

NIJ Expert System Testbed Project

GeneMapper ID	FSS-i3	TrueAllele	Rule	Threshold	Rule fires when:
	AMELO	AMELO	Amelo		Allele designations at this locus are other than XX or XY.
CC	KP	CC	Control Concordance Known Profiles Check Control		Allele calls for Positive control samples do not match expected designations.
OVL	XO		Overlap		
	DEG		Crossover Degradation		An allele for one locus may have crossed over into an adjacent locus window of the same color. Degradation ratio between lowest and highest MW loci.
	S/N	DISP	Signal-to-noise Dispersion	S/N = 90% Dispersion = 60%	The main peaks contain less than a certain percentage of the total signal in the allelic window.
SPU	PU	D2D/OVL	Spectral Pull Up Pull Up Dye to dye/Overlap	SPU = 40% ($\pm 1dp$) PU = 40% ($\pm 0.2bp$) D2D/OVL = 150%	Extra peaks in window may be caused by other dyes at that location (aka pull-up or bleed-through).
AN	XP/XA	XA/3P	Allele number Extra Peak/Extra allele Extra Allele/3rd Peak	AN = More than 2 XP/XA = 50 RFU XA/3rd Peak \Rightarrow 20%	There are more than two significant peaks within the allelic window.
	Minus A	Hi N	Minus A High N peak	Minus A $>25\%$ ($\pm 0.3bp$) High N = 25%	The height of the n (-A) peak is too high relative to the n+1 (+A; true peak) peak.
OS	HS	HS	Off Scale High signal	OS = 8192 (raw data) HS = 9000	The height of one or more peaks exceeds the user-defined limit.
LPH	LHo	LHo	Low Peak Height Low Homozygote	LPH (LHo = 200) LHo = 200	The height of the single designated peak in the window is too low.
LPH	LHt	Lsig	Low Peak Height Low Heterozogote Low Signal	LPH (LHt = 100) LHt = 100 Lsig = 100	The height of one or more peaks is less than the user-defined limit.
CC	NEG	NEG	Control Concordance Negative		Peaks were detected in the designated negative control lanes.
BIN	OL	OL/OPL/UNEX	Out Of Bin Allele Off Ladder Off Ladder/Off Physical Ladder/Unexpected	BIN 20% OL = $\geq \pm 0.4bp$ OL = $\geq 0.4bp$ /OPL = 0 bp/UNEX = $\geq 20\%$	One or more designated alleles are outside bin/template of the physical/virtual ladder.
	Noise	Noise	Noise		No peaks were detected in the sample at this locus.
BD	Morph	Morph/Spike	Broad Peak Peak morphology Peak morphology/Spike	BD = 1.5 bp Morph = >2.0 ; <0.04 Morph = 0.6-1.8/Spike = 0.35	The designated peaks have peak fit quality less than a user-defined threshold.
	Rare	Rare	Rare	Rare = OL,R,<,>	One or more designated peaks match user defined flag.
PHR	Pref Amp	RelHgt	Peak Height Ratio Preferential Amplification Relative Height	PHR = 50% Pref Amp = 50% Rel Hgt = 50%	The height of the smaller peak is less than the expected amount relative to the larger peak.
	SP		Split Peak		Allele split into two distinct peaks.
	Stu	Stu	Stutter Stutter	Stu = 15% ($\pm 0.1bp$)* Stu = 20%	* FSS-i3 - Set specifically for each locus (Generally 15%) The area of the stutter peak is too high relative to the peak that is one repeat larger.
	UNC	UNC	Uncorrelated	UNC = 0.45	The two designated peaks appear to migrate in opposite directions relative to the ladder.