SUPPLEMENTARY MATERIAL

SUPPLEMENTARY METHODS

Differential expression analysis of RNA-seq data from discoidin domain receptor (DDR) animal models

Cell lines used in this analysis were previously described. NA13 was a murine C57B6 bladder cancer line [1] and T24 were human bladder cancer (BCa) cells [2]. RNA-seq analysis was done through the standard Illumina RNA-seq protocol. The sequenced reads were put into the STAR-RSEM RNA-seq data analysis pipeline [3,4] to quantify gene-level expression. We generated RNA-seq data from 4 *DDR1* overexpression and 4 Control mice. To this end, we used Rag2/Il2rg Double Knockout mice (TACONIC TRANSGENIC MODELS™) at 6-week of age as the host for tumor cell engraftment for these experiments. Tumor cells were allowed to engraft for 6 weeks before sacrifice for RNA isolation, library prep and RNA-seq. *DDR1* data were aligned with Human Genome GRCh38 version, while *DDR2* data were aligned with Mouse Genome 19 version. Read counts were normalized by TMM normalization method [5] and Negative Binomial test [6] was applied to identify differentially expressed genes (DEGs) of these comparisons including *DDR1* overexpression versus control and sh*DDR2* versus IgG control. False discovery rate (FDR) was estimated with Storey's method [7]. DEGs were selected with FDR<.05 and log2-fold-change ≥1.

TCGA BCa sample selection

Out of 407 TCGA BCa patient records retrieved from the UCSC Xena browser [8], we selected 259 sample data for further analysis. The samples which met the following criteria were excluded from our analysis: 1) stage other than T2-4; 2) variant histology (n=52, 42 squamous, 4 small cell/neuroendocrine, 2 micropapillary, 4 plasmacytoid), pure squamous cell carcinomas (n=3), squamous cell carcinoma of non-bladder origin (n=1) and adenocarcinoma (n=1); 3) prior intravesical immunotherapy with Bacille Calmette-Guerin (n=35); 4) neoadjuvant chemotherapy (NAC) (n=12); and 5) low histological grade (n=21).

Subtype assignment of BCa tumor samples

To assign the BCa tumor samples into one of 5 molecular subtypes, we used the consensus MIBC R package (https://github.com/cit-bioinfo/consensusMIBC). Normalized log2 expression data were used as an input.

Gene set enrichment analysis (GSEA) of DDR high and low groups

To investigate the biological consequences of high expression of *DDR1/2* in BCa, we performed gene set enrichment analysis (GSEA) and digital dissection analyses to identify the cellular processes and immune cell components that are enriched in each of these types of tumors. We first stratified TCGA-BCa tumors by *DDR1* or *DDR2* expression at their median level and then compared the high and low groups. Finally, normalized enrichment scores of 50 hallmark genesets [9] were separately computed for *DDR1* and *DDR2*. Enriched gene sets were selected with nominal *P*<.05 and FDR<.1.

Digital dissection analysis using cancer transcriptome

We performed digital dissection analysis via a transcriptome-based cell type quantification method using MCP-Counter [10] to estimate how the presence of various immune cell types correlates with *DDR1/2* expression. Gene signatures for various immune cells and stromal components were obtained from CIBERSORT [11], MCP-Counter [10] and xCell [12]. If the genes overlapped between different immune cell type signatures, only the cell type-specific genes were retained. For example, if the B cell subsets such as Memory B cell and Naïve B cells had overlapping genes in the original signatures, we removed the overlapping genes from both signatures to represent subset-specific expression. Thus, resulting signatures had no overlap, with 11 memory B cell and 14 Naïve B cell signatures. Finally, we refined gene signatures for 23 immune cell types including Memory B cell, Naïve B cell, Memory CD4 T cell, Activated Memory CD4 T cell, Naïve CD4 T cell, CD8 T cell, Cytotoxic T lymphocytes, Activated Dendritic cells, Eosinophil, M0 Macrophage, M1 Macrophage, M2 Macrophage, Activated Mast cell, Monocyte, Activated NK cell, Neutrophil, Plasma cell, Activated Dysregulated T cell, Dysregulated T cell, Exhausted T cell, Follicular Helper T cell, Gamma Delta T cell and Regulatory T cell (**Supplementary Table 1**). Given these gene sets for immune cell types, we computed the immune score using MCP-counter method [10].

T-cell-inflamed gene-expression profile (GEP) score in the TCGA pan-cancer cohort

The T-cell-inflamed GEP score was used as an estimation for assessing the immune tumor microenvironment (TME), and its correlation with *DDR1* and *DDR2* gene expression was evaluated using transcriptomic data of the TCGA pan-cancer cohort (TCGA-pancan; n=10,323) obtained from the UCSC Xena browser [8]. Patients were stratified by *DDR1* and *DDR2* gene expression levels and T-cell-inflamed GEP scores (median) using cutoffs equivalent in prevalence to those used to define the clinical response groups in the TCGA-pancan.

Computation of DDR signature score

A Z-score method [13] was employed to compute *DDR* signature scores in individual tumors with the *DDR1* and *DDR2* gene signature. Prior to the score calculation, patient gene expression data were centered by the median of all the samples. The score represents the difference between the error-weighted mean of the expression values of the genes in the *DDR* signature and the error-weighted mean of all genes in a sample. The result reflects both the magnitude and relative direction of *DDR* downstream genes.

Differential expression analysis of distinct response groups in IMvigor210

The IMvigor210 data can be found in http://research-pub.gene.com/IMvigor210CoreBiologies/. Log2-scaled and TMM normalized expression data were employed to test differential expression of the genes by a Negative Binomial testing method [6]. FDR was estimated by Storey's method [7].

Refinement of DDR gene signatures for predicting response to PD-L1 therapy

We started with upregulated genes from *DDR1* RNA-seq data and selected genes that satisfied two criteria: 1) Cox Proportional Hazard Regression of overall survival P-value<0.05 and HR>1 and 2) log2-fold-change<-0.3, which are 95 percentile cutoffs of differential expression between stable disease/partial disease (SD/PD) and complete response/partial response (CR/PR) in the IMvigor210 cohort. This yielded a 10-gene signature (CS-10). In a different fashion, we also performed backward feature selection based on Cox regression of OS with 42 genes detected in IMvigor210 data. Comparisons of the full model with all 42 genes and the reduced model with a subset of the 42 genes were conducted with a log-likelihood test and 19 genes were selected for optimal subset for the *DDR1* Cox model (CS-19). Using the same method for DDR2, we selected 4 genes (CS-4) and 25 genes (CS-25) for the Z-score and Cox model, respectively. Finally, four gene signatures were developed: a 10-gene signature based on the Z-score model (CS-10) and 19-gene signature based on the Cox model (CS-19) for *DDR1*, and a 4-gene signature based on the Z-score model (CS-4) and 25-gene signature based on the Cox model (CS-25) for *DDR2*.

Non-small cell lung cancer (NSCLC) sample selection

For the independent blinded validation study, two de-identified health records of NSCLC patients treated with FDA-approved ICT or ICT plus chemotherapy were selected from the Caris and Tempus databases and transcriptomic data were compiled from formalin-fixed, paraffin-embedded previously sequenced tumor samples. Progression-free survival (PFS), defined as the number of days from ICT start to the first documented tumor progression event, censored on the last known physician encounter, was used as the primary endpoint in survival analysis.

Assessing an association between DDR1/2 expression and PD-L1 expression/HLA defects/tumor mutational burden

We used cBioPortal data (https://www.cbioportal.org/). Using the "Query by Gene" functionality, we put these gene names including DDR1, DDR2, PD-L1 (CD274), HLA-A, HLA-B, and HLA-C with the selection of "Bladder Urothelial Carcinoma TCGA Firehose Legacy" data or "TCGA PanCancer Atlas" study data. We then selected patient samples with both mutation profiles and transcriptome profiles for the use of "Plots" function to assess association between the DDR1/2 expression and PD-L1 expression/HLA defects/tumor mutational burden using scatter plot with regression and box plot analysis.

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Supplementary Table 1, Lists of genes (Entrez Gene IDs) for individual immune cell types used to estimate abundance of cell types with cancer transcriptome.

Memory B cell	**Naïve B cell**	**Memory CD4 T cell**	**Activated Memory CD4 T cell**	**Naïve CD4 T cell**	**CD8 T cell**	**Cytotoxic T lymphocytes**	**Activated Dendritic cells**	**Eosinophil**	**M0 Macrophage**	**M1 Macrophage**	**M2 Macrophage**	**Activated Mast cell**	**Monocyte**	**Activated NK cell**	**Neutrophil**	**Plasma cell**	**Activated Dysregulated T cell**	**Dysregulated T cell**	**Exhausted T cell**	**Folicular Helper T cell**	**Gamma Delta T cell**	**Regulatory T cell**
9447	5244	2035	993	9744	926	925	58504	597	79365	43	6358	3198	55803	762	60489	23457	226	355	123	767	631	8538
240	605	2113	3605	79722	925	8320	330	27202	6354	80833	6368	3552	1436	1084	894	270	302	602	419	1117	9024	921
9629	79656	55336	55801	55086		83888	941	1602	1296	408	1414	3553	2359	3577	1021	51378	506	604	466	7976	1234	970
9750	673	57326	3565	2041		10578	942	23604	1435	958	55691	3567	8942	3579	356	6315	515	784	699	3382	11314	752014
3446	3566	140801	3578	79667		3823	56548	9681	6374	4283	2952	81698	7941	4051	3805	79703	811	817	760	59067	1010	29121
3574	283876	28670	4998	79690		8302	2117	2015	81501	1594	3269	115123	83937	2215	3809	2826	822	901	832	23178	8292	1946
440348	4224	28662	9136	2587		3824	3593	22905	2239	643314	80896	7006	22797	3034	5008	3012	1400	930	836	5133	10663	50943
11262	57553	678	220134	5871			9175	2696	8685	6504	5973			3772		8339	1465	972	837	56301	2996	83786
23495	55335			26297			9242	1880	4318	54795	81029			1955		3497	1786	1236	924	28951	10219	3090
9618	5670			50853			8013	8477	5473	968	9332			51312		3738	1846	1453	928	7253	442236	203510
27033	6402			7476			81796	3568	3684					79689		26251	2023	1912	953	65986	3973	55243
	8115			7754			8792	4033						9895		4121	2597	2308	1359		4110	3904
	54576			25799			3687	27334						7090		79694	2617	2625	1376		643503	23547
	57335							5029						8794		22983	3015	2859	1419		79973	126987
								5146						55350		374977	3054	3164	1493			4861
								27039								51237	3070	3561	1690			4917
								23223								5081	3326	3682	2107			56143
								64092								5163	3490	3717	2820			9651
								55512								25780	3516	4602	3394			5793
								27293								5972	3559	4723	3604			6261
								140803								6676	3587	4853	3627			25956
								7673								27090	3939	5283	3669			5413
																9333	3956	5450	3685			9806
																7367	3978	5609	3718			6756
																81030	4085	5641	3902			7299
																7718	4175	5862	4223			
																	5230	5914	4288			
																	5315	5971	4622			
																	5426	6641	4772			
																	5499	8315	4929			
																	5524	8665	5074			
																	5557	8897	5090			
																	5781	9063	5179			
																	5934	9114	5359			
																	5962	9153	5414			
																	6187	9520	5445			
																	6240	9589	5653			
																	6275	9770	5732			
																	6675	10019	5734			
																	7027	10039	5783			
																	7112	10252	5954			
																	7167	10318	6004			
																	7227	10427	6284			
																	7293	10437	6348			
																	7533	10672	6351			
																	8079	10678	6629			
																	8318	10765	6696			
																	8352	10957	6845			
																	8467	11182	6919			
																	8553	22807	6988			
																	8676	23030	7132			
																	9123	23075	7280			
																	9125	23479	7462			
																	9282	23608	7706			

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Supplementary Table 2. Differentially expressed genes in DDR1 overexpression xenografts.

			DDR1 OE vs Ctrl	
EntrezID	**Symbol**	**Description**	**log2FC**	**FDR**
28	ABO	ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase	1.48	0.01
41	ASIC1	acid sensing ion channel subunit 1	1.2	0.03
135	ADORA2A	adenosine A2a receptor	1.5	0.03
218	ALDH3A1	aldehyde dehydrogenase 3 family member	2.28	<0.01
286	ANK1	ankyrin 1	1.3	<0.01
341	APOC1	apolipoprotein C1	1.46	0.01
360	AQP3	aquaporin 3 (Gill blood group)	2.22	<0.01
627	BDNF	brain derived neurotrophic factor	1.08	0.04
771	CA12	carbonic anhydrase 12	1.95	<0.01
780	DDR1	discoidin domain receptor tyrosine kinase 1	1.53	<0.01
793	CALB1	calbindin 1	1.34	0.01
810	CALML3	calmodulin like 3	1.54	<0.01
875	CBS	cystathionine beta-synthase	1.06	0.02
1113	CHGA	chromogranin A	2.18	<0.01
1116	CHI3L1	chitinase 3 like 1	2.21	<0.01
1152	CKB	creatine kinase B	1.49	0.01
1201	CLN3	CLN3 lysosomal/endosomal transmembrane protein, battenin	2.54	<0.01
1293	COL6A3	collagen type VI alpha 3 chain	1.02	<0.01
1388	ATF6B	activating transcription factor 6 beta	2.48	<0.01
1396	CRIP1	cysteine rich protein 1	2.05	<0.01
1397	CRIP2	cysteine rich protein 2	1.03	<0.01
1464	CSPG4	chondroitin sulfate proteoglycan 4	1.28	0.01
1525	CXADR	CXADR Ig-like cell adhesion molecule	1.36	<0.01
1551	CYP3A7	cytochrome P450 family 3 subfamily A	1.22	0.05
1555	CYP2B6	cytochrome P450 family 2 subfamily B	1.63	<0.01
1556	CYP2B7P	cytochrome P450 family 2 subfamily B member 7, pseudogene	1.44	0.02
1645	AKR1C1	aldo-keto reductase family 1 member C1	1.05	<0.01
1646	AKR1C2	aldo-keto reductase family 1 member C2	1.05	0.01
1672	DEFB1	defensin beta 1	2.23	<0.01
1917	EEF1A2	eukaryotic translation elongation factor 1	1.89	<0.01
1953	MEGF6	multiple EGF like domains 6	1.77	<0.01
2036	EPB41L1	erythrocyte membrane protein band 4.1 like	1.41	<0.01
2078	ERG	ETS transcription factor ERG	1.49	<0.01
2261	FGFR3	fibroblast growth factor receptor 3	2.07	<0.01
2295	FOXF2	forkhead box F2	1.13	0.04
2304	FOXE1	forkhead box E1	1.95	<0.01
2331	FMOD	fibromodulin	1.21	0.03
2354	FOSB	FosB proto-oncogene, AP-1 transcription factor subunit	1.15	<0.01
2624	GATA2	GATA binding protein 2	1.2	0.03

2657	GDF1	growth differentiation factor 1	1.43	0.04
2687	GGT5	gamma-glutamyltransferase 5	1.32	0.01
2696	GIPR	gastric inhibitory polypeptide receptor	1.14	0.04
2752	GLUL	glutamate-ammonia ligase	1.13	<0.01
3037	HAS2	hyaluronan synthase 2	1.27	0.01
3398	ID2	inhibitor of DNA binding 2	1.28	<0.01
3485	IGFBP2	insulin like growth factor binding protein 2	1.98	0.01
3557	IL1RN	interleukin 1 receptor antagonist	1.14	0.04
3560	IL2RB	interleukin 2 receptor subunit beta	1.87	<0.01
3705	ITPK1	inositol-tetrakisphosphate 1-kinase	1.21	<0.01
3776	KCNK2	potassium two pore domain channel subfamily K member 2	1.15	0.01
3853	KRT6A	keratin 6A	1.32	<0.01
3860	KRT13	keratin 13	1.4	<0.01
3861	KRT14	keratin 14	1.23	<0.01
3934	LCN2	lipocalin 2	1.03	<0.01
3958	LGALS3	galectin 3	1	<0.01
4046	LSP1	lymphocyte specific protein 1	2.08	<0.01
4128	MAOA	monoamine oxidase A	1.21	<0.01
4143	MAT1A	methionine adenosyltransferase 1A	1.44	0.01
4210	MEFV	MEFV innate immuity regulator, pyrin	1.4	0.02
4549	RNR1	s-rRNA	2.05	<0.01
4550	RNR2	l-rRNA	1.76	<0.01
4582	MUC1	mucin 1, cell surface associated	1.38	0.01
4586	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	1.58	<0.01
4588	MUC6	mucin 6, oligomeric mucus/gel-forming	1.17	0.04
4680	CEACAM6	CEA cell adhesion molecule 6	1.16	<0.01
4856	CCN3	cellular communication network factor 3	1.21	<0.01
4883	NPR3	natriuretic peptide receptor 3	1.62	0.01
4923	NTSR1	neurotensin receptor 1	1.33	0.01
5064	PALM	paralemmin	1.68	<0.01
5081	PAX7	paired box 7	2.18	<0.01
5138	PDE2A	phosphodiesterase 2A	1.2	0.03
5187	PER1	period circadian regulator 1	1.17	<0.01
5360	PLTP	phospholipid transfer protein	1.17	0.04
5583	PRKCH	protein kinase C eta	1.1	<0.01
5625	PRODH	proline dehydrogenase 1	2.15	<0.01
5797	PTPRM	protein tyrosine phosphatase receptor type	1.89	<0.01
5909	RAP1GAP	RAP1 GTPase activating protein	1.58	<0.01
6217	RPS16	ribosomal protein S16	1.18	<0.01
6317	SERPINB3	serpin family B member 3	1.51	0.02
6337	SCNN1A	sodium channel epithelial 1 subunit alpha	1.06	0.01
6338	SCNN1B	sodium channel epithelial 1 subunit beta	2.36	<0.01
6340	SCNN1G	sodium channel epithelial 1 subunit gamma	1.54	<0.01
6563	SLC14A1	solute carrier family 14 member 1 (Kidd blood group)	1.12	<0.01
6564	SLC15A1	solute carrier family 15 member 1	1.11	0.04
6755	SSTR5	somatostatin receptor 5	1.28	0.03

6781	STC1	stanniocalcin 1	1.16	<0.01
6899	TBX1	T-box transcription factor 1	1.38	0.04
7031	TFF1	trefoil factor 1	4.44	<0.01
7033	TFF3	trefoil factor 3	2.1	<0.01
7045	TGFBI	transforming growth factor beta induced	1.19	<0.01
7051	TGM1	transglutaminase 1	1.63	<0.01
7062	TCHH	trichohyalin	1.29	0.02
7136	TNNI2	troponin I2, fast skeletal type	1.33	<0.01
7140	TNNT3	troponin T3, fast skeletal type	1.64	<0.01
7356	SCGB1A1	secretoglobin family 1A member 1	1.91	<0.01
8170	SLC14A2	solute carrier family 14 member 2	1.68	0.04
8436	CAVIN2	caveolae associated protein 2	1.29	0.03
8515	ITGA10	integrin subunit alpha 10	1.34	<0.01
8581	LY6D	lymphocyte antigen 6 family member D	1.42	<0.01
8645	KCNK5	potassium two pore domain channel subfamily K member 5	1.21	0.01
8857	FCGBP	Fc fragment of IgG binding protein	3.24	<0.01
9145	SYNGR1	synaptogyrin 1	1.58	<0.01
9249	DHRS3	dehydrogenase/reductase 3	1.35	<0.01
9252	RPS6KA5	ribosomal protein S6 kinase A5	1	<0.01
9351	SLC9A3R2	SLC9A3 regulator 2	1.01	<0.01
9537	TP53I11	tumor protein p53 inducible protein 11	2.82	<0.01
10516	FBLN5	fibulin 5	2.14	<0.01
10529	NEBL	nebulette	2.85	<0.01
10551	AGR2	anterior gradient 2, protein disulphide isomerase family member	2.02	<0.01
10562	OLFM4	olfactomedin 4	1.75	<0.01
10595	ERN2	endoplasmic reticulum to nucleus signaling	1.97	<0.01
10811	NOXA1	NADPH oxidase activator 1	1.85	0.01
10863	ADAM28	ADAM metallopeptidase domain 28	2.5	<0.01
11199	ANXA10	annexin A10	3.29	<0.01
11247	NXPH4	neurexophilin 4	2.47	<0.01
23213	SULF1	sulfatase 1	1	0.01
23242	COBL	cordon-bleu WH2 repeat protein	1.05	0.05
23508	TTC9	tetratricopeptide repeat domain 9	1.28	0.02
23584	VSIG2	V-set and immunoglobulin domain	1.57	0.01
25803	SPDEF	SAM pointed domain containing ETS transcription factor	2.07	<0.01
25825	BACE2	beta-secretase 2	1.45	<0.01
25891	PAMR1	peptidase domain containing associated with muscle regeneration 1	1.24	0.01
27132	CPNE7	copine 7	2.19	<0.01
50614	GALNT9	polypeptide N-	2.33	<0.01
51162	EGFL7	EGF like domain multiple 7	1.38	<0.01
51286	CEND1	cell cycle exit and neuronal differentiation 1	1.36	0.04
51297	BPIFA1	BPI fold containing family A member 1	1.86	<0.01
51673	TPPP3	tubulin polymerization promoting protein family member 3	1.23	0.01

54848	ARHGEF38	Rho guanine nucleotide exchange factor 38	1.68	<0.01
54873	PALMD	palmdelphin	1.27	<0.01
55068	ENOX1	ecto-NOX disulfide-thiol exchanger 1	1.47	0.02
55089	SLC38A4	solute carrier family 38 member 4	1.25	0.01
55107	ANO1	anoctamin 1	1.08	<0.01
55638	SYBU	syntabulin	1.25	0.02
56103	PCDHGB2	protocadherin gamma subfamily B, 2	1.05	0.05
56172	ANKH	ANKH inorganic pyrophosphate transport regulator	1.2	<0.01
56241	SUSD2	sushi domain containing 2	1.21	<0.01
56704	JPH1	junctophilin 1	1.49	0.02
56901	NDUFA4L2	NDUFA4 mitochondrial complex associated	2.47	<0.01
56924	PAK6	p21 (RAC1) activated kinase 6	1.38	<0.01
57016	AKR1B10	aldo-keto reductase family 1 member B10	1.77	<0.01
57161	PELI2	pellino E3 ubiquitin protein ligase family	1.42	<0.01
57537	SORCS2	sortilin related VPS10 domain containing receptor 2	1.86	<0.01
64115	VSIR	V-set immunoregulatory receptor	1.03	0.01
64714	PDIA2	protein disulfide isomerase family A	1.76	0.02
79007	DBNDD1	dysbindin domain containing 1	1.2	0.04
79812	MMRN2	multimerin 2	1.51	<0.01
79838	TMC5	transmembrane channel like 5	1.37	0.01
80195	TMEM254	transmembrane protein 254	1.12	<0.01
80726	IQCN	IQ motif containing N	1.61	<0.01
81693	AMN	amnion associated transmembrane protein	1.91	<0.01
83481	EPPK1	epiplakin 1	1.73	<0.01
83643	CCDC3	coiled-coil domain containing 3	1.15	0.03
83872	HMCN1	hemicentin 1	2.1	<0.01
84152	PPP1R1B	protein phosphatase 1 regulatory inhibitor subunit 1B	1.55	<0.01
84525	HOPX	HOP homeobox	1.33	0.02
84871	AGBL4	ATP/GTP binding protein like 4	1.5	0.02
84969	TOX2	TOX high mobility group box family member	1.84	<0.01
85358	SHANK3	SH3 and multiple ankyrin repeat domains 3	1.29	<0.01
85379	KIAA1671	KIAA1671	1.02	<0.01
89874	SLC25A21	solute carrier family 25 member 21	1.26	0.03
90019	SYT8	synaptotagmin 8	1.32	<0.01
90523	MLIP	muscular LMNA interacting protein	2.57	<0.01
90632	LINC00473	long intergenic non-protein coding RNA 473	1.17	0.05
90865	IL33	interleukin 33	3.16	<0.01
90993	CREB3L1	cAMP responsive element binding protein 3	2.01	<0.01
93010	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	1.12	<0.01
93429	LOC93429	uncharacterized LOC93429	1.64	0.01
94122	SYTL5	synaptotagmin like 5	1.28	0.04
94234	FOXQ1	forkhead box Q1	1.99	<0.01
112399	EGLN3	egl-9 family hypoxia inducible factor 3	1.08	<0.01
114784	CSMD2	CUB and Sushi multiple domains 2	2.49	<0.01

115650	TNFRSF13C	TNF receptor superfamily member 13C	1.4	0.01
116154	PHACTR3	phosphatase and actin regulator 3	1.37	0.01
120224	TMEM45B	transmembrane protein 45B	2.59	<0.01
122622	ADSS1	adenylosuccinate synthase 1	1.79	<0.01
130576	LYPD6B	LY6/PLAUR domain containing 6B	1.64	<0.01
136288	C7orf57	chromosome 7 open reading frame 57	2.06	<0.01
139065	SLITRK4	SLIT and NTRK like family member 4	1.69	<0.01
140825	NEURL2	neuralized E3 ubiquitin protein ligase 2	1.42	0.03
145482	PTGR2	prostaglandin reductase 2	1.11	0.02
146336	SSTR5-AS1	SSTR5 antisense RNA 1	1.48	<0.01
146802	SLC47A2	solute carrier family 47 member 2	1.23	0.01
151473	SLC16A14	solute carrier family 16 member 14	1.64	<0.01
161247	FITM1	fat storage inducing transmembrane protein	1.39	0.02
163688	CALML6	calmodulin like 6	1.56	0.04
191585	PLAC4	placenta enriched 4	1.22	0.04
196051	PLPP4	phospholipid phosphatase 4	1.32	0.02
202151	RANBP3L	RAN binding protein 3 like	1.34	0.01
256158	HMCN2	hemicentin 2	2.39	<0.01
260293	CYP4X1	cytochrome P450 family 4 subfamily X	1.3	0.02
283120	H19	H19 imprinted maternally expressed	1.51	<0.01
283848	CES4A	carboxylesterase 4A	1.84	<0.01
283897	C16orf54	chromosome 16 open reading frame 54	1.19	0.05
284021	MILR1	mast cell immunoglobulin like receptor 1	1.19	0.02
284339	TMEM145	transmembrane protein 145	1.69	0.01
286343	LURAP1L	leucine rich adaptor protein 1 like	1.05	0.03
319085	ITPK1-AS1	ITPK1 antisense RNA 1	1.24	0.03
340113	LINC02120	long intergenic non-protein coding RNA	1.41	0.04
342574	KRT27	keratin 27	1.4	<0.01
343578	ARHGAP40	Rho GTPase activating protein 40	1.48	0.02
353194	KRT16P6	keratin 16 pseudogene 6	1.17	<0.01
374378	GALNT18	polypeptide N-	1.13	<0.01
374918	IGFL1	IGF like family member 1	2.27	<0.01
388743	CAPN8	calpain 8	2.45	<0.01
389197	C4orf50	chromosome 4 open reading frame 50	1.51	0.01
400916	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	1.22	<0.01
401093	MBNL1-AS1	MBNL1 antisense RNA 1	1.45	<0.01
401546	C9orf152	chromosome 9 open reading frame 152	1.46	0.01
441058	LINC01667	long intergenic non-protein coding RNA	2.98	<0.01
441425	ANKRD20A3F	ankyrin repeat domain 20 family member A3, pseudogene	1.34	0.01
494470	RNF165	ring finger protein 165	1.27	<0.01
642954	RBBP4P1	RBBP4 pseudogene 1	1.38	0.01
643596	RNF224	ring finger protein 224	1.64	0.03
644809	C15orf56	chromosome 15 open reading frame 56	1.42	0.02
767557	SYS1-DBNDD	SYS1-DBNDD2 readthrough (NMD	1.36	0.03
100008587	RNA5-8SN5	RNA, 5.8S ribosomal N5	2.6	<0.01
100133545	MRPL23-AS1	MRPL23 antisense RNA 1	1.81	<0.01

100500872	MIR3911	microRNA 3911	1.44	0.03
100505817	LINC02582	long intergenic non-protein coding RNA	1.16	<0.01
100507487	LINC02615	long intergenic non-protein coding RNA	3.51	<0.01
100533483	DNAAF4-CCP	DNAAF4-CCPG1 readthrough (NMD	1.3	0.01
101927501	PINCR	p53-induced noncoding RNA	1.6	<0.01
102724788	LOC1027247	proline dehydrogenase 1, mitochondrial	1.96	<0.01
105379194	LOC1053791	uncharacterized LOC105379194	1.57	0.05
10630	PDPN	podoplanin	-5.85	<0.01
109729169	LINC02154	long intergenic non-protein coding RNA	-4.66	<0.01
51438	MAGEC2	MAGE family member C2	-3.72	<0.01
6262	RYR2	ryanodine receptor 2	-3.35	<0.01
392636	AGMO	alkylglycerol monooxygenase	-3.29	<0.01
101928336	LOC1019283	uncharacterized LOC101928336	-3.23	<0.01
5778	PTPN7	protein tyrosine phosphatase non-receptor	-3.18	<0.01
57101	ANO2	anoctamin 2	-3.15	<0.01
388015	RTL1	retrotransposon Gag like 1	-3.11	<0.01
445582	POTEE	POTE ankyrin domain family member E	-3.08	<0.01
4620	MYH2	myosin heavy chain 2	-2.96	<0.01
969	CD69	CD69 molecule	-2.96	<0.01
7373	COL14A1	collagen type XIV alpha 1 chain	-2.95	<0.01
286499	FAM133A	family with sequence similarity 133 member	-2.91	<0.01
3290	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	-2.89	<0.01
440910	LOC440910	uncharacterized LOC440910	-2.89	<0.01
2567	GABRG3	gamma-aminobutyric acid type A receptor subunit gamma3	-2.89	<0.01
4118	MAL	mal, T cell differentiation protein	-2.85	<0.01
339260	LOC339260	uncharacterized LOC339260	-2.84	<0.01
4619	MYH1	myosin heavy chain 1	-2.83	<0.01
7293	TNFRSF4	TNF receptor superfamily member 4	-2.81	<0.01
100289574	HERC2P4	hect domain and RLD 2 pseudogene 4	-2.8	<0.01
101927513	LOC10192751	uncharacterized LOC101927513	-2.72	<0.01
56999	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif 9	-2.72	<0.01
10584	COLEC10	collectin subfamily member 10	-2.69	<0.01
101927528	LINC01204	long intergenic non-protein coding RNA	-2.64	<0.01
101928687	LNCAROD	lncRNA activating regulator of DKK1	-2.62	<0.01
81792	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif 12	-2.53	<0.01
4318	MMP9	matrix metallopeptidase 9	-2.52	<0.01
3174	HNF4G	hepatocyte nuclear factor 4 gamma	-2.48	<0.01
58	ACTA1	actin alpha 1, skeletal muscle	-2.46	<0.01
440915	POTEKP	POTE ankyrin domain family member K, pseudogene	-2.46	<0.01
84856	LINC00839	long intergenic non-protein coding RNA 839	-2.46	<0.01
23636	NUP62	nucleoporin 62	-2.38	<0.01
9023	CH25H	cholesterol 25-hydroxylase	-2.37	<0.01
441389	LINC01239	long intergenic non-protein coding RNA	-2.37	<0.01

400110	ANKRD20A19	ankyrin repeat domain 20 family member A19, pseudogene	-2.35	<0.01
347468	OR13H1	olfactory receptor family 13 subfamily H member 1	-2.28	<0.01
3684	ITGAM	integrin subunit alpha M	-2.28	<0.01
3887	KRT81	keratin 81	-2.26	<0.01
729298	PCNPP3	PEST containing nuclear protein	-2.24	<0.01
728957	ZNF705D	zinc finger protein 705D	-2.24	<0.01
6098	ROS1	ROS proto-oncogene 1, receptor tyrosine	-2.24	<0.01
402429	KRT8P8	keratin 8 pseudogene 8	-2.21	<0.01
5789	PTPRD	protein tyrosine phosphatase receptor type	-2.21	<0.01
343450	KCNT2	potassium sodium-activated channel subfamily T member 2	-2.18	<0.01
58529	MYOZ1	myozenin 1	-2.17	<0.01
101929222	DISC1FP1	DISC1 fusion partner 1	-2.15	<0.01
107075116	MIR3142HG	MIR3142 host gene	-2.15	<0.01
114548	NLRP3	NLR family pyrin domain containing 3	-2.15	<0.01
55879	GABRQ	gamma-aminobutyric acid type A receptor subunit theta	-2.14	<0.01
4481	MSR1	macrophage scavenger receptor 1	-2.14	<0.01
115701	ALPK2	alpha kinase 2	-2.14	<0.01
101928767	LINC02328	long intergenic non-protein coding RNA	-2.13	0.01
105369848	LNCOG	lncRNA osteogenesis associated	-2.12	<0.01
8842	PROM1	prominin 1	-2.11	<0.01
441461	STX17-AS1	STX17 antisense RNA 1	-2.1	0.01
57393	CLTRN	collectrin, amino acid transport regulator	-2.1	<0.01
644684	BMS1P12	BMS1 pseudogene 12	-2.07	<0.01
644100	ARL14EPL	ADP ribosylation factor like GTPase 14 effector protein like	-2.07	<0.01
84561	SLC12A8	solute carrier family 12 member 8	-2.07	<0.01
100873793	PHF2P2	PHD finger protein 2 pseudogene 2	-2.05	<0.01
6489	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	-2.05	<0.01
4102	MAGEA3	MAGE family member A3	-2.05	<0.01
653089	NaN	NaN	-2.02	<0.01
27283	TINAG	tubulointerstitial nephritis antigen	-2.02	<0.01
1602	DACH1	dachshund family transcription factor 1	-2.01	<0.01
51302	CYP39A1	cytochrome P450 family 39 subfamily A member 1	-2.01	<0.01
101928845	LINC01842	long intergenic non-protein coding RNA	-2	<0.01
8745	ADAM23	ADAM metallopeptidase domain 23	-2	<0.01
157695	TDRP	testis development related protein	-2	<0.01
114827	FHAD1	forkhead associated phosphopeptide binding domain 1	-1.99	<0.01
344901	OSTN	osteocrin	-1.99	<0.01
100874094	ZNF197-AS1	ZNF197 antisense RNA 1	-1.98	0.05
101805492	CASC9	cancer susceptibility 9	-1.97	<0.01
387597	ILDR2	immunoglobulin like domain containing	-1.96	<0.01

2556	GABRA3	gamma-aminobutyric acid type A receptor subunit alpha3	-1.94	<0.01
116442	RAB39B	RAB39B, member RAS oncogene family	-1.94	<0.01
80034	CSRNP3	cysteine and serine rich nuclear protein 3	-1.94	<0.01
654790	PCP4L1	Purkinje cell protein 4 like 1	-1.94	0.01
50617	ATP6V0A4	ATPase H+ transporting V0 subunit a4	-1.94	<0.01
10761	PLAC1	placenta enriched 1	-1.94	0.04
105372840	LINC01694	long intergenic non-protein coding RNA	-1.93	<0.01
100216479	FAR2P2	fatty acyl-CoA reductase 2 pseudogene 2	-1.92	<0.01
90161	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	-1.92	0.01
7070	THY1	Thy-1 cell surface antigen	-1.92	<0.01
9381	OTOF	otoferlin	-1.91	<0.01
7456	WIPF1	WAS/WASL interacting protein family	-1.91	0.01
6503	SLA	Src like adaptor	-1.91	0.03
114788	CSMD3	CUB and Sushi multiple domains 3	-1.9	<0.01
55553	SOX6	SRY-box transcription factor 6	-1.89	<0.01
157	GRK3	G protein-coupled receptor kinase 3	-1.88	<0.01
4023	LPL	lipoprotein lipase	-1.87	<0.01
101928122	LINC01483	long intergenic non-protein coding RNA	-1.85	<0.01
221687	RNF182	ring finger protein 182	-1.85	<0.01
7772	ZNF229	zinc finger protein 229	-1.85	<0.01
3575	IL7R	interleukin 7 receptor	-1.83	<0.01
170692	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif 18	-1.83	<0.01
100506465	LINC01234	long intergenic non-protein coding RNA	-1.83	<0.01
54549	SDK2	sidekick cell adhesion molecule 2	-1.83	<0.01
401115	C4orf48	chromosome 4 open reading frame 48	-1.81	<0.01
5239	PGM5	phosphoglucomutase 5	-1.8	<0.01
100216001	MANCR	mitotically associated long non coding RNA	-1.8	<0.01
6101	RP1	RP1 axonemal microtubule associated	-1.8	<0.01
7335	UBE2V1	ubiquitin conjugating enzyme E2 V1	-1.8	<0.01
84176	MYH16	myosin heavy chain 16 pseudogene	-1.8	<0.01
7490	WT1	WT1 transcription factor	-1.79	<0.01
284759	SIRPB2	signal regulatory protein beta 2	-1.79	<0.01
3899	AFF3	AF4/FMR2 family member 3	-1.78	0.04
157381	LINC00964	long intergenic non-protein coding RNA 964	-1.77	<0.01
5806	PTX3	pentraxin 3	-1.77	<0.01
6546	SLC8A1	solute carrier family 8 member A1	-1.76	<0.01
391174	FAM96AP2	family with sequence similarity 96 member A pseudogene 2	-1.76	0.01
54847	SIDT1	SID1 transmembrane family member 1	-1.76	<0.01
80070	ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif 20	-1.76	<0.01
3263	HPX	hemopexin	-1.75	0.02
8578	SCARF1	scavenger receptor class F member 1	-1.74	<0.01
91133	L3MBTL4	L3MBTL histone methyl-lysine binding	-1.74	<0.01
6422	SFRP1	secreted frizzled related protein 1	-1.74	<0.01
1780	DYNC1I1	dynein cytoplasmic 1 intermediate chain 1	-1.74	<0.01

6328	SCN3A	sodium voltage-gated channel alpha	-1.74	<0.01
440854	CAPN14	calpain 14	-1.74	<0.01
7526	YES1P1	YES1 pseudogene 1	-1.73	<0.01
10082	GPC6	glypican 6	-1.73	0.03
9235	IL32	interleukin 32	-1.73	<0.01
116372	LYPD1	LY6/PLAUR domain containing 1	-1.73	<0.01
645715	EEF1A1P24	eukaryotic translation elongation factor 1 alpha 1 pseudogene 24	-1.72	<0.01
1573	CYP2J2	cytochrome P450 family 2 subfamily J	-1.72	<0.01
3694	ITGB6	integrin subunit beta 6	-1.72	<0.01
100506258	LOC10050625	uncharacterized LOC100506258	-1.72	0.01
10330	CNPY2	canopy FGF signaling regulator 2	-1.71	<0.01
4886	NPY1R	neuropeptide Y receptor Y1	-1.7	<0.01
9723	SEMA3E	semaphorin 3E	-1.7	<0.01
255130	IGFBP7-AS1	IGFBP7 antisense RNA 1	-1.7	0.02
10878	CFHR3	complement factor H related 3	-1.7	0.01
4101	MAGEA2	MAGE family member A2	-1.69	<0.01
23043	TNIK	TRAF2 and NCK interacting kinase	-1.69	<0.01
149773	APCDD1L-DT	APCDD1L divergent transcript	-1.69	<0.01
3936	LCP1	lymphocyte cytosolic protein 1	-1.69	<0.01
399942	TUBAP2	tubulin alpha pseudogene 2	-1.69	<0.01
7096	TLR1	toll like receptor 1	-1.69	0.01
84251	SGIP1	SH3GL interacting endocytic adaptor 1	-1.67	<0.01
283316	CD163L1	CD163 molecule like 1	-1.67	<0.01
1437	CSF2	colony stimulating factor 2	-1.66	<0.01
23705	CADM1	cell adhesion molecule 1	-1.66	<0.01
4311	MME	membrane metalloendopeptidase	-1.65	<0.01
2566	GABRG2	gamma-aminobutyric acid type A receptor subunit gamma2	-1.65	0.01
285382	C3orf70	chromosome 3 open reading frame 70	-1.65	0.01
106479468	RN7SL674P	RNA, 7SL, cytoplasmic 674, pseudogene	-1.64	<0.01
1879	EBF1	EBF transcription factor 1	-1.62	0.01
100128055	SMARCA5-AS	SMARCA5 antisense RNA 1	-1.62	0.02
50486	G0S2	G0/G1 switch 2	-1.62	<0.01
776	CACNA1D	calcium voltage-gated channel subunit	-1.62	<0.01
54830	NUP62CL	nucleoporin 62 C-terminal like	-1.62	0.01
27342	RABGEF1	RAB guanine nucleotide exchange factor 1	-1.62	<0.01
81406	OR2W6P	olfactory receptor family 2 subfamily W member 6 pseudogene	-1.62	0.01
80201	HKDC1	hexokinase domain containing 1	-1.61	0.01
30061	SLC40A1	solute carrier family 40 member 1	-1.61	0.03
27253	PCDH17	protocadherin 17	-1.6	0.01
5629	PROX1	prospero homeobox 1	-1.6	<0.01
387104	SOGA3	SOGA family member 3	-1.6	<0.01
440905	FAR2P1	fatty acyl-CoA reductase 2 pseudogene 1	-1.59	<0.01
101926925	LINC01358	long intergenic non-protein coding RNA	-1.59	0.01
81697	OR2B2	olfactory receptor family 2 subfamily B	-1.59	0.01
1794	DOCK2	dedicator of cytokinesis 2	-1.58	<0.01

55799	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	-1.58	<0.01
723788	MIG7	mig-7	-1.57	<0.01
102725191	LOC10272519	uncharacterized LOC102725191	-1.57	0.02
81030	ZBP1	Z-DNA binding protein 1	-1.57	<0.01
53353	LRP1B	LDL receptor related protein 1B	-1.57	0.01
285051	STPG4	sperm-tail PG-rich repeat containing 4	-1.56	0.01
139716	GAB3	GRB2 associated binding protein 3	-1.56	0.01
400046	LINC02389	long intergenic non-protein coding RNA	-1.56	<0.01
3439	IFNA1	interferon alpha 1	-1.55	0.01
88	ACTN2	actinin alpha 2	-1.55	0.02
641364	SLC7A11-AS1	SLC7A11 antisense RNA 1	-1.55	0.01
3773	KCNJ16	potassium inwardly rectifying channel subfamily J member 16	-1.55	0.01
95	ACY1	aminoacylase 1	-1.54	0.01
9308	CD83	CD83 molecule	-1.54	<0.01
4319	MMP10	matrix metallopeptidase 10	-1.54	<0.01
10202	DHRS2	dehydrogenase/reductase 2	-1.54	<0.01
100271871	RBM22P2	RNA binding motif protein 22 pseudogene 2	-1.54	0.04
1950	EGF	epidermal growth factor	-1.53	0.01
8512	MBL1P	mannose binding lectin 1, pseudogene	-1.53	0.01
952	CD38	CD38 molecule	-1.52	0.02
3604	TNFRSF9	TNF receptor superfamily member 9	-1.52	0.01
9079	LDB2	LIM domain binding 2	-1.51	0.01
27071	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1	-1.51	<0.01
6447	SCG5	secretogranin V	-1.51	0.01
27112	FAM155B	family with sequence similarity 155 member	-1.51	0.01
8972	MGAM	maltase-glucoamylase	-1.51	0.02
101101772	LINC00601	long intergenic non-protein coding RNA 601	-1.5	0.04
93986	FOXP2	forkhead box P2	-1.49	0.01
221806	VWDE	von Willebrand factor D and EGF domains	-1.49	<0.01
6916	TBXAS1	thromboxane A synthase 1	-1.49	<0.01
54084	TSPEAR	thrombospondin type laminin G domain and EAR repeats	-1.49	0.03
3552	IL1A	interleukin 1 alpha	-1.49	<0.01
7837	PXDN	peroxidasin	-1.48	<0.01
10750	GRAP	GRB2 related adaptor protein	-1.48	0.01
6326	SCN2A	sodium voltage-gated channel alpha	-1.48	0.01
4684	NCAM1	neural cell adhesion molecule 1	-1.48	0.02
100303491	ZEB2-AS1	ZEB2 antisense RNA 1	-1.48	0.03
50940	PDE11A	phosphodiesterase 11A	-1.47	0.02
63951	DMRTA1	DMRT like family A1	-1.47	0.01
5764	PTN	pleiotrophin	-1.47	0.02
2591	GALNT3	polypeptide N-	-1.47	<0.01
647333	NaN	NaN	-1.47	<0.01
153163	MGC32805	uncharacterized LOC153163	-1.47	0.02
1903	S1PR3	sphingosine-1-phosphate receptor 3	-1.47	0.01

389903	CSAG3	CSAG family member 3	-1.46	<0.01
29119	CTNNA3	catenin alpha 3	-1.46	<0.01
7075	TIE1	tyrosine kinase with immunoglobulin like and EGF like domains 1	-1.46	0.03
154860	FEZF1-AS1	FEZF1 antisense RNA 1	-1.46	0.02
131909	FAM172BP	family with sequence similarity 172 member B, pseudogene	-1.46	0.03
101927311	LINC02185	long intergenic non-protein coding RNA	-1.45	0.03
131450	CD200R1	CD200 receptor 1	-1.45	0.01
10659	CELF2	CUGBP Elav-like family member 2	-1.45	0.01
57408	LRTM1	leucine rich repeats and transmembrane domains 1	-1.44	0.03
340017	LINC02433	long intergenic non-protein coding RNA	-1.44	0.03
63876	PKNOX2	PBX/knotted 1 homeobox 2	-1.44	0.02
866	SERPINA6	serpin family A member 6	-1.43	0.02
730755	KRTAP2-3	keratin associated protein 2-3	-1.43	0.01
8995	TNFSF18	TNF superfamily member 18	-1.43	0.01
51191	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	-1.42	<0.01
645668	TUFMP1	Tu translation elongation factor, mitochondrial pseudogene 1	-1.42	0.03
54538	ROBO4	roundabout guidance receptor 4	-1.42	0.03
375061	FAM89A	family with sequence similarity 89 member	-1.42	0.01
100132463	CLDN24	claudin 24	-1.41	0.03
7226	TRPM2	transient receptor potential cation channel subfamily M member 2	-1.41	0.01
1520	CTSS	cathepsin S	-1.41	<0.01
3553	IL1B	interleukin 1 beta	-1.41	<0.01
8840	CCN4	cellular communication network factor 4	-1.41	0.02
401138	AMTN	amelotin	-1.4	0.01
330	BIRC3	baculoviral IAP repeat containing 3	-1.4	<0.01
116071	BATF2	basic leucine zipper ATF-like transcription	-1.4	0.01
55340	GIMAP5	GTPase, IMAP family member 5	-1.4	0.02
10501	SEMA6B	semaphorin 6B	-1.39	0.03
6515	SLC2A3	solute carrier family 2 member 3	-1.39	<0.01
91461	PKDCC	protein kinase domain containing,	-1.39	0.02
645280	SMPD4P1	sphingomyelin phosphodiesterase 4 pseudogene 1	-1.39	0.02
2250	FGF5	fibroblast growth factor 5	-1.39	<0.01
100420259	GDI2P2	GDP dissociation inhibitor 2 pseudogene 2	-1.39	0.03
56133	PCDHB2	protocadherin beta 2	-1.38	0.01
56892	TCIM	transcriptional and immune response	-1.38	0.01
115362	GBP5	guanylate binding protein 5	-1.38	0.01
2719	GPC3	glypican 3	-1.38	0.03
50509	COL5A3	collagen type V alpha 3 chain	-1.37	0.02
100128888	RPSAP36	ribosomal protein SA pseudogene 36	-1.37	0.03
85449	KIAA1755	KIAA1755	-1.37	0.04
645864	MAGEB17	MAGE family member B17	-1.36	0.03

56156	TEX13B	testis expressed 13B	-1.36	0.03
348751	FTCDNL1	formiminotransferase cyclodeaminase N-terminal like	-1.36	0.04
27147	DENND2A	DENN domain containing 2A	-1.35	0.01
100130418	CECR7	cat eye syndrome chromosome region, candidate 7	-1.34	0.03
5672	PSG4	pregnancy specific beta-1-glycoprotein 4	-1.34	0.02
1768	DNAH6	dynein axonemal heavy chain 6	-1.33	0.03
105376261	TTLL11-IT1	TTLL11 intronic transcript 1	-1.33	0.04
257194	NEGR1	neuronal growth regulator 1	-1.33	<0.01
1837	DTNA	dystrobrevin alpha	-1.32	0.03
25780	RASGRP3	RAS guanyl releasing protein 3	-1.31	0.02
4857	NOVA1	NOVA alternative splicing regulator 1	-1.31	0.02
1850	DUSP8	dual specificity phosphatase 8	-1.31	0.05
618	BCYRN1	brain cytoplasmic RNA 1	-1.31	<0.01
102724094	MUC12-AS1	MUC12 antisense RNA 1	-1.31	0.03
129099	CPSF1P1	cleavage and polyadenylation specific factor 1 pseudogene 1	-1.3	0.03
100132077	LOC10013207	uncharacterized LOC100132077	-1.3	0.03
7124	TNF	tumor necrosis factor	-1.3	<0.01
23475	QPRT	quinolinate phosphoribosyltransferase	-1.3	0.02
408186	OVOS	alpha-2-macroglobulin like 1 pseudogene	-1.3	0.04
3624	INHBA	inhibin subunit beta A	-1.3	<0.01
53840	TRIM34	tripartite motif containing 34	-1.29	0.03
100133612	LINC01134	long intergenic non-protein coding RNA	-1.29	0.05
81704	DOCK8	dedicator of cytokinesis 8	-1.29	0.02
646627	LYPD8	LY6/PLAUR domain containing 8	-1.29	0.04
2925	GRPR	gastrin releasing peptide receptor	-1.29	0.04
283008	NUTM2E	NUT family member 2E	-1.28	0.03
152404	IGSF11	immunoglobulin superfamily member 11	-1.28	0.04
133396	IL31RA	interleukin 31 receptor A	-1.28	0.04
5332	PLCB4	phospholipase C beta 4	-1.27	0.03
4208	MEF2C	myocyte enhancer factor 2C	-1.27	0.02
255231	MCOLN2	mucolipin 2	-1.26	0.02
91543	RSAD2	radical S-adenosyl methionine domain containing 2	-1.26	<0.01
3778	KCNMA1	potassium calcium-activated channel subfamily M alpha 1	-1.25	0.02
80310	PDGFD	platelet derived growth factor D	-1.25	0.03
57580	PREX1	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1	-1.25	0.01
199920	FYB2	FYN binding protein 2	-1.24	0.05
10333	TLR6	toll like receptor 6	-1.24	0.02
344875	COL6A4P1	collagen type VI alpha 4 pseudogene 1	-1.24	0.04
101927661	LOC10192766	uncharacterized LOC101927661	-1.23	0.04
79674	VEPH1	ventricular zone expressed PH domain containing 1	-1.23	0.01
90139	TSPAN18	tetraspanin 18	-1.23	0.03

9407	TMPRSS11D	transmembrane serine protease 11D	-1.23	0.04
4753	NELL2	neural EGFL like 2	-1.23	0.03
1295	COL8A1	collagen type VIII alpha 1 chain	-1.22	<0.01
51816	ADA2	adenosine deaminase 2	-1.22	0.05
51200	CPA4	carboxypeptidase A4	-1.22	<0.01
3800	KIF5C	kinesin family member 5C	-1.22	<0.01
5157	PDGFRL	platelet derived growth factor receptor like	-1.21	0.03
347716	USP32P3	ubiquitin specific peptidase 32 pseudogene	-1.21	0.04
101928978	LOC10192897	uncharacterized LOC101928978	-1.21	0.04
401024	FSIP2	fibrous sheath interacting protein 2	-1.21	0.01
129607	CMPK2	cytidine/uridine monophosphate kinase 2	-1.2	<0.01
100288413	ERVMER34-1	endogenous retrovirus group MER34 member 1, envelope	-1.2	0.03
84141	EVA1A	eva-1 homolog A, regulator of programmed cell death	-1.2	<0.01
9734	HDAC9	histone deacetylase 9	-1.2	0.02
646208	NUS1P2	NUS1 pseudogene 2	-1.2	0.03
646324	LINC00607	long intergenic non-protein coding RNA 607	-1.2	0.05
9839	ZEB2	zinc finger E-box binding homeobox 2	-1.19	<0.01
5452	POU2F2	POU class 2 homeobox 2	-1.19	0.03
2863	GPR39	G protein-coupled receptor 39	-1.19	0.03
200162	SPAG17	sperm associated antigen 17	-1.19	0.03
2191	FAP	fibroblast activation protein alpha	-1.19	0.04
9119	KRT75	keratin 75	-1.18	0.01
10673	TNFSF13B	TNF superfamily member 13b	-1.17	0.04
8869	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	-1.17	0.01
57126	CD177	CD177 molecule	-1.17	0.03
388	RHOB	ras homolog family member B	-1.17	<0.01
6352	CCL5	C-C motif chemokine ligand 5	-1.16	<0.01
23231	SEL1L3	SEL1L family member 3	-1.16	<0.01
677847	SNORA81	small nucleolar RNA, H/ACA box 81	-1.15	<0.01
3038	HAS3	hyaluronan synthase 3	-1.15	<0.01
57105	CYSLTR2	cysteinyl leukotriene receptor 2	-1.14	<0.01
101	ADAM8	ADAM metallopeptidase domain 8	-1.14	<0.01
5896	RAG1	recombination activating 1	-1.13	0.04
9404	LPXN	leupaxin	-1.13	<0.01
27185	DISC1	DISC1 scaffold protein	-1.13	0.03
84659	RNASE7	ribonuclease A family member 7	-1.13	0.04
152573	SHISA3	shisa family member 3	-1.13	0.01
4111	MAGEA12	MAGE family member A12	-1.12	<0.01
50944	SHANK1	SH3 and multiple ankyrin repeat domains 1	-1.12	0.05
414899	BLID	BH3-like motif containing, cell death inducer	-1.12	0.05
54033	RBM11	RNA binding motif protein 11	-1.12	0.04
79739	TTLL7	tubulin tyrosine ligase like 7	-1.11	0.02
89795	NAV3	neuron navigator 3	-1.11	0.02
4794	NFKBIE	NFKB inhibitor epsilon	-1.11	0.01
3075	CFH	complement factor H	-1.11	<0.01

6364	CCL20	C-C motif chemokine ligand 20	-1.11	0.01
63970	TP53AIP1	tumor protein p53 regulated apoptosis inducing protein 1	-1.11	0.04
1435	CSF1	colony stimulating factor 1	-1.11	0.01
8638	OASL	2'-5'-oligoadenylate synthetase like	-1.1	<0.01
51761	ATP8A2	ATPase phospholipid transporting 8A2	-1.1	0.01
85441	HELZ2	helicase with zinc finger 2	-1.09	<0.01
8482	SEMA7A	semaphorin 7A (John Milton Hagen blood	-1.09	0.01
8642	DCHS1	dachsous cadherin-related 1	-1.09	0.05
7098	TLR3	toll like receptor 3	-1.08	0.01
26851	SNORD3B-1	small nucleolar RNA, C/D box 3B-1	-1.08	<0.01
8997	KALRN	kalirin RhoGEF kinase	-1.07	0.05
11274	USP18	ubiquitin specific peptidase 18	-1.07	<0.01
5649	RELN	reelin	-1.07	0.01
828	CAPS	calcyphosine	-1.07	<0.01
347	APOD	apolipoprotein D	-1.06	0.01
164312	LRRN4	leucine rich repeat neuronal 4	-1.06	0.01
57559	STAMBPL1	STAM binding protein like 1	-1.06	0.03
4599	MX1	MX dynamin like GTPase 1	-1.05	<0.01
3481	IGF2	insulin like growth factor 2	-1.04	<0.01
5099	PCDH7	protocadherin 7	-1.04	<0.01
55287	TMEM40	transmembrane protein 40	-1.03	<0.01
23414	ZFPM2	zinc finger protein, FOG family member 2	-1.03	0.03
7367	UGT2B17	UDP glucuronosyltransferase family 2 member B17	-1.03	0.03
84059	ADGRV1	adhesion G protein-coupled receptor V1	-1.02	0.02
387845	EEF1A1P16	eukaryotic translation elongation factor 1 alpha 1 pseudogene 16	-1.02	0.02
2706	GJB2	gap junction protein beta 2	-1.02	<0.01
2152	F3	coagulation factor III, tissue factor	-1.01	<0.01
389136	VGLL3	vestigial like family member 3	-1.01	0.01
8613	PLPP3	phospholipid phosphatase 3	-1.01	0.01
80144	FRAS1	Fraser extracellular matrix complex subunit	-1	0.01
79683	ZDHHC14	zinc finger DHHC-type palmitoyltransferase	-1	0.05

Supplementary Table 3. Differentially expressed genes in NA13 DDR2 mouse model.

			shDDR2 vs. Ctrl	
EntrezID	**Symbol**	**Description**	**log2FC**	**FDR**
225642	Grp	gastrin releasing peptide	-2.96	<0.01
11656	Alas2	aminolevulinic acid synthase 2, erythroid	-2.57	<0.01
15122	Hba-a1	hemoglobin alpha, adult chain 1	-2.51	<0.01
217328	Myo15b	myosin XVB	-2.42	<0.01
12985	Csf3	colony stimulating factor 3 (granulocyte)	-2.36	<0.01
110257	Hba-a2	hemoglobin alpha, adult chain 2	-2.3	<0.01
16165	Il13ra2	interleukin 13 receptor, alpha 2	-2.3	<0.01
11687	Alox15	arachidonate 15-lipoxygenase	-2.28	<0.01
11684	Alox12	arachidonate 12-lipoxygenase	-2.14	<0.01
20311	Cxcl5	chemokine (C-X-C motif) ligand 5	-2.05	<0.01
16017	Ighg1	immunoglobulin heavy constant gamma 1 (G1m marker)	-2.04	<0.01
217733	Tmem63c	transmembrane protein 63c	-2	0.01
20310	Cxcl2	chemokine (C-X-C motif) ligand 2	-1.94	<0.01
546144	Wdr72	WD repeat domain 72	-1.86	<0.01
228564	Frmd5	FERM domain containing 5	-1.84	0.03
14917	Gucy2c	guanylate cyclase 2c	-1.84	<0.01
26878	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-1.81	<0.01
216643	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi	-1.76	<0.01
19016	Pparg	peroxisome proliferator activated receptor gamma	-1.74	<0.01
330627	Trim66	tripartite motif-containing 66	-1.64	0.03
100727	Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	-1.6	0.04
15112	Hao1	hydroxyacid oxidase 1, liver	-1.6	0.04
21990	Tph1	tryptophan hydroxylase 1	-1.59	0.02
20202	S100a9	S100 calcium binding protein A9 (calgranulin B)	-1.55	<0.01
330122	Cxcl3	chemokine (C-X-C motif) ligand 3	-1.52	<0.01
140919	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	-1.51	0.01
12981	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	-1.5	0.05
11571	Crisp1	cysteine-rich secretory protein 1	-1.49	0.03
381651	Odaph	odontogenesis associated phosphoprotein	-1.49	0.01
11685	Alox12e	arachidonate lipoxygenase, epidermal	-1.48	<0.01
70918	Nsun7	NOL1/NOP2/Sun domain family, member 7	-1.43	0.05
16691	Krt8	keratin 8	-1.43	<0.01

53897	Gal3st1	galactose-3-O-sulfotransferase 1	-1.42	0.03
72077	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	-1.38	<0.01
16175	Il1a	interleukin 1 alpha	-1.35	<0.01
56221	Ccl24	chemokine (C-C motif) ligand 24	-1.34	<0.01
226610	Fam78b	family with sequence similarity 78, member B	-1.32	0.02
628324	S100a2	S100 calcium binding protein A2	-1.32	0.03
18703	Pigr	polymeric immunoglobulin receptor	-1.32	0.03
53624	Cldn7	claudin 7	-1.31	<0.01
20297	Ccl20	chemokine (C-C motif) ligand 20	-1.31	0.04
17384	Mmp10	matrix metallopeptidase 10	-1.3	<0.01
14600	Ghr	growth hormone receptor	-1.3	<0.01
18413	Osm	oncostatin M	-1.29	0.04
21946	Pglyrp1	peptidoglycan recognition protein 1	-1.29	<0.01
22249	Unc13b	unc-13 homolog B	-1.27	0.05
20755	Sprr2a1	small proline-rich protein 2A1	-1.25	<0.01
12351	Car4	carbonic anhydrase 4	-1.25	0.03
114142	Foxp2	forkhead box P2	-1.24	0.03
17002	Ltf	lactotransferrin	-1.24	<0.01
17829	Muc1	mucin 1, transmembrane	-1.22	<0.01
14825	Cxcl1	chemokine (C-X-C motif) ligand 1	-1.19	<0.01
14133	Fcna	ficolin A	-1.18	0.03
57349	Ppbp	pro-platelet basic protein	-1.16	0.03
70894	Efcab3	EF-hand calcium binding domain 3	-1.16	0.03
110310	Krt7	keratin 7	-1.15	<0.01
69993	Chn2	chimerin 2	-1.15	0.03
70350	Basp1	brain abundant, membrane attached signal protein 1	-1.15	<0.01
93961	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-1.14	<0.01
22317	Vamp1	vesicle-associated membrane protein 1	-1.14	0.01
78906	Misp	mitotic spindle positioning	-1.13	0.04
66889	Rnf128	ring finger protein 128	-1.1	0.01
213948	Atg9b	autophagy related 9B	-1.09	<0.01
72269	Cda	cytidine deaminase	-1.09	0.05
13522	Adam28	a disintegrin and metallopeptidase domain 28	-1.08	0.01
70835	Prss22	protease, serine 22	-1.08	0.01
56312	Nupr1	nuclear protein transcription regulator 1	-1.06	<0.01
16669	Krt19	keratin 19	-1.03	<0.01
20201	S100a8	S100 calcium binding protein A8 (calgranulin A)	-1	0.02
18295	Ogn	osteoglycin	1.01	0.05
14590	Ggh	gamma-glutamyl hydrolase	1.01	<0.01
69542	2300002M23	RIKEN cDNA 2300002M23 gene	1.02	0.04
259277	Klk8	kallikrein related-peptidase 8	1.03	<0.01

26357	Abcg2	ATP binding cassette subfamily G member 2 (Junior blood group)	1.03	0.01
219151	Scara3	scavenger receptor class A, member 3	1.03	0.03
66469	Prxl2b	peroxiredoxin like 2B	1.05	0.02
27357	Gyg	glycogenin	1.06	0.02
116847	Prelp	proline arginine-rich end leucine-rich repeat	1.06	0.01
214425	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	1.07	<0.01
14178	Fgf7	fibroblast growth factor 7	1.08	0.01
71932	Ephx3	epoxide hydrolase 3	1.08	0.04
64817	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.09	<0.01
59091	Jph2	junctophilin 2	1.1	0.01
64661	Krtdap	keratinocyte differentiation associated protein	1.1	<0.01
12295	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	1.11	0.05
17189	Mb	myoglobin	1.13	0.02
22403	Ccn5	cellular communication network factor 5	1.15	<0.01
67733	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	1.15	0.05
16661	Krt10	keratin 10	1.17	<0.01
240633	Lipk	lipase, family member K	1.17	<0.01
11790	Speg	SPEG complex locus	1.17	0.03
56188	Fxyd1	FXYD domain-containing ion transport regulator 1	1.17	0.05
80892	Zfhx4	zinc finger homeodomain 4	1.17	0.02
23796	Aplnr	apelin receptor	1.21	<0.01
66283	Gkn1	gastrokine 1	1.22	0.01
70061	Sdr9c7	4short chain dehydrogenase/reductase family 9C, member 7	1.23	0.01
22239	Ugt8a	UDP galactosyltransferase 8A	1.24	0.03
16678	Krt1	keratin 1	1.24	<0.01
12773	Ccr4	chemokine (C-C motif) receptor 4	1.25	<0.01
14264	Fmod	fibromodulin	1.26	<0.01
20459	Ptk6	PTK6 protein tyrosine kinase 6	1.27	0.04
626870	Gm11992	predicted gene 11992	1.27	0.03
12491	Cd36	CD36 molecule	1.29	<0.01
19752	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)	1.29	0.04
74055	Plce1	phospholipase C, epsilon 1	1.29	0.04
56437	Rrad	Ras-related associated with diabetes	1.3	0.01
216049	Zfp365	zinc finger protein 365	1.31	0.02
14077	Fabp3	fatty acid binding protein 3, muscle and heart	1.32	0.05

16531	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1.34	0.03
52250	Reep1	receptor accessory protein 1	1.34	0.02
105298	Epdr1	ependymin related protein 1 (zebrafish)	1.34	0.02
118449	Synpo2	synaptopodin 2	1.35	0.01
11807	Apoa2	apolipoprotein A-II	1.36	0.05
16002	Igf2	insulin-like growth factor 2	1.37	<0.01
108897	Aif1l	allograft inflammatory factor 1-like	1.37	0.02
14051	Eya4	EYA transcriptional coactivator and phosphatase 4	1.37	0.04
282619	Sbsn	suprabasin	1.38	<0.01
435529	Adgrf2	adhesion G protein-coupled receptor F2	1.39	0.02
12338	Capn6	calpain 6	1.39	0.05
22370	Vtn	vitronectin	1.39	0.04
243912	Hspb6	heat shock protein, alpha-crystallin-related, B6	1.39	<0.01
20129	Rptn	repetin	1.4	<0.01
386463	Cdsn	corneodesmosin	1.4	<0.01
68828	Sync	syncoilin	1.41	0.03
244198	Olfml1	olfactomedin-like 1	1.42	0.05
11537	Cfd	complement factor D (adipsin)	1.42	0.04
209378	Itih5	inter-alpha (globulin) inhibitor H5	1.44	<0.01
12335	Capn3	calpain 3	1.46	0.01
19011	Endou	endonuclease, polyU-specific	1.46	<0.01
21952	Tnni1	troponin I, skeletal, slow 1	1.49	<0.01
241113	Prkag3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	1.49	0.02
14199	Fhl1	four and a half LIM domains 1	1.5	<0.01
101533	Klk9	kallikrein related-peptidase 9	1.5	<0.01
109314	Prr9	proline rich 9	1.5	<0.01
76942	Lypd5	Ly6/Plaur domain containing 5	1.5	<0.01
21922	Clec3b	C-type lectin domain family 3, member b	1.52	<0.01
387314	Tmtc1	transmembrane and tetratricopeptide repeat containing 1	1.52	0.01
626048	Rps12-ps16	ribosomal protein S12, pseudogene 16	1.53	0.03
75572	Acyp2	acylphosphatase 2, muscle type	1.53	0.01
239853	Adgrg7	adhesion G protein-coupled receptor G7	1.53	<0.01
73230	Bmper	BMP-binding endothelial regulator	1.54	0.01
74116	Pi16	peptidase inhibitor 16	1.54	<0.01
67516	Kctd4	potassium channel tetramerisation domain containing 4	1.55	0.01
20289	Scx	scleraxis	1.57	0.01
225638	Alpk2	alpha-kinase 2	1.57	0.02
13482	Dpp4	dipeptidylpeptidase 4	1.58	0.01
639634	Aadacl2	arylacetamide deacetylase like 2	1.58	0.01
320040	Rnf222	ring finger protein 222	1.59	0.01

17260	Mef2c	myocyte enhancer factor 2C	1.59	<0.01
433091	Pnpla1	patatin-like phospholipase domain containing 1	1.59	0.01
232413	Clec12a	C-type lectin domain family 12, member a	1.59	0.01
21908	Tlx1	T cell leukemia, homeobox 1	1.59	0.02
19713	Ret	ret proto-oncogene	1.6	0.02
16716	Ky	kyphoscoliosis peptidase	1.6	0.05
71755	Dhdh	dihydrodiol dehydrogenase (dimeric)	1.61	0.01
216961	Coro6	coronin 6	1.62	0.02
57911	Gsdma	gasdermin A	1.62	<0.01
94045	P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	1.64	0.03
242642	Hpdl	4-hydroxyphenylpyruvate dioxygenase-like	1.66	0.05
12845	Comp	cartilage oligomeric matrix protein	1.67	0.03
16515	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	1.67	0.01
27494	Amot	angiomotin	1.68	<0.01
320590	Svopl	SV2 related protein homolog (rat)-like	1.7	0.04
194597	Tmprss11a	transmembrane protease, serine 11a	1.7	<0.01
73284	Ddit4l	DNA-damage-inducible transcript 4-like	1.7	0.02
52187	Rragd	Ras-related GTP binding D	1.71	<0.01
72607	Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3)	1.72	<0.01
24004	Rai2	retinoic acid induced 2	1.73	0.04
14025	Bcl11a	B cell CLL/lymphoma 11A (zinc finger protein)	1.76	<0.01
12955	Cryab	crystallin, alpha B	1.77	<0.01
54159	Rnase2b	ribonuclease, RNase A family, 2B (liver, eosinophil-derived neurotoxin)	1.78	<0.01
15451	Hpn	hepsin	1.78	<0.01
15360	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	1.79	0.03
216616	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	1.83	<0.01
20339	Sele	selectin, endothelial cell	1.84	0.03
237611	Stac3	SH3 and cysteine rich domain 3	1.85	<0.01
80796	Calm4	calmodulin 4	1.85	<0.01
233335	Synm	synemin, intermediate filament protein	1.87	<0.01
11932	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	1.87	<0.01
16500	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	1.87	<0.01
11812	Apoc1	apolipoprotein C-I	1.89	<0.01
74175	Crct1	cysteine-rich C-terminal 1	1.91	<0.01
74407	Ttc25	tetratricopeptide repeat domain 25	1.94	0.02
59006	Myoz2	myozenin 2	1.96	<0.01

399548	Scn4b	sodium channel, type IV, beta	1.96	<0.01
81877	Tnxb	tenascin XB	1.96	<0.01
69253	Hspb2	heat shock protein 2	1.99	<0.01
107765	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	1.99	<0.01
12323	Camk2b	calcium/calmodulin-dependent protein kinase II, beta	2	<0.01
142687	Asb14	ankyrin repeat and SOCS box-containing 14	2	0.01
12160	Bmp5	bone morphogenetic protein 5	2.01	0.01
54403	Slc4a4	solute carrier family 4 (anion exchanger), member 4	2.04	<0.01
18670	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	2.04	<0.01
239134	Gucy1b2	guanylate cyclase 1, soluble, beta 2	2.05	<0.01
21828	Thbs4	thrombospondin 4	2.06	<0.01
74165	Fbxl22	F-box and leucine-rich repeat protein 22	2.07	<0.01
100302565	Snord68	small nucleolar RNA, C/D box 68	2.11	0.04
382864	Colq	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	2.12	<0.01
27389	Dusp13	dual specificity phosphatase 13	2.19	<0.01
17896	Myl4	myosin, light polypeptide 4	2.22	<0.01
17751	Mt3	metallothionein 3	2.24	<0.01
22229	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	2.25	<0.01
67855	Asprv1	aspartic peptidase, retroviral-like 1	2.26	<0.01
433619	Kprp	keratinocyte expressed, proline-rich	2.26	<0.01
384061	Fndc5	fibronectin type III domain containing 5	2.29	<0.01
17879	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	2.32	<0.01
56012	Pgam2	phosphoglycerate mutase 2	2.32	<0.01
217012	Unc45b	unc-45 myosin chaperone B	2.34	<0.01
26549	Itgb1bp2	integrin beta 1 binding protein 2	2.34	<0.01
68794	Flnc	filamin C, gamma	2.36	<0.01
20568	Slpi	secretory leukocyte peptidase inhibitor	2.36	<0.01
73720	Cst6	cystatin E/M	2.37	<0.01
106393	Srl	sarcalumenin	2.38	<0.01
17929	Myom1	myomesin 1	2.43	<0.01
14955	H19	H19, imprinted maternally expressed transcript	2.44	<0.01
65256	Asb2	ankyrin repeat and SOCS box-containing 2	2.45	<0.01
225443	Gm94	predicted gene 94	2.49	<0.01
11464	Actc1	actin, alpha, cardiac muscle 1	2.51	<0.01
74249	Lrrc2	leucine rich repeat containing 2	2.56	<0.01
231148	Ablim2	actin-binding LIM protein 2	2.58	<0.01
21955	Tnnt1	troponin T1, skeletal, slow	2.59	<0.01

26971	Pla2g2f	phospholipase A2, group IIF	2.61	<0.01
69520	Lce3f	late cornified envelope 3F	2.64	<0.01
21924	Tnnc1	troponin C, cardiac/slow skeletal	2.74	<0.01
17349	Mlf1	myeloid leukemia factor 1	2.74	<0.01
378431	Txlnb	taxilin beta	2.74	<0.01
24052	Sgcd	sarcoglycan, delta (dystrophin-associated glycoprotein)	2.77	<0.01
12322	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	2.79	<0.01
70788	Klhl30	kelch-like 30	2.86	<0.01
69354	Slc38a4	solute carrier family 38, member 4	2.88	<0.01
15464	Hrc	histidine rich calcium binding protein	2.9	<0.01
12350	Car3	carbonic anhydrase 3	2.98	<0.01
13505	Dsc1	desmocollin 1	3	<0.01
23993	Klk7	kallikrein related-peptidase 7 (chymotryptic, stratum corneum)	3	<0.01
14555	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	3.02	<0.01
68854	Asb11	ankyrin repeat and SOCS box-containing 11	3.03	<0.01
98660	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	3.08	<0.01
11811	Apobec2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	3.1	<0.01
50874	Tmod4	tropomodulin 4	3.12	<0.01
13346	Des	desmin	3.12	<0.01
241431	Xirp2	xin actin-binding repeat containing 2	3.12	<0.01
78321	Ankrd23	ankyrin repeat domain 23	3.15	<0.01
13808	Eno3	enolase 3, beta muscle	3.25	<0.01
434246	Trim72	tripartite motif-containing 72	3.27	<0.01
67252	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	3.32	<0.01
22138	Ttn	titin	3.39	<0.01
18767	Pkia	protein kinase inhibitor, alpha	3.47	<0.01
12292	Cacna1s	calcium channel, voltage-dependent, L type, alpha 1S subunit	3.48	<0.01
240892	Dusp27	dual specificity phosphatase 27 (putative)	3.51	<0.01
21953	Tnni2	troponin I, skeletal, fast 2	3.57	<0.01
53412	Ppp1r3c	protein phosphatase 1, regulatory subunit 3C	3.6	<0.01
228003	Klhl41	kelch-like 41	3.6	<0.01
18682	Phkg1	phosphorylase kinase gamma 1	3.63	<0.01
20190	Ryr1	ryanodine receptor 1, skeletal muscle	3.64	<0.01
21818	Tgm3	transglutaminase 3, E polypeptide	3.64	<0.01
12299	Cacng1	calcium channel, voltage-dependent, gamma subunit 1	3.68	<0.01
17996	Neb	nebulin	3.79	<0.01

29818	Hspb7	heat shock protein family, member 7 (cardiovascular)	3.86	<0.01
53318	Pdlim3	PDZ and LIM domain 3	3.93	<0.01
50795	Sh3bgr	SH3-binding domain glutamic acid-rich protein	3.97	<0.01
17907	Mylpf	myosin light chain, phosphorylatable, fast skeletal muscle	3.98	<0.01
229665	Ampd1	adenosine monophosphate deaminase 1	4.01	<0.01
11733	Ank1	ankyrin 1, erythroid	4.07	<0.01
24131	Ldb3	LIM domain binding 3	4.13	<0.01
66175	Mustn1	musculoskeletal, embryonic nuclear protein 1	4.15	<0.01
17901	Myl1	myosin, light polypeptide 1	4.22	<0.01
12372	Casq1	calsequestrin 1	4.25	<0.01
11459	Acta1	actin, alpha 1, skeletal muscle	4.44	<0.01
18175	Nrap	nebulin-related anchoring protein	4.54	<0.01
22437	Xirp1	xin actin-binding repeat containing 1	4.61	<0.01
21925	Tnnc2	troponin C2, fast	4.7	<0.01
76469	Cmya5	cardiomyopathy associated 5	4.74	<0.01
11474	Actn3	actinin alpha 3	4.74	<0.01
21957	Tnnt3	troponin T3, skeletal, fast	4.78	<0.01
27273	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	4.96	<0.01
19309	Pygm	muscle glycogen phosphorylase	5.19	<0.01
11937	Atp2a1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	5.54	<0.01
19293	Pvalb	parvalbumin	5.55	<0.01
12715	Ckm	creatine kinase, muscle	6.03	<0.01
17884	Myh4	myosin, heavy polypeptide 4, skeletal muscle	6.92	<0.01

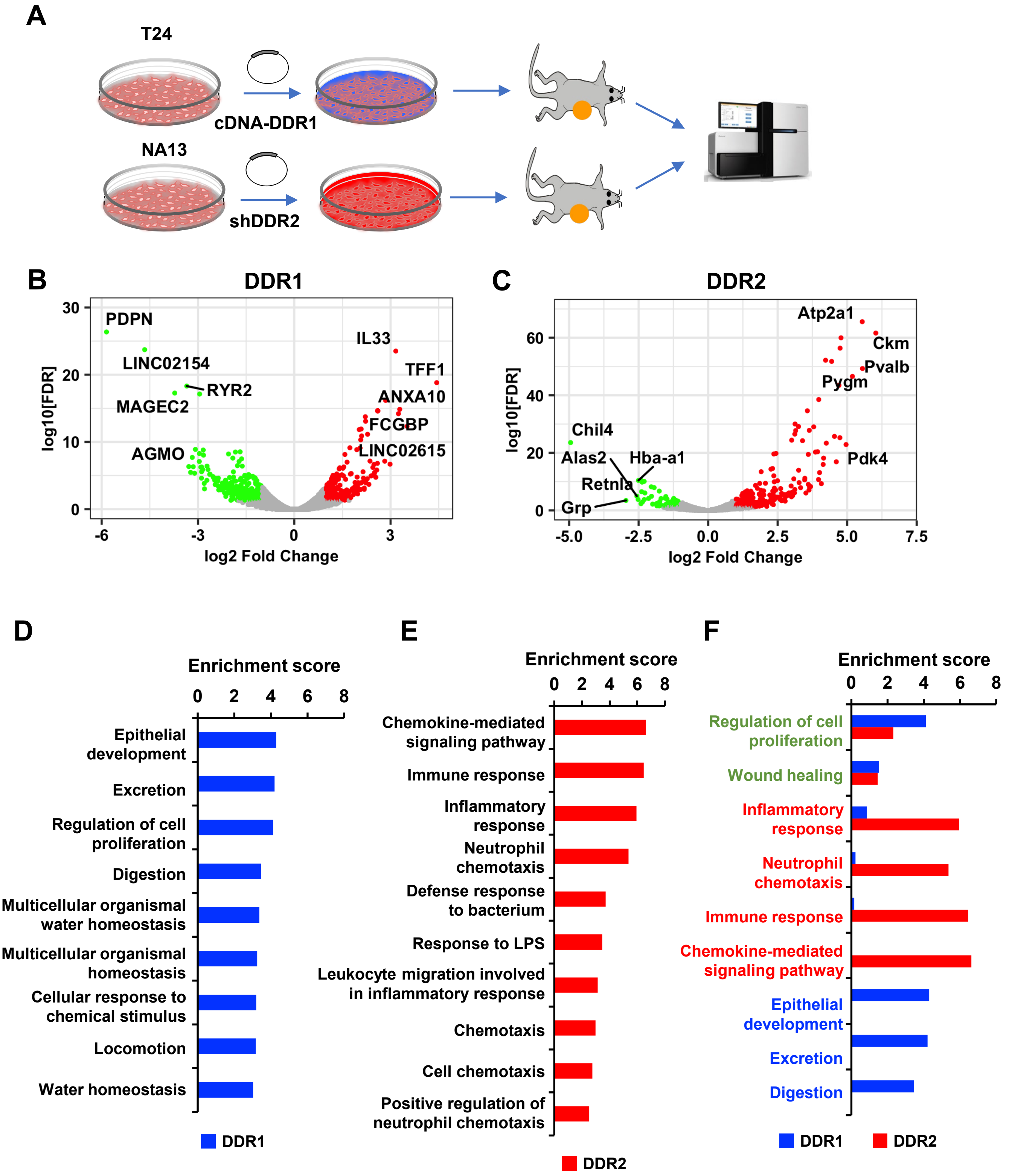
Supplementary Table 4. Clinical characteristics for the Tempus and Caris non-small cell lung cancer datasets treated with immune checkpoint blockade.

Characteristic	Caris	Tempus
No. of patients	259	196
Age, Median, years (range)	67 (36-89)	67 (26-90)
Sex, male, n (%)	136 (52)	95 (48)
Race, Non-Hispanic White n (%)	not available	106 (54)
Site of primary tumor, n (%)		
Lung	259 (100)	196 (100)
ECOG PS, n (%)		
0	not available	19 (10)
1	not available	36 (18)
Other (2,3,4)	not available	21 (11)
Unknown	not available	120 (61)
Tobacco use, n (%)		
Current	not available	38 (19)
Never	not available	30 (15)
Previous	not available	110 (56)
Unknown	not available	18 (9)
Metastatic sites at baseline, n (%)		
Visceral*	135 (52)	131 (67)
Liver	18 (7)	16 (8)
Lymph node only	37 (14)	12 (6)
Time from prior chemotherapy ≤3 months, n (%)	31 (12)	8 (4)
Prior therapy regimen, n (%)		
Platinum-based chemotherapy	36 (14)	88 (45)
Taxane	17 (7)	44 (22)
Tyrosine Kinase Inhibitor	4 (2)	16 (8)
Chemoradiation	90 (35)	33 (17)
Targeted therapy**	6 (2)	37 (19)
Pemetrexed	18 (7)	72 (37)
Other	40 (15)	30 (15)
PD-L1 status in tumor-infiltrating immune cells (Proportion of PD-L1-stained tumor-infiltrating immune cells within the tumor area)		
≥5% of the tumor area	129 (50)	56 (29)
<5% of the tumor area	130 (50)	80 (41)
Unknown	0 (0)	60 (31)

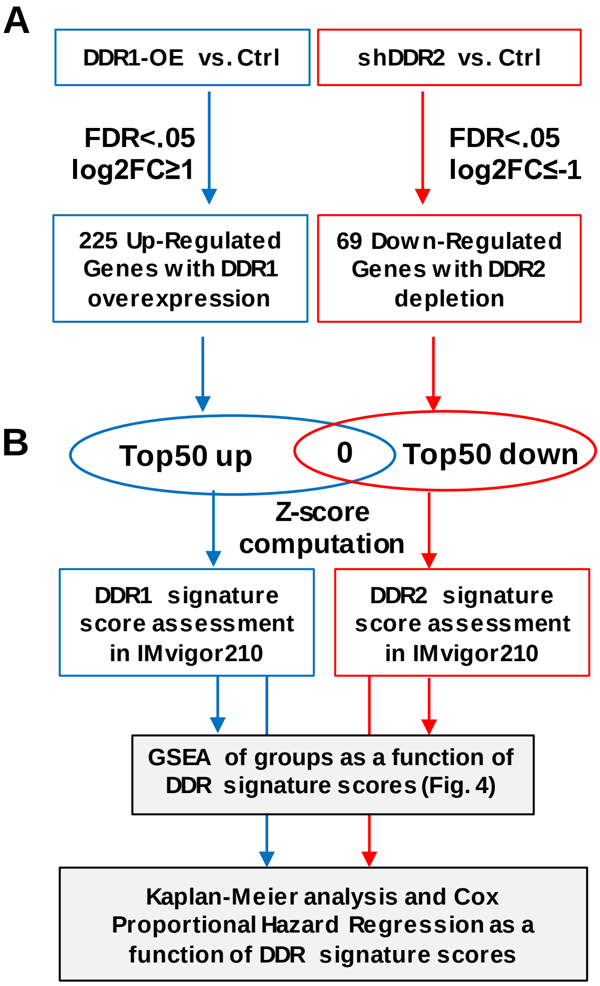
*Visceral metastases defined as liver, lung, bone, or any nonlymph node or soft tissue metastasis.

** VEGF targeted therapy + TKI

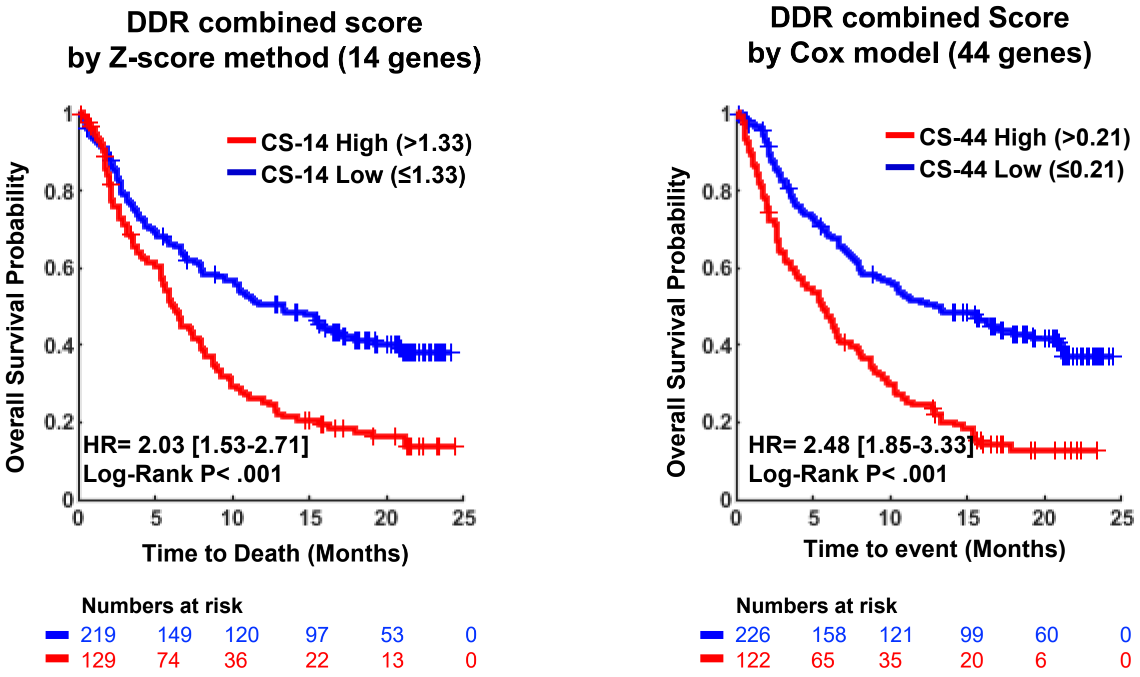
Supplementary Figure 1. Differentially expressed genes in response to DDR1 and DDR2 expression changes in mouse bladder cancer models. A. Generation of tumors with enforced expression of DDR1 and controls based on T24 human bladder tumor cells, and NA13 mouse bladder tumor treated with shDDR2 and control scrambles. B and C. Volcano plots depict differential expression of the genes perturbed by DDR1 (B) or DDR2 (C) in murine models. D. Bar chart shows uniquely enriched hallmark gene sets by the up-regulated genes by DDR1 overexpression. E. Bar chart shows uniquely enriched hallmark gene sets by the downregulated genes by DDR2 deletion. F. Common and differentially enriched hallmark gene sets by upregulated genes by DDR1 overexpression and downregulated genes by DDR2 depletion.



Supplementary Figure 2. Development and characterization of DDR gene expression signatures and their scores. A. A flow chart shows the selection process of the differentially expressed genes perturbed by DDR1 or DDR2 in separate models. B. The flow chart continues, showing the functional evaluation process of the top 50 genes from the DDR1 or DDR2 model through pathway analysis and survival analysis.

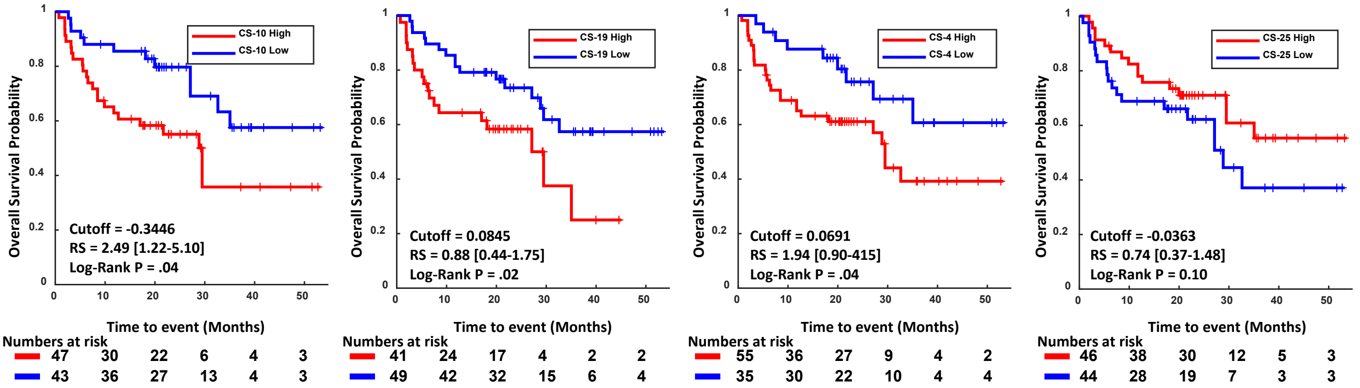


Supplementary Figure 3. Survival association of combined DDR1 and DDR2 gene models. Kaplan-Meier curves show survival rate difference between combined DDR gene model score high and low groups.

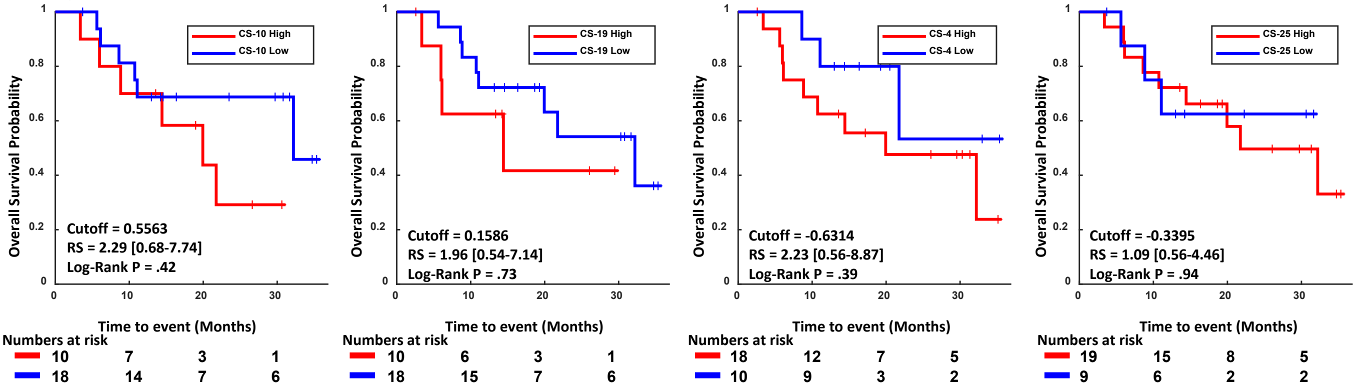


Supplementary Figure 4. Survival association of DDR1 or DDR2 gene models in independent cohorts

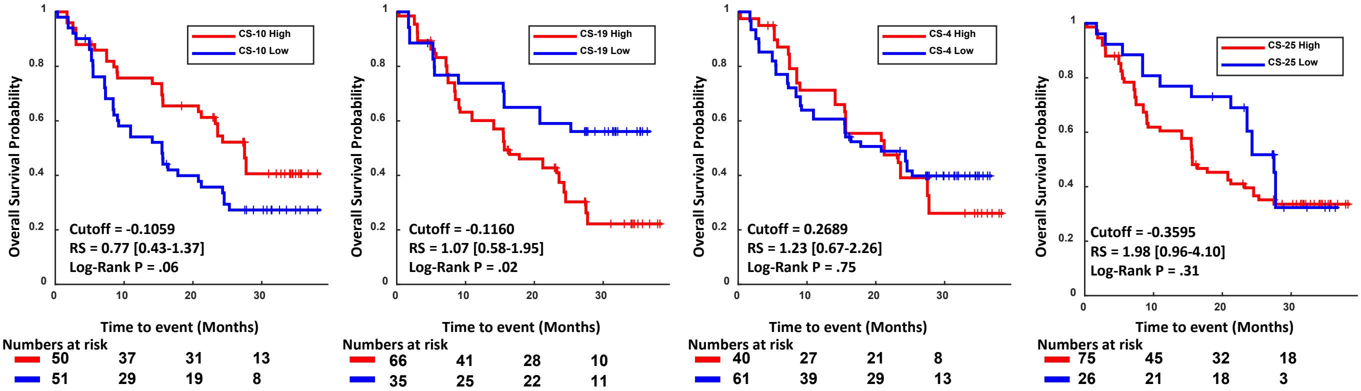
Gide cohort (Melanoma)



Hugo cohort (Melanoma)

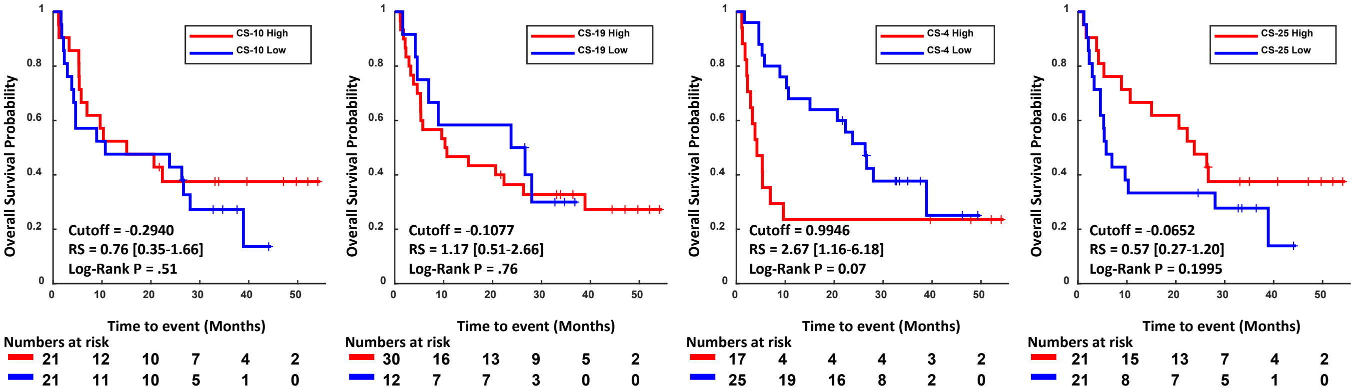


Riaz cohort (Melanoma)

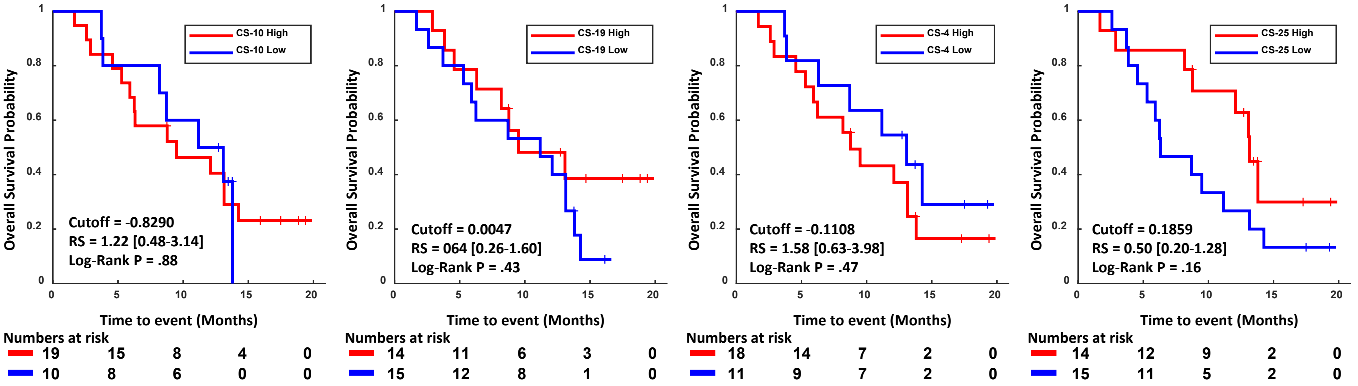


Supplementary Figure 4. Survival association of DDR1 or DDR2 gene models in independent cohorts (cont.)

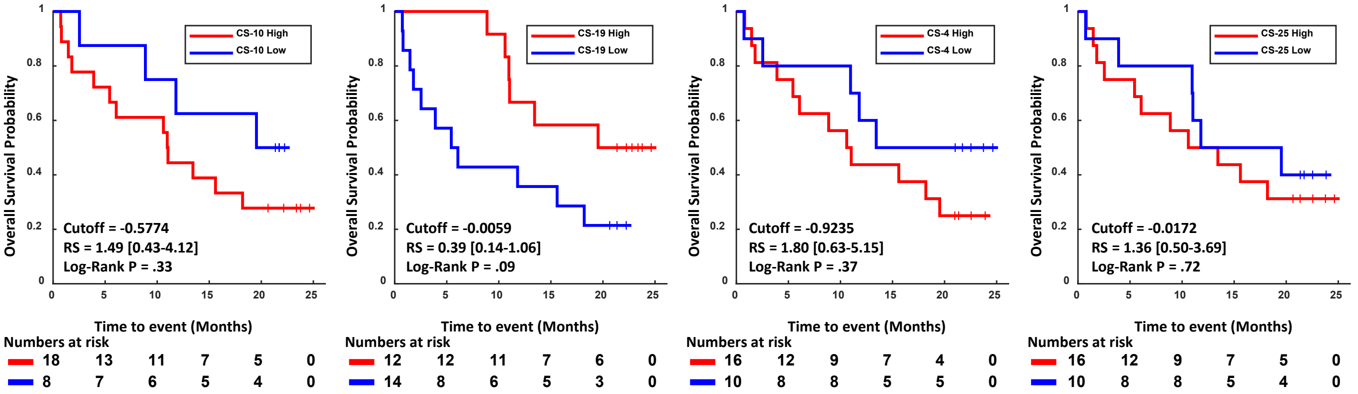
Van Allen cohort (Melanoma)



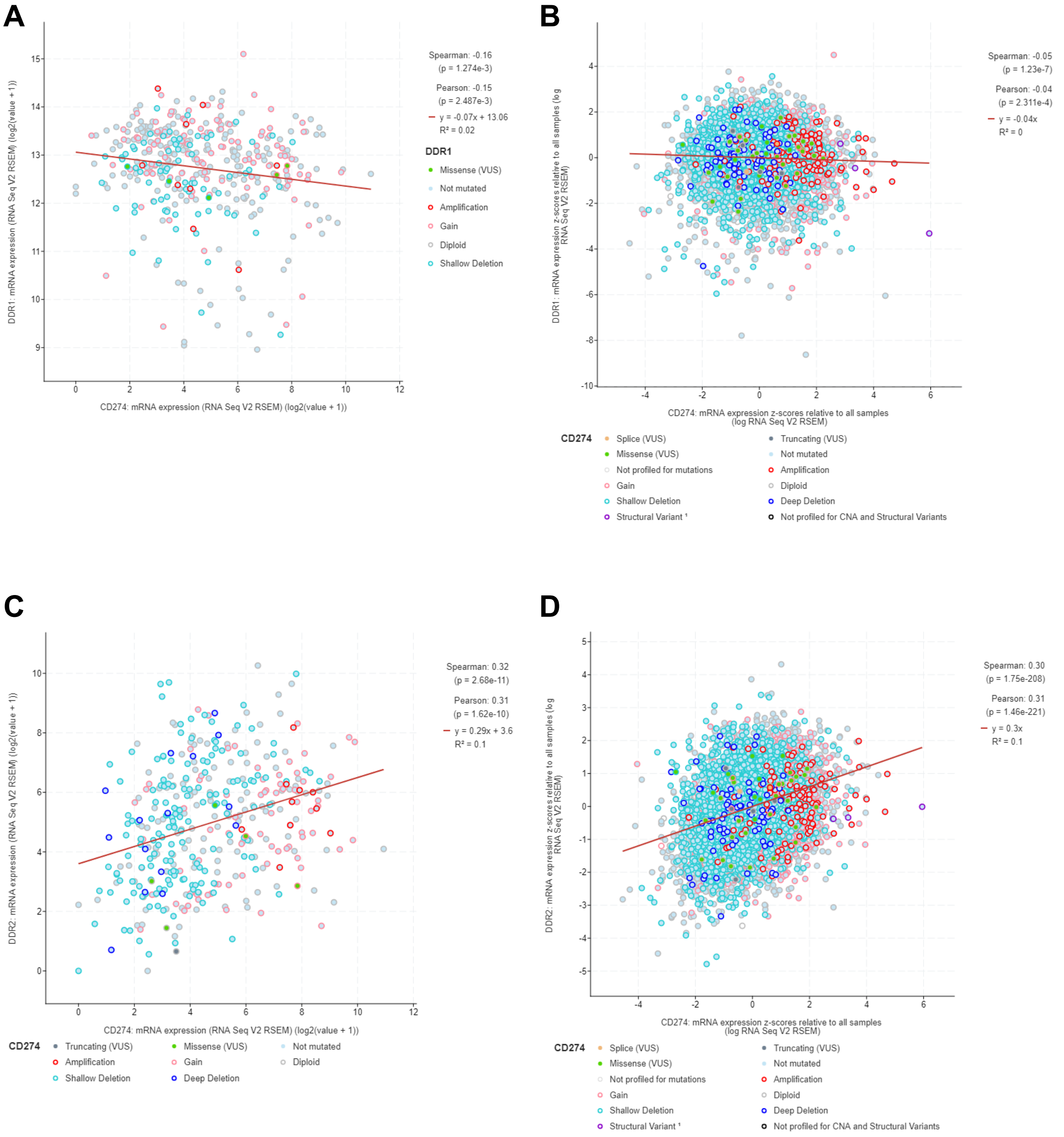
Prins cohort (Glioblastoma)



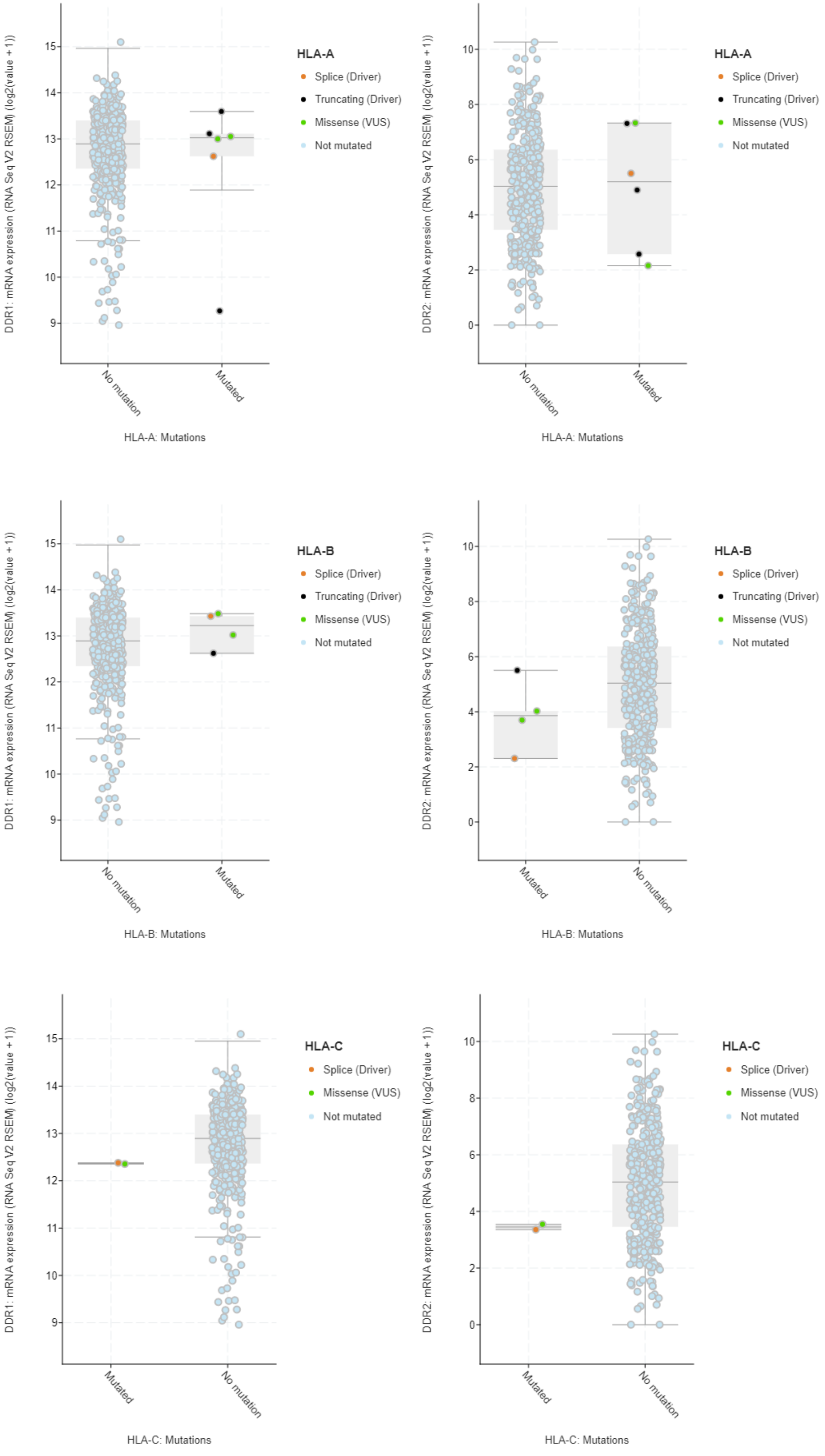
Snyder cohort (Age, Sex corrected RS)



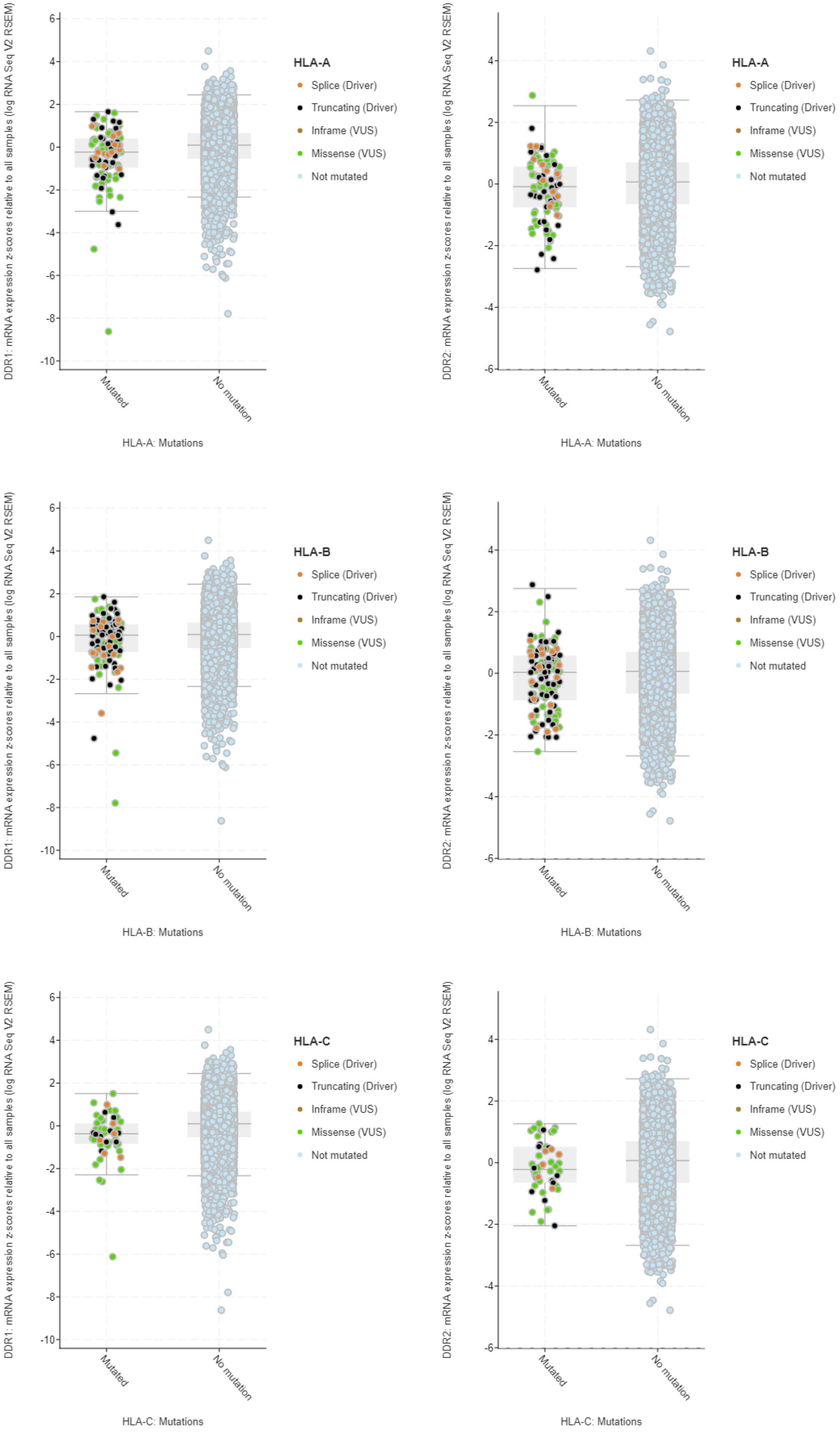
Supplementary Figure 5. DDR1/2 expression versus PD-L1 expression



Supplementary Figure 6. DDR1/2 expression versus HLA mutations



Supplementary Figure 7. DDR1/2 expression versus HLA mutations (Pan-cancer)



Supplementary Figure 8. DDR1/2 expression versus TMB