

Supplementary Table S1. Genetic, functional, and clinical characteristics of patients with antithrombin type I deficiency carrying a single nucleotide variation or a small insertion/deletion who were evaluated by MLPA. Genetic variants are related to transcript NM_000488.4.

| Mutation cDNA | Protein modification | Thromb | Age 1st | Rec | AntiFXa activity | Antigen levels | Pathogenic prediction (ACMG) |
|--------------------------|-----------------------------|---------------|----------------|------------|-------------------------|-----------------------|---|
| c.334C>T | p.Pro112Ser | Yes | 18 | Yes | 50% | 55% | Likely Pathogenic |
| c.394C>T | p.Gln132Ter | Yes | 22 | Yes | 50% | 51% | Likely Pathogenic |
| c.839 C>A | p.Ser280Ter | Yes | 25 | No | 50% | 50% | Likely Pathogenic |
| c.1332_1336del | p.Arg445Serfs*18 | Yes | 20 | Yes | 50% | 50% | Pathogenic |
| c.398A>C | p.Gln133Pro | Yes | 32 | Yes | 60% | 52% | Pathogenic |
| c.685C>T | p.Arg229Ter | Yes | 52 | No | 50% | 53% | Pathogenic |
| c.89T>A c.951G>C | p.Val30Glu p.Leu317Phe | Yes | ND | Yes | 50% | 51% | Likely Benign Uncertain Significance |
| c.1218+1G>A | Splicing | Yes | ND | Yes | 60% | 50% | Likely Pathogenic |
| c.750del | p.Ile251Phefs*32 | Yes | 41 | No | 47% | 50% | Pathogenic |
| c.814dup | p.Tyr272Leufs*3 | Yes | 57 | Yes | 50% | 48% | Pathogenic |
| c.470A>G | p.Lys157Arg | Yes | 25 | Yes | 57% | 56% | Pathogenic |
| c.763-2A>C | Splicing | Yes | 27 | Yes | 55% | 50% | Pathogenic |
| c.1219-3C>A | Splicing | Yes | 35 | No | 59% | 56% | Likely Pathogenic |
| c.1141T>C | p.Ser381Pro | Yes | 16 | No | 56% | 66% | Uncertain Significance |
| c.42-2A>C | Splicing | Yes | 21 | Yes | 17% | 69% | Likely Pathogenic |
| c.341G>A | p.Ser114Asn | Yes | 17 | No | 48% | 49% | Pathogenic |
| c.1218+1G>T | Splicing | Yes | 40 | No | 38% | 44% | Likely Pathogenic |
| c.1246G>T c.1190C>T | p.Ala416Ser p.Ser397Leu | Yes | 39 | No | 52% | 52% | Pathogenic Likely Pathogenic |
| c.1233dup | p.Ser412Glnfs*1 | Yes | 50 | No | 56% | 53% | Likely Pathogenic |
| c.998_999insC | p.Glu334Profs*9 | Yes | 15 | No | 43% | 44% | Likely Pathogenic |
| c.1332_1333del | p.Ile444Metfs*19 | No | - | - | 42% | 44% | Likely Pathogenic |
| c.537T>G | p.Phe179Leu | No | - | - | 62% | 56% | Likely Pathogenic |
| c.243G>A | p.Trp81Ter | Yes | 19 | No | 52% | 63% | Likely Pathogenic |
| c.464T>C | p.Phe155Ser | Yes | 20 | Yes | 51% | 55% | Pathogenic |
| c.409-2A>T c.1246 G>T | Splicing p.Ala416Ser | Yes | 31 | No | 35% | 44% | Likely Pathogenic Pathogenic |
| c.1033_1035del | p.Glu345del | Yes | 32 | Yes | 59% | 52% | Uncertain Significance |
| c.1154-2A>T | Splicing | Yes | ND | No | 46% | 48% | Likely Pathogenic |
| c.94T>C | p.Cys32Arg | Yes | 25 | No | 45% | 49% | Uncertain Significance |
| c.495del | p.Ala166Profs*6 | Yes | 18 | No | 44% | 43% | Pathogenic |
| c.42-1060_1057dup | Regulatory | Yes | 46 | No | 68% | 65% | ND |
| c.3G>T | p.Met1Ile | Yes | 16 | Yes | 49% | 50% | Likely Pathogenic |
| c.1154-14G>A | Splicing | No | - | - | 52% | 63% | Pathogenic |
| c.592T>A | p.Tyr198Ans | Yes | 23 | No | 55% | 60% | Pathogenic |
| c.286del | p.His97Trpfs*16 | Yes | 40 | No | 56% | 52% | Likely Pathogenic |
| c.1219-1_1248del | Splicing | Yes | 29 | No | 58% | 62% | Pathogenic |
| c.490C>T | p.Arg164Ter | Yes | 22 | No | 42% | 51% | Likely Pathogenic |
| c.1126T>C | p.Phe408Leu | Yes | 19 | No | 42% | 53% | Likely Pathogenic |

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|------------------|--------------------------|-----|----|-----|-----|-----|------------------------|
| c.551_553del | p.Ile218del | Yes | 30 | Si | 42% | 45% | Likely Pathogenic |
| c.409-1G>C | Splicing | Yes | 29 | No | 33% | 41% | Pathogenic |
| c.779dup | p.Lys260Lysfs*4 | Yes | 36 | No | 47% | 45% | Likely Pathogenic |
| c.265C>A | p.Arg89Ser | Yes | 57 | Yes | 53% | 61% | Likely Pathogenic |
| c.749C>T | p.Thr250Ile | No | - | - | 78% | 82% | Likely Pathogenic |
| c.1171dup | p.Arg391Profs*3 | No | - | - | 40% | 42% | Likely Pathogenic |
| c.1012G>T | p.Glu338Ter | Yes | ND | Yes | 18% | 31% | Likely Pathogenic |
| c.352G>C | p.Ala118Pro | Yes | ND | Yes | 33% | 38% | Likely Pathogenic |
| c.1373_1384del | p.Val458_Cys462delinsGly | No | - | - | 75% | 50% | Pathogenic |
| c.41+3A>G | Splicing | Yes | 65 | No | 56% | 52% | Uncertain Significance |
| c.667T>C | p.Ser223Pro | Yes | 10 | Yes | 52% | 43% | Uncertain Significance |
| c.344T>A | p.Ile115Asn | Yes | 1 | Yes | 65% | 50% | Likely Pathogenic |
| c.175G>T | p.Glu59Ter | Yes | 24 | No | 45% | 45% | Likely Pathogenic |
| c.666del | p.Ser223Profs*61 | Yes | 43 | Yes | 43% | 48% | Likely Pathogenic |
| c.1115T>C | p.Leu372Pro | Yes | 57 | No | 48% | 50% | Likely Pathogenic |
| c.1322T>C | p.Leu441Pro | Yes | 37 | No | 41% | 38% | Pathogenic |
| c.1171C>T | p.Arg391Ter | Yes | 40 | No | 40% | 45% | Likely Pathogenic |
| c.763-1G>C | Splicing | Yes | 14 | Yes | 37% | 42% | Pathogenic |
| c.462_464del | p.Phe155del | Yes | 31 | No | 25% | 35% | Pathogenic |
| c.495delA | p.Ala166Profs*7 | Yes | 40 | Yes | 29% | 38% | Pathogenic |
| c.1157T>C | p.Ile386Thr | No | - | - | 51% | 56% | Likely Pathogenic |
| c.580A>G | p.Ser194Gly | No | - | - | 71% | 78% | Likely Pathogenic |
| c.962 insG | p.Lys322Glufs*21 | Yes | 41 | Yes | 44% | 52% | Likely Pathogenic |
| c.1319_1320insTT | p.Leu441Serfs*5 | Yes | 16 | Yes | 59% | 60% | Pathogenic |

Thromb: Thrombosis; Rec: Recurrence. ND: Not determined.

Supplementary Table S2. Location of the genetic variants identified in patients with antithrombin deficiency that could affect the MLPA probes used for SV detection in *SERPINC1*. The MLPA result obtained in each case is also shown.

| Mutation cDNA | EXON | MLPA PROBE AFFECTED | POSITION | MLPA RESULT |
|---------------------------------------|-------------|------------------------------------|-----------------|------------------------|
| c.41 +3 A>G | 1 | RPO | +7 | Negative |
| c.302 C>G | 2 | LPO | -8 | Negative |
| c.286del | 2 | LPO | -24 | Negative |
| c.334 C>T | 2 | RPO | +25 | Negative |
| c.335 C>T | 2 | RPO | +26 | Negative |
| c.341 G>A | 2 | RPO | +32 | Negative |
| c.344 T>A | 2 | RPO | +35 | Negative |
| c.352 G>C | 2 | RPO | +43 | Negative |
| c.592 T>A | 3 | RPO | +24 | Negative |
| c.700 A>T | 4 | LPO | -21 | Negative |
| c.716 T>C | 4 | LPO | -5 | Negative |
| c.720 T>G | 4 | LPO | -1 | False positive |
| c.722_725 delins [731_751;GAACCAG] | 4 | RPO | +2/+5 | False positive |
| c.749 C>T | 4 | RPO | +29 | Negative |
| c.750del | 4 | RPO | +30 | Negative |
| c.1115 T>C | 5 | RPO | +28 | Negative |
| c.1126 T>C | 5 | RPO | +39 | Negative |
| c.1171 C>T | 6 | LPO | -28 | Negative |
| c.1171dup | 6 | LPO | -28 | Negative |
| c.1190 C>T | 6 | LPO | -8 | Negative |
| c.1198 T>G | 6 | LPO | -1 | False positive |
| c.1201 C>T | 6 | RPO | +3 | Negative |
| c.1206 G >A | 6 | RPO | +8 | Negative |

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|----------------|---|-----|---------|----------|
| c.1218+1 G>T | 6 | RPO | +21 | Negative |
| c.1218+1 G>A | 6 | RPO | +21 | Negative |
| c.1246 G>C | 7 | LPO | -14 | Negative |
| c.1246 G>T | 7 | LPO | -14 | Negative |
| c.1272_1274del | 7 | RPO | +13/+15 | Negative |
| c.1277 C>T | 7 | RPO | +18 | Negative |
| c.1273 C>T | 7 | RPO | +14 | Negative |
| c.1274 G>A | 7 | RPO | +15 | Negative |
| c.1297 A>T | 7 | RPO | +38 | Negative |