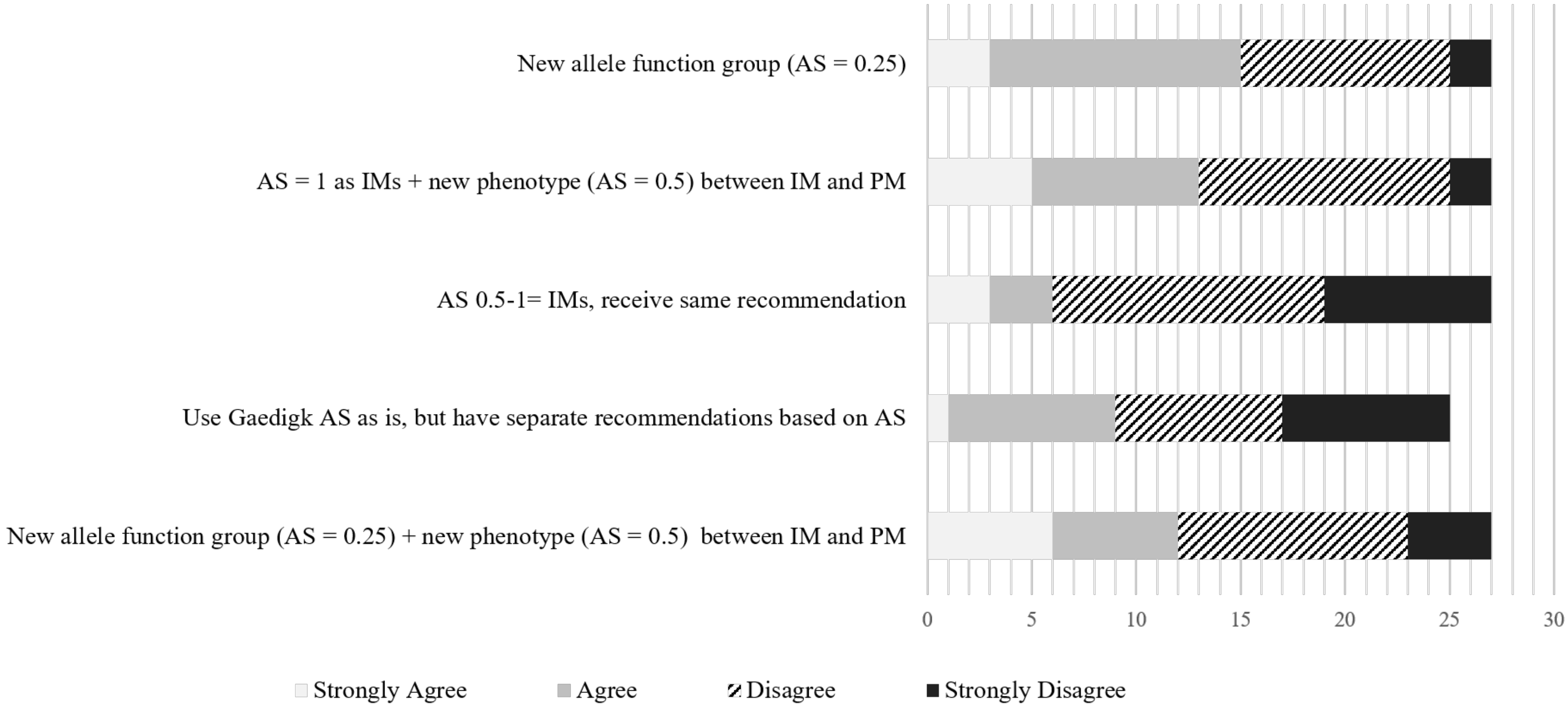

Figure S1. Results from Survey 1 showing level of agreement on *CYP2D6* genotype to phenotype methods

Table S1. Refinement phase survey results

Activity score	Expert response	
0.25	IM 56% (n=14)	PM 44% (n=11)
2.25	UM 52% (n=13)	NM 48% (n=12)
1.25	NM 60% (n=15)	IM 40% (n=10)
ranges	Option 1 52% (n=14)	Option 2 41% (n=11)

Option 1: UM >2.25; NM 1.25-2.25; IM 0.25-1; PM 0

Option 2: UM >2; NM 1.25-2; IM 0.25-1; PM 0

Table S2. Comparison of CPIC genotype to phenotype translations across CYP enzymes

Phenotype	**CYP2B6**	**CYP2C9**	**CYP2C19**	**CYP2D6**
UM	increased + increased	n/a	increased + increased	>2 copies of normal (AS > 2)
RM	normal + increased	n/a	normal + increased	n/a
NM	normal + normal	normal + normal	normal + normal	normal + normal (AS=2) normal + decreased (AS=1.5)
IM	normal + decreased normal + no function increased + decreased increased + no function	normal + decreased normal + no function normal + possible decreased ("possible IM")	normal + decreased ("likely IM") normal + no function increased + decreased ("likely IM") increased + no function decreased + decreased ("likely IM")	normal + no function (AS=1) decreased + decreased (AS=1) decreased + no function (AS=0.5)
PM	decreased + decreased no function + no function decreased + no function	decreased + decreased no function + no function decreased + no function decreased + possible decreased ("possible PM") possible decreased + possible decreased ("possible PM")	no function + no function decreased + no function ("likely PM")	no function + no function (AS=0)

Increased, increased function allele; normal, normal function allele; decreased, decreased function allele; no function, no function allele

UM, ultrarapid metabolizer; RM, rapid metabolizer; NM, normal metabolizer; IM, intermediate metabolizer; PM, poor metabolizer