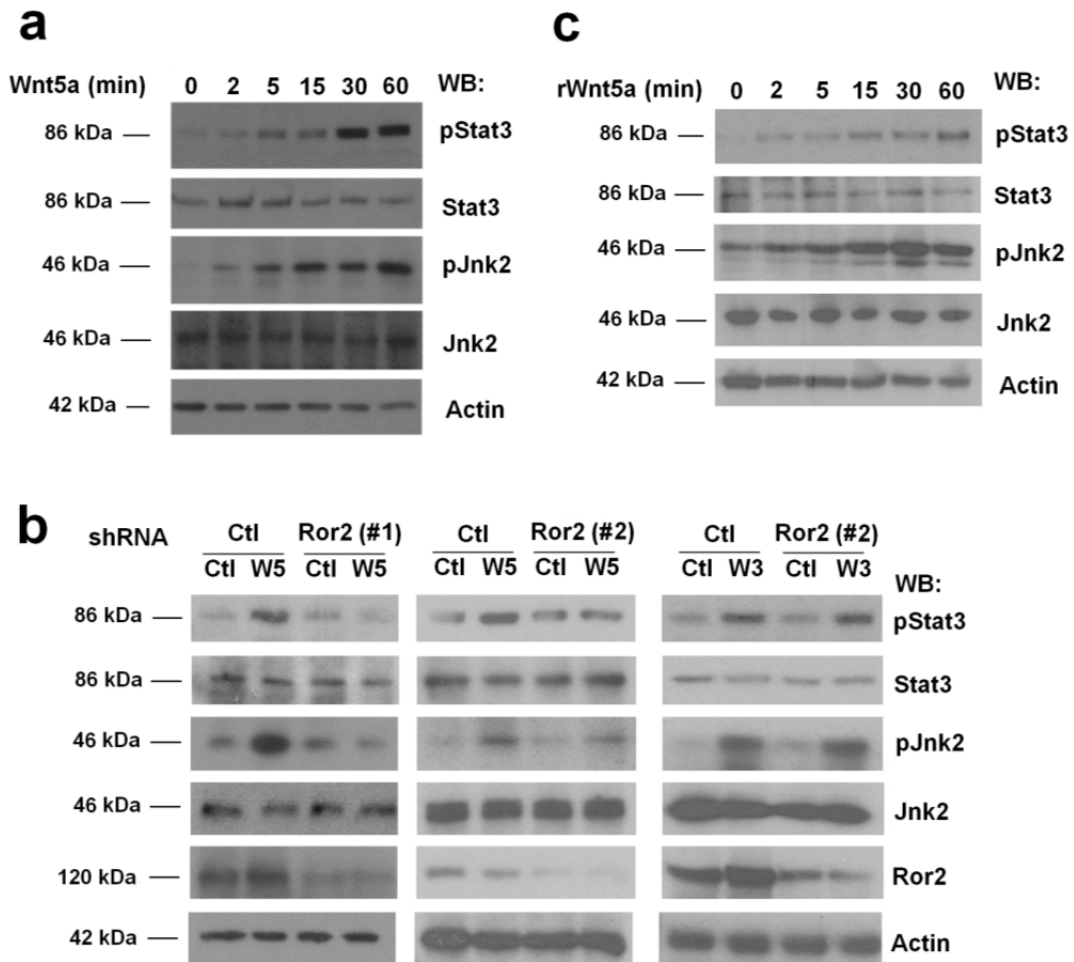


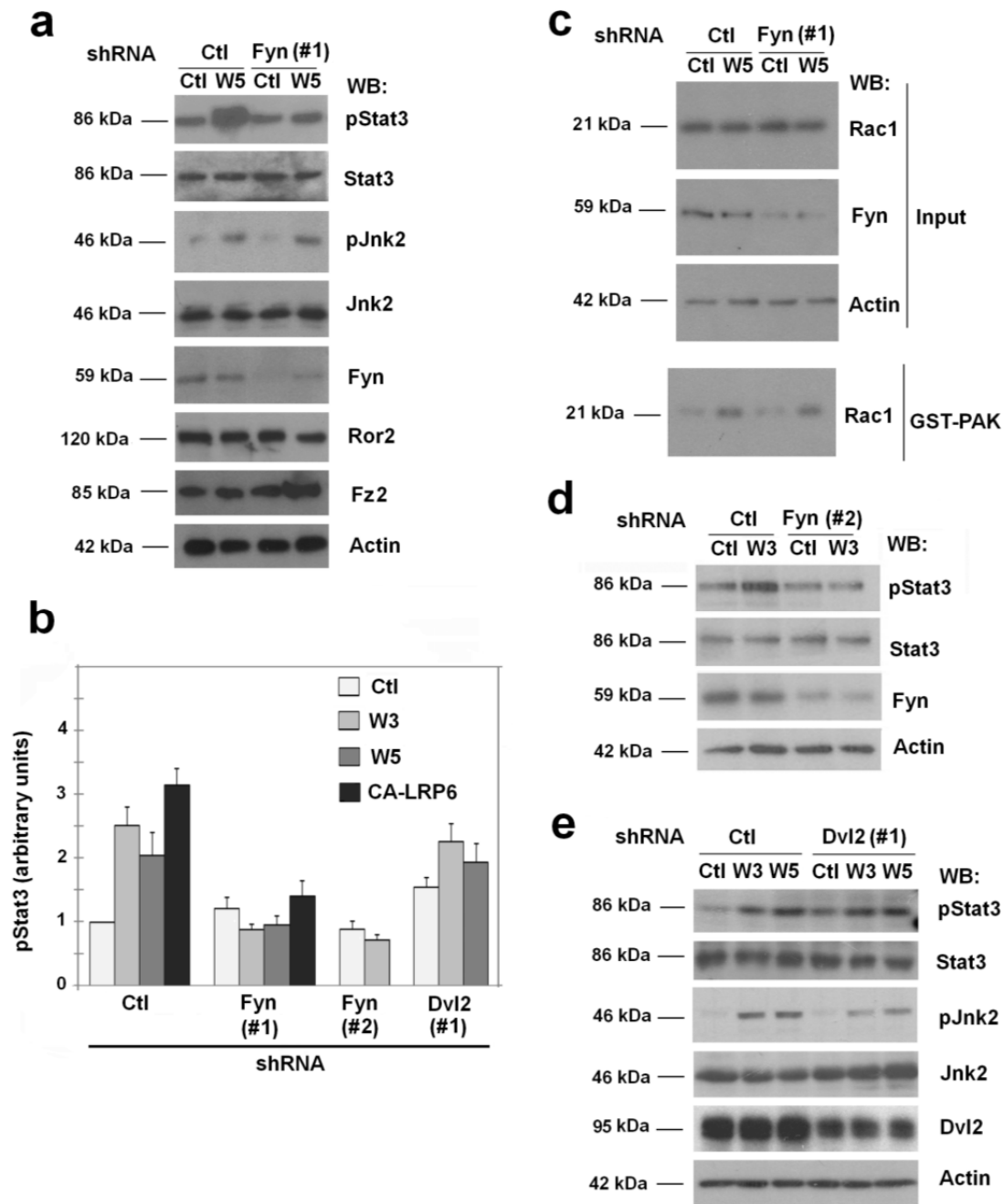
Supplementary Information to

Src and Fyn define a new signaling cascade activated by canonical and non-canonical Wnt ligands and required for gene transcription and cell invasion

Aida Villarroel, Beatriz del Valle-Pérez, Guillem Fuertes, Josué Curto, Neus Ontiveros, Antonio García de Herreros, and Mireia Duñach

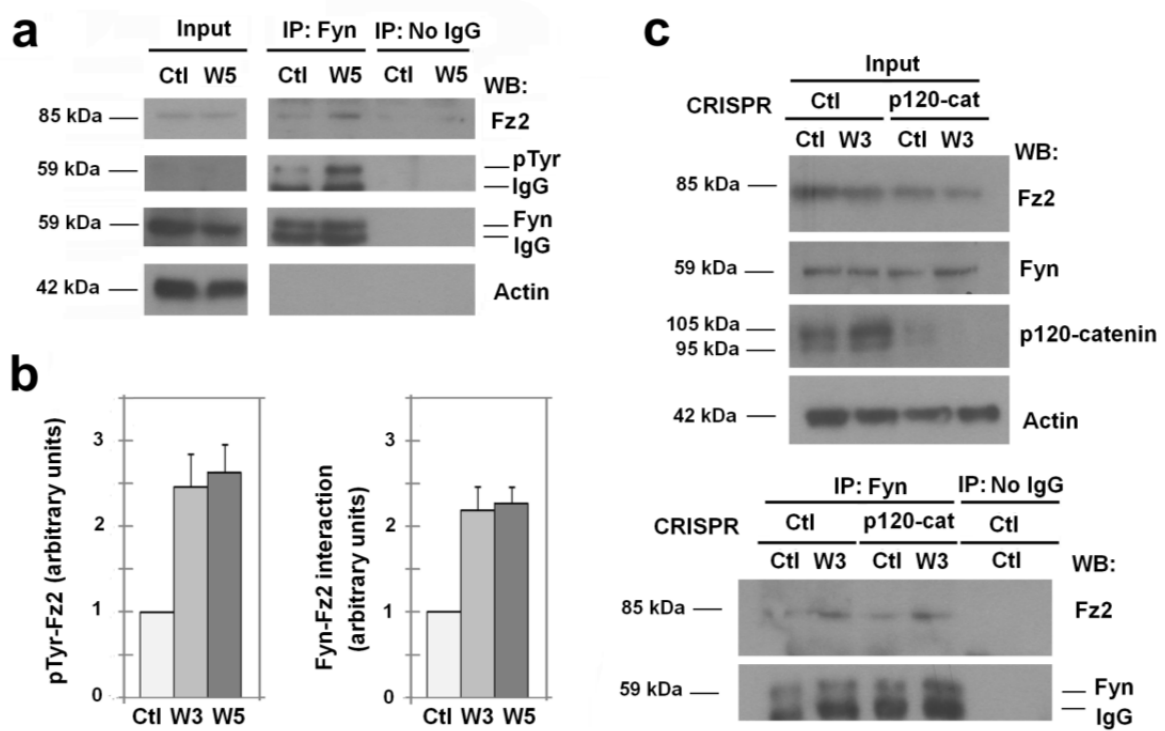


Suppl. Fig. 1. Wnt3a and Wnt5a stimulate Stat3 phosphorylation. (a) HEK293T cells were stimulated with control or Wnt5a-conditioned medium for the indicated times. Cells were lysed and proteins were analyzed by WB with specific antibodies. Jnk2 and Stat3 phosphorylation was determined with anti-phospho antibodies against Jnk (Thr183/Tyr185, Thr221/Tyr223) or Stat3 (Tyr705). (b) HEK293T cells, depleted of Ror2 with two specific shRNA or transfected with the corresponding control shRNA, were stimulated for 30 minutes with control, Wnt3a- or Wnt5a-conditioned medium as indicated. Cells were lysed and Jnk2 and Stat3 phosphorylation was determined as above. (c) Cells were incubated for the indicated times with recombinant Wnt5a (50 ng/ml) and cell extracts analyzed by WB.

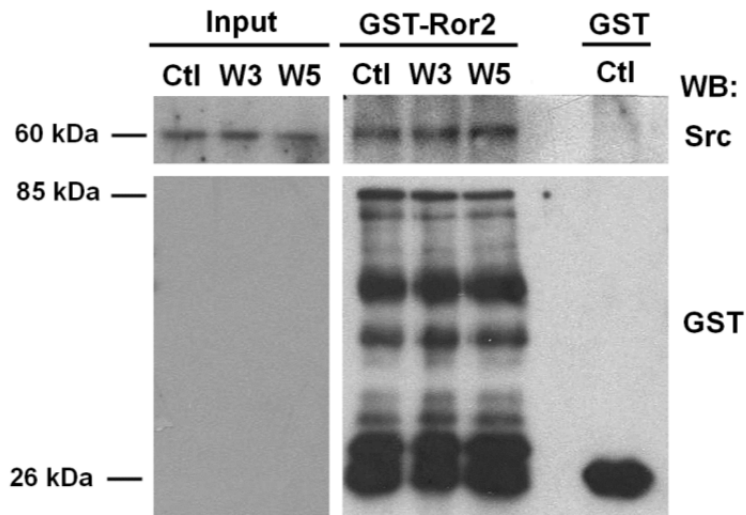


Suppl. Fig. 2. Fyn is required for Wnt3a and Wnt5a-induced Stat3 phosphorylation. (a-d) HEK293T cells depleted of Fyn using two specific shRNAs or a non-targeting control were treated for 30 min with control, Wnt3a- or Wnt5a-conditioned medium, as indicated. Cells were lysed and Stat3 and Jnk2 phosphorylation was analyzed by WB with specific antibodies; a GST-PAK pull-down assay was performed in c and active Rac1 was determined by WB. In b a quantification of three independent experiments carried out as in a, d, e and Figures 2a

and b is represented. Mean \pm SD is shown. (e) HEK293T cells were down-regulated of Dvl2 using shRNA #1 or a control shRNA and stimulated with control, Wnt3a- or Wnt5a- conditioned medium for 30 min. Cells were lysed and Stat3 phosphorylation was analyzed by WB.

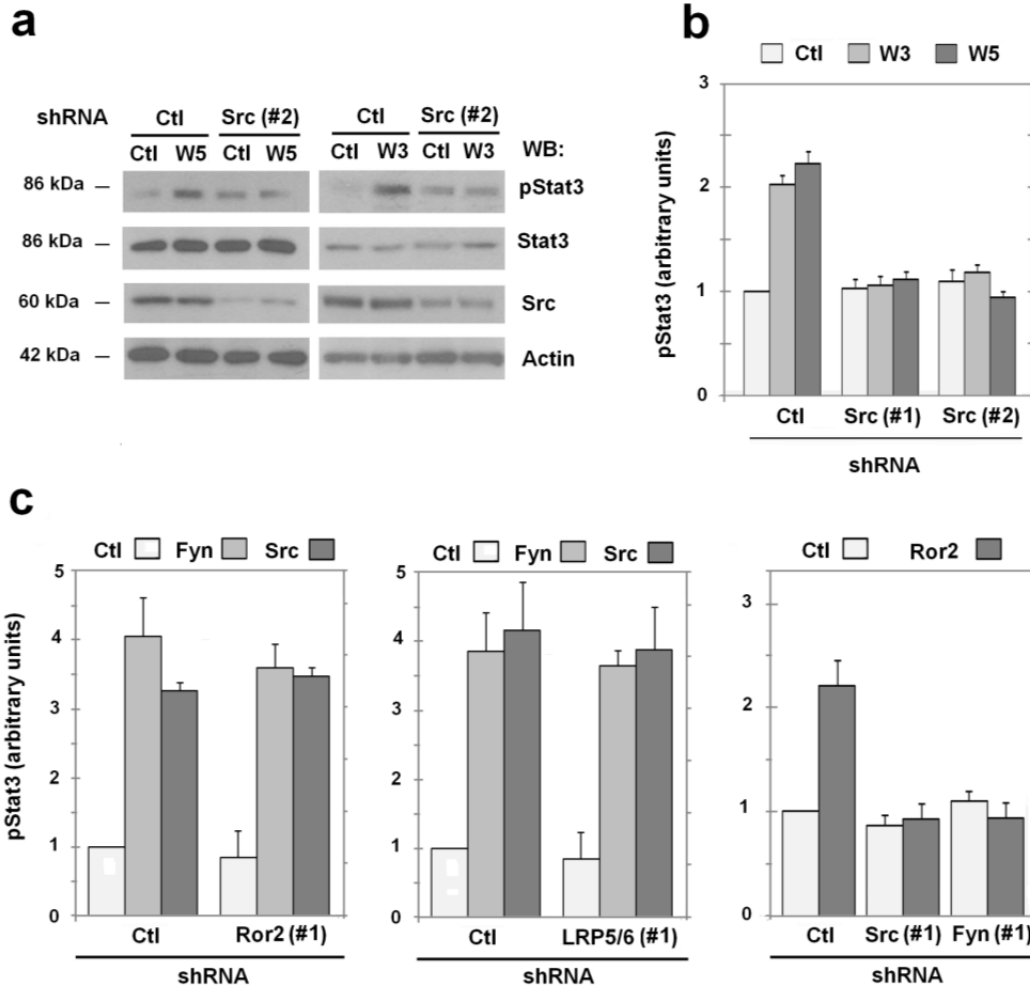


Suppl. Fig. 3. Canonical and non-canonical Wnt promote Fyn phosphorylation and binding to Fz2. HEK293T cells, either control (**a**) or CRISPR-deleted in p120-catenin (**c**) were treated with Wnt3a- or Wnt5a-conditioned-medium for 30 minutes. Fyn was immunoprecipitated from total cell extracts and Fyn phosphorylation and association with Fz2 was determined by WB. In (**b**) signals from the different experiments as in panels **a** and **c** and Figures 2e and f were densitometered and represented. The mean \pm SD of three different experiments is shown.



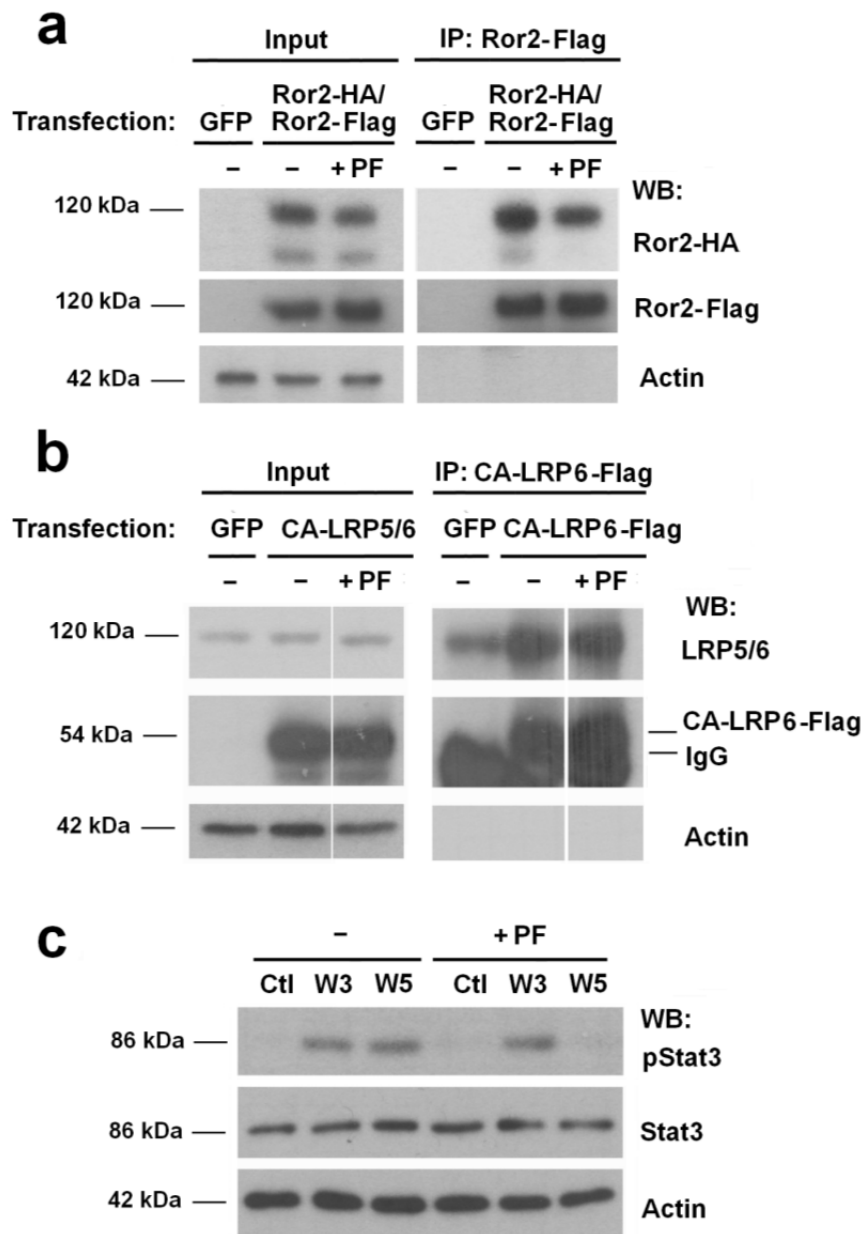
Suppl. Fig. 4. Src directly binds to Ror2 and Wnt does not affect this interaction.

A pull-down assay was performed incubating 700 µg of total cell extracts with 10 pmol of GST-cytoRor2 or GST. Protein complexes were affinity purified and analyzed by WB.

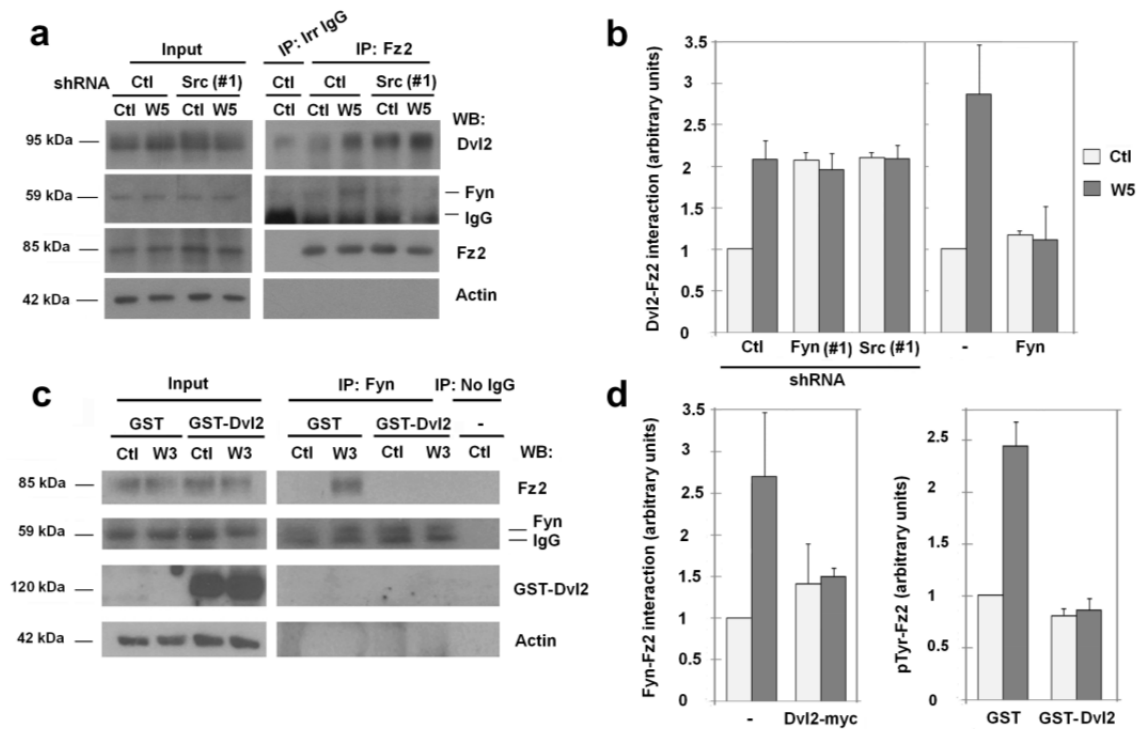


Suppl. Fig. 5. Src is required for Wnt3a or Wnt5a-induced Stat3 phosphorylation.

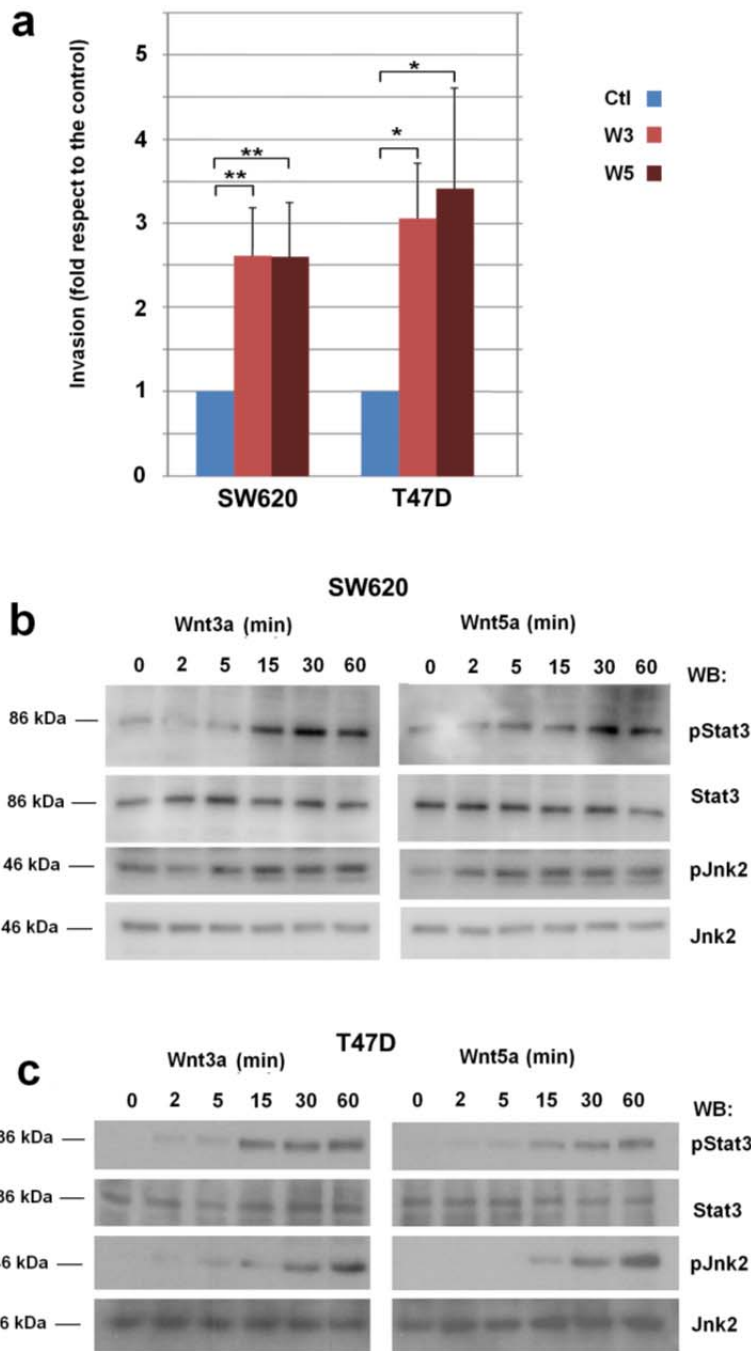
(a) HEK293T cells depleted of Src with shRNA #2 or a non-targeting control were treated with control, Wnt3a- or Wnt5a-conditioned medium for 30 min, lysed and Stat3 phosphorylation was analyzed by WB. (b) Signal was densitometered and represented. The quantification of three different experiments, as well as those corresponding to Figures 3f and g, is shown (mean \pm SD). In (c) the quantification of the different experiments performed as in Figures 4a-c is shown (mean \pm SD). The ectopically expressed proteins are presented above the graphs.



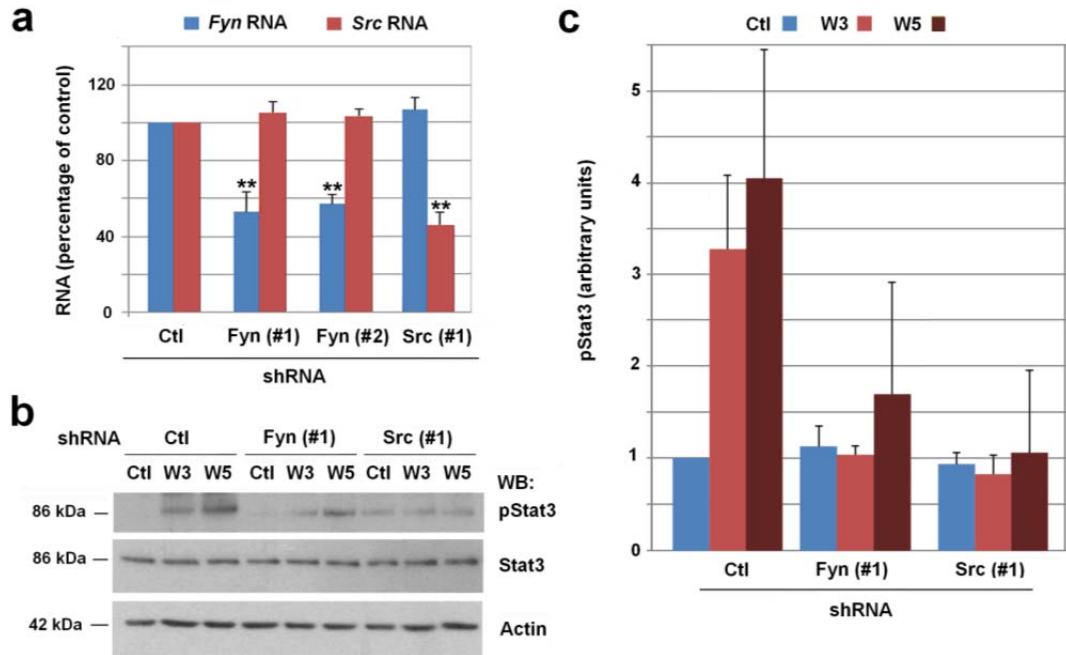
Suppl. Fig. 6. CK1 ϵ activity is required for Ror2 dimerization and Stat3 phosphorylation induced by Wnt5a. (a) Ror2-HA, Ror2-Flag or empty vector were overexpressed in HEK293T cells. After 48 hours, cells were treated with PF5006739 (PF) (50 nM) for 1 h. Ror2-flag was immunoprecipitated and association with Ror2-HA was analyzed by WB with anti HA antibody. (b) HEK293T cells overexpressing CA-LRP6-Flag or empty vector were treated with PF for 1 h. CA-LRP6-Flag was immunoprecipitated from total extracts with anti-Flag antibody and associated LRP5/6 was determined by WB. (c) HEK293T cells were treated with PF for 1 h, total cell extracts were prepared and Stat3 phosphorylation was analyzed by WB.



Suppl. Fig. 7. The two Wnt-induced signaling pathways involving Fz2 interaction with Fyn or Dvl2 are mutually excluding. (a) HEK293T cells transfected with a shRNA control or shRNA Src were stimulated with control or Wnt5a-conditioned medium for 30 min. Fz2 was immunoprecipitated from total cell extracts and associated proteins were analyzed by WB. The extent of Src down-regulation is presented in Fig. 3f. (b) Quantification of the different experiments of Dvl2-Fz2 association performed as in panel a or as in Figures 5a and b. The mean \pm SD is shown. (c) HEK293T cells overexpressing GST-Dvl2 or a control vector were treated with control or Wnt3a-conditioned medium for 30 min. Fyn was immunoprecipitated from total cell extracts and associated Fz2 was analyzed by WB. (d) Quantification of the different experiments of Fyn-Fz2 association and Fz2 tyrosine phosphorylation performed as in panel c or as in Figures 5c and d. The mean \pm SD is shown.



Suppl. Fig. 8. Wnt3a and Wnt5a also increase cellular invasion and Stat3 phosphorylation in SW620 and T47D tumor cell lines. Colon SW620 (**a, b**) and breast T47D (**a, c**) tumor cell lines were treated with Wnt3a or Wnt5a-conditioned medium for 24 h (**a**) or the indicated times (**b, c**); collagen 1 invasion (**a**) or Stat3 phosphorylation (**b, c**) were assessed as described. In **a**, the mean \pm SD is shown. **, $p < 0.01$; *, $p < 0.05$.



Suppl. Fig. 9 Fyn and Src are required for Stat3 phosphorylation by Wnt3a or Wnt5a in MSC. (a) RNA was isolated from control, Src-, or Fyn-depleted MSC. Expression of *Fyn* (blue bars) and *Src* (red bars) RNA was assessed by quantitative RT-PCR. Results are presented as mean \pm SD from three independent experiments. **, $p < 0.01$. (b) MSC, control, Src-, or Fyn-depleted MSC, were treated with control, Wnt3a- or Wnt5a-conditioned medium for 30 min, lysed and Stat3 phosphorylation was analyzed by WB. (c) A quantification of the three independent Stat3 phosphorylation analysis performed in **b** is represented (mean \pm SD).

Gene	Primer Sequence (5'-3')
<i>AXIN2 (Homo sapiens)</i>	FW: TGTCTTAAAGGTCTTGAGGGTTGAC RV: CAACAGATCATCCCATCCAACA
<i>SIAH2 (Homo sapiens)</i>	FW: TTTGCCATCGTCCTGCTCAT RV: GGCTGTGTCGAAAACAAG
<i>CCND1 (Homo sapiens)</i>	FW: CTCAGACTTGCGCGTCACAG RV: CAGAACACGGCTCACGCTTA
<i>MMP7 (Homo sapiens)</i>	FW: TGTGGGGCAAAGAGATCCCC RV: CCTCGCGCAAAGCCAATC
<i>THBS1 (Homo sapiens)</i>	FW: GAGCTGGCCTGCGAGTTC RV: TGTGTGTACCGGAGCGC
<i>MMP9 (Homo sapiens)</i>	FW: TTCAGGGAGACGCCCATTTTC RV: TGGGTGTAGAGTCTCTCGCT
<i>MMP13 (Homo sapiens)</i>	FW: AAGGACCCTGGAGCACTCAT RV: CCTGGACCATAGAGAGACTGGA
<i>SNAI1 (Homo sapiens)</i>	FW: GTGCCTCGACCACTATGCC RV: GCTGCTGGAAGGTAAACTCTGG
<i>TCF7 (Homo sapiens)</i>	FW: ACCAAGAATCCACCACAGAGAC RV: TCACATCTGCACCAAGGCAA
<i>PUM1 (Homo sapiens)</i>	FW: GACCAGCAGAATGAGATGGTTC RV: CATAAGGATGTGTGGATAAGGCA
<i>Fyn (Mus musculus)</i>	FW: GGAAAAAGGATCCGGAAGAG RV: GCAGGCTCTCACAGGTTTTTC
<i>Src (Mus musculus)</i>	FW: GCTGTATGCTGGTGTCCG RV: CAGTGGGGTAGCCGCAAATA
<i>Pum1 (Mus musculus)</i>	FW: CAGGTAATTAACGAGATGGTGCG RV: ACGGGTGCGTAGACAAAGC

Table S1: Oligonucleotides used in the RT-PCR analysis.