

实验中心发表主要论著

	Individualized identification of disease-associated pathways with disrupted coordination of gene expression.	Brief Bioinform, 2015, pii: bbv030
	Individual-level analysis of differential expression of genes and pathways for personalized medicine.	Bioinformatics , 2015, 31(1) 62-68
	The BRCA1/2-directed miRNA signature predicts a good prognosis in ovarian cancer patients with wild-type BRCA1/2	Oncotarget, 2015, 6(4) 2397-2406
	Autophagy-related prognostic signature for breast cancer.	Molecular Carcinogenesis . 2015, doi: 10.1002/mc.22278.
	Effects of ER α -specific antagonist on mouse preimplantation embryo development and zygotic genome activation	J Steroid Biochem Mol Biol, 2015, 145(1):13-20
	Identification of reproducible drug-resistance-related dysregulated genes in small-scale cancer cell line experiments	Sci Rep, 2015 , Doi: 10.1038/srep11895
	Application of the rank-based method to DNA methylation for	Gene , 2015, 555: 203-207

	cancer diagnosis	
	Hepatitis B virus core protein inhibits Fas-mediated apoptosis of hepatoma cells via regulation of mFas/FasL and sFas expression	FASEB J, 2015, 29: 1113-1123
	Transcriptional regulation of the apolipoprotein F (ApoF) gene by ETS and C/EBPalpha in hepatoma cells	Biochimie, 2015, 112: 1-9
	Hepatitis B virus X protein increases the IL-1beta-induced NF-kappaB activation via interaction with evolutionarily conserved signaling intermediate in Toll pathways (ECSIT)	Virus Res, 2015, 195: 236-245
	A relative ordering-based predictor for tamoxifen-treated estrogen receptor-positive breast cancer patients: multi-laboratory cohort validation.	Breast Cancer Research and Treatment, 2013;142(3):505-14
	Deconvolution of the gene expression profiles of valuable banked blood specimens for studying the prognostic values of altered peripheral immune cell proportions in cancer patients	PLoS One, 2014 , 9(6):e100934
	Similar blood-borne DNA methylation alterations in cancer and inflammatory	Br J Cancer, 2014 , 111(3):525-31

	diseases determined by subpopulation shifts in peripheral leukocytes	
	Similar source of differential blood mRNAs in lung cancer and pulmonary inflammatory diseases: calls for improved strategy for identifying cancer-specific biomarkers	PLoS One, 2014 , 9(9):e108104
	MTTP polymorphisms and susceptibility to non-alcoholic fatty liver disease in a Han Chinese population	Liver Int, 2014, 34: 118-128
	Establishment of and comparison between orthotopic xenograft and subcutaneous xenograft models of gallbladder carcinoma	Asian Pac J Cancer Prev, 2014, 15(8):3747-52
	Helicobacter pylori outer inflammatory protein DNA vaccine-loaded bacterial ghost enhances immune protective efficacy in C57BL/6 mice	Vaccine, 2014, (32):6054-6060
	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure	Journal of Biomedical Informatics, 2014,49: 187-197
	Functional comparison between genes dysregulated in ulcerative colitis and colorectal carcinoma	PLoS One, 2013, 8(8):e71989-e71989

	Genes Dysregulated to Different Extent or Oppositely in Estrogen Receptor-Positive and Estrogen Receptor-Negative Breast Cancers	PLos One, 2013, 8(7):1-10
	Rank-based predictors for response and prognosis of neoadjuvant taxane-anthracycline-based chemotherapy in breast cancer.	Breast Cancer Res Treat, 2013, 139(2):361-9
	An Integrated Approach to Uncover Driver Genes in Breast Cancer Methylation Genomes	PLos One, 2013, 8(4):1-15
	Network analysis of genomic alteration profiles reveals co-altered functional modules and driver genes for glioblastoma	Molecular Biosystems, 2013, 9(3):467-477
	Separate enrichment analysis of pathways for up- and downregulated genes	Journal of the Royal Society Interface, 2013, 11(92):1-12.