Supplemental information SI2. Unadjusted and multivariate Cox proportional hazard models for biochemical relapse by GST genotypes.

Genotypes	**HR** (95% CI)	**HR**$_{adj}^{a}$ (95% CI)	**HR**$_{adj}^{b}$ (95% CI)	**HR**$_{adj}^{c}$ (95% CI)	**HR**$_{adj}^{d}$ (95% CI)	**HR**$_{adj}^{e}$ (95% CI)	**HR**$_{adj}^{f}$ (95% CI)
GSTT1							
Present	1.00 (reference)		1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	
Null	1.69 (0.81-3.53)		1.87 (0.89-3.91)	1.88 (0.88-4.01)	2.05 (0.92-4.54)	1.86 (0.85-4.09)	
p-value	0.164	NA	0.099	0.103	0.078	0.121	NA
GSTM1							
Present	1.00 (reference)		1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	
Null	1.26 (0.64-2.47)		1.26 (0.64-2.48)	1.08 (0.54-2.18)	0.97 (0.47-2.01)	1.14 (0.57-2.28)	
p-value	0.503	NA	0.496	0.823	0.937	0.703	NA
GSTP1 c.313 A>G							
AA	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)
AG	1.16 (0.54-2.52)	1.13 (0.52-2.47)	1.20 (0.55-2.60)	1.12 (0.49-2.56)	0.85 (0.33-2.17)	0.93 (0.39-2.17)	1.00 (0.42-2.40)
p-value (AG *vs* AA)	0.702	0.756	0.649	0.793	0.729	0.847	0.996
GG	**3.38 (1.40-8.16)**	**3.01 (1.27-7.55)**	**2.96 (1.19-7.33)**	2.63 (0.96-7.16)	2.73 (0.89-8.38)	2.55 (0.88-7.36)	2.49 (0.88-7.03)
p-value (GG *vs* AA)	**0.007**	**0.013**	**0.019**	0.059	0.079	0.084	0.085
GSTP1 c.313 A>G							
AA+AG	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)
GG	**3.16 (1.41-7.06)**	**2.92 (1.31-6.57)**	**2.73 (1.19-6.28)**	**2.48 (1.00-6.13)**	**3.01 (1.13-8.02)**	**2.68 (1.07-6.75)**	**2.49 (1.00-6.23)**
p-value	**0.005**	**0.009**	**0.018**	**0.049**	**0.028**	**0.036**	**0.050**
GSTP1 c.313 A>G + GSTT1 null + GSTM1 null [g]							
0 risk allele	1.00 (reference)		1.00 (reference)	1.00 (reference)	1.00 (reference)	1.00 (reference)	
1 risk allele	0.97 (0.43-2.21)		1.04 (0.46-2.37)	0.99 (0.42-2.32)	0.74 (0.30-1.84)	0.88 (0.37-2.12)	
p-value (1 *vs* 0)	0.994	NA	0.929	0.974	0.512	0.782	NA
2+ risk alleles	**2.82 (1.23-6.49)**		**3.04 (1.30-7.09)**	**2.66 (1.08-6.56)**	**3.06 (1.20-7.80)**	**2.94 (1.18-7.32)**	
p-value (2+ *vs* 0)	**0.015**	NA	**0.010**	**0.034**	**0.019**	**0.020**	NA

Statistical significant associations are bolded (p≤0.050).

[a] *GSTP1* analysis adjusted for *GSTT1* and *GSTM1* genotypes

[b] adjusted for margin

[c] adjusted for margin, Gleason score (low-risk *vs* high-risk) and pathological T stage (pT2 *vs* pT3)

[d] adjusted for margin, Gleason score (low-risk *vs* high-risk), pathological T stage (pT2 *vs* pT3), PSA level at diagnosis (≤4 *vs* >4-10 *vs* >10), family history of PCa, smoking status (never *vs* former *vs* current) and age at diagnosis (continuous variable)

[e] adjusted for margin, Gleason score (low-risk *vs* high-risk), PSA level at diagnosis (≤4 *vs* >4-10 *vs* >10), family history of PCa, smoking status (never *vs* former *vs* current), and age at diagnosis (continuous variable).

[f] *GSTP1* analysis adjusted for *GSTT1* and *GSTM1* genotypes, margin, Gleason score (low-risk *vs* high-risk), PSA level at diagnosis (≤4 *vs* >4-10 *vs* >10), family history of PCa, smoking status (never *vs* former *vs* current), and age at diagnosis (continuous variable).
[g] for GSTP1 c.313 A>G the recessive model was considered

Abbreviations: NA; not applicable