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Subject: quick notes on lab sequencing from discussion with JW
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Budgeted for full time operation of HiSeq through 2013

- 1) Establish operational baseline on HiSeq
Amy 2x100 @ 300bp fragments, 30-40x WGS + Exome, modern chemistry
- 2) Establish Personalis Mainstream Diversity Panel (PMDP = likely customer ethnic profiles)
Set of high quality, good coverage genomes of common ethnicities:
European, Chinese, Japanese, Indian, African American, Hispanic American
Balance male / female
Attempt to start with members of trios (preferably having 1kG coverage and/or exomes to augment)
Start with single members and later expand to full trios
Outsource sequencing if internal resources too occupied with #3 below
- 3) Develop and Demo Personalis WGS+ and Exome+
Develop pullouts to extend coverage of interpretable content (exome + custom pullout)
SV junction pullout for sequencing (include jens and insert/del)
Problem-specific pullouts and libraries (Compressions, SD, STR, Homopolymers) - may require long fragments
Optimize sequencer parameters for accuracy and not necessarily cost (e.g. read length, density)
Prepare for longer reads from ILMN in fall
- 4) Customers and collaborations
Probably most exome on 3Q
Move quickly - ASHG?