## Supplementary Figure 1

## A



B


## Supplementary Figure 2



## Supplementary Figure 3

A

| + NRG (10nM) |  |  |  |
| :---: | :---: | :---: | :---: |
|  | A3 | A6 |  |
| $5 x^{2}$ |  |  |  |
| 1. | -1:1 | 19 | pY1289HER3 |
|  | \| +1 | 11 | Total HER3 |
|  |  |  |  |
| - | $\cdots$ | 4-4, | pS473AKT |
|  |  |  | Total AKT |
|  |  |  | Tubulin |
| \# | \# $=$ | = | pERK1/2 |
| 5 F |  | $\pm=$ | Total ERK1/2 |

B


C


## Supplementary Figure 4



## Supplementary Figure 5



## Supplementary Figure 6

A


B


## Supplementary Table 1

|  | Experimental design | Compounds | Hit selection | Controls ( $\mathrm{Tm}\left({ }^{\circ} \mathrm{C}\right) \pm$ SD) | RZ factor |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Stage I-HER3 screening cascade |  |  |  |  |  |
| Step 1 - Primary screening | Pools of 4 compounds/ well at $30 \mu \mathrm{M}$ each, $\mathrm{n}=1$ | 107,008 | $\Delta T m>3^{\circ} \mathrm{C}$ | TmApo $34.71 \pm 0.44$ <br> TmATP $47.75 \pm 0.33$ | 0.88 |
| Step 2 - Deconvolution screening | Deconvoluted compounds at $30 \mu \mathrm{M}, \mathrm{n}=2$ | 3,119 | $\Delta T m>3^{\circ} \mathrm{C}$ | TmApo $35.60 \pm 0.45$ <br> TmATP $47.46 \pm 0.28$ | 0.88 |
| Step 3 - Potency screening | Dose-response at $30,10,3,1 \mu \mathrm{M}, \mathrm{n}=2$ | 338 | $\Delta \mathrm{Tm}>3^{\circ} \mathrm{C}$ and potency<10 $\mu \mathrm{M}$ | TmApo $35.09 \pm 1.56$ <br> TmATP $47.63 \pm 0.76$ | 0.87 |
| Step 4 - Near neighbours screening | Dose-response at $30,10,3,1 \mu \mathrm{M}, \mathrm{n}=2$ | 663 | $\Delta \mathrm{Tm}>3^{\circ} \mathrm{C}$ | TmApo $33.47 \pm 0.58$ <br> TmATP $48.45 \pm 0.29$ | 0.83 |
| Stage II - HER2 counter screening | Dose-response at $30,10,3,1 \mu \mathrm{M}, \mathrm{n}=2$ | 555 | $\Delta T m>2^{\circ} \mathrm{C}$ | TmApo $38.64 \pm 0.31$ <br> TmLapatinib $52.67 \pm 0.28$ | 0.93 |

## Supplementary Table 2

|  | Concentration, $\mu \mathbf{M}$ | $\Delta \mathbf{T m}\left({ }^{\circ} \mathbf{C}\right) \pm \mathbf{S D}$ |
| :---: | :---: | :---: |
| HER3 primary screen, pools of 4 compounds | 30 each | 6.6 |
| HER3 deconvolution screen | 30 | $3.65 \pm 0.25$ |
| HER3 potency screen | 30 | $3.2 \pm 0.24$ |
|  | 10 | $3.28 \pm 0.62$ |
|  | 3 | $1.27 \pm 0.51$ |
|  | 1 | $-1.34 \pm 0.48$ |
| HER2 counter screen | 30 | $1.95 \pm 0.25$ |
|  | 10 | $1.56 \pm 0.26$ |
|  | 3 | $0.48 \pm 0.52$ |
|  | 1 | $-0.75 \pm 0.18$ |

## Supplementary Table 3

| Compound ID | Activity against HER2, $\mathbf{I C}_{50}(\mu \mathbf{M})$ |
| :---: | :---: |
| C5 | 0.54 |
| B1 | 0.84 |
| A3 | 0.88 |
| A6 | 1.13 |
| AC3573 | $>10$ |

Supplementary Table 4

| Kinase Name | Mean Inhibition (\%) |
| :---: | :---: |
| AAK1 | 54 |
| ABL1 | 73 |
| ABL2 (Arg) | 67 |
| ACVR1 (ALK2) | 12 |
| ACVR1B (ALK4) | 6 |
| ACVR2A | 1 |
| ACVR2B | 15 |
| ACVRL1 (ALK1) | 7 |
| ADCK3 | -1 |
| ADRBK1 (GRK2) | -2 |
| ADRBK2 (GRK3) | -4 |
| AKT1 (PKB alpha) | 4 |
| AKT2 (PKB beta) | 1 |
| AKT3 (PKB gamma) | 19 |
| ALK | 5 |
| AMPK (A1/B1/G2) | 2 |
| AMPK (A1/B1/G3) | 7 |
| AMPK (A1/B2/G1) | 7 |
| AMPK (A1/B2/G2) | 8 |
| AMPK (A1/B2/G3) | 5 |
| AMPK (A2/B1/G2) | 6 |
| AMPK (A2/B1/G3) | 5 |
| AMPK (A2/B2/G1) | 10 |
| AMPK (A2/B2/G2) | 0 |
| AMPK (A2/B2/G3) | 8 |
| AMPK A1/B1/G1 | -8 |
| AMPK A2/B1/G1 | 4 |
| ANKK1 | 15 |
| AURKA (Aurora A) | 5 |
| AURKB (Aurora B) | 2 |
| AURKC (Aurora C) | 9 |
| AXL | 4 |
| BLK | 34 |
| BMPR1A (ALK3) | 2 |
| BMPR1B (ALK6) | 7 |
| BMPR2 | 54 |
| BMX | 12 |
| BRAF | 7 |
| BRSK1 (SAD1) | 22 |
| BRSK2 | -10 |
| BTK | 13 |
| CAMK1 (CaMK1) | -20 |


| CAMK1G (CAMKI gamma) | 6 |
| :---: | :---: |
| CAMK2A (CaMKII alpha) | 9 |
| CAMK2B (CaMKII beta) | -3 |
| CAMK2D (CaMKII delta) | 11 |
| CAMK2G (CaMKII gamma) | -2 |
| CAMK4 (CaMKIV) | 3 |
| CAMKK1 (CAMKKA) | 6 |
| CAMKK2 (CaMKK beta) | 30 |
| CASK | -3 |
| CDC42 BPA (MRCKA) | 3 |
| CDC42 BPB (MRCKB) | 2 |
| CDC42 BPG (MRCKG) | 1 |
| CDC7/DBF4 | 23 |
| CDK1/cyclin B | 15 |
| CDK11 (Inactive) | 10 |
| CDK11/cyclin C | 7 |
| CDK13/cyclin K | 20 |
| CDK14 (PFTK1)/cyclin Y | -5 |
| CDK16 (PCTK1)/cyclin Y | 7 |
| CDK17/cyclin Y | 5 |
| CDK18/cyclin Y | 4 |
| CDK2/cyclin A | 20 |
| CDK2/cyclin A1 | 36 |
| CDK2/cyclin E1 | -8 |
| CDK3/cyclin E1 | 17 |
| CDK4/cyclin D1 | 12 |
| CDK4/cyclin D3 | 1 |
| CDK5 (Inactive) | 17 |
| CDK5/p25 | 12 |
| CDK5/p35 | 15 |
| CDK6/cyclin D1 | 6 |
| CDK7/cyclin H/MNAT1 | 7 |
| CDK8/cyclin C | 7 |
| CDK9 (Inactive) | 65 |
| CDK9/cyclin K | 54 |
| CDK9/cyclin T1 | 83 |
| CDKL5 | 11 |
| CHEK1 (CHK1) | 4 |
| CHEK2 (CHK2) | 1 |
| CHUK (IKK alpha) | 1 |
| CLK1 | 3 |
| CLK2 | 18 |
| CLK3 | 8 |
| CLK4 | 30 |
| CSF1R (FMS) | 47 |
| CSK | 1 |
| CSNK1A1 (CK1 alpha 1) | 3 |
| CSNK1A1L | 2 |


| CSNK1D (CK1 delta) | 10 |
| :---: | :---: |
| CSNK1E (CK1 epsilon) | 5 |
| CSNK1G1 (CK1 gamma 1) | -2 |
| CSNK1G2 (CK1 gamma 2) | 6 |
| CSNK1G3 (CK1 gamma 3) | 7 |
| CSNK2A1 (CK2 alpha 1) | 20 |
| CSNK2A2 (CK2 alpha 2) | 32 |
| CSNK2A2 (CK2 alpha 2) | 32 |
| DAPK1 | 2 |
| DAPK2 | 5 |
| DAPK3 (ZIPK) | 1 |
| DCAMKL1 (DCLK1) | 3 |
| DCAMKL2 (DCK2) | 10 |
| DDR1 | 10 |
| DDR2 | 0 |
| DDR2 | -3 |
| DMPK | 2 |
| DNA-PK | 37 |
| DYRK1A | 19 |
| DYRK1B | 10 |
| DYRK2 | 79 |
| DYRK3 | 27 |
| DYRK4 | 17 |
| EEF2K | 4 |
| EGFR (ErbB1) | 49 |
| EIF2AK2 (PKR) | 3 |
| EPHA1 | 38 |
| EPHA2 | 21 |
| EPHA3 | -12 |
| EPHA4 | 10 |
| EPHA5 | 0 |
| EPHA5 | 14 |
| EPHA6 | 6 |
| EPHA7 | -3 |
| EPHA8 | 6 |
| EPHB1 | 21 |
| EPHB2 | 14 |
| EPHB3 | 8 |
| EPHB4 | 8 |
| ERBB2 (HER2) | 3 |
| ERBB4 (HER4) | 14 |
| ERN1 | -15 |
| ERN2 | -3 |
| FER | 9 |
| FES (FPS) | 4 |
| FGFR1 | 5 |
| FGFR1 V561M | 9 |
| FGFR2 | 2 |


| FGFR3 | -4 |
| :---: | :---: |
| FGFR4 | -4 |
| FGR | 47 |
| FLT1 (VEGFR1) | -3 |
| FLT3 | 24 |
| FLT4 (VEGFR3) | -2 |
| FRAP1 (mTOR) | 11 |
| FRK (PTK5) | 7 |
| FYN | 10 |
| FYN A | 38 |
| GAK | 58 |
| GRK1 | 6 |
| GRK4 | -25 |
| GRK5 | -4 |
| GRK6 | -18 |
| GRK7 | 3 |
| GSG2 (Haspin) | 6 |
| GSK3A (GSK3 alpha) | 5 |
| GSK3B (GSK3 beta) | 12 |
| HCK | 39 |
| HIPK1 (Myak) | 0 |
| HIPK2 | 8 |
| HIPK3 (YAK1) | 9 |
| HIPK4 | 8 |
| HUNK | 21 |
| ICK | 5 |
| IGF1R | 2 |
| IKBKB (IKK beta) | -3 |
| IKBKE (IKK epsilon) | 1 |
| INSR | 3 |
| INSRR (IRR) | -3 |
| IRAK1 | 62 |
| IRAK3 | 48 |
| IRAK4 | 14 |
| ITK | 1 |
| JAK1 | 10 |
| JAK2 | -1 |
| JAK3 | -4 |
| KDR (VEGFR2) | 8 |
| KIT | 1 |
| KSR2 | 8 |
| LATS2 | 17 |
| LCK | 27 |
| LIMK1 | 40 |
| LIMK2 | 33 |
| LRRK2 | 29 |
| LRRK2 FL | 35 |
| LTK (TYK1) | -1 |


| LYN A | 28 |
| :---: | :---: |
| LYN B | 61 |
| MAP2K1 (MEK1) | -5 |
| MAP2K2 (MEK2) | 5 |
| MAP2K4 (MEK4) | 14 |
| MAP2K5 (MEK5) | 20 |
| MAP2K6 (MKK6) | 4 |
| MAP2K6 (MKK6) | -1 |
| MAP3K10 (MLK2) | 26 |
| MAP3K11 (MLK3) | 10 |
| MAP3K14 (NIK) | -4 |
| MAP3K19 (YSK4) | 8 |
| MAP3K2 (MEKK2) | -18 |
| MAP3K3 (МЕКK3) | -21 |
| MAP3K5 (ASK1) | -26 |
| MAP3K7/MAP3K7IP1 (TAK1-TAB1) | 18 |
| MAP3K8 (COT) | 11 |
| MAP3K9 (MLK1) | 13 |
| MAP4K1 (HPK1) | 10 |
| MAP4K2 (GCK) | 17 |
| MAP4K3 (GLK) | 9 |
| MAP4K4 (HGK) | 63 |
| MAP4K5 (KHS1) | -8 |
| MAPK1 (ERK2) | 11 |
| MAPK10 (JNK3) | 11 |
| MAPK11 (p38 beta) | 11 |
| MAPK12 (p38 gamma) | 10 |
| MAPK13 (p38 delta) | 8 |
| MAPK14 (p38 alpha) | 4 |
| MAPK15 (ERK7) | 84 |
| MAPK3 (ERK1) | 12 |
| MAPK7 (ERK5) | 3 |
| MAPK8 (JNK1) | 17 |
| MAPK9 (JNK2) | 2 |
| МАРКАРК2 | 6 |
| MAPKAPK3 | 7 |
| MAPKAPK5 (PRAK) | 4 |
| MARK1 (MARK) | 6 |
| MARK2 | 14 |
| MARK3 | 4 |
| MARK4 | -7 |
| MASTL | -4 |
| MATK (HYL) | 8 |
| MELK | 36 |
| MERTK (cMER) | 3 |
| MET (cMet) | 8 |
| MINK1 | 50 |
| MKNK1 (MNK1) | 41 |


| MKNK2 (MNK2) | 63 |
| :---: | :---: |
| MKNK2 (MNK2) | 57 |
| MLCK (MLCK2) | 26 |
| MLK4 | 31 |
| MST1R (RON) | -1 |
| MST4 | 7 |
| MUSK | -2 |
| MYLK (MLCK) | 3 |
| MYLK2 (skMLCK) | 0 |
| MYLK4 | 50 |
| MYO3A (MYO3 alpha) | 9 |
| MYO3B (MYO3 beta) | 13 |
| NEK1 | 7 |
| NEK2 | -6 |
| NEK2 | 2 |
| NEK4 | 10 |
| NEK6 | 5 |
| NEK8 | 3 |
| NEK9 | -2 |
| NIM1K | 8 |
| NLK | 16 |
| NTRK1 (TRKA) | 6 |
| NTRK2 (TRKB) | 7 |
| NTRK3 (TRKC) | 3 |
| NUAK1 (ARK5) | 24 |
| NUAK2 | 29 |
| PAK1 | 9 |
| PAK2 (PAK65) | 10 |
| PAK3 | 1 |
| PAK4 | 6 |
| PAK6 | 11 |
| PAK7 (KIAA1264) | 1 |
| PASK | 5 |
| PDGFRA (PDGFR alpha) | 13 |
| PDGFRB (PDGFR beta) | 11 |
| PDK1 | 8 |
| PEAK1 | 9 |
| PHKG1 | 11 |
| PHKG2 | 1 |
| PI4K2A (PI4K2 alpha) | 3 |
| PI4K2B (PI4K2 beta) | -2 |
| PI4KA (PI4K alpha) | 10 |
| PI4KB (PI4K beta) | 57 |
| PIK3C2A (PI3K-C2 alpha) | 6 |
| PIK3C2B (PI3K-C2 beta) | 5 |
| PIK3C2G (PI3K-C2 gamma) | 17 |
| PIK3C3 (hVPS34) | 1 |
| PIK3CA/PIK3R1 (p110 alpha/p85 alpha) | 10 |


| PIK3CA/PIK3R3 (p110 alpha/p55 gamma) | 30 |
| :---: | :---: |
| PIK3CB/PIK3R1 (p110 beta/p85 alpha) | -3 |
| PIK3CB/PIK3R2 (p110 beta/p85 beta) | 0 |
| PIK3CD/PIK3R1 (p110 delta/p85 alpha) | -6 |
| PIK3CG (p110 gamma) | 20 |
| PIM1 | 37 |
| PIM2 | 5 |
| PIM3 | -7 |
| PIP4K2A | 79 |
| PIP5K1A | 48 |
| PIP5K1B | 93 |
| PIP5K1C | 91 |
| PKMYT1 | 15 |
| PKN1 (PRK1) | 3 |
| PKN2 (PRK2) | 9 |
| PLK1 | 6 |
| PLK2 | -2 |
| PLK3 | -22 |
| PLK4 | 26 |
| PRKACA (PKA) | 0 |
| PRKACB (PRKAC beta) | 12 |
| PRKACG (PRKAC gamma) | 2 |
| PRKCA (PKC alpha) | 2 |
| PRKCB1 (PKC beta I) | 1 |
| PRKCB2 (PKC beta II) | 16 |
| PRKCD (PKC delta) | -5 |
| PRKCE (PKC epsilon) | -2 |
| PRKCG (PKC gamma) | 0 |
| PRKCH (PKC eta) | 11 |
| PRKCI (PKC iota) | -16 |
| PRKCN (PKD3) | 20 |
| PRKCQ (PKC theta) | 11 |
| PRKCZ (PKC zeta) | 14 |
| PRKD1 (PKC mu) | 31 |
| PRKD2 (PKD2) | 8 |
| PRKG1 | 4 |
| PRKG2 (PKG2) | 5 |
| PRKX | 10 |
| PTK2 (FAK) | 9 |
| PTK2B (FAK2) | 14 |
| PTK6 (Brk) | 73 |
| RAF1 (cRAF) Y340D Y341D | 4 |
| RET | 6 |
| RIPK2 | 17 |
| RIPK3 | 46 |
| ROCK1 | -4 |
| ROCK2 | -7 |


| ROS1 | 18 |
| :---: | :---: |
| RPS6KA1 (RSK1) | 8 |
| RPS6KA2 (RSK3) | 28 |
| RPS6KA3 (RSK2) | 8 |
| RPS6KA4 (MSK2) | 14 |
| RPS6KA5 (MSK1) | 7 |
| RPS6KA6 (RSK4) | 35 |
| RPS6KB1 (p70S6K) | 3 |
| RPS6KB2 (p70S6Kb) | 1 |
| SBK1 | 6 |
| SGK (SGK1) | 5 |
| SGK (SGK1) | 3 |
| SGK2 | 6 |
| SGKL (SGK3) | 6 |
| SIK1 | 32 |
| SIK3 | 24 |
| SLK | 5 |
| SNF1LK2 | 13 |
| SPHK1 | 9 |
| SPHK2 | -6 |
| SRC | 23 |
| SRMS (Srm) | 27 |
| SRPK1 | 7 |
| SRPK2 | -6 |
| STK16 (PKL12) | -2 |
| STK17A (DRAK1) | 30 |
| STK17B (DRAK2) | 47 |
| STK22B (TSSK2) | 5 |
| STK22D (TSSK1) | 13 |
| STK23 (MSSK1) | 4 |
| STK24 (MST3) | 6 |
| STK25 (YSK1) | 7 |
| STK3 (MST2) | 8 |
| STK32B (YANK2) | 1 |
| STK32C (YANK3) | -1 |
| STK33 | 18 |
| STK38 (NDR) | 15 |
| STK38L (NDR2) | -22 |
| STK39 (STLK3) | 6 |
| STK4 (MST1) | 1 |
| SYK | 11 |
| TAOK1 | 18 |
| TAOK2 (TAO1) | 4 |
| TAOK3 (JIK) | -5 |
| TBK1 | 11 |
| TEC | 4 |
| TEK (Tie2) | 8 |
| TESK1 | 6 |


| TESK2 | -4 |
| :---: | :---: |
| TGFBR1 (ALK5) | 2 |
| TGFBR2 | 44 |
| TLK1 | 0 |
| TLK2 | 31 |
| TNIK | 47 |
| TNK1 | 17 |
| TNK2 (ACK) | 48 |
| TTK | 16 |
| TXK | 25 |
| TYK2 | 1 |
| TYRO3 (RSE) | 25 |
| ULK1 | -1 |
| ULK2 | 6 |
| ULK3 | 15 |
| VRK2 | 14 |
| WEE1 | 34 |
| WNK1 | 5 |
| WNK2 | 8 |
| WNK3 | 4 |
| YES1 | 30 |
| ZAK | 5 |
| ZAP70 | -5 |

## Supplementary Figures and Tables Legends

## Supplementary Figure 1 <br> Differential scanning fluorimetry multiplex screening set up.

A) Signal window and DMSO tolerance of the thermal shift assay. Recombinant HER3 kinase domain in absence of any ligand (ApoHER3) was used as a neutral control and recombinant HER3 kinase domain in the presence of $200 \mu \mathrm{M} \mathrm{ATP} / 10 \mathrm{mM} \mathrm{MgCl}_{2}\left(\mathrm{ATP} / \mathrm{MgCl}_{2}\right)$ was used as positive control. Assays were performed with an increasing percentage of DMSO. Data showed a large signal window between the neutral and positive controls (shift in HER3 Tm of $13.5^{\circ} \mathrm{C}$ without DMSO) and which was not significantly reduced at the DMSO concentration used in the screening (shift in HER3 Tm of $12.5^{\circ} \mathrm{C}$ between ApoHER3 and HER3 $+\mathrm{ATP} / \mathrm{MgCl}_{2}$ at $1.25 \%$ DMSO). B) Thermal shift binding assay of recombinant HER3 kinase domain with selected kinase inhibitors. Recombinant HER3 kinase domain was assayed in absence of any ligand (ApoHER3), or in presence of $200 \mu \mathrm{M} \mathrm{ATP} / 10 \mathrm{mM} \mathrm{MgCl}_{2}\left(\mathrm{ATP} / \mathrm{MgCl}_{2}\right)$ or in presence of $1 \mu \mathrm{M}$ of bosutinib alone or in combination with a mixture of 4 other inhibitors at $1 \mu \mathrm{M}$ each (BLU577, MG-132, LY294002, CRT6854) or in combination with a mixture of 9 other inhibitors at $1 \mu \mathrm{M}$ each (BLU577, BIM1, BX-912, LY294002, staurosporine, MG-132, bortezomib, MG-132, CRT0066854). Data showed that HER3-binding compounds, e.g. bosutinib, could be identified from pools of compounds, as the shift in HER3 Tm induced by bosutinib was not affected as a result of pooling compounds.

## Supplementary Figure 2

Differential scanning fluorimetry data obtained for the proof-of-concept compound AC3573 at all the steps of the screening cascade.
A) Primary screening thermal denaturation profiles of recombinant HER3 kinase domain, in the presence of $1.2 \%$ DMSO (ApoHER3 control, in the absence of any ligand), $\mathrm{ATP} / \mathrm{MgCl}_{2}$ (ATP control) and the pool of 4 compounds containing AC3573. Compounds were tested at $30 \mu \mathrm{M}$ each. B) Deconvolution screening thermal denaturation profiles of recombinant HER3 kinase domain, in presence of $0.3 \%$ DMSO (ApoHER3 control), ATP $/ \mathrm{MgCl}_{2}$ (ATP control) and the deconvoluted compounds at $30 \mu \mathrm{M}$. Representative curves obtained from two separate fluorescence profiling experiments are shown. C) Correlation of shift in HER3 Tm value induced by compounds tested at 4 concentrations ( $1,3,10$ and $30 \mu \mathrm{M} ; \mathrm{n}=2$ ). ApoHER3 was used for all DSF analyses and $\mathrm{ATP} / \mathrm{MgCl}_{2}$ was used as positive control. Proof-of-concept
compound AC3573 is highlighted. D) Correlation of shift in HER2 Tm value induced by compounds at $1,3,10$ and $30 \mu \mathrm{M}$ for HER2 counter screening ( $\mathrm{n}=2$ ). ApoHER2 (HER2 in the absence of any ligand) was used for all DSF analyses and $1 \mu \mathrm{M}$ lapatinib was used as a positive control. Proof-of-concept compound AC3573 is highlighted.

## Supplementary Figure 3

Dose-response effects of the 5 compounds identified in the single dose cell-based screen on NRG-induced HER3 phosphorylation and downstream signalling.

SK-BR-3 cells were serum-starved for 16 h and treated for 1 h with either DMSO, or the indicated concentrations of compounds A3 or A6 (A), or B1 or C5 (B) or G3 (C) or $1 \mu \mathrm{M}$ lapatinib and subjected or not to 15 min NRG stimulation (10nM). After lysis, whole-cell extracts were immunoblotted with the indicated primary antibodies for assessment of effects of compounds on NRG-induced signalling. Western blots shown are representative of two independent experiments. Compounds A3, A6, B1 and C5 prevented HER2-HER3 activation in response to NRG stimulation below $10 \mu \mathrm{M}$, while compound G 3 did not show any inhibition on HER3 downstream signalling below $30 \mu \mathrm{M}$.

## Supplementary Figure 4

In vitro kinase assay of the HER2 kinase domain against AC3573 performed at the Km for ATP conducted by ThermoFisher.

## Supplementary Figure 5 <br> HER3 peptide mapping for HDX-MS.

Peptide mapping was obtained by using non-deuterated samples in triplicate and only unique peptides present in all three data files were selected for deuterium uptake data analysis. Protein digests provided a list of 2,000 peptides. 146 peptides were selected for HDX analysis providing $>96 \%$ sequence coverage with many overlapping peptides.

## Supplementary Figure 6

AC3573 compound disrupts HER2-HER3 heterodimers but does not induce HER3 homodimers.
A) Differences in probability of HER2-HER3 nearest neighbour distances. Cluster measurements from STORM data taken from SK-BR-3 cells labelled with HER2-Alexa488

Affibody and HER3-CF640R SE Affibody (HER2-HER3) or NRG-CF640R SE (HER2-NRG) $\pm 1 \mu \mathrm{M}$ lapatinib or $30 \mu \mathrm{M} \mathrm{AC} 3573$ compound. Graphs show near neighbour distribution of HER2 and HER3 molecules as Y condition (right-hand side) - X condition (top). A positive difference indicates that it is more likely to find a HER2 at the corresponding distance from a HER3 under Y condition than under X condition. B) HER3 cluster size (radii, left box plot) and number of HER3 molecules per cluster (right box plot) measurements from STORM data taken from SK-BR-3 cells labelled with HER3-CF640R SE Affibody in presence of $30 \mu \mathrm{M}$ AC 3573 compound or DMSO. The graphs show radii and number of molecules per cluster of 1007 clusters for DMSO treated cells and 630 clusters for AC3573 treated cells. The median values are shown. AC3573 compound did not alter either the size of HER3 clusters (median radii 29.3 nm for DMSO treated cells versus 29.7 nm for AC3573 treated cells), or the number of HER3 molecules per cluster which remained the same between control (DMSO) and AC3573-treated cells.

## Supplementary Movie 1

A $360^{\circ}$ rotation of HER3 bound to AMP-PNP (PDB:3KEX) showing the binding site of AC3573 (highlighted).

## Supplementary Table 1

Detailed assay workflow for the identification of HER3 binders through the screening of a 107, 008 compound library by differential scanning fluorimetry.

Overview of the complete compound screening strategy, including all the compound screening stages and steps, experimental design, hit selection criteria, Tm of controls (ApoHER3 with no ligand and $200 \mu \mathrm{M} \mathrm{ATP} / 10 \mathrm{mM} \mathrm{MgCl}_{2}$ for HER3 screening, ApoHER2 without any ligand and $1 \mu \mathrm{M}$ lapatinib for HER2, as means $\pm$ SD calculated from all the plates assayed at each step of screening) and RZ factor (calculated from all the plates assayed at each step of screening).

## Supplementary Table 2

Thermal shift results for the proof-of-concept compound AC3573 at the different stages of the screening cascade.
$\Delta \mathrm{Tm}$ values are reported as mean $\pm \mathrm{SD}$ obtained from at least two independent experiments, except for the HER3 primary screen $(\mathrm{N}=1)$.

## Supplementary Table 3

$\mathrm{IC}_{50}$ values of proof-of-concept compound AC3573 and compounds A3, A6, B1 and C5 against HER2 kinase domain were determined by an in vitro kinase assay performed at the Km for ATP (assay conducted by ThermoFisher).

## Supplementary Table 4

Profiling of AC3573 at $1 \mu \mathrm{M}$ against a panel of 400 kinases performed at the ATP Km conducted by ThermoFisher.

