Tejedor et al. Role of Six Single Nucleotide Polymorphisms, Risk Factors in Coronary Disease, in *OLR1* Alternative Splicing

Supplementary Tables and Figure legends.

Table S1. Single Nucleotide Polymorphisms characterized in the OLR1 gene in the genomic region spanning from exon 4 to the end of the 3' Untranslated Region (UTR) in terminal exon 6 (relevant to Table 1). Shadowed rows indicate SNPs in linkage disequilibrium analyzed in this study. Sequence coordinates correspond to the hg18 version of the NCBI genome browser (dsSNP 130).

Table S2. Raw data of endogenous OLR1 AS changes upon knockdown of splicing and chromatin factors (relevant to Table 2). Data include information about the knocked down genes, the corresponding siRNA pools, quantification of alternative isoforms by semiquantitative PCR and high-throughput capillary electrophoresis, and percentage of exon inclusion (PSI index) for each of the three biological replicas as well as the median, standard deviation, p value and z-scores for the knockdown triplicates compared to control samples. Additional information is provided in Figure S2. Analyses were carried out as described in Papasaikas et al, 2015).

Table S3. Raw and processed information from mass spectrometry analysis (relevant to Table 3).

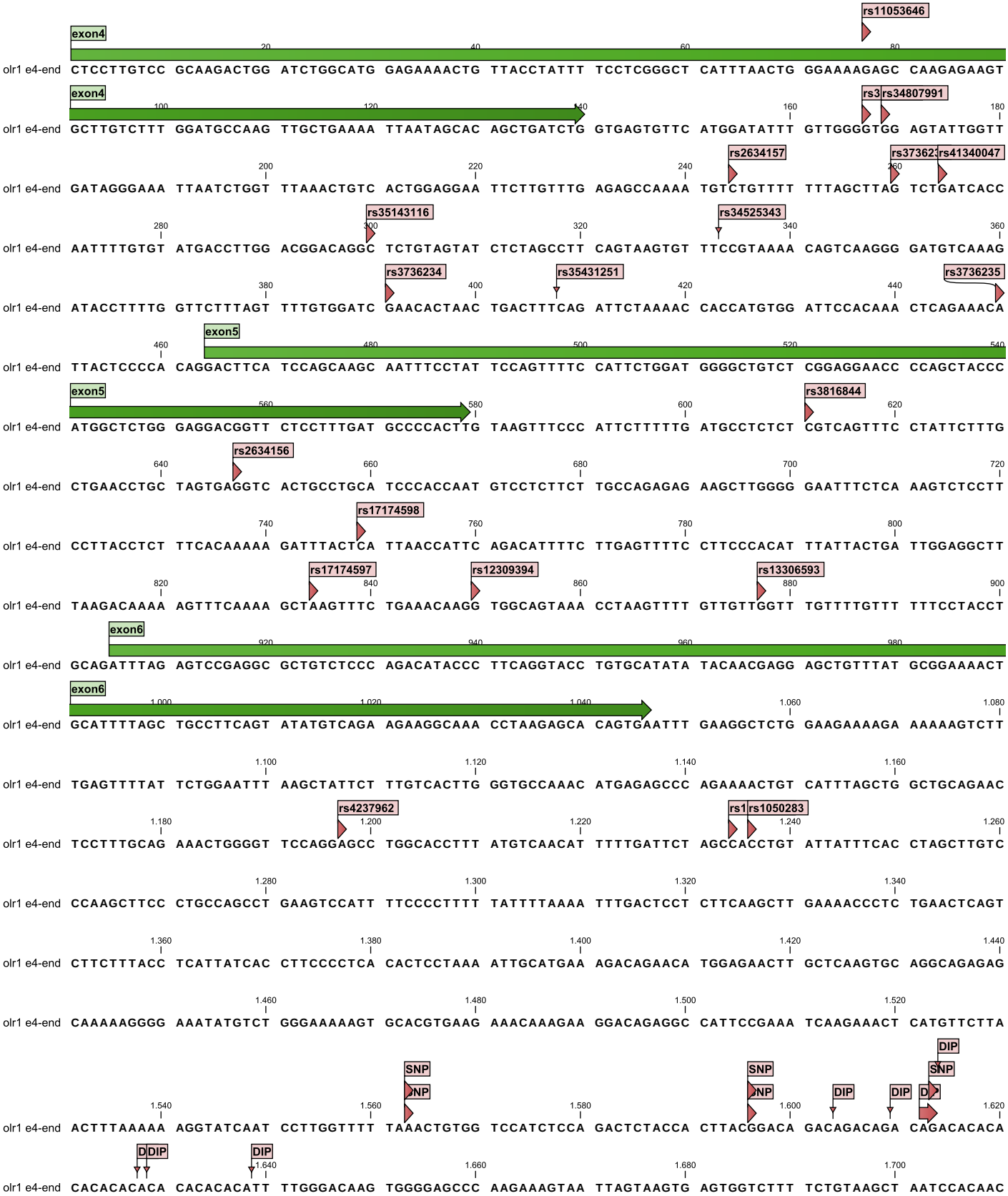
Figure S1. OLR1 genomic sequence used in this study (relevant to Table 1). Exons, SNPs and polyadenylations sites are highlighted.

Figure S2. A. Similar alternative splicing patterns from endogenous and minigene-derived transcripts. OLR1 alternative splicing patterns from endogenous RNAs or minigene-derived transcripts (different amounts of low risk and high risk minigenes transfected) were analyzed by RT and semi-quantitative PCR and amplification products resolved by conventional polyacrylamide gel electrophoresis. **B. Z-score distribution of changes in ORL1 alternative splicing upon knock down of ~280 factors by siRNA.** Y axis shows Robust Z-scores for the different siRNA treatments indicated in the X axis. Positive Z-scores indicate more inclusion of endogenous OLR1 exon 5 upon siRNA knockdown, negative Z-scores indicate more skipping upon siRNA knockdown. Horizontal lines above and below the x axis represent and arbitrary cutoff of 3 Z-scores comparing siRNA treatments with control samples. See also Table S2.

TABLE S1. Tejedor et al.

TABLE 1. SNPs characterized in the OLR1 gene (from exon4 to 3'UTR)

dbSNP	Position	Band	Function	Strand	Observed	Reference alelle	Average heterozygosity	Appeareance in - strand	Position in pre-mRNA
rs1053646	chr12:10204715	12p13.2	exon	+	C/G	C	0.287 +/- 0.247	G/C	11443
rs3736232	chr12:10204625	12p13.2	intron	-	C/G	G	0.389 +/- 0.208	G/C	11533
rs34807991	chr12:10204623	12p13.2	intron	-	A/G	G	0062 +/- 0.165	A/G	11535
rs2634157	chr12:10204548	12p13.2	intron	+	C/G	G	n.d.	G/C	11610
rs3736233	chr12:10204532	12p13.2	intron	-	A/G	G	0.400 +/-0.200	A/G	11626
rs41340047	chr12:10204528	12p13.2	intron	-	G/T	G	0.039 +/- 0.134	G/T	11630
rs35143116	chr12:10204492	12p13.2	intron	-	C/T	C	0.021 +/- 0.100	C/T	11666
rs34525343	chr12:10204460	12p13.2	intron	+	_/A	-	n.d.	_/T	11699
rs3736234	chr12:10204401	12p13.2	intron	-	C/T	C	0.043 +/- 0.198	C/T	11757
rs35431251	chr12:10204385	12p13.2	intron	+	_/A	-		_/T	11774
rs3736235	chr12:10204342	12p13.2	intron	-	A/G	A	0.405 +/- 0.196	A/G	11816
rs3816844	chr12:10204181	12p13.2	intron	-	C/T	C	0.398 +/- 0.202	C/T	11977
rs2634156	chr12:10204145	12p13.2	intron	+	C/T	C	0.010 +/- 0.068	G/A	12013
rs17174598	chr12:10204043	12p13.2	intron	+	A/G	G	0.427 +/- 0.177	T/C	12115
rs17174597	chr12:10203958	12p13.2	intron	+	C/T	T	0.427 +/- 0.177	A/G	12200
rs12309394	chr12:10203942	12p13.2	intron	+	C/T	C	0.134 +/- 0.221	G/A	12216
rs13306593	chr12:10203915	12p13.2	intron	-	G/T	G	0.427 +/- 0.177	G/T	12244
rs4237962	chr12:10203595	12p13.2	intron	+	A/T	T		T/A	12563
rs12316150	chr12:10203558	12p13.2	intron	+	A/T	A	0.045 +/- 0.144	T/A	12600
rs1050283	chr12:10203556	12p13.2	intron	-	C/T	C	0.421 +/- 0.182	C/T	12602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rs2634157
rs373623 rs41340047
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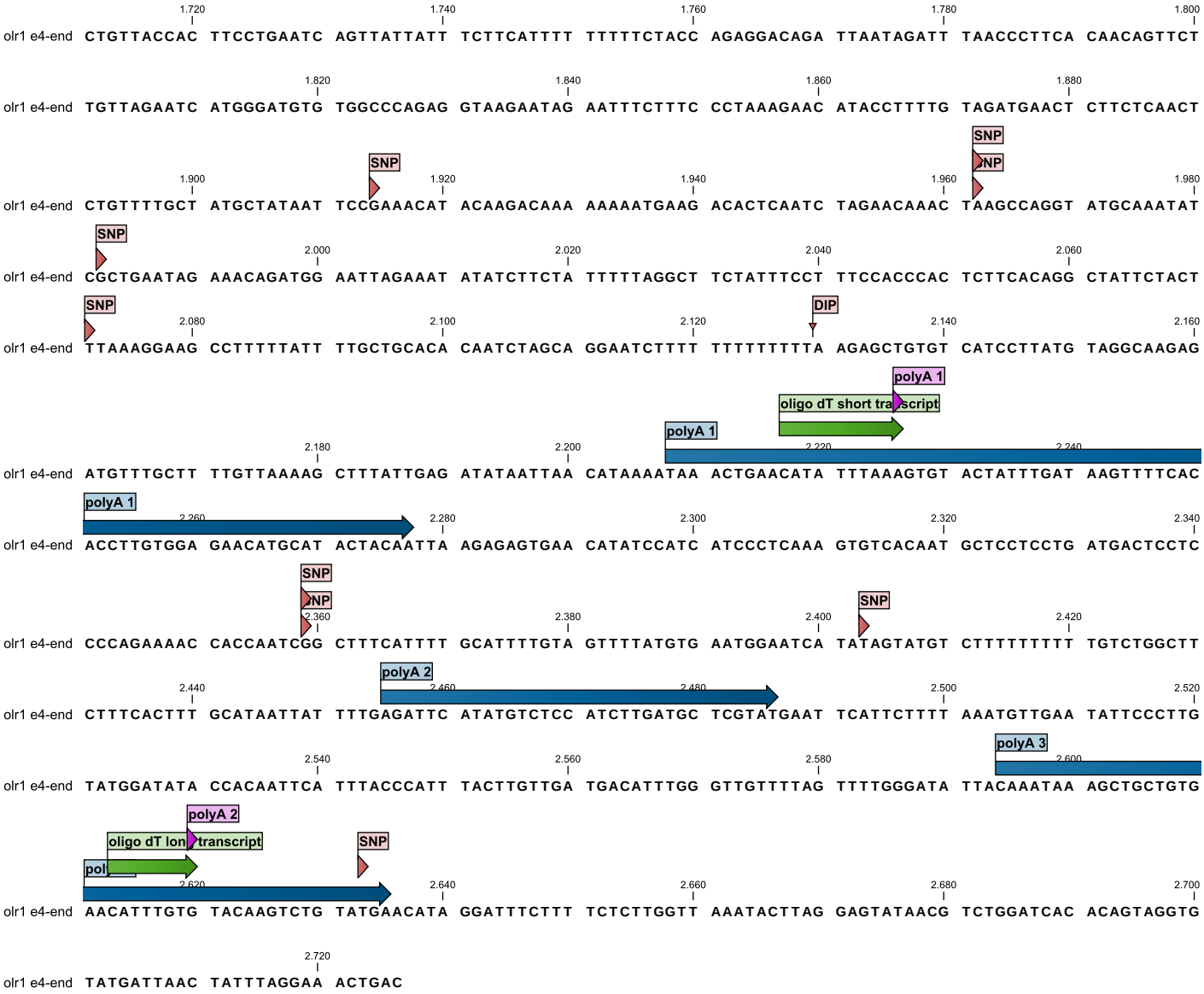
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Figure S2. Tejedor et al.