

# Summary of Mx, pref amp and Homozygote drop-out rules within i-STReam software

## 2 peak locus:

Cont1	Cont. 2	i-STReam (RH column) Mx †	Pref amp rule
AA	BB	$\frac{\phi_R}{\phi_L + \phi_R}$	No info
BB	AA		
AB	AA	$\frac{\phi_S - \phi_U}{\phi_U + \phi_S}$	$PAT * \phi_U \leq \phi_S$
AB	BB		
AA	AB	$\frac{2\phi_U}{\phi_U + \phi_S}$	$PAT \leq \frac{\phi_A}{\phi_B} \leq \frac{1}{PAT}$
BB	AB		
AB	AB	No info	

Key: Cont. - Contributor, L- left column allele, R – right column allele, S – shared allele, U – unshared allele, HomT – homozygous threshold, MxP – mixing proportion for whole profile, MxT – mixing proportion tolerance (swing currently  $\pm 0.35$ ), F – failed allele,  $\phi$  - peak area of allele, PAT – pref amp tolerance. † if  $Mx \geq MxP - MxT$  and if  $Mx \leq MxP + MxT$ , then accept, else reject the pair

## 3 peak locus:

Cont. 1	Cont. 2	i-STReam (RH column) Mx †	Pref amp rule
AA	BC	$\frac{\phi_2 + \phi_3}{\phi_2 + \phi_3 + \phi_{HOM}}$	$PAT \leq \frac{\phi_2}{\phi_3} \leq \frac{1}{PAT}$ Where 2&3 correspond to areas of alleles in right hand column
BB	AC		
CC	AB	$\frac{\phi_{HOM}}{\phi_{HOM} + \phi_1 + \phi_2}$	$PAT \leq \frac{\phi_1}{\phi_2} \leq \frac{1}{PAT}$ Where 1&2 correspond to areas of alleles in left hand column
BC	AA		
AC	BB	$\frac{3\phi_{UR} - \phi_{UL} + \phi_S}{2(\phi_{UL} + \phi_{UR} + \phi_S)}$	$PAT \leq \frac{\phi_S}{\phi_{UL} + \phi_{UR}} \leq \frac{1}{PAT}$
AB	CC		
AB	AC		
AB	BC		

Key: Hom – homozygous allele, UL – unshared allele in left column, UR – unshared allele in right column, S – shared allele, HomT – homozygous threshold, F – failed allele,  $\phi$  - peak area of allele, PAT – pref amp tolerance, H – homozygous allele. † if  $Mx \geq MxP - MxT$  and if  $Mx \leq MxP + MxT$ , then accept, else reject the pair

#### 4 peak locus:

Cont .1	Cont. 2	i-STReam (RH column) Mx †	Pref amp rule (RH column)	Pref amp rule (LH column)
AB	CD	$\frac{\phi_3 + \phi_4}{\phi_1 + \phi_2 + \phi_3 + \phi_4}$ where 3&4 correspond to alleles in right hand column	$PAT \leq \frac{\phi_3}{\phi_4} \leq \frac{1}{PAT}$	$PAT \leq \frac{\phi_1}{\phi_2} \leq \frac{1}{PAT}$ 1&2 correspond to alleles in left hand column
AC	BD			
AD	BC			
BC	AD			
BD	AC			
CD	AB			

Key: Cont. - Contributor,  $\phi$  - peak area of allele, PAT – pref amp tolerance. † if  $Mx \geq MxP - MxT$  and if  $Mx \leq MxP + MxT$ , then accept, else reject the pair