					17	10.33%	5.80%	4.01%	16.4	5.51%	7.34%	
18	11.02%	3.46%	1.62%	18	17	16.02%	1.99%	2.99%													17	5.73%	1.14%	
18.1	11.19%	2.92%	2.67%	18.3	13	12.14%	1.94%	3.01%													17.4	5.80%	7.36%	
18.2	11.27%	2.94%	2.67%	19		15.00%	5.79%	3.05%													18	6.05%	27.09%	
18.3	11.35%	2.95%	2.67%	19.3	14	13.11%	1.18%	3.07%													19	5.94%	1.52%	
19	11.91%	3.05%	2.70%	20.3		15.63%	5.75%	3.12%													20	6.58%	7.40%	
20	12.71%	3.19%	2.73%	21		15.96%	5.73%	3.16%													21	8.09%	1.13%	
20.1	12.79%	3.21%	2.73%																		22	8.59%	7.44%	
21	13.51%	3.33%	2.76%																		23	7.34%	7.45%	
																					24	7.77%	7.47%	
																					25	8.07%	7.49%	

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D16S539				D18S51				D2S1338				CSF1PO				Penta D				D18S51 continued			
Allele	BS	FS	HBS	Allele	BS	FS	HBS	Panel	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS
4	2.54%	2.00%		7	4.05%	1.64%	1.55%	10	5.61%	10.21%	0.56%	5	2.40%			2.2	0.81%			18.1	11.95%	2.48%	1.18%
5	3.26%	2.15%		8	4.76%	1.72%	1.52%	11	6.09%	10.22%	0.66%	6	3.27%			3.2	1.05%			18.2	12.02%	2.48%	1.18%
6	3.98%	2.30%		9	5.48%	1.79%	1.49%	12	6.57%	10.23%	0.75%	7	4.14%			5	1.48%			19	12.59%	1.83%	0.68%
7	4.70%	2.45%		9.2	5.62%	1.81%	1.48%	13	7.04%	10.24%	0.85%	7.3	4.40%			6	1.71%			19.2	12.74%	2.56%	1.14%
8	5.42%	2.60%		10	6.19%	1.87%	1.45%	14	7.52%	10.25%	0.95%	8	5.00%			6.4	1.81%			20	13.30%	4.82%	1.11%
8.3	5.64%	2.64%		10.2	6.33%	1.88%	1.45%	15	8.00%	10.26%	1.05%	8.1	5.09%			7	1.95%			20.2	13.45%	2.63%	1.11%
9	6.15%	1.06%		11	6.90%	1.94%	1.42%	16	8.66%	0.73%	1.14%	8.3	5.27%			7.4	2.05%			21	14.02%	2.69%	1.08%
9.3	6.36%	2.79%		11.2	7.04%	1.96%	1.41%	17	7.30%	20.48%	1.24%	9	5.87%			8	2.65%			21.1	14.09%	2.70%	1.08%
10	6.87%	1.97%		12	7.61%	2.69%	2.30%	18	8.73%	10.29%	1.34%	9.1	5.96%			8.2	2.24%			21.2	14.16%	2.71%	1.07%
10.3	7.08%	2.94%		12.2	7.75%	2.03%	1.38%	18.3	9.57%	10.30%	1.37%	10	6.74%			9	1.45%			22	14.73%	3.84%	1.05%
11	7.59%	5.00%		12.3	7.82%	2.04%	1.37%	19	9.24%	2.80%	1.43%	10.1	6.83%			9.2	2.48%			22.2	14.87%	2.78%	1.04%
11.3	7.80%	3.09%		13	8.32%	1.61%	1.17%	19.3	10.04%	10.31%	1.46%	10.2	6.91%			9.4	2.52%			23	15.44%	2.84%	1.01%
12	8.31%	3.90%		13.1	8.39%	2.10%	1.35%	20	10.50%	11.77%	1.53%	10.3	7.00%			10	2.53%			23.2	15.58%	2.86%	1.01%
12.1	8.38%	3.21%		13.2	8.47%	2.11%	1.34%	21	11.58%	3.98%	1.63%	11	7.61%			11	2.32%			24	16.15%	2.92%	0.98%
12.2	8.45%	3.23%		13.3	8.54%	2.12%	1.34%	22	9.85%	4.80%	1.72%	11.1	7.69%			11.1	2.93%			24.2	16.29%	2.93%	0.97%
13	9.03%	2.87%		14	9.03%	1.29%	0.96%	22.2	11.42%	10.34%	1.74%	11.3	7.87%			11.2	2.95%			25	16.86%	2.99%	0.95%
13.3	9.24%	3.39%		14.2	9.18%	2.18%	1.31%	23	11.69%	2.12%	1.82%	12	8.47%			12	2.43%			26	17.57%	3.07%	0.91%
14	9.75%	1.99%		15	9.75%	1.43%	0.81%	23.2	11.90%	10.35%	1.84%	12.1	8.56%			12.1	3.17%			27	18.29%	3.14%	0.88%
15	10.47%	3.64%		15.2	9.89%	2.26%	1.28%	23.3	11.95%	10.35%	1.85%	12.3	8.73%			12.2	3.19%						
16	11.19%	3.79%		15.3	9.96%	2.27%	1.27%	24	13.02%	4.45%	1.92%	13	9.34%			13	2.70%						
				16	10.46%	1.53%	0.77%	24.2	12.38%	10.36%	1.94%	13.3	9.60%			13.4	3.47%						
				16.1	10.53%	2.33%	1.25%	25	13.30%	16.07%	2.01%	14	10.21%			14	4.26%						
				16.2	10.60%	2.33%	1.24%	26	16.31%	10.38%	2.11%	15	11.07%			14.1	3.64%						
				16.3	10.67%	2.34%	1.24%	27	13.71%	10.39%	2.21%	16	11.94%			14.4	3.71%						
				17	11.17%	1.92%	0.85%	28	14.18%	10.40%	2.31%					15	4.38%						
				17.2	11.31%	2.41%	1.21%	29	14.66%	10.41%	2.40%					16	4.09%						
				17.3	11.38%	2.42%	1.21%									17	4.33%						
				18	11.88%	3.34%	0.69%									18	4.57%						

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TH01				vWA				D21S11				D7S820				D5S818				TPOX				
Allele	LUS	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS	Allele	BS	FS	HBS
3	3	1.71%		1.32%	10	3.87%	6.71%		23.2	9.50%	3.03%		5	1.99%	3.58%	2.55%	5	1.27%	1.99%		4	0.93%		
4	4	2.27%		1.32%	11	4.83%	6.60%		23.3	9.54%	3.03%		5.2	2.16%	3.57%	2.54%	6	2.25%	2.13%		5	1.53%		
5	5	2.82%		1.31%	12	5.63%	6.48%		24	9.76%	3.05%		6	2.85%	3.55%	2.49%	7	3.24%	2.27%		6	2.13%		
5.3		4.13%		1.31%	13	6.76%	6.36%		24.2	9.83%	3.06%		6.3	3.10%	3.54%	2.48%	8	4.22%	2.41%		7	2.73%		
6	6	3.37%		1.07%	14	7.83%	11.80%		24.3	9.86%	3.06%		7	3.70%	3.52%	2.44%	9	5.20%	2.56%		7.1	2.79%		
6.1		4.16%		1.31%	15	8.46%	0.87%		25	10.09%	3.08%		7.1	3.79%	3.52%	2.44%	10	6.18%	2.10%		7.3	2.91%		
6.3	3	1.71%		1.31%	15.2	8.88%	6.11%		25.2	10.15%	3.09%		7.3	3.96%	3.52%	2.43%	10.1	6.28%	2.71%		8	2.78%		
7	7	3.92%		0.91%	16	6.41%	6.02%		25.3	10.18%	3.09%		8	4.56%	3.01%	2.26%	11	7.16%	2.84%		9	3.93%		
7.1		4.21%		1.30%	16.1	9.75%	6.01%		26	10.41%	3.11%		8.1	4.65%	3.49%	2.39%	11.1	7.26%	2.85%		10	4.53%		
7.3		4.22%		1.30%	17	9.42%	1.76%		26.2	10.48%	3.11%		8.2	4.73%	3.49%	2.38%	12	8.14%	2.62%		10.1	4.59%		
8	8	4.48%		1.70%	18	10.80%	8.98%		27	10.73%	3.14%		8.3	4.82%	3.49%	2.38%	12.1	8.24%	3.00%		10.3	4.71%		
8.3	5	2.82%		1.30%	18.2	11.78%	5.76%		27.1	10.77%	3.14%		9	5.42%	3.47%	1.45%	12.3	8.43%	3.03%		11	5.38%		
9	9	5.03%		0.88%	18.3	11.88%	5.75%		27.2	10.80%	3.14%		9.1	5.50%	3.46%	2.34%	13	9.12%	3.25%		12	7.12%		
9.1		4.30%		1.29%	19	12.19%	1.89%		28	7.85%	6.31%		9.2	5.59%	3.46%	2.33%	14	10.10%	3.27%		13	6.33%		
9.3	6	3.37%		1.51%	20	12.23%	1.76%		28.1	11.09%	3.17%		9.3	5.67%	3.46%	2.33%	15	11.08%	5.71%		14	6.93%		
10	10	5.58%		1.29%	21	11.17%	5.44%		28.2	11.12%	3.17%		10	6.28%	4.37%	2.08%	16	12.06%	3.55%		15	7.53%		
10.3	6	3.37%		1.29%	22	15.45%	5.32%		28.3	11.16%	3.17%		10.1	6.36%	3.44%	2.29%	17	13.04%	3.69%		16	8.13%		
11	11	6.13%		1.29%	23	16.41%	5.21%		29	10.19%	2.89%		10.3	6.53%	3.43%	2.28%	18	14.02%	3.84%					
13.3	8	4.48%		1.28%	24	17.38%	5.09%		29.1	11.42%	3.20%		11	7.13%	3.51%	1.75%	19	15.01%	3.98%					
					25	18.34%	4.97%		29.2	11.45%	3.20%		11.1	7.22%	3.41%	2.24%								
									29.3	11.48%	3.20%		11.2	7.30%	3.41%	2.23%								
									30	13.62%	2.41%		11.3	7.39%	3.40%	2.23%								
									30.1	11.74%	3.22%		12	7.99%	2.20%	2.04%								
									30.2	11.23%	2.47%		12.1	8.08%	3.38%	2.19%								
									30.3	11.80%	3.23%		12.3	8.25%	3.38%	2.18%								
									31	12.03%	3.25%		13	8.85%	3.36%	2.14%								
									31.1	12.06%	3.25%		13.1	8.93%	3.35%	2.14%								
									31.2	11.87%	2.62%		14	9.70%	3.33%	2.09%								
									31.3	12.13%	3.26%		14.1	9.79%	3.32%	2.09%								
									32	11.47%	3.28%		15	10.56%	3.30%	2.04%								
									32.1	12.39%	3.28%		16	11.42%	3.27%	1.99%								

D21S11 continued			
Allele	BS	FS	HBS
32.2	9.58%	2.22%	
32.3	12.45%	3.29%	
33	12.68%	3.31%	
33.1	12.71%	3.31%	
33.2	11.91%	6.69%	
33.3	12.78%	3.31%	
34	13.00%	3.33%	
34.1	13.04%	3.34%	
34.2	13.07%	3.34%	
34.3	13.10%	3.34%	
35	13.33%	3.36%	
35.1	13.36%	3.37%	
35.2	11.09%	3.37%	
36	13.65%	3.39%	
36.1	13.69%	3.39%	
36.2	13.72%	3.40%	
37	13.98%	3.42%	
37.2	14.04%	3.43%	
38	14.30%	3.45%	
38.2	14.37%	3.45%	
39	14.63%	3.48%	

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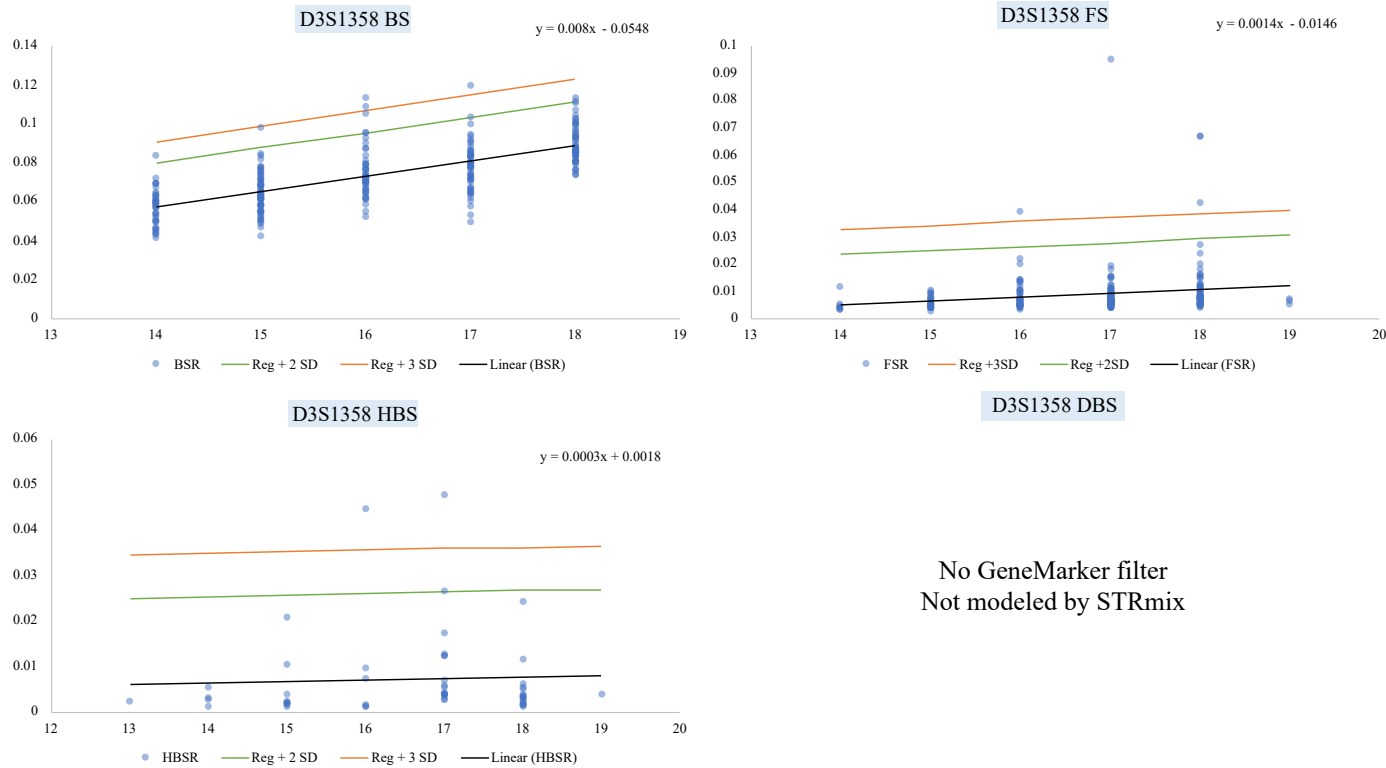
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6	7.00%	2.87%		13	5.59%	3.40%		5.2	4.09%	16.66%		12.2	5.32%	4.79%		6	0.61%	9.37%		25	10.50%	7.63%	
7	7.50%	2.89%		14	6.74%	3.49%		6	4.68%	16.00%		13	5.69%	5.03%		7	2.08%	10.10%		25.1	11.24%	8.76%	
8	5.10%	2.91%		15	7.89%	3.58%		6.2	4.83%	15.83%		14	6.15%	5.34%		8	3.56%	10.83%		25.2	11.28%	8.79%	
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12	10.54%	4.18%		17.3	10.55%	3.79%		9	6.92%	13.49%		16.2	7.15%	6.02%		12	9.45%	16.28%		26.2	11.74%	9.10%	
12.3	10.16%	2.98%		18	11.35%	4.84%		9.2	7.07%	13.33%		17	7.52%	6.26%		13	10.93%	14.47%		26.3	11.79%	9.13%	
13	9.94%	3.32%		18.1	11.47%	3.86%		10	7.67%	12.66%		17.2	7.61%	6.33%		14	12.40%	7.11%		27	12.11%	9.34%	
13.2	10.61%	3.00%		18.3	11.70%	3.88%		10.2	7.82%	12.49%		18	7.98%	6.57%		15	13.88%	18.23%		27.2	12.20%	9.40%	
13.3	10.66%	3.00%		19	12.51%	3.94%		11	4.13%	11.82%		18.2	8.07%	6.63%		16	15.35%	15.12%		27.3	12.24%	9.43%	
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15	10.44%	2.45%		20	13.66%	2.70%		12	10.62%	10.99%		19.2	8.53%	6.94%		19	19.77%	18.85%		28.3	12.70%	9.74%	
15.1	11.56%	3.03%		20.1	13.77%	4.04%		12.1	9.24%	10.91%		19.3	8.58%	6.97%		20	21.25%	19.58%		29	13.02%	9.96%	
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18	13.91%	1.35%		22	15.96%	2.66%		13.2	10.06%	9.99%		20.3	9.03%	7.28%						30.2	13.57%	10.33%	
19	13.51%	3.10%		22.3	16.31%	4.23%		14	9.47%	4.62%		21	8.87%	7.50%						31	13.94%	10.57%	
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								19	14.38%	5.15%		24.2	10.82%	8.48%						49.2	22.29%	16.18%	
								19.2	14.53%	4.98%		24.3	10.87%	8.51%						50.2	22.75%	16.48%	
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# FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

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Table 4. Stutter ratio (SR) data collected for each location, allele, and stutter type. GeneMarker® filters were determined using a value two standard deviations above either the average value, the allele regression line, or the LUS regression line. Graphs show the stutter ratio on the y-axis and allele number of the parent allele or LUS value on the x-axis.



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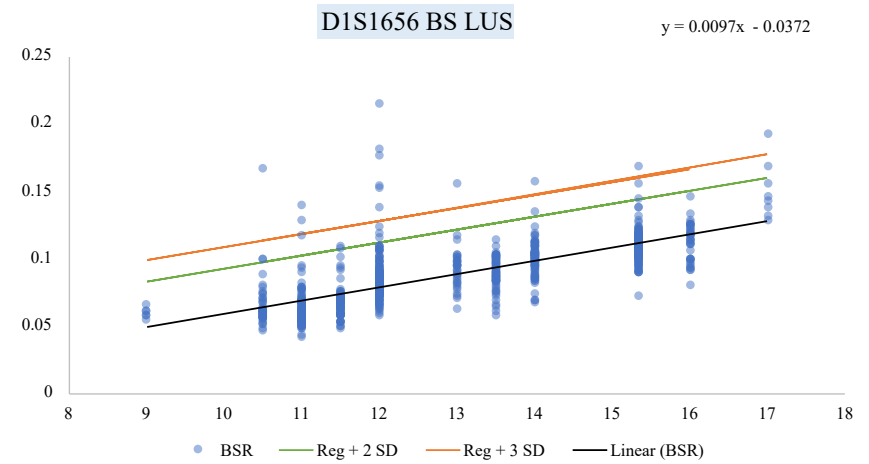
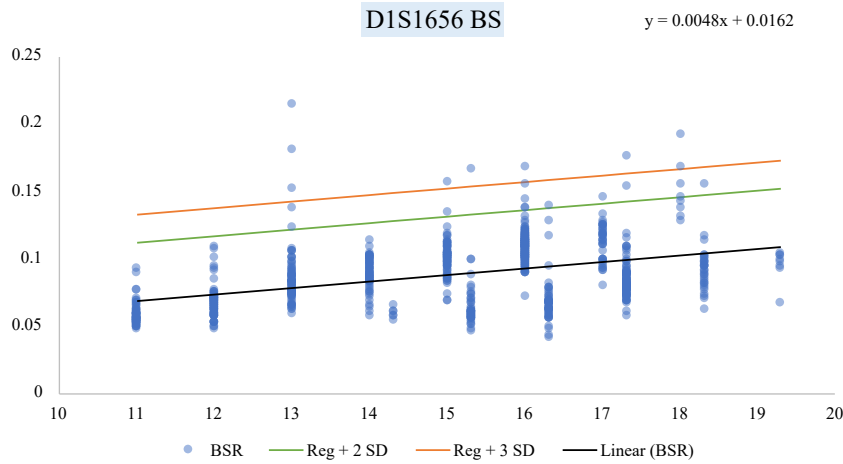
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Allele	LUS Allele
11	11
12	11.5
13	12
14	13.5
14.3	9
15	14
15.3	10.5
16	15.33
16.3	11
17	16
17.3	12
18	17
18.3	13
19.3	14

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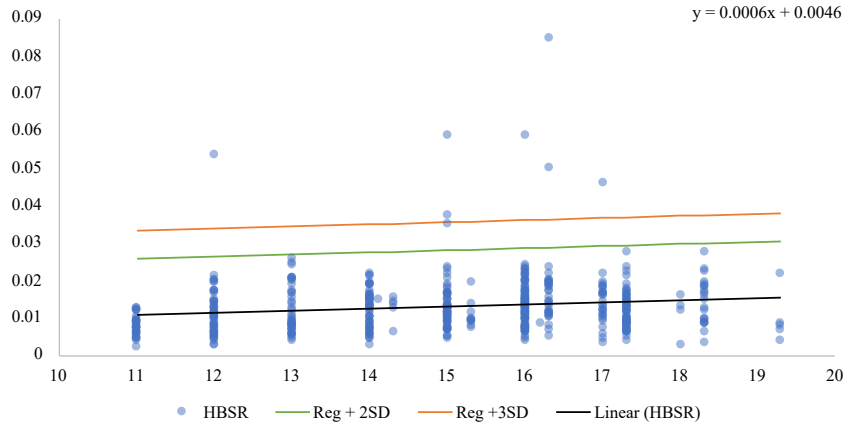
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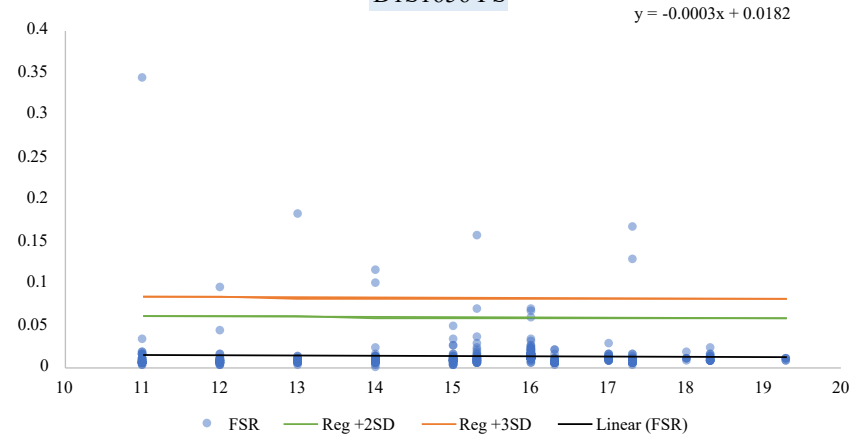
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(See LUS for BS)

**DIS1656 HBS**

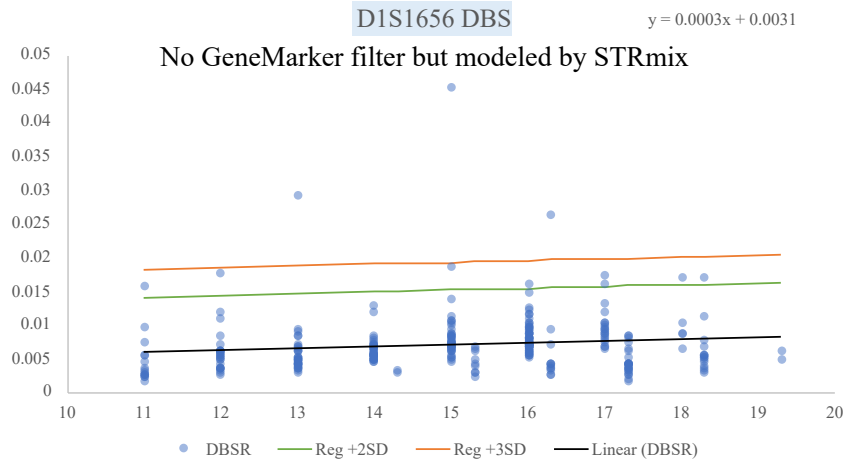


**D1S1656 FS**



**D1S1656 DBS**

No GeneMarker filter but modeled by STRmix



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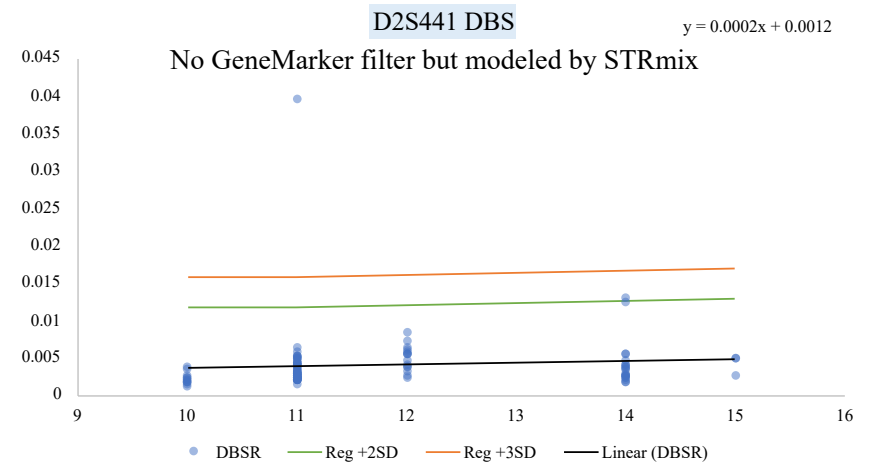
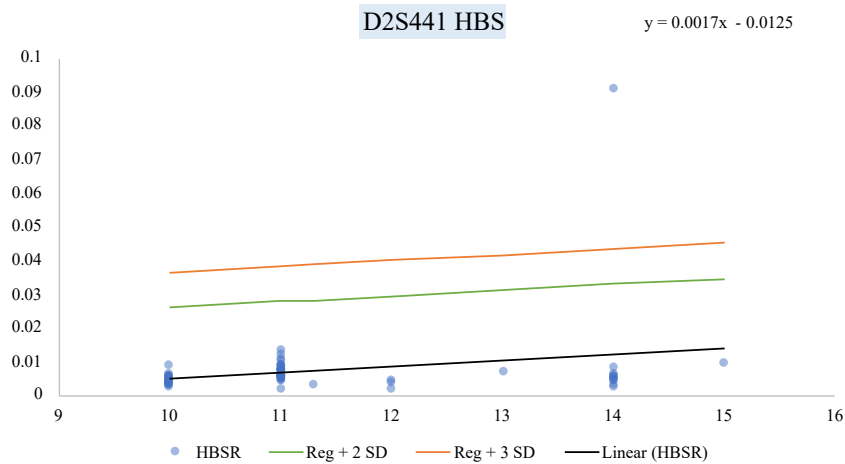
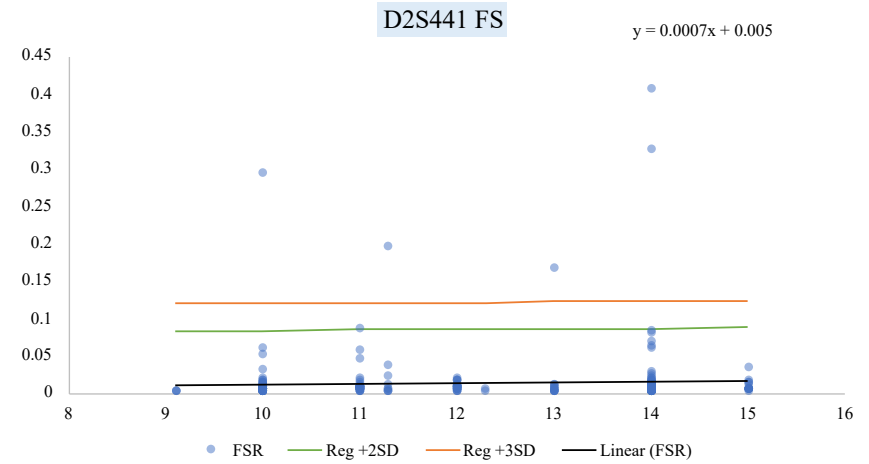
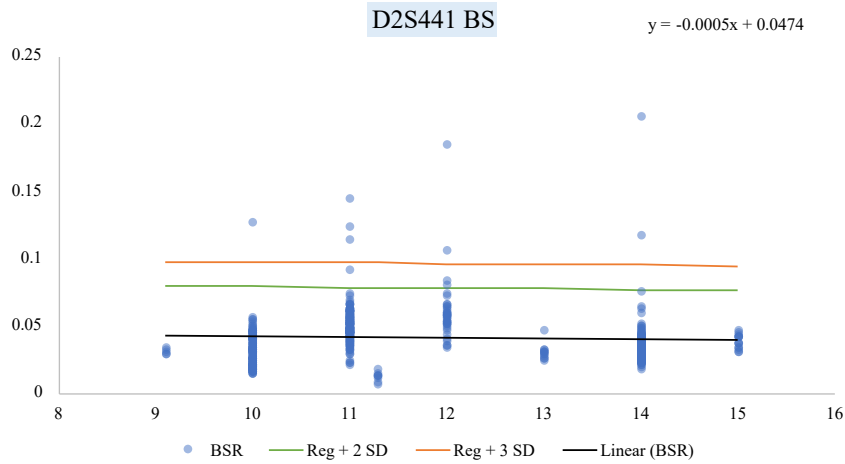
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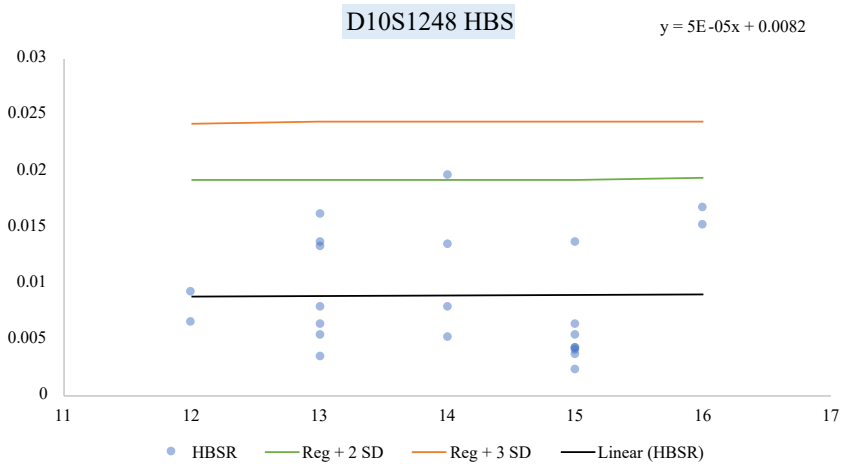
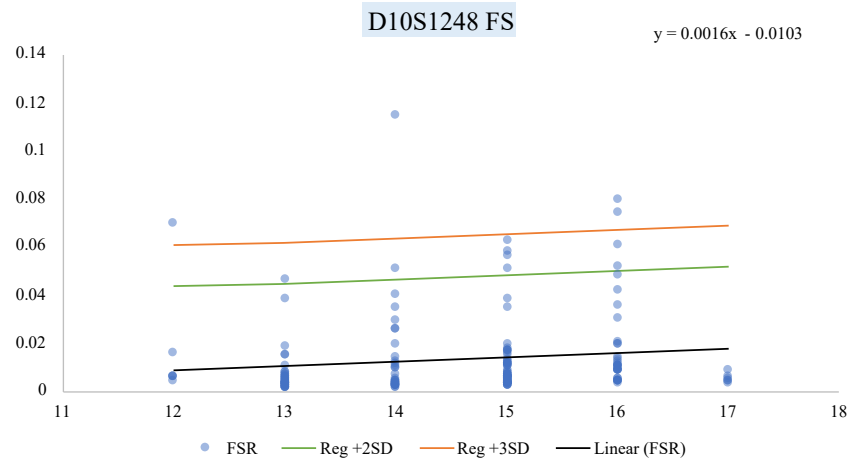
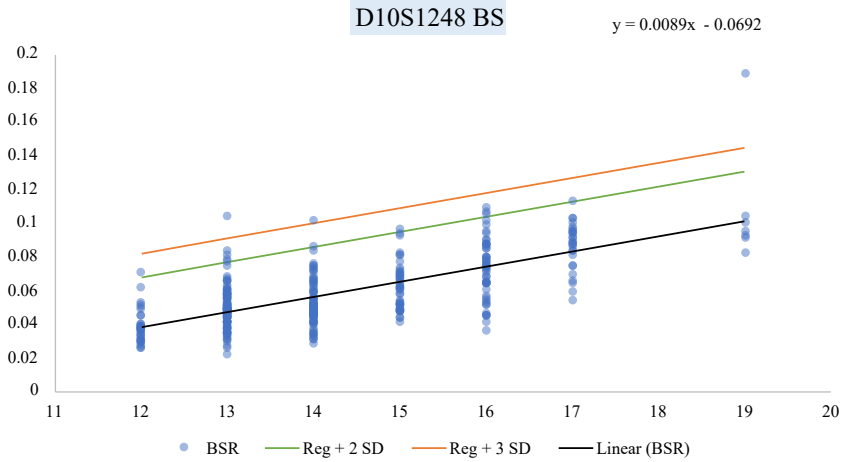
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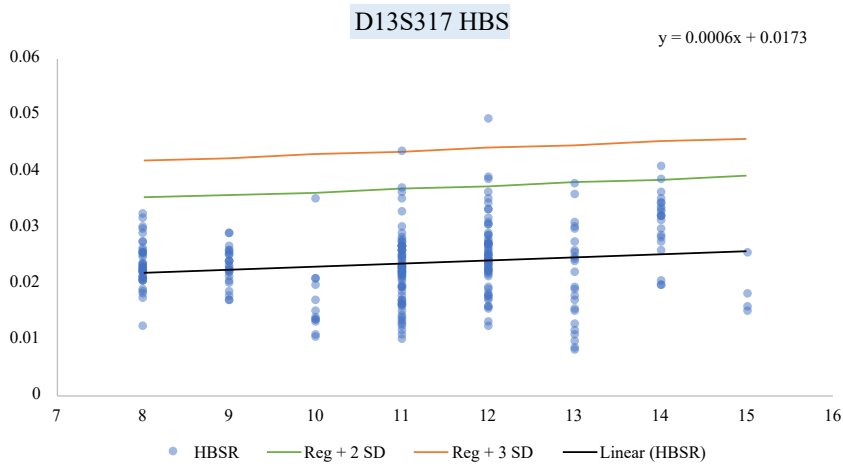
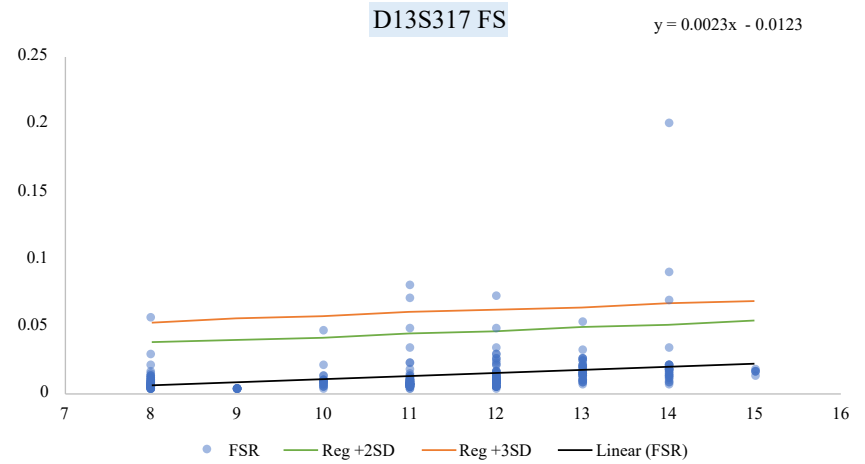
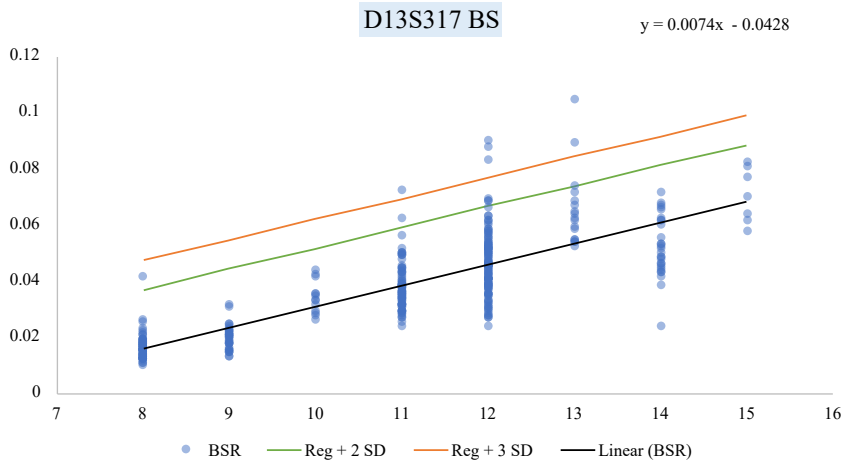
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Not modeled by STRmix

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**D13S317 DBS**

No GeneMarker filter  
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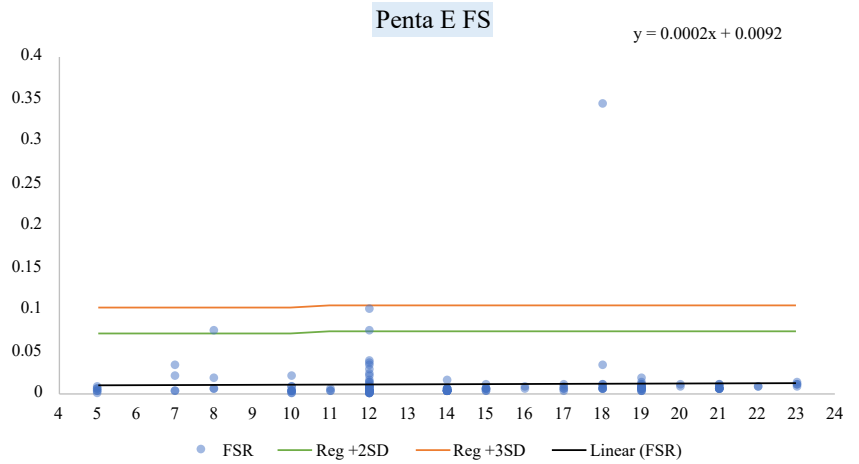
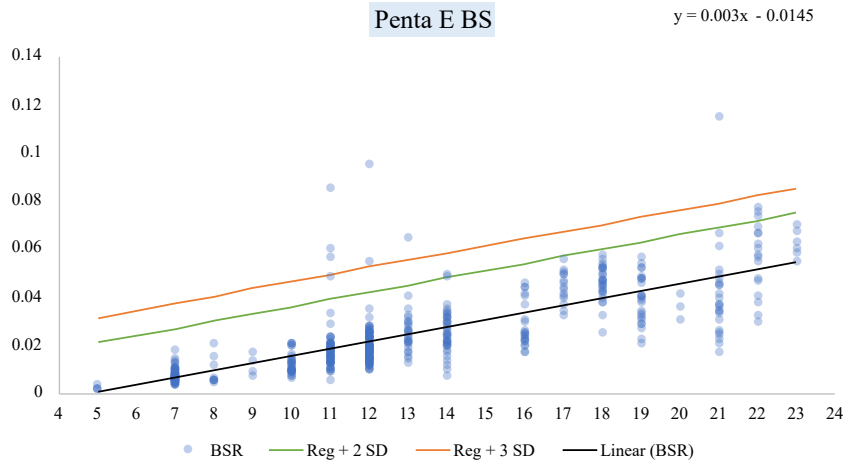
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Penta E HBS

Penta E DBS

No GeneMarker filter  
Not modeled by STRmix

No GeneMarker filter  
Not modeled by STRmix

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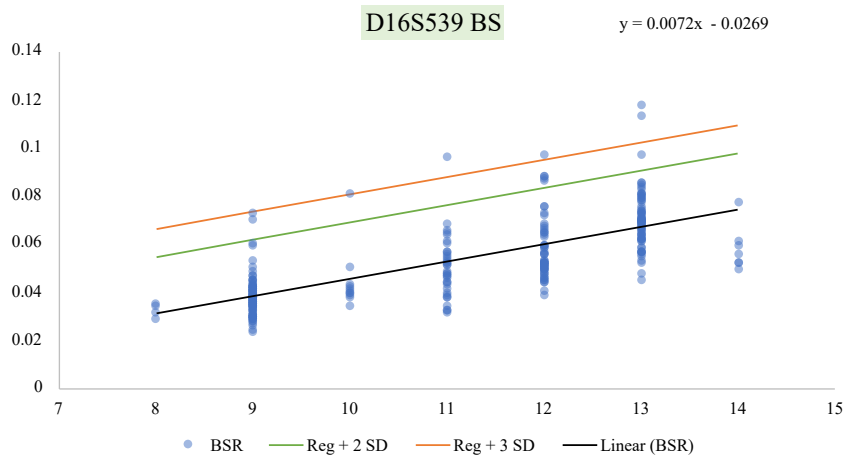
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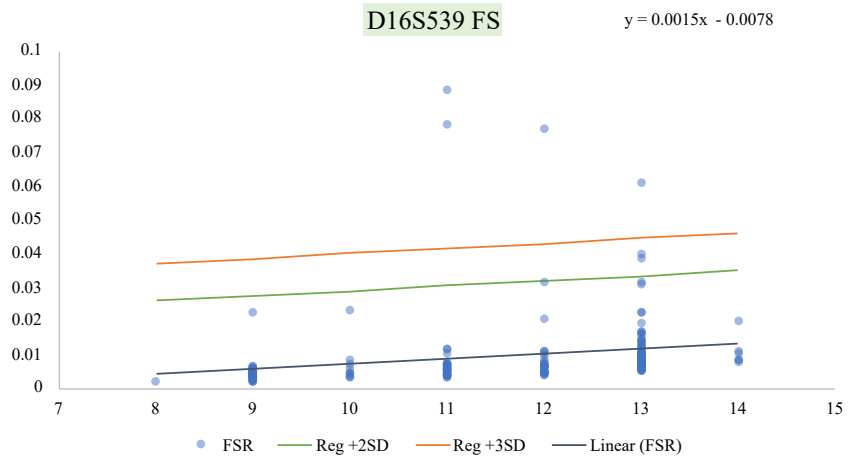
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**D16S539 HBS**

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**D16S539 DBS**

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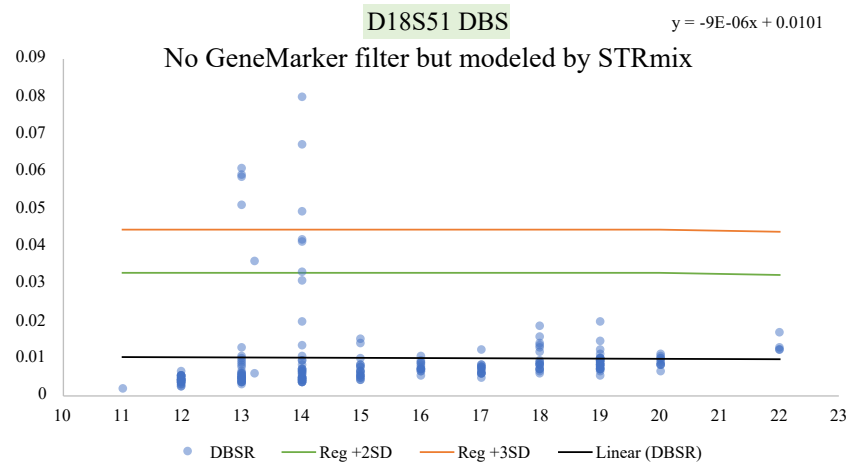
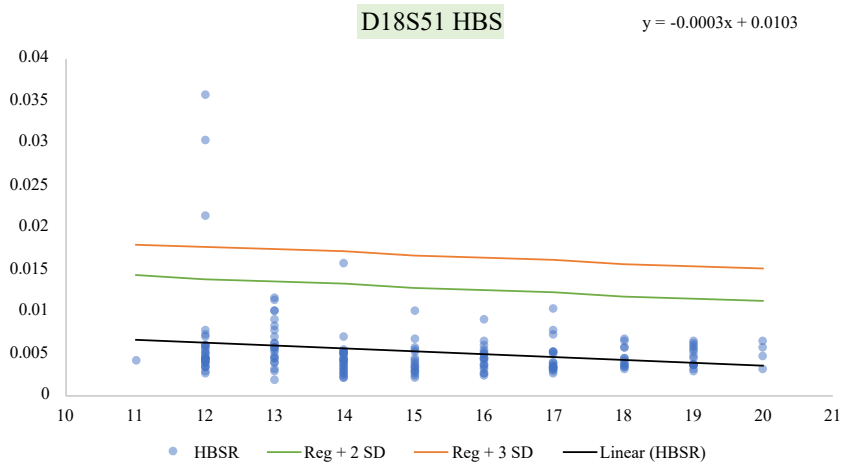
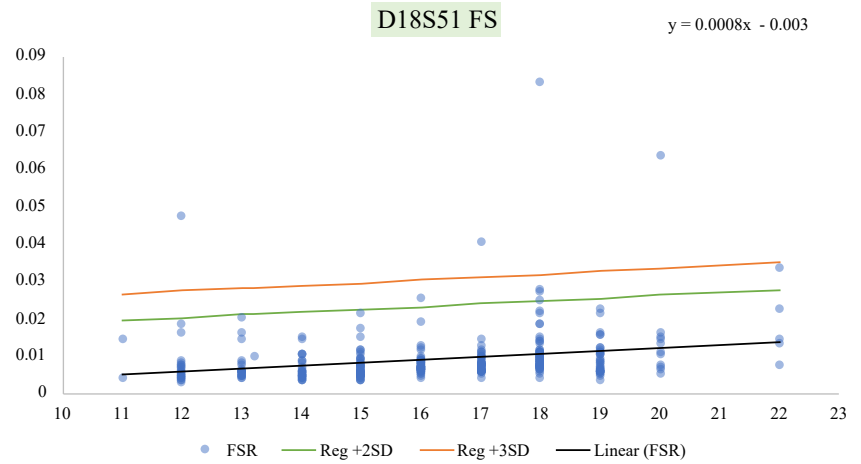
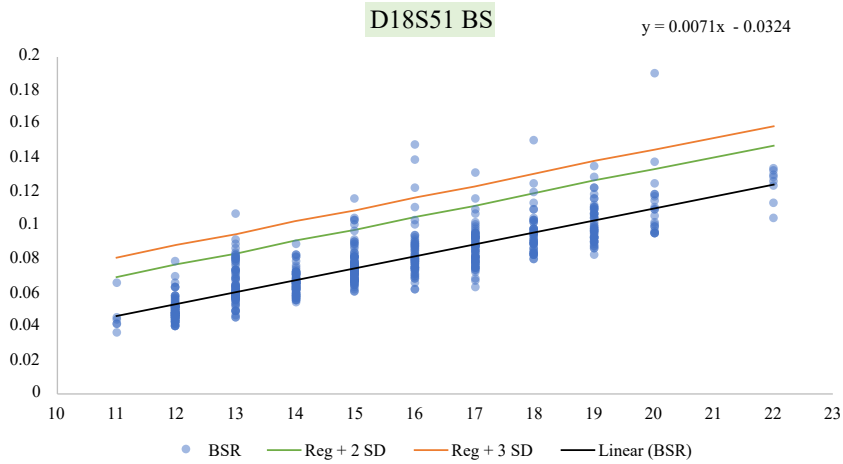
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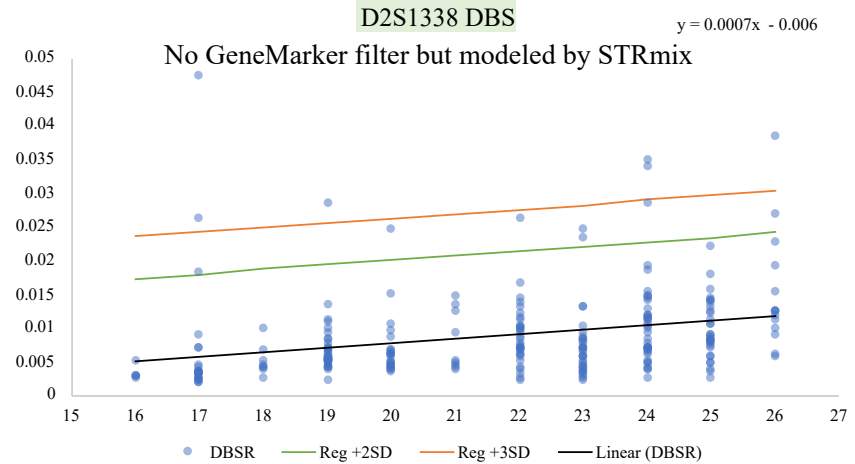
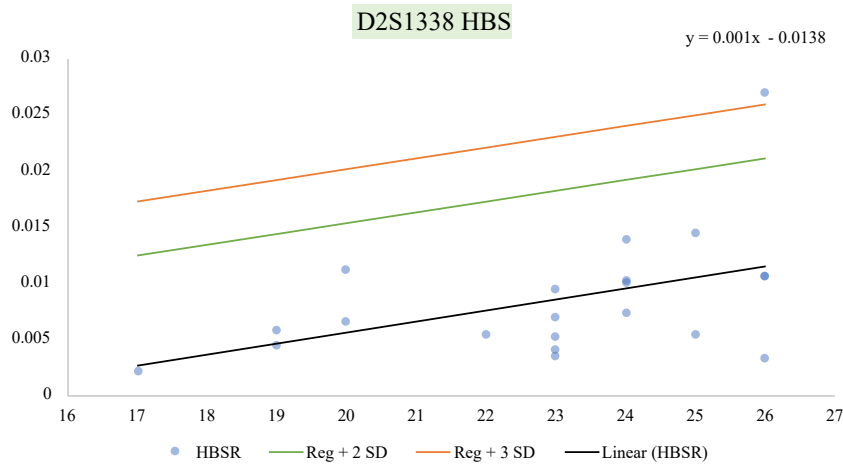
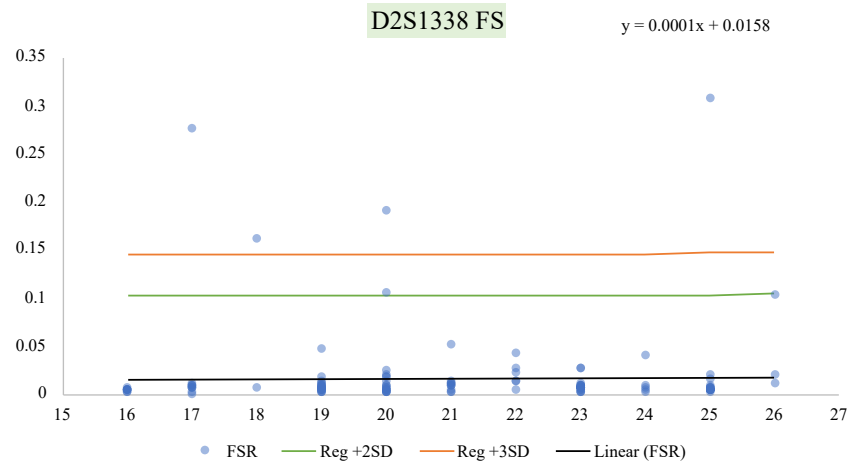
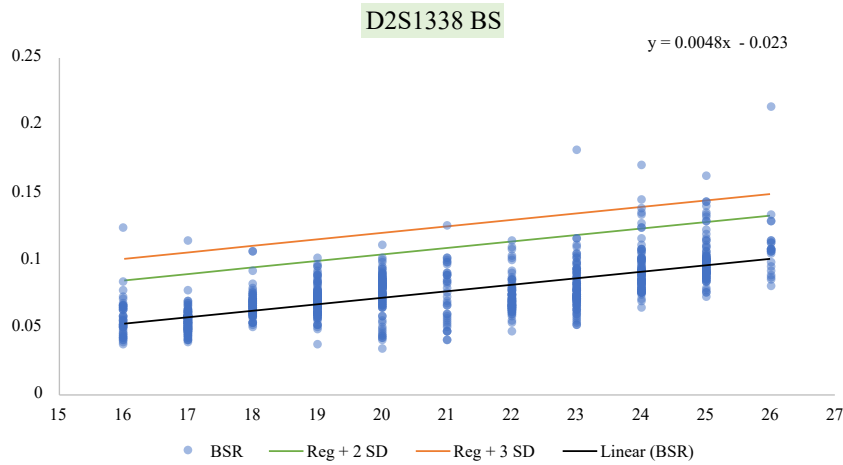
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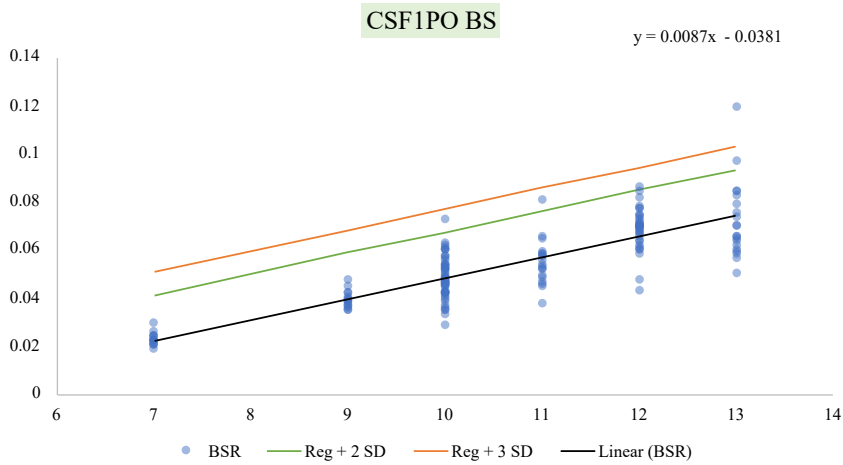


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**CSF1PO FS**

No GeneMarker filter  
Not modeled by STRmix

**CSF1PO HBS**

No GeneMarker filter  
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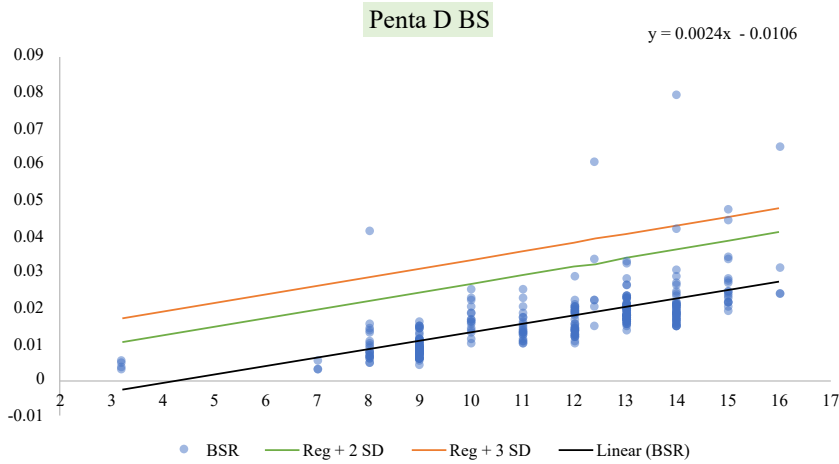
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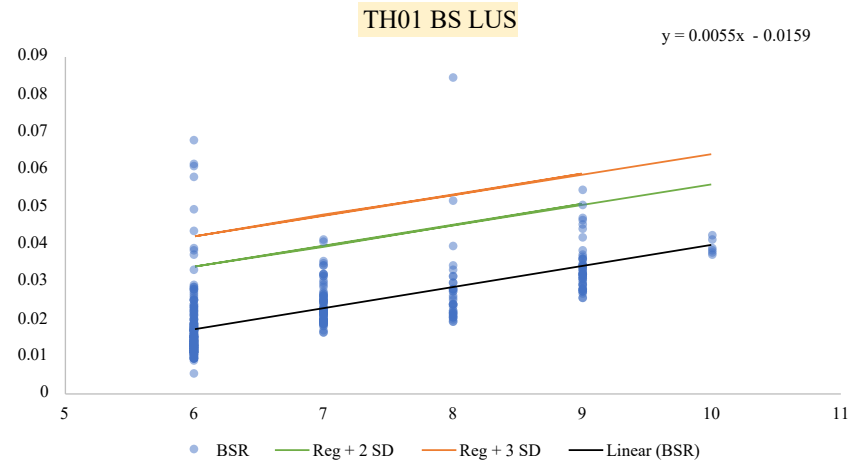
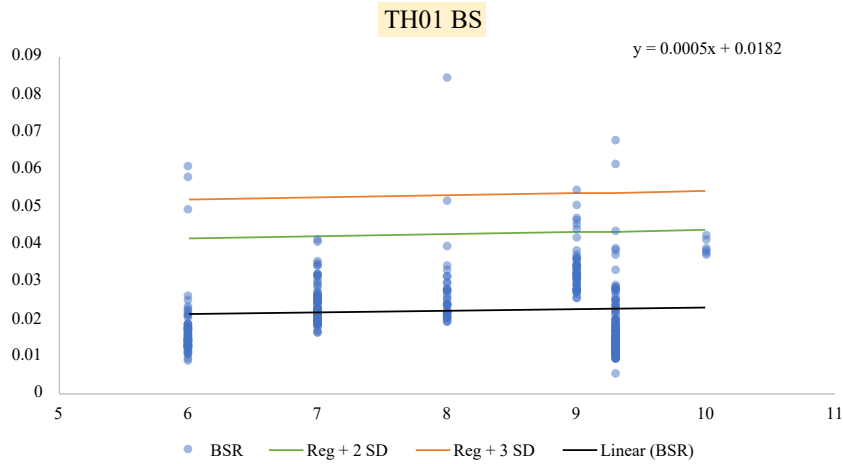
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Allele	LUS Allele
6	6
7	7
8	8
9	9
9.3	6
10	10

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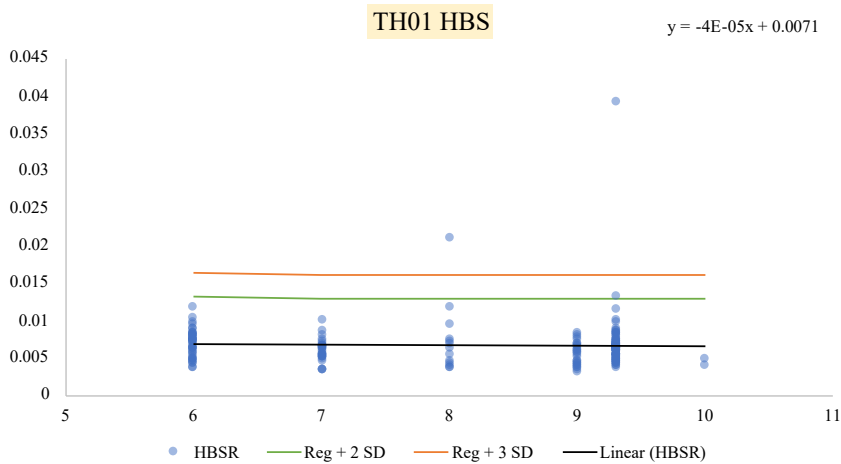
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TH01 FS

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TH01 DBS

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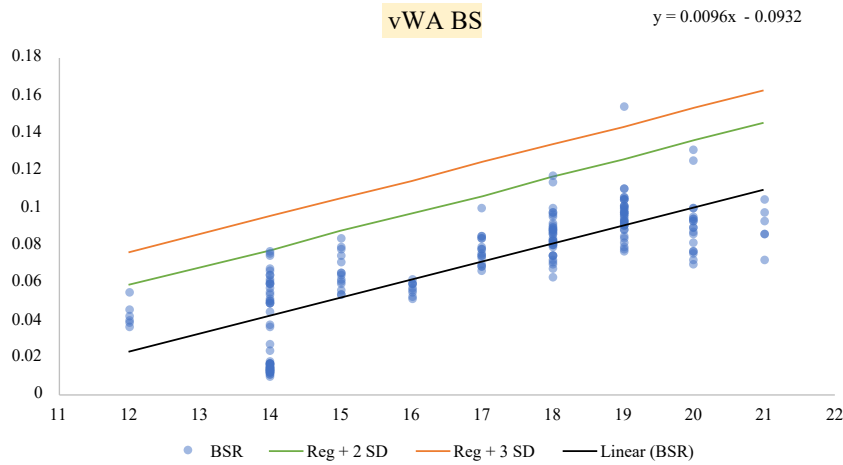
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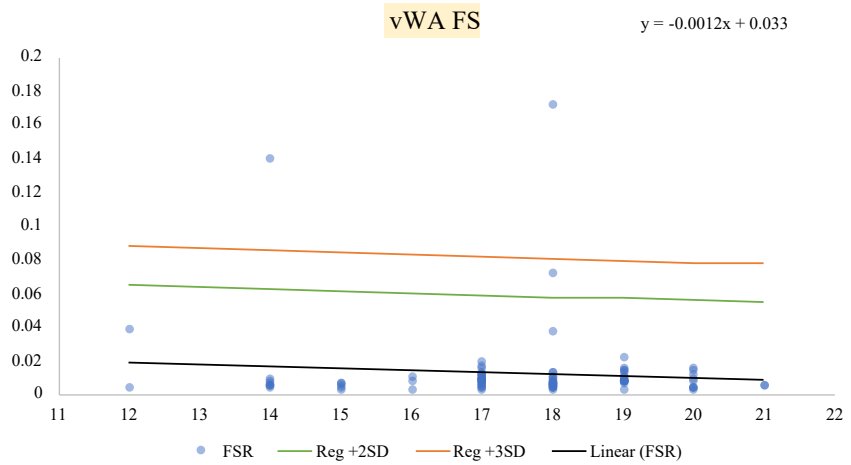
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**vWAHBS**

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**vWADBS**

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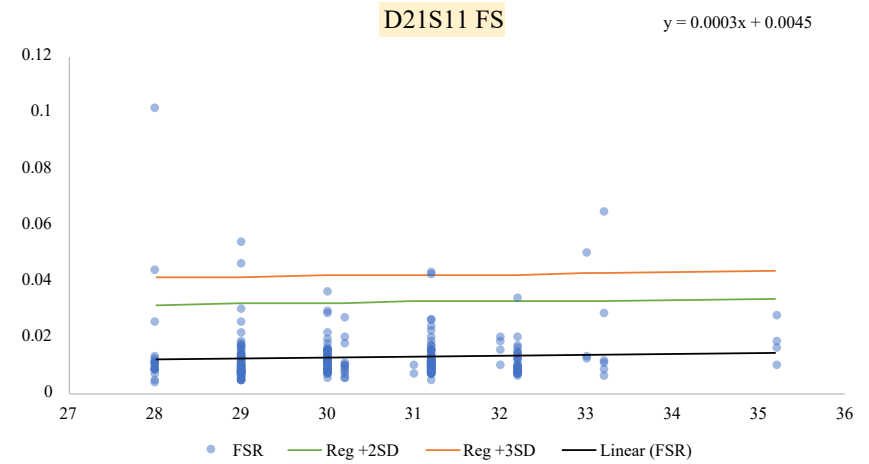
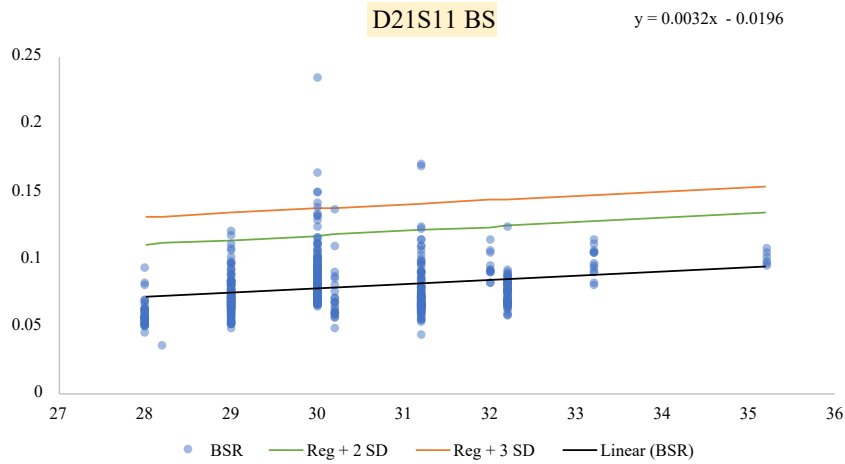
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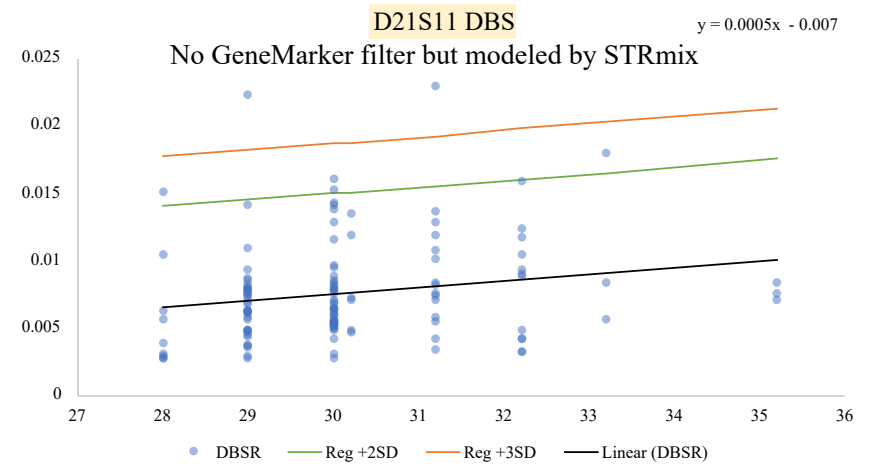
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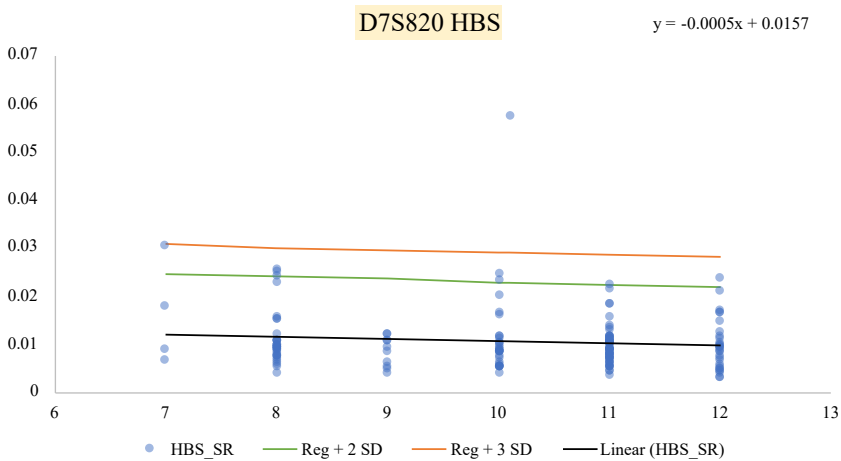
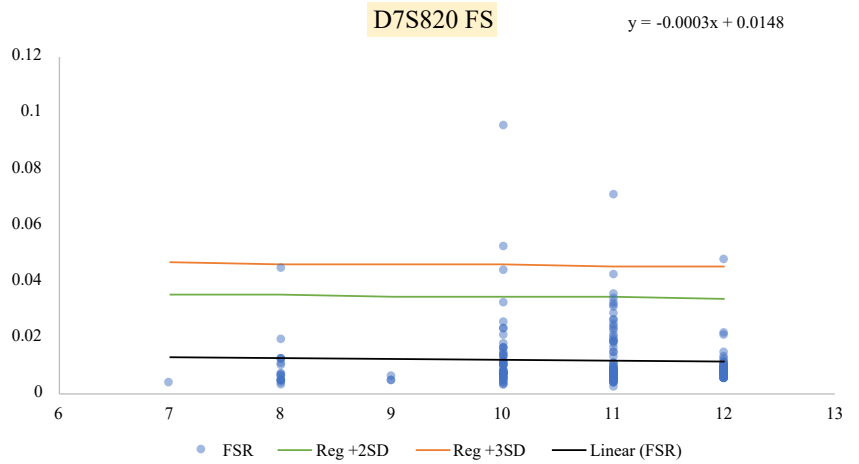
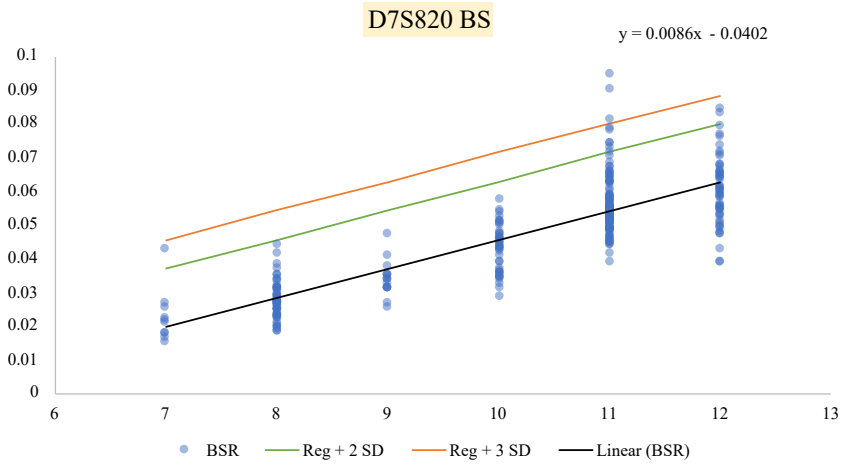
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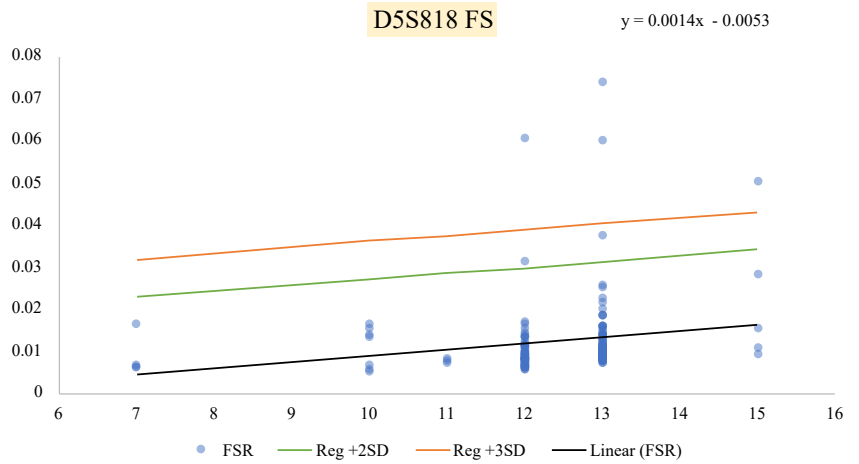
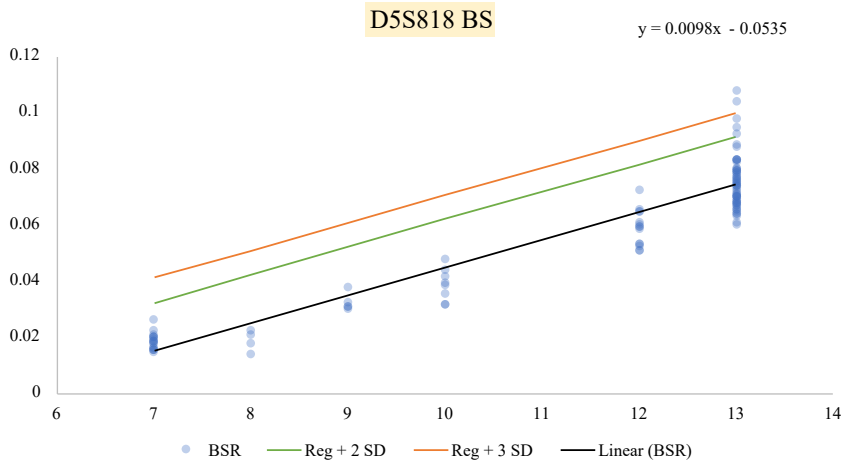
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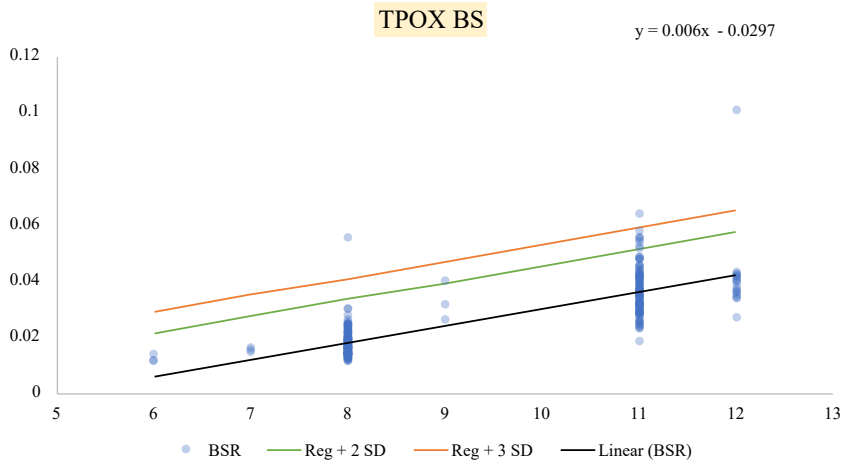
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**TPOX HBS**

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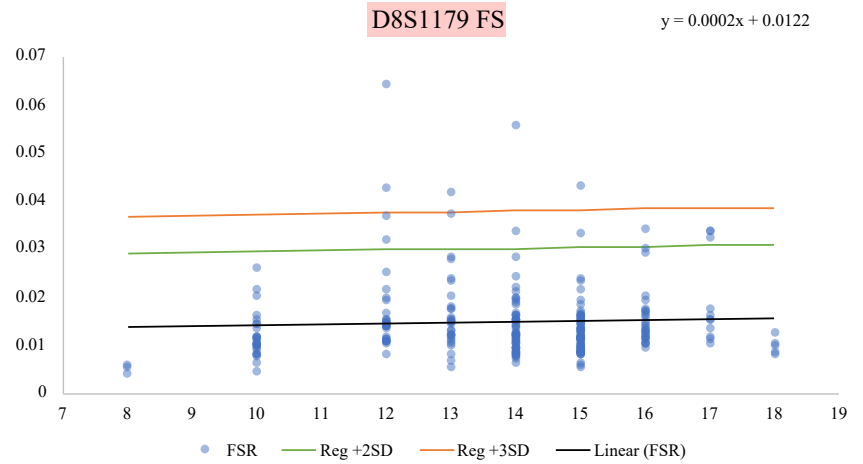
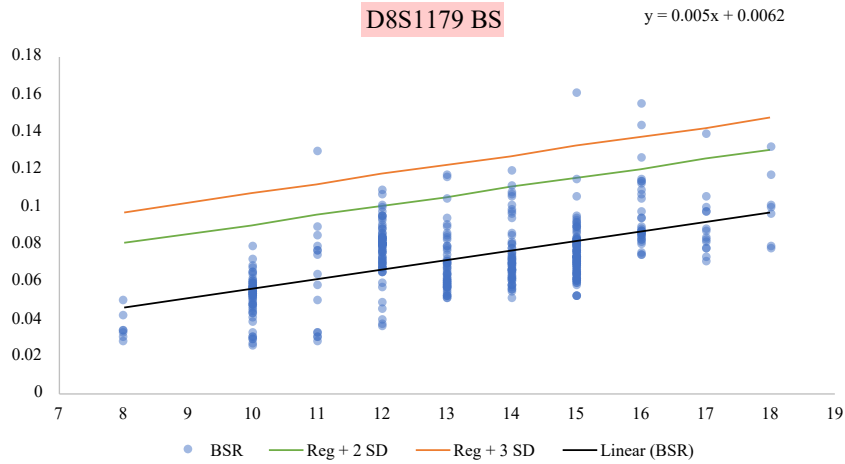
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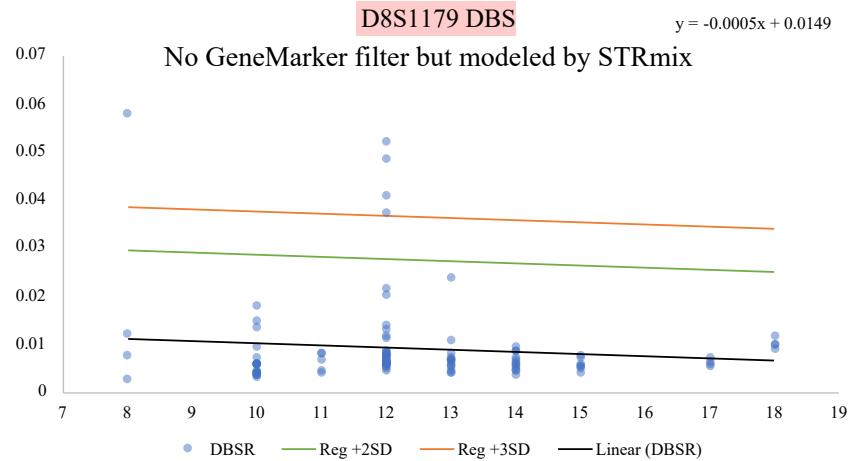
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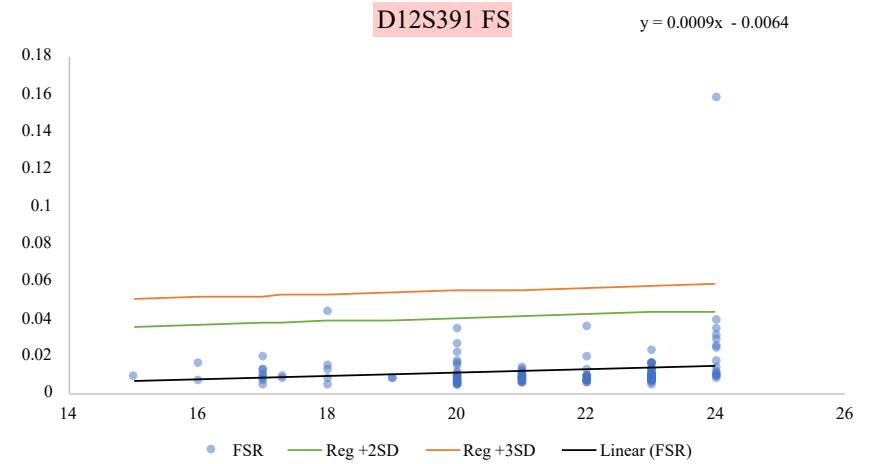
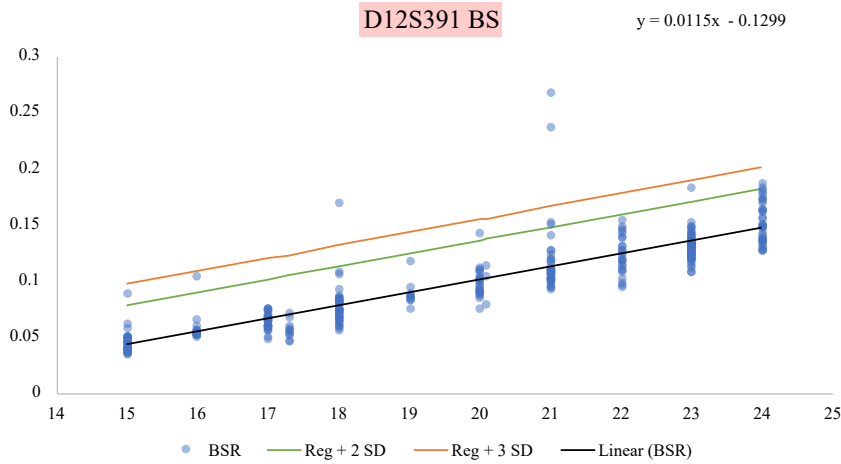
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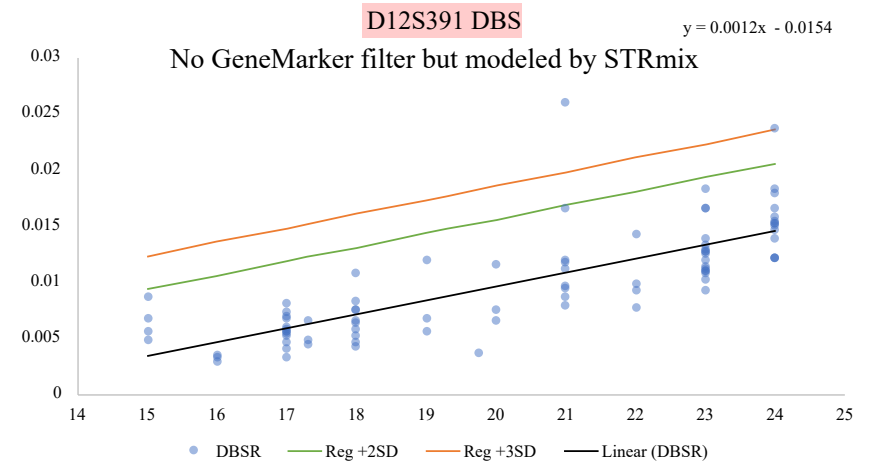
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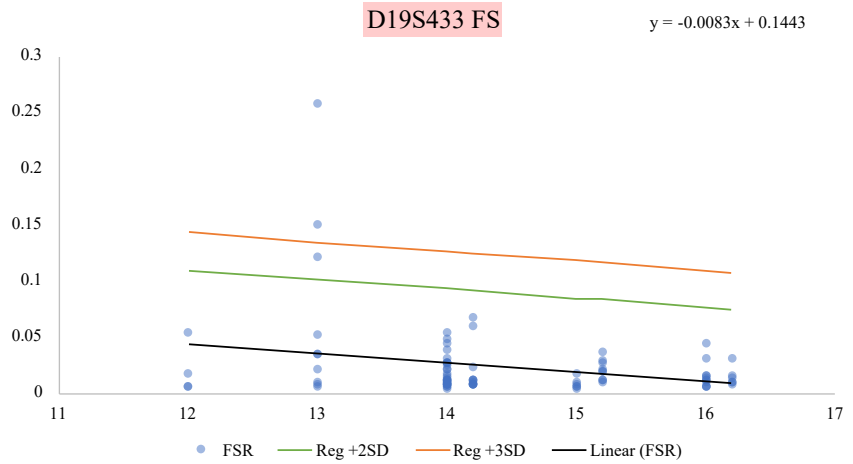
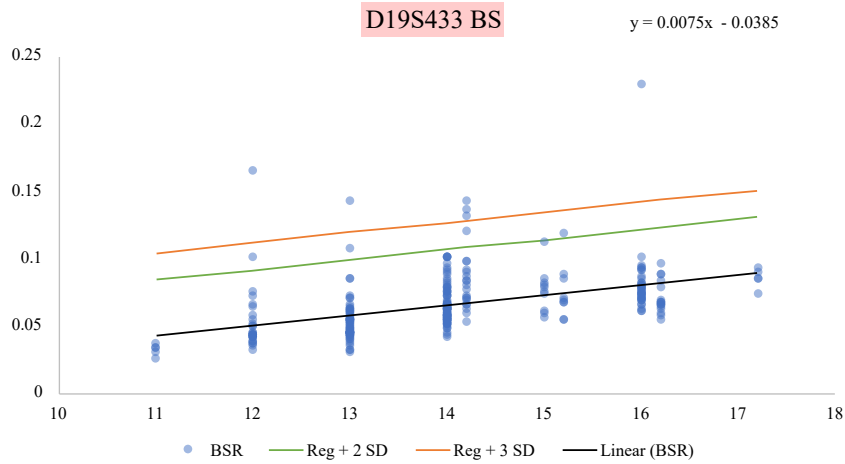
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**D19S433 HBS**

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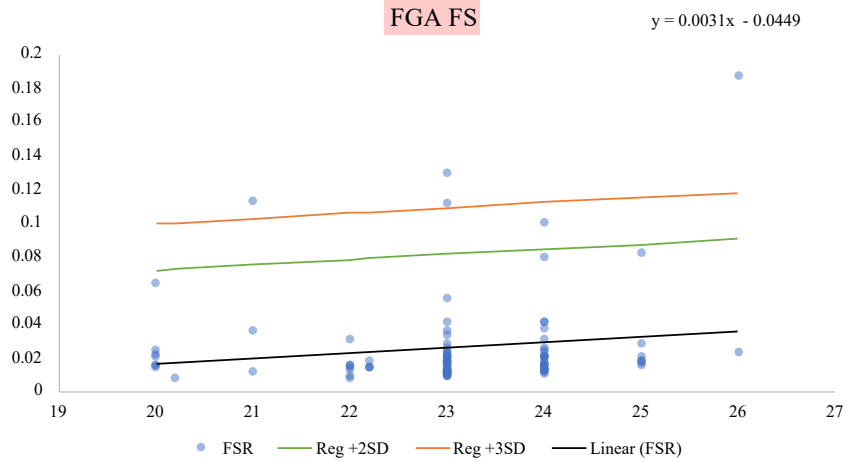
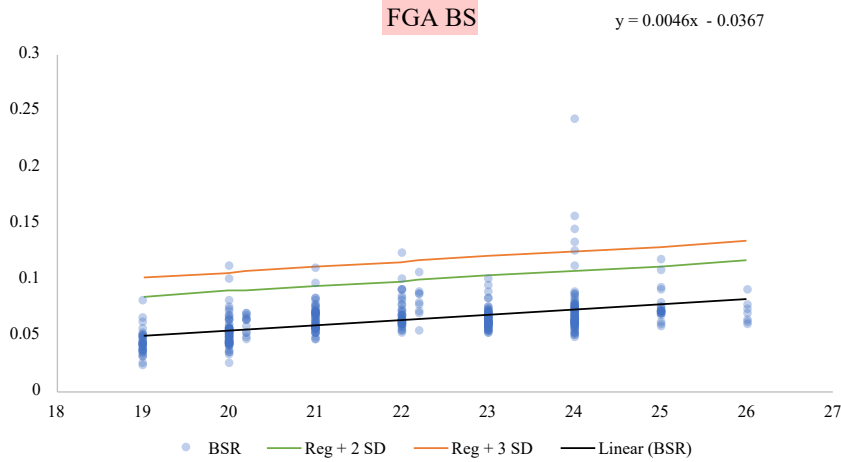
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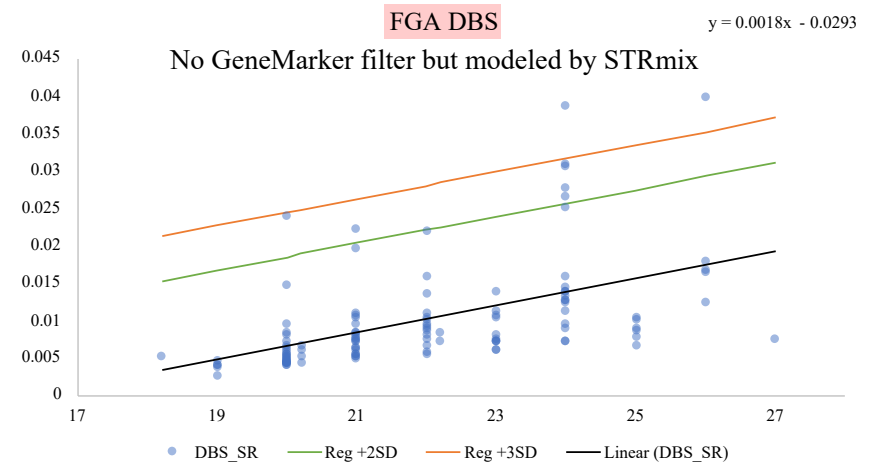
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**FGA HBS**

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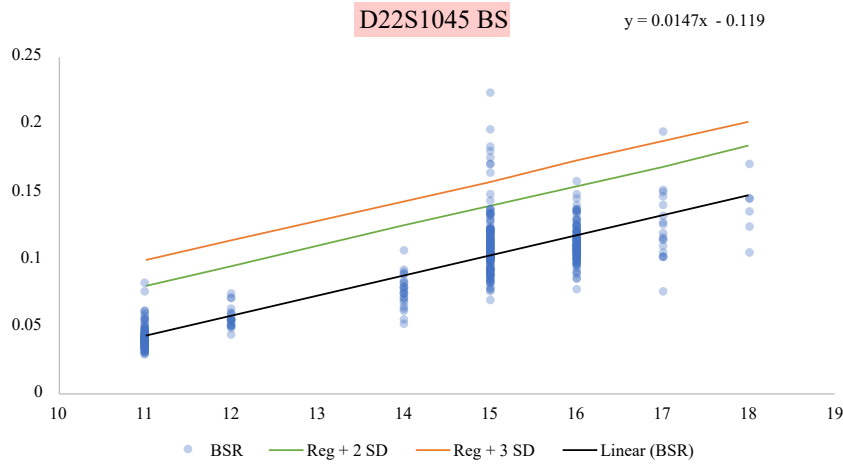
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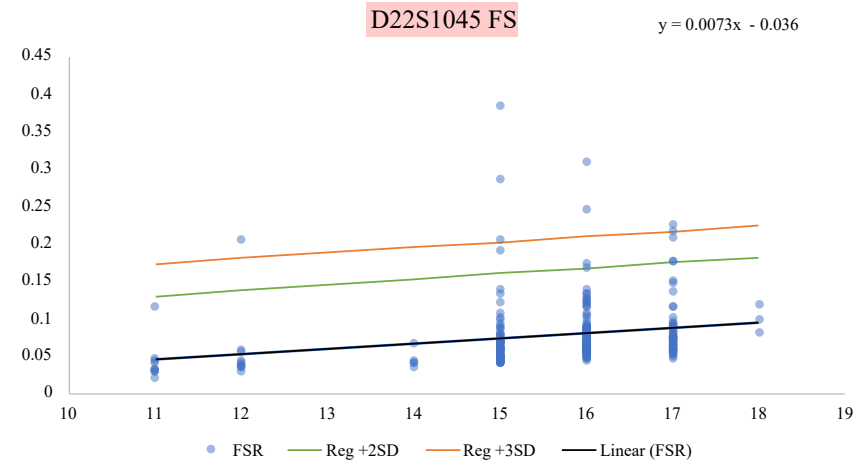
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### References

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- 2 NYC OCME Stutter Study for GeneMarker® HID 3.0.0 and STRmix™ Version 2.7-; PowerPlex® Fusion Data run on 3500xl Genetic Analyzers
- 3 Estimation of STRmix™ parameters for OCME New York Laboratory
- 4 Internal Validation of STRmix™ V2.4 for Fusion NYC OCME