Table 2. Pairwise comparison of SNP array data using the GeneChip Human Mapping 250K array for the 11 cell lines exhibiting greatest sensitivity to erlotinib.

	PC-9	**H3255**	**PC-14**	**NUGC-4**	**NCI-H2170**	**KYSE-520**	**OE21**	**KYSE-450**	**KHM-3S**	**HCC-827**	**JPC-3**
PC-9	1	0.615	0.957	0.660	0.615	0.690	0.639	0.678	0.671	0.632	0.659
H3255	0.615	1	0.609	0.604	0.635	0.622	0.648	0.622	0.610	0.653	0.677
PC-14	0.957	0.609	1	0.660	0.612	0.683	0.636	0.672	0.671	0.626	0.618
NUGC-4	0.660	0.604	0.660	1	0.605	0.662	0.612	0.665	0.662	0.614	0.650
NCI-H2170	0.615	0.635	0.612	0.605	1	0.624	0.646	0.617	0.614	0.649	0.663
KYSE-520	0.690	0.622	0.683	0.662	0.624	1	0.646	0.679	0.681	0.648	0.649
OE21	0.639	0.648	0.636	0.612	0.646	0.646	1	0.638	0.629	0.664	0.669
KYSE-450	0.678	0.622	0.672	0.665	0.617	0.679	0.638	1	0.670	0.634	0.631
KHM-3S	0.671	0.610	0.671	0.662	0.614	0.681	0.629	0.670	1	0.633	0.655
HCC-827	0.632	0.653	0.626	0.614	0.649	0.648	0.664	0.634	0.633	1	0.622
JPC-3	0.640	0.655	0.623	0.670	0.622	0.652	0.623	0.670	0.684	0.663	1.000

Pairs of lines with an identity greater than 70% (0.7) are likely to have been derived from the same individual and therefore most are probably derivatives of each other. Note that PC-9 and PC-14 cells are genomically closely related; however, by cytogenetic analysis (not shown), we have determined that they exhibit distinct chromosome features, raising the possibility that they were isolated from distinct tumors in the same patient, or from the same patient before and after treatment.