

ORIGINAL ARTICLE

Spectrum of EGFR aberrations and potential clinical implications: insights from integrative pan-cancer analysis

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Abstract

Background: Human epidermal growth factor receptor (*EGFR*) is an oncogenic gene and one of top targets of precision therapy in lung cancer with *EGFR* mutations. Although there are many reports for some individual cancers, comprehensive profiling of *EGFR* mutations, overexpression, amplification, DNA methylation, and their clinical associations across many different cancers simultaneously was not available. This study aimed to fill the gap and provide insights to the alteration spectrum of *EGFR* and its therapeutic and prognostic implications.

Methods: The Cancer Genome Atlas (TCGA) datasets for 32 cancer types involving 11,314 patients were analyzed for alterations (mutations and amplification/deletion), abnormal expression and DNA methylation in *EGFR* gene. Mutation frequency, genomic location distribution, functional impact, and clinical targeted therapy implication were compared among different cancer types, and their associations with patient survival were analyzed.

Results: *EGFR* alteration frequency, mutation sites across functional domains, amplification, overexpression, and DNA methylation patterns differed greatly among different cancer types. The overall mutation frequency in all cancers combined was relatively low. Targetable mutations, mainly in lung cancer, were primarily

Abbreviations: aa, amino acid; ACC, adrenocortical carcinoma; ACMG, American College of Medical Genetics and Genomics; AML, acute myeloid lymphoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CCLE, Cancer Cell Line Encyclopedia; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; CNV, copy number variant; COAD, colon adenocarcinoma; DFS, disease-free survival; DLBC, lymphoid neoplasm diffuse large B-cell lymphoma; EGFR, epidermal growth factor receptor; ESCA, esophageal carcinoma; FDA, Food and Drug Administration; GBM, glioblastoma multiforme; GDC, Genomic Data Commons; GTEx, Genotype-Tissue Expression; HNSC, head and neck squamous cell carcinoma; ICGC, the International Cancer Genome Consortium; Indel, insertion/deletion; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LGG, brain lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MAPK, mitogen-activated protein kinase; MESO, mesothelioma; NSCLC, non-small-cell lung cancer; OS, overall survival; OV, ovarian serous cystadenocarcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PI3K, phosphoinositide 3-kinase; PKB, protein kinase B; PRAD, prostate adenocarcinoma; RAF, rapidly accelerated fibrosarcoma; RAS, rat sarcoma; RTK, receptor tyrosine kinases; SARC, sarcoma; SKCM, skin cutaneous melanoma; SNV, single nucleotide variant; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; TGCT, testicular germ cell tumors; THCA, thyroid carcinoma; THYM, thymoma; TKIs, tyrosine-kinase inhibitors; TPM, transcripts per million; UCEC, uterine corpus endometrial carcinoma; UCS, uterine carcinosarcoma; UVM, uveal melanoma.

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found in the Pkinase_Tyr domain. Glioblastoma multiforme had the highest rate of alterations, but it was dominated by gene amplification and most mutations were in the Furin-like domain where targeted therapy was less effective. Low-grade glioma often had gene amplification and increased *EGFR* expression which was associated with poor outcome. Colon and pancreatic adenocarcinoma had very few *EGFR* mutations; however, high *EGFR* expression was significantly associated with short patient survival. Squamous cell carcinoma regardless of their sites (the head and neck, lung, or esophagus) exhibited similar characteristics with an alteration frequency of about 5.0%, was dominated by gene amplification, and had increased *EGFR* expression generally associated with short patient survival. DNA methylation was highly associated with *EGFR* expression and patient outcomes in some cancers.

Conclusions: *EGFR* aberration type, frequency, distribution in functional domains, and expression vary from cancer to cancer. While mutations in the Pkinase_Tyr domain are more important for treatment selection, increased expression from amplification or deregulation affects more tumor types and leads to worse outcome, which calls for new treatment strategies for these *EGFR*-driven tumors.

KEY WORDS

EGFR expression, *EGFR* mutation, epidermal growth factor receptor, pan-cancer profiling, patient survival, targeted therapy, The Cancer Genome Atlas (TCGA)

1 | BACKGROUND

The human epidermal growth factor receptor (*EGFR*) family, also known as the HER family of receptor tyrosine kinases (RTK), consists of four members—*EGFR*, *ERBB2*, *ERBB3*, and *ERBB4* [1, 2]. Five functional domains are characterized for *EGFR* according to the database of protein families (Pfam, <http://pfam.xfam.org/protein/P00533>): Recep_L (57-168aa), Furin-like (177-338aa), Recep_L (361-481aa), GF_recep_IV (505-637aa), and Pkinase_Tyr domains (712-968aa). The Recep_L domains contain ligand binding sites; the Furin-like domain is a cysteine rich region involved in signal transduction and receptor aggregation; the GF_recep_IV domain regulates the binding of a ligand to the Recep_L domains; and the Pkinase_Tyr domain performs the phosphorylation function [3].

Upon stimulation by its ligands, dimerization (both homodimerization and heterodimerization) of *EGFR* results in its intracellular tyrosine kinase activation and autophosphorylation at multiple tyrosine residues, which activates a number of downstream signaling cascades that not only promote proliferation, growth, and survival of normal cells but also contribute to processes that are crucial to cancer progression, including angiogenesis, metastasis, and apoptosis [4, 5]. The best known involved pathways include the rat sarcoma (Ras)/mitogen-activated protein kinase (MAPK) and phosphoinositide 3-kinase (PI3K)/protein kinase B (PKB)

signaling pathways, whose roles in promoting tumor growth, survival, and progression are well characterized [6].

EGFR is one of the first few identified oncogenes and is a key treatment target in clinical oncology [7-10]. It is frequently activated by gene mutation, amplification, or overexpression through abnormal regulation in human cancers. Among *EGFR*-associated cancers, pancreatic adenocarcinoma (PAAD) has an extremely poor prognosis, which usually results in death within several months after diagnosis [11, 12]. In cancers like non-small-cell lung cancer (NSCLC) [13] and colon adenocarcinoma (COAD) [14], *EGFR* mutation status is considered as a poor prognostic factor, which is often associated with a more aggressive behavior and decreased patient survival.

Because of the critical roles of *EGFR* in cancers, various treatment strategies, including tyrosine kinase inhibitors (TKIs, small-molecule inhibitors, which bind to the ligand-binding site on the extracellular domain) [15], antibody-based therapy [16], immunotherapy [17], and preclinical trials of RNA interference therapies [18], have been developed to inhibit its activities and thus control tumor growth and progression. When the ligand binding with *EGFR* is prevented by monoclonal antibodies or TKIs, it dampens signal transduction through pathways such as the RAS/rapidly accelerated fibrosarcoma (RAF)/MAPK and PI3K/PKB cascades [2, 19]. Such treatments are very effective and provide significantly improved patient outcomes, particularly

for lung adenocarcinoma (LUAD) patients with *EGFR* mutations [20, 21]. However, successful applications of TKIs to other cancers are less certain [22]. Although many literature reports are available on *EGFR* mutation, overexpression, or amplification for particular cancer types [12-14, 23, 24], a simultaneous comprehensive profiling over multiple cancer types to explore their similarity and difference is not available. Such information is important to understand what other cancers are more likely to benefit from such targeted therapy and what role *EGFR* plays among different cancers.

Taking advantage of the large datasets from The Cancer Genome Atlas (TCGA), we systematically profiled the mutation, copy number, expression, and DNA methylation patterns of *EGFR* across 32 cancer types. We first examined the patterns of *EGFR* mutations, including single nucleotide variant (SNV) and short insertion/deletion (indel), across tumors and their implications for targeted therapies. Copy number variants (CNVs) and their impact on gene expression and clinical outcomes were investigated next. For cancers without gene amplification, we further looked into gene expression patterns, their association with clinical outcomes, contribution of DNA methylation to gene abnormal expression, and impact of DNA methylation on patient overall survival (OS).

2 | DATA SOURCES AND METHODS

2.1 | *EGFR* mutation and CNV data from TCGA provisional dataset

Mutation data from whole exome sequencing, CNVs from GISTIC for *EGFR* gene, and clinical data were downloaded and formatted from the cBioportal (<https://www.cbioportal.org/>), a web resource for exploring, visualizing, and analyzing multidimensional cancer genomics databases, such as TCGA [25], the International Cancer Genome Consortium (ICGC) [26], Cancer Cell Line Encyclopedia (CCLE) [27]. We selected the more inclusive TCGA provisional cohort, which was retrieved on Feb 26th, 2019 consisting of 11,314 patients with 11,410 samples across 32 histopathologic cancer types and representing most major classes of human adult cancers [28, 29]. The mutation data included SNVs, indels, and CNVs (defined by GISTIC 2.0 as following for log ratio value: $-2/-1$ = deletion; 0 = diploid; 1 = gain; 2 = amplification).

2.2 | *EGFR* expression and methylation data in normal and cancer tissues

EGFR expression in normal tissues was examined in RNA sequencing (RNA-seq) data from The Genotype-Tissue Expression (GTEx) (<https://www.gtexportal.org/home/>),

which consisted of 11,688 samples from 53 tissue types/organs. Transcripts per million (TPM) was used to compare the relative expression levels of *EGFR* from different organs or sub-locations of an organ. Expression and DNA methylation data in tumors and their paired normal samples were obtained from TCGA Genomic Data Commons (GDC) portal (<https://portal.gdc.cancer.gov/>), which included data for 32 cancer types. The expression data was pre-processed and normalized using upper quartile of 1000. The genome-wide profile of human DNA methylation was generated using Infinium Human Methylation 450K BeadChip (Illumina, San Diego, CA, USA).

2.3 | Data analysis

For differential expression of *EGFR* between tumors and their paired normal samples in each cancer type, the expression data was log₂ transformed, and two-group *t* test was performed for those tumor types with at least two normal samples (22 out of 32 tumor types). The log₂ fold change and significant *P* value (minus log₁₀) were plotted by using the Volcano plot for each cancer type. As TCGA had a limited number of paired normal samples or not at all for several tumor types, we further examined the differential expression data from Gene Expression Profiling Interactive Analysis (GEPIA, <http://gepia.cancer-pku.cn/index.html>) [30], a web server for exploring and analyzing RNA-seq data of 9736 tumor samples and 8,587 normal samples from TCGA and the GTEx projects using a uniform processing pipeline and normalization method.

OS and disease-free survival (DFS), defined as the duration from diagnosis to death or recurrence, were analyzed using the Kaplan-Meier method. The hazard ratio and 95% confidence intervals were plotted by R package 'forestplot'. Each CpG's methylation correlation with *EGFR* expression was analyzed using Pearson correlation. The prognostic values of *EGFR* alterations and its CpG methylation were analyzed with Cox proportional hazard model.

All data analyses were conducted using the R package, version 3.5.3 (<https://www.r-project.org/>) unless specifically stated.

3 | RESULTS

3.1 | *EGFR* somatic mutation patterns across tumor types

The overall *EGFR* mutation frequency was 2.8% (320/11,410) for all tumor samples and 2.4% (268/11,314) for all patients across the 32 tumor types. The most common tumors with *EGFR* mutations were glioblastoma multiforme (GBM,

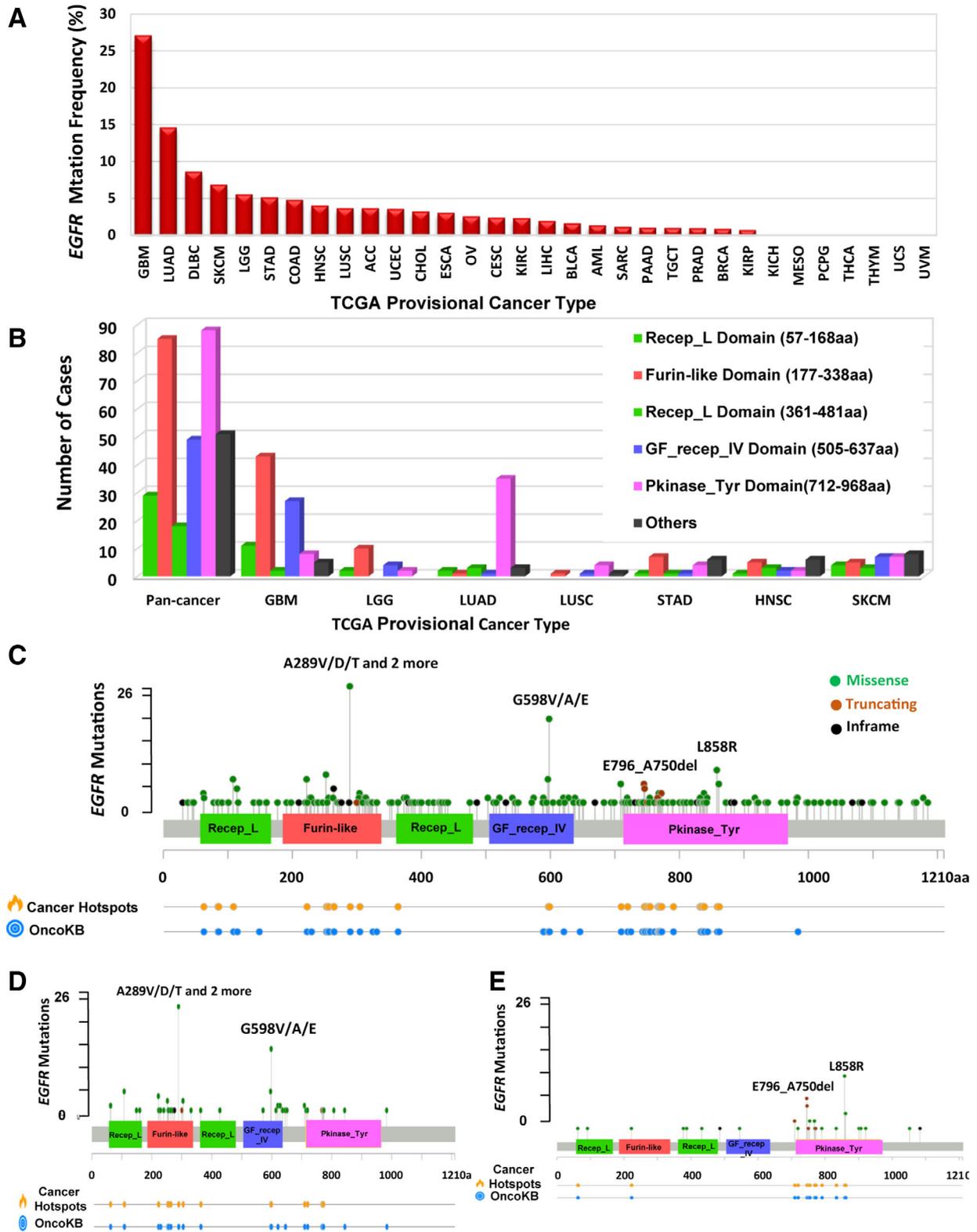


FIGURE 1 EGFR mutation distribution in different cancer types and protein functional domains. **A** EGFR mutation frequency in 32 TCGA provisional cancer types. **B** EGFR mutations in different functional domains in all and top 7 cancer types. **C** EGFR mutation distribution over different functional domains of EGFR for all cancers together. **D** EGFR mutation distribution over different functional domains of EGFR in GBM. **E** EGFR mutation distribution over different functional domains of EGFR in LUAD. Abbreviations: aa: amino acid; ACC: adrenocortical carcinoma; AML: acute myeloid lymphoma; BLCA: bladder urothelial carcinoma; BRCA: breast invasive carcinoma; CESC: cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL: cholangiocarcinoma; COAD: colon adenocarcinoma; DLBC: lymphoid neoplasm diffuse large B-cell lymphoma; EGFR: epidermal growth factor receptor; ESCA: esophageal carcinoma; GBM: glioblastoma multiforme; HNSC: head and neck

26.8%), LUAD (14.4%), diffuse large B-cell lymphoma (DLBC, 8.3%), and skin cutaneous melanoma (SKCM, 6.5%). On the contrary, kidney chromophobe cell carcinoma (KICH), mesothelioma (MESO), pheochromocytoma and paraganglioma (PCPG), thymoma (THYM), thyroid carcinoma (THCA), uterine carcinosarcoma (UCS), and uveal melanoma (UVM) showed almost no *EGFR* mutations (Figure 1A). The total number of samples for each cancer type varied from 48 (DLBC) to 1105 (breast invasive carcinoma [BRCA]), and those with too few samples might not reflect the complete picture of *EGFR* mutation status (Supplementary Table S1).

The 320 *EGFR* somatic mutations (from 268 tumor samples) were observed across all cancer types and were widely distributed along different functional domains of *EGFR* gene. The most common ones were the Pkinase_Tyr domain (88 samples) and the Furin-like domain (85 samples), followed by the GF_recep_IV domain (45 samples). The location distribution of these *EGFR* mutations was dramatically different among different cancers (Figure 1B, Supplementary Table S2). Mutations in GBM and brain lower-grade glioma (LGG) were most commonly located in the Furin-like domain, about 5 times more than the mutations located in the Pkinase_Tyr domain. On the contrary, mutations in NSCLC were primarily in the Pkinase_Tyr domain, especially for LUAD, which amounted to four fifths of all mutations. Mutations in stomach adenocarcinoma (STAD), head and neck squamous cell carcinoma (HNSC), and SKCM were mostly in other domains whose functions were less known.

From functional impact on protein coding, these 320 *EGFR* mutations were classified into three categories: missense (280 mutations), truncating (21 mutations), and in-frame insertion/deletions (19 mutations) (Figure 1C). The 289aa in the Furin-like domain was the most frequently mutated position, which was observed in 27 samples (3 samples with A289D, 1 with A289I, 1 with A289N, 6 with A289T, 15 with A289V, and 1 with A289Rfs*9). The mutations at this position almost exclusively occurred in GBM samples (25/27) (Figure 1D). A289V is known to be oncogenic, while other mutation types (A289D/T/N/I) are likely oncogenic. None of these mutations are known to be targetable. The only other tumor with mutations at this position was HNSC (1 sample with A289T and 1 with A289Rfs*9), and their importance was little known to this cancer. The second most mutated position was 598aa in the GF_recep_IV domain: 16 GBMs had G598V, 2 GBMs had G598A, and 1 esophageal squamous cell carcinoma (ESCC)

had G598E. These mutations might affect ligand-receptor binding and are likely oncogenic. Most mutations in LUAD (35 of 45 mutations) were located in the Pkinase_Tyr domain, especially at the positions of 858aa (8 samples with L858R) and 746-750aa (6 with E746_A750del, 2 with L747_E749del, and 1 with L747_T751del) (Figure 1E).

Each somatic gene mutation can be classified by their oncogenic effect and predictive significance [31]. As shown in Figure 2, 83 (25.9%) *EGFR* mutations were oncogenic, 34 (10.6%) likely oncogenic, 27 (8.4%) predicted oncogenic, 5 (1.6%) likely neutral, 3 (0.9%) inconclusive, and 168 (52.5%) unknown. Over half of them were in the unknown class, highlighting the challenge in mutation interpretation.

According to clinical targeted therapy implication [32], the 320 *EGFR* mutations could be divided into 7 levels (Supplementary Table S1): Level 1 (30 mutations), Level 2B (5 mutations), Level 3A (1 mutation), Level 3B (5 mutations), Level 4 (33 mutations), Level NA (244 mutations), and Level R1 (2 mutations). Only Level 1 and Level R1 mutations were indicated for or against targeted therapy currently with a Food and Drug Administration (FDA)-approved drug [33]. All Level 1 mutations were found in NSCLC (28 in LUAD and 2 in lung squamous cell carcinoma [LUSC]), and these mutations were concentrated in exons 19-21, which included L858R, L861Q, G719A, S768I, L833F, E796_A750del, L747_E749del, E709_T710delinsD, L747_T751del, and T751_E758del (Figure 3). LUAD harbored the highest proportion of oncogenic/likely oncogenic mutations (66.7%), and almost all were Level 1 mutations (28 of 30 mutations). Although the oncogenic/likely oncogenic mutations accounted for 57.9% and 50.0% of GBM and LGG samples, respectively, most of them were in Level 4 and Level NA without treatment implications.

3.2 | *EGFR* CNVs in different tumor types

The overall *EGFR* CNV frequency was about 5.0% (detected in 569 of 11,410 samples). Almost all were amplification (in 549 of 569 samples), only 20 samples with deletion (Figure 4A). The most common solid tumors with *EGFR* CNVs were GBM (43.9%), ESCA (14.1%), HNSC (10.9%), LUSC (7.6%), and LGG (7.4%). DLBC, kidney renal clear cell carcinoma (KIRC), MESO, THCA, THYM, UCS, and UVM were not affected with any CNV (Figure 4A). Among the 320 samples with *EGFR* mutations described above, 213 also had

squamous cell carcinoma; KICH: kidney chromophobe; KIRC: kidney renal clear cell carcinoma; KIRP: kidney renal papillary cell carcinoma; LGG: brain lower-grade glioma; LIHC: liver hepatocellular carcinoma; LUAD: lung adenocarcinoma; LUSC: lung squamous cell carcinoma; MESO: mesothelioma; OV: ovarian serous cystadenocarcinoma; PAAD: pancreatic adenocarcinoma; PCPG: pheochromocytoma and paraganglioma; PRAD: prostate adenocarcinoma; SARC: sarcoma; SKCM: skin cutaneous melanoma; STAD: stomach adenocarcinoma; TCGA: The Cancer Genome Atlas; TGCT: testicular germ cell tumors; THCA: thyroid carcinoma; THYM: thymoma; UCEC: uterine corpus endometrial carcinoma; UCS: uterine carcinosarcoma; UVM: uveal melanoma

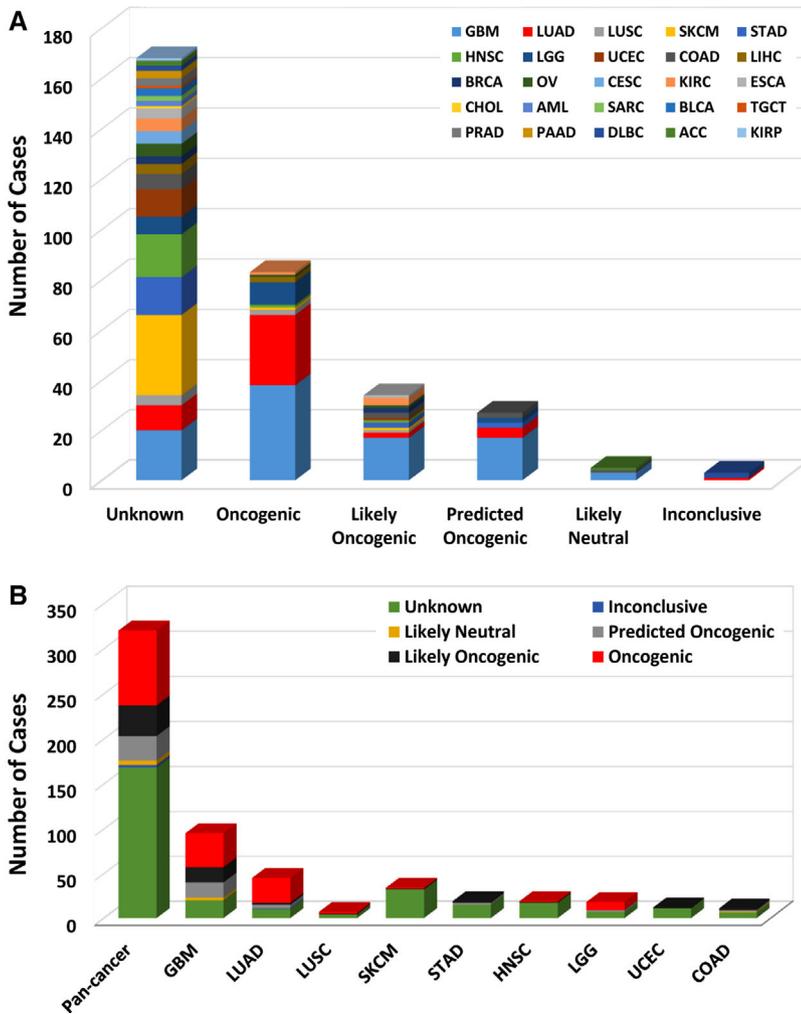


FIGURE 2 *EGFR* mutation classification by functional impacts. **A** *EGFR* mutations by functional impact on all tumors combined. **B** Functional impact class distribution of *EGFR* mutations for all cancer types together and for top 9 cancer types. According to the guideline of the American College of Medical Genetics and Genomics (ACMG), gene mutations are divided into 6 groups: oncogenic, likely oncogenic, predicted oncogenic, likely neutral, inconclusive, and unknown. Abbreviations as in Figure 1

EGFR CNV changes (Figure 4B, Supplementary Table S1), of which 108 with amplification, 101 with gain, and 4 with deletion. GBM and LUAD were two cancer types with the highest numbers of amplification or gain (Figure 4B).

3.3 | Combined *EGFR* alterations (mutation and CNV) in different cancer types

The combined *EGFR* mutation and CNV frequency in all tumors was about 7.0% (746 of 11,314 patients, 748 of 11,410 samples). However, the frequency among different cancers was dramatically different (Figure 5A). While KICH, MESO, THCA, THYM, USS, and UVM had neither *EGFR* mutation nor *EGFR* CNV, 273 of 591 (46.2%) GBM cases had CNV (33.2%), mutation (3.4%), or both (9.6%). Other cancers with dominant *EGFR* amplification but at much lower amplification rate included ESCA (13.0%), HNSC (9.4%), STAD (5.2%), LGG (5.4%), LUSC (6.4%), and BLCA (4.4%). Mutation was more common in DLBC (8.3% vs. 0.0%) and SKCM (5.2% vs. 0.2%). Although *EGFR* alteration frequencies of two lung cancer subtypes (LUAD and LUSC) were

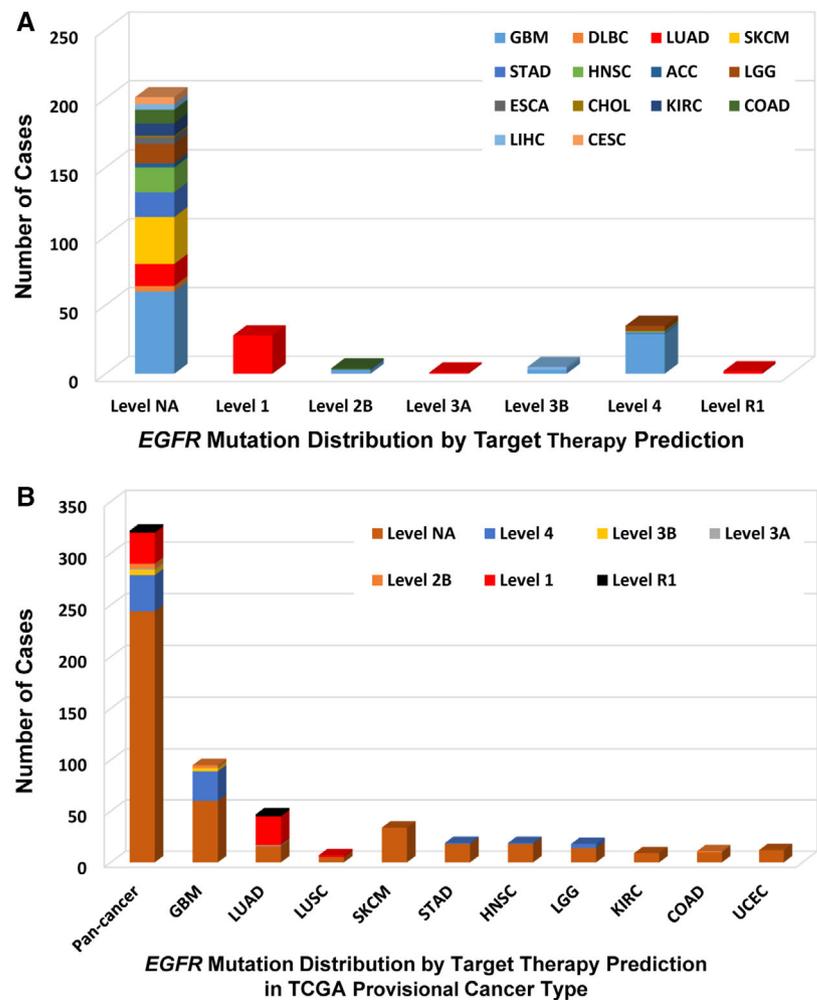
similar, the mutation frequency was slightly higher than that of amplification in LUAD (4.7% vs. 3.7%), while amplification was much more common than mutation in LUSC (6.4% vs. 0.6%).

Mutation location and CNV occurrence appeared to be associated. Over half of the mutations (47 of 82 mutations) in the Furin-like domain were accompanied by *EGFR* amplification, while nearly half of mutations (40 of 85 mutations) in the Pkinase_Tyr domain had copy gain. Mutations in the Recep_L domains and other function-unknown domains rarely had concurrent CNVs (Figure 5B).

3.4 | *EGFR* alterations and patient survival

In order to evaluate the clinical significance of *EGFR* alterations, we analyzed patient survival for pan-cancer and for each cancer type separately by alteration status (mutations and CNVs alone or in combination). When all tumors were analyzed together, patients with any *EGFR* alteration had significantly shorter median OS and DFS than those without *EGFR* alteration (both $P < 0.001$, Supplementary Figure S1). When

FIGURE 3 *EGFR* mutation distribution by targeted treatment implications as annotated in OncoKB among all tumor types and top cancer types. A *EGFR* mutation distribution of OncoKB therapeutic levels of evidence in all TCGA provisional cancer types. B *EGFR* mutation distribution of OncoKB therapeutic levels in top 10 cancer types. OncoKB therapeutic levels: “Level 1: Food and Drug Administration (FDA)-recognized biomarker predictive of response to an FDA-approved drug in this indication; Level 2B: Standard care biomarker predictive of response to an FDA-approved drug in another indication, but not standard care for this indication; Level 3A: Compelling clinical evidence supports the biomarker as being predictive of response to a drug in this indication; Level 3B: Compelling clinical evidence supports the biomarker as being predictive of response to a drug in another indication; Level 4: Compelling biological evidence supports the biomarker as being predictive of response to a drug; Level R1: Standard care biomarker predictive of resistance to an FDA-approved drug in this indication” [32]. Abbreviations as in Figure 1



analysis was performed for CNV and mutation separately, the presence of either aberration was associated with shortened patients' OS and DFS (all $P < 0.001$, Supplementary Figure S2 and S3).

For survival association in individual cancer types, only those cancer types with at least 10 tumor samples containing either *EGFR* mutations or CNVs were included in the analysis. Among patients with HNSC, LGG, or LUAD, *EGFR* amplification was associated with short survival (Figure 6A). However, *EGFR* somatic SNV/indel mutations appeared not affecting patient survival although only 5 cancer types with at least 10 samples containing *EGFR* mutations could be analyzed (Figure 6B). This low mutation frequency might lead to an insufficient power to detect the small effect of mutations on survival. Not surprisingly, *EGFR*-amplified tumors had significantly higher *EGFR* expression than those without *EGFR* amplification in all 9 cancers types (all $P < 0.001$, Figure 6C); however, there was no much *EGFR* expression difference between tumors with or without *EGFR* mutations except that *EGFR* mutation status was associated with significantly increased *EGFR* expression in GBM ($P = 0.024$) and LUAD ($P = 0.001$, Figure 6D).

3.5 | *EGFR* abnormal expression and clinical implications

The low *EGFR* mutation frequency in most cancer types made it difficult to assess its impact on patient survival yet, and the increased expression of *EGFR* wide type could be oncogenic driver for tumor development and progression and have a negative impact on patient survival. For this we were interested in the tumors with abnormal *EGFR* expression compared with their paired normal samples across different cancer types. We first examined *EGFR* expression in 53 types of normal tissues in GTEx samples. As shown in Figure 7A, the expression of *EGFR* was quite variable across different types of tissues, with the medians ranging from 2.22 TPM (the brain-spinal cord) to 73.91 TPM (the skin on the sun-exposed, lower leg). EBV-transformed lymphocytes and whole blood virtually barely had *EGFR* expression. The skin (both sun-exposed and not exposed) had the highest expression.

We then compared *EGFR* expression between tumors and their paired normal samples profiled in TCGA. Among the 32 tumor types, 22 had at least two normal samples. Differential expression was found in 10 cancer types (all $P < 0.01$), with

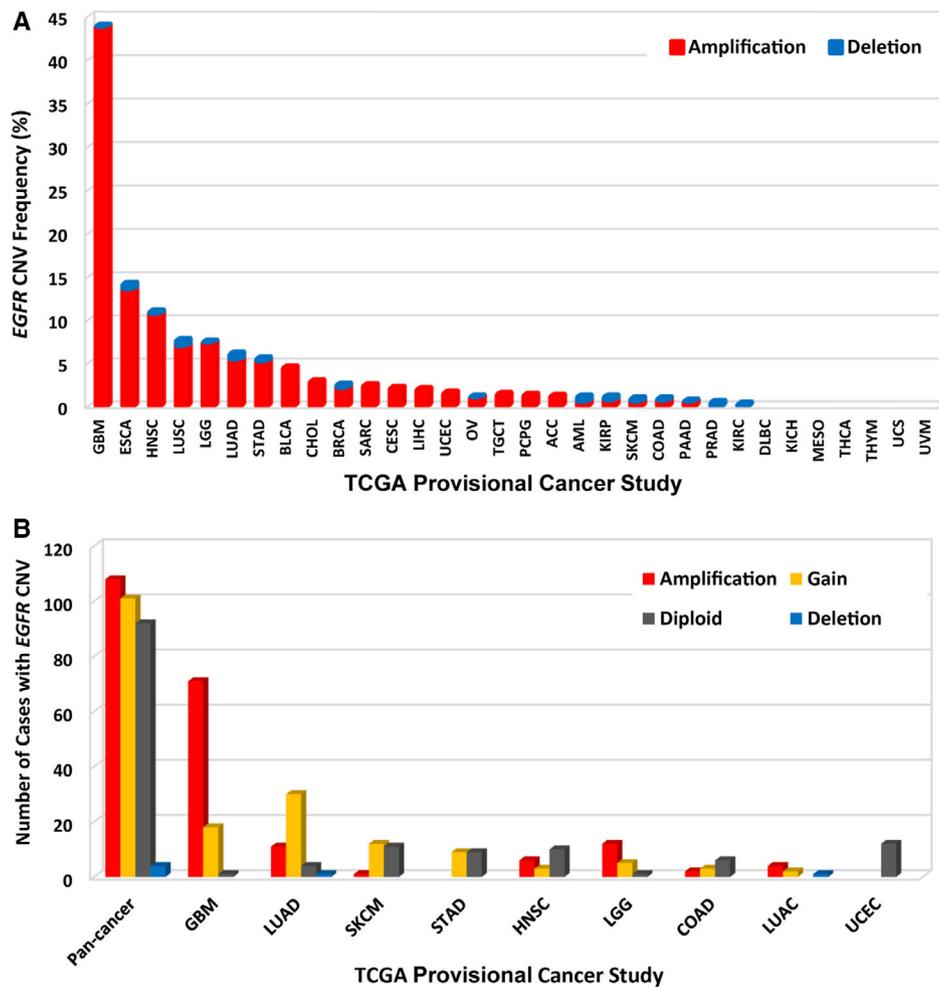


FIGURE 4 *EGFR* CNV distribution across all and selected top cancer types. A *EGFR* CNV frequency in 32 TCGA provisional cancer types. B *EGFR* CNV distribution in top 9 cancer types for the cases with *EGFR* mutations. Abbreviations: CNV: copy number variant; other abbreviations as in Figure 1. CNV is defined by GISTIC 2.0 as following: -2/-1 = deletion; 0 = diploid; 1 = gain; 2 = amplification

3 cancer types up-regulated (HNSC, LUSC, and KIRC) and 7 down-regulated (BRCA, cholangiocarcinoma [CHOL], uterine corpus endometrial carcinoma [UCEC], liver hepatocellular carcinoma [LIHC], COAD, prostate adenocarcinoma [PRAD], and kidney renal papillary cell carcinoma [KIRP]) (Figure 7B). The most noticeable was BRCA whose *EGFR* expression was reduced over 8 folds (\log_2 fold change = -3). The cancer type with the most increased expression was KIRC with over 2-fold increase. As some cancer types in TCGA did not have paired normal tissues or had too few, we further analyzed the data using GTEx normal samples as reference. Among different cancer types, GBM, LGG, KIRC, HNSC, ESCA, and LUSC all had higher *EGFR* expression than other cancer types (Supplementary Figure S4). Differential expression analysis from this expanded normal reference dataset showed similar results to the analysis of TCGA dataset. However, it revealed several additional cancer types with *EGFR* differential expression. *EGFR* expression was up-regulated in GBM, LGG, KIRC, and THYM but

down-regulated in adrenocortical carcinoma (ACC), BRCA, ovarian serous cystadenocarcinoma (OV), PCPG, SKCM, UCEC, and UCS (all $P < 0.01$, Figure 7C). In the normal brain tissues, *EGFR* had minimal expression; however, its expression in GBM and LGG was dramatically increased (20-fold increase for GBM and more than 10-fold increase for LGG). KIRC also had nearly 4-fold increase as compared with normal kidney tissues. Both ESCA and LUSC had a higher level of *EGFR* expression (about 2 folds) than their matching normal tissues. *EGFR* expression in SKCM was dramatically reduced relative to normal skin tissues; however, SKCM is thought to originate from melanocytes, and normal skin tissues have few such cells.

Survival association analysis using all tumors regardless of mutation or CNV status showed that increased *EGFR* expression was associated with short patient OS in bladder urothelial carcinoma (BLCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), COAD, HNSC, LGG, PAAD, SKCM, and STAD. Interestingly, increased

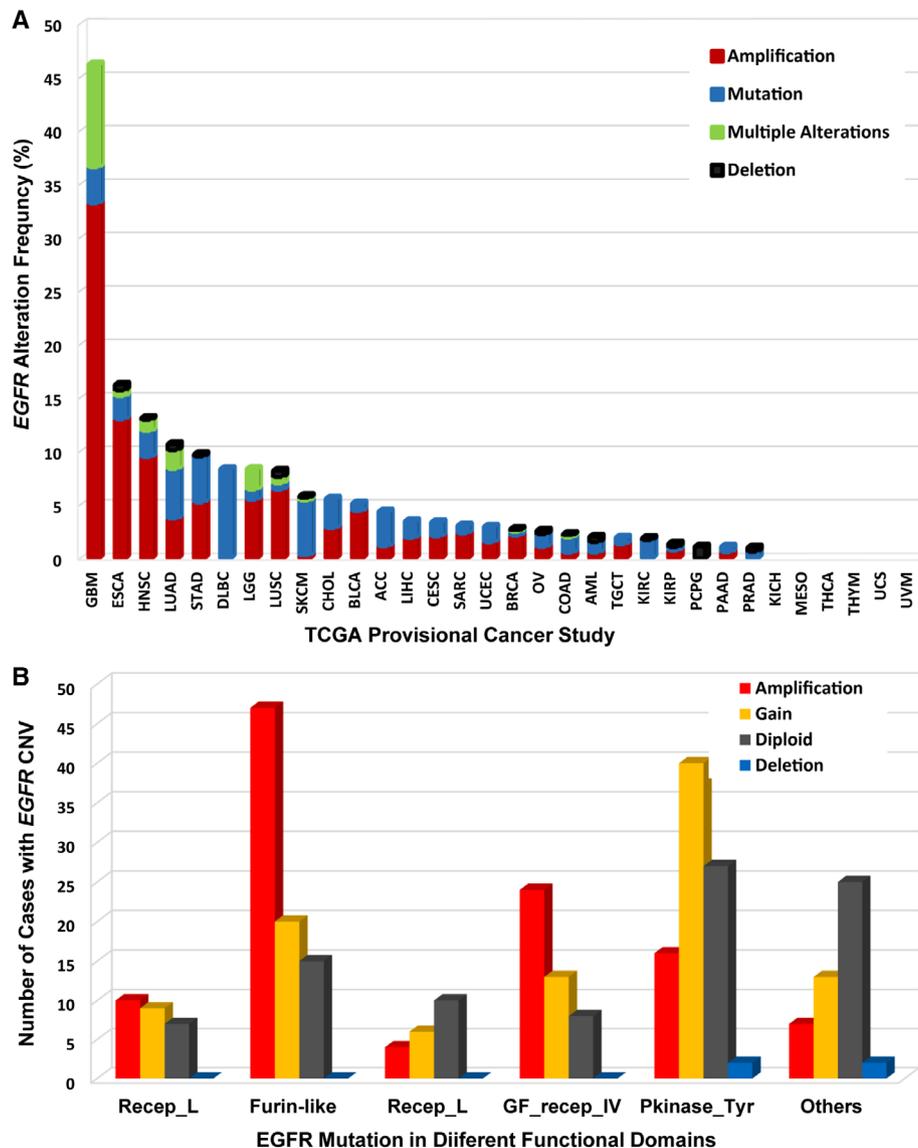


FIGURE 5 Combined *EGFR* alteration frequencies and their relationship. A Combined *EGFR* alteration (mutations and CNVs) frequency in 32 TCGA cancer types. B The relationship of *EGFR* mutation types and CNV types. C The distribution of CNV types along with mutations located in different domains. *EGFR* functional domains: Recep_L (57-168aa), Furin-like (177-338aa), Recep_L (361-481aa), GF_recep_IV (505-637aa), and Pkinase_Tyr domains (712-968aa). Abbreviations are the same as in Figure 1

EGFR expression was associated with better prognosis for KIRC (Figure 8A). As gene amplification is a major driver for increased expression, we then limited analysis to those samples without amplification (tumors with unknown CNV status were also excluded). The same association held for BLCA, CESC, COAD, PAAD, SKCM, and KIRC (Figure 8B).

3.6 | Associations of CpG methylation with *EGFR* expression and patient survival

For the tumors without *EGFR* amplification, we were interested in knowing if DNA methylation changes were responsible for or associated with abnormal expression of *EGFR*.

Therefore, we extracted the methylation data of the 49 CpG sites associated with *EGFR* for the same set of patients. We analyzed the associations of each CpG site with *EGFR* RNA expression for all tumors together (7,913 samples) and for each tumor type separately. Among the 49 CpG sites, 46 were significantly associated with *EGFR* expression after Bonferroni multiple testing correction ($P < 0.001$). Interestingly, all CpGs around the promoter region of *EGFR* (7 CpGs in TSS \pm 1500 or 5' UTR region) were negatively correlated with *EGFR* expression, while almost all (except 4) in the gene body were positively correlated with *EGFR* expression (Figure 9A). In individual cancer type analysis, most tumor types had the similar patterns of methylation association with gene expression in promoter and gene body, but a few

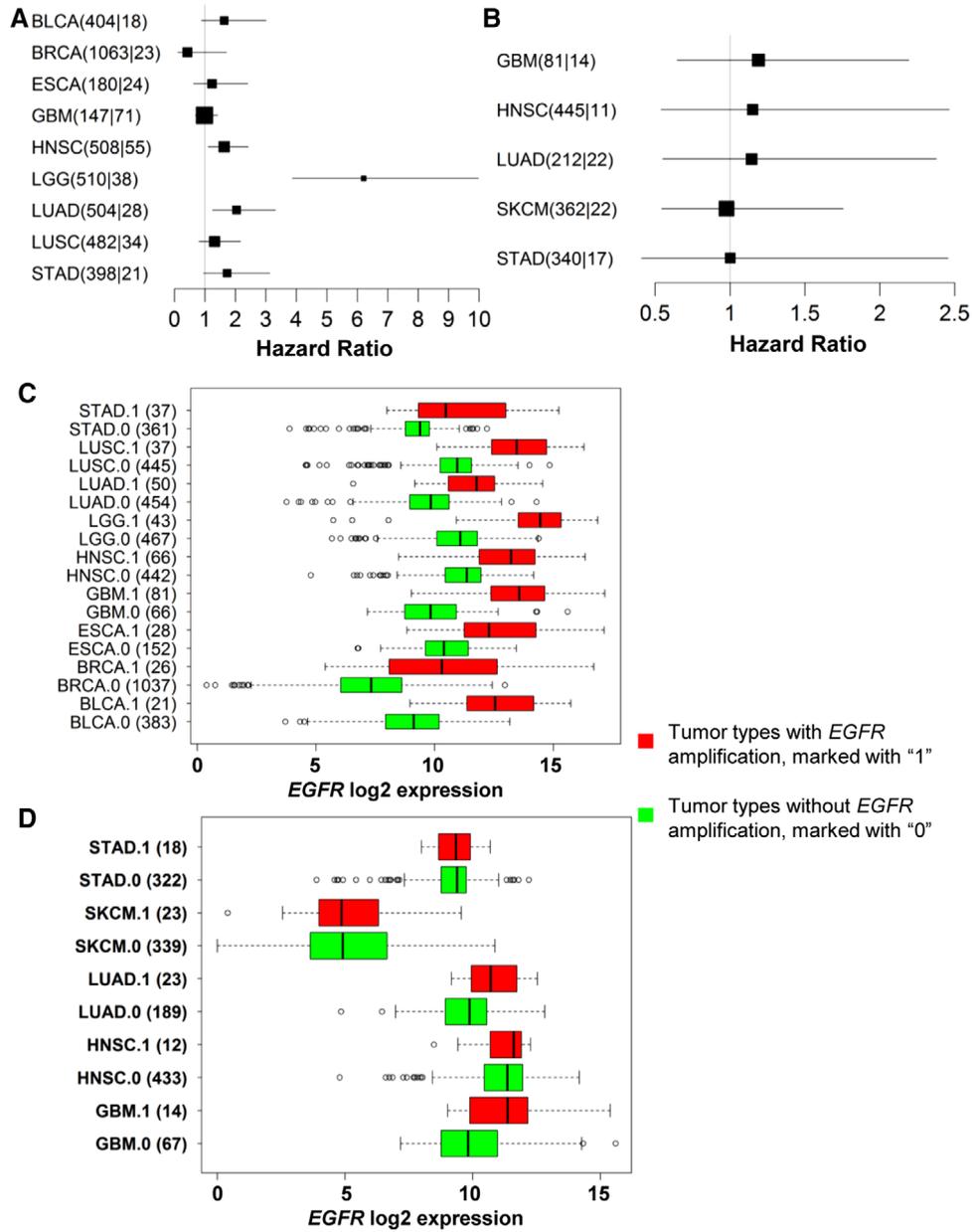
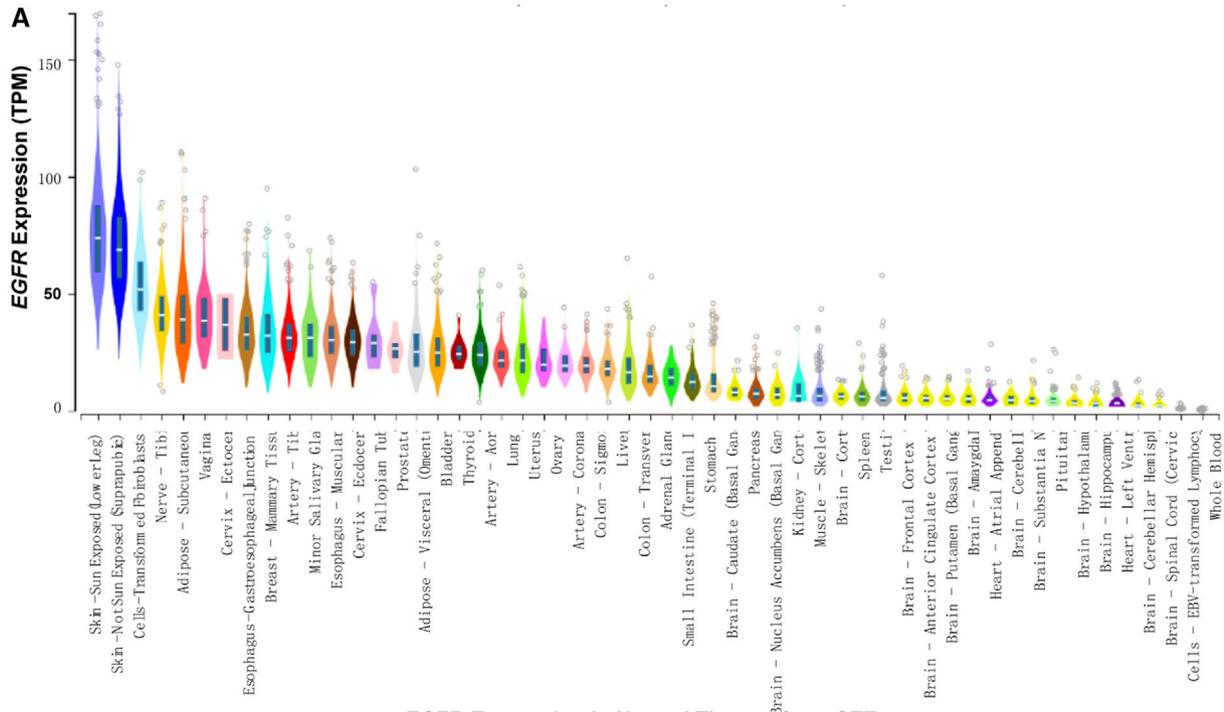
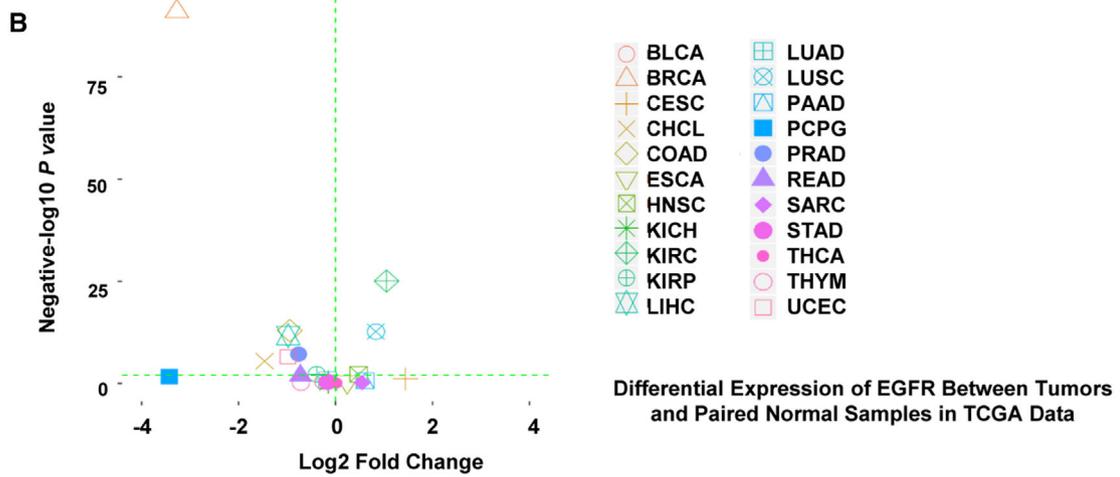


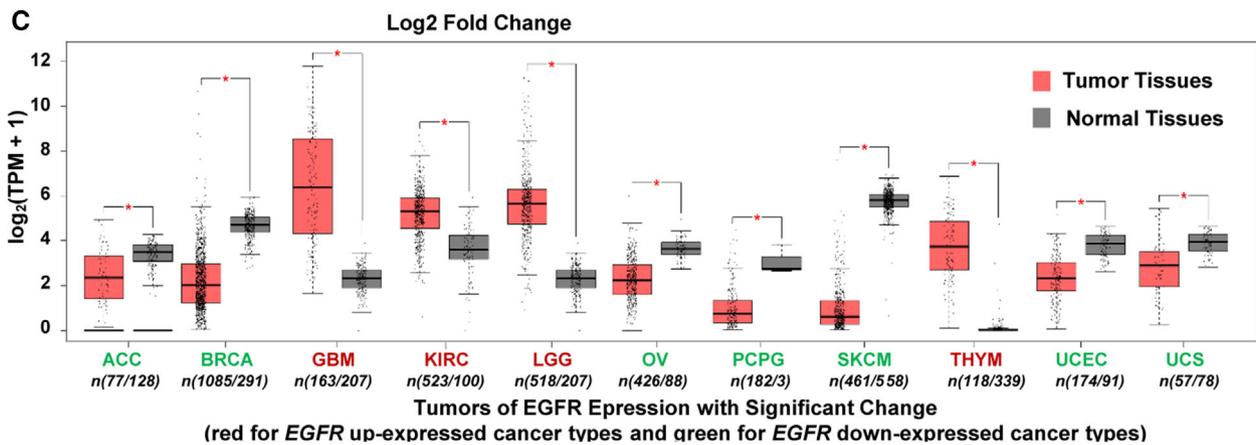
FIGURE 6 Association of *EGFR* amplification and somatic mutations with patient survival and *EGFR* expression. A Forest plot for the association between *EGFR* amplification and patient overall survival (OS). Only cancer types with at least 10 tumor samples containing amplification were analyzed. The sample size (number of samples without amplification | number of samples with amplification) of each cancer type is presented in parentheses. B Forest plot for the association between *EGFR* mutation status (SNVs and indels) and patient OS. Only cancer types with at least 10 tumor samples containing mutations were analyzed. Samples with CNVs were excluded from the analysis. The sample size (number of samples without mutations | number of samples with mutations) of each cancer type is presented in parentheses. Black boxes represent hazard ratio, and horizontal lines represent 95% confidence intervals. C *EGFR* expression in samples with and without *EGFR* amplification. Tumor types with *EGFR* amplification are marked with "1", and their data are presented as red boxes; tumor types without *EGFR* amplification are marked with "0", and their data are presented as green boxes. The numbers in parentheses are the sample sizes of indicated cancer types. *EGFR*-amplified tumors have significantly higher *EGFR* expression than those without *EGFR* amplification in all 9 cancers types (all $P < 0.001$). D *EGFR* expression in tumors with (marked with "1" and red box) and without (marked with "0" and green box) *EGFR* mutations. The numbers in parentheses are the sample sizes of indicated cancer types. There is no significant *EGFR* expression difference between tumors with or without *EGFR* mutations except that *EGFR* mutations was associated with slightly increased *EGFR* expression in GBM ($P = 0.024$) and LUAD ($P = 0.001$)



EGFR Expression in Normal Tissues from GTEx



Differential Expression of EGFR Between Tumors and Paired Normal Samples in TCGA Data



Tumors of EGFR Epression with Significant Change (red for EGFR up-expressed cancer types and green for EGFR down-expressed cancer types)

FIGURE 7 EGFR expression in normal and cancer tissues. A EGFR expression across 53 types of normal tissues. B Differential expression of EGFR between tumors and paired normal samples in TCGA datasets. C Differential expression of EGFR between tumors and normal samples using combined data from TCGA and GTEx datasets. EGFR expression is up-regulated in GBM, LGG, KIRC, and THYM, but down-regulated in ACC, BRCA, OV, SKCM, UCEC, and UCS (all $P < 0.01$). The sample size (number of tumor samples/number of normal samples) of each cancer type is presented in parentheses. Abbreviations: TPM, transcripts per million; other abbreviations as in Figure 1

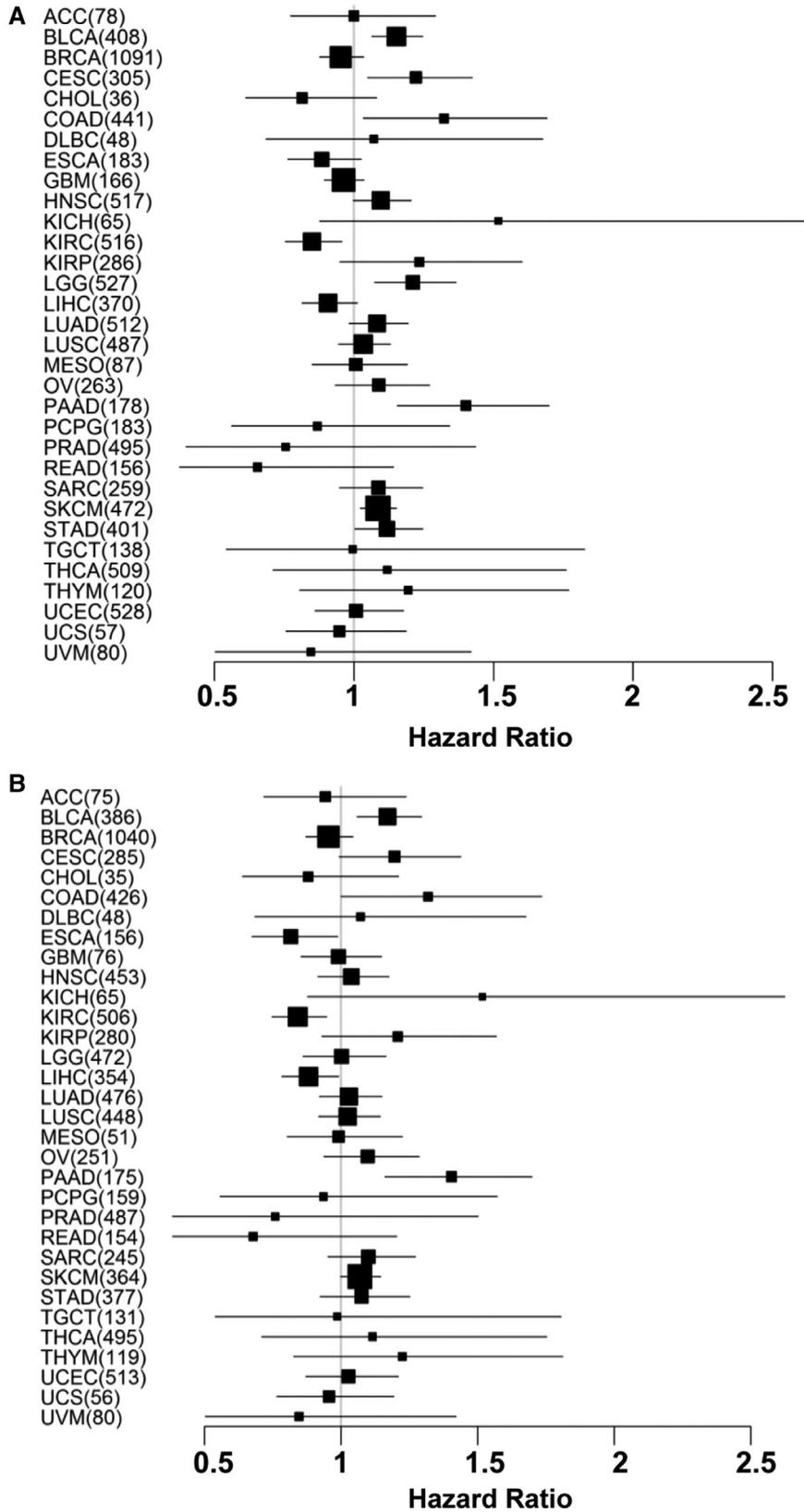


FIGURE 8 Association between *EGFR* expression and patient OS. A Forest plot of *EGFR* expression association with patient OS regardless of *EGFR* amplification status. B Forrest plot of *EGFR* expression association with patient OS for tumors without *EGFR* amplification. Black boxes represent hazard ratio, and horizontal lines represent 95% confidence intervals. The sample size of each cancer type is presented in parentheses. Abbreviations: OS: overall survival

others had predominant hypomethylation in both regions, such as GBM, LUSC, PRAD, THYM, KIRC, and KICH (Supplementary Figure S5). Survival analysis for all tumors with tumor type as a covariate only found 2 CpG sites

(cg07311521 and cg16751451) significantly associated with OS, and both were in the promoter region (TSS1500). Association analysis for each tumor type separately found 13 tumor types with at least 2 CpGs that were significantly associated

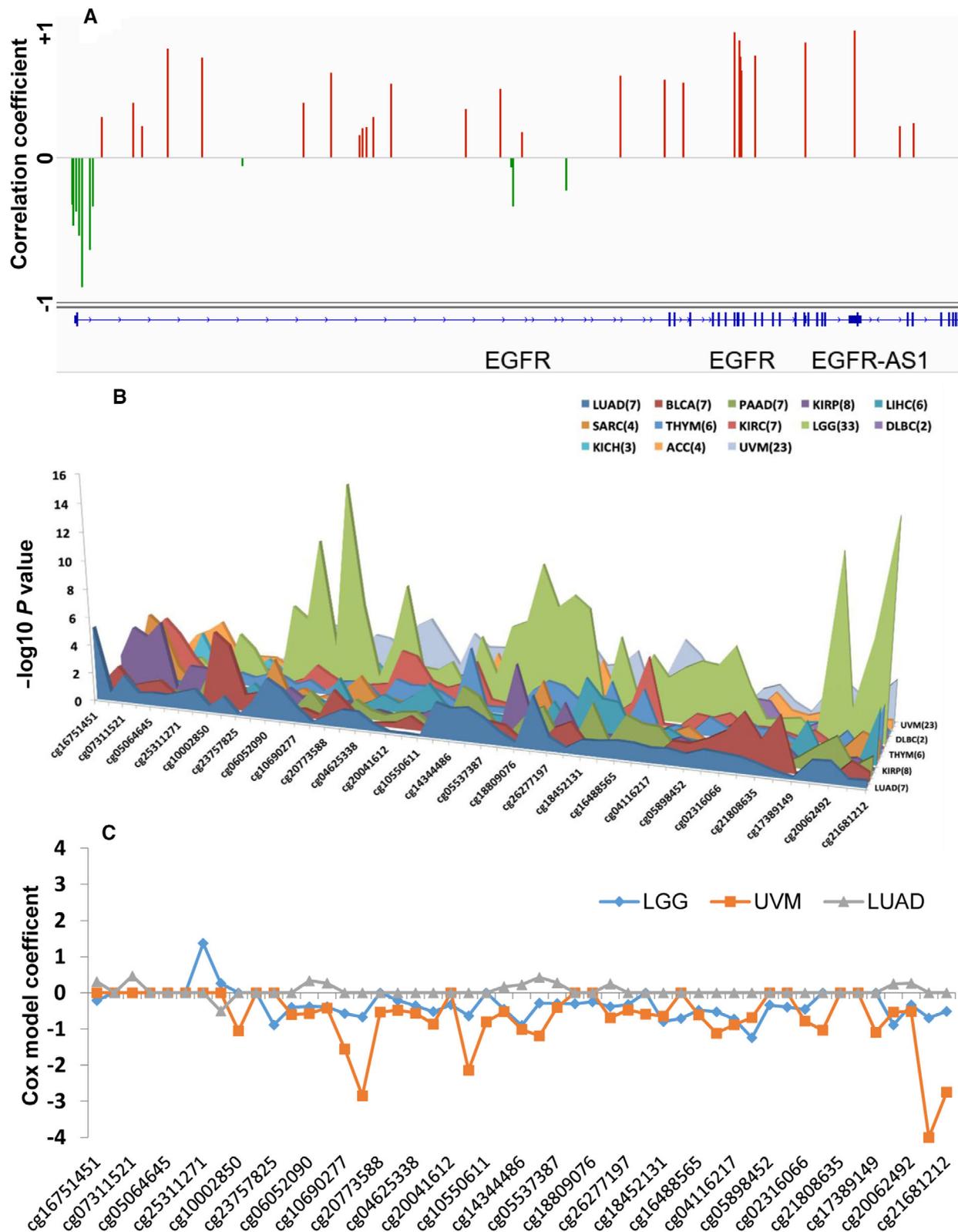


FIGURE 9 Associations of CpG methylation with EGFR expression and patient survival. **A** Correlation of CpG methylation with *EGFR* gene expression for all tumor types. CpGs in *EGFR* promoter are negatively correlated with *EGFR* expression, while CpGs in the gene body are positively correlated with gene expression with a few exceptions. **B** Survival association *P* value ($-\log_{10} P$ value) of each CpG site of *EGFR* gene for each tumor type. LGG and UVM have the highest numbers of CpGs significantly associated with patient survival. **C** Survival association direction and effect size (Cox model coefficient) for three selected tumor types (LGG, UVM, and LUAD). CpGs with *P* value greater than 0.05 are plotted as 0 for effect size (non-significance)

with OS (Figure 9B). LGG and UVM had the highest numbers of CpGs associated with patient survival (33 and 23 CpGs, respectively). For both cancer types, the CpGs with significant associations were mostly located in the gene body, where higher CpG methylation was associated with a better outcome. Higher methylation of one CpG in the promoter region was significantly associated with worse outcome of LGG. However, for LUAD (with 7 significant CpGs), their associations were mostly in opposite directions: hypermethylation of CpGs in the gene body was associated with worse outcome, while hypermethylation of one CpG in the promoter region was associated with better outcome (Figure 9C).

4 | DISCUSSION

Our analyses showed that *EGFR* mutation frequency, locations, and amplification differed greatly among different cancer types, which had important clinical implications. GBM had the highest rate of *EGFR* alterations, and amplification was the primary alteration. Somatic mutations generally occurred in the non-targetable Furin-like domain. Paradoxically, although *EGFR* expression in GBM was significantly increased, either by gene amplification or DNA methylation change, the expression level was not associated with patient OS. Other common tumor types with *EGFR* alterations include ESCA, HNSC, LGG, LUSC, and BLCA, all with similar characteristics: alteration frequency of about 5.0% and amplification as a dominant type. Except LGG, they were squamous or similar transitional cell origin. LUAD and STAD had similar frequencies of alternations, but their mutation and amplification patterns differed. On the other side of the spectrum, tumors such as DLBC and SKCM mainly had SNV mutations but rarely CNV; tumors including KIRC, MESO, THCA, THYM, UCS and UVM almost had no *EGFR* alterations.

Mutations in the Furin-like and Pkinase_Tyr domains accounted for most of *EGFR* single nucleotide or indel mutations. However, the Pkinase_Tyr domain was far more important in terms of targeted therapy with TKIs as 90% *EGFR* mutations in LUAD occurred in this region, particularly the exon 19 deletion and the L858R point mutation in exon 21. Mutations in these regions are proven predictive markers for effective TKI therapy for NSCLC in clinical practice [7, 33-35], with significantly prolonged survival as compared with traditional combination chemotherapy [21, 36, 37]. The mutation rate of NSCLC in this TCGA cohort appeared consistent with the previous report that these two mutations accounted for 85% to 90% of all *EGFR*-mutated NSCLC tumors [38, 39]. For other uncommon *EGFR* mutations in NSCLC, targeted therapy generated inconsistent results [34, 40-42]. It is clear that different *EGFR* mutations have very different implications, and only those resulting in destabilization of the equi-

librium between the active and inactive states of *EGFR* kinase activity may benefit from *EGFR* targeted therapy [43, 44].

The clinical significance of *EGFR* mutations in other regions of the gene is less defined. *EGFR* was first linked to the oncogenesis of GBM [45]. In this large TCGA dataset, the combined alteration rate (amplification, deletion, or mutation) reached 67.3% in GBM. However, this high alteration rate was mainly driven by a high frequency of gene amplification. Compared with LUAD, most *EGFR* mutations in GBM were located in extracellular domain or single-span transmembrane segment, which was known to be associated with tumorigenesis but not responsiveness to TKIs. Although *EGFR* amplification was a predictor of poor prognosis for several cancer types, it was not significantly associated with GBM, consistent with the paradox phenomenon reported in the literature [46]. Similarly, *EGFR* expression level was not prognostic in this dataset although some reports suggested otherwise [47]. The disagreement could be the results of multiple factors. The absence of well-known responsive mutations and presence of redundant and alternative compensatory pathways were among the most important escape mechanisms [48].

The prognostic role of *EGFR* in LGG appears clear. Both amplification and high expression of *EGFR* were correlated with short patient survival in this dataset as reported previously [49, 50]. More interestingly, we found that LGG had the highest number of CpGs whose methylation level was associated with patient survival (i.e., hypermethylation of CpGs in the gene body with better survival), which has not been reported before.

COAD and PAAD had very few *EGFR* mutations in this TCGA dataset. However, high *EGFR* expression was significantly associated with short patient survival. Studies have shown that inhibition of *EGFR* by TKIs or antibodies either alone or in combination with chemotherapy provided extended survival for patients with these cancers [51-53]. Unfortunately, the clinical benefit is generally not big enough for routine application.

Squamous cell carcinomas in the head and neck (HNSC), lung (LUSC), and esophagus (ESCA) have some commonalities: significantly increased *EGFR* expression, high frequency of *EGFR* amplification, and low rate of SNV/indel mutations. Targeted therapy with cetuximab or necitumumab (a monoclonal antibody targeting *EGFR*), along with radiotherapy or chemotherapy, have demonstrated promising efficacy and prolonged OS for locally advanced or recurrent and/or metastatic HNSC [54], ESCA [55-57], and LUSC [58, 59], which is now a new first-line treatment option in squamous NSCLC. The clear correlation between *EGFR* abnormal expression and treatment benefit highlights the importance of molecular profiling and predictive biomarkers for treatment selection.

This study profiled 32 cancer types. However, some rare cancer types did not have sufficient samples to capture the

full *EGFR* alteration and expression spectrum and establish small and moderate associations. The low frequency of *EGFR* mutation or amplification also made analysis challenging. It was mostly a pan-cancer global survey without deep dive on each cancer type. Several important leads revealed from this study are the directions of our future investigations.

5 | CONCLUSIONS

Our analysis provides a comprehensive view of *EGFR* mutation, abnormal expression, DNA methylation, and their interplay and clinical implications for 32 cancer types covering over ten thousand tumor samples. While some alternations are involved more in tumorigenesis, others are more therapeutic. Some cancer types have a higher frequency of *EGFR* alternations where mutation, amplification, or abnormal expression is associated with outcome or indicated for clinical action. Genomic profiling may provide guidance for their use in targeted therapy.

DECLARATIONS

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AUTHORS' CONTRIBUTIONS

HJL and ZFS conceived the study, performed the data analyses, interpreted the results, and wrote the manuscript. BZ provided suggestions and feedbacks to the design and implementation of the study. All authors read and approved the final manuscript.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

CONSENT FOR PUBLICATION

Not applicable.

COMPETING INTERESTS

The authors declare that they have no competing interests.

AVAILABILITY OF DATA AND MATERIALS

The datasets analyzed for this study are all publicly available as indicated in the Method section.

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SUPPORTING INFORMATION

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