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		Bioinformatics	6	Briefings in Bioinformatics	3	Human Mutation
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	4	81271822	X L-FABP NQO1			2013- 2016	95
	5	81201293	TGF 1I1			2013- 2016	23
	6	81271784	1-integrin			2013- 2016	80
	7	2012ZX1 0002002 -004-006				2012- 2015	46
	8	81401657	USP15 X			2015- 2017	23
	9	2012J011 30				2012- 2014	4
	10	2012J013 65	X ECSIT 1b(IL-1b)			2012- 2014	4

	11	20123518 120003	X 1b			2013- 2015	4
	12	WKJ-FJ- 29				2013- 2016	27
	13	81170624				2012- 2015	65
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		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.	
		-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 cancer diagnosis	Gene , 2015, 555: 203-207
	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 diseases determined by subpopulation shifts in peripheral leukocytes	Br J Cancer, 2014 , 111(3):525-31
	Similar source of differential blood mRNAs in lung cancer and pulmonary inflammatory diseases: calls for	PLoS One, 2014 , 9(9):e108104

		improved strategy for identifying cancer-specific biomarkers	
		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	Molecular Biosystems, 2013, 9(3):467-477

		glioblastoma		
		Separate enrichment analysis of pathways for up- and downregulated genes		Journal of the Royal Society Interface, 2013, 11(92):1-12.
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