

Table S8. Correlations of expression of imprinted and non-imprinted genes at 20q11-q13.32 with log(IC50) satisfying Spearman $|\rho| > 0.25$

Gene	Agent	Spearman ρ	p_0	p_{FDR}	$ \rho > 0.3$ and $p_{FDR} < 0.05$	Sample size	Imprinted or non-imprinted gene
<i>SGK2</i>	Nilotinib	0.3343	2.40E-09	2.80E-07	*	303	Imprinted
<i>L3MBTL1</i>	Nilotinib	0.3067	5.05E-08	2.96E-06	*	303	Imprinted
<i>NNAT</i>	TG101348 (fedratinib)	0.3005	0.00578	0.04507	*	83	Imprinted
<i>GNAS</i>	TG101348 (fedratinib)	0.2777	0.01103	0.06454		83	Imprinted
<i>GNAS</i>	Lestaurtinib (CEP-701)	0.2747	0.01366	0.06948		80	Imprinted
<i>SGK2</i>	Panobinostat	0.2705	0.00202	0.02361		128	Imprinted
<i>GNAS</i>	Nilotinib	0.2669	2.45E-06	9.54E-05		303	Imprinted
<i>ZNF217</i>	Lenalidomide	0.2606	0.00883	0.06454		100	Non-imprinted
<i>GNAS</i>	Lenalidomide	-0.3197	0.00118	0.01540	*	100	Imprinted
<i>SGK2</i>	Lenalidomide	-0.3208	0.00114	0.01540	*	100	Imprinted

All correlations satisfying $|\rho| > 0.25$ had $p_{FDR} < 0.1$.

An asterisk (*) shows correlations satisfying more stringent criteria of Spearman $|\rho| > 0.3$ and $p_{FDR} < 0.1$.

Correlations are highlighted in shades of pink or blue according to the direction of association (positive or negative, respectively).

Sample size, number of cell lines with available data used in correlation analysis

Spearman ρ , Spearman correlation coefficient

p_0 , p -value prior to FDR adjustment

p_{FDR} , p -value after FDR adjustment