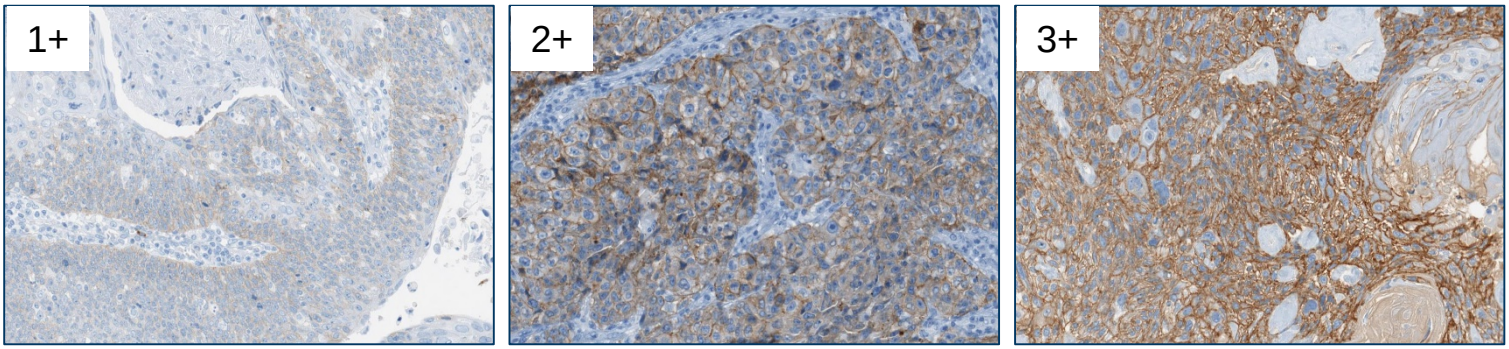
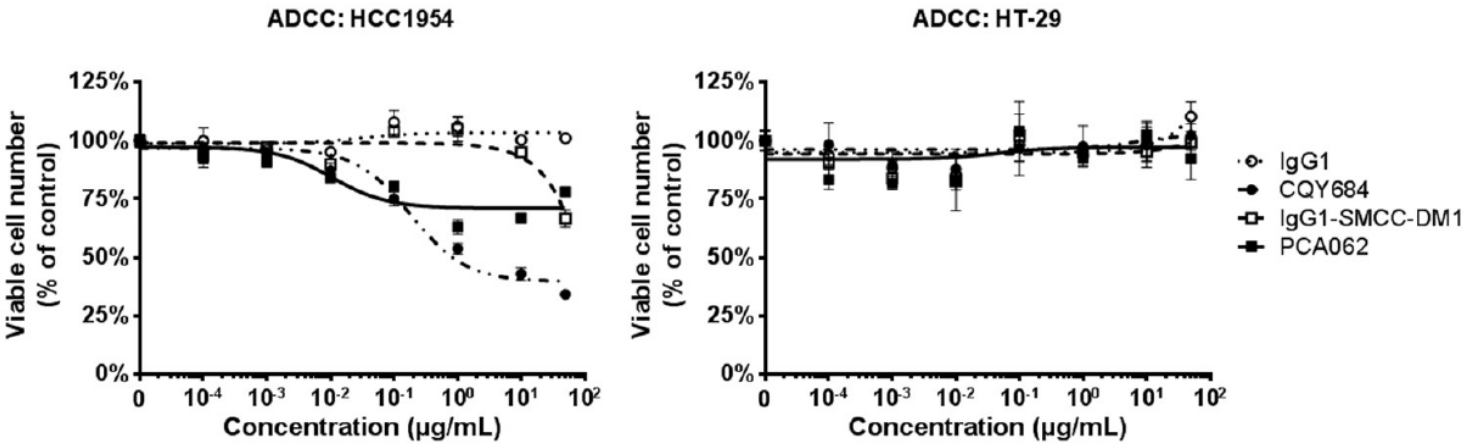
Supplemental Figure 1.  Examples of PCAD IHC staining intensity




Illustrated are Examples of PCAD IHC staining of 1+, 2+ and 3+ intensity In patient tumor samples

# Supplemental Figure 2. Assessment of ADCC activity of PCA062 and CQY684



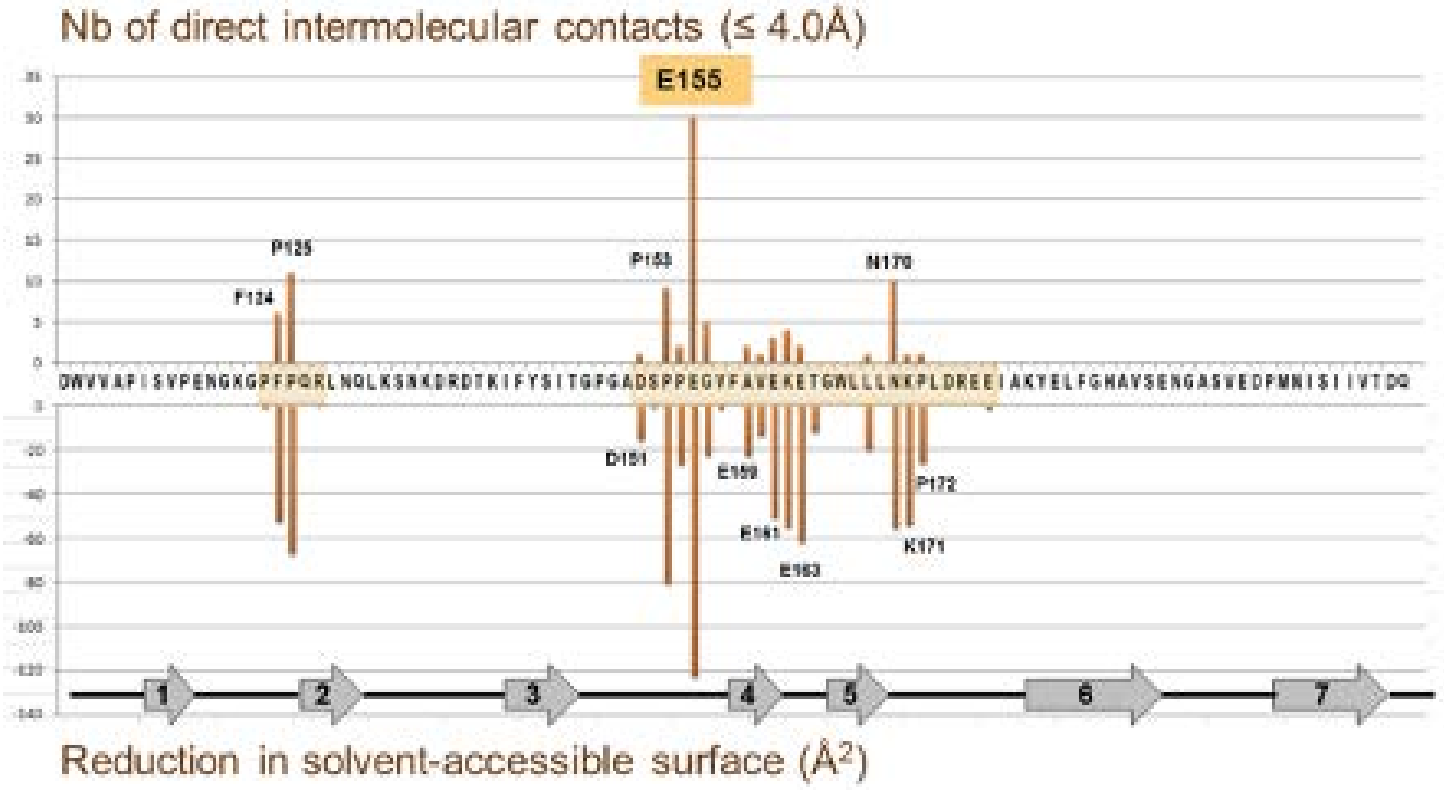

Assessment of ADCC capacity of PCA062 and CQY684 in HCC1954 and HT29 cells. Target cells were incubated with a fixed number of fresh human NK effector cells (5:1 effector to target cell ratio) and increasing amounts of CQY684 (closed circles), IgG1 control antibody (open circles), PCA062 (closed squares) or IgG1-SMCC-DM1 (open squares). All samples were run in triplicate; cell viability was assessed after 48 hrs.

# Supplemental Table 1. X-ray data collection and refinement statistics

| | human P-cadherin EC1_EC2 | CQY684 Fab | CQY684 Fab complex |
|---|---|---|---|
| Data collection | | | |
| Space group | C2 | $P2_12_12_1$ | $P2_12_12$ |
| a, b, c (Å) | 120.89, 76.52, 46.21 | 65.33, 109.38, 139.27 | 172.69, 77.79, 133.41 |
| α, β, γ (°) | 90.00, 107.79, 90.00 | 90.00, 90.00, 90.00 | 90.00, 90.00, 90.00 |
| Resolution (Å) | 1.40 (1.44-1.40) | 1.55 (1.59-1.55) | 2.10 (2.15-2.10) |
| $R_{sym}$ or $R_{merge}$ | 0.022 (0.523) | 0.056 (0.520) | 0.199 (2.39) |
| I / σ(I) | 23.72 (2.06) | 20.56 (3.52) | 7.97 (0.88) |
| $CC^{1/2}$ | - | - | 99.5% (39.6%) |
| Completeness (%) | 99.2 (99.6) | 100.0 (100.0) | 100.0 (100.0) |
| Redundancy | 3.3 (3.4) | 7.1 (6.8) | 6.7 (7.0) |
| | | | |
| Refinement | | | |
| Resolution (Å) | 57.55-1.40 | 69.63-1.55 | 72.49-2.10 |
| No. reflections | 78,177 | 144,980 | 105,437 |
| $R_{work}$ / $R_{free}$ | 0.198/ 0.213 | 0.188 / 0.207 | 0.192 / 0.221 |
| No. atoms | | | |
| Protein | 1,670 | 6,729 | 9,990 |
| Metal ions | 3 $Ca^{2+}$, 4 $Na^{+}$ | 0 | 6 $Ca^{2+}$ |
| Waters | 340 | 767 | 622 |
| B-factors (Å$^2$) | | | |
| Ab light-chain (chains B/L) | - / - | 18.9 / 20.1 | 47.8 / 50.5 |
| Ab heavy-chain (chains A/H) | - / - | 20.5 / 20.5 | 46.8 / 47.2 |
| P-cadherin (chains I/J) | 29.0 / - | - / - | 61.1 / 67.0 |
| Metal ions ($Ca^{2+}$ / $Na^{+}$ ) | 18.6 / 32.6 | - / - | 33.4 / - |
| Waters (chain W) | 39.5 | 28.1 | 46.4 |
| R.m.s. deviations | | | |
| Bond lengths (Å) / angles (°) | 0.010 / 1.13 | 0.010 / 1.11 | 0.010 / 1.18 |

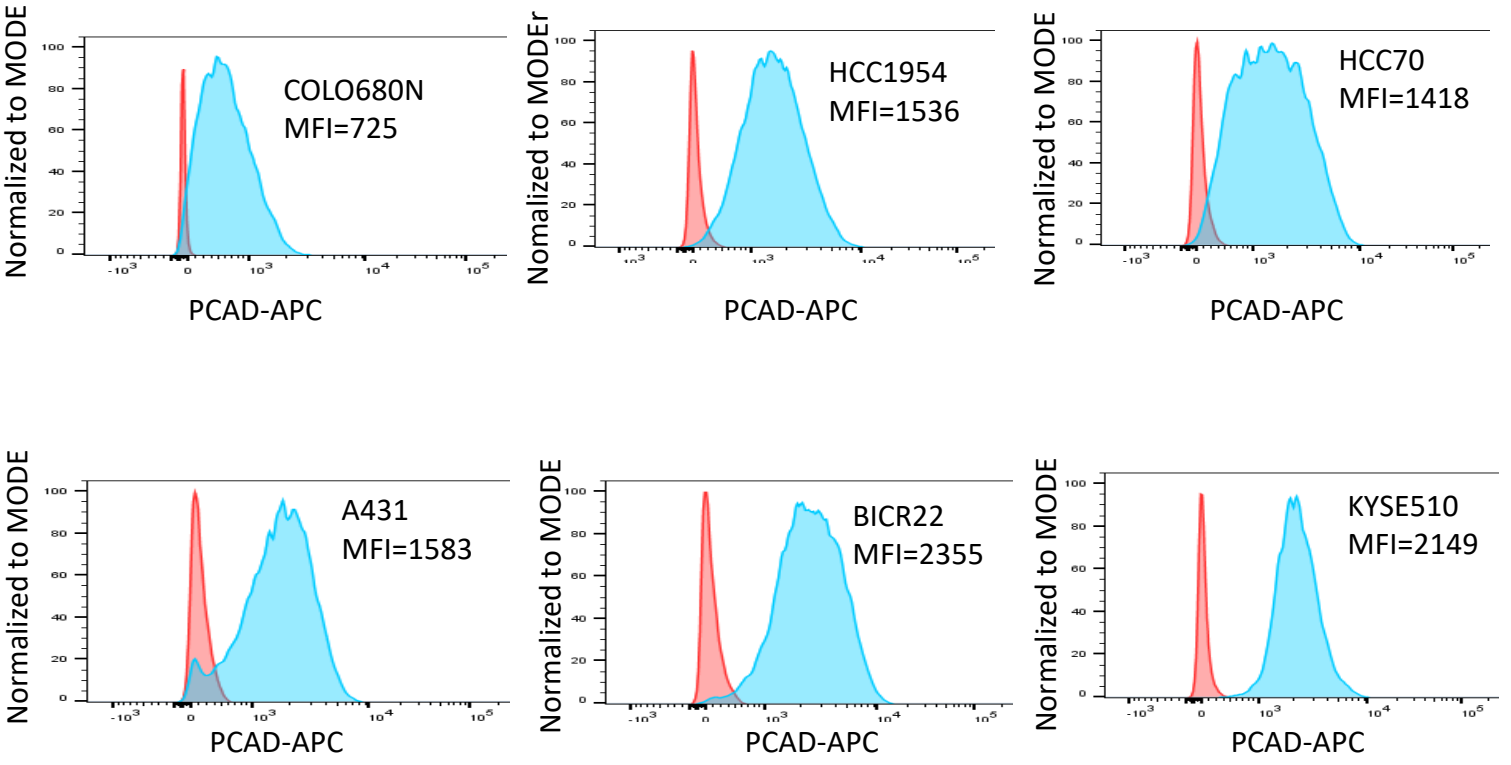
Diffraction data and refinement statistics. Numbers in brackets correspond to the high-resolution shell.

# Supplemental Figure 3. P-cadherin epitope recognized by CQY684/PCA062




Human P-cadherin epitope bound by CQY684. The amino acid sequence of the human P-cadherin EC1 domain is displayed on the horizontal axis. The upper part of the graph shows the number of direct intermolecular contacts between the protein antigen and the antibody, as identified by the program NCONT using a cut-off distance of 4.0Å between non-hydrogen atoms. The lower part of the graph shows the reduction in solvent-accessible surface (in Å2) incurred by P-cadherin residues upon antibody binding, as calculated by the program AREAIMOL. The β-barrel structure of the EC1 domain is schematically shown as a string of arrows with labels corresponding to the numbering of the β-strands.

# Supplemental Figure 4. Flow cytometry analysis of P-cadherin expression on cell surface of a panel of human cancer cell lines




Cell surface P-cadherin expression is measured by an APC-conjugated anti-P-cadherin antibody using via flow cytometry (blue peak). Control IgG antibody is cell surface staining illustrated in red.