

Supplementary Table S3: P-values for sequence kernel association test (SKAT) for remaining genes, by mutation type							
Gene	KIT exon 11 codon 557-8 deletion	KIT exon 11 insertion	KIT exon 11 other deletion	KIT exon 11 point mutation	Other KIT mutation	PDGFRA mutation	Wild type
ADH1A	0.8	1.0	0.1	0.6	0.1	0.1	0.3
ADH1B	0.1	0.6	0.4	0.9	0.5	0.2	0.3
ADH1C	0.1	0.3	0.4	0.5	0.2	0.5	0.2
AHR	0.8	0.7	0.8	0.1	0.5	0.5	0.3
ALDH18A1	0.6	0.8	0.1	0.4	0.9	0.3	0.9
ALDH1A1	0.5	0.7	1.0	0.4	0.2	1.0	1.0
ALDH1A2	0.3	0.7	0.6	0.4	0.9	0.5	0.5
ALDH1A3	0.6	0.3	0.2	0.8	0.4	0.8	0.7
ALDH1B1	0.6	0.5	0.4	0.7	0.8	0.7	1.0
ALDH1L1	0.4	0.2	0.3	0.8	1.0	0.4	0.1
ALDH1L2	0.5	0.2	0.2	0.9	0.6	0.9	0.01
ALDH2	0.5	0.03	0.9	0.6	0.7	0.2	0.2
CYP1A2	0.1	0.3	0.6	0.5	0.9	0.3	0.9
CYP2B6	0.4	0.2	1.0	0.1	0.9	0.5	0.1
CYP2C8	0.4	0.4	0.1	0.7	0.8	0.9	0.2
CYP2C9	0.5	0.9	0.3	0.3	0.6	0.4	0.1
CYP2D6	0.7	0.3	0.02	0.3	1.0	0.8	0.2
CYP2E1	0.5	0.5	0.9	0.9	0.04	0.3	0.7
CYP3A4	0.2	0.4	0.4	0.7	0.3	0.9	0.6
ERCC5	0.1	0.9	0.7	1.0	0.7	0.7	0.9
G6PC	0.6	0.1	0.5	0.2	0.5	0.4	0.4
GSTP1	0.5	0.5	0.9	0.3	0.4	0.3	0.9
GSTT1	0.2	0.6	0.02	0.1	0.7	0.04	0.8
HIF1A	0.4	0.7	0.3	0.5	0.8	0.2	0.8
HNF4A	0.6	1.0	0.4	0.1	0.3	0.6	0.7
MDM2	0.2	0.7	0.2	0.7	0.3	0.6	0.4
NAT2	0.4	1.0	0.3	0.6	0.2	0.3	0.1
NFE2L2	0.8	0.7	0.1	0.4	0.3	0.7	0.5
NOS2A	0.3	0.5	0.2	0.2	0.3	0.2	0.7
NQO1	0.9	0.5	0.03	0.5	0.8	0.5	0.1
PTGS2	0.3	0.6	0.6	0.2	0.1	0.1	0.4
SULT1A1	0.3	0.1	0.1	0.9	0.3	1.0	0.3
TP53	0.1	0.2	0.2	0.5	0.2	0.1	1.0
XPA	0.8	0.2	0.3	1.0	0.9	0.6	0.7
XPC	0.6	0.6	0.1	0.3	0.1	0.2	1.0