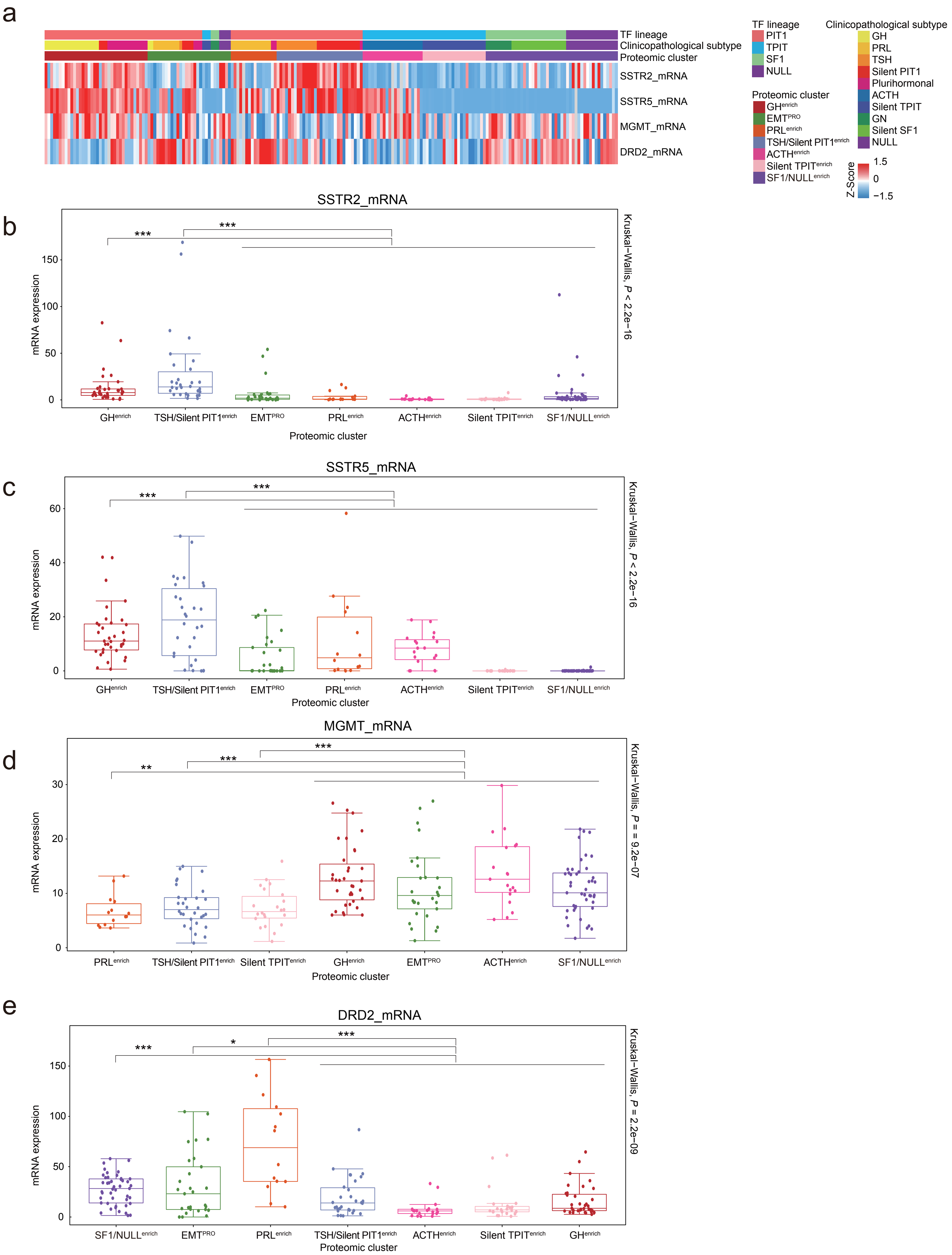
a
TF lineage
Clinicopathological subtype
Proteomic cluster
SSTR2_mRNA
SSTR5_mRNA
MGMT_mRNA
DRD2_mRNA
TF lineage
PIT1
TPIT
SF1
NULL
Proteomic cluster
GHenrich
EMTPRO
PRLenrich
TSH/Silent PIT1enrich
ACTHenrich
Silent TPITenrich
SF1/NULLenrich
Clinicopathological subtype
GH
PRL
TSH
Silent PIT1
Plurihormonal
ACTH
Silent TPIT
GN
Silent SF1
NULL
Z-Score
1.5
0
−1.5
b
SSTR2_mRNA
***
***
150
100
50
0
mRNA expression
GHenrich
TSH/Silent PIT1enrich
EMTPRO
PRLenrich
ACTHenrich
Silent TPITenrich
SF1/NULLenrich
Proteomic cluster
Kruskal−Wallis, P < 2.2e−16
c
SSTR5_mRNA
***
***
60
40
20
0
mRNA expression
GHenrich
TSH/Silent PIT1enrich
EMTPRO
PRLenrich
ACTHenrich
Silent TPITenrich
SF1/NULLenrich
Proteomic cluster
Kruskal−Wallis, P < 2.2e−16
d
MGMT_mRNA
***
***
**
30
20
10
0
mRNA expression
PRLenrich
TSH/Silent PIT1enrich
Silent TPITenrich
GHenrich
EMTPRO
ACTHenrich
SF1/NULLenrich
Proteomic cluster
Kruskal−Wallis, P = 9.2e−07
e
DRD2_mRNA
***
*
***
150
100
50
0
mRNA expression
SF1/NULLenrich
EMTPRO
PRLenrich
TSH/Silent PIT1enrich
ACTHenrich
Silent TPITenrich
GHenrich
Proteomic cluster
Kruskal−Wallis, P = 2.2e−09

Supplementary information, Fig. S9 The mRNA expression levels of targets of FDA-approved drugs in all 200 PitNETs, related to Fig. 6.

a Heatmap comparing the mRNA expression of *SSTR2*, *SSTR5*, *MGMT* and *DRD2* among the seven proteomic clusters.

b, c Boxplot showing mRNA expression of *SSTR2* **(b)** and *SSTR5* **(c)** was significantly elevated in GH$^{\mathrm{enrich}}$ and TSH/silent PIT1$^{\mathrm{enrich}}$ than in other proteomic clusters (Wilcoxon rank-sum test, $^{***}P < 0.001$). Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant.

d Boxplot showing mRNA expression of *MGMT* was significantly lower in PRL$^{\mathrm{enrich}}$, TSH/silent PIT1$^{\mathrm{enrich}}$, and silent TPIT$^{\mathrm{enrich}}$ than in other proteomic clusters, respectively (Wilcoxon rank-sum test, $^{**}P < 0.001$, $^{***}P < 0.001$). Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant.

e Boxplot showing mRNA expression of *DRD2* was significantly elevated in SF1/NULL$^{\mathrm{enrich}}$, EMT$^{\mathrm{PRO}}$, and PRL$^{\mathrm{enrich}}$ than in other proteomic clusters, respectively (Wilcoxon rank-sum test, $^{*}P < 0.05$, $^{***}P < 0.001$). Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant.