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Full name:	Thyroid disgenesis (38 genes) - VUB
Description:	(in-silico subpanel of Mendeliome) https://www.brightcore.be/gene-panels/mendeliome---thyroid-disorders---v11 Kit used : Roche SeqCap EZ custom design
Type of panel:	Custom panel
Provider:	home made
Version number:	V11
Laboratory:	Centrum Medische Genetica - UZ Brussel VUB
Created:	17 Jul 2019 - 11:05
Changed:	01 Sep 2022 - 15:17

Related Diseases

- Athyreosis
- Autosomal dominant hypocalcemia
- Bartter syndrome with hypocalcemia
- Brain-lung-thyroid syndrome
- Cushing syndrome due to bilateral macronodular adrenocortical disease
- Familial gestational hyperthyroidism
- Familial hyperthyroidism due to mutations in TSH receptor
- Familial hypocalciuric hypercalcemia type 1
- Familial hypocalciuric hypercalcemia type 2
- Familial hypocalciuric hypercalcemia type 3
- Familial thyroid dyshormonogenesis
- Generalized resistance to thyroid hormone
- Genetic transient congenital hypothyroidism
- Hypothyroidism due to TSH receptor mutations
- Neonatal severe primary hyperparathyroidism
- Peripheral resistance to thyroid hormones

- Pituitary resistance to thyroid hormone
- Pseudohypoparathyroidism type 1A
- Pseudohypoparathyroidism type 1B
- Pseudohypoparathyroidism type 1C
- Resistance to thyroid hormone due to a mutation in thyroid hormone receptor alpha
- Thyroid ectopia
- Thyroid hypoplasia

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
AP2S1	100.00	0	No comment
CASR	100.00	0	No comment
CDCA8	100.00	0	No comment
DUOX1	100.00	0	No comment
DUOX2	100.00	0	No comment
DUOXA2	100.00	0	No comment
DYRK1A	100.00	0	No comment
ELN	100.00	0	No comment
FOXE1	60.48	0	No comment
GAS1	62.99	0	No comment
GLIS3	100.00	0	No comment
GNA11	99.51	0	No comment
GNAS	98.96	0	No comment
GNAS-AS1	100.00	0	No comment
IYD	100.00	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
JAG1	99.66	0	No comment
KAT6B	100.00	0	No comment
KDM6A	100.00	0	No comment
KMT2D	100.00	0	No comment
NKX2-1	92.46	0	No comment
NKX2-5	100.00	0	No comment
NTN1	95.84	0	No comment
PAX8	100.00	0	No comment
SALL1	100.00	0	No comment
SECISBP2	98.68	0	No comment
SLC11A2	100.00	0	No comment
SLC26A4	99.99	0	No comment
SLC26A7	100.00	0	No comment
SLC5A5	100.00	0	No comment
STX16	100.00	0	No comment
TBX1	77.39	0	No comment
TG	100.00	0	No comment
THPO	99.84	0	No comment
THRA	100.00	0	No comment
THRB	100.00	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
TSHR	100.00	0	No comment
TUBB1	100.00	0	No comment
URB1	99.99	0	No comment