Whole Exome Sequencing
Gene package Disorders of Sex Development (DSD), version 4, 8-7-2016

Technical information
After DNA was enriched using Agilent Sureselect Clinical Research Exome (CRE) Capture, samples were run on the Illumina Hiseq platform. The aim is to obtain 50 million total reads per exome with a mapped fraction >0.98. The average coverage of the exome is ~50x. Data are demultiplexed by Illumina software bcl2fastq. Reads are mapped to the genome using BWA (reference: http://bio-bwa.sourceforge.net/). Variant detection is performed by Genome Analysis Toolkit (reference: http://www.broadinstitute.org/gatk/). Analysis is performed in Cartagenia using The Variant Calling File (VCF) followed by filtering. It is not excluded that pathogenic mutations are being missed using this technology. At this moment, there is not enough information about the sensitivity of this technique with respect to the detection of deletions and duplications of more than 5 nucleotides and of somatic mosaic mutations (all types of sequence changes).

Erasmus MC
University Medical Center Rotterdam

Dept. Clinical Genetics

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	Transcript	median depth	% covered >10x	% covered >20x
AMH	Persistent Mullerian duct syndrome, type I, 261550	600957	NM_000479.3	47	100	83
AMHR2	Persistent Mullerian duct syndrome, type II, 261550	600956	NM_020547.2	98	100	100
AR	Androgen insensitivity, 300068 Spinal and bulbar muscular atrophy of Kennedy, 313200 Androgen insensitivity, partial, with or without breast cancer, 312300 {Prostate cancer, susceptibility to}, 176807 Hypospadias 1, X-linked, 300633	313700	NM_000044.3	46	96	89
ATRX	Alpha-thalassemia/mental retardation syndrome, 301040 Alpha-thalassemia myelodysplasia syndrome, somatic, 300448 Mental retardation-hypotonic facies syndrome, X-linked, 309580	300032	NM_000489.4	38	98	83
BMP15	Ovarian dysgenesis 2, 300510 Premature ovarian failure 4, 300510	300247	NM_005448	56	100	100
CBX2	?46XY sex reversal 5, 613080	602770	NM_005189.2	63	100	97
CYP11A1	Adrenal insufficiency, congenital, with 46XY sex reversal, partial or complete, 613743	118485	NM_000781.2	77	100	99
CYP17A1	17-alpha-hydroxylase/17,20-lyase deficiency, 202110 17,20-lyase deficiency, isolated, 202110	609300	NM_000102.3	77	100	100
CYP19A1	Aromatase deficiency, 613546 Aromatase excess syndrome, 139300	107910	NM_031226.2	96	100	100
DHCR7	Smith-Lemli-Opitz syndrome, 270400	602858	NM_001360.2	114	100	100

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	Transcript	median depth	% covered >10x	% covered >20x
DHH	46XY partial gonadal dysgenesis, with minifascicular neuropathy, 607080 46XY sex reversal 7, 233420	605423	NM_021044.2	83	100	100
DMRT1	No OMIM phenotype	602424	NM_021951.2	67	100	100
DMRT2	No OMIM phenotype	604935	NM_006557.6	32	96	78
FAM58A	STAR syndrome, 300707	300708	NM_152274.4	32	76	64
FSHB	Hypogonadotropic hypogonadism 24 without anosmia, 229070	136530	NM_000510.2	52	100	100
FSHR	Ovarian dysgenesis 1, 233300 Ovarian response to FSH stimulation, 276400 Ovarian hyperstimulation syndrome, 608115	136435	NM_000145.3	60	100	100
GATA4	Atrial septal defect 2, 607941 Ventricular septal defect 1, 614429 Atrioventricular septal defect 4, 614430 ?Testicular anomalies with or without congenital heart disease, 615542 Tetralogy of Fallot, 187500	600576	-	60	77	62
HOXA13	Hand-foot-uterus syndrome, 140000 Guttmacher syndrome, 176305	142959	NM_000522.4	60	80	72
HSD17B3	Pseudohermaphroditism, male, with gynecomastia, 264300	605573	NM_000197.1	73	100	100
HSD3B2	3-beta-hydroxysteroid dehydrogenase, type II, deficiency, 201810	613890	NM_000198.3	136	100	100
LHCGR	Precocious puberty, male, 176410 Leydig cell hypoplasia with pseudohermaphroditism, 238320 Leydig cell hypoplasia with hypergonadotropic hypogonadism, 238320 Luteinizing hormone resistance, female, 238320 Leydig cell adenoma, somatic, with precocious puberty, 176410	152790	NM_000233.3	78	100	91
MAMLD1	Hypospadias 2, X-linked, 300758	300120	NM_001177465.2	54	100	99
MCM8	?Premature ovarian failure 10, 612885	608187	-	43	98	87
MCM9	Ovarian dysgenesis 4, 616185	610098	NM_017696	76	100	96
NR0B1	Adrenal hypoplasia, congenital, with hypogonadotropic hypogonadism, 300200 46XY sex reversal 2, dosage-sensitive, 300018	300473	NM_000475.4	55	100	100
NR5A1	46XY sex reversal 3, 612965 Premature ovarian failure 7, 612964 Adrenocortical insufficiency Spermatogenic failure 8, 613957	184757	NM_004959.4	67	100	99
NUP107	Nephrotic syndrome, type 11, 616730	607617	NM_020401	42	95	78
POR	Antley-Bixler syndrome with genital anomalies and disordered steroidogenesis, 201750 Disordered steroidogenesis due to cytochrome P450 oxidoreductase, 613571	124015	NM_000941.2	94	100	100
PSMC3IP	Ovarian dysgenesis 3, 614324	608665	NM_016556	54	100	100
RSPO1	Palmoplantar hyperkeratosis with squamous cell carcinoma of skin and sex reversal, 610644 Palmoplantar hyperkeratosis and true hermaphroditism, 610644	609595	NM_001038633.3	67	100	100

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	Transcript	median depth	% covered >10x	% covered >20x
SOX9	Campomelic dysplasia with autosomal sex reversal, 114290 Acampomelic campomelic dysplasia, 114290 Campomelic dysplasia, 114290	608160	NM_000346.3	73	98	91
SRD5A2	Pseudovaginal perineoscrotal hypospadias, 264600	607306	NM_000348.3	67	100	100
SRY	46XY sex reversal 1, 400044 46XX sex reversal 1, 400045	480000	NM_003140.2	92	100	100
STAG3	?Premature ovarian failure 8, 615723	608489	NM_012447	40	91	81
STAR	Lipoid adrenal hyperplasia, 201710	600617	NM_000349.2	88	100	100
SYCE1	No OMIM phenotype	611486	NM_001143763	51	100	93
TSPYL1	Sudden infant death with dysgenesis of the testes syndrome, 608800	604714	NM_003309.3	99	100	100
WNT4	SERKAL syndrome, 611812 Mullerian aplasia and hyperandrogenism, 158330	603490	NM_030761.4	125	96	92
WT1	Wilms tumor, type 1, 194070 Denys-Drash syndrome, 194080 Nephrotic syndrome, type 4, 256370 Frasier syndrome, 136680 Meacham syndrome, 608978 Mesothelioma, somatic, 156240	607102	NM_024426.4	61	99	90
ZFPM2	Tetralogy of Fallot, 187500 Diaphragmatic hernia 3, 610187 46XY sex reversal 9, 616067	603693	NM_012082	78	100	100

- Gene symbols according HGCN
- OMIM release used: 17-3-2016
- "No OMIM phenotypes" indicates a gene without a current OMIM association
- OMIM phenotypes between "[ ]", indicate "nondiseases," mainly genetic variations that lead to apparently abnormal laboratory test values
- OMIM phenotypes between "{}", indicate risk factors
- OMIM phenotypes with a question mark, "?", before the disease name indicates an unconfirmed or possibly spurious mapping.
- The statistics above are based on a set of 50 samples
- Median depth is the median of the mean sequence depth over the protein coding exons of the transcript
- % Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x
- % Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x