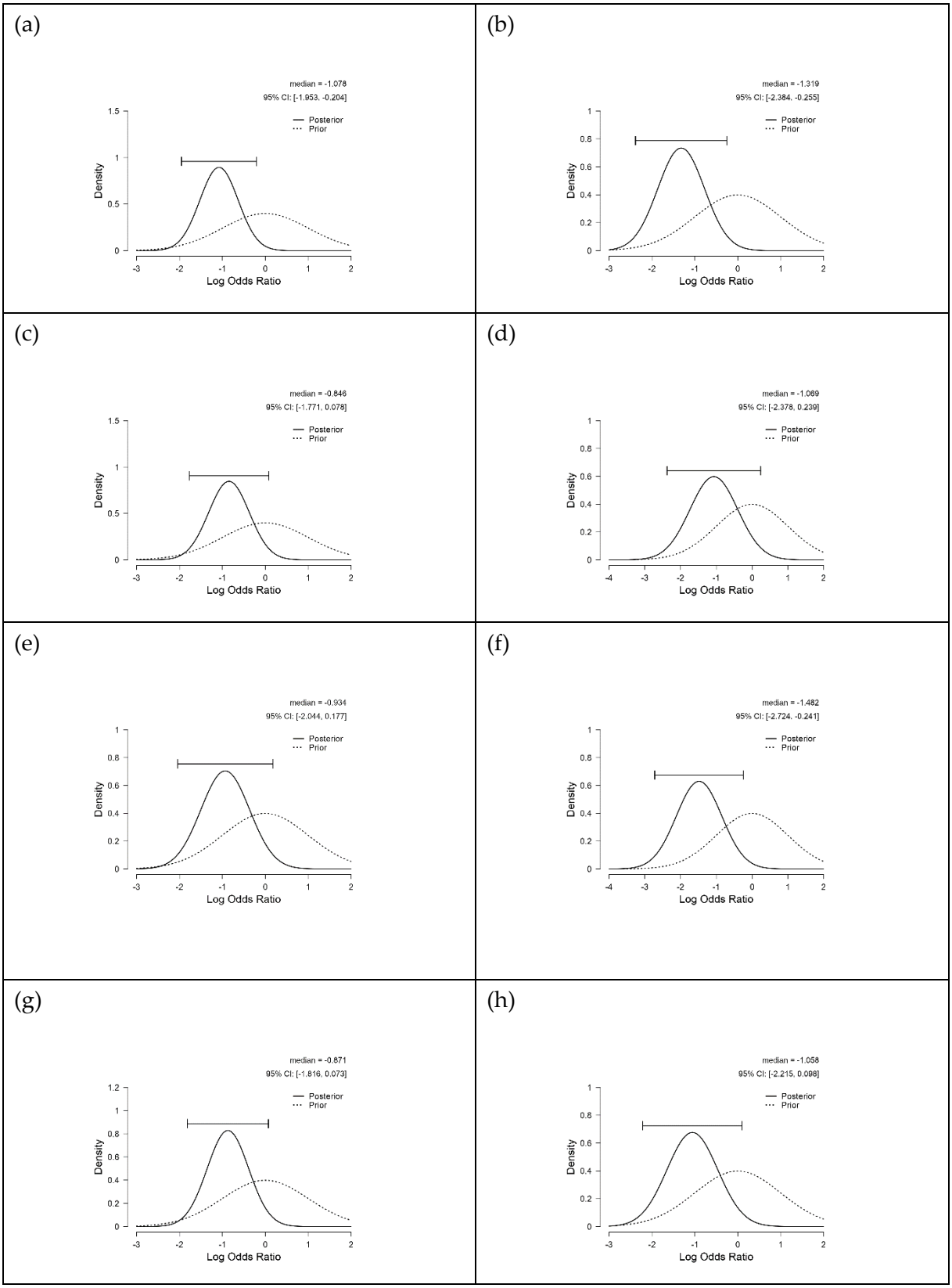
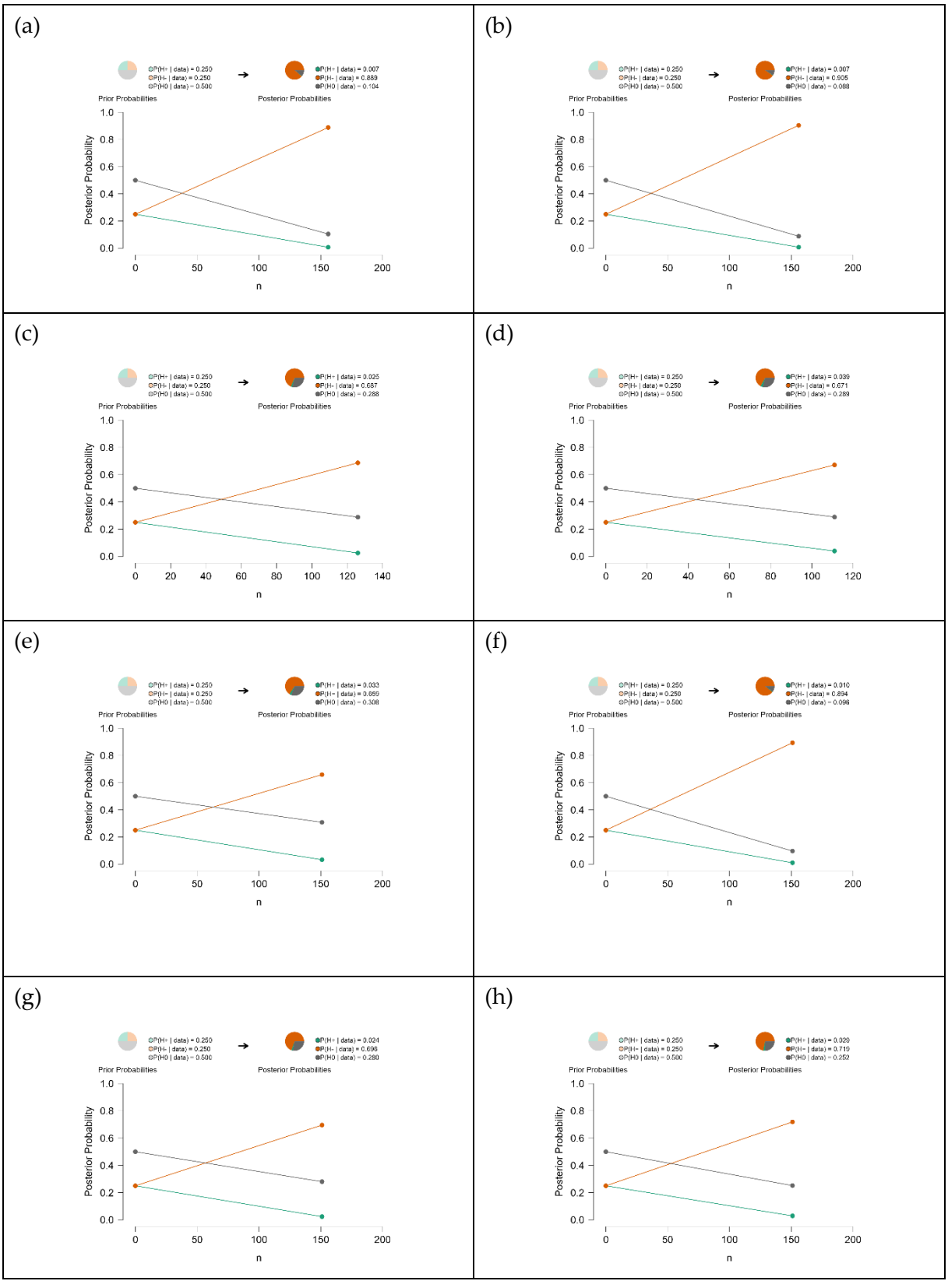
Figure S1: Posterior distribution of the odds log ratio for the relationships between clinicopathological features and CHK2 expression, *TP53* gene status, and p53 expression together with *TP53* gene status in tumor tissues from PTC patients with and without *CHEK2* germline mutations




(a) CHK2 expression and response to therapy; (b) CHK2 expression and final follow-up; (c) CHK2 expression and tumor diameter; (d) CHK2 expression and PTC histologic variant; (e) *TP53* gene status and age; (f) *TP53* gene status and vascular invasion; (g) p53

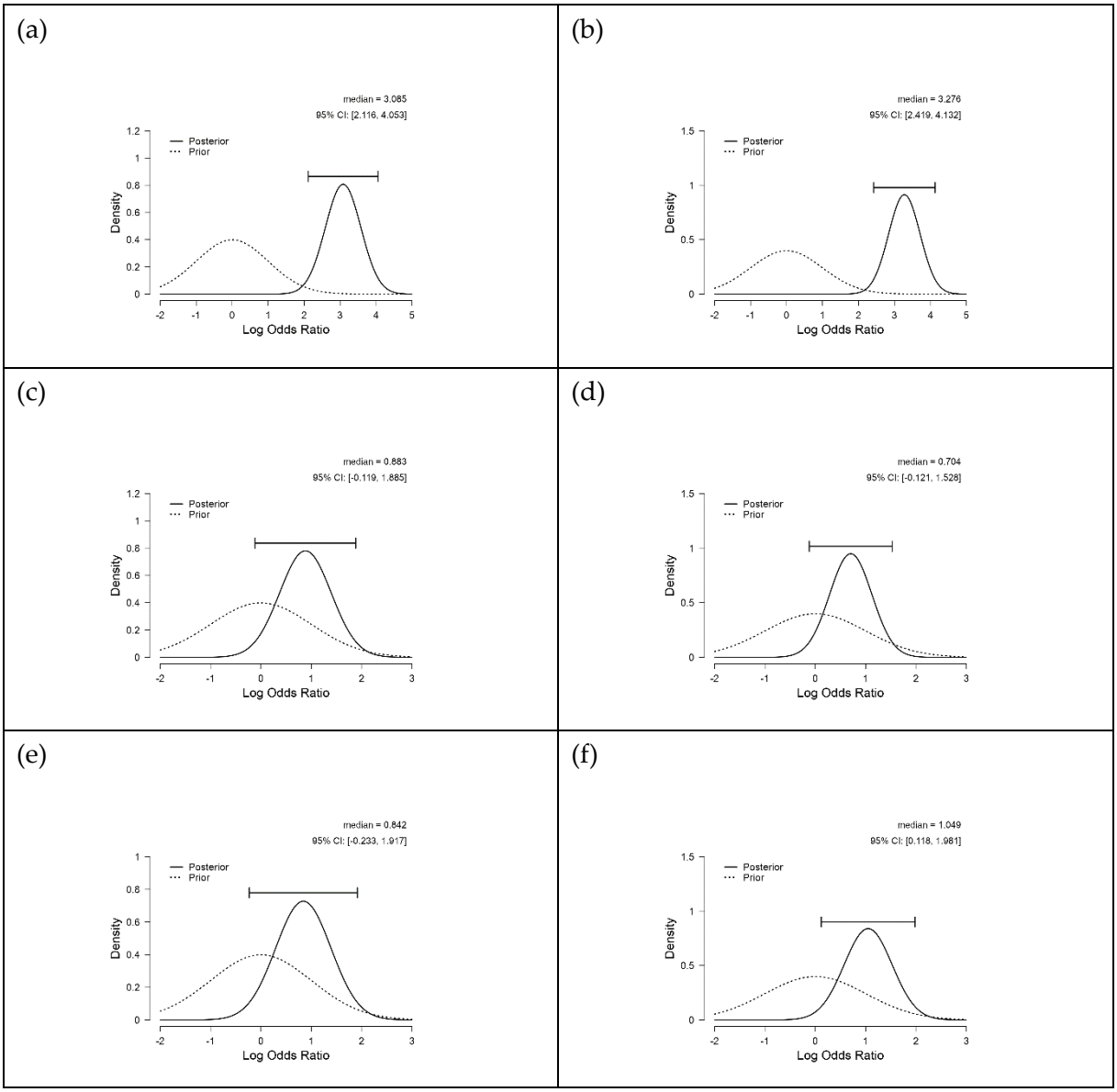
expression + *TP53* gene status and age; (h) p53 expression and *TP53* gene status and vascular invasion. Abbreviation: 95% CI, 95% credible interval.

Figure S2: Sequential analysis for the relationships between clinicopathological features and CHK2 expression, *TP53* gene status, and p53 expression together with *TP53* gene status in the tumor tissues of PTC patients with and without *CHEK2* germline mutations



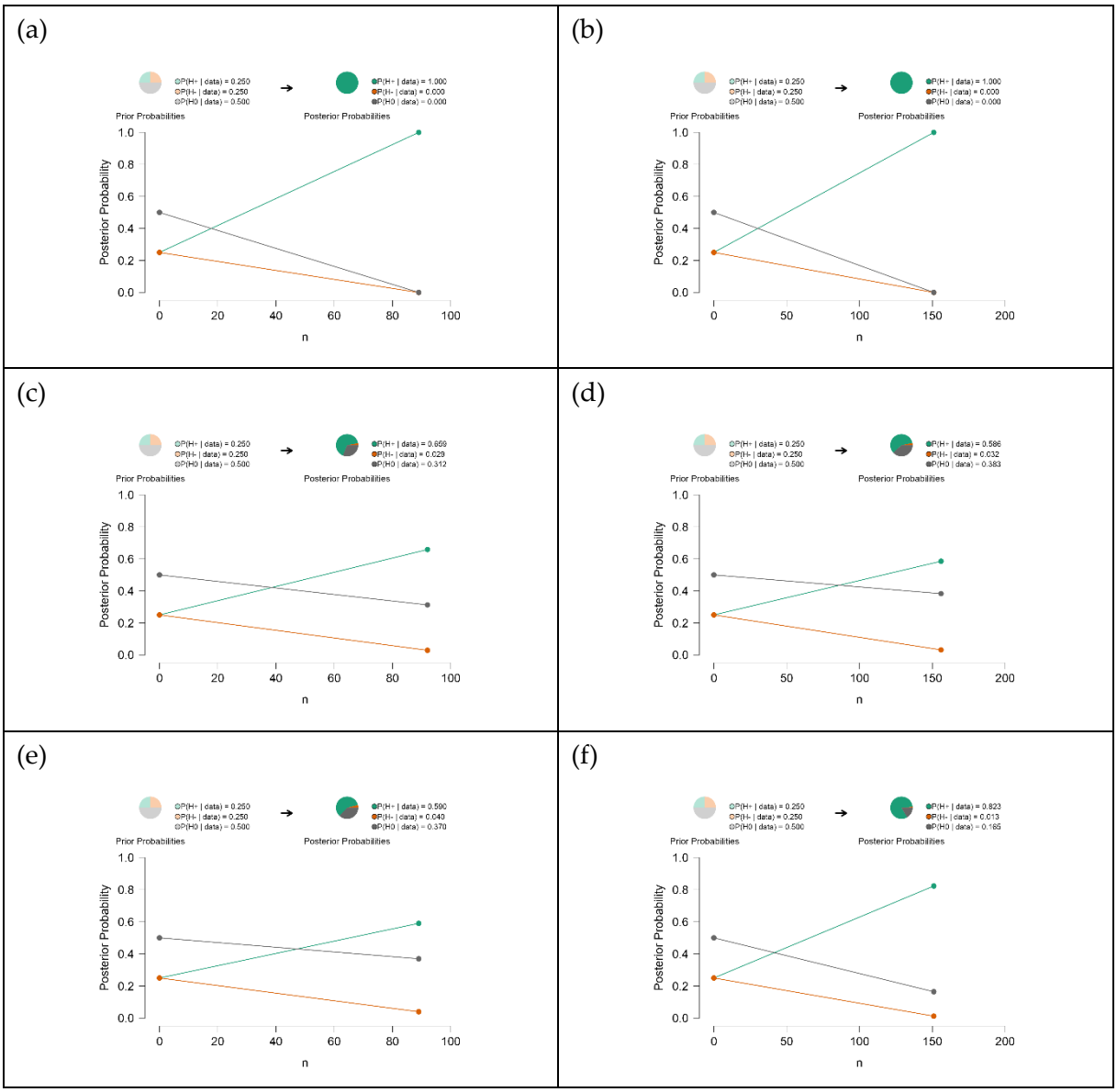
(a) CHK2 expression and response to therapy; (b) CHK2 expression and final follow-up; (c) CHK2 expression and tumor diameter; (d) CHK2 expression and PTC histologic variant; (e) *TP53* gene status and age; (f) *TP53* gene status and vascular invasion; (g) p53 expression together with *TP53* gene status and age; (h) p53 expression together with *TP53* gene status and vascular invasion. Abbreviations: P(H+|data), the probability of hypothesis H+ given the data; P(H-|data), the probability of hypothesis H- given the data; P(H0|data), the probability of hypothesis H0 given the data.

Figure S3: Posterior distribution of the odds log ratio for the association between *CHEK2* gene status, CHK2 expression, and the p53 expression together with *TP53* gene status in tumor tissues from PTC patients with and without the *CHEK2* germline mutations




(a) *CHEK2* gene status vs. *CHEK2* truncating mutation and WT; (b) *CHEK2* gene status vs. *CHEK2* truncating mutation and WT group + missense I157T mutation group; (c) *CHEK2* expression vs. *CHEK2* truncating mutation and WT; (d) *CHEK2* expression vs. *CHEK2* truncating and WT group + missense I157T mutation group; (e) p53 expression and *TP53* gene status vs. *CHEK2* truncating mutation and WT; (f) p53 expression and *TP53* gene status vs. *CHEK2* expression vs. *CHEK2* truncating mutation and WT group + missense I157T mutation group Abbreviations: 95% CI, 95% credible interval; *CHEK2* gene status, no loss/deletion of a *CHEK2* gene copy; *TP53* gene status, no loss/deletion of a *TP53* gene copy as determined by FISH; FISH, fluorescence in situ hybridization; p53 expression, negative/positive as determined by IHC; IHC, immunohistochemistry; *CHEK2* truncating, germline heterozygous truncating *CHEK2* mutation variants (1100delC, IVS2+1G>A, del5395); WT, wild type.

Figure S4: Sequential analysis of the associations between *CHEK2* gene status, CHK2 expression as determined by IHC, and p53 expression together with *TP53* gene status as determined by FISH in tumor tissues from PTC patients with and without the *CHEK2* germline mutations




(a) *CHEK2* gene status vs. *CHEK2* truncating mutation and WT; (b) *CHEK2* gene status vs. *CHEK2* truncating mutation and WT group + missense I157T mutation group ; (c) *CHEK2* expression vs. *CHEK2* truncating mutation and WT; (d) *CHEK2* expression vs. *CHEK2* truncating mutation and WT group + missense I157T mutation group; (e) p53 expression and *TP53* gene status vs. *CHEK2* truncating mutation and WT; (f) p53 expression and *TP53* gene status vs. *CHEK2* expression vs. *CHEK2* truncating mutation and WT group + missense I157T mutation group.Abbreviations: 95% CI, 95% credible interval; *CHEK2* gene status, no loss/deletion of a *CHEK2* gene copy; *TP53* gene status, no loss/deletion of a *TP53* gene copy; FISH, fluorescence in situ hybridization; p53 expression, negative/positive as determined by IHC; IHC, immunohistochemistry; *CHEK2* truncating, germline heterozygous truncating *CHEK2* mutation variants (1100delC, IVS2+1G>A, del5395); WT, wild type; P(H+|data), the probability of hypothesis H+ given the data; P(H-|data), the probability of hypothesis H- given the data; P(H0|data), the probability of hypothesis H0 given the data.

Figure S5: CHK2 expression levels in primary papillary thyroid cancer tissue and lymph node metastases.

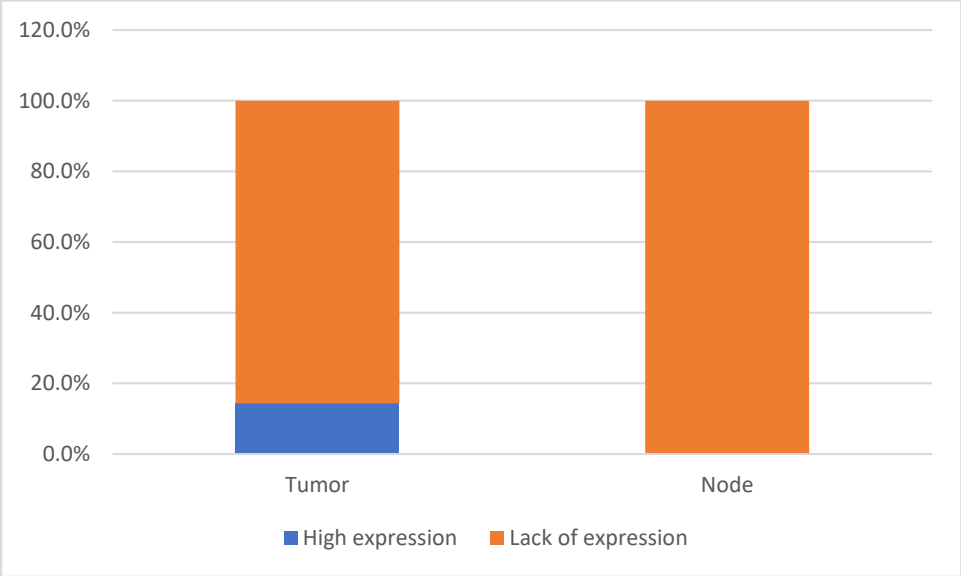



Table S1: Predictive values of the tested hypotheses for the relationships between clinicopathological features, treatment response, and disease outcome and level of CHK2 expression and *TP53* gene status, and p53 expression together with *TP53* status in tumor tissues from PTC patients with and without *CHEK2* germline mutations.

| Variables | Models | P(M) | P(M\|data) | $BF_{10}$ |
|---|---|---|---|---|
| CHK2 expression and response to therapy | Log odds ratio = 0 | 0.500 | 0.104 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.007 | 0.135 |
| | Log odds ratio < 0 | 0.250 | 0.889 | 17.031 |
| CHK2 expression and final follow-up | Log odds ratio = 0 | 0.500 | 0.088 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.007 | 0.168 |
| | Log odds ratio < 0 | 0.250 | 0.905 | 20.554 |
| CHK2 expression and tumor diameter | Log odds ratio = 0 | 0.500 | 0.288 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.025 | 0.174 |
| | Log odds ratio < 0 | 0.250 | 0.687 | 4.766 |
| CHK2 expression and PTC histologic variant | Log odds ratio = 0 | 0.500 | 0.289 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.039 | 0.273 |
| | Log odds ratio < 0 | 0.250 | 0.671 | 4.646 |
| *TP53* gene status and age | Log odds ratio = 0 | 0.500 | 0.308 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.033 | 0.212 |
| | Log odds ratio < 0 | 0.250 | 0.659 | 4.280 |
| *TP53* gene status and vascular invasion | Log odds ratio = 0 | 0.500 | 0.096 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.010 | 0.208 |
| | Log odds ratio < 0 | 0.250 | 0.894 | 18.553 |
| p53 expression + *TP53* gene status and age | Log odds ratio = 0 | 0.500 | 0.280 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.024 | 0.170 |
| | Log odds ratio < 0 | 0.250 | 0.696 | 4.962 |
| p53 expression + *TP53* gene status and vascular invasion | Log odds ratio = 0 | 0.500 | 0.252 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.029 | 0.233 |
| | Log odds ratio < 0 | 0.250 | 0.719 | 5.713 |

Abbreviations: P(M), prior model probability; P(M|data), posterior model probability; $BF_{10}$, Bayes factor giving the evidence for H1 over H0; CHK2 expression, CHK2 expression (loss/low/high) as determined by IHC; *TP53* gene status, *TP53* no loss/deletion of a gene copy in tumor tissue as determined by FISH; FISH, fluorescence in situ hybridization; p53, positive/negative p53 expression as determined by IHC; IHC, immunohistochemistry

Table S2: Predictive value of tested hypotheses for the association between *CHEK2* gene status, CHK2 expression, and p53 expression together with *TP53* gene status in PTC patients with and without the *CHEK2* germline mutations

| Variable | | *CHEK2* truncating and WT | | | *CHEK2* truncating and WT + missense I157T | | |
|---|---|---|---|---|---|---|---|
| | Models | P(M) | P(M\|data) | $BF_{10}$ | P(M) | P(M\|data) | $BF_{10}$ |
| *CHEK2* gene status | Log odds ratio = 0 | 0.500 | 1.123e-10 | 1.000 | 0.500 | 1.898e-15 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 1.000 | 1.781e+10 | 0.250 | 1.000 | 1.054e+15 |
| | Log odds ratio < 0 | 0.250 | 2.610e-12 | 0.046 | 0.250 | 3.282e-17 | 0.035 |
| CHK2 expression | Log odds ratio = 0 | 0.500 | 0.312 | 1.000 | 0.500 | 0.383 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.659 | 4.215 | 0.250 | 0.586 | 3.058 |
| | Log odds ratio < 0 | 0.250 | 0.029 | 0.185 | 0.250 | 0.032 | 0.165 |
| p53 expression and *TP53* gene status | Log odds ratio = 0 | 0.500 | 0.370 | 1.000 | 0.500 | 0.165 | 1.000 |
| | Log odds ratio > 0 | 0.250 | 0.590 | 3.194 | 0.250 | 0.823 | 9.999 |
| | Log odds ratio < 0 | 0.250 | 0.040 | 0.215 | 0.250 | 0.013 | 0.152 |

Abbreviations: *CHEK2* gene status, no loss/deletion of a *CHEK2* gene copy; *TP53* gene status, no loss/deletion of a *TP53* gene copy as determined by FISH; FISH, fluorescence in situ hybridization; p53 expression, negative/positive as determined by IHC; IHC, immunohistochemistry; *CHEK2* truncating, germline heterozygous truncating *CHEK2* mutation variants (1100delC, IVS2+1G>A, del5395); WT, wild type.