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Title: The long non-coding MALAT-1 stimulates cellular growth, migration and proliferation

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Body: Introduction: In non small cell lung cancer, the expression levels of the large non-coding RNA (lncRNA) MALAT-1 are associated both with patient survival and with tumor promoting effects. Here, we focus on the molecular genetic impact of MALAT-1 on cellular gene regulation. Methods: Gene expression was studied in murine fibroblasts (NIH 3T3) either transduced with PINCO::MALAT-1 expression vector or with empty control vector using Next Generation Sequencing (Mouse Gene 1.0 ST array, Affymetrix, CA). Differentially expressed genes were analyzed by the Ingenuity Pathway Analysis (IPA) software (Ingenuity Systems, Inc. Redwood City, CA). Results: Out of 29.000 genes, 250 genes were significantly (at least twofold) up-regulation or down-regulation. Differentially expressed genes were categorized into "Top Bio Functions" groups. The three most important groups were "cellular growth and proliferation" (n=90), "cellular movement" (n=75), and "inflammatory response" (n=65). The observation of a positive association of MALAT-1 gene expression with cellular growth, migration and proliferation was confirmed in vitro with migration assays, colony assays, and scratch assays (p<0.01, all comparisons). Conclusions: These data demonstrate that enhanced MALAT-1 expression levels stimulate cellular migration, colony formation and wound healing and contribute to the idea of multidimensional effects of MALAT-1 ncRNA on important cellular functions in malignant lung cells.