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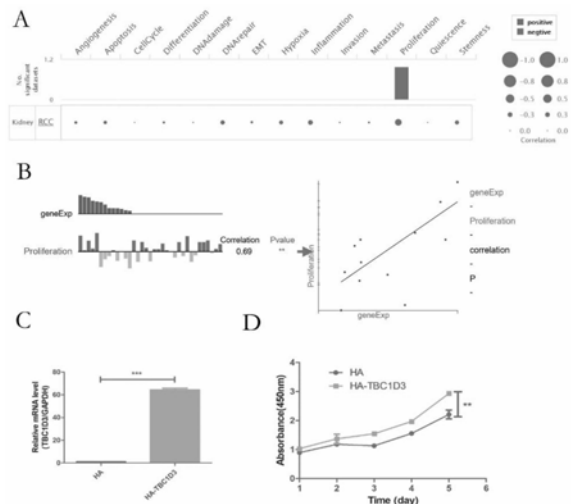
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(54) 发明名称

TBC1D3及其家族在制备肿瘤诊断药物与预后判断药物中的应用

(57) 摘要

本发明提供了TBC1D3及其家族在制备肿瘤诊断药物与预后判断药物中的应用,属于生物医药技术领域。本发明发现肾透明细胞癌组织中TBC1D3及其家族蛋白的表达显著高于癌旁正常组织;肾透明细胞癌中TBC1D3及其家族蛋白的表达水平与患者的预后密切相关。本发明提出TBC1D3可作为肾透明细胞癌诊断和预后判断的分子标记及治疗药物的靶标。TBC1D3家族成员可以作为肾透明细胞癌的免疫治疗靶点。



1. TBC1D3、TBC1D3B、TBC1D3C、TBC1D3D、TBC1D3E、TBC1D3F、TBC1D3G或TBC1D3H作为肿瘤诊断及预后标记物的应用。

2. 根据权利要求1中所述的应用,其特征在于,所述TBC1D3、TBC1D3B、TBC1D3C、TBC1D3D、TBC1D3E、TBC1D3F、TBC1D3G和TBC1D3H的核苷酸序列分别如SEQ ID NO.1-SEQ ID NO.8所示。

3. 根据权利要求1所述的应用,其特征在于,所述肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌或甲状腺癌。

4. TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G和TBC1D3H的RNA干扰靶点序列分别如SEQ ID NO.9-SEQ ID NO.14所示。

5. 如权利要求4所述的TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G或TBC1D3H的RNA干扰靶点序列在制备治疗肿瘤药物中的应用。

6. 根据权利要求5所述的应用,其特征在于,所述的肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌或甲状腺癌。

7. 一种抗肿瘤的药物,其特征在于,所述药物中含有权利要求4中所述TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G或TBC1D3H的RNA干扰靶点序列。

8. 根据权利要求7中所述的药物,其特征在于,所述药物还包括CD4+T细胞或T细胞耗竭的抑制剂。

9. 根据权利要求7所述的药物,其特征在于,所述的肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌或甲状腺癌。

TBC1D3及其家族在制备肿瘤诊断药物与预后判断药物中的应用

技术领域

[0001] 本发明属于生物医药技术领域,尤其是指TBC1D3及其家族在制备肿瘤诊断药物与预后判断药物中的应用。

背景技术

[0002] 肾透明细胞癌是肾癌中最常见的恶性肿瘤,占原发性肾脏恶性肿瘤的75-82%。在各种临床和基因组研究中,肾透明细胞癌被证明是一种高度免疫浸润的肿瘤,是最早的免疫治疗肿瘤之一。由于肾透明细胞癌对常规放疗和化疗不敏感,其治疗主要依赖于靶向治疗和免疫治疗。靶向治疗包括酪氨酸激酶抑制剂,如舒尼替尼和索拉非尼。然而,肿瘤异质性、动态变化和对治疗的适应细胞死亡相关信号通路的改变显著限制了靶向药物在肾透明细胞癌治疗中的应用。

发明内容

[0003] 本发明通过在线数据库发现肾透明细胞癌组织中TBC1D3及其家族基因的表达显著高于癌旁正常组织;肾透明细胞癌中TBC1D3及其家族蛋白的表达水平与患者的预后密切相关,肾透明细胞癌组织中TBC1D3及其家族蛋白表达水平高的患者总的生存率低于表达低的患者。同时我们构建TBC1D3质粒,转染肾透明细胞癌细胞,发现可以促进其细胞增殖。同时发现TBC1D3家族成员与免疫浸润相关。

[0004] RNA干扰(RNA interference, RNAi)是指内源性或外源性双链RNA介导的细胞内mRNA发生特异性降解,导致靶基因的表达沉默,产生相应的功能表型缺失。它可高效、特异地阻断体内特定基因的表达,导致其降解,从而引起生物体内特异基因的沉默,使细胞表现出某种基因表型的缺失,是近年来新兴的一种常用的研究基因功能、寻找疾病治疗方法的实验室技术。目前, RNAi特异性的抑制基因表达,已应用于基因病、病毒感染性疾病、癌症的基因治疗等方面。

[0005] TBC1D3、TBC1D3B、TBC1D3C、TBC1D3D、TBC1D3E、TBC1D3F、TBC1D3G 或TBC1D3H作为肿瘤诊断及预后标记物的应用。

[0006] 在本发明的一个实施例中,所述TBC1D3、TBC1D3B、TBC1D3C、TBC1D3D、TBC1D3E、TBC1D3F、TBC1D3G或TBC1D3H的核苷酸序列分别如SEQ ID NO.1-SEQ ID NO.8所示。

[0007] 在本发明的一个实施例中,所述肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌和甲状腺癌。

[0008] TBC1D3、TBC1D3B、TBC1D3C、TBC1D3D、TBC1D3E、TBC1D3F、TBC1D3G 或TBC1D3H的RNA干扰靶点序列分别如SEQ ID NO.9-SEQ ID NO.14所示。

[0009] 所述的TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G或TBC1D3H的RNA干扰靶点序列在制备治疗肿瘤药物中的应用。

[0010] 在本发明的一个实施例中,所述肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺

腺癌、肺鳞状细胞癌或甲状腺癌。

[0011] 一种抗肿瘤的 药物,所述药物中含有所述TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G或TBC1D3H的RNA干扰靶点序列。

[0012] 在本发明的一个实施例中,所述药物还包括抑制CD4+T细胞或T细胞耗竭的抑制剂。

[0013] 在本发明的一个实施例中,所述肿瘤为肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌或甲状腺癌。

[0014] 在本发明的一个实施例中,所述TBC1D3、TBC1D3B、TBC1D3C、TBC1D3F、TBC1D3G或TBC1D3H的RNA干扰靶点序列分别如SEQ ID NO.9-SEQ ID NO.14所示。

[0015] 本发明的上述技术方案相比现有技术具有以下优点:

[0016] 本发明首次证实TBC1D3及其家族是一个肾透明细胞癌预后标记物,首次发现TBC1D3可作为肾透明细胞癌诊断和预后判断的分子标记及治疗药物的靶标。TBC1D3 家族成员可以作为肾透明细胞癌的免疫治疗靶点。

附图说明

[0017] 为了使本发明的内容更容易被清楚的理解,下面根据本发明的具体实施例并结合附图,对本发明作进一步详细的说明,其中

[0018] 图1-1与图1-2是本发明TBC1D3泛癌表达分析,TBC1D3家族在TCGA数据库中的表达。

[0019] 图2是本发明中TBC1D3家族成员的基因组改变以及TBC1D3家族基因的基因-基因和蛋白质-蛋白质相互作用网络。

[0020] 图3-1、图3-2与图3-3是本发明中TBC1D3家族成员在肾透明细胞癌中预后表达。

[0021] 图4是本发明中TBC1D3家族成员在肾透明细胞癌中的功能。

[0022] 图5-1、图5-2、图5-3与图5-4是本发明中TBC1D3家族蛋白与免疫抑制剂的相关性。

[0023] 图6-1、图6-2、图6-3、图6-4与图6-5是本发明中TBC1D3家族成员蛋白与肾透明细胞癌免疫浸润相关性。

[0024] 图7-1、图7-2与图7-3是本发明中肾透明细胞癌免疫浸润水平与TBC1D3家族成员不同体细胞拷贝数改变的相关性。

具体实施方式

[0025] 下面结合附图和具体实施例对本发明作进一步说明,以使本领域的技术人员可以更好地理解本发明并能予以实施,但所举实施例不作为对本发明的限定。

[0026] 实施例1 TBC1D3及其家族在肾功能透明细胞癌中的表达

[0027] 通过GSCA数据库分析,TBC1D3在肾透明细胞癌中的表达。发现TBC1D3表达在肾透明细胞癌、肾乳头状细胞癌、肝癌、肺腺癌、肺鳞状细胞癌和甲状腺癌中高表达,在头颈部鳞状细胞癌中低表达。我们同时通过UALCAN数据库和下载肾透明细胞癌TCGA 数据,通过R语言分析数据,发现TBC1D3家族(TBC1D3,TBC1D3B,TBC1D3C,TBC1D3D,TBC1D3E,TBC1D3F,TBC1D3G,TBC1D3H)在肾透明细胞癌中相比于癌旁组织都高表达。

[0028] 实施例2 TBC1D3及其家族的基因和蛋白网络的基因改变

[0029] 我们使用cBioportal数据库来确定TCGA KIRC样本中TBC1D3家族改变的类型和频率。结果显示TBC1D3家族成员很少发生突变(少于5个频率),这是高度保守的(结果见图2-A)。然后,我们使用cBioportal的“相关分析”对TBC1D3家族的五个成员进行分析,结果表明,TBC1D3家族成员之间的关联呈正相关,但TBC1D3C与TBC1D3G呈负相关(结果见图2-D)。利用GeneMANIA和STRING生成的基因-基因和蛋白质-蛋白质相互作用网络显示,20个潜在靶基因和11个潜在靶蛋白与TBC1D3家族相互作用(结果见图2-B与图2-C)。

[0030] 实施例3 TBC1D3家族成员在肾透明细胞癌中预后表达

[0031] 使用GSCA、TISIDB、LinkedOmics和Kaplan-Meier绘图仪评估TBC1D3家族表达对生存率的影响。GSCA分析显示,TBC1D3在KIRC多发性肿瘤中的表达与OS和PFS呈正相关。此外,高表达的TBC1D3存活时间短(结果见图3-1)。TISIDB和LinkedOmics的总生存率分析表明,TBC1D3家族成员高表达的患者总生存期较短(结果见图3-2与图3-3)。为了进一步探讨TBC1D3在KIRC临床特征中的作用,我们使用Kaplan-Meier绘图仪研究了TBC1D3表达与KIRC临床病理特征之间的关系。如表1所示,TBC1D3和TBC1D3B的高表达与I期、II期、III期、IV期、3级和4级患者的OS恶化相关。为了探讨TBC1D3表达是否是KIRC患者总生存率的独立预测因素,我们进行了单变量和多变量Cox回归分析。单因素Cox回归分析显示,年龄、分级、分期、TNM分级均为OS的独立危险因素($p=0.012$ 、 $3.61E-08$ 、 $1.26E-10$ 、 $2.69E-08$ 、 $2.76E-10$ 和 0.001);在多变量Cox回归分析中,年龄、年级和TBC1D3表达是OS的独立危险因素(分别 $p=0.0003$ 、 0.014 和 0.013) (结果见表2)。

[0032] 表1

临床参数	总存活(530)					
	TBC1D3			TBC1D3B		
	N	Hazard ratio	p-value	N	Hazard ratio	p-value
分期						
[0033] 女	186	2.18(1.32-3.6)	0.0019	186	1.79(1.07-2.01)	0.024
男	344	1.92(1.31-2.83)	0.00075	344	1.85(1.25-2.74)	0.0018
分期						
1	67	3.88(1.1-13.74)	0.024	265	1.94(1.07-3.52)	0.025
2	57	6.57(1.73-25.01)	0.0018	57	7.72(2.33-25.58)	9.6E-05
3	123	2.18(1.23-3.86)	0.0061	123	1.8(1-3.26)	0.048
4	82	2.01(1.21-3.36)	0.0064	82	1.43(0.84-2.42)	0.19
分级						
[0034] 1	\	\	\	\	\	\
2	227	1.35(0.75-2.45)	0.32	227	2.32(1.2-4.51)	0.01
3	206	2.37(1.47-3.81)	0.00027	206	1.72(1.07-2.75)	0.023
4	75	1.85(1.04-3.29)	0.033	75	1.93(1.06-3.53)	0.03

[0035] 注:粗体字表示 $p<0.05$ 。

[0036] 表2

因素	单变量分析		多变量分析	
	HR (95%CI)	P value	HR (95%CI)	P value
年龄	1.023(1.004-1.041)	0.012	1.037(1.017-1.059)	0.0003
性别	1.013(0.666-1.541)	0.95	1.272(0.813-1.992)	0.292
分期	2.242(1.682-2.988)	3.61E-08	1.508(1.086-2.095)	0.014
分级	1.862(1.541-2.251)	1.26E-10	1.416(0.839-2.389)	0.192
T 分期	1.943(1.538-2.456)	2.69E-08	0.992(0.604-1.628)	0.974
M 分期	4.073(2.634-6.301)	2.76E-10	1.877(0.832-4.238)	0.129
N 分期	2.932(1.516-5.668)	0.001	1.67(0.804-3.47)	0.169
TBC1D3	379.35(0.01-1.17E8)	0.26	23299.765(7.84-6.92E8)	0.013

[0037] 注:粗体字表示 $p < 0.05$ 。

[0038] 表3

	Gene markers	KIRC			
		None		Purity	
		Cor	P	Cor	P
CD8 + T cell	CD8A	0.077	ns	0.062	ns
	CD8B	0.061	ns	0.053	ns
T cell(general)	CD3D	0.072	ns	0.054	ns
	CD3E	0.101	*	0.085	ns
B cell	CD2	0.111	*	0.093	*
	CD19	0.133	*	0.117	*
Monocyte	CD79A	-0.022	ns	-0.014	ns
	CD86	0.051	ns	0.072	ns
TAM	CD115 (CSF1R)	0.099	ns	0.112	*
	CCL2	-0.008	ns	-0.028	ns
M1 Macrophage	CD68	0.006	ns	0.031	ns
	IL10	0.068	ns	0.18	ns
	INOS(NOS2)	-0.003	ns	-0.002	ns
	IRF5	0.365	***	0.358	***
	COX2(PTGS2)	-0.001	ns	-0.044	ns

[0041]

M2 Macrophage	CD163	0.034	ns	0.067	ns
	VSIG4	0.054	ns	0.079	ns
	MS4A4A	0.031	ns	0.049	ns
Neutrophils	CD66b(CEACAM8)	0.169	***	0.166	***
	CD11B(ITGAM)	0.151	***	0.168	***
	CCR7	0.088	ns	0.09	ns
Natural killer cell	KIR2DL1	0.022	ns	0.018	ns
	KIR2DL3	0.049	ns	0.07	ns
	KIR2DL4	0.061	ns	0.067	ns
	KIR3DL1	-0.02	ns	-0.017	ns
	KIR3DL2	0.004	ns	-0.009	ns
	KIR3DL3	-0.002	ns	-0.016	ns
	KIR2DS4	-0.027	ns	-0.029	ns
Dendritic cell	HLA-DPB1	0.011	ns	0.025	ns
	HLA-DQB1	0.056	ns	0.065	ns
	HLA-DRA	0	ns	0.02	ns
	HLA-DPA1	0.023	ns	0.032	ns
	BDCA-1(CD1C)	0.043	ns	0.057	ns
	BDCA-4(NRP1)	0.041	ns	0.065	ns
	CD11c(ITGAX)	0.424	***	0.436	ns
Th1	T-bet (TBX21)	0.241	***	0.24	***
	STAT4	0.366	***	0.363	***
	STAT1	0.079	ns	0.082	ns
	IFN- γ (IFNG)	0.176	***	0.172	***
	TNF- α (TNF)	0.249	***	0.245	***
Th2	GATA3	0.062	ns	0.065	ns
	STAT6	0.357	***	0.383	***
	STAT5A	0.163	***	0.177	***
	IL13	0.36	***	0.327	***
Tfh	BCL6	0.347	***	0.332	***
	IL21	0.069	ns	0.071	ns
Th17	STAT3	0.093	ns	0.012	**
	IL17A	0.002	ns	-0.023	ns
Treg	FOXP3	0.2	***	0.187	***
	CCR8	0.187	***	0.199	***
	STAT5B	0.163	***	0.177	***
	TGF β (TGFB1)	0.017	ns	0.011	ns
T cell exhaustion	PD-1(PDCD1)	0.171	**	0.15	**
	CTLA4	0.33	***	0.314	***
	TIM-3(HAVCR2)	-0.024	ns	-0.015	ns
	GZMB	0.046	ns	0.05	ns
	LAG3	0.167	***	0.141	***
	PDL1(CD274)	0.106	**	0.099	*

[0042] 注：TAM, 肿瘤相关巨噬细胞；Th, T辅助细胞；Tfh, 卵泡辅助性T细胞；Treg, 调节性T细胞；*P<0.01；**P<0.001；***P<0.0001。

[0043] 实施例4 TBC1D3在肾透明细胞癌中的功能

[0044] 为了研究TBC1D3家族在KIRC中的功能,我们使用CancerSEA进行了单细胞分析。结果表明,TBC1D3D正调控KIRC细胞的增殖,负调控炎症(图4A-B)。我们构建了 TBC1D3质粒并转染Caki-1细胞,结果显示TBC1D3能促进肾透明细胞癌细胞的增殖(结果见图4-C)。TBC1D3的生物学过程通过过表达富集分析(ORA)进行鉴定,结果表明 TBC1D3的表达与免疫应答密切相关(结果见图4-D)。

[0045] 实施例5 TBC1D3家族表达与免疫抑制剂在肾透明细胞癌中的相关性

[0046] 选择TISIDB数据库研究TBC1D3家族表达与免疫抑制效应之间的关系。因此,TBC1D3、TBC1D3B、TBC1D3C和TBC1D3G是TBC1D3家族的四个成员,分别与CD160、CTLA4、CD244、KDR、LAG3、PDCD1、PDCD1LG2和TIGIT相关。此外,TGFBR1 和HAVCR2与TBC1D3、TBC1D3B和TBC1D3G相关。CD274与TBC1D3B、TBC1D3C 和TBC1D3G相关。此外,TBC1D3与LGALS9相关。TBC1D3B与CD274相关。TBC1D3C 与CD96和LGALS9相关。TBC1D3G与IL10RB和PVRL2相关(结果见图5-1,图5-2,图5-3,图5-4)。

[0047] 实施例6 TBC1D3家族表达与免疫浸润在肾透明细胞癌中的相关性

[0048] 采用TIMER数据库探讨TBC1D3家族表达与肾透明细胞癌浸润淋巴细胞的关系。TBC1D3家族表达与CD4+T细胞浸润水平呈正相关。此外,巨噬细胞浸润水平仅与 TBC1D3表达显著相关,树突状细胞浸润水平与TBC1D3B表达呈负相关。中性粒细胞 浸润水平与TBC1D3和TBC1D3H表达呈正相关(结果见图6-1,图6-2,图6-3,图6-4,图6-5)。为了进一步证实TBC1D3在KIRC中的表达与免疫细胞浸润水平之间的关系,我们使用TIMER数据库来探讨TBC1D3表达与各种免疫浸润相关标记物之间的关系。我们的结果显示,TBC1D3的表达与大多数中性粒细胞、Th1、Th2、Treg和T细胞衰竭 的标志物之间存在显著相关性(结果见表3)。特别是T细胞衰竭,结果与DISTIB分析 一致。体细胞拷贝数改变(SCNA)模块显示TBC1D3家族成员的臂水平缺失与肾透明 细胞癌中的免疫细胞浸润水平显著相关(结果见图7-1,图7-2,图7-3)。

[0049] 显然,上述实施例仅仅是为清楚地说明所作的举例,并非对实施方式的限定。对于所属领域的普通技术人员来说,在上述说明的基础上还可以做出其它不同形式变化或变动。这里无需也无法对所有的实施方式予以穷举。而由此所引申出的显而易见的变化或变动仍处于本发明创造的保护范围之内。

SEQUENCE LISTING

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<120> TBC1D3及其家族在制备肿瘤诊断药物与预后判断药物中的应用

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<211> 2077

<212> RNA

<213> (人工合成)

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 aauguauuaa gaaagagugc agcucgagag agauucagag auggaacaca ccagaccca 1920
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<210> 9

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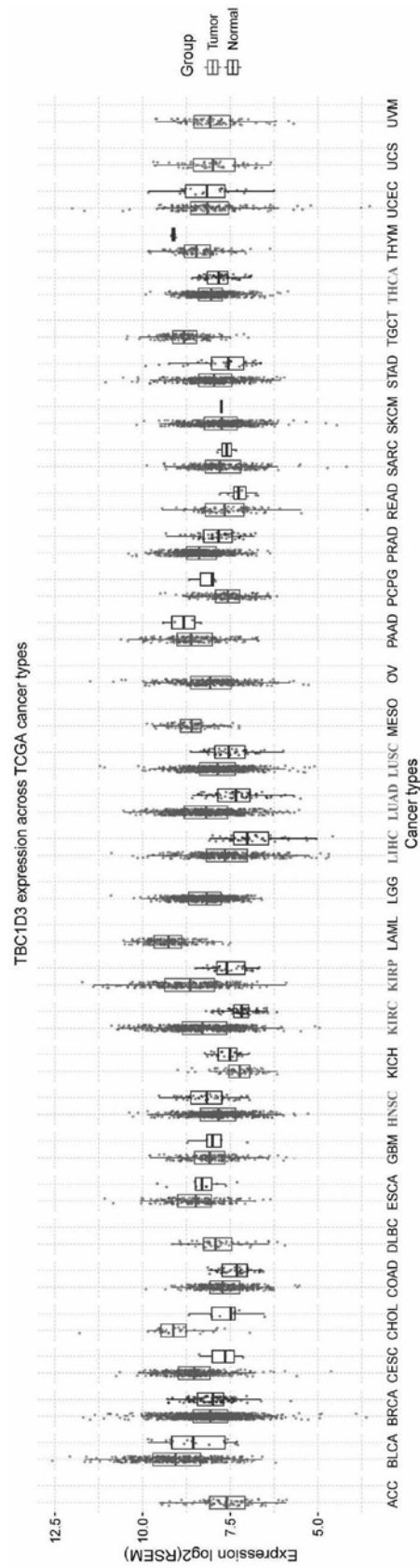


图1-1

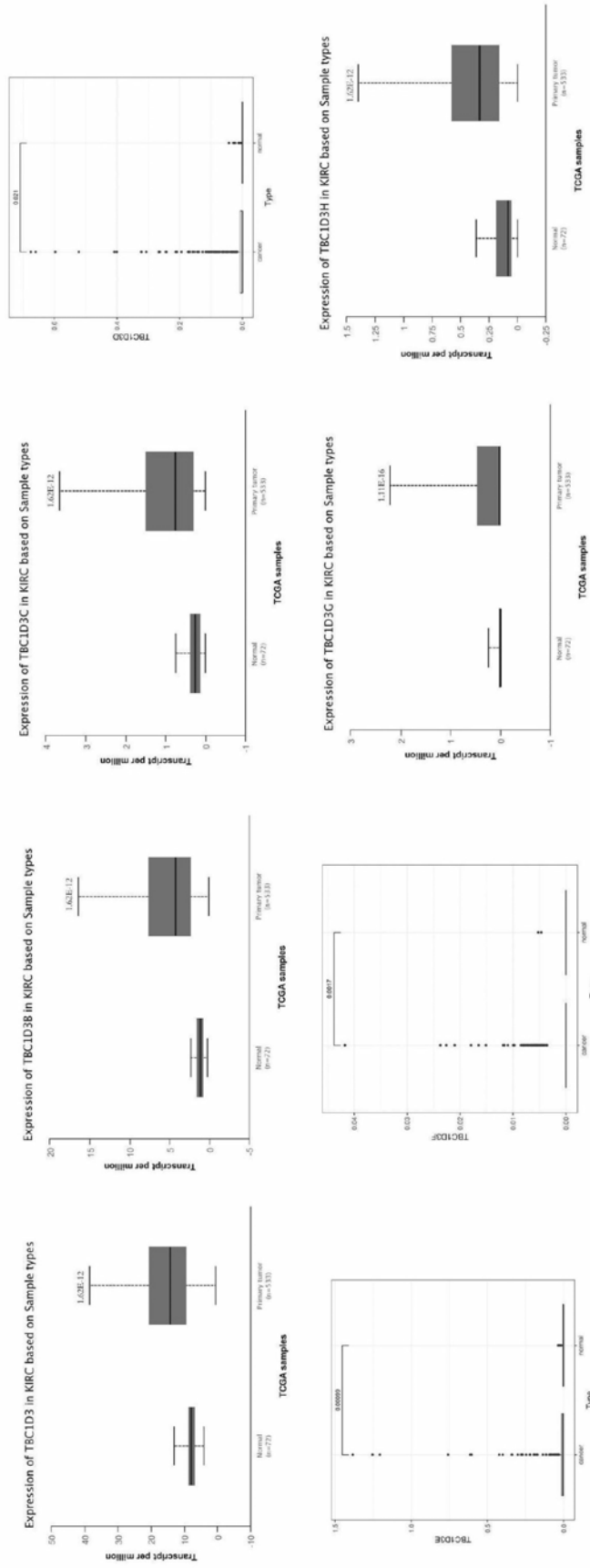


图1-2

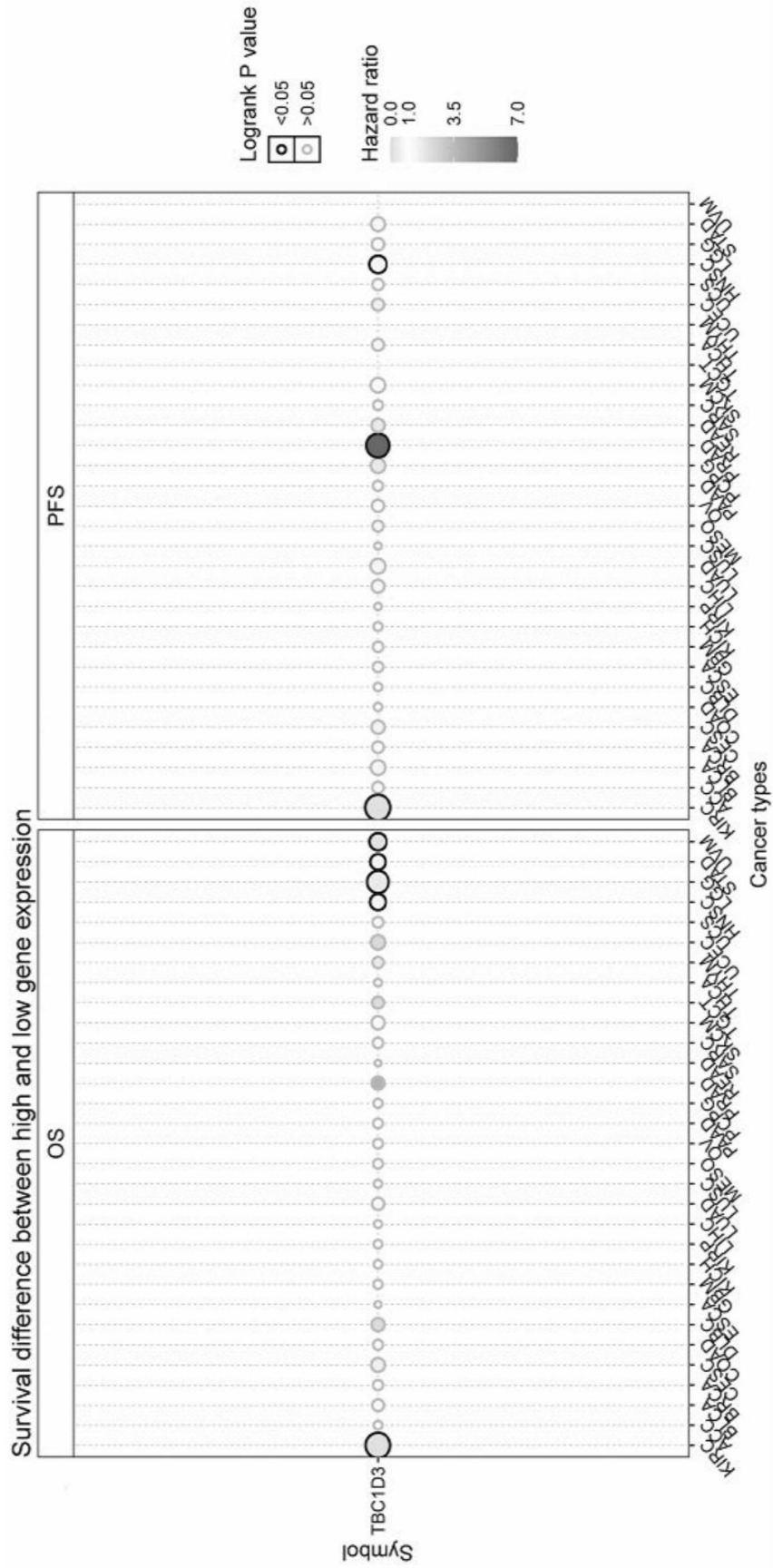


图3-1

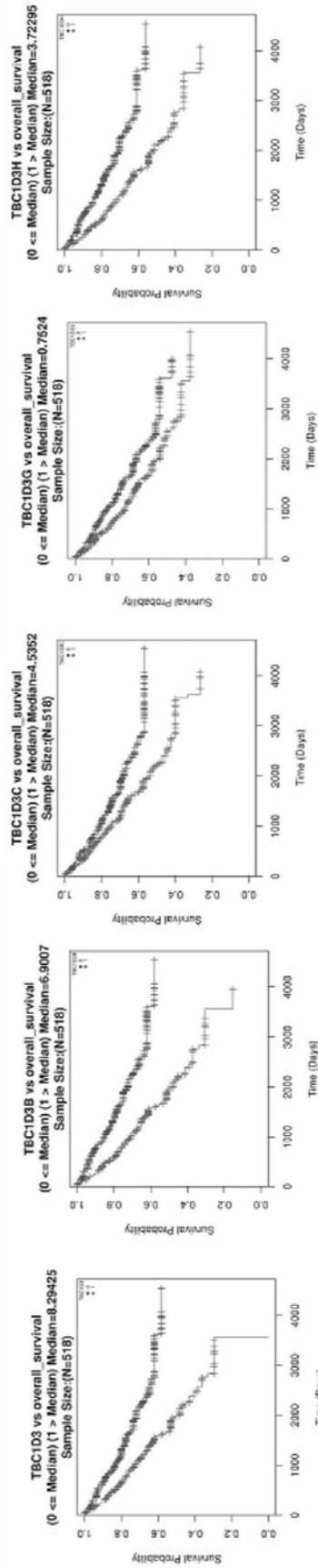


图3-2

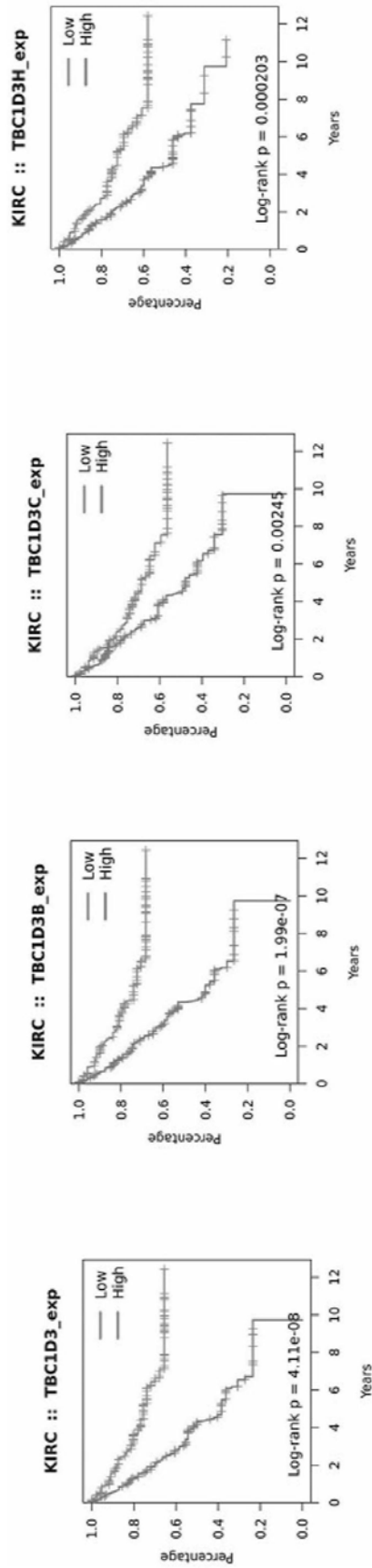


图3-3

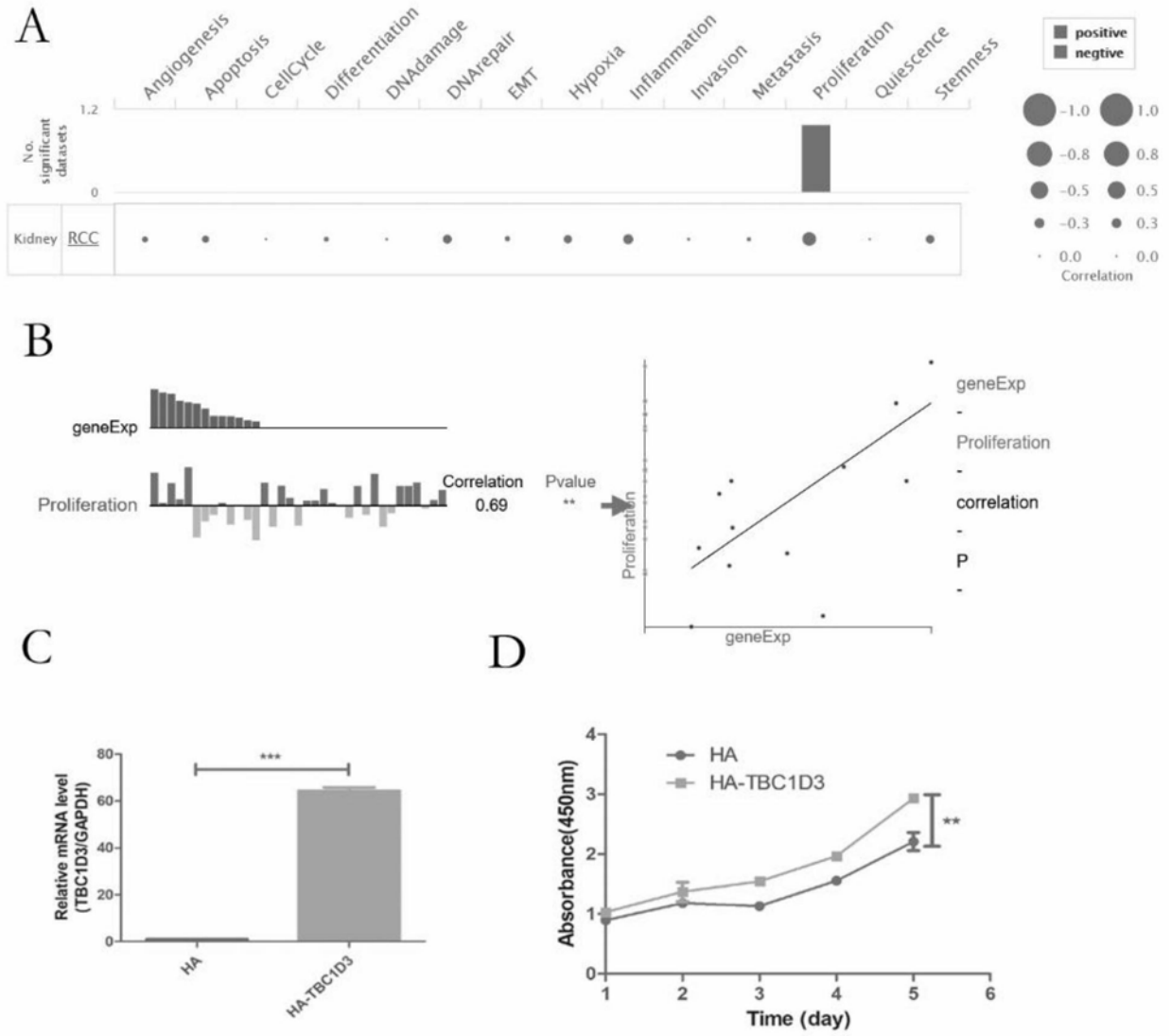


图4

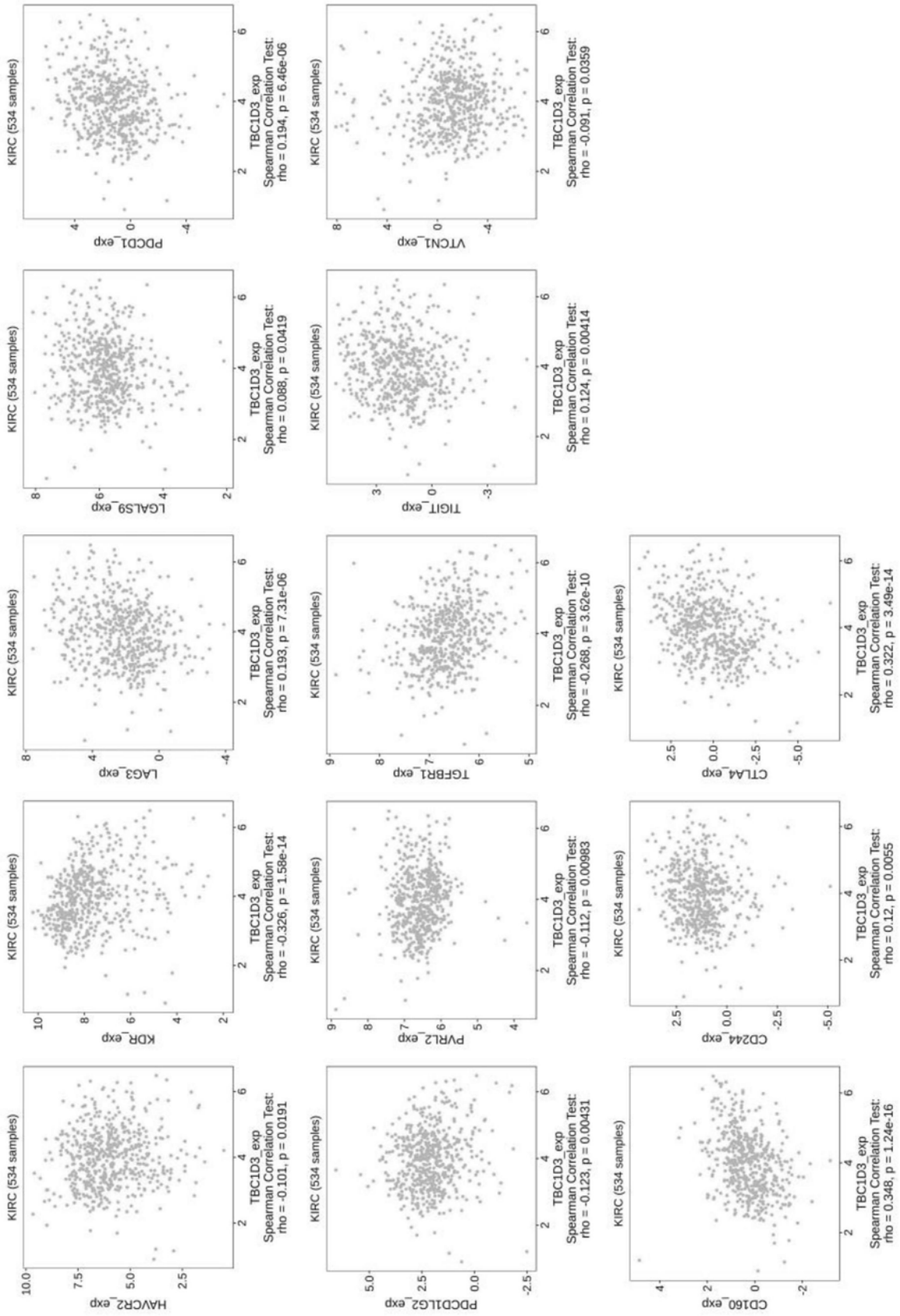


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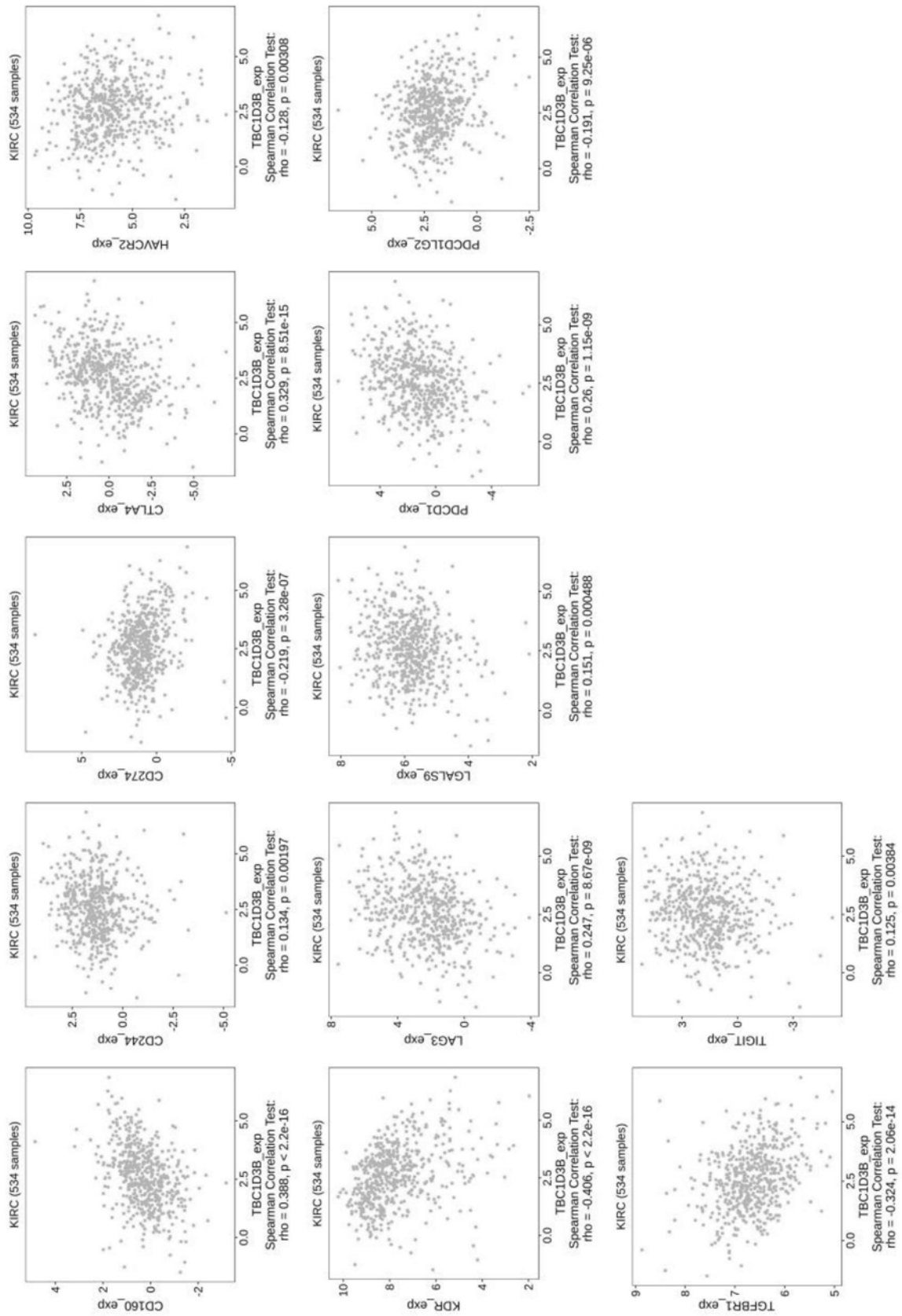


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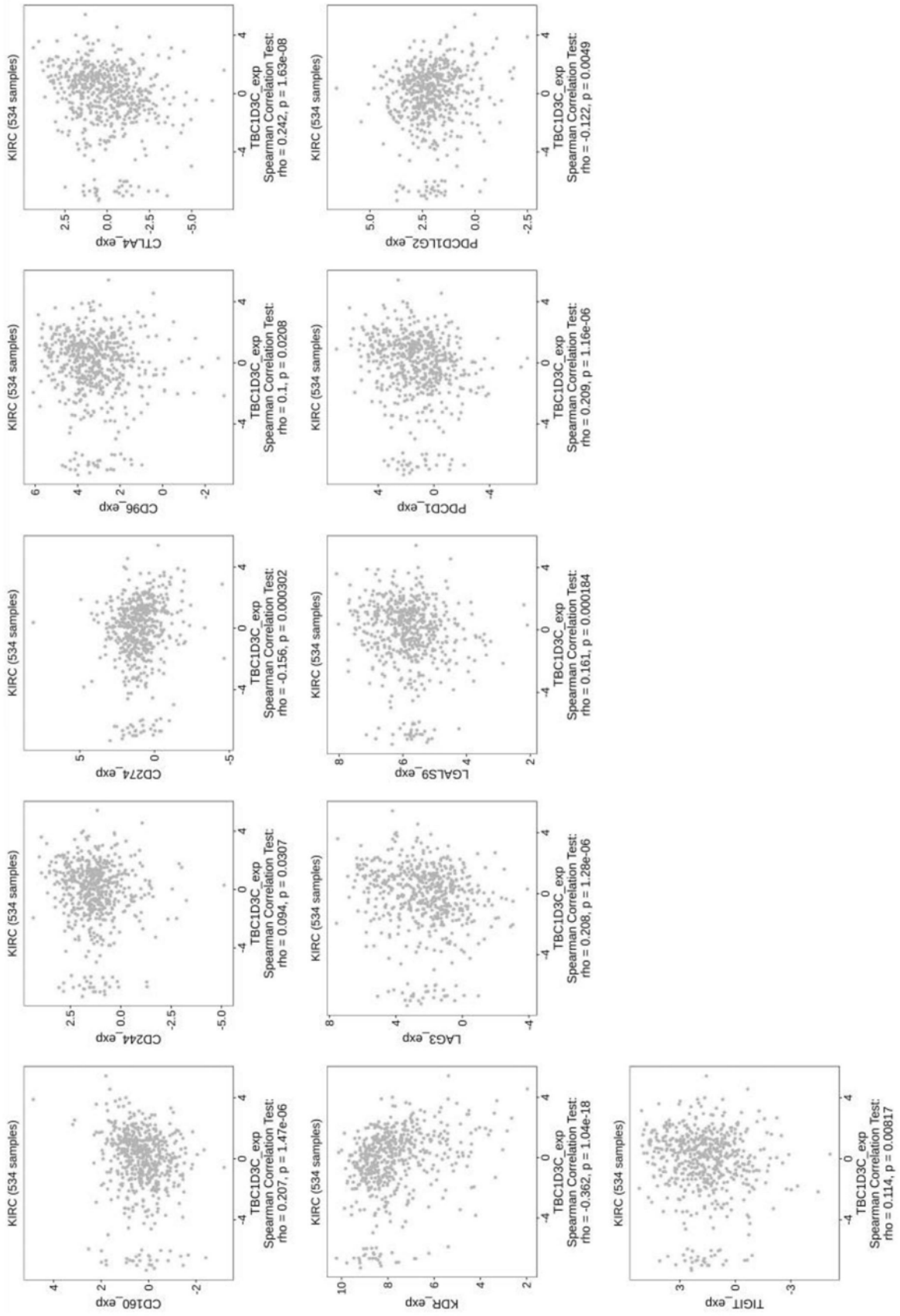


图5-3

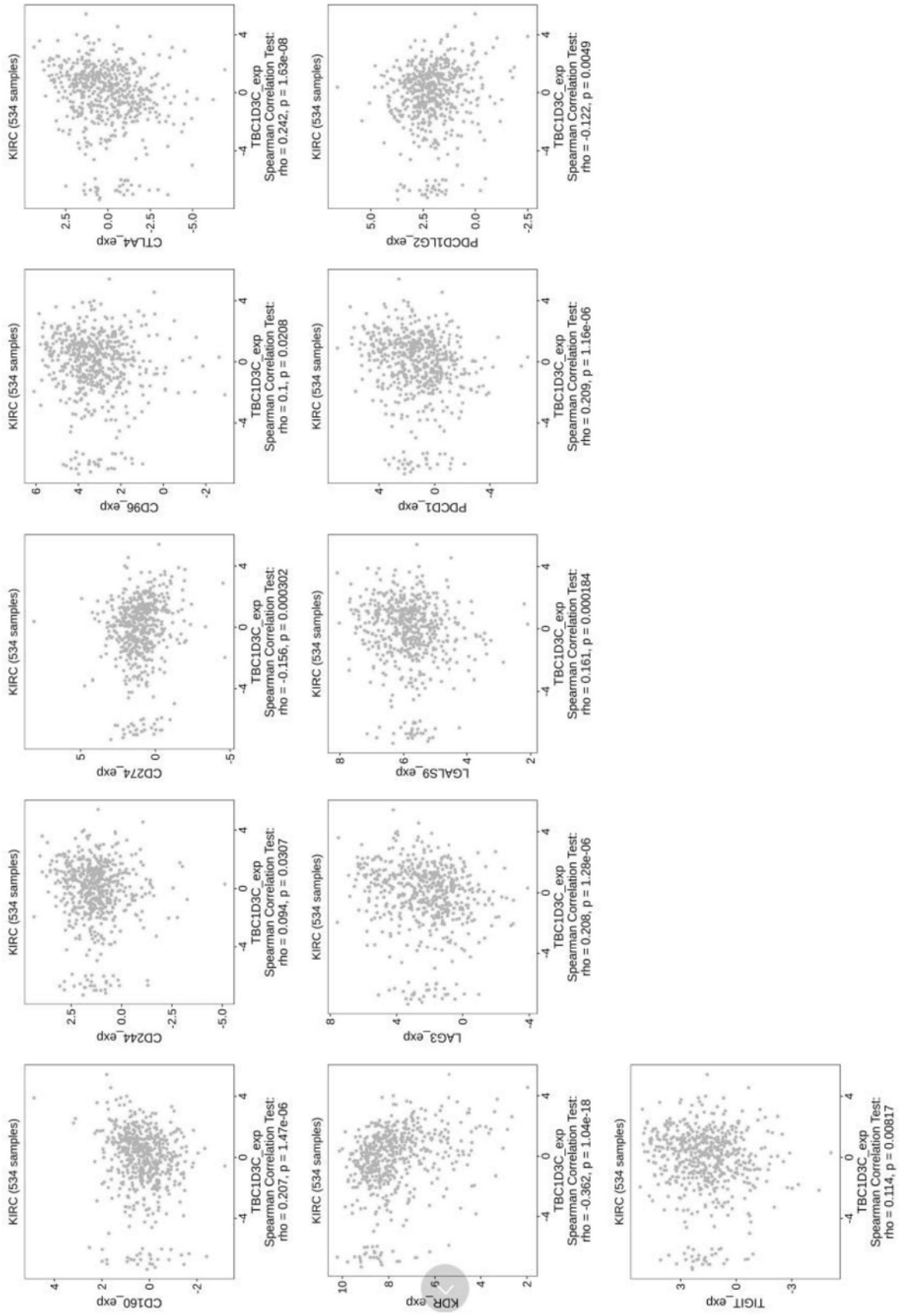


图5-4

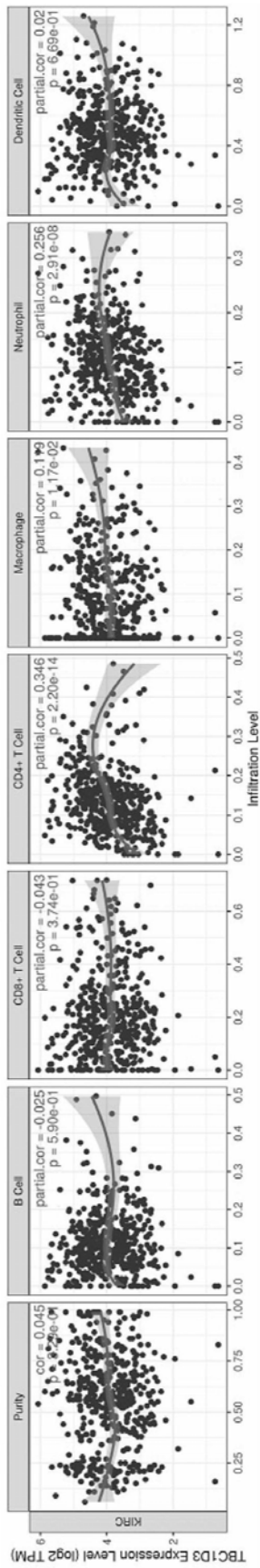


图6-1

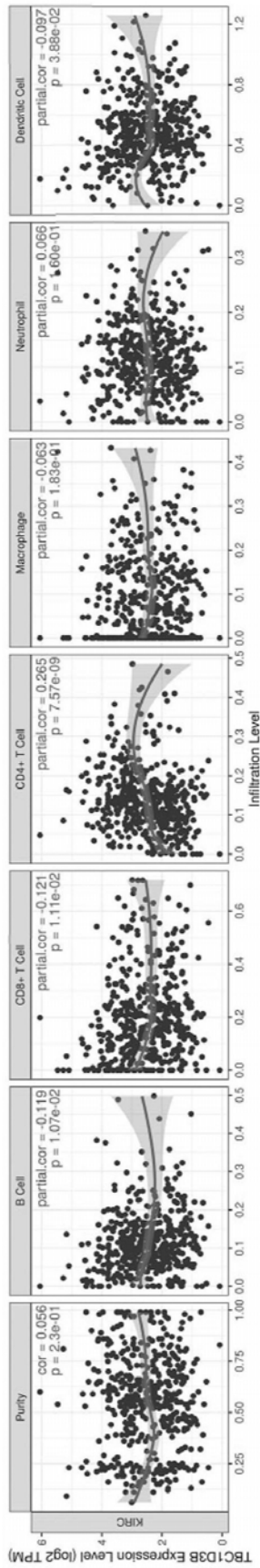


图6-2

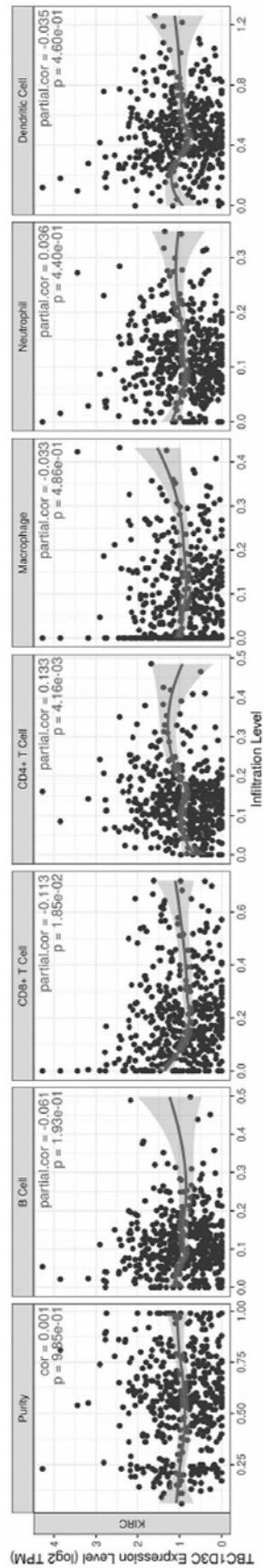


图6-3

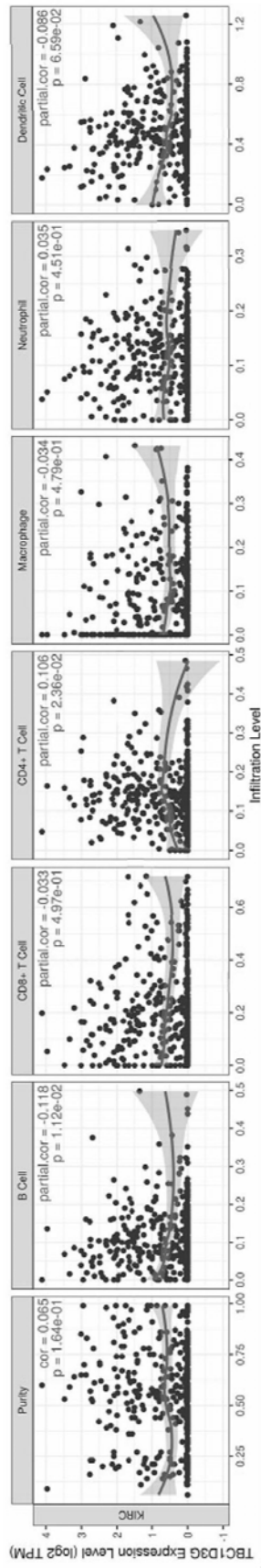


图6-4

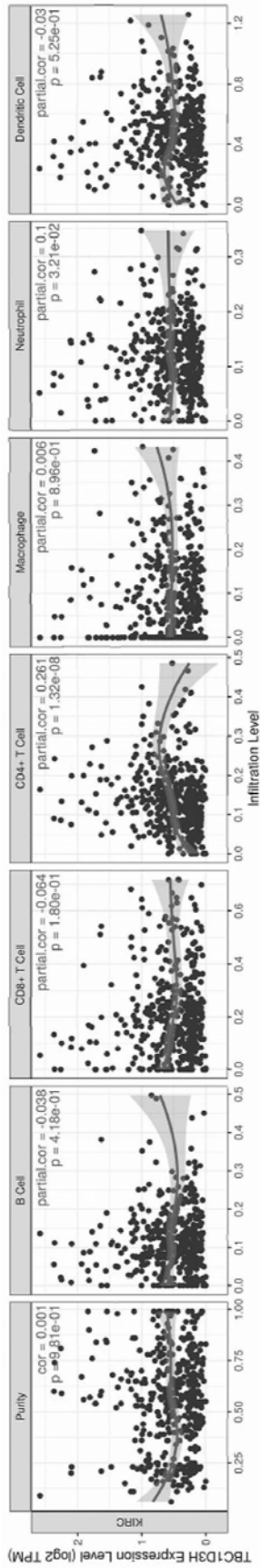


图6-5

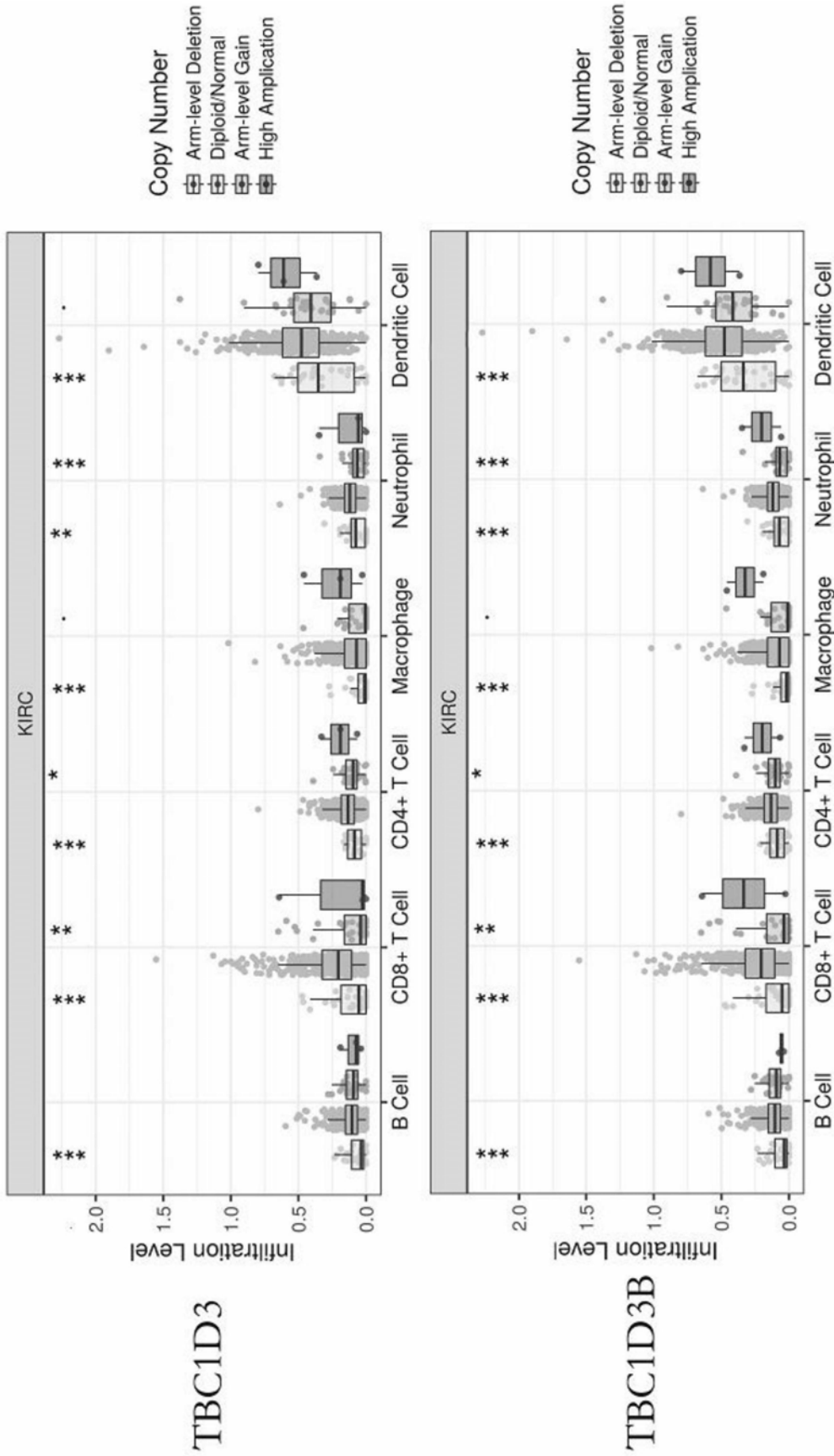


图7-1

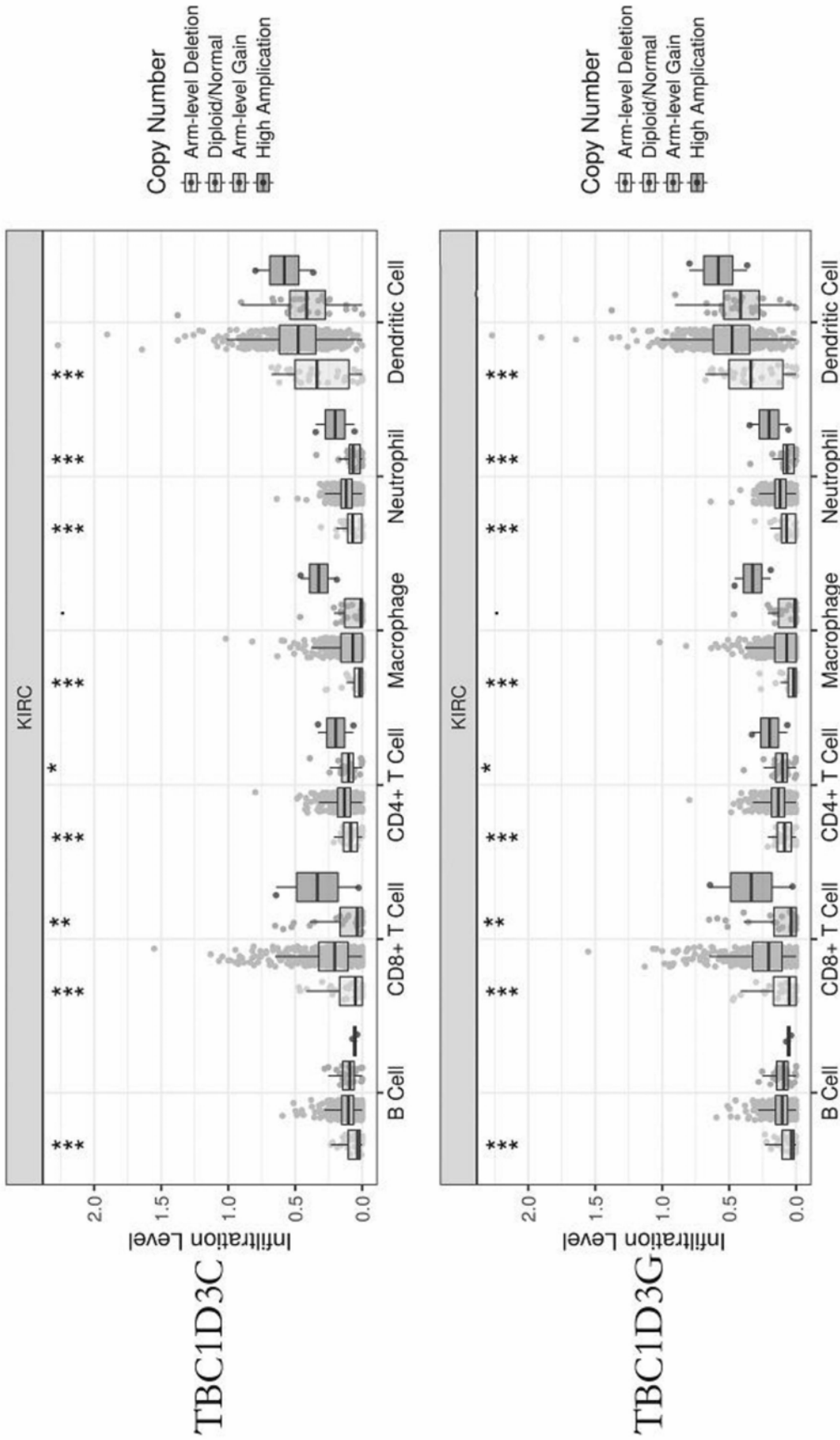


图7-2

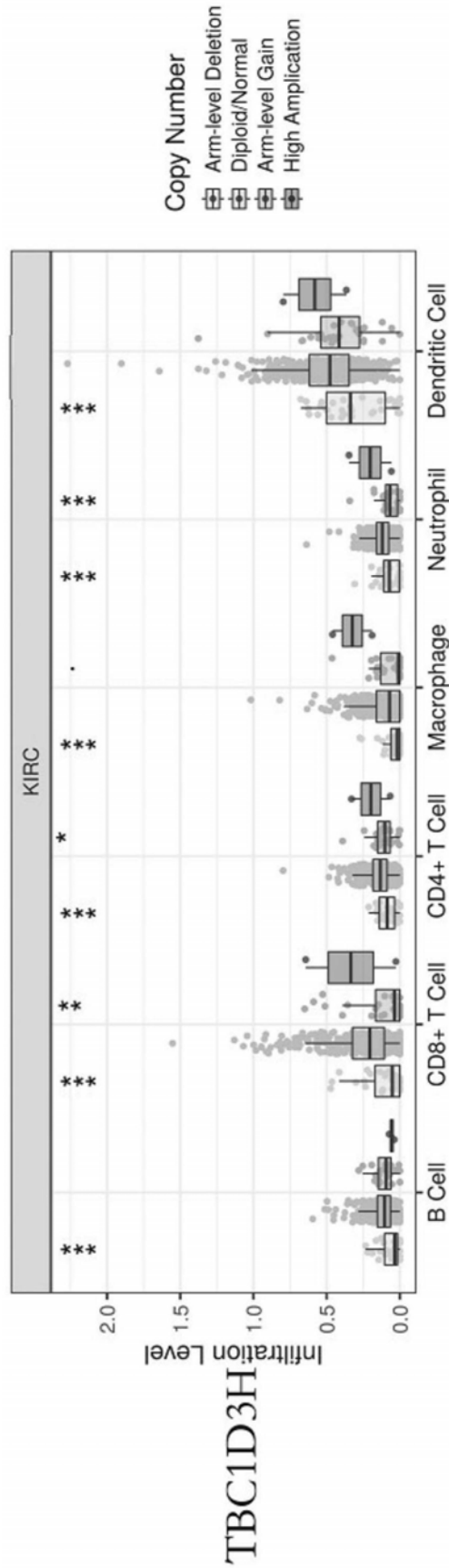


图7-3