

Supplementary data

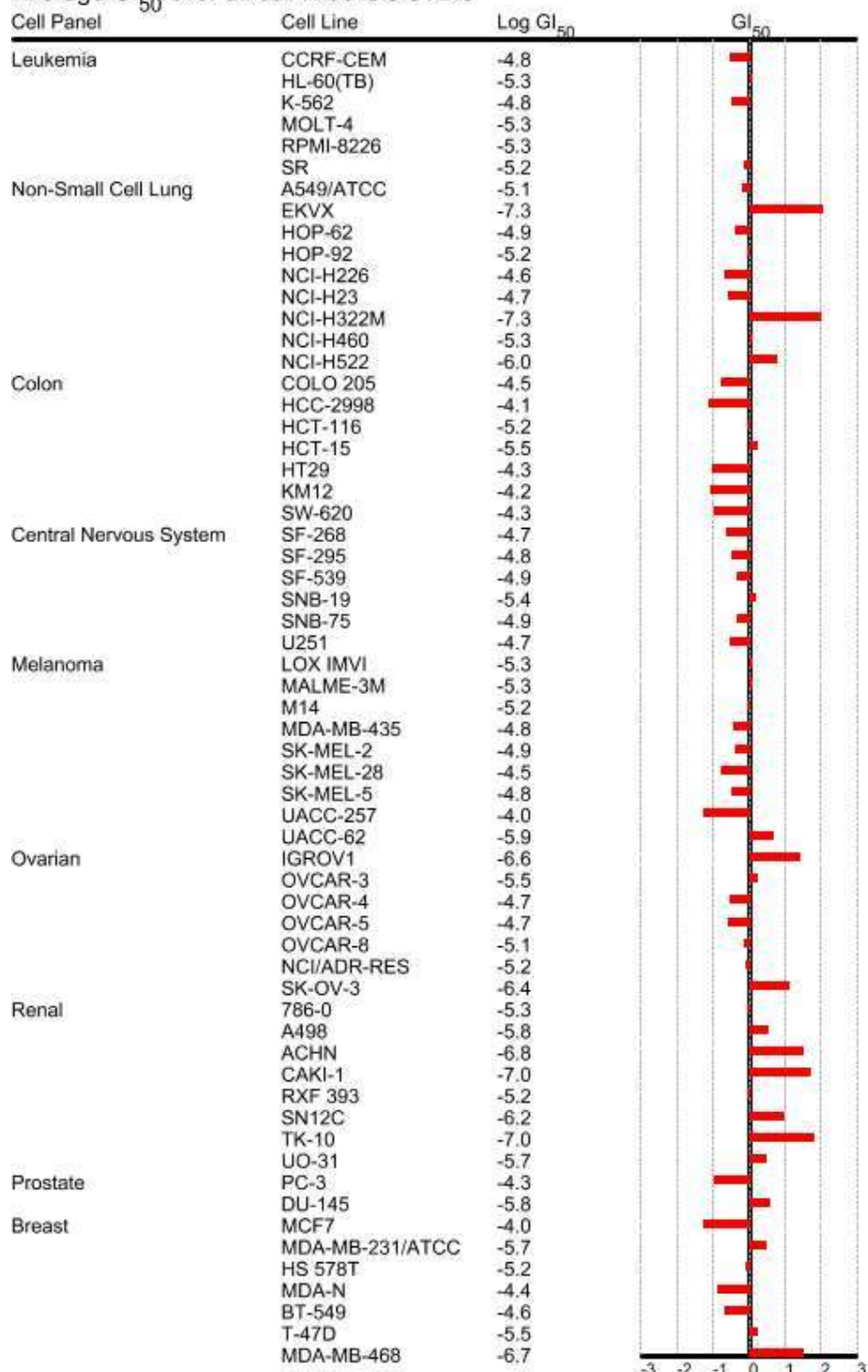
S1. The explanation for the Mean Graph of GI₅₀: the mean GI₅₀ graph demonstrated the selective nature of growth inhibition of human derived cancer cell lines. The positive and negative values means resistance and sensitivity of a particular cell line, respectively.

Erlotinib

GI₅₀ Mean Graph for Compound 718781

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 5.51E-6

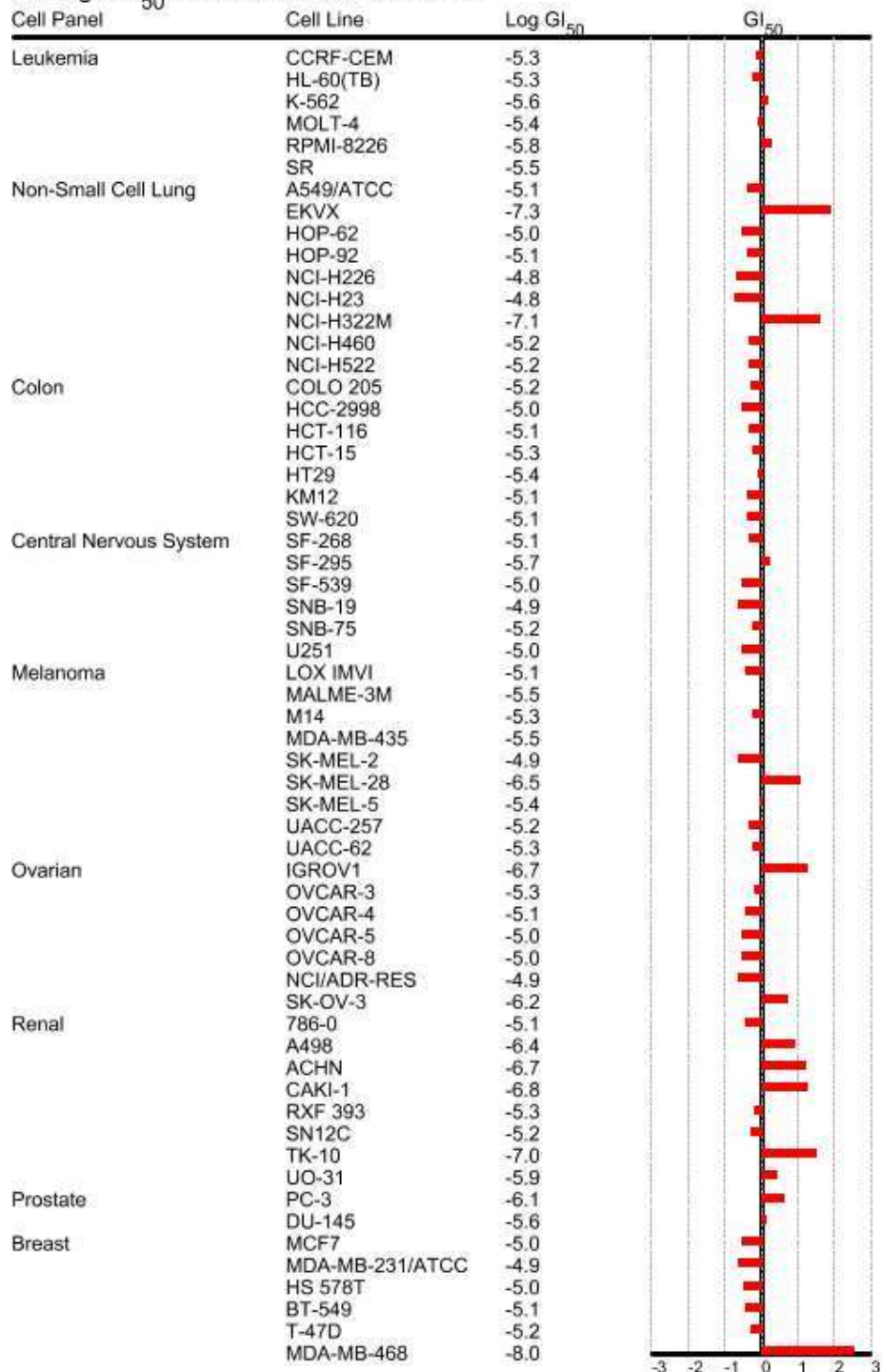


Gefitinib

GI₅₀ Mean Graph for Compound 715055

NCI Cancer Screen Current Data, October 2009

Average GI₅₀ over all cell lines is 3.24E-6

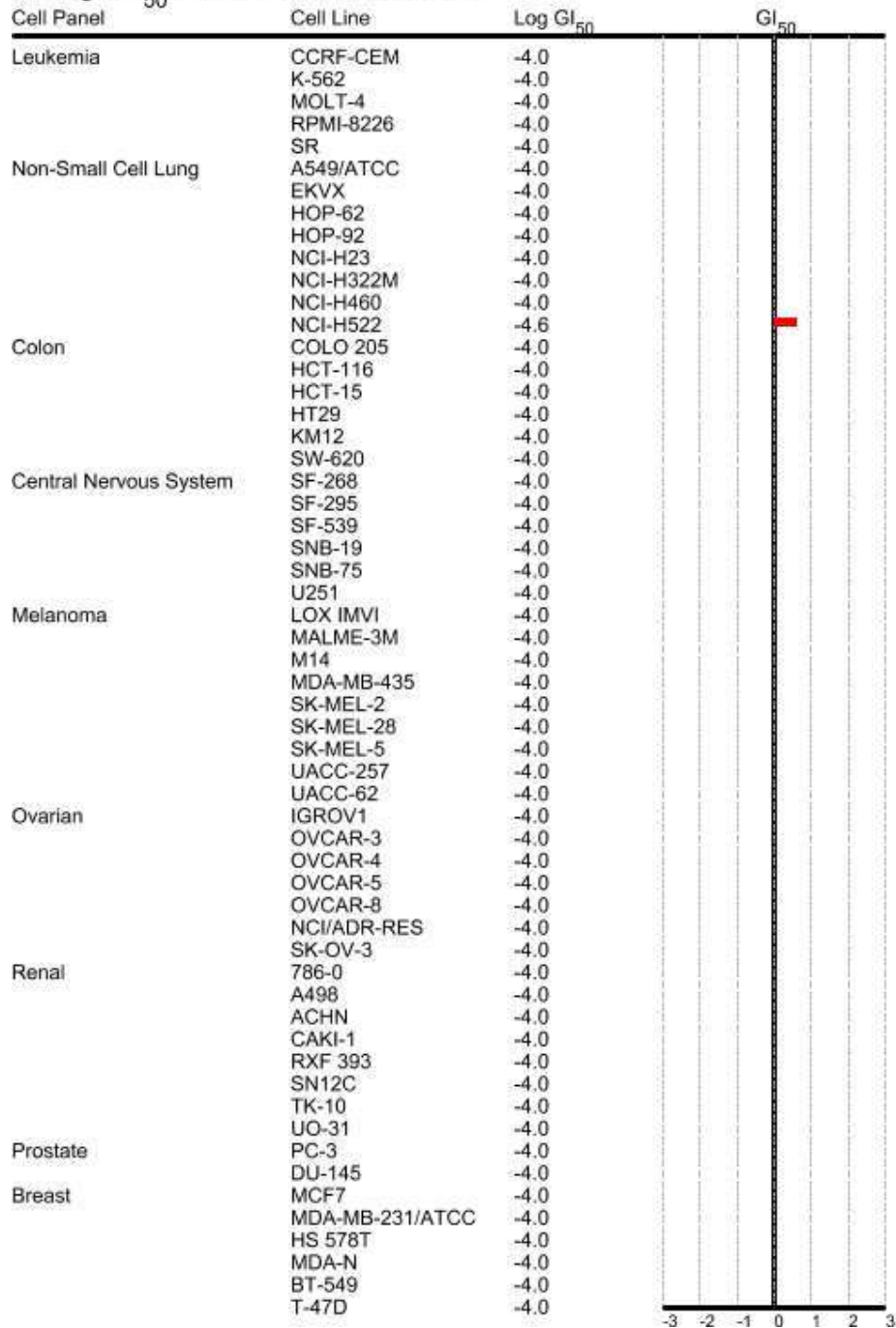


Compound B

GI₅₀ Mean Graph for Compound 48283

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 9.76E-5

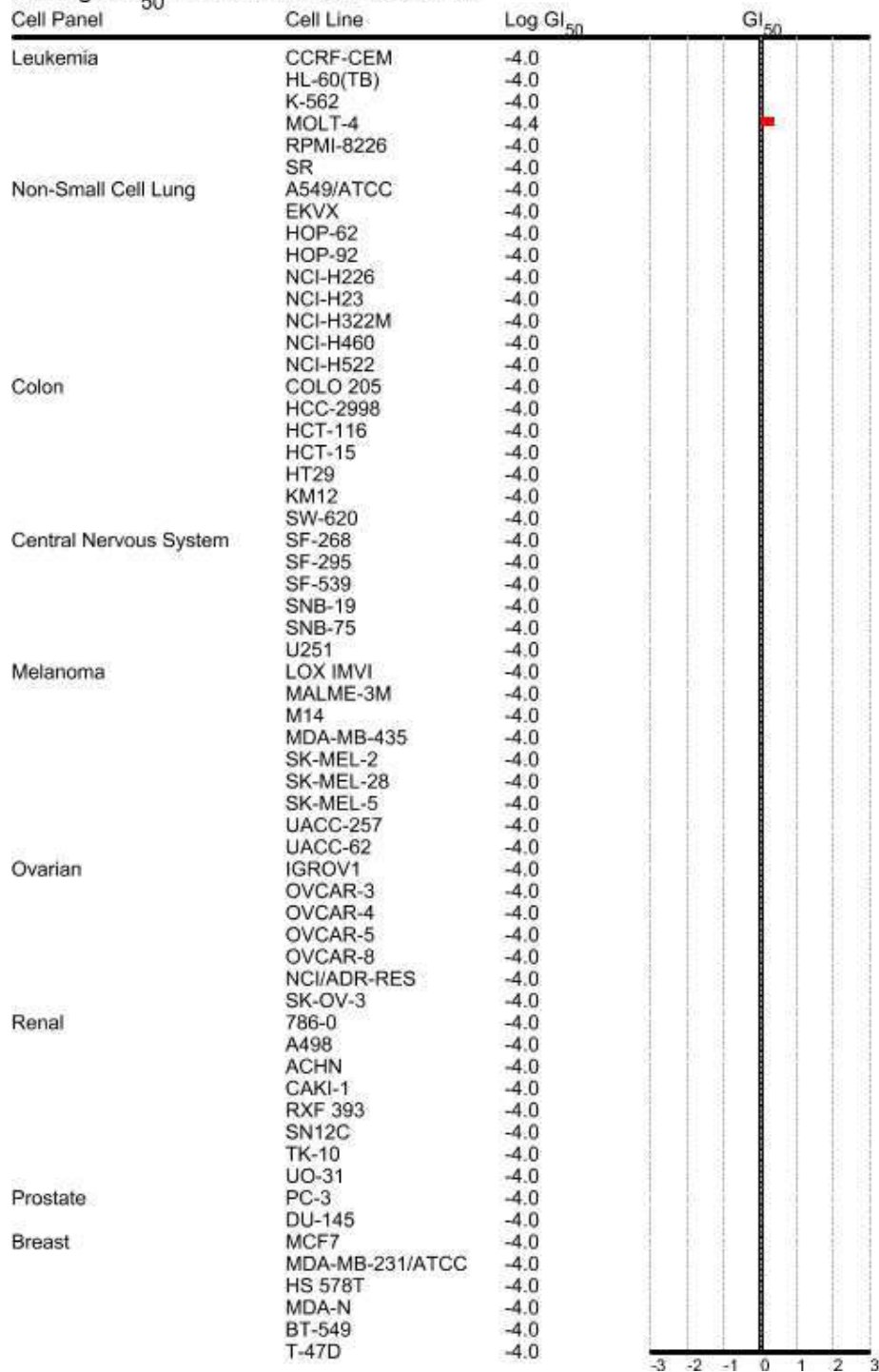


Compound G

GI₅₀ Mean Graph for Compound 125910

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 9.86E-5

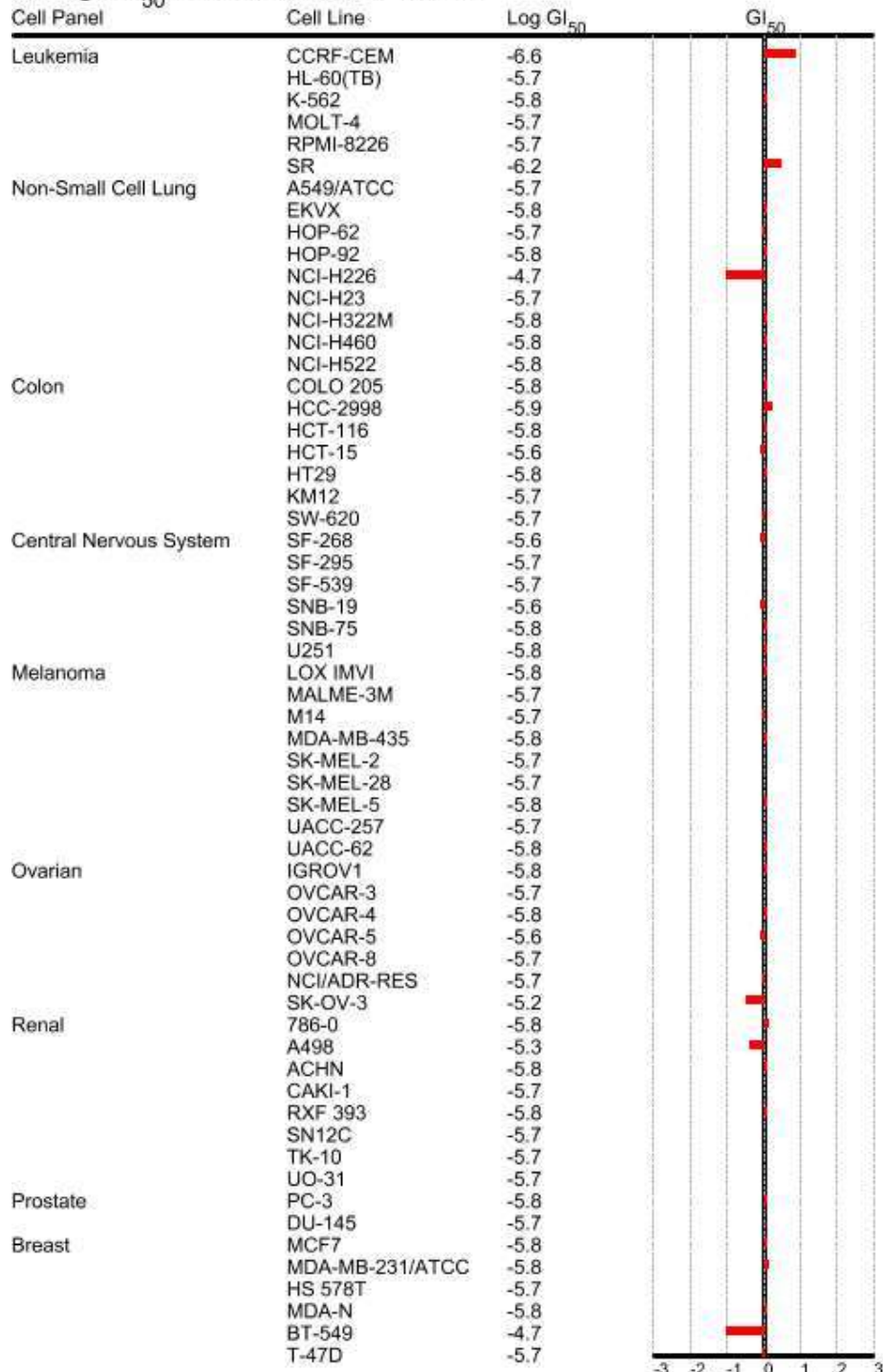


Compound H

GI₅₀ Mean Graph for Compound 130813

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 1.94E-6

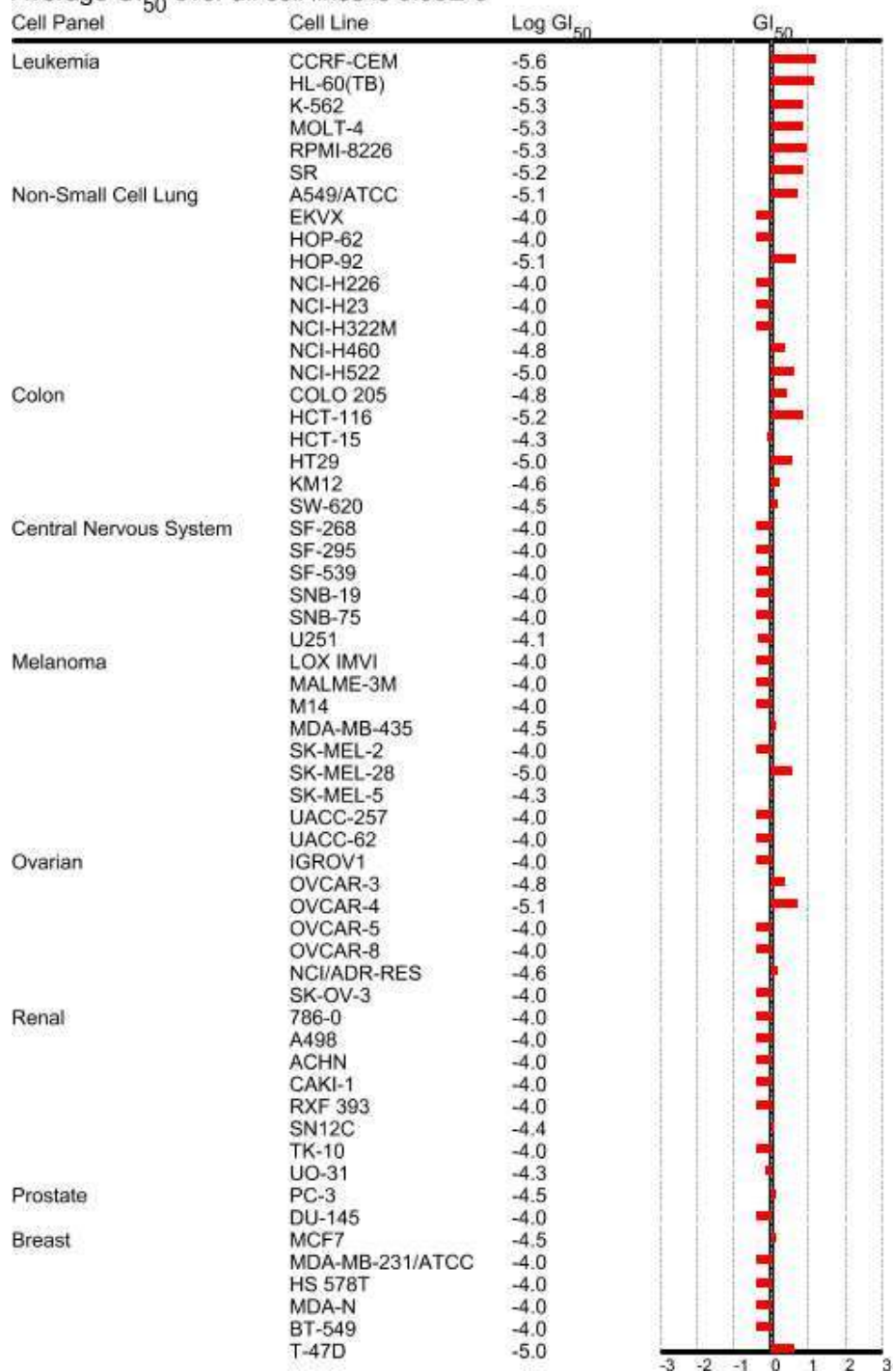


Compound I

GI₅₀ Mean Graph for Compound 135371

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 3.95E-5

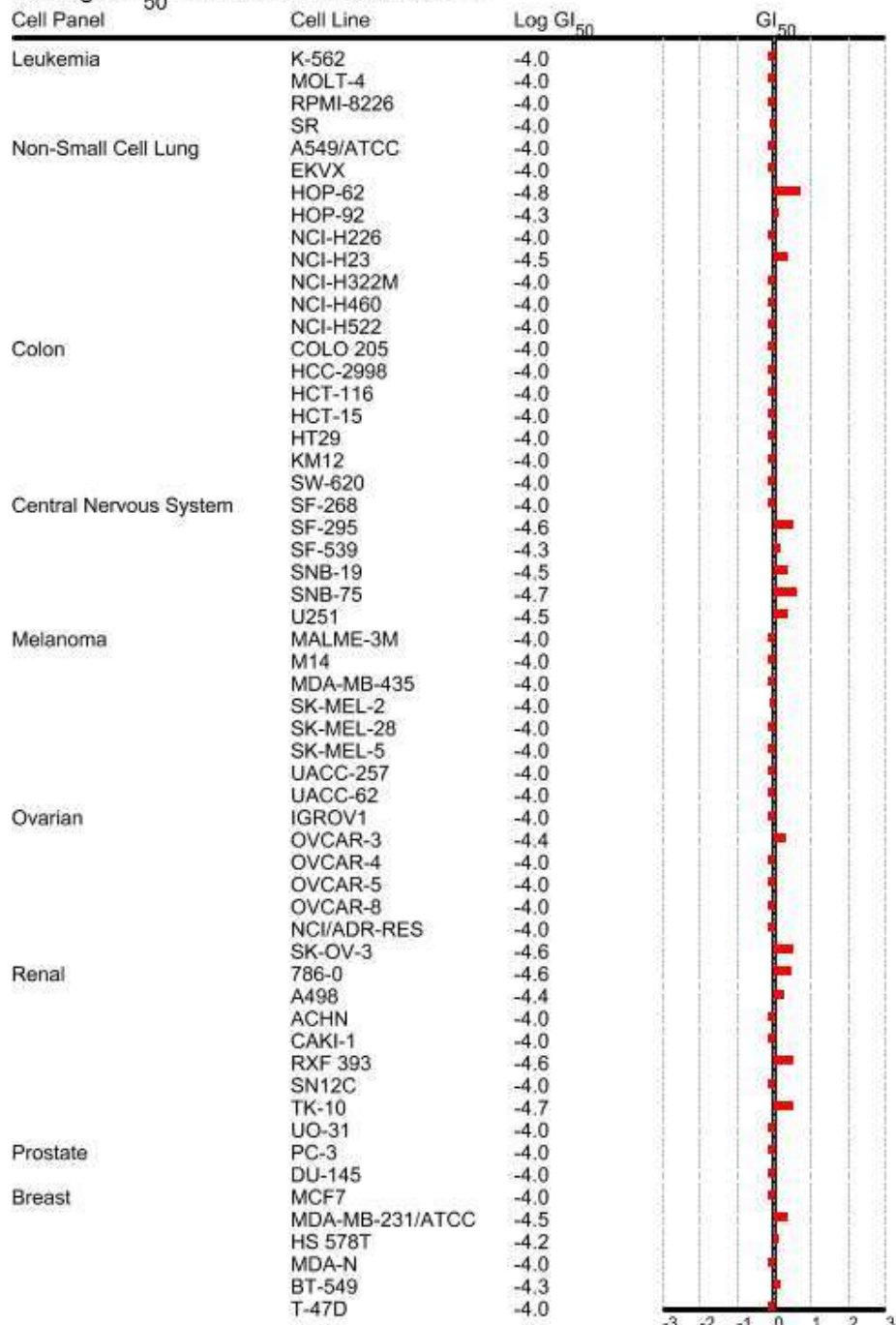


Compound J

GI₅₀ Mean Graph for Compound 299137

NCI Cancer Screen Current Data, May 2009

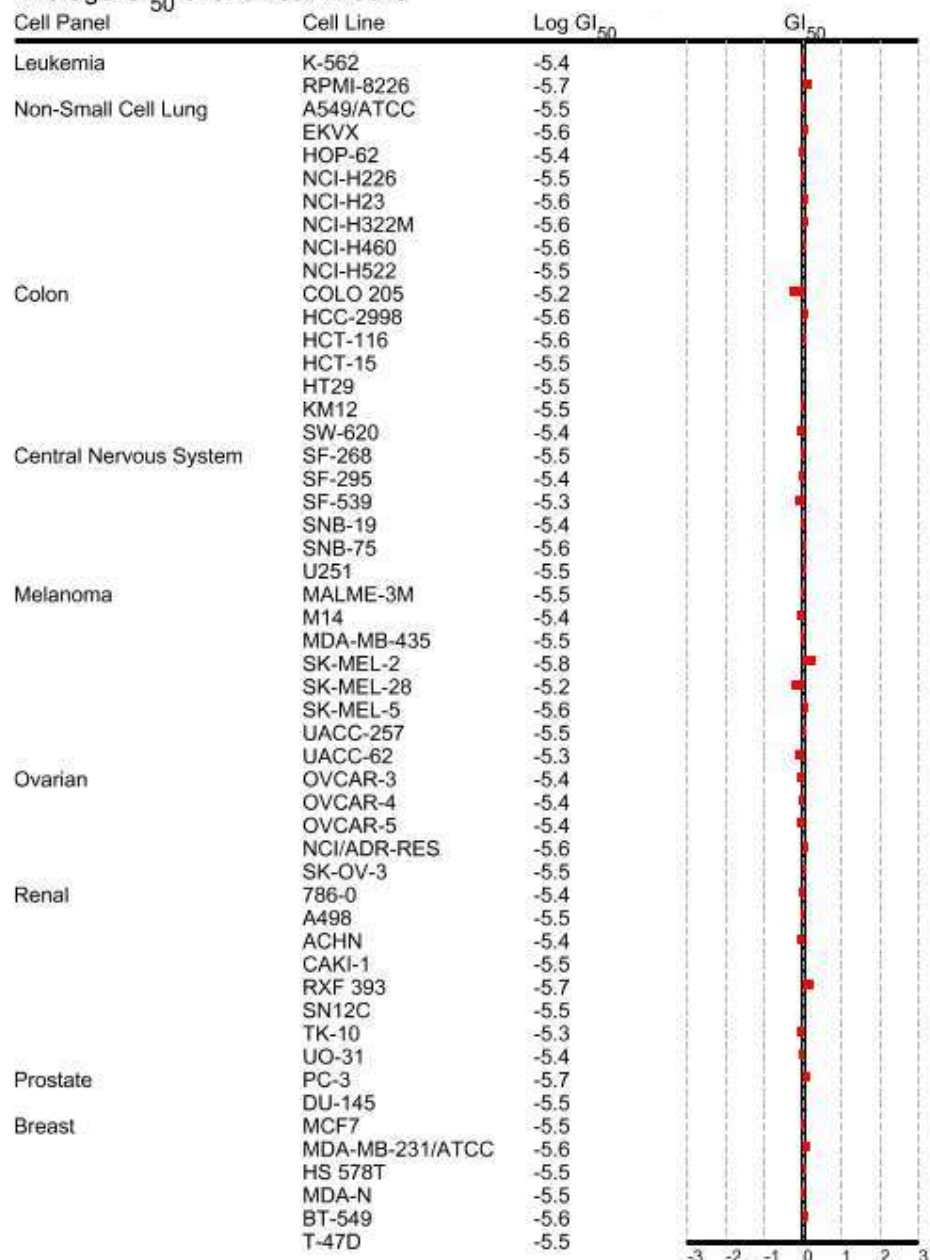
Average GI₅₀ over all cell lines is 7.03E-5



Compound K

GI₅₀ Mean Graph for Compound 306698

NCI Cancer Screen Current Data, May 2009

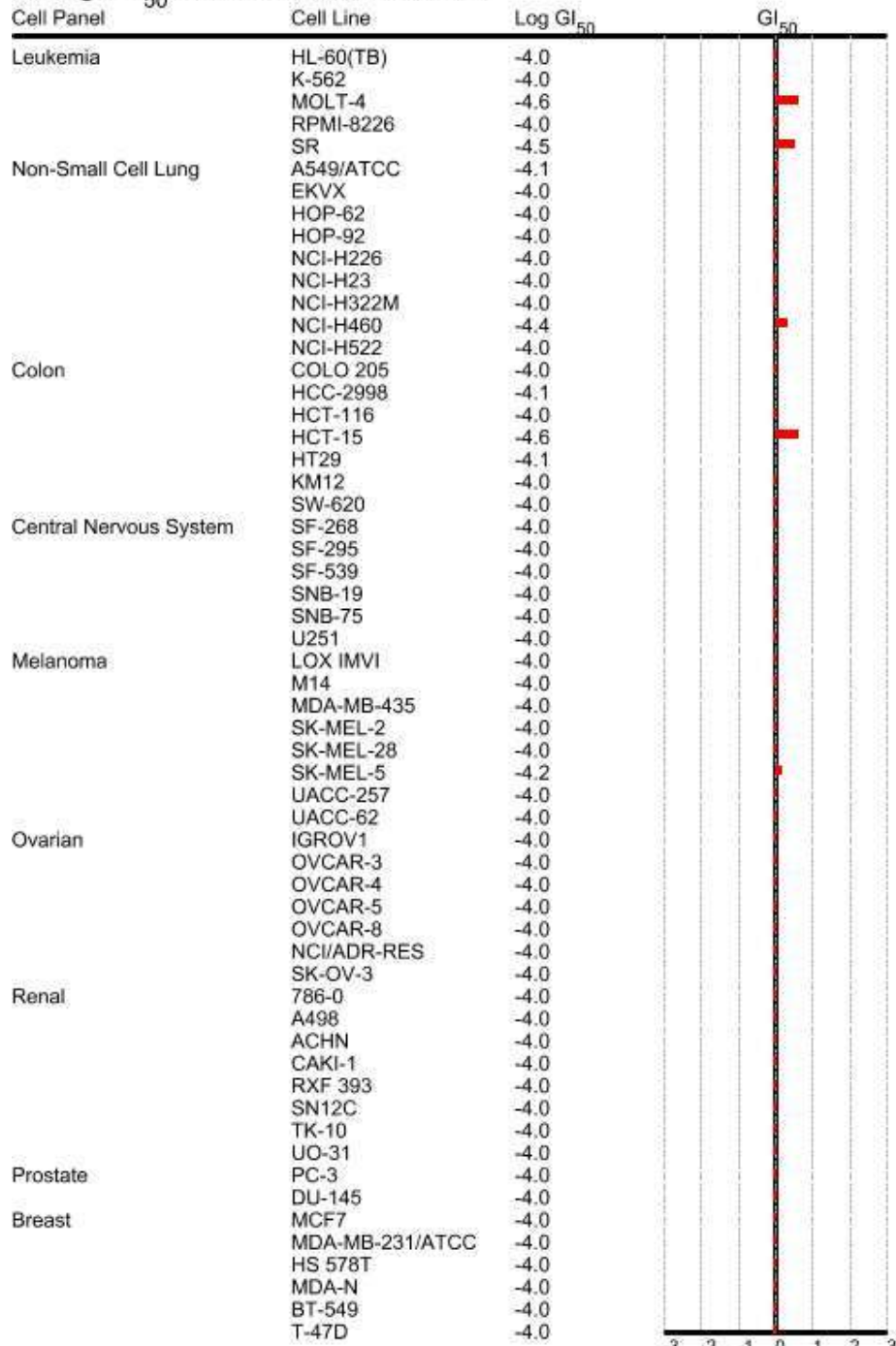
Average GI₅₀ over all cell lines is 3.25E-6

Compound L

GI₅₀ Mean Graph for Compound 351123

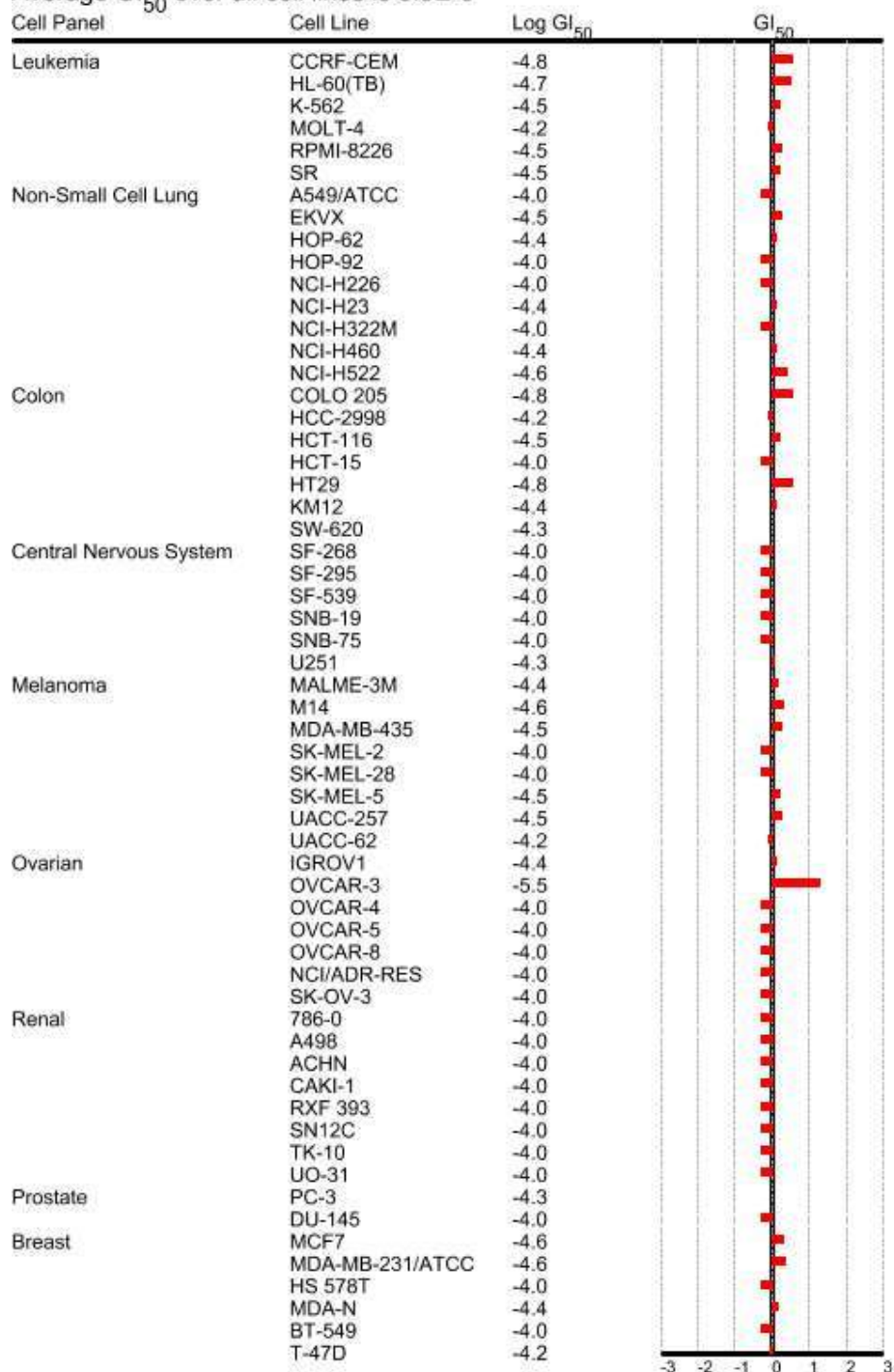
NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 9.02E-5



Compound M**GI₅₀ Mean Graph for Compound 402959**

NCI Cancer Screen Current Data, May 2009

Average GI₅₀ over all cell lines is 5.5E-5

Sample Availability: Samples are available from the authors.

S2. Diagram showing the interaction between the EGFR-TK and the eight candidate compounds using Ligand Interactions module in MOE package.

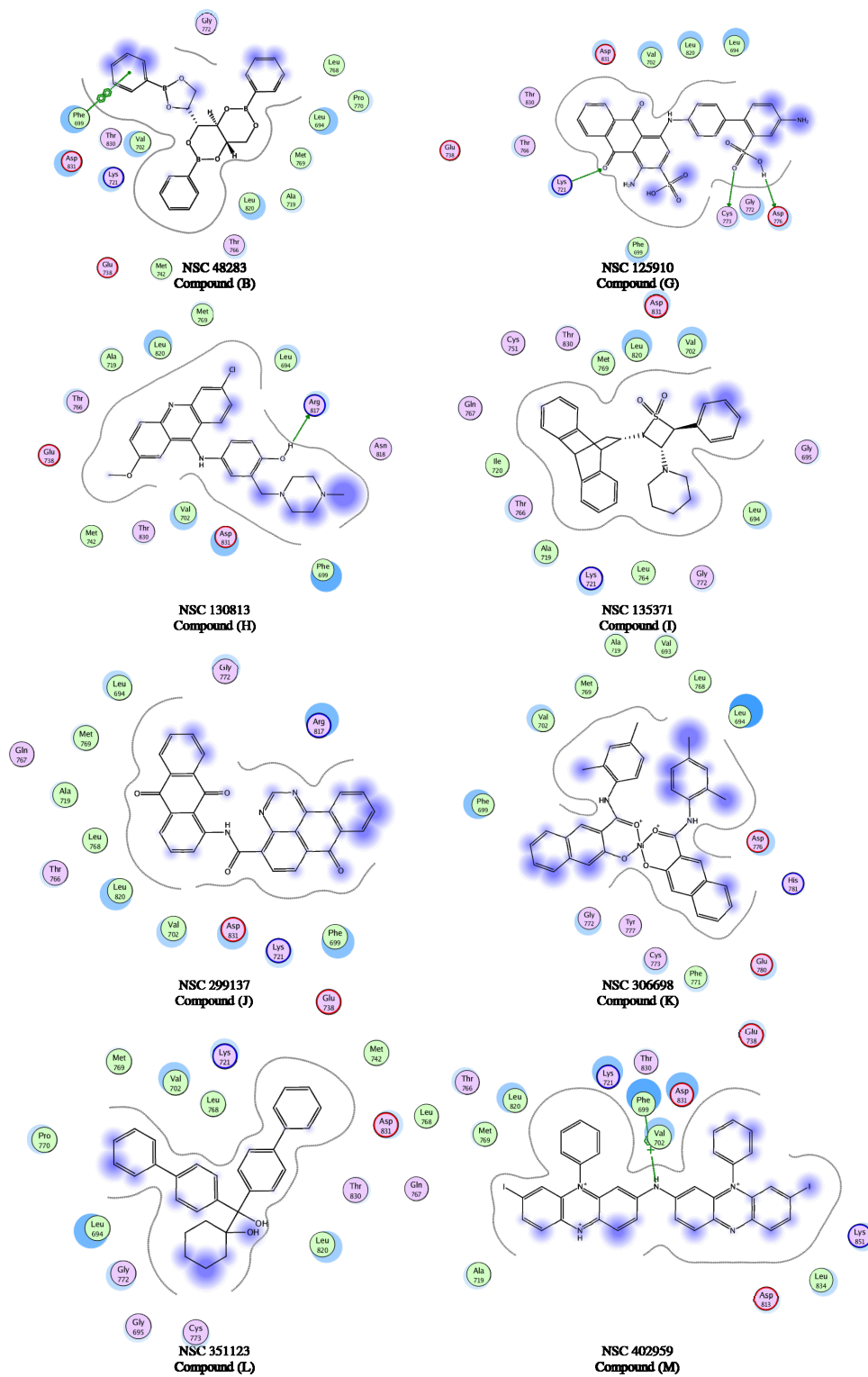
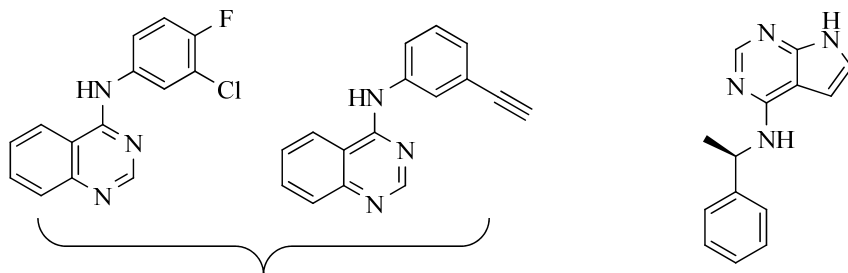


Table S1. The binding free energy and the score fitness value of the 3 known inhibitors from GOLD docking and scoring calculations.

Compounds	NSC no.	RMSD (Å)	RMSD (Å)	KCS score fitness value	GOLD			$\Delta G(\text{kJ/mol})$	Average GI_{50}^{\dagger} ($\mu\text{g/ml}$)
		All heavy atom	Core structure		Hbond [§]	Lipo [‡]	DE Clash [*]		
Gefitinib	715055	3.67	0.81	30.05	0.70	229.62	0.26	-31.00	3.24×10^{-6}
Erlotinib	718781	1.74	0.34	28.65	0.61	237.36	1.49	-31.03	5.51×10^{-6}
AEE788	N/A	1.37	0.68	32.55	1.65	220.57	0.80	-34.04	N/A

[†]The average GI_{50} overall cell line from NCI Cancer Screen Current Data, May 2009. The GI_{50} means drug concentration causing 50% cell-growth inhibition; [§] and [‡] refer to protein-ligand H-bond and lipophilic contribution to the chemscore values, respectively, and ^{*} refer to protein-ligand clash penalty to the chemscore value.

S3. The core structure of the known inhibitors that used for calculate the RMSD values, the aniline-quinazoline group from gefitinib and erlotinib and the phenethyl-amino-pyrrolopyrimidine group from AEE 788.



anilino-quinazoline group from gefitinib (left) and erlotinib (right) core structure of AEE 788