

SUPPLEMENTARY INFORMATION GUIDE

Tumour DDR1 Promotes Collagen Fibre Alignment to Instigate Immune Exclusion

Xiujie Sun^{1#}, Bogang Wu^{1#}, Huai-Chin Chiang^{1#}, Hui Deng², Xiaowen Zhang¹, Wei Xiong², Junquan Liu², Aaron M. Rozeboom³, Brent Harris³, Eline Blommaert⁴, Antonio Gomez⁵, Roderic Espin Garcia⁴, Yufan Zhou⁶, Payal Mitra⁷, Madeleine Prevost¹, Deyi Zhang⁸, Debarati Banik¹, Claudine Isaacs³, Deborah Berry³, Catherine Lai³, Krysta Chaldekis³, Patricia S. Latham⁹, Christine A. Brantner¹⁰, Anastas Popratiloff¹⁰, Victor X. Jin⁶, Ningyan Zhang², Yanfen Hu⁷, Miguel Angel Pujana^{4*}, Tyler J. Curiel^{8*}, Zhiqiang An^{2*}, Rong Li^{1*}

¹Department of Biochemistry & Molecular Medicine,

⁷Department of Anatomy & Cell Biology, ⁹Department of Pathology,
School of Medicine & Health Sciences,

¹⁰GW Nanofabrication and Imaging Center,

The George Washington University, Washington, DC 20037, USA

²Texas Therapeutics Institute, Brown Foundation Institute of Molecular Medicine,
The University of Texas Health Science Center at Houston, Houston, TX 77030, USA

³Lombardi Comprehensive Cancer Center,

Georgetown University, Washington, DC 20007, USA

⁴ProCURE, Catalan Institute of Oncology, Oncobell, Bellvitge Institute for Biomedical
Research (IDIBELL), L'Hospitalet del Llobregat, Barcelona, Catalonia, Spain

⁵Rheumatology Department and Rheumatology Research Group, Vall d'Hebron Hospital
Research Institute, Barcelona, Spain

⁶Department of Molecular Medicine, ⁸Department of Medicine, The Mays Cancer Center,
University of Texas Health San Antonio, San Antonio, TX 78229, USA

Running Title: Breaking down DDR1-dependent immune exclusion

#These authors contributed equally to the work

*Correspondence to: R.L. (rli69@gwu.edu), Z.A. (Zhiqiang.An@uth.tmc.edu), T.J.C. (curielt@uthscsa.edu), M.A.P. (mapujana@iconcologia.net)

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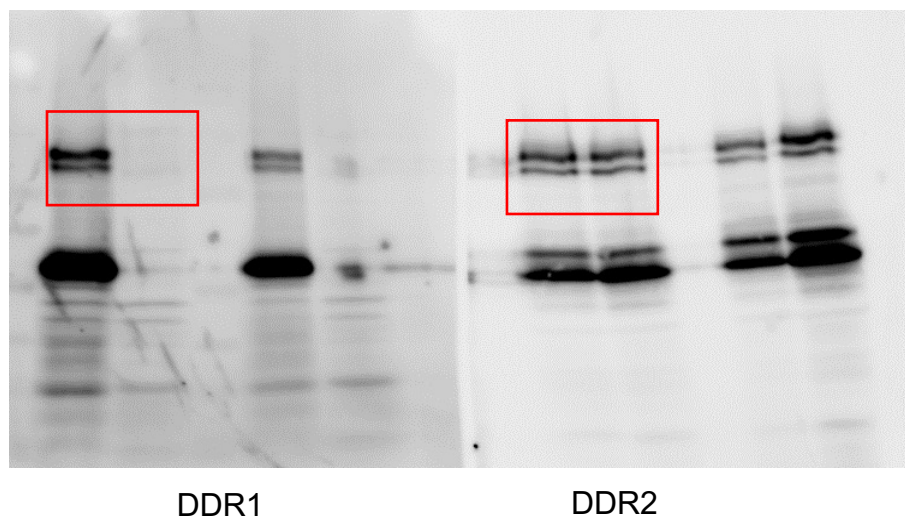
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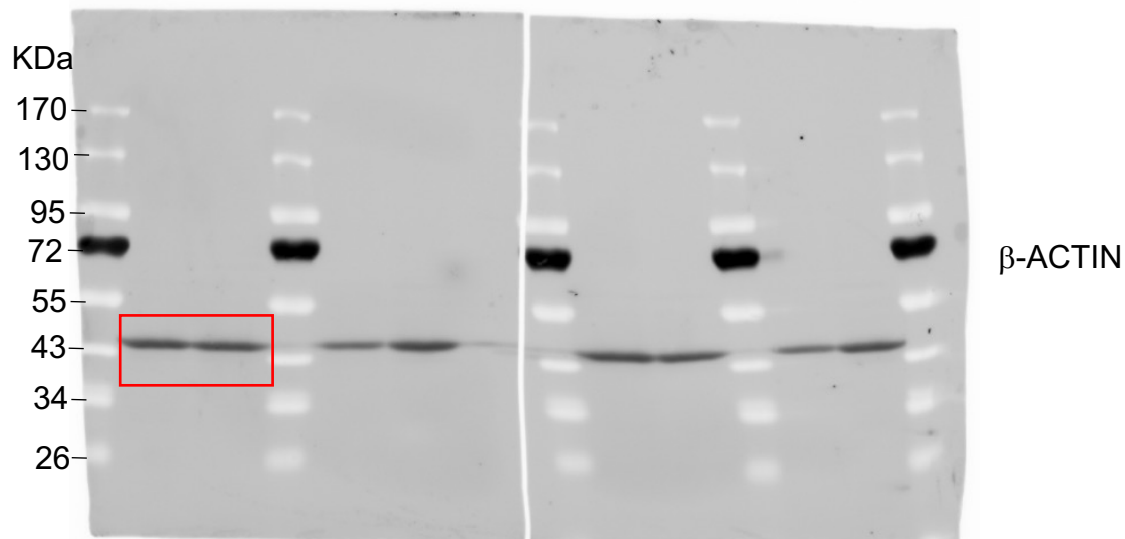
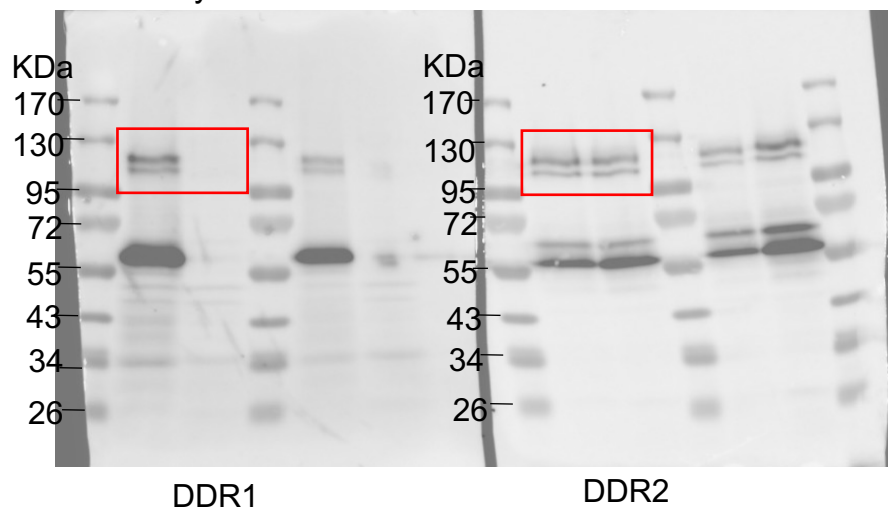
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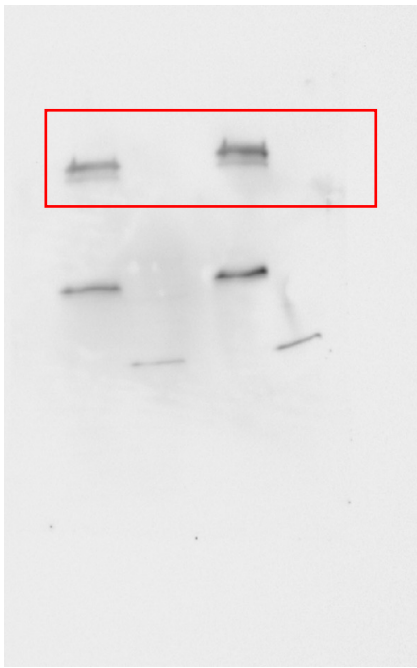
Supplementary Figure 1. Gel source data for Main Figure 1a



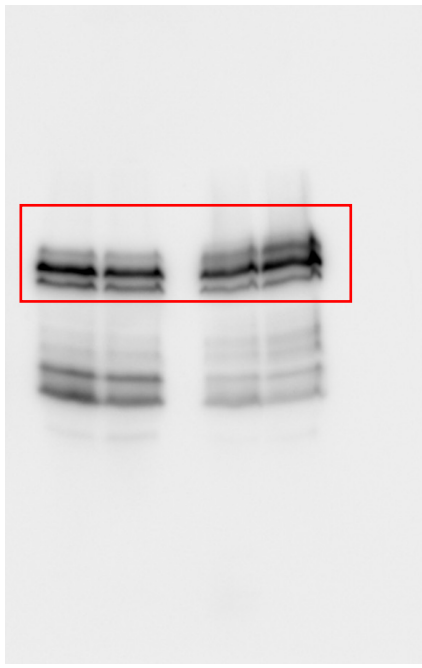
Overlay with marker



Supplementary Figure 2. Gel source data for Extended Data Figure 1a

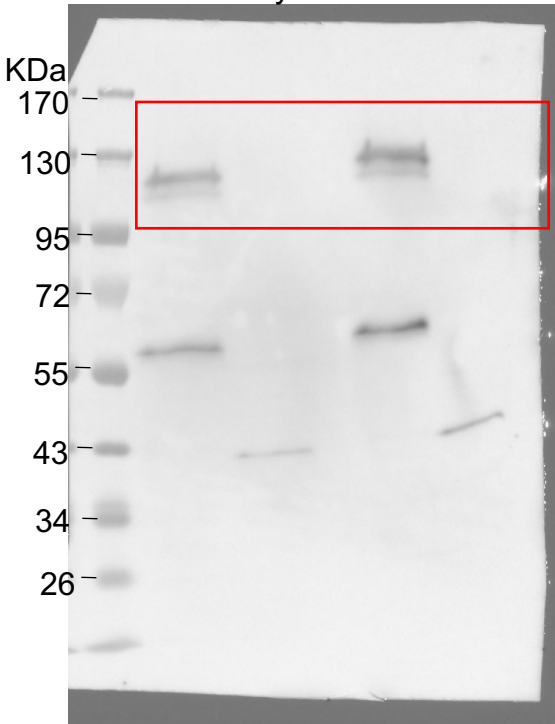


DDR1

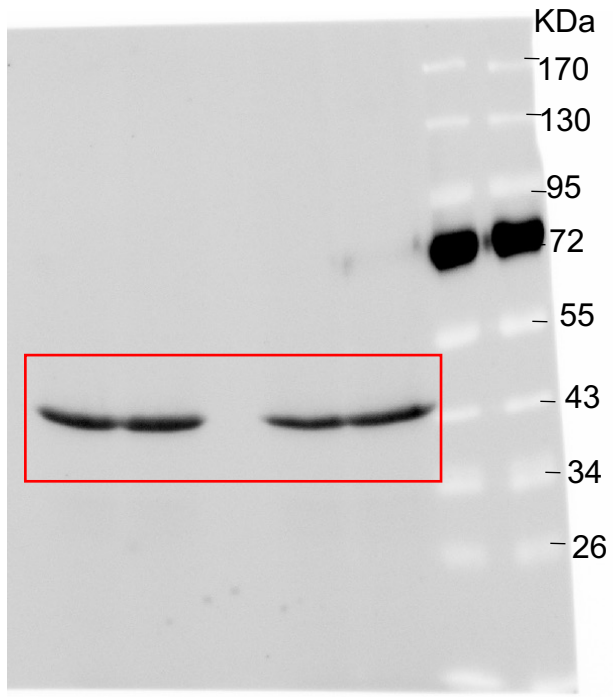


DDR2

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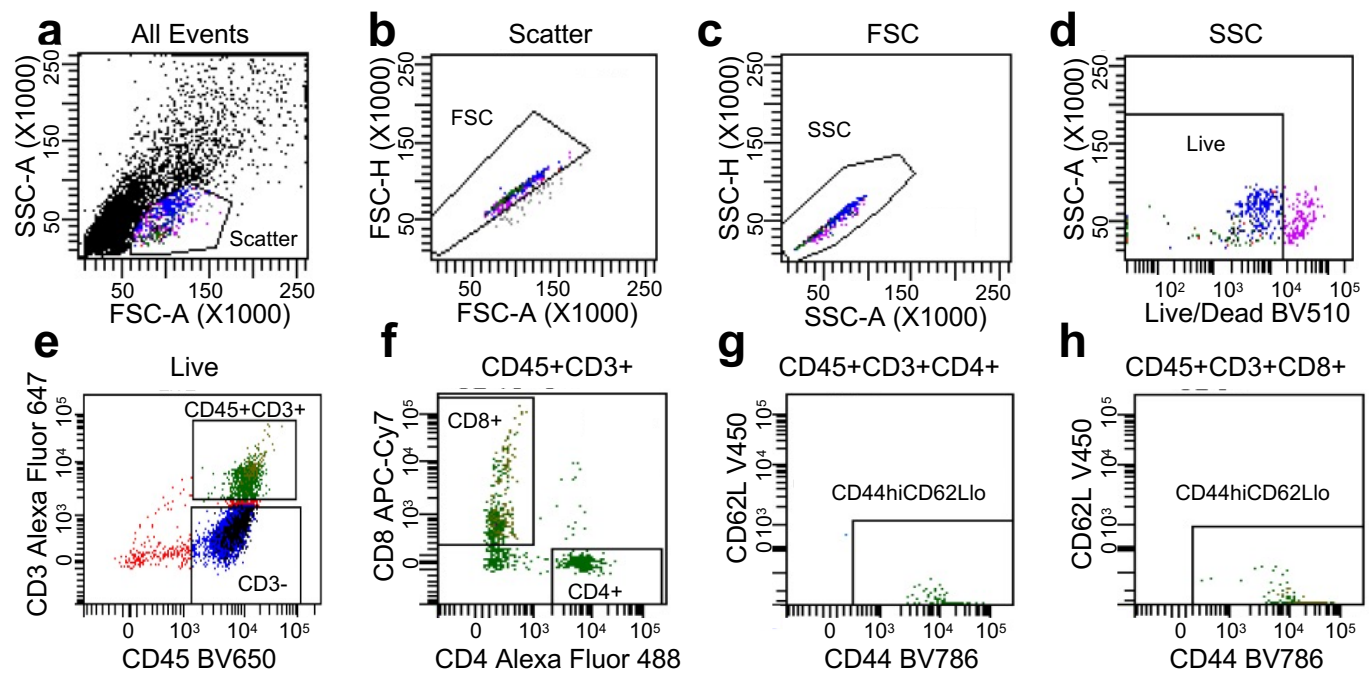


DDR1



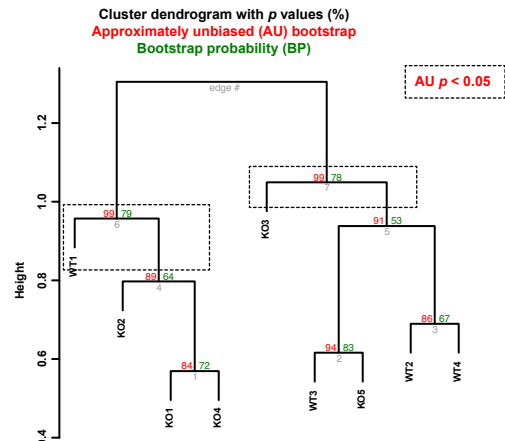
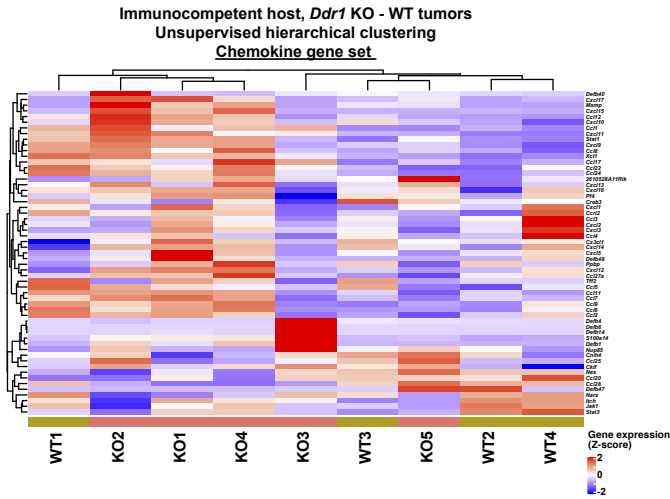
β -ACTIN

Supplementary Figure 3. Representative gating strategies for flow cytometry analysis of TILs used in this study.

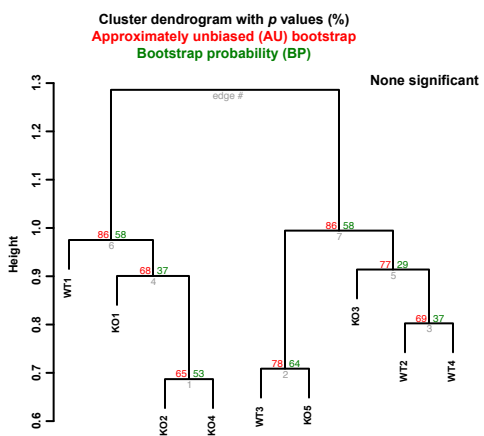
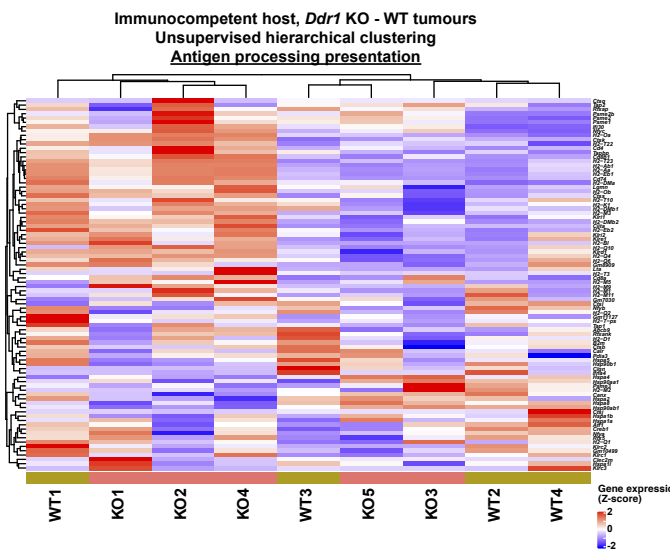


Supplementary Figure 4. Immune-related transcriptomic changes

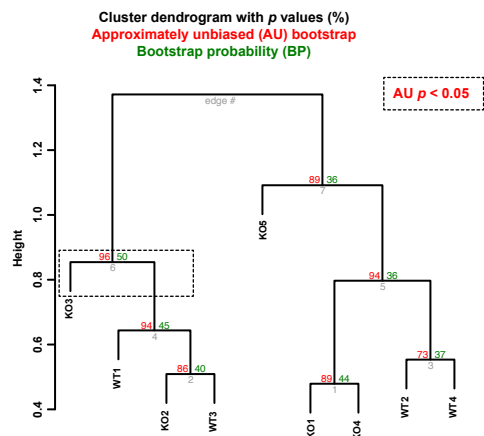
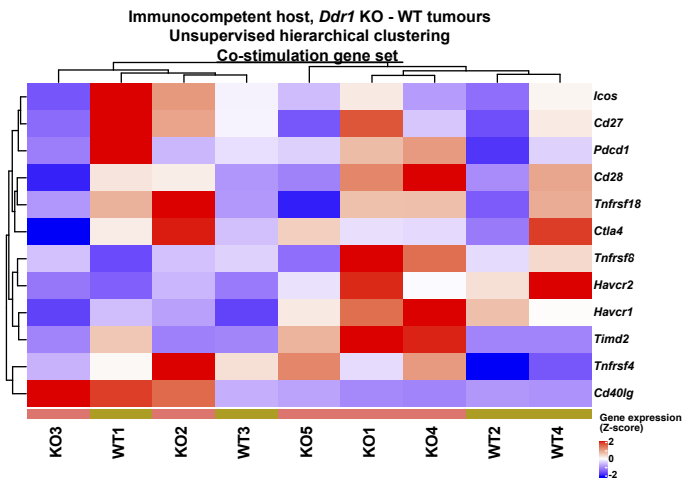
a



b



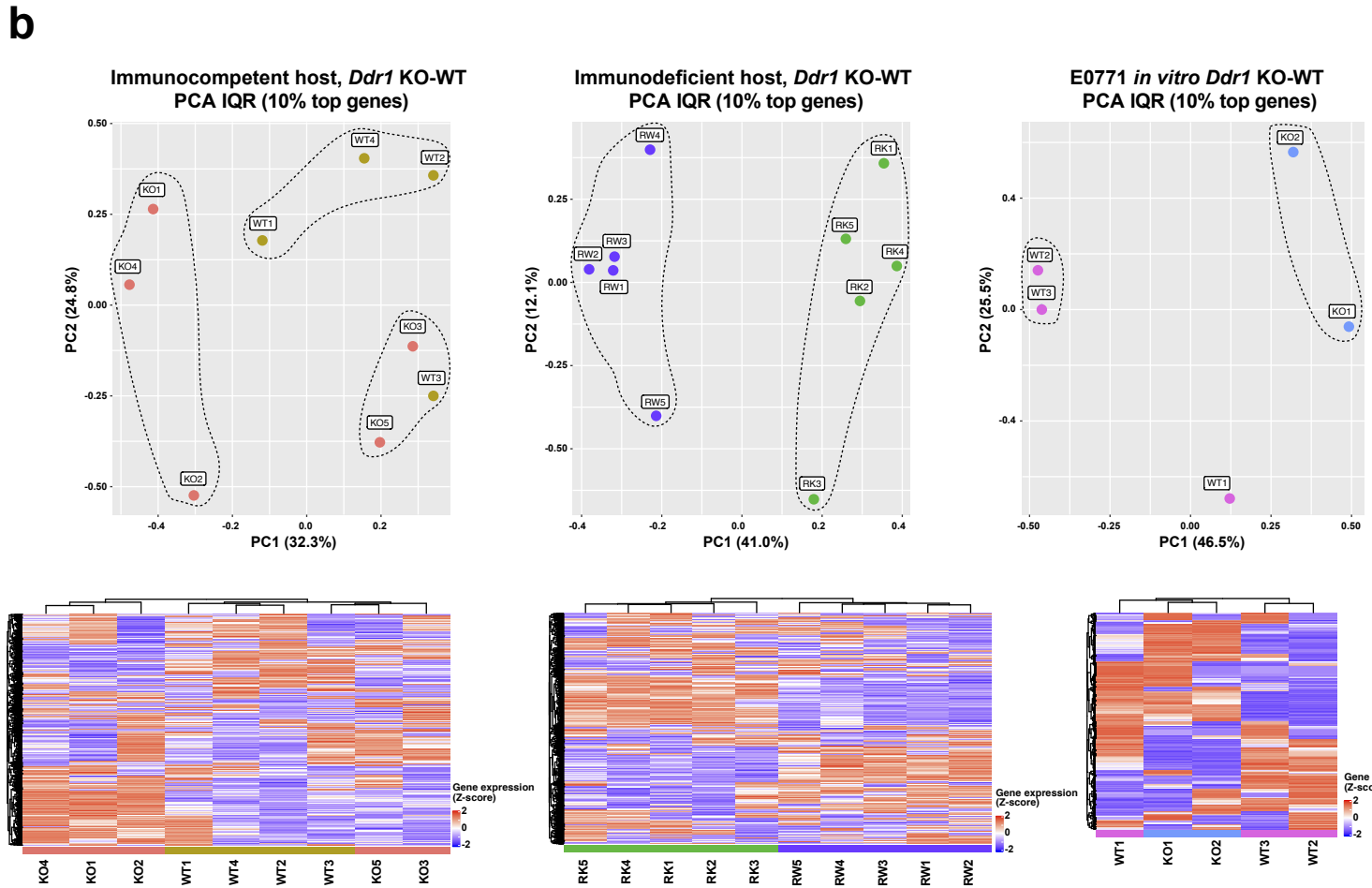
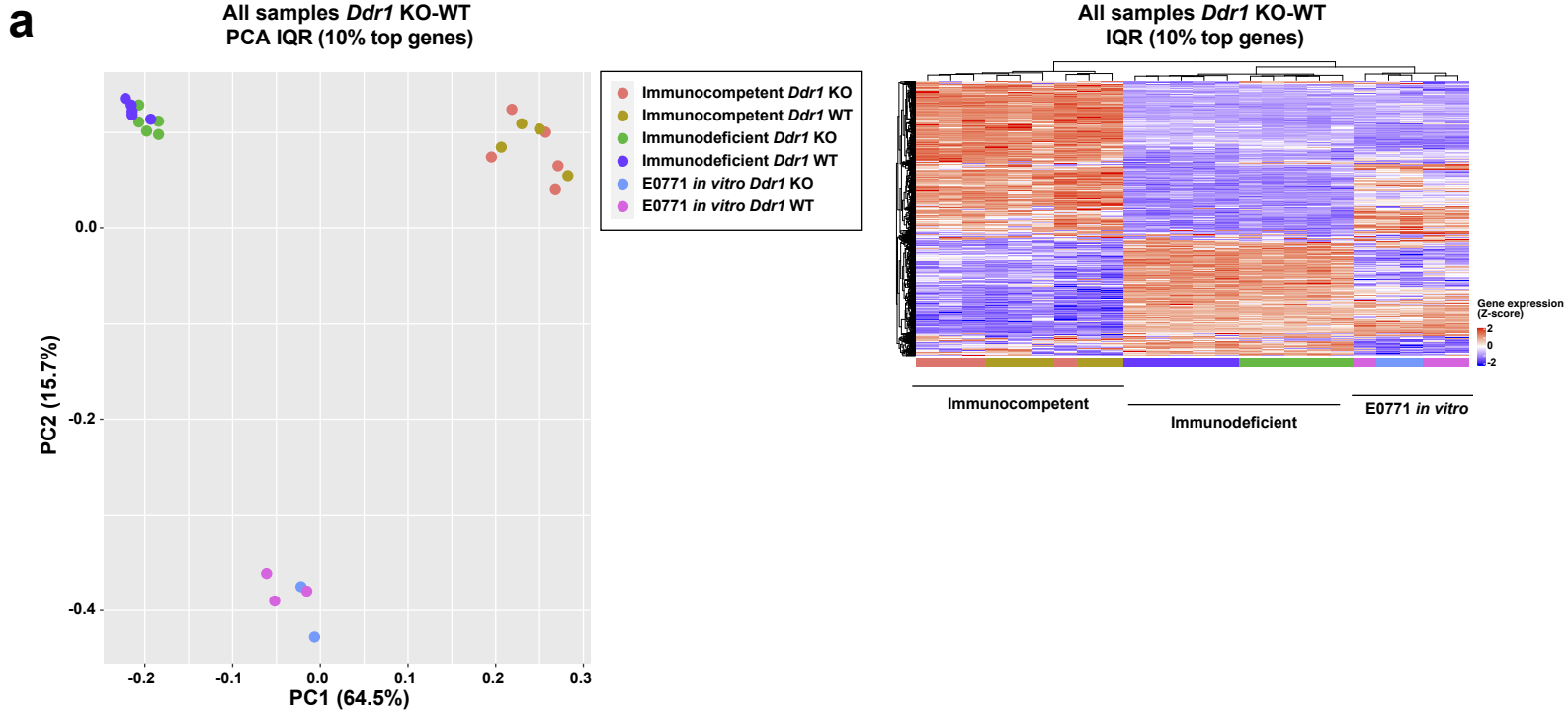
c



Supplementary Figure 4. Immune-related transcriptomic changes.

(a-c) Left panels, unsupervised hierarchical clustering of the expression of immune-related gene sets in *Ddr1*-WT and KO tumours from immunocompetent hosts: chemokine genes (a); genes involved in antigen processing/presentation (b); and co-stimulation genes (c). Right panels, hierarchical clustering performed for the gene sets using the R package Pvcust. Values at branches are approximately unbiased (AU) p values (left, red font) and bootstrap probability (BP) values (right, green font). The clusters considered significant (AU $p < 0.05$) are marked by dashed rectangles.

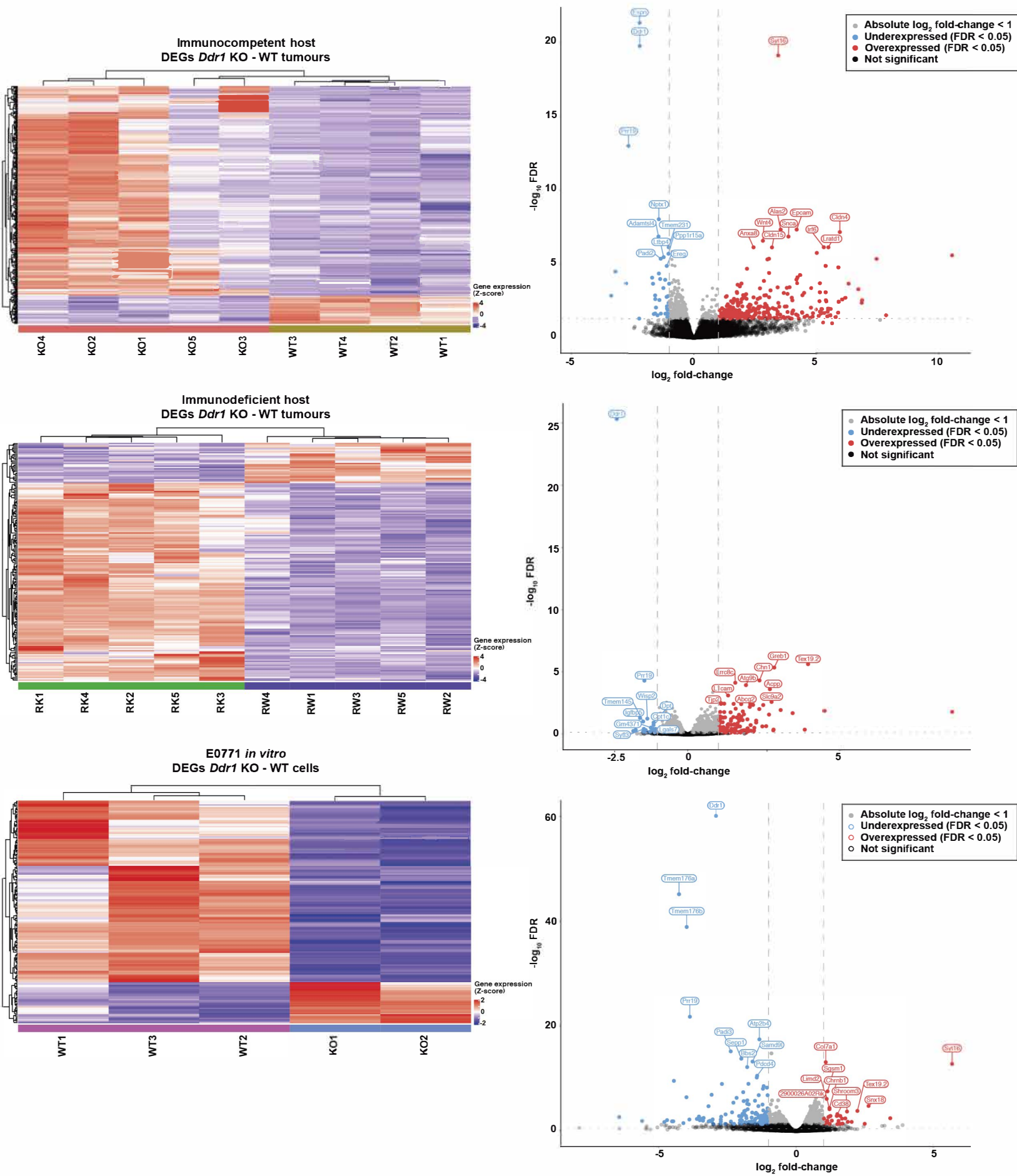
Supplementary Figure 5. PCA of transcriptome profiles across studies and samples



Supplementary Figure 5. PCA of transcriptome profiles across studies and samples. (a)

Left panel, PCA plot including all tumours/cells analysed by RNA-seq. Right panel, unsupervised hierarchical clustering of the genes with the highest (10% top) IQR. The gene list is provided in Extended Data Table 1. **(b)** Top panels, PCA plots of the tumours/cells analysed by RNA-seq in each setting. Bottom panels, unsupervised hierarchical clustering of the genes with the highest (10% top) IQR in each setting. The gene lists are provided in Supplementary Table 1.

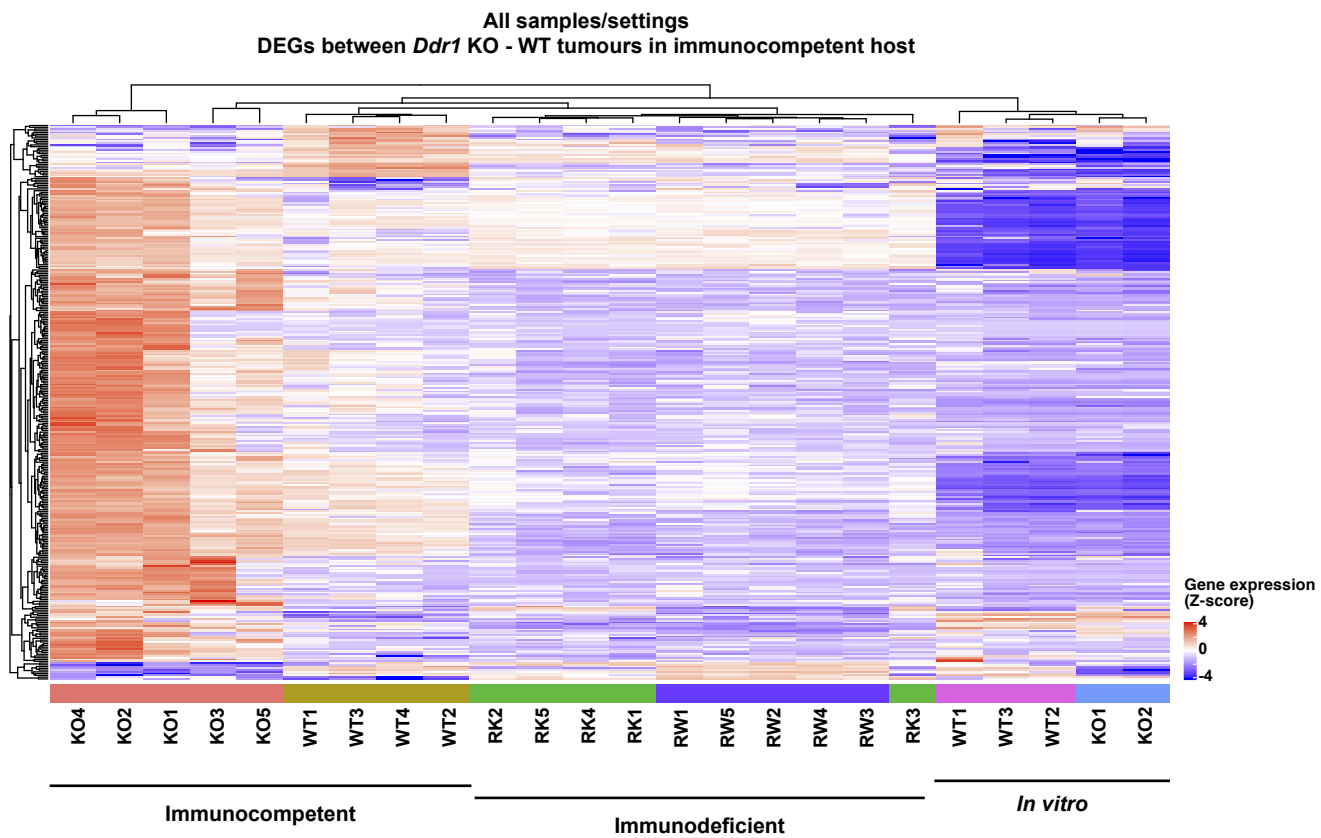
Supplementary Figure 6. DEGs between *Ddr1*-KO and WT tumours/cells



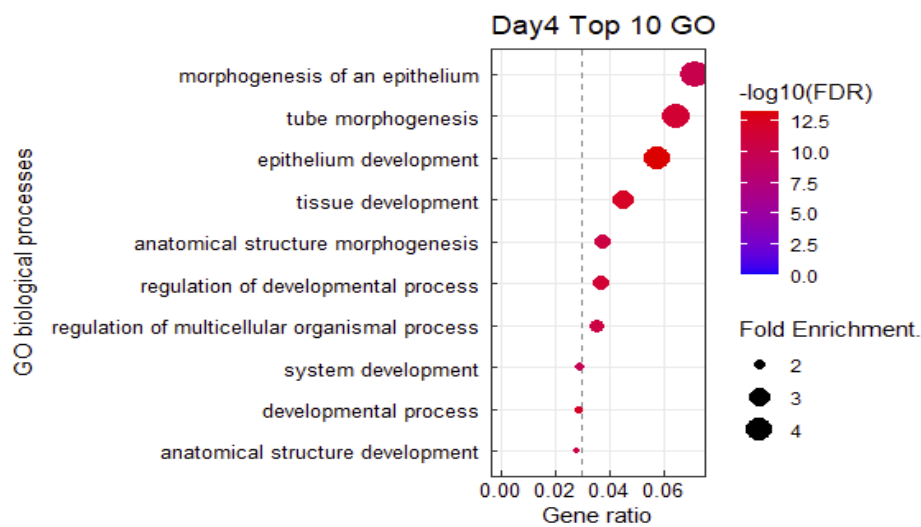
Supplementary Figure 6. DEGs between *Ddr1*-KO and WT tumours/cells. Left panels, unsupervised hierarchical clustering of DEGs (FDR-adjusted $p < 0.05$) in each setting (top, immunocompetent host; middle, immunodeficient host; bottom, E0771 cells *in vitro*). Right panels, Volcano plots of differential gene expression between *Ddr1*-KO and WT tumours/cells. Genes are plotted in different colours depending on their significance and absolute \log_2 fold-change (inset). The names of the 10-top differentially expressed genes in each direction and setting are indicated. The complete lists of DEGs are provided in Supplementary Table 2.

Supplementary Figure 7. Profiles of DEGs from immunocompetent host tumours and GO annotations

a



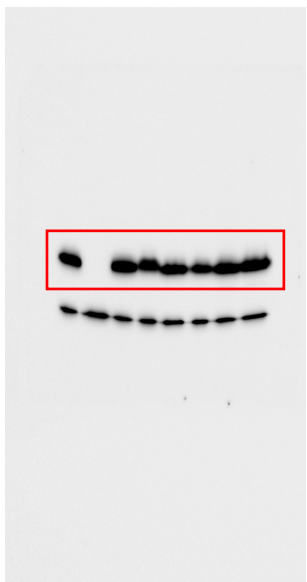
b



Supplementary Figure 7. Profiles of DEGs from immunocompetent host tumours and GO annotations. (a) Unsupervised hierarchical clustering of all settings/samples using DEGs identified in the comparison between *Ddr1*-KO and WT tumours developed in immunocompetent host. (b) GO analysis of immunocompetent host-unique DEGs.

Supplementary Figure 8. Gel source data for Extended Data Figure 5c

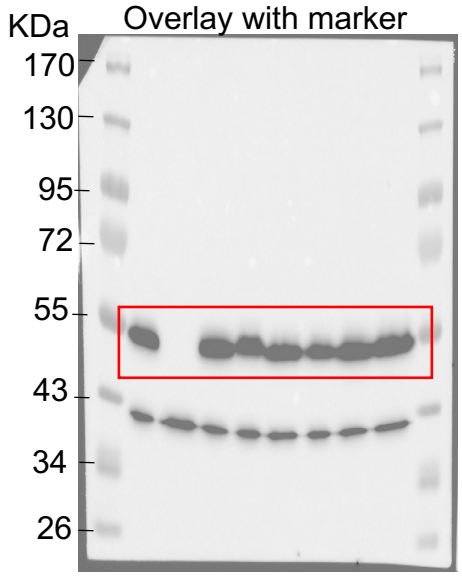
M-Wnt



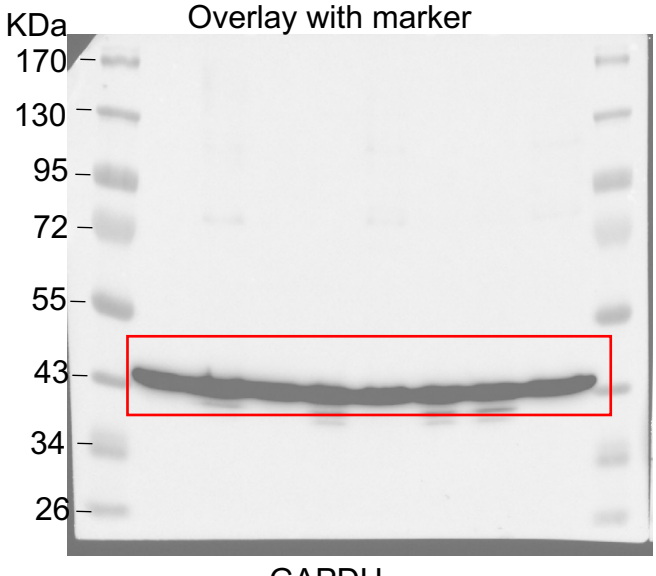
Flag



GAPDH



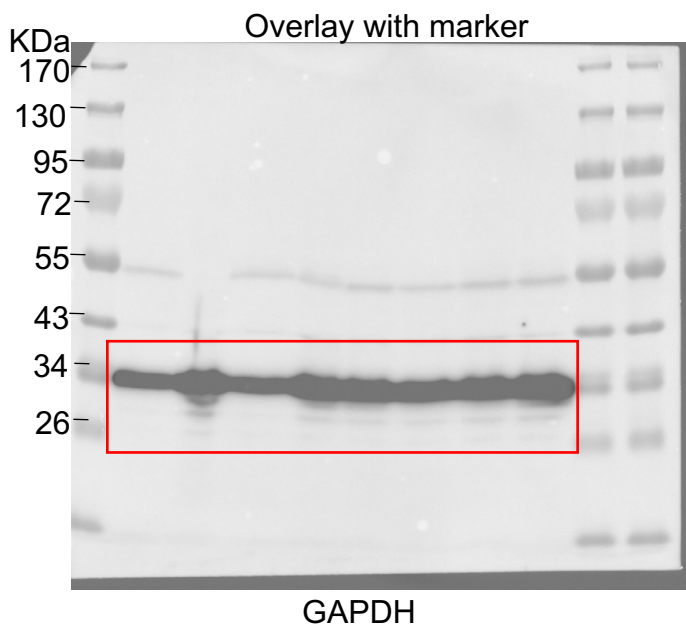
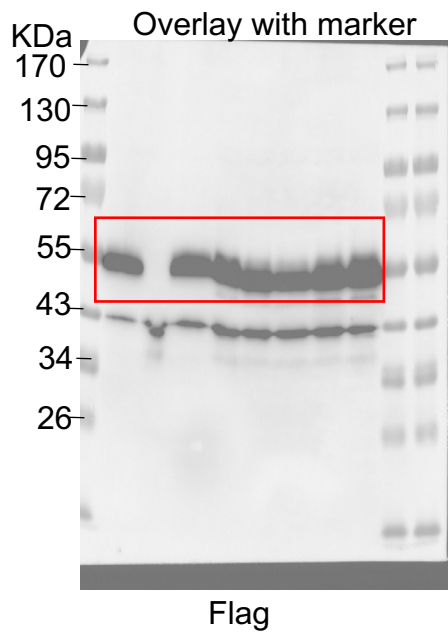
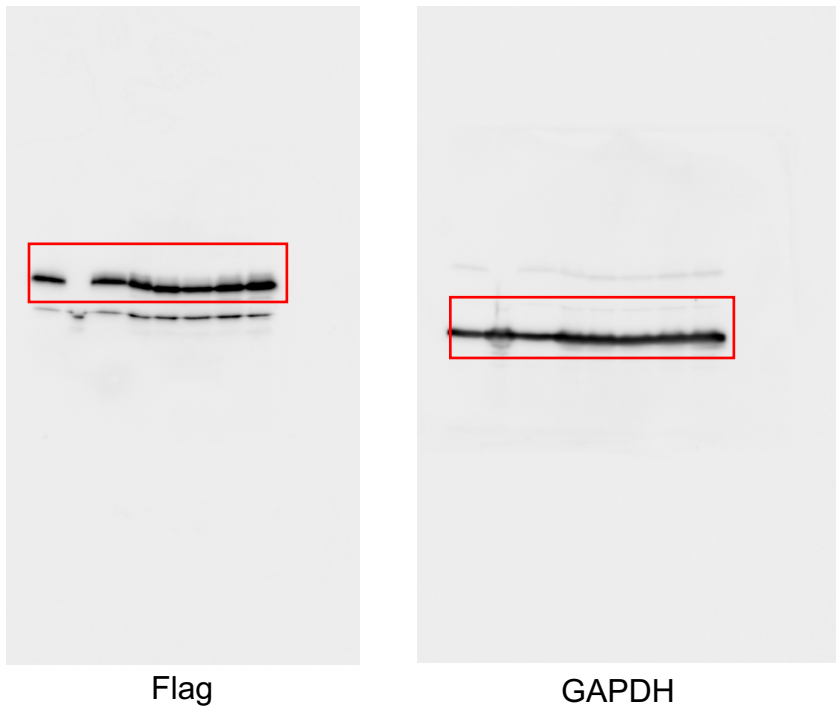
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GAPDH

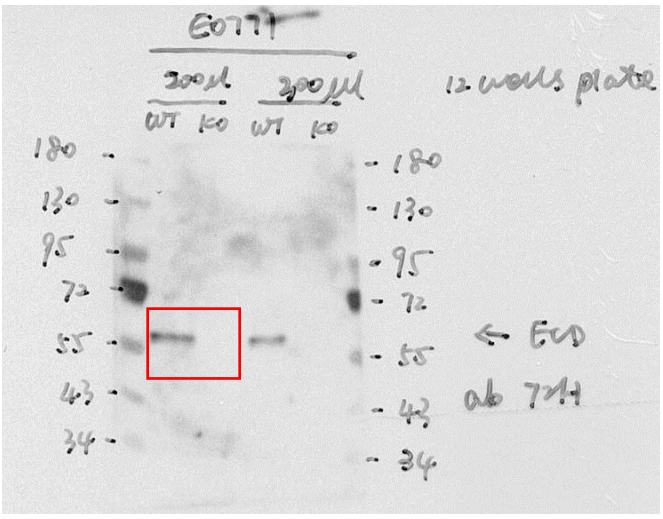
Supplementary Figure 9. Gel source data for Extended Data Figure 5d

AT-3

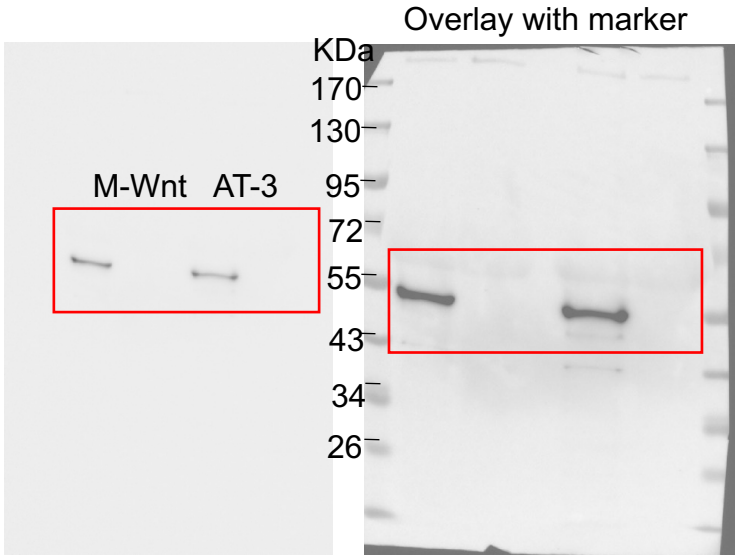


Supplementary Figure 10. Gel source data for Extended Data Figure 5g

Conditioned Medium:

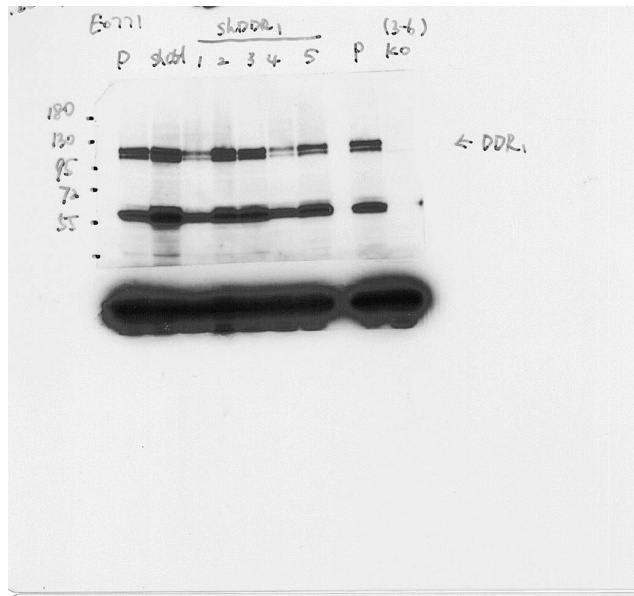


DDR1 ECD

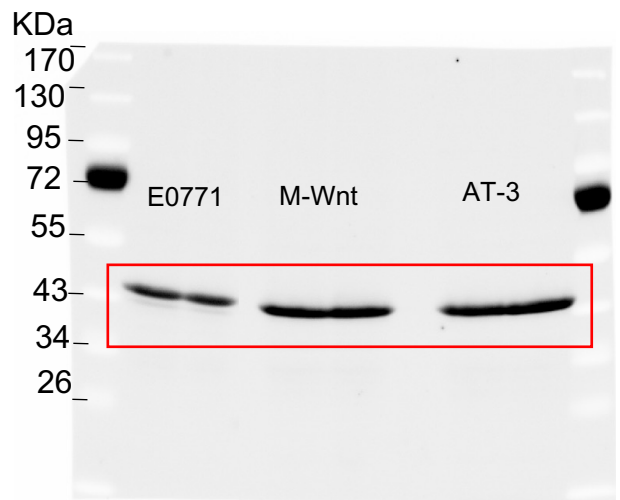
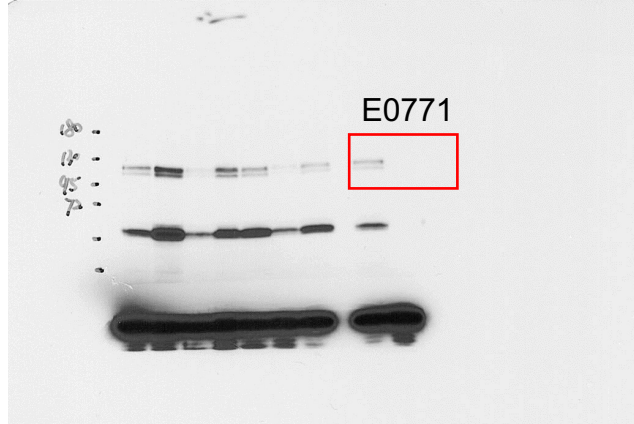
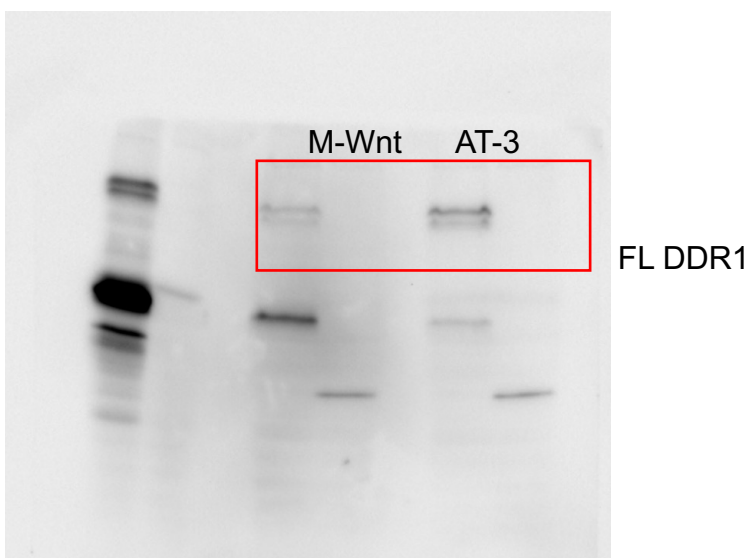


DDR1 ECD

DDR1 ECD



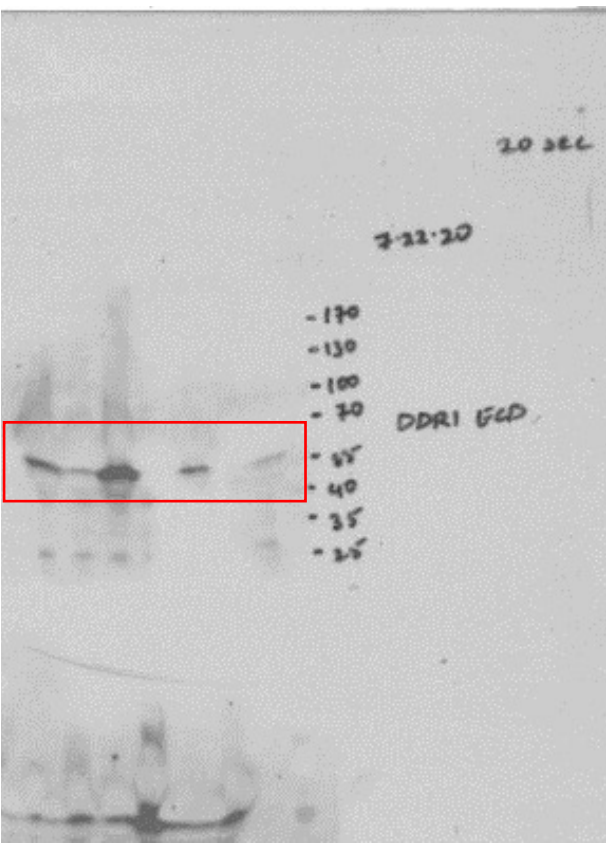
FL DDR1



beta-ACTIN

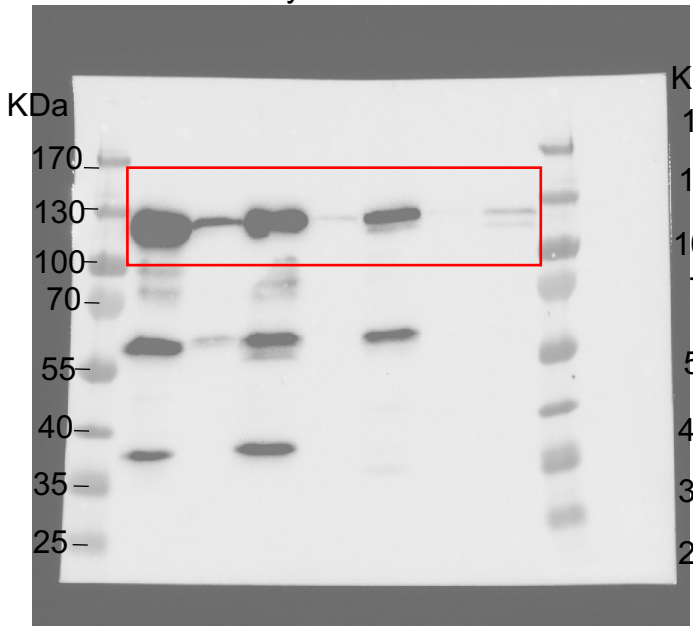
Supplementary Figure 11. Gel source data for Extended Data Figure 5h

Conditioned Medium



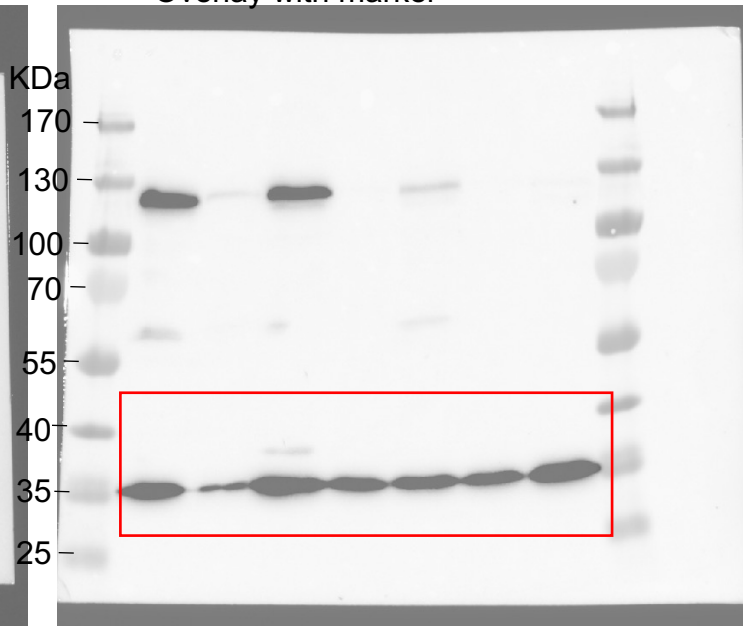
DDR1 ECD

Overlay with marker

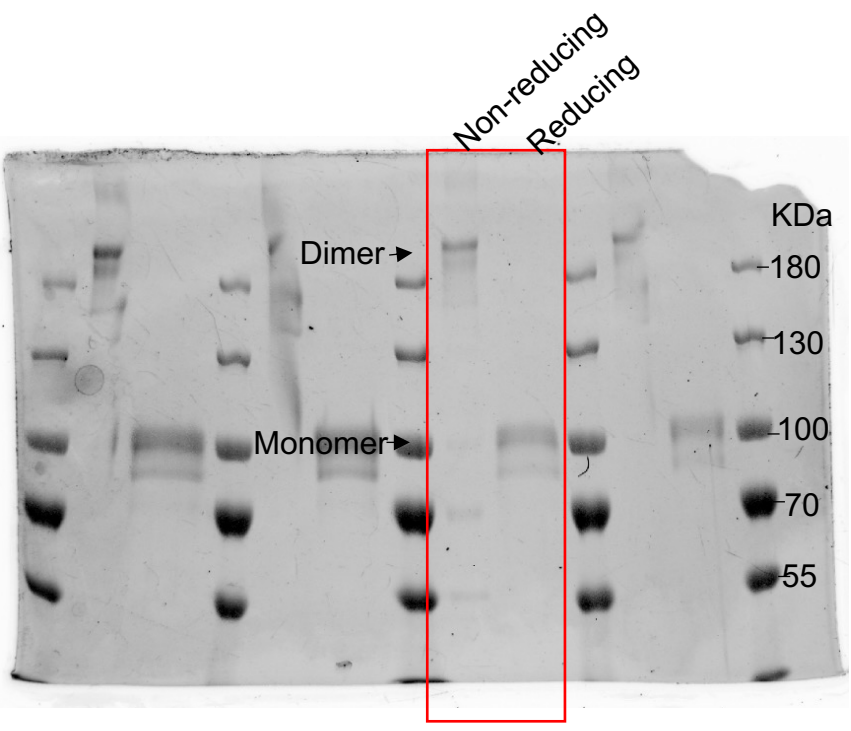


FL DDR1

Overlay with marker

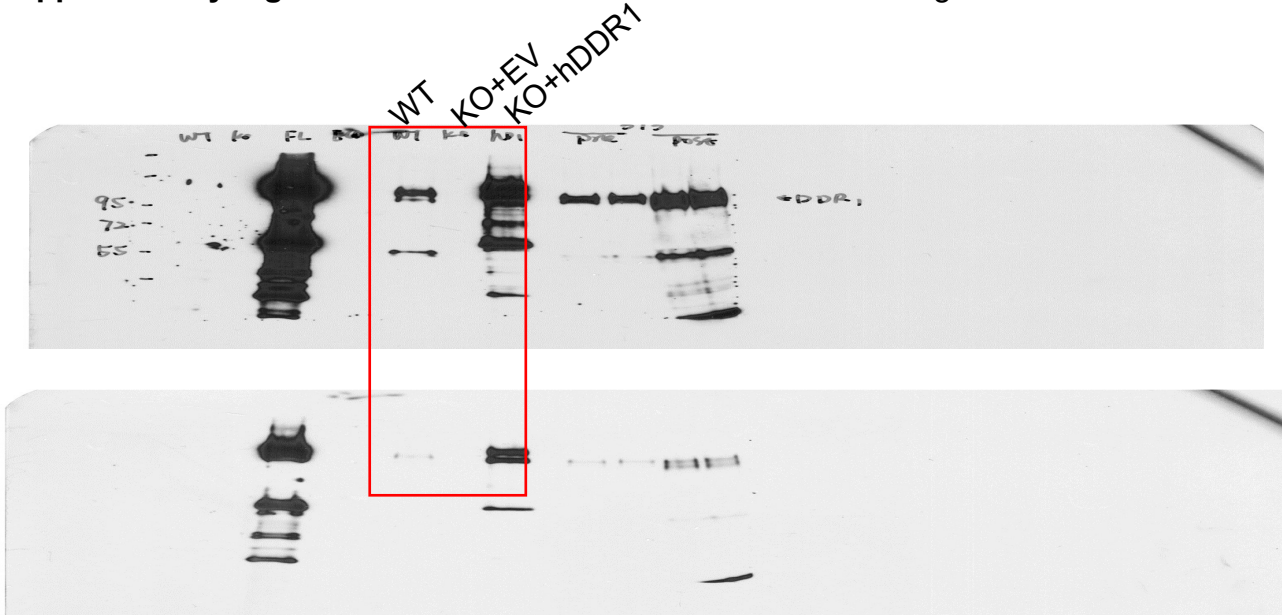


GAPDH (probed after stripping)

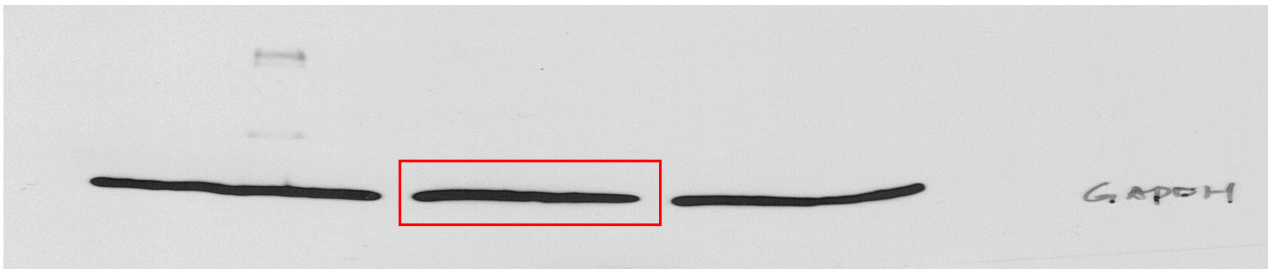


Coomassie Gel Staining

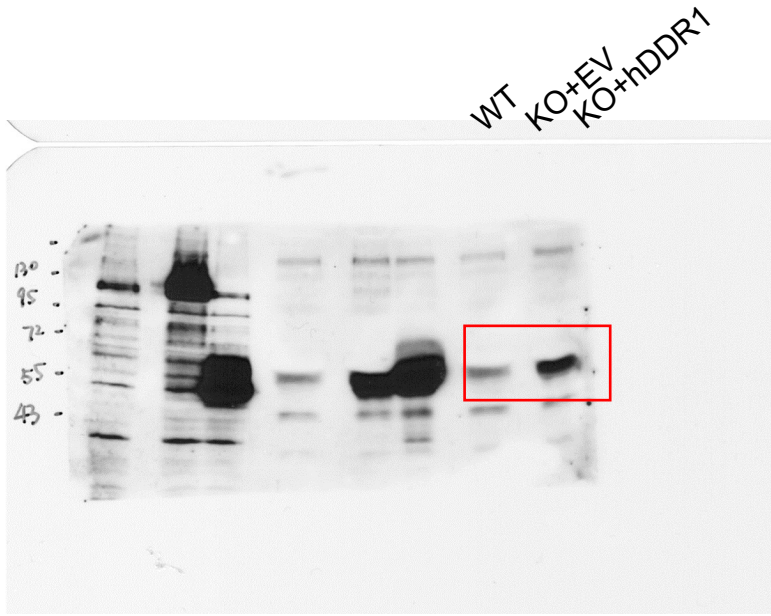
Supplementary Figure 13. Gel source data for Extended Data Figure 7a



FL DDR1



GAPDH



DDR1 ECD

Supplementary Figure 14. GO analysis of DEGs from RNA-seq of E0771 KO+huDDR1 tumours, treated with control IgG and anti-DDR1 antibody (#9) (n=4 each group; harvested on day 6 after antibody administration).

