

Table S3. Information on GO enrichment analysis

Category	Term	Count	Ratio	P Value	Genes	FDR
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stim	11	21.56862745	4.85E-10	RET, HSP90AA1, ABCB1, SRC, MGMT, CASP3, MMP2,	5.43E-07
GOTERM_BP_DIRECT	GO:0042493~response to drug	10	19.60784314	5.48E-08	RET, LGALS1, ABCB1, SRC, MGMT, CASP3, CD38, PPA	3.07E-05
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene	10	19.60784314	8.63E-08	PIK3CA, KDR, PPARG, PTPN22, LGALS9, MMP8, HRAS,	3.22E-05
GOTERM_BP_DIRECT	GO:0051897~positive regulation of protei	7	13.7254902	9.88E-07	RET, HSP90AA1, PIK3CA, SRC, TNF, MET, PIK3CG	2.76E-04
GOTERM_BP_DIRECT	GO:0032729~positive regulation of interf	6	11.76470588	1.85E-06	TLR9, PTPN22, LGALS9, HRAS, TNF, IL2	4.14E-04
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK	7	13.7254902	3.47E-06	RET, TLR9, KDR, MMP8, HRAS, TNF, ADRA2A	5.25E-04
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	8	15.68627451	3.67E-06	PIK3CA, MMP2, FN1, KDR, MAPK14, PTGS2, PIK3CG, T	5.25E-04
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	5	9.803921569	3.75E-06	MMP12, MMP13, MMP2, MMP8, MMP9	5.25E-04
GOTERM_BP_DIRECT	GO:0042307~positive regulation of protei	5	9.803921569	5.00E-06	HSP90AA1, PRKCD, PTPN22, MAPK14, PTGS2	6.22E-04
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disasse	5	9.803921569	5.99E-06	MMP12, MMP13, MMP2, MMP8, MMP9	6.71E-04
GOTERM_CC_DIRECT	GO:0005576~extracellular region	20	39.21568627	2.30E-07	ACHE, HSP90AA1, MMP2, PRKCD, FN1, KLK3, MAPK1	3.15E-05
GOTERM_CC_DIRECT	GO:0005615~extracellular space	18	35.29411765	1.62E-06	ACHE, MMP2, FN1, KLK3, MMP8, TNF, MMP9,	1.11E-04

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GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	17	33.33333333	4.35E-05	HSP90AA1, PTPRS, ABCB1, PRKCB, SRC, PRKCD, FN1,	0.001986
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytopl	10	19.60784314	8.22E-05	ACHE, HSP90AA1, PIK3CA, SRC, ALOX5, PRKCD, PPAR	0.002598
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	26	50.98039216	9.48E-05	RET, ACHE, PTPRS, ABCB1, SRC, ITGAL, TNF, PIK3CG,	0.002598
GOTERM_CC_DIRECT	GO:0009986~cell surface	9	17.64705882	1.41E-04	LGALS3, ACHE, HSP90AA1, LGALS1, ABCB1, CD38, ITG	0.003223
GOTERM_CC_DIRECT	GO:0005829~cytosol	26	50.98039216	3.89E-04	PTPRS, SRC, PTPN22, TYMS, PIK3CG, AURKA, TYMP, L	0.007616
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	26	50.98039216	4.74E-04	SRC, PTPN22, TYMS, PTGS2, PIK3CG, PTGS1, LGALS3,	0.00811
GOTERM_CC_DIRECT	GO:0043235~receptor complex	5	9.803921569	0.001900383	RET, KDR, PPARG, MET, ADRA2A	0.028928
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membra	5	9.803921569	0.002696132	HSP90AA1, CA2, TLR9, CD38, ADRA2A	0.035673
GOTERM_MF_DIRECT	GO:0004175~endopeptidase activity	6	11.76470588	3.34E-06	MMP12, MMP13, MMP2, KLK3, MMP8, MMP9	7.46E-04
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	9	17.64705882	6.32E-06	RET, SRC, PRKCB, PRKCD, MAPK14, MET, MAP3K14, PI	7.46E-04
GOTERM_MF_DIRECT	GO:0005518~collagen binding	5	9.803921569	3.14E-05	MMP12, ACHE, MMP13, FN1, MMP9	0.002466
GOTERM_MF_DIRECT	GO:0019903~protein phosphatase bindin	5	9.803921569	1.07E-04	LGALS3, HSP90AA1, PPARG, MAPK14, MET	0.006317
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase	6	11.76470588	1.55E-04	MMP12, MMP13, MMP2, KLK3, MMP8, MMP9	0.007317

GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor pr	5	9.803921569	2.51E-04	RET, SRC, PRKCD, KDR, MET	0.009037
GOTERM_MF_DIRECT	GO:0004222~metalloendopeptidase activi	5	9.803921569	2.68E-04	MMP12, MMP13, MMP2, MMP8, MMP9	0.009037
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	10	19.60784314	4.26E-04	MMP12, CA1, MMP13, CA2, PRKCB, MMP2, ALB, PPA	0.011172
GOTERM_MF_DIRECT	GO:0016702~oxidoreductase activity, acti	3	5.882352941	5.27E-04	ALOX5, PTGS2, PTGS1	0.011172
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	7	13.7254902	5.53E-04	SRC, PRKCD, FN1, PPARG, LGALS9, MAPK14, PTGS2	0.011172
