

Supplementary Materials: A Genomic Study of Myxomatous Mitral Valve Disease in Cavalier King Charles Spaniels

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Table S1. Proportion of cases and controls showing a run of homozygosity in regions flanking selected genes.

Gene	Cases (<i>n</i> = 16)	Controls (<i>n</i> = 17)	Difference between cases and controls
<i>STEAP2</i>	0.55	0.09	0.46
<i>HEPACAM2</i>	0.50	0.05	0.45
<i>CDK6</i>	0.50	0.06	0.44
<i>ARNT2</i>	0.80	0.42	0.38
<i>KIAA1024</i>	0.79	0.41	0.38
<i>FAH</i>	0.80	0.42	0.38
<i>BCAR1</i>	0.44	0.10	0.34
<i>RAB10</i>	0.38	0.12	0.26
<i>PPP2R2C</i>	0.65	0.40	0.25
<i>LATS1</i>	0.57	0.34	0.23
<i>PDE1A</i>	0.62	0.43	0.19
<i>NRG1</i>	0.50	0.32	0.18
<i>TBC1D14</i>	0.59	0.44	0.15
<i>RAB3GAP1</i>	0.08	0.05	0.03
<i>UBXN4</i>	0.04	0.01	0.02
<i>ZRANB3</i>	0.04	0.02	0.01
<i>PLCB2</i>	0.19	0.17	0.01
<i>PDE3A</i>	0.32	0.32	0.00
<i>ADCY9</i>	0.00	0.00	0.00
<i>AXIN1</i>	0.00	0.00	0.00
<i>CACNA1H</i>	0.00	0.00	0.00
<i>CREBBP</i>	0.00	0.00	0.00
<i>PDPK1</i>	0.00	0.00	0.00
<i>SLC8A2</i>	0.00	0.00	0.00
<i>TRAP1</i>	0.00	0.00	0.00
<i>TCF7L1</i>	0.26	0.27	-0.01
<i>SMAD3</i>	0.20	0.24	-0.04
<i>TLN2</i>	0.30	0.35	-0.05
<i>WNT2</i>	0.08	0.18	-0.10
<i>CTNNAL1</i>	0.18	0.27	-0.10
<i>ADCYAP1R1</i>	0.06	0.18	-0.11
<i>FRRS1L</i>	0.17	0.28	-0.12
<i>EPB41L4B</i>	0.17	0.29	-0.12
<i>LPAR1</i>	0.17	0.29	-0.12
<i>CTNNA3</i>	0.06	0.20	-0.14
<i>PRKD1</i>	0.22	0.38	-0.17
<i>ADCY2</i>	0.25	0.43	-0.18
<i>ITPR2</i>	0.35	0.57	-0.22