

Solve-RD: systematic pan-European data sharing and collaborative analysis to solve rare diseases

ZUREK, Birte, ELLWANGER, Kornelia, VISSERS, Lisenka E. L. M., SCHÜLE, Rebecca, SYNOFZIK, Matthis, TÖPF, Ana, DE VOER, Richarda M., LAURIE, Steven, MATALONGA, Leslie, GILISSEN, Christian, OSSOWSKI, Stephan, 'T HOEN, Peter A. C., VITOBELLO, Antonio, SCHULZE-HENTRICH, Julia M., RIESS, Olaf, BRUNNER, Han G., BROOKES, Anthony J., RATH, Ana, BONNE, Gisèle, GUMUS, Gulcin, VERLOES, Alain, HOOGERBRUGGE, Nicoline, EVANGELISTA, Teresinha, HARMUTH, Tina, SWERTZ, Morris, SPALDING, Dylan, HOISCHEN, Alexander, BELTRAN, Sergi, GRAESSNER, Holm, HAACK, Tobias B., ZUREK, Birte, ELLWANGER, Kornelia, DEMIDOV, German, STURM, Marc, KESSLER, Christoph, WAYAND, Melanie, WILKE, Carlo, TRASCHÜTZ, Andreas, SCHÖLS, Ludger, HENGEL, Holger, HEUTINK, Peter, BRUNNER, Han, SCHEFFER, Hans, STEYAERT, Wouter, SABLASKAS, Karolis, DE VOER, Richarda M., KAMSTEEG, Erik-Jan, VAN DE WARRENBURG, Bart, VAN OS, Nienke, TE PASKE, Iris, JANSSEN, Erik, DE BOER, Elke, STEEHOUWER, Marloes, YALDIZ, Burcu, KLEEFSTRA, Tjitske, VEAL, Colin, GIBSON, Spencer, WADSLEY, Marc, MEHTARIZADEH, Mehdi, RIAZ, Umar, WARREN, Greg, DIZJIKAN, Farid Yavari, SHORTER, Thomas, STRAUB, Volker, BETTOLO, Chiara Marini, SPECHT, Sabine, CLAYTON-SMITH, Jill, BANKA, Siddharth, ALEXANDER, Elizabeth, JACKSON, Adam, FAIVRE, Laurence, THAUVIN, Christel, VITOBELLO, Antonio, DENOMMÉ-PICHON, Anne-Sophie, DUFFOURD, Yannis, TISSERANT, Emilie, BRUEL, Ange-Line, PEYRON, Christine, PÉLISSIER, Aurore, BELTRAN, Sergi, GUT, Ivo Glynne, LAURIE, Steven, PISCIA, Davide, MATALONGA, Leslie, PAPAKONSTANTINO, Anastasios, BULLICH, Gemma, CORVO, Alberto, GARCIA, Carles, FERNANDEZ-CALLEJO, Marcos, HERNÁNDEZ, Carles, PICÓ, Daniel, PARAMONOV, Ida, LOCHMÜLLER, Hanns, GUMUS, Gulcin, BROS-FACER, Virginie, HANAUER, Marc, OLRÝ, Annie, LAGORCE, David, HAVRYLENKO, Svitlana, IZEM, Katia, RIGOUR, Fanny, STEVANIN, Giovanni, DURR, Alexandra, DAVOINE, Claire-Sophie, GUILLOT-NOEL, Léna, HEINZMANN, Anna, COARELLI, Giulia, ALLAMAND, Valérie, NELSON, Isabelle, YAOU, Rabah Ben, METAY, Corinne, EYMARD, Bruno, COHEN, Enzo, ATALAIA, Antonio, STOJKOVIC, Tanya, MACEK, Milan, TURNOVEC, Marek, THOMASOVÁ, Dana, KREMLIKOVÁ, Radka Pourová, FRANKOVÁ, Vera, HAVLOVICOVÁ, Markéta, KREMLIK, Vlastimil, PARKINSON, Helen, KEANE, Thomas, SENF, Alexander, ROBINSON, Peter, DANIS, Daniel, ROBERT, Glenn, COSTA, Alessia, PATCH, Christine, HANNA, Mike, HOULDEN, Henry, REILLY, Mary,

VANDROVCOVA, Jana, MUNTONI, Francesco, ZAHARIEVA, Irina, SARKOZY, Anna, TIMMERMAN, Vincent, BAETS, Jonathan, VAN DE VONDEL, Liedewei, BEIJER, Danique, DE JONGHE, Peter, NIGRO, Vincenzo, BANFI, Sandro, TORELLA, Annalaura, MUSACCHIA, Francesco, PILUSO, Giulio, FERLINI, Alessandra, SELVATICI, Rita, ROSSI, Rachele, NERI, Marcella, ARETZ, Stefan, SPIER, Isabel, SOMMER, Anna Katharina, PETERS, Sophia, OLIVEIRA, Carla, PELAEZ, Jose Garcia, MATOS, Ana Rita, JOSÉ, Celina São, FERREIRA, Marta, GULLO, Irene, FERNANDES, Susana, GARRIDO, Luzia, FERREIRA, Pedro, CARNEIRO, Fátima, SWERTZ, Morris A., JOHANSSON, Lennart, VAN DER VELDE, Joeri K., VAN DER VRIES, Gerben, NEERINCX, Pieter B., ROELOFS-PRINS, Dieuwke, KÖHLER, Sebastian, METCALFE, Alison <<http://orcid.org/0000-0002-6466-918X>>, VERLOES, Alain, DRUNAT, Séverine, ROORYCK, Caroline, TRIMOUILLE, Aurelien, CASTELLO, Raffaele, MORLEO, Manuela, PINELLI, Michele, VARAVALLO, Alessandra, DE LA PAZ, Manuel Posada, SÁNCHEZ, Eva Bermejo, MARTÍN, Estrella López, DELGADO, Beatriz Martínez, DE LA ROSA, F. Javier Alonso García, CIOLFI, Andrea, DALLAPICCOLA, Bruno, PIZZI, Simone, RADIO, Francesca Clementina, TARTAGLIA, Marco, RENIERI, Alessandra, BENETTI, Elisa, BALICZA, Peter, MOLNAR, Maria Judit, MAVER, Ales, PETERLIN, Borut, MÜNCHAU, Alexander, LOHMANN, Katja, HERZOG, Rebecca, PAULY, Martje, MACAYA, Alfons, MARCÉ-GRAU, Anna, OSORIO, Andres Nacimiento, DE BENITO, Daniel Natera, LOCHMÜLLER, Hanns, THOMPSON, Rachel, POLAVARAPU, Kiran, BEESON, David, COSSINS, Judith, CRUZ, Pedro M. Rodriguez, HACKMAN, Peter, JOHARI, Mridul, SAVARESE, Marco, UDD, Bjarne, HORVATH, Rita, CAPELLA, Gabriel, VALLE, Laura, HOLINSKI-FEDER, Eike, LANER, Andreas, STEINKE-LANGE, Verena, SCHRÖCK, Evelin and RUMP, Andreas

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Solve-RD analysis projects for existing exome and genome data

Title	DITF	WG
Solve-RD QC analysis: Perform quality control on all Solve-RD samples	All	Several WGs
Solve-RD ancestry and admixture analysis: For all Solve-RD samples, determine ancestry and admixture	All	Several WGs
Solve-RD variant annotation: Annotate all Solve-RD samples using multiple databases	All	WG1 SNV/indel
Automated SNV and Indel filtering and prioritisation	All	WG1 SNV/indel
Prevalence of pathogenic variant in genes associated in with known tumour risk syndromes	GENTURIS	WG1 SNV/indel & WG5 Meta-analysis
Detection of mitochondrial DNA variants from WES/WGS	All	WG1 SNV/indel
Landscape of rare genetic variants in titin gene	EURO NMD	WG1 SNV/indel
Clinvar class IV-V mutational burden analysis of exome negative (unsolved) patients with intellectual disability (ID)	ITHACA	WG1 SNV/indel & WG5 Meta-analysis
Detection of Copy Number Variants in WES and WGS data experiment in the Solve-RD re-analysis cohort	All	WG2 CNV
Solve-RD CNV analysis using Conifer: detect possible copy-number variations using multiple CNV tools	All	WG2 CNV
Identification and Interpretation of rare structural variants in WES-based rare-disease diagnostics	All	WG2 CNV
Solve-RD STR analysis: detect aberrant short tandem repeats	All	WG2 CNV
Solve-RD UPD analysis: detect possible uniparental disomies	All	WG2 CNV
Run of homozygosity, consanguinity, relatedness and ancestry analysis	All	WG3 RoH / relatedness
Solve-RD de novo variant calling in patient-parent trios	All	WG4 <i>De novo</i> mutations
Solve-RD meta-analysis: Compare case and control cohorts to find novel disease genes based on statistical enrichment and overlap analysis	All	WG5 Meta-analysis