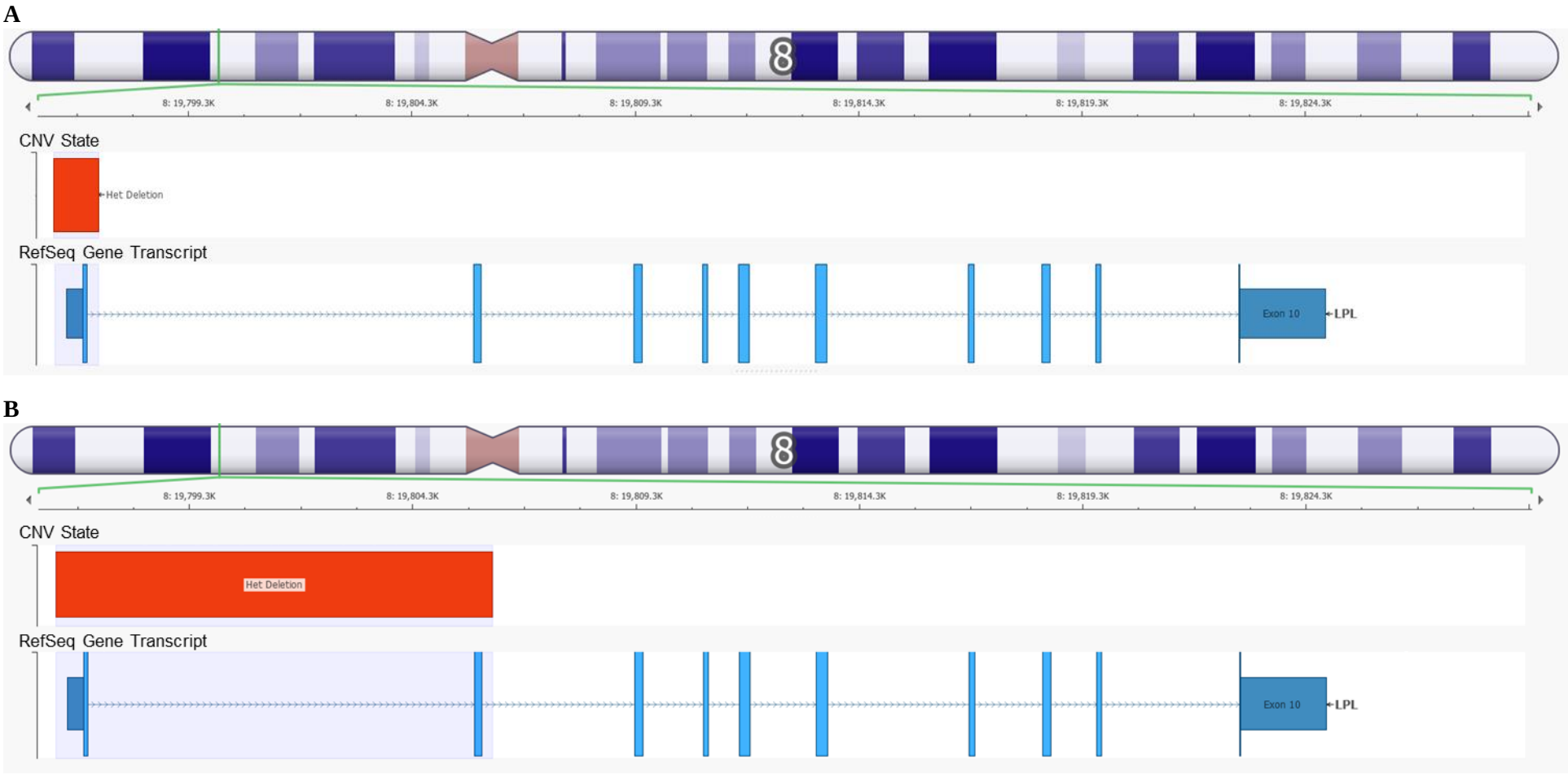
Supplemental Table S1: Screening primers for *LPL* CNVs.

CNV	Breakpoint	Primer direction	Primer sequence (5' to 3')	Annealing temp (°C)	Primer labels in Figure 1 and 2
5'UTR – exon 1	Upstream	F	TTGTAGGTTAGAGTGAACGTGCACAG	60	P2
		R	CATTATGCTGATGCTGCACAACTCTG	60	P3
	Downstream	F	TTCACACTTGATGGTCTCATTCAGTGG	60	P4
		R	GATCAGACTGAATTGATTGGTCTGTTCAG	60	P5
5' UTR – exon 2	Upstream	F	CTCTATTGGACGTGCTAATGGCACAG	60	P1
		R	CATTATGCTGATGCTGCACAACTCTG	60	P3
	Downstream	F	ACTGACATGCTGACATGCCAGATG	60	P6
		R	CATCTGTGTGAATTCTGTTAGTAGTAG	60	P7

The primers listed were designed to flank the two breakpoints for each CNV. The "Breakpoint" listed is relative to the deleted section of the gene. The sequence orientation for P1-P7 are relative to *LPL*. Highlighted primer sequences are the same. Abbreviations: CNV = copy-number variant; F = forward; R = reverse; UTR = untranslated region.



Supplemental Figure S1. Identification of *LPL* CNVs using the VarSeq-CNV® caller algorithm on targeted sequencing data. Chr8:19,795,931-19,829,369 (hg19 genome build) is the region visualized in each panel. **A)** Subject 1, carrier of a heterozygous deletion spanning the 5'UTR and exon 1 of *LPL*. **B)** Subject 2 to 4, carriers of a heterozygous deletion spanning the 5'UTR, exon 1 and exon 2 of *LPL*. Abbreviations: chr = chromosome; CNV = copy-number variant; UTR = untranslated region.