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MDPI

*Supplementary Material*

**Table S1.** NGS sequencing coverage of RPGR orf15 exon in the analyzed samples. When a specific coverage was not identified in any patient, "/" was reported as Mean exone taget hole.

| Coverage range | Mean exone target hole (bp) | Number of patients |
|---|---|---|
| 47.5-50.0 % | 899 | 1 |
| 50.0-52.5 % | 845 | 5 |
| 52.5-55.0 % | 800 | 8 |
| 55.0-57.5 % | 754 | 19 |
| 57.5-60.0 % | 709 | 22 |
| 60.0-62.5 % | 669 | 12 |
| 62.5-65.0 % | 623 | 7 |
| 65.0-67.5 % | 599 | 1 |
| 67.5-70.0 % | / | 0 |
| 70.0-72.5 % | / | 0 |
| 72.5-75.0 % | / | 0 |
| 75.0-77.5 % | / | 0 |
| 77.5-80.0 % | / | 0 |
| 80.0-82.5 % | 329 | 2 |

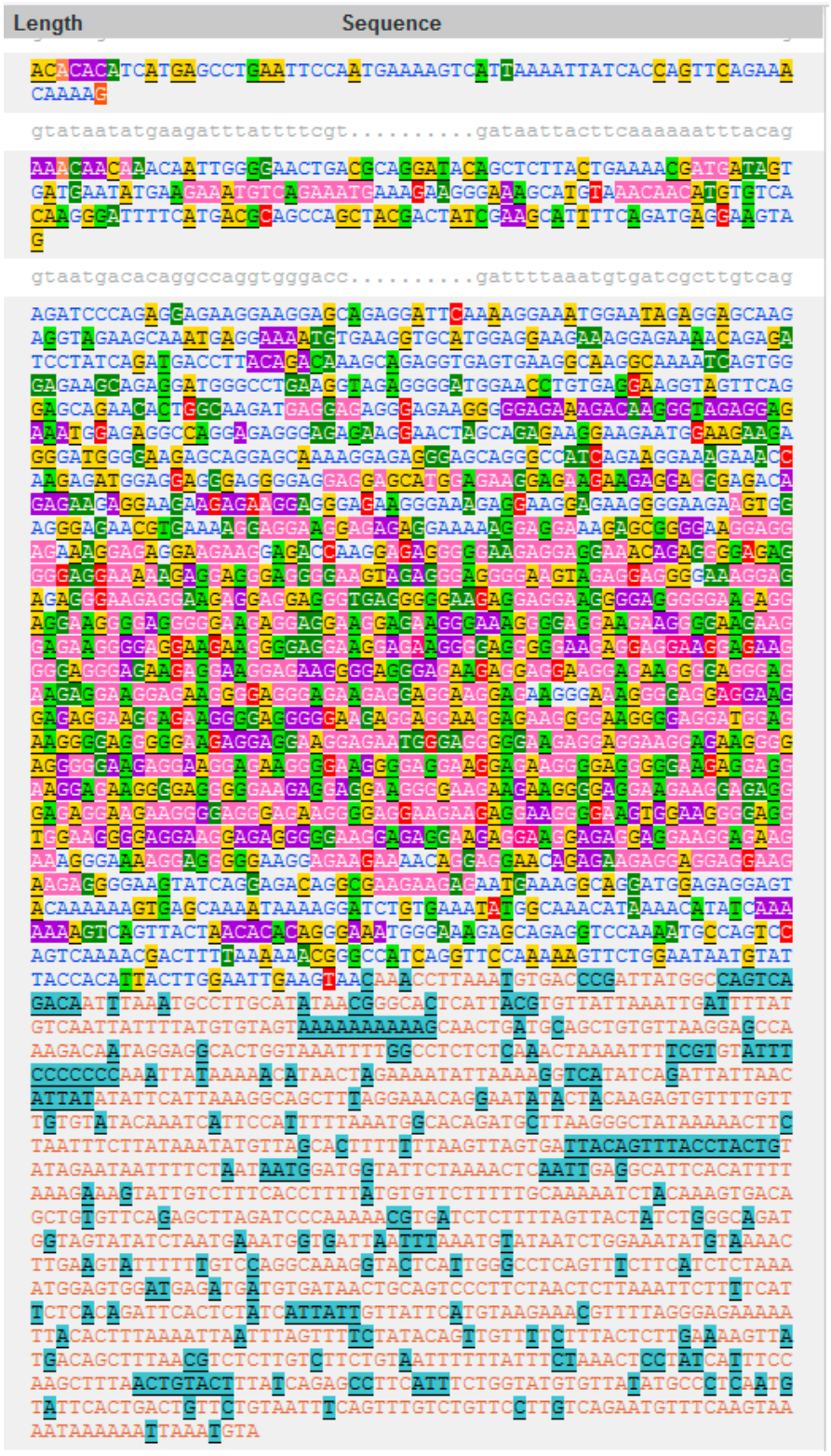


**Figure S1.** RPGRORF15 exon 15 sequence on Ensembl database. Colored residues represent residues in which genetic variants are found (ORF15 is a mutation hotspot of RPGR). Light blue: 3 prime UTR variants; Green: Coding sequence variants; Violet: Frameshift variants; Pink: Inframe deletions variants; Yellow: Missense variants; Dark Pink: Protein altering variants; Orange: Splice donor variants; Light orange: Splice region variants; Red: Stop gained variants; Light green: Synonymous variants.

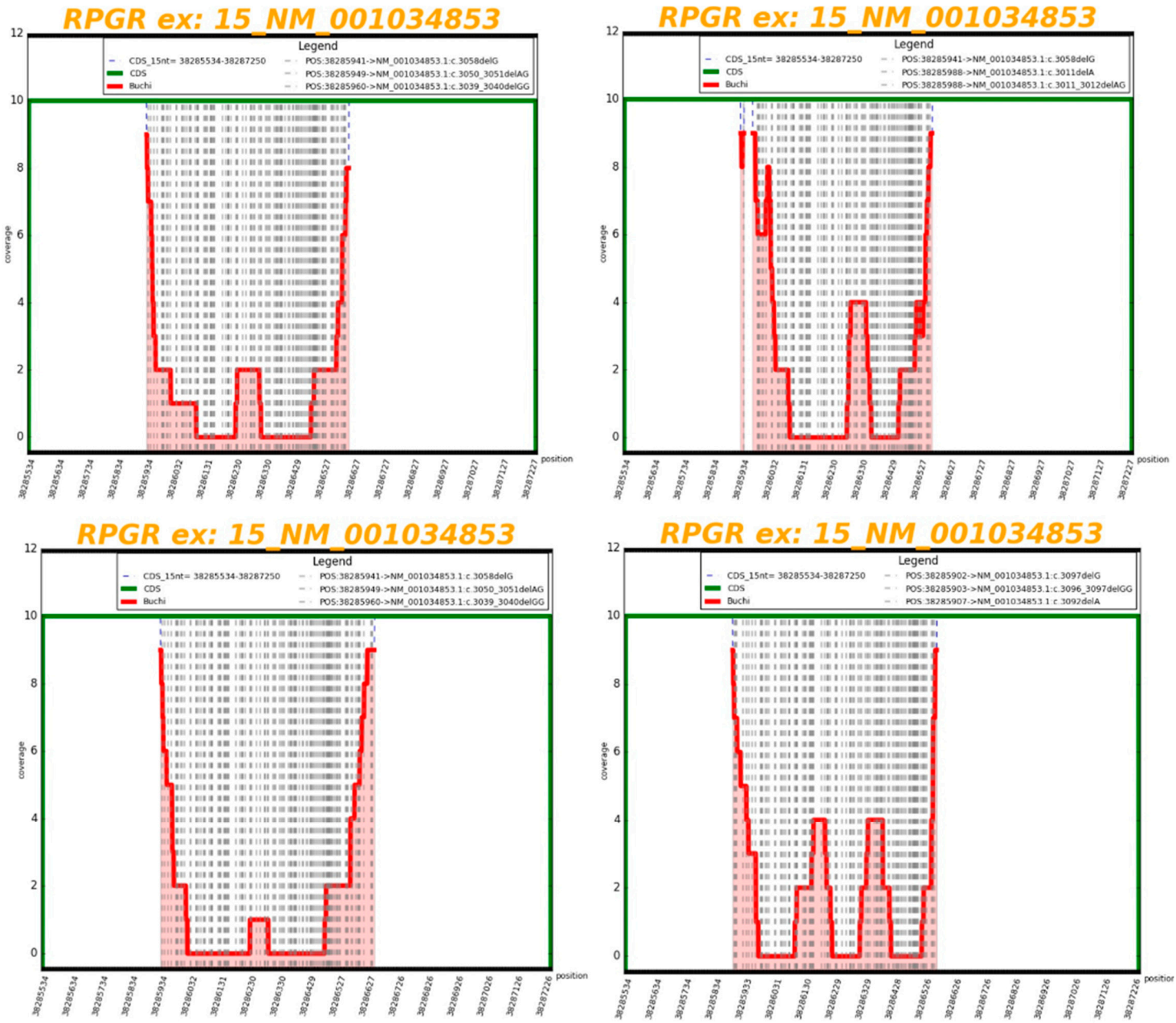


**Figure S2.** Examples of NGS sequencing coverage pitfalls in RPGRORF15 exon 15. Average coverage of RPGR is 60X, while orf15 region has a coverage lower than 10X. X axes represent nucleotide position, while Y axes represent coverage.

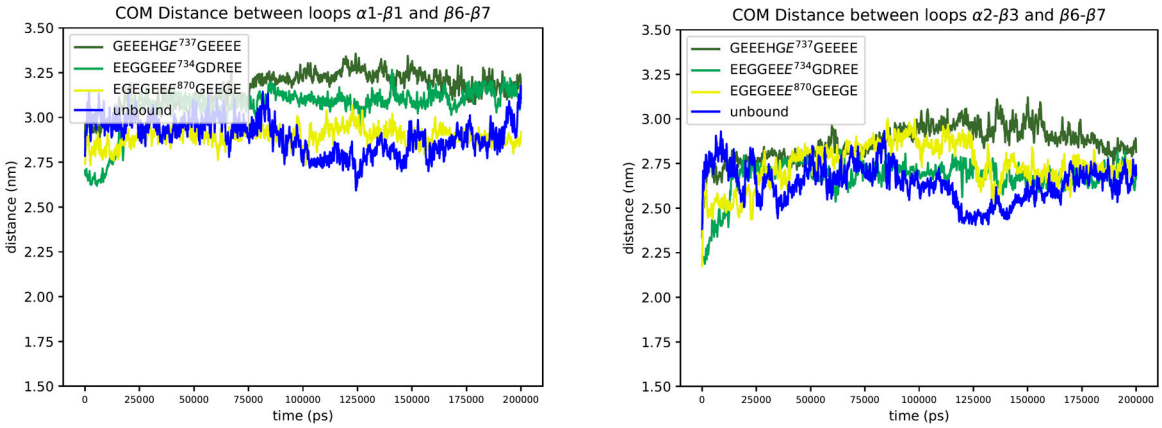


**Figure S3.** COM distance between the respective loops forming the binding cavity. Both the distances conform to a narrow stance in the free (unbound) TTLL5 as compared to the bound complex.