

Supplementary Table 1

Genetic profile of the KDP.PVG-*RT1^{a/u}* and PVG.KDP-*Cblb* congenic strains

Chr	Locus	cM ^a	Chr: Position (bp) ^b	Genotype ^c	
				KDP.PVG- <i>RT1^{a/u}</i>	PVG.KDP- <i>Cblb</i>
1	<i>D1Rat1</i>	8.9	1:10615276-10615404	KDP	PVG.R23
1	<i>D1Rat258</i>	30.4	ND	KDP	PVG.R23
1	<i>D1Rat51</i>	81.1	1:159782446-159782631	KDP	PVG.R23
1	<i>D1Rat290</i>	103.2	1:195105753-195105954	KDP	PVG.R23
1	<i>D1Rat90</i>	154.5	1:267110926-267111087	KDP	PVG.R23
2	<i>D2Rat10</i>	16.8	2:35874554-35874746	KDP	PVG.R23
2	<i>D2Rat118</i>	84.5	2:214988989-214989202	KDP	PVG.R23
2	<i>D2Rat185</i>	103.2	2:238139979-238140155	KDP	PVG.R23
3	<i>D3Rat82</i>	13.4	3:29749287-29749474	KDP	PVG.R23
3	<i>D3Rat169</i>	48.1	ND	KDP	PVG.R23
3	<i>D3Rat147</i>	65.6	3:143492509-143492676	KDP	PVG.R23
3	<i>D3Rat137</i>	85.5	3:163335008-163335184	KDP	PVG.R23
4	<i>D4Rat143</i>	4.2	ND	KDP	PVG.R23
4	<i>D4Rat128</i>	45.6	ND	KDP	PVG.R23
4	<i>D4Rat66</i>	92.1	4:161023443-161023565	KDP	PVG.R23
5	<i>D5Rat121</i>	4.4	5:9396685-9396878	KDP	PVG.R23
5	<i>D5Rat70</i>	20.9	5:36386127-36386391	KDP	PVG.R23
5	<i>D5Rat154</i>	60.6	ND	KDP	PVG.R23
6	<i>D6Rat105</i>	23.2	6:18615952-18616170	KDP	PVG.R23
6	<i>D6Rat130</i>	48.8	ND	KDP	PVG.R23
6	<i>D6Rat79</i>	87.5	6:131029752-131029973	KDP	PVG.R23
7	<i>D7Rat32</i>	11.1	7:21790656-21790795	KDP	PVG.R23
7	<i>D7Rat102</i>	63.2	ND	KDP	PVG.R23
7	<i>D7Rat94</i>	91.9	7:142816043-142816152	KDP	PVG.R23
8	<i>D8Rat49</i>	23.9	ND	KDP	PVG.R23
8	<i>D8Rat71</i>	89.9	8:127907014-127907265	KDP	PVG.R23
9	<i>D9Rat44</i>	3.8	9:2948883-2949051	KDP	PVG.R23
9	<i>D9Rat13</i>	46.7	9:62957528-62957638	KDP	PVG.R23
9	<i>D9Rat4</i>	62.3	9:90696863-90697021	KDP	PVG.R23
10	<i>D10Rat51</i>	11.7	ND	KDP	PVG.R23
10	<i>D10Rat98</i>	53.1	10:70191315-70191541	KDP	PVG.R23
11	<i>D11Rat21</i>	6.2	11:25035084-25035273	KDP	PVG.R23
11	<i>D11Rat26</i>	7.7	11:27193145-27193293	KDP	PVG.R23
11	<i>D11Rat18</i>	ND	11:29928014-29928167	KDP	PVG.R23
11	<i>D11Rat13</i>	10.8	11:31820215-31820348	KDP	PVG.R23
11	<i>D11Rat68</i>	24.6	11:46793415-46793584	KDP	PVG.R23
11	<i>D11M16Mit46</i>	26.1	ND	KDP	KDP/PVG
11	<i>D11Yok1</i>	27.6	ND	KDP	KDP/PVG
11	<i>Cblb</i>	29.1	11:49690402-49856762	KDP	KDP/PVG
11	<i>D11M16Mit14</i>	30.6	ND	KDP	KDP/PVG
11	<i>D11Rat34</i>	ND	11:63814024-63814155	KDP	KDP/PVG
11	<i>D11Rat37</i>	ND	11:74026445-74026604	KDP	PVG.R23
11	<i>D11Rat50</i>	ND	11:84840964-84841212	KDP	PVG.R23
12	<i>D12Rat5</i>	19.2	ND	KDP	PVG.R23
12	<i>D12Rat79</i>	44	12:36223812-36224036	KDP	PVG.R23
13	<i>D13Rat1</i>	0	13:10555731-10556042	KDP	PVG.R23
13	<i>D13Rat111</i>	4.4	13:32030140-32030259	KDP	PVG.R23
13	<i>D13Rat32</i>	30.9	13:78189257-78189364	KDP	PVG.R23
14	<i>D14Rat10</i>	22.3	14:33157433-33157602	KDP	PVG.R23
14	<i>D14Rat37</i>	44.4	14:81448327-81448566	KDP	PVG.R23
14	<i>D14Rat22</i>	68.4	14:102509228-102509397	KDP	PVG.R23

Supplementary Table 1
Continued

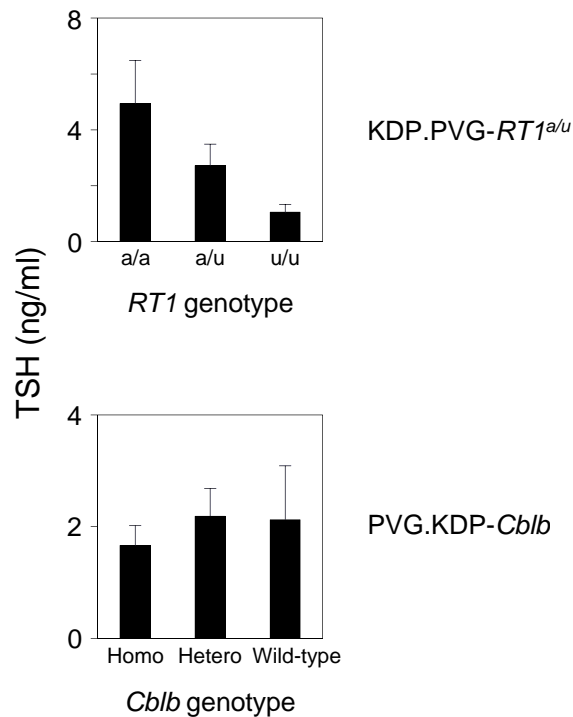
Chr	Locus	cM ^a	Chr: Position (bp) ^b	Genotype ^c	
				KDP.PVG- <i>RT1</i> ^{a/u}	PVG.KDP- <i>Cblb</i>
15	<i>D15Rat54</i>	10.1	15:14072030-14072252	KDP	PVG.R23
15	<i>D15Rat123</i>	37.9	15:58412002-58412138	KDP	PVG.R23
15	<i>D15Rat106</i>	69.3	15:106177704-106177917	KDP	PVG.R23
16	<i>D16Rat12</i>	4	16:350122-350232	KDP	PVG.R23
16	<i>D16Rat67</i>	21.6	16:50115924-50116143	KDP	PVG.R23
16	<i>D16Rat28</i>	27	16:60211076-60211297	KDP	PVG.R23
17	<i>D17Rat117</i>	15.8	17:31007409-31007601	KDP	PVG.R23
17	<i>D17Rat47</i>	45.5	ND	KDP	PVG.R23
18	<i>D18Rat29</i>	4.9	18:13904418-13904577	KDP	PVG.R23
18	<i>D18Arb3</i>	25.3	18:58175228-58175596	KDP	PVG.R23
18	<i>D18Rat44</i>	53.2	18:86863207-86863412	KDP	PVG.R23
19	<i>D19Rat34</i>	2.2	19:2265038-2265293	KDP	PVG.R23
19	<i>D19Rat82</i>	7.8	19:12290643-12290775	KDP	PVG.R23
19	<i>D19Rat96</i>	17.7	ND	KDP	PVG.R23
19	<i>D19Rat68</i>	29.3	ND	KDP	PVG.R23
19	<i>D19Rat67</i>	35.9	ND	KDP	PVG.R23
20	<i>D20Rat46</i>	1	20:3040047-3040188	KDP/PVG	PVG.R23
20	<i>RT1-Db</i>	ND	20:4671513-4681035	KDP/PVG	PVG.R23
20	<i>RT1-Bb</i>	ND	20:4730560-4736186	KDP/PVG	PVG.R23
20	<i>D20Rat48</i>	5.7	ND	KDP/PVG	PVG.R23
20	<i>D20Rat31</i>	11.5	20:10410005-10410227	KDP/PVG	PVG.R23
20	<i>D20Rat60</i>	ND	20:14605697-14605852	KDP	PVG.R23
X	<i>DXRat8</i>	6.7	X:41386879-41387039	KDP	PVG.R23
X	<i>DXRat104</i>	44.4	X:143448612-143448759	KDP	PVG.R23

Abbreviations: Chr, chromosome; cM, centiMorgan; bp, base pair; ND, not determined.

^aDistances (in cM) were based on the genetic map for chromosome 11²² or on the Genome-Wide Screening Set (Invitrogen, Carlsbad, CA) for other chromosomes.

^bPositions (in bp) were based on the RGSC 3.4 assembly (Ensembl Genome Browser, <http://www.ensembl.org/index.html>).

^cKDP, homozygous for the KDP allele; PVG.R23, homozygous for the PVG.R23 allele; KDP/PVG, heterozygous for the KDP and PVG.R23 alleles.



Supplementary Figure 1

The serum TSH values (mean \pm S.E.) in the KDP.PVG-RT1^{a/u} and PVG.KDP-Cblb congenic strains.

Data were obtained from the a/a homozygous (n = 6), a/u heterozygous (n = 15) and u/u homozygous (n = 6) animals in the KDP.PVG-RT1^{a/u} congenic strain, all of which harbor the homozygous *Cblb* mutation, and from the animals homozygous (n = 15), heterozygous (n = 5), and wild-type (n = 4) for the *Cblb* mutation in the PVG.KDP-Cblb congenic strain. There is no statistical difference among three genotypes in both congenic strains by Tukey-Kramer method. There was one *Cblb* homozygous mutant animal in the PVG.KDP-Cblb congenic strain exhibiting an exceptionally high TSH value of more than 200 ng/ml that was excluded from the figure as an outlier.