

Agilent SureSelect CD

Sanger Model Organism Panels

Designs by experts, available to the community



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Targeted next-generation sequencing for investigation of model organisms

Agilent Community Designs (CD) for targeted next-generation sequencing (NGS) are developed in collaboration with subject matter experts in different research fields. These NGS design files are available in Agilent's SureDesign webtool and as custom, made-to-order panels that provide you with robust and cost-effective sequencing results that focus on your genes or regions of interest.

This family of Agilent SureSelect Community Designs were designed by scientists in the Adam's Group at the Wellcome Sanger Institute. The aim of Dr. Louise van der Weyden's and the Adams Group's research is to understand the genetics of cancer, using a combination of genomic studies, mouse models, and comparative oncology approaches. These panels have been used to study spontaneously developed cancer in animals, both as alternative models of human cancer and for the benefit of the animals themselves.¹⁻³

For example, these panels were used to compare hemangiosarcoma in dogs and cats to angiosarcoma in humans², as well as urinary bladder urothelial carcinoma in dogs, cats, and cows to muscle invasive urothelial carcinoma in humans.³ The panels identified several driver genes were recurrently mutated in both the dog and cow species.¹

"Collaborating with the design experts at Agilent ensured we developed high-quality whole-exome and targeted bait sets with optimal target enrichment, to ensure we were able to maximize our ability to effectively interrogate our genes of interest."

Features of the SureSelect CD Canine and Feline Oncogenome designs

- Standard Agilent SureSelect boosting used in design for deeper sequencing of oncology samples.
- Canine Oncogenome design contains 962 cancer-associated genes (6.33 Mb).²
- Feline Oncogenome design contains 986 cancer-associated genes(6.35 Mb).²

Features of the SureSelect CD Canine, Feline, and Bovine Exome designs

- Design features a sleeker bait coverage, allowing for economies not normally associated with large designs.
- Canine: 45.3 Mb target size; 53.4 Mb total covered regions; 451,108 total unique probes.^{1,3}
- Feline: 44.0 Mb target size; 53.6 Mb total covered regions; 454,721 total unique probes.³
- Bovine: 44.5 Mb target size; 53.8 Mb total covered regions, 446,232 total unique probes.³

Table 1. Ordering information for Agilent SureSelect Community Design Model Organism panels.

Product	Part Number
SureSelect CD Bovine Exome 16	5280-0075
SureSelect CD Bovine Exome 96	5280-0076
SureSelect CD Bovine Exome 96 Auto	5280-0077
SureSelect CD Feline Oncogenome 16	5280-0078
SureSelect CD Feline Oncogenome 96	5280-0079
SureSelect CD Feline Oncogenome 96 Auto	5280-0080
SureSelect CD Canine Oncogenome 16	5280-0081
SureSelect CD Canine Oncogenome 96	5280-0082
SureSelect CD Canine Oncogenome 96 Auto	5280-0083
SureSelect CD Feline Exome 16	5282-0092
SureSelect CD Feline Exome 96	5282-0093
SureSelect CD Feline Exome 96 Auto	5282-0094
SureSelect CD Canine Exome 16	5282-0095
SureSelect CD Canine Exome 96	5282-0096
SureSelect CD Canine Exome 96 Auto	5282-0097

Note: Part numbers cover the capture probe libraries only. Library preparation and target enrichment kits must be purchased separately.

Disclaimer: Agilent has not performed verification and validation on these panels.

References

1. Wong, K.; van der Weyden, L.; Schott, C. R.; Foote, A.; Constantino-Casas, F.; Smith, S.; Dobson, J. M.; Murchison, E. P.; Wu, H.; Yeh, I.; Fullen, D. R.; Joseph, N.; Bastian, B. C.; Patel, R. M.; Martincorena, I.; Robles-Espinoza, C. D.; Iyer, V.; Kuijjer, M. L.; Arends, M. J.; Brenn, T. Cross-Species Genomic Landscape Comparison of Human Mucosal Melanoma with Canine Oral and Equine Melanoma. *Nature Communications* **2019**, 10 (1). <https://doi.org/10.1038/s41467-018-08081-1>.
2. Wong, K.; Ludwig, L.; Krijgsman, O.; Adams, D. J.; Wood, G. A.; van der Weyden, L. Comparison of the Oncogenomic Landscape of Canine and Feline Hemangiosarcoma Shows Novel Parallels with Human Angiosarcoma. *Disease Models & Mechanisms* **2021**, 14 (7). <https://doi.org/10.1242/dmm.049044>.
3. Wong, K.; Abascal, F.; Ludwig, L.; Aupperle-Lellbach, H.; Grassinger, J. M.; Wright, C. W.; Allison, S. J.; Pinder, E.; Phillips, R. M.; Romero, L.; Gal, A.; Roady, P. J.; Pires, I.; Franco Guscetti; Munday, J. S.; Peleteiro, M. C.; Pinto, C.; Carvalho, T.; João Bettencourt Cota; Elizabeth. Cross-Species Oncogenomics Offers Insight into Human Muscle-Invasive Bladder Cancer. *Genome Biology* **2023**, 24 (1). <https://doi.org/10.1186/s13059-023-03026-4>.

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