

Genetic polymorphisms in glycolytic pathway are associated with the prognosis of patients with early stage non-small cell lung cancer

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Supplementary Table 1. List of analyzed SNPs and the association with survival outcomes.

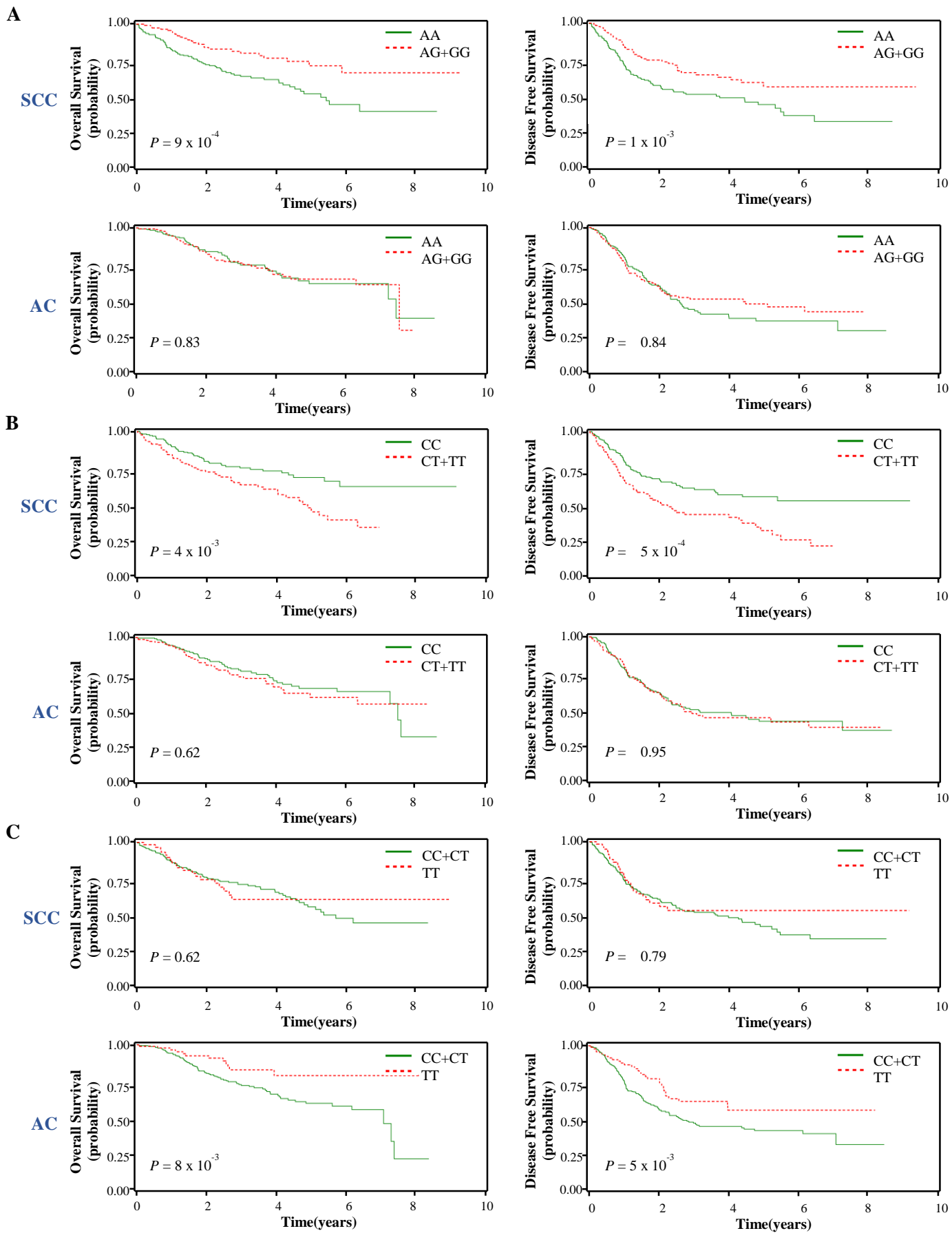
SNP ID	Gene	Base change	MAF	P^a for Overall survival			P^a for Disease-free survival		
				Dominant	Recessive	Codominant	Dominant	Recessive	Codominant
rs2274971	ENO1	A>G	0.23	0.02	0.16	0.02	0.01	0.40	0.02
rs11168417	PFKM	C>T	0.22	0.02	0.82	0.05	0.04	0.76	0.10
rs1132173	PFKP	C>T	0.47	0.72	0.11	0.24	0.74	0.02	0.12
rs3785921	PDK2	G>A	0.33	0.10	0.39	0.10	0.003	0.22	0.01
rs7971637	GAPDH	C>T	0.28	0.17	0.05	0.05	0.24	0.10	0.10
rs2986408	PDHX	A>C	0.15	0.35	0.31	0.26	0.43	0.10	0.23
rs2071064	TPI1	C>T	0.30	0.08	0.51	0.30	0.44	0.87	0.61
rs8192431	PKM	C>T	0.36	0.83	0.31	0.72	0.56	0.08	0.64
rs4880592	PFKP	G>A	0.47	0.63	0.56	0.98	0.80	0.09	0.25
rs656489	HK2	G>A	0.30	0.29	0.48	0.65	0.19	0.08	0.87
rs7231	PDHB	G>C	0.24	0.56	0.11	0.25	0.76	0.10	0.35
rs17032801	ENO1	A>G	0.42	0.25	0.41	0.75	0.50	0.25	0.84
rs1057034	PFKL	C>T	0.36	0.52	0.30	0.33	0.55	0.16	0.25
rs4757650	LDHA	C>T	0.09	0.29	0.72	0.35	0.47	0.77	0.54
rs8112853	GAPDHS	G>C	0.27	0.56	0.63	0.51	0.19	0.26	0.13
rs1053000	PFKP	C>T	0.23	0.92	0.42	0.79	0.96	0.46	0.73
rs6489721	GAPDH	T>C	0.39	0.50	0.10	0.68	0.51	0.16	0.76
rs7100037	PFKP	T>C	0.36	0.55	0.63	0.51	0.19	0.69	0.26
rs12302749	TPI1	C>T	0.21	0.60	0.43	0.48	0.41	0.73	0.54
rs2306302	PFKP	G>A	0.09	0.72	0.22	0.54	0.48	0.64	0.59
rs4908519	ENO1	C>T	0.16	0.74	0.22	0.53	0.20	0.34	0.35
rs1803621	GAPDH	C>T	0.49	0.37	0.35	0.98	0.35	0.51	0.86
rs7128549	LDHA	C>G	0.36	0.46	0.48	0.86	0.17	0.52	0.50
rs7176223	ADPGK	T>G	0.24	0.83	0.92	0.83	0.54	0.66	0.73
rs4806173	GAPDHS	C>G	0.29	0.46	0.63	0.43	1.00	0.58	0.82
rs10492080	PFKM	C>T	0.46	0.38	0.22	0.20	0.46	0.12	0.16
rs2956107	PDHX	C>T	0.27	0.17	0.32	0.14	0.50	0.21	0.29
rs11064436	TPI1	G>C	0.19	0.35	0.29	0.25	0.80	0.56	0.69
rs10181851	PDK1	A>G	0.21	0.61	0.20	0.38	0.38	0.24	0.25
rs7248411	GPI	C>G	0.18	0.72	0.60	0.63	0.50	0.72	0.64
rs2229626	HK2	C>T	0.46	0.53	0.58	0.47	0.34	0.92	0.50
rs4760619	PFKM	A>T	0.23	0.75	0.35	0.55	0.66	0.57	0.85
rs1052309	PFKP	G>A	0.19	0.38	0.33	0.30	0.97	0.96	0.96
rs608112	HK2	G>A	0.23	0.57	0.62	0.79	0.37	0.26	0.79
rs4806174	GAPDHS	G>C	0.37	0.33	0.80	0.41	0.68	0.50	0.96

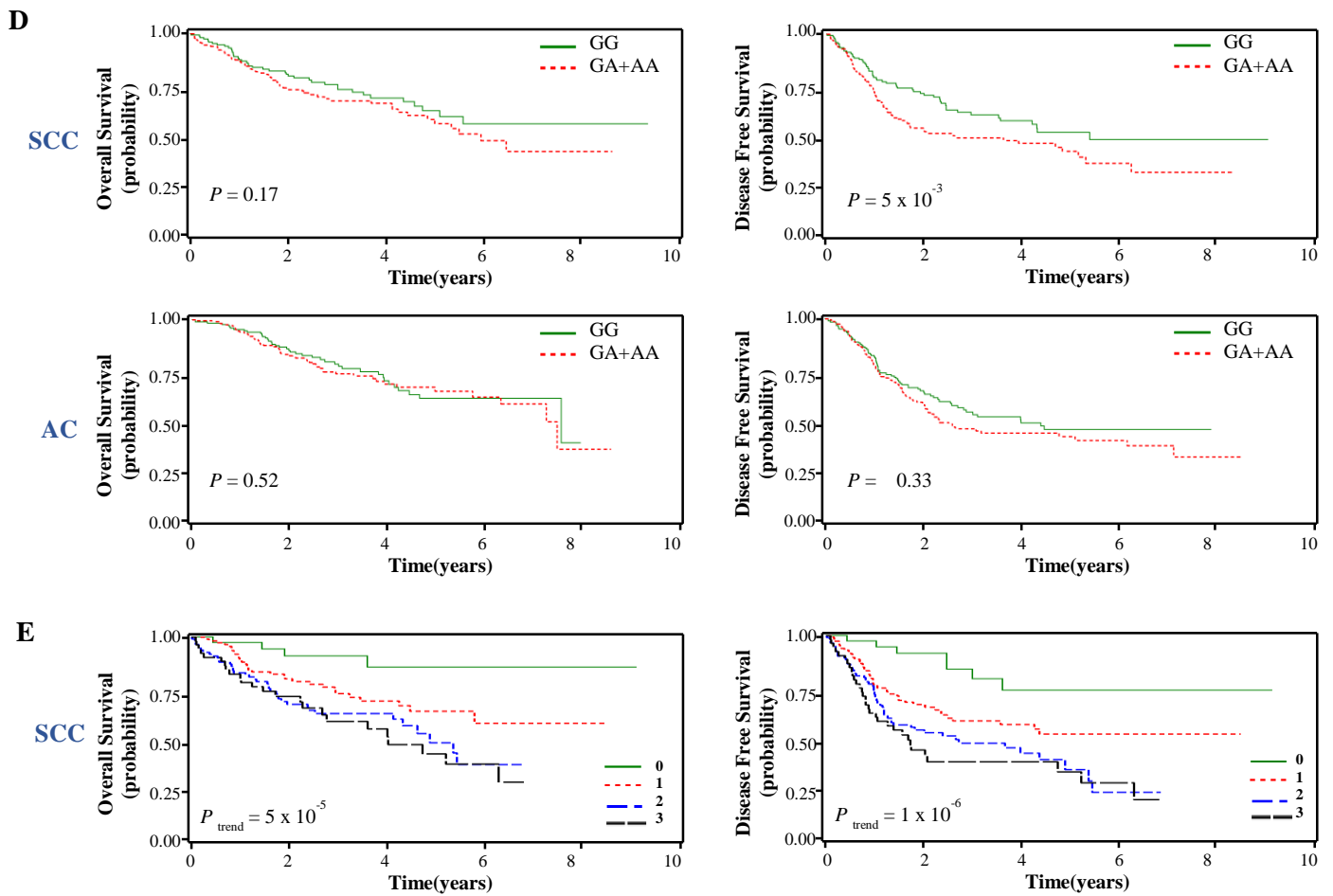
Supplementary Table 1. Continued.

SNP ID	Gene	Base change	MAF	<i>P</i> ^a for Overall survival			<i>P</i> ^a for Disease-free survival		
				Dominant	Recessive	Codominant	Dominant	Recessive	Codominant
rs2073436	PFKL	C>G	0.21	0.95	0.80	0.97	0.84	0.76	0.79
rs12276735	PDHX	G>A	0.11	0.18	0.98	0.35	0.84	0.71	0.92
rs3807891	PDK4	C>G	0.30	0.62	0.17	0.32	0.62	0.73	0.60
rs2001004	TPI1	A>G	0.46	0.30	0.94	0.49	0.38	0.79	0.48
rs3732298	HK2	T>C	0.12	0.57	0.14	0.33	0.64	0.20	0.95
rs8040828	PKM	C>A	0.39	0.57	0.75	0.83	0.22	0.70	0.31
rs8023358	ADPGK	A>G	0.22	0.65	0.25	0.95	0.61	0.13	0.33
rs1346165	ADPGK	C>T	0.21	0.96	0.39	0.78	0.41	0.17	0.24
rs2278543	ADPGK	G>A	0.46	0.58	0.62	0.95	0.63	0.65	0.57

MAF, minor allele frequency

^a *P*-values calculated using multivariate Cox proportional hazard models, adjusted for age, gender, smoking status, tumor histology, pathologic stage, and adjuvant therapy.





Supplementary Figure 1. Overall survival and disease free survival curves according to *ENO1* rs2274971A>G (A), *PFKM* rs11168417C>T (B), *PFKP* rs1132173C>T (C), and *PDK2* rs3785921G>A (D) genotypes in SCC and AC, and according to the number of bad genotypes of *ENO1* rs2274971A>G, *PFKM* rs11168417C>T, and *PDK2* rs3785921G>A (E). P values in the multivariate Cox hazard models. SCC, squamous cell carcinoma; AC, adenocarcinoma.