

MET gene amplification in different cell lines and primary cells derived from human tumors of different origin

Cell line	Tumor origin	Fold Amplification
A549	Lung	1 <sup>#</sup> ± 0.06
EBC-1	Lung	11.9 *
GTL-16	Stomach	10.42 <sup>#</sup> ± 0.69
Hs746T	Stomach	17.9*
NCI-H1993	Lung	7.8*
NCI-H226	Lung	1.13 <sup>#</sup> ± 0.07
NCI-H441	Lung	2.37 <sup>#</sup> ± 0.15
Caki-I	Kidney	2.14 <sup>#</sup> ± 0.04
GTR-164	Stomach	0.96 <sup>^</sup> ± 0.13
GTR-498	Stomach	1.4 <sup>^</sup> ± 0.12
GTR-210	Stomach	1.13 <sup>^</sup> ± 0.41
L1.13	CUP	19.8 <sup>§</sup>
GTL-16_Res	Stomach	2-3 folds higher than GTL-16 <sup>@</sup>

# Fold change in MET gene copy number with respect to the diploid cell line A549, determined by real-time qPCR.

<sup>^</sup> Fold change in MET gene copy number with respect to the diploid cell line 293T, determined by real-time qPCR.

\*Data from Pennacchietti et al., Can Res 2014; PMID: 25217525

<sup>§</sup> Data from Virzi et al. PNAS 2016; PMID: 30224486

<sup>@</sup>Data from Cepero et al., Cancer Res 2010; PMID: 20841479