

SUPPLEMENTARY INFORMATION

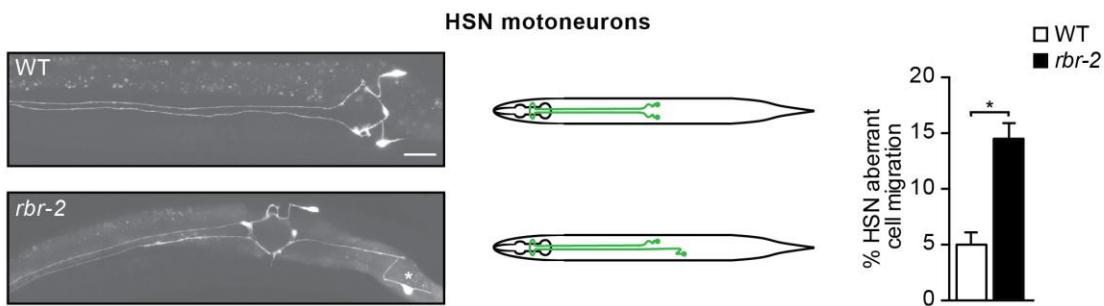
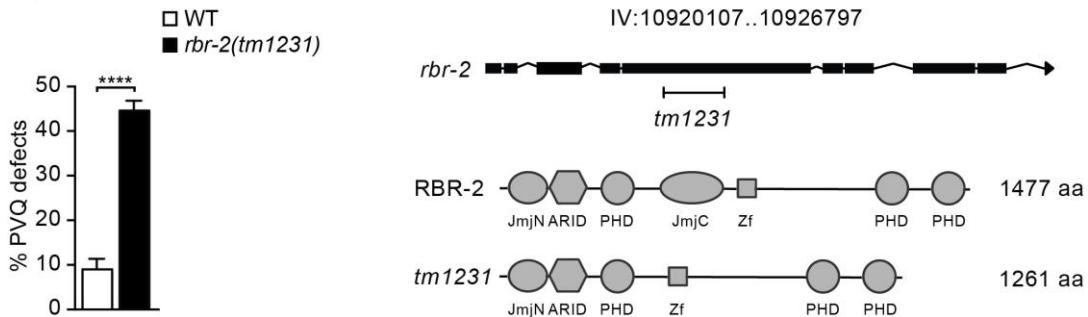
A**B**

Fig. S1. (A) Left: Representative images of HSN neurons in wild-type (WT) and *rbr-2(tm3141)* adult animals, visualized using the transgene *rpEx6*. Ventral views, anterior to the left. Scale bar, 20 μ m. Asterisk indicates aberrant position of the cell body. Center: Schematic diagrams of HSN neurons in wild-type and *rbr-2(tm3141)* mutant animals. Right: Quantification of HSN aberrant cell migration in *rbr-2(tm3141)* adult animals. $n>100$, *p<0.05 (Fisher's exact test). Error bars represent standard error of proportion. (B) Left: Quantification of PVQ axonal cross-over defects in *rbr-2(tm1231)* mutant animals. $n=100$, ****p<0.0001 (Fisher's exact test). Error bars represent standard error of proportion. Right, top: Genomic organization of *rbr-2*. Black H-shaped line indicates the position of the *tm1231* deletion. Right, bottom: RBR-2 and putative *tm1231* protein. JmjN, Jumonji N domain; ARID, AT-rich interacting domain; PHD, plant homeodomain zinc-finger domain; JmjC, Jumonji C domain; Zf, zinc-finger.

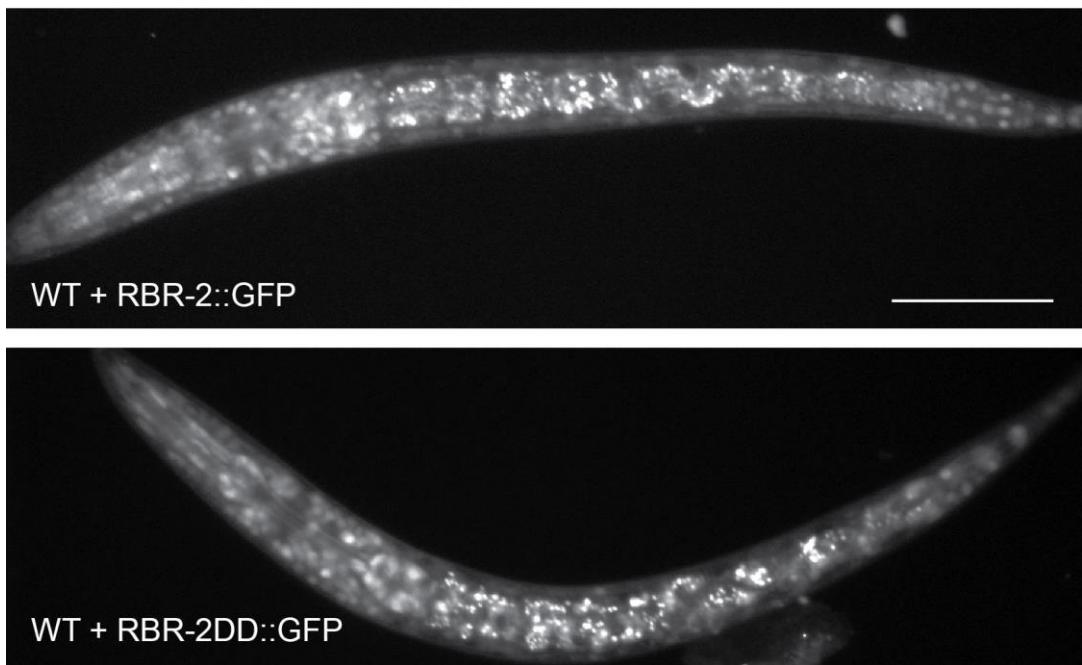


Fig. S2. Representative images of wild-type (WT) L1 animals expressing GFP-tagged RBR-2 or catalytically inactive RBR-2 (RBR-2DD). Ventral view, anterior to the left. Scale bar, 35 μ m.

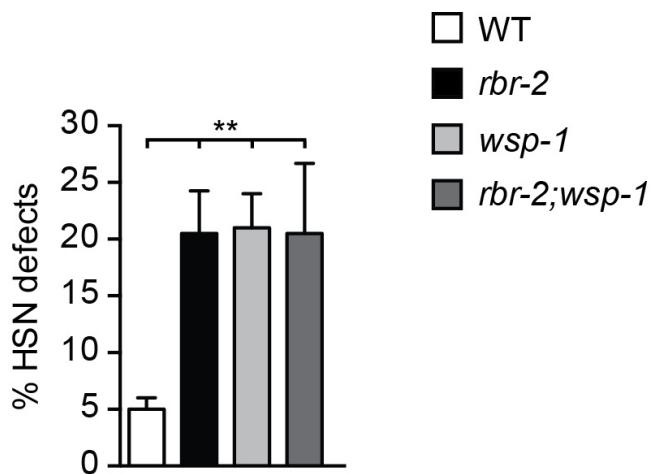


Fig. S3. Quantification of HSN axonal cross-over defects in *rbr-2(tm3141)*, *wsp-1(gm324)* and double mutant. $n>100$, ** $p<0.01$ (one-way ANOVA followed by Tukey's multiple-comparison test). Error bars represent standard error of proportion.

Table S1. *rbr-2* genetically interacts with the main pathways involved in axon guidance

Genotype	Defective animals (%)
WT	9 (n=162)
<i>rbr-2(tm3141)</i>	22 (n=296)
<i>unc-5(e53)</i>	25 (n=200)
<i>rbr-2(tm3141);unc-5(e53)</i>	33 (n=200) n.s.
<i>sax-3(ky123)</i>	52 (n=96)
<i>rbr-2(tm3141);sax-3(ky123)</i>	45 (n=112) n.s.
<i>slt-1(eh15)</i>	23 (n=150)
<i>rbr-2(tm3141);slt-1(eh15)</i>	27 (n=150) n.s.
<i>vab-1(dx31)</i>	27 (n=210)
<i>rbr-2(tm3141);vab-1(dx31)</i>	26 (n=218) n.s.
<i>vab-2(ju1)</i>	15 (n=100)
<i>rbr-2(tm3141);vab-2(ju1)</i>	19 (n=200) n.s.
<i>efn-3(ev696)</i>	34 (n=50)
<i>rbr-2(tm3141);efn-3(ev696)</i>	34 (n=200) n.s.
<i>vab-2(ju1);efn-3(ev696)</i>	32 (n=100)
<i>rbr-2(tm3141);vab-2(ju1);efn-3(ev696)</i>	39 (n=200) n.s.
<i>hse-5(tm472)</i>	45 (n=150)
<i>rbr-2(tm3141);hse-5(tm472)</i>	40 (n=150) n.s.
<i>sdn-1(zh20)</i>	47 (n=150)
<i>rbr-2(tm3141);sdn-1(zh20)</i>	42 (n=150) n.s.
<i>plx-2(ev773)</i>	27 (n=200)
<i>rbr-2(tm3141);plx-2(ev773)</i>	20 (n=200) n.s.

Quantification of PVQ axonal cross-over defects in the indicated strains. Statistical significance of the difference between double mutants and the corresponding single mutant with the highest penetrance was assessed with one-way ANOVA followed by Tukey's multiple-comparison test. n.s., not significant.

Table S2. Mammalian PHD-containing proteins binding to H3K4me3 and their *C. elegans* homologs

Mammalian protein	<i>C. elegans</i> homolog	Allele
BPTF	NURF-1	<i>nurf-1(n4295)</i>
ING1/5	LSY-13 ING-3 Y43H11AL.1	<i>lsy-13(ok1475)</i> <i>ing-3(tm2530)</i> not available
KDM7A/C	JMJD-1.1 JMJD-1.2	<i>jmjd-1.1(tm3980)</i> <i>jmjd-1.2(tm3713)</i>
RAG2	-	-
TAF3	TAF-3	not available

List of plant homeodomain (PHD)-containing proteins reported to bind H3K4me3 in mammals (Fortschegger and Shiekhattar, 2011), homologs in *C. elegans* and mutant alleles used in this study.

Table S3. Loss of *nurf-1* restores correct PVQ guidance in *rbr-2(tm3141)* mutants

Genotype	Defective animals (%)
WT	9 (n=162)
<i>rbr-2(tm3141)</i>	22 (n=296)
<i>nurf-1(n4295)</i>	14 (n=150)
<i>rbr-2(tm3141);nurf-1(n4295)</i>	12 (n=150) **
<i>ing-3(tm2530)</i>	14 (n=100)
<i>rbr-2(tm3141);ing-3(tm2530)</i>	23 (n=100) n.s.
<i>lsy-13(ok1475)</i>	9 (n=100)
<i>rbr-2(tm3141);lsy-13(ok1475)</i>	17 (n=150) n.s.
<i>jmjd-1.1(tm3980)</i>	n.d.
<i>rbr-2(tm3141);jmjd-1.1(tm3980)</i>	26 (n=100) n.s.
<i>jmjd-1.2(tm3713)</i>	22 (n=200)
<i>rbr-2(tm3141);jmjd-1.2(tm3713)</i>	17 (n=200) n.s.

Quantification of PVQ axonal cross-over defects in the indicated strains. Statistical significance of the difference between *rbr-2(tm3141)* and double mutants was assessed with one-way ANOVA followed by Tukey's multiple-comparison test. **p<0.01, n.s., not significant, n.d., not determined. For unclear reasons, it was not possible to obtain the single mutant *jmjd-1.1(tm3980)* carrying a transgenic marker for the PVQs.

Table S4. Transgenic strains

Strain	Genotype
ZR241	N2; <i>zrEx48 Ex(Prbr-2::rbr-2::GFP)</i>
ZR246	<i>rbr-2(tm3141); oyIs14; zrEx48 Ex(Prbr-2::rbr-2::GFP)</i>
ZR848	<i>rbr-2(tm3141); oyIs14; zrEx289 Ex(Prbr-2::rbr-2::GFP)</i>
ZR849	<i>rbr-2(tm3141); oyIs14; zrEx290 Ex(Prbr-2::rbr-2::GFP)</i>
ZR248	<i>rbr-2(tm3141); oyIs14; zrEx51 Ex(PF25B3.3::rbr-2::GFP)</i>
ZR412	<i>rbr-2(tm3141); oyIs14; zrEx87 Ex(PF25B3.3::rbr-2::GFP)</i>
ZR413	<i>rbr-2(tm3141); oyIs14; zrEx88 Ex(PF25B3.3::rbr-2::GFP)</i>
ZR249	<i>rbr-2(tm3141); oyIs14; zrEx50 Ex(Pmyo-3::rbr-2::GFP)</i>
ZR408	<i>rbr-2(tm3141); hdIs26; zrEx83 Ex(Pmyo-3::rbr-2::GFP)</i>
ZR409	<i>rbr-2(tm3141); hdIs26; zrEx84 Ex(Pmyo-3::rbr-2::GFP)</i>
ZR851	<i>rbr-2(tm3141); oyIs14; zrEx291 Ex(Pdpy-7::rbr-2::GFP)</i>
ZR852	<i>rbr-2(tm3141); oyIs14; zrEx292 Ex(Pdpy-7::rbr-2::GFP)</i>
ZR594	<i>rbr-2(tm3141); oyIs14; zrEx175 Ex(Psra-6::rbr-2::GFP)</i>
ZR595	<i>rbr-2(tm3141); oyIs14; zrEx176 Ex(Psra-6::rbr-2::GFP)</i>
ZR597	<i>rbr-2(tm3141); oyIs14; zrEx178 Ex(Psra-6::rbr-2::GFP)</i>
ZR242	N2; <i>zrEx49 Ex(Prbr-2::rbr-2DD::GFP)</i>
ZR247	<i>rbr-2(tm3141); oyIs14; zrEx49 Ex(Prbr-2::rbr-2DD::GFP)</i>
ZR293	<i>rbr-2(tm3141); hdIs26; zrEx66 Ex(Prbr-2::rbr-2DD::GFP)</i>
ZR294	<i>rbr-2(tm3141); hdIs26; zrEx67 Ex(Prbr-2::rbr-2DD::GFP)</i>
ZR850	N2; <i>Is(Prbr-2::rbr-2::GFP)</i>
ZR677	N2; <i>oyIs14; zrEx217 Ex(PF25B3.3::wsp-1a cDNA)</i>
ZR679	N2; <i>oyIs14; zrEx219 Ex(PF25B3.3::wsp-1a cDNA)</i>

Strain	Genotype
ZR680	N2; <i>oyIs14</i> ; <i>zrEx220</i> Ex(<i>PF25B3.3::wsp-1a</i> cDNA)
ZR839	N2; <i>oyIs14</i> ; <i>zrEx280</i> Ex(<i>Pmyo-3::wsp-1a</i> cDNA)
ZR840	N2; <i>oyIs14</i> ; <i>zrEx281</i> Ex(<i>Pmyo-3::wsp-1a</i> cDNA)
ZR842	N2; <i>oyIs14</i> ; <i>zrEx283</i> Ex(<i>Pmyo-3::wsp-1a</i> cDNA)
ZR846	<i>rbr-2(tm3141);wsp-1(gm324); oyIs14; zrEx217</i> Ex(<i>PF25B3.3::wsp-1a</i> cDNA)
ZR847	<i>rbr-2(tm3141);wsp-1(gm324); oyIs14; zrEx288</i> Ex(<i>PF25B3.3::wsp-1a</i> cDNA::GFP)
ZR900	N2; <i>oyIs14</i> ; <i>zrEx321</i> Ex(<i>PF25B3.3::VCA</i> cDNA::GFP)
ZR901	N2; <i>oyIs14</i> ; <i>zrEx322</i> Ex(<i>PF25B3.3::VCA</i> cDNA::GFP)
ZR902	N2; <i>oyIs14</i> ; <i>zrEx323</i> Ex(<i>PF25B3.3::VCA</i> cDNA::GFP)
ZR905	N2; <i>oyIs14</i> ; <i>zrEx326</i> Ex(<i>Psra-6::VCA</i> cDNA::GFP)
ZR906	N2; <i>oyIs14</i> ; <i>zrEx327</i> Ex(<i>Psra-6::VCA</i> cDNA::GFP)
ZR910	N2; <i>oyIs14</i> ; <i>zrEx331</i> Ex(<i>Psra-6::VCA</i> cDNA::GFP)]

List of transgenic strains used in this study: names and genotypes are indicated.