Supplementary Table 1: Demographics of tissue donors

Case ID	Age (years)	Sex	PMI	Ethnicity	Brain RIN	Cause of death
5238	37.2	M	10.5	AA	8.9	Multiple blunt force injuries
5298	50.3	M	12.5	AA	8.7	Multiple injuries
5346	25.1	F	24.5	AS	8.3	Multiple injuries

PMI: postmortem interval; RIN: RNA Integrity Number; M: male; F: female; AA: African American; AS: Asian

Supplementary table 2: Samples and reads in each sequencing run

Sample	Barcode	Run	Run1 reads	Run2 reads
5238 cingulate	BC001	1, 2	4836	6752
5238 DLPFC	BC002	1, 2	7227	10484
5238 occipital	BC003	1	4630	
5238 parietal	BC004	1	6024	
5238 cerebellum	BC003	2		3735
5238 striatum	BC004	2		8778
5298 cingulate	BC005	1, 2	6287	9329
5298 DLPFC	BC006	1, 2	5660	8849
5298 occipital	BC007	1	2729	
5298 parietal	BC008	1	2729	
5298 cerebellum	BC007	2		6725
5298 striatum	BC008	2		8116
5246 cingulate	BC009	1, 2	1760	2421
5346 DLPFC	BC010	1, 2	2572	3403
5346 occipital	BC011	1	4859	
5346 parietal	BC012	1	3681	
5346 cerebellum	BC011	2		7609
5346 striatum	BC012	2		4130

Supplementary table 3: Sequencing metrics for each nanopore sequencing run

	Run1	Run2
Flowcell	R9.0 (MIN105)	R9.4 (MIN106)
Basecalling	Epi2Me v1.125	Albacore V1.1.0
Total reads	112024	126314
Pass, barcoded reads	52994	80331
Yield (Mb)	315	480
Median length (pass, barcoded reads only)	6363	6451
Median Q-score (pass reads only)	12.75	15.89
DNA calibration strand added	Y	N

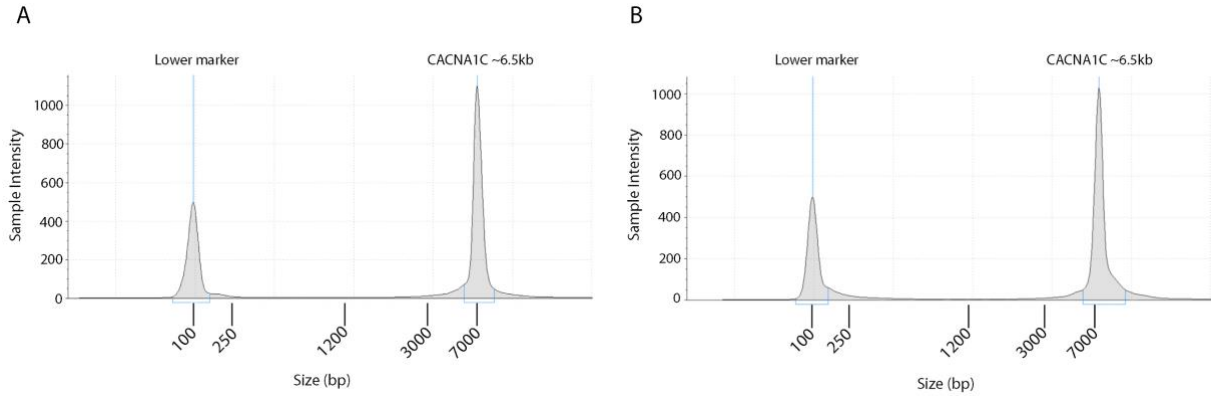
Supplementary Table 4: primers and PCR conditions used to confirm novel exons and junctions.

Novel exon/junction		Forward primer		Reverse primer		Annealing temperature
Novel exon A	5' confirmation (round 1)	Exon 1B F2	GGTCAATGA GAATACGAG GATG	Exon A R2	AGCCTCGTG TCATTCTGCT	53
	5' confirmation (round 2)	Exon 1B F	GAATCAGGT AATCGTCGG CGG	Exon A R	TGAAGACAG CATCTGCGT C	53
	3' confirmation (round 1)	Exon A F2	CCTCATCCT GGTCCCCAG C	Exon 2 R2	CTGCCCATC AGCTTAGCC TG	53
	3' confirmation (round 2)	Exon A F	AGCAGAATG ACACGAGGC T	Exon 2 R	AGCTGACTG TGGAGATGG TC	53
Novel Exon B	5' confirmation (round 1)	Exon 3 F2	ACGCCACCA ATTCCAACCT G	Exon B R2	TCTCCAATCT GGGATGTTC CTC	50

	5’ confirmation (round 2)	Exon 3 F	TTGCCAATTGTGTGGCCTTAG	Exon B R	CTACTCTAGTTGGGCTGAGTT	50
	3’ confirmation (round 1)	Exon B F2	AACTCAGCCCAACTAGAGTAG	Exon 4 R2	GGTGAAAGAGGAGTCCATAGG	50
	3’ confirmation (round 2)	Exon B F	GAGGAACATCCCAGATTGGAGA	Exon 4 R	TCTAGTAGGTTCCAGCCGTTG	50
Novel Exon D	5’ confirmation (round 1)	Exon 7 F2	CAGTGCATCACCATGGAGG	Exon D R2	TCTGCCTCAAGAGGAATCACTCT	53
	5’ confirmation (round 2)	Exon 7 F	GCACGGCATCACCAACTT	Exon D R	CTCCTGTGACCGAAGGGGAC	53
	3’ confirmation (round 1)	Exon D F2	GTCCCCTTCGGTCACAGGAG	Exon 8 R2	CAGGGTAACTCATAGCCCATAGC	53
	3’ confirmation (round 2)	Exon D F	AGAGTGATTCCTCTTGAGGCAGA	Exon 8 R	CGCTCAACACACCGAGAACCA	53
Novel Exon 9-13 junction		Exon junction 9.13 F	CCCGAAACAACACGGCAAACA	Exon 13 R	ACACACGACGAAGCAGTCAAA	55
Novel Exon 14-23 junction		Exon 14 F2	CATCCTTGCTGAACTCTGTGC	Exon junction 14.23 R	AGCAGTCATCTGAAACACAGTGA	53
Novel Exon 37-44 junction		Exon 37 F	TGAAACACCCTGTGGTAGCAG	Exon 37.44 R	GCCCTCAGGAAGGCACAGA	55

Supplementary Figure 1: Full-length, highly pure pooled CACNA1C amplicons.

A) Run1 B) Run2. Slight apparent shift of amplicon to a larger size is due to slight inaccuracy inherent in gDNA screentape where there is only a lower marker for sizing.



Supplementary Figure 2: Mapping pipeline for the annotation of novel exons and novel transcripts