Quantitative proteomics reveals that distant recurrenceassociated protein R-Ras and Transgelin predict post-surgical survival in patients with Stage III colorectal cancer

SUPPLEMENTARY DATA

REFERENCES

- 1. Bassorgun, C.I, et al., S100A8 and S100A9 Positive Cells in Colorectal Carcinoma: Clinicopathological Analysis. Gastroenterol Res Pract, 2014. 2014:p. 943175.
- 2. Duan, L., et al., S100A8 and S100A9 are associated with colorectal carcinoma progression and contribute to colorectal carcinoma cell survival and migration via Wnt/ beta-catenin pathway. PLoS One, 2013. 8:p. e62092.
- 3. Kim, H.J., et al., Identification of S100A8 and S100A9 as serological markers for colorectal cancer. J Proteome Res, 2009. 8:p. 1368-79.
- 4. Kim, J.H., et al., The role of myofibroblasts in upregulation of S100A8 and S100A9 and the differentiation of myeloid cells in the colorectal cancer microenvironment. Biochem Biophys Res Commun, 2012. 423:p. 60-6.
- 5. Krasnov, G.S., et al., Identification of proteins with altered expression in colorectal cancer by means of 2D-proteomics. Molecular Biology, 2009. 43:p. 321-328.
- 6. Spitzner, M., et al., A gene expression signature for chemoradiosensitivity of colorectal cancer cells. Int J Radiat Oncol Biol Phys, 2010. 78:p. 1184-92.
- 7. Wilding, J.L., et al., Replication error deficient and proficient colorectal cancer gene expression differences caused by 3'UTR polyT sequence deletions. Proc Natl Acad Sci U S A, 2010. 107:p. 21058-63.
- 8. Aychek, T., et al., E-selectin regulates gene expression in metastatic colorectal carcinoma cells and enhances HMGB1 release. Int J Cancer, 2008. 123:p. 1741-50.
- 9. Lee, H., et al., Diagnostic significance of serum HMGB1 in colorectal carcinomas. PLoS One, 2012. 7:p. e34318.
- 10. Li, W., et al., HMGB1 recruits myeloid derived suppressor cells to promote peritoneal dissemination of colon cancer after resection. Biochem Biophys Res Commun, 2013. 436:p. 156-61.
- 11. Liu, W., et al., HMGB1-mediated autophagy modulates sensitivity of colorectal cancer cells to oxaliplatin via MEK/ERK signaling pathway. Cancer Biol Ther, 2015. 16:p. 511-7.
- 12. Luo, Y., et al., HMGB1 attenuates anti-metastatic defence of the liver in colorectal cancer. Eur J Cancer, 2010. 46:p. 791-9.
- 13. Moriwaka, Y., et al., HMGB1 attenuates anti-metastatic defense of the lymph nodes in colorectal cancer. Pathobiology, 2010. 77:p. 17-23.
- 14. Suren, D., et al., The role of high mobility group box 1 (HMGB1) in colorectal cancer. Med Sci Monit, 2014. 20: p. 530-7.
- 15. Ueda, M., et al., Prognostic significance of high mobility group box 1 (HMGB1) expression in patients with colorectal cancer. Anticancer Res, 2014. 34:p. 5357-62.
- 16. Yao, X., et al., Overexpression of high-mobility group box 1 correlates with tumor progression and poor prognosis in human colorectal carcinoma. J Cancer Res Clin Oncol, 2010. 136:p. 677-84.
- 17. Zhang, C.C., et al., The HMGB1 protein sensitizes colon carcinoma cells to cell death triggered by pro-apoptotic agents. Int J Oncol, 2015. 46:p. 667-76.
- 18. Zhang, Z., et al., Increased HMGB1 and cleaved caspase-3 stimulate the proliferation of tumor cells and are correlated with the poor prognosis in colorectal cancer. J Exp Clin Cancer Res, 2015. 34:p. 51.
- 19. Kang, U.B., et al., Expression profiling of more than 3500 proteins of MSS-type colorectal cancer by stable isotope labeling and mass spectrometry. J Proteomics, 2012. 75:p. 3050-62.
- 20. Hostetter, R.B., et al., Carcinoembryonic Antigen as a Selective Enhancer of Colorectal-Cancer Metastasis. Journal of the National Cancer Institute, 1990. 82:p. 380-385.
- 21. Koprowski, H., et al., Specific antigen in serum of patients with colon carcinoma. Science, 1981. 212:p. 53-5.
- 22. Bruin, S.C., et al., Molecular alterations associated with liver metastases development in colorectal cancer patients. Br J Cancer, 2011. 105:p. 281-7.
- 23. Pimiento, J.M., et al., Targeting CSE1L in colorectal cancer. Journal of the American College of Surgeons, 2012. 215:p. S127-S127.
- 24. Puerta-Garcia, E., M. Canadas-Garre, M.A. Calleja-Hernandez, Molecular biomarkers in colorectal carcinoma. Pharmacogenomics, 2015:p. 1-33.
- 25. Sethi, M.K., et al., Quantitative proteomic analysis of paired colorectal cancer and non-tumorigenic tissues reveals signature proteins and perturbed pathways involved in CRC progression and metastasis. J Proteomics, 2015. 126:p. 54-67.
- 26. Tai, C.J., et al., Correlations between cytoplasmic CSE1L in neoplastic colorectal glands and depth of tumor penetration and cancer stage. J Transl Med, 2013. 11:p. 29.
- 27. Meisenberg, C., et al., Clinical and cellular roles for TDP1 and TOP1 in modulating colorectal cancer response to irinotecan. Mol Cancer Ther, 2015. 14:p. 575-85.
- 28. Romer, M.U., et al., TOP1 gene copy numbers in colorectal cancer samples and cell lines and their association to *in vitro* drug sensitivity. Scand J Gastroenterol, 2012. 47:p. 68-79.
- 29. Romer, M.U., et al., Topoisomerase 1(TOP1) gene copy number in stage III colorectal cancer patients and its relation to prognosis. Mol Oncol, 2013. 7:p. 101-11.
- 30. Smith, D.H., et al., Mechanisms of topoisomerase I (TOP1) gene copy number increase in a stage III colorectal cancer patient cohort. PLoS One, 2013. 8:p. e60613.
- 31. Sonderstrup, I.M.H., et al., Topoisomerase-1 and-2A gene copy numbers are elevated in mismatch repairproficient colorectal cancers. Molecular Oncology, 2015. 9:p. 1207-1217.
- 32. Knol, J.C., et al., Proteomics of differential extraction fractions enriched for chromatin-binding proteins from colon adenoma and carcinoma tissues. Biochim Biophys Acta, 2014. 1844:p. 1034-43.
- 33. Lu, H., V. Goodell, M.L. Disis, Targeting serum antibody for cancer diagnosis: a focus on colorectal cancer. Expert Opin Ther Targets, 2007. 11:p. 235-44.
- 34. Staub, E., et al., A genome-wide map of aberrantly expressed chromosomal islands in colorectal cancer. Mol Cancer, 2006. 5:p. 37.
- 35. Sakai, K., et al., Chemoradiation provides a physiological selective pressure that increases the expansion of aberrant TP53 tumor variants in residual rectal cancerous regions. Oncotarget, 2014. 5:p. 9641-9649.
- 36. Shin, Y.J., et al., High-mobility group box 2 (HMGB2) modulates radioresponse and is downregulated by p53 in colorectal cancer cell. Cancer Biol Ther, 2013. 14:p. 213-21.
- 37. Kim, M.S., et al., Expressional analysis of NOLA1, NOLA2, NOLA3 and DKC1, the core proteins in H/ACA riboproteins, in gastric and colorectal cancers. Pathology, 2012. 44:p. 576-7.
- 38. Choi, D.S., et al., Quantitative proteomics of extracellular vesicles derived from human primary and metastatic colorectal cancer cells. J Extracell Vesicles, 2012. 1.
- 39. Yan, X.B., et al., Knockdown of Yboxbinding protein1 inhibits the malignant progression of HT29 colorectal

adenocarcinoma cells by reversing epithelialmesenchymal transition. Mol Med Rep, 2014. 10:p. 2720-8.

- 40. Hao, J.M., et al., A five-gene signature as a potential predictor of metastasis and survival in colorectal cancer. J Pathol, 2010. 220:p. 475-89.
- 41. Gerner, E.W., et al., A comprehensive strategy to combat colon cancer targeting the adenomatous polyposis coli tumor suppressor gene. Ann N Y Acad Sci, 2005. 1059: p. 97-105.
- 42. Chen, H., et al., Protein-protein interaction analysis of distinct molecular pathways in two subtypes of colorectal carcinoma. Mol Med Rep, 2014. 10:p. 2868-74.
- 43. Raeisossadati, R., et al., Aberrant expression of DPPA2 and HIWI genes in colorectal cancer and their impacts on poor prognosis. Tumour Biol, 2014. 35:p. 5299-305.
- 44. Kim, M.S., et al., Frameshift mutations of chromosome cohesion-related genes SGOL1 and PDS5B in gastric and colorectal cancers with high microsatellite instability. Hum Pathol, 2013. 44:p. 2234-40.
- 45. Deb, S., et al., RAD21 cohesin overexpression is a prognostic and predictive marker exacerbating poor prognosis in KRAS mutant colorectal carcinomas. British Journal of Cancer, 2014. 110:p. 1606-1613.
- 46. Karl, J., et al., Improved diagnosis of colorectal cancer using a combination of fecal occult blood and novel fecal protein markers. Clin Gastroenterol Hepatol, 2008. 6:p. 1122-8.
- 47. Thierolf, M., et al., Towards a comprehensive proteome of normal and malignant human colon tissue by 2-D-LC-ESI-MS and 2-DE proteomics and identification of S100A12 as potential cancer biomarker. Proteomics Clin Appl, 2008. 2:p. 11-22.
- 48. Babel, I., et al., Identification of MST1/STK4 and SULF1 proteins as autoantibody targets for the diagnosis of colorectal cancer by using phage microarrays. Mol Cell Proteomics, 2011. 10:p. M110 001784.
- 49. Zhai, X.H., et al., Identification of a new protein biomarker for colorectal cancer diagnosis. Mol Med Rep, 2012. 6:p. 444-8.
- 50. Krzystek-Korpacka, M., et al., Tumor location determines midkine level and its association with the disease progression in colorectal cancer patients: a pilot study. Int J Colorectal Dis, 2012. 27:p. 1319-24.
- 51. Krzystek-Korpacka, M., et al., Circulating midkine in malignant and non-malignant colorectal diseases. Cytokine, 2013. 64:p. 158-64.
- 52. Slattery, M.L., et al., Gene expression in colon cancer: A focus on tumor site and molecular phenotype. Genes Chromosomes Cancer, 2015. 54:p. 527-41.
- 53. Wang, B., et al., A novel all-trans retinoid acid derivatives inhibits the migration of breast cancer cell lines MDA-MB-231 via myosin light chain kinase involving

p38-MAPK pathway. Biomed Pharmacother, 2013. 67:p. 357-62.

- 54. Ma, Y., et al., Proteomics identification of desmin as a potential oncofetal diagnostic and prognostic biomarker in colorectal cancer. Mol Cell Proteomics, 2009. 8:p. 1878-90.
- 55. Mikula, M., et al., Integrating proteomic and transcriptomic high-throughput surveys for search of new biomarkers of colon tumors. Functional & Integrative Genomics, 2011. 11:p. 215-224.
- 56. Yasui, Y., T. Tanaka, Protein expression analysis of inflammation-related colon carcinogenesis. J Carcinog, 2009. 8:p. 10.
- 57. Park, S.Y., et al., KITENIN-targeting microRNA-124 suppresses colorectal cancer cell motility and tumorigenesis. Mol Ther, 2014. 22:p. 1653-64.
- 58. Ang, C.S., E.C. Nice, Targeted in-gel MRM: a hypothesis driven approach for colorectal cancer biomarker discovery in human feces. J Proteome Res, 2010. 9:p. 4346-55.
- 59. Lv, J., et al., Identification of Differentially Expressed Proteins of Normal and Cancerous Human Colorectal Tissues by Liquid Chromatograph-Mass Spectrometer Based on iTRAQ Approach. Cancer Invest, 2015:p. 1-9.
- 60. Zhu, Y., et al., Gut microbiota and probiotics in colon tumorigenesis. Cancer Lett, 2011. 309:p. 119-27.
- 61. Ma, Y., et al., Searching for consistently reported upand down-regulated biomarkers in colorectal cancer: a systematic review of proteomic studies. Mol Biol Rep, 2012. 39:p. 8483-90.
- 62. Wang, N., et al., Selenium-binding protein 1 is associated with the degree of colorectal cancer differentiation and is regulated by histone modification. Oncol Rep, 2014. 31:p. 2506-14.
- 63. Lascorz, J., K. Hemminki, A. Forsti, Systematic enrichment analysis of gene expression profiling studies identifies consensus pathways implicated in colorectal cancer development. J Carcinog, 2011. 10:p. 7.
- 64. Gao, H., et al., Anterior gradient 2: a new target to treat colorectal cancer. Med Hypotheses, 2013. 80:p. 706-8.
- 65. Riener, M.O., et al., Loss of anterior gradient-2 expression is an independent prognostic factor in colorectal carcinomas. Eur J Cancer, 2014. 50:p. 1722-30.
- 66. Valladares-Ayerbes, M., et al., Evaluation of the adenocarcinoma-associated gene AGR2 and the intestinal stem cell marker LGR5 as biomarkers in colorectal cancer. Int J Mol Sci, 2012. 13:p. 4367-87.
- 67. Traicoff, J.L., et al., Characterization of the human polymeric immunoglobulin receptor (PIGR) 3'UTR and differential expression of PIGR mRNA during colon tumorigenesis. J Biomed Sci, 2003. 10:p. 792-804.
- 68. Bianchini, M., et al., Comparative study of gene expression by cDNA microarray in human colorectal cancer tissues and normal mucosa. Int J Oncol, 2006. 29:p. 83-94.
- 69. Bongaerts, B.W., et al., Alcohol consumption, alcohol dehydrogenase 1C (ADH1C) genotype, and risk of colorectal cancer in the Netherlands Cohort Study on diet and cancer. Alcohol, 2011. 45:p. 217-25.
- 70. Yang, H.Y., et al., Comparative proteomic analysis of cysteine oxidation in colorectal cancer patients. Mol Cells, 2013. 35:p. 533-42.
- 71. Crous-Bou, M., et al., Polymorphisms in alcohol metabolism genes ADH1B and ALDH2, alcohol consumption and colorectal cancer. PLoS One, 2013. 8:p. e80158.
- 72. Guo, X.F., et al., Meta-analysis of the ADH1B and ALDH2 polymorphisms and the risk of colorectal cancer in East Asians. Intern Med, 2013. 52:p. 2693-9.
- 73. Gao, Z.H., et al., ILEI: a novel marker for epithelialmesenchymal transition and poor prognosis in colorectal cancer. Histopathology, 2014. 65:p. 527-38.
- 74. Lind, G.E., et al., Identification of an epigenetic biomarker panel with high sensitivity and specificity for colorectal cancer and adenomas. Mol Cancer, 2011. 10:p. 85.
- 75. Takemasa, I., et al., Potential biological insights revealed by an integrated assessment of proteomic and transcriptomic data in human colorectal cancer. Int J Oncol, 2012. 40:p. 551-9.
- 76. Wang, H.Y., et al., Expression status of S100A14 and S100A4 correlates with metastatic potential and clinical outcome in colorectal cancer after surgery. Oncol Rep, 2010. 23:p. 45-52.
- 77. Gormley, J.A., et al., The role of Cathepsin S as a marker of prognosis and predictor of chemotherapy benefit in adjuvant CRC: a pilot study. British Journal of Cancer, 2011. 105:p. 1487-1494.
- 78. Kuester, D., et al., The cathepsin family and their role in colorectal cancer. Pathology Research and Practice, 2008. 204:p. 491-500.
- 79. Choi, D.S., et al., Proteomic analysis of microvesicles derived from human colorectal cancer ascites. Proteomics, 2011. 11:p. 2745-51.
- 80. Kim, S.W., et al., Abrogation of galectin-4 expression promotes tumorigenesis in colorectal cancer. Cell Oncol (Dordr), 2013. 36:p. 169-78.
- 81. Rechreche, H., et al., Cloning and expression of the mRNA of human galectin-4, an S-type lectin down-regulated in colorectal cancer. European Journal of Biochemistry, 1997. 248:p. 225-230.
- 82. Satelli, A., et al., Galectin-4 functions as a tumor suppressor of human colorectal cancer. International Journal of Cancer, 2011. 129:p. 799-809.
- 83. Ye, H., et al., Meta-analysis of human colorectal cancer transcriptome. Int J Colorectal Dis, 2012. 27:p. 1125-8.
- 84. Perilli, L., et al., Circulating miR-182 is a biomarker of colorectal adenocarcinoma progression. Oncotarget, 2014. 5:p. 6611-6619.
- 85. Pizzini, S., et al., Impact of microRNAs on regulatory networks and pathways in human colorectal carcinogenesis and development of metastasis. BMC Genomics, 2013. 14: p. 589.
- 86. Groschl, B., et al., Iqgap2 is downregulated in colorectal cancer (crc) and involved in cellular migration. Cancer Research, 2014. 74:p. 5004-5004.
- 87. Roepman, P., et al., Colorectal cancer intrinsic subtypes predict chemotherapy benefit, deficient mismatch repair and epithelial-to-mesenchymal transition. International Journal of Cancer, 2014. 134:p. 552-562.
- 88. Zhang, C., et al., Lack of association of SULT1A1 R213H polymorphism with colorectal cancer: a meta-analysis. PLoS One, 2011. 6:p. e19127.
- 89. Otero-Estevez, O., et al., Decreased Expression of Alpha-L-Fucosidase Gene FUCA1 in Human Colorectal Tumors. International Journal of Molecular Sciences, 2013. 14:p. 16986-16998.
- 90. Hong, Y., et al., A 'metastasis-prone' signature for earlystage mismatch-repair proficient sporadic colorectal cancer patients and its implications for possible therapeutics. Clinical & Experimental Metastasis, 2010. 27:p. 83-90.
- 91. Soreide, K., et al., Trypsin in colorectal cancer: molecular biological mechanisms of proliferation, invasion, and metastasis. J Pathol, 2006. 209:p. 147-56.
- 92. Chen, Q., et al., Microarray analyses reveal liver metastasisrelated genes in metastatic colorectal cancer cell model. J Cancer Res Clin Oncol, 2013. 139:p. 1169-78.
- 93. Fernandez-Rozadilla, C., et al., Pharmacogenomics in colorectal cancer: a genome-wide association study to predict toxicity after 5-fluorouracil or FOLFOX administration. Pharmacogenomics J, 2013. 13:p. 209-17.
- 94. Gylfe, A.E., et al., Identification of candidate oncogenes in human colorectal cancers with microsatellite instability. Gastroenterology, 2013. 145:p. 540-3 e22.
- 95. Yeh, C.S., et al., Fatty acid metabolism pathway play an important role in carcinogenesis of human colorectal cancers by Microarray-Bioinformatics analysis. Cancer Lett, 2006. 233:p. 297-308.
- 96. Yi, J.M., et al., Genomic and epigenomic integration identifies a prognostic signature in colon cancer. Clin Cancer Res, 2011. 17:p. 1535-45.
- 97. McHugh, S.M., J. O'Donnell, P. Gillen, Genomic and oncoproteomic advances in detection and treatment of colorectal cancer. World J Surg Oncol, 2009. 7:p. 36.
- 98. Chik, J.H.L., et al., Comprehensive glycomics comparison between colon cancer cell cultures and tumours:

Implications for biomarker studies. Journal of Proteomics, 2014. 108:p. 146-162.

- 99. Schafer, H., et al., TGF-beta 1-dependent L1CAM expression has an essential role in macrophage-induced apoptosis resistance and cell migration of human intestinal epithelial cells. Oncogene, 2013. 32:p. 180-189.
- 100. Lee, S., et al., Identification of GABRA1 and LAMA2 as new DNA methylation markers in colorectal cancer. International Journal of Oncology, 2012. 40:p. 889-898.
- 101. Hansen, A.G., et al., Elevated ALCAM shedding in colorectal cancer correlates with poor patient outcome. Cancer Res, 2013. 73:p. 2955-64.
- 102. Tachezy, M., et al., Activated leukocyte cell adhesion molecule (CD166)-Its prognostic power for colorectal cancer patients. Journal of Surgical Research, 2012. 177: p. E15-E20.
- 103. Budinska, E., et al., Gene expression patterns unveil a new level of molecular heterogeneity in colorectal cancer. J Pathol, 2013. 231:p. 63-76.
- 104. Dou, R., et al., Multi-microarray identifies lower AQP9 expression in adjuvant chemotherapy nonresponders with stage III colorectal cancer. Cancer Lett, 2013. 336:p. 106-13.
- 105. Birkenkamp-Demtroder, K., et al., Keratin23 (KRT23) knockdown decreases proliferation and affects the DNA damage response of colon cancer cells. PLoS One, 2013. 8:p. e73593.
- 106. Tian, X., et al., Screening of potential diagnostic markers and therapeutic targets against colorectal cancer. Onco Targets Ther, 2015. 8:p. 1691-9.
- 107. Yeh, C.S., et al., Significance of the glycolytic pathway and glycolysis related-genes in tumorigenesis of human colorectal cancers. Oncol Rep, 2008. 19:p. 81-91.
- 108. Koike, Y., et al., Preoperative C-Reactive Protein as a Prognostic and Therapeutic Marker for Colorectal Cancer. Journal of Surgical Oncology, 2008. 98:p. 540-544.
- 109. Shiu, Y.C., et al., Is C-reactive protein a prognostic factor of colorectal cancer? Dis Colon Rectum, 2008. 51:p. 443-9.
- 110. Tsilidis, K.K., et al., C-reactive protein and colorectal cancer risk: a systematic review of prospective studies. Int J Cancer, 2008. 123:p. 1133-40.
- 111. Lin, Y., et al., Association of the actin-binding protein transgelin with lymph node metastasis in human colorectal cancer. Neoplasia, 2009. 11:p. 864-73.
- 112. Peng, J.Y., et al., A rat-to-human search for proteomic alterations reveals transgelin as a biomarker relevant to colorectal carcinogenesis and liver metastasis. Electrophoresis, 2009. 30:p. 2976-2987.

Supplementary Figure S1: Quantitative MS identified 146 DEPs associated with distant recurrence. A. 2,383 proteins were identified in both IIIB and IIIC groups. Additionally, 839 IIIB-specific proteins and 435 IIIC-specific proteins were also identified. **B.** Out of the total 3,657 proteins, 146 proteins were differentially expressed between good outcome and distant recurrence. About half of them had a score more than 10. (DR, distant recurrence).

A R-RAS (UniProt_AC P10301)

Supplementary Figure S2: MS/MS spectra of R-Ras and Transgelin unique peptides. A. MS/MS spectra of R-Ras aa177- 188 (m/z = 831.45) in the MS experiments of IIIB and IIIC groups. **B.** MS/MS spectra of Transgelin aa109-121 (m/z = 995.52) in the MS experiments of IIIB and IIIC groups. The TMT reporter signals were also shown.

Supplementary Figure S3: Representative photos (amplification: 100) of anti-R-Ras IHC with regions zoomed in (amplification: 400). Top panel: R-Ras dense staining is observed in epithelial cells of longitudinally cut mucosa crypts of paratumor tissue. Medium panel: positive R-Ras staining of poorly differentiated adenocarcinoma. Bottom panel: well differentiated adenocarcinoma with negative R-Ras staining.

Supplementary Figure S4: Representative photos (amplification: 100) of anti-Transgelin IHC with regions zoomed in (amplification: 400). Top panel: Transgelin dense staining is observed around tangentially cut mucosa crypts of para-tumor tissue. Medium panel: moderately differentiated tumor tissue of positive Transgelin staining. Bottom panel: Transgelin-negative tumor tissue shows desmoplasia. Necrotic debris can be observed in glandular lumina.

Supplementary Figure S5: R-Ras has no effect on CRC cells proliferation. (A) SW480 and (B) HCT116 were stably transfected with pLv-CP06 vector and pLv-CP06-Flag-RRAS (left panel); pLv-shRNA-KP Ctrl, pLv-shRNA-KP-sh1, and pLv-shRNA-KP-sh2 (right panel), respectively. Monolayer growth rates of cells were determined by CCK8 assay. Results are presented as means±SD (n=4).

Supplementary Table S1:

See Supplementary File 1

Supplementary Table S2: Manual search in literature databases found that the relevance of 66 DEPs with CRC has been reported previously

See Supplementary File 2

Supplementary Table S3: R-Ras and Transgelin expression in tumor and para-tumor tissue of Stage III CRC

Supplementary Table S4: DEPs expression measurement information IIIB

See Supplementary File 3