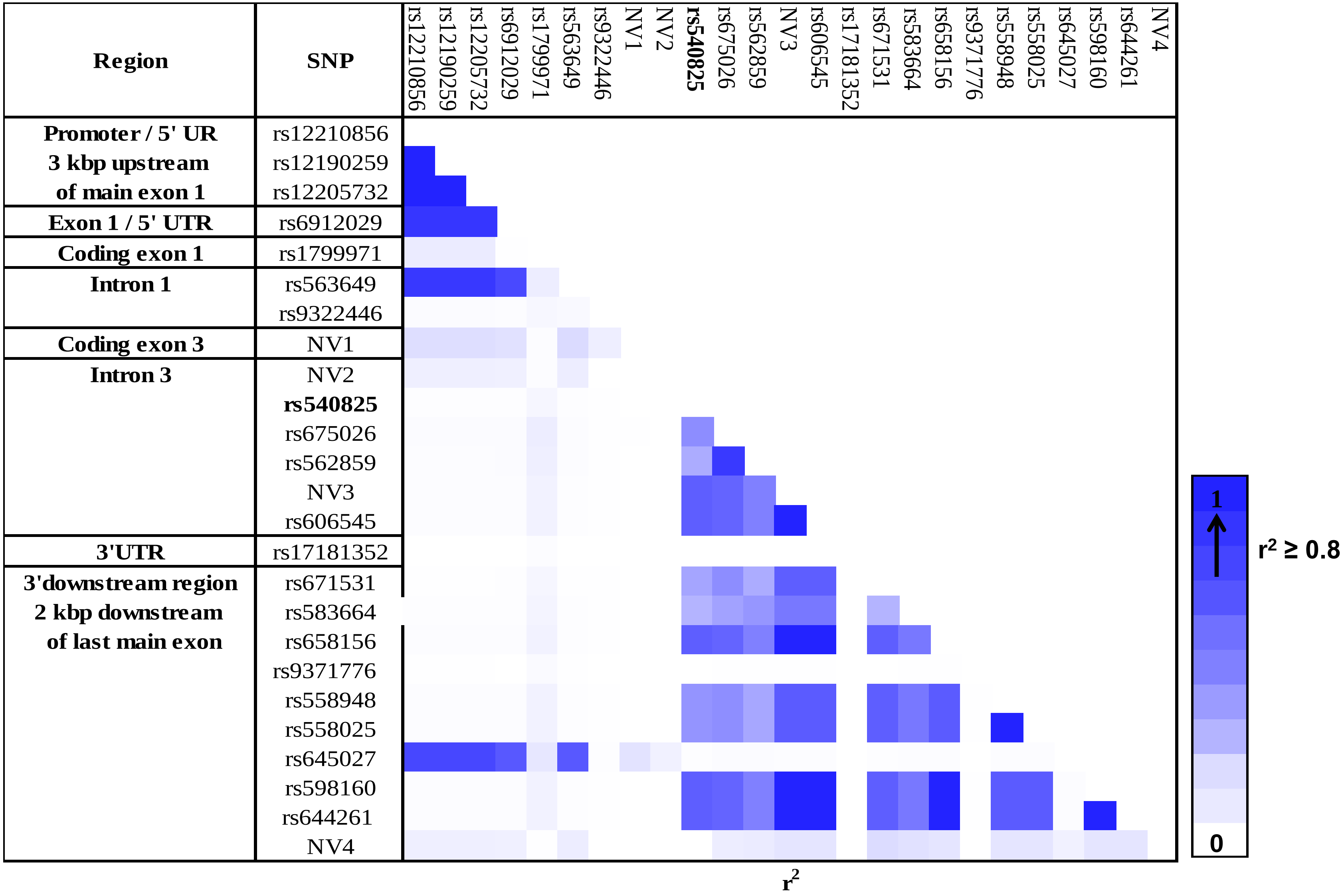
**Supplementary Figure 3: Pairwise linkage disequilibrium (LD) pattern of the following sequenced regions of *OPRM1*; 3 kbp of the promoter region, exons coding for the main mu-opioid receptor transcript (MOR1), 14 alternative exons of *OPRM1* that code for 12 mu-opioid receptor splice variants and 2 kbp of the 3' region downstream of *OPRM1*. SNPs with $r^2 \geq 0.8$ indicates high LD between the 2 SNPs as reflected by the increased colour intensities in the LD plot. SNP rs540825 (in bold) which was significantly associated with fentanyl induced emesis, has low LD with other SNPs. There are 4 groups of SNPs with high LD and 11 SNPs who are not in high LD with other SNPs identified during sequencing. Abbreviations:**
**UR: upstream region, UTR: untranslated region, NV: novel variant kbp: kilobase pair**



| Region | SNP |
|---|---|
| **Promoter / 5' UR 3 kbp upstream of main exon 1** | rs12210856 |
| | rs12190259 |
| | rs12205732 |
| **Exon 1 / 5' UTR** | rs6912029 |
| **Coding exon 1** | rs1799971 |
| **Intron 1** | rs563649 |
| | rs9322446 |
| **Coding exon 3** | NV1 |
| **Intron 3** | NV2 |
| | **rs540825** |
| | rs675026 |
| | rs562859 |
| | NV3 |
| | rs606545 |
| **3'UTR** | rs17181352 |
| **3'downstream region 2 kbp downstream of last main exon** | rs671531 |
| | rs583664 |
| | rs658156 |
| | rs9371776 |
| | rs558948 |
| | rs558025 |
| | rs645027 |
| | rs598160 |
| | rs644261 |
| | NV4 |