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General research subject: breast cancer, colorectal cancer, genomics, prognostic and predictive markers, RNA sequencing, CTC, ctDNA, DNA methylation

Group website: https://www.erasmusmc.nl/interne_oncologie/research/

Publications:

1. French JD, Ghossaini M, Edwards SL, Meyer KB, Michailidou K, Ahmed S, Khan S, Maranian MJ, O'Reilly M, Hillman KM, Betts JA, Carroll T, Bailey PJ, Dicks E, Beesley J, Tyrer J, Maia AT, Beck A, Knoblauch NW, Chen C, Kraft P, Barnes D, González-Neira A, Alonso MR, Herrero D, Tessier DC, Vincent D, Bacot F, Luccarini C, Baynes C, Conroy D, Dennis J, Bolla MK, Wang Q, Hopper JL, Southey MC, Schmidt MK, Broeks A, Verhoef S, Cornelissen S, Muir K, Lophatananon A, Stewart-Brown S, Siriwanarangsarn P, Fasching PA, Loehberg CR, Ekici AB, Beckmann MW, Peto J, dos Santos Silva I, Johnson N, Aitken Z, Sawyer EJ, Tomlinson I, Kerin MJ, Miller N, Marme F, Schneeweiss A, Sohn C, Burwinkel B, Guénel P, Truong T, Laurent-Puig P, Menegaux F, Bojesen SE, Nordestgaard BG, Nielsen SF, Flyger H, Milne RL, Zamora MP, Arias Perez JI, Benitez J, Anton-Culver H, Brenner H, Müller H, Arndt V, Stegmaier C, Meindl A, Lichtner P, Schmutzler RK, Engel C, Brauch H, Hamann U, Justenhoven C; GENICA Network, Aaltonen K, Heikkilä P, Aittomäki K, Blomqvist C, Matsuo K, Ito H, Iwata H, Sueta A, Bogdanova NV, Antonenkova NN, Dörk T, Lindblom A, Margolin S, Mannermaa A, Kataja V, Kosma VM, Hartikainen JM; kConFab Investigators, Wu AH, Tseng CC, Van Den Berg D, Stram DO, Lambrechts D, Peeters S, Smeets A, Floris G, Chang-Claude J, Rudolph A, Nickels S, Flesch-Janys D, Radice P, Peterlongo P, Bonanni B, Sardella D, Couch FJ, Wang X, Pankratz VS, Lee A, Giles GG, Severi G, Baglietto L, Haiman CA, Henderson BE, Schumacher F, Le Marchand L, Simard J, Goldberg MS, Labrèche F, Dumont M, Teo SH, Yip CH, Ng CH, Vithana EN, Kristensen V, Zheng W, Deming-Halverson S, Shrubsole M, Long J, Winqvist R, Pylkäs K, Jukkola-Vuorinen A, Grip M, Andrulis IL, Knight JA, Glendon G, Mulligan AM, Devilee P, Seynaeve C, García-Closas M, Figueroa J, Chanock SJ, Lissowska J, Czene K, Klevebring D, Schoof N, Hooning MJ, **Martens JW**, Collée JM, Tilanus-Linthorst M, Hall P, Li J, Liu J, Humphreys K, Shu XO, Lu W, Gao YT, Cai H, Cox A, Balasubramanian SP, Blot W, Signorello LB, Cai Q, Pharoah PD, Healey CS, Shah M, Pooley KA, Kang D, Yoo KY, Noh DY, Hartman M, Miao H, Sng JH, Sim X, Jakubowska A, Lubinski J, Jaworska-Bieniek K, Durda K, Sangrajrang S, Gaborieau V, McKay J, Toland AE, Ambrosone CB, Yannoukakos D, Godwin AK, Shen CY, Hsiung CN, Wu PE, Chen ST, Swerdlow A, Ashworth A, Orr N, Schoemaker MJ, Ponder BA, Nevanlinna H, Brown MA, Chenevix-Trench G, Easton DF, Dunning AM. Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. *Am J Hum Genet.* (2013) 92:489-503.
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